



United States Department of State

Washington, D.C. 20520

April 24, 2023

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 March 13, 2023, we are processing your request for material under the Freedom of Information Act ("FOIA"), 5 U.S.C. § 552. The Department of State has identified an additional seven responsive records subject to the FOIA. We have determined all seven 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 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 cursive script that reads "Jeanne Miller". The signature is written in black ink and is positioned below the word "Sincerely,".

Jeanne Miller
Chief, Programs and Policies Division
Office of Information Programs and Services

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

From: (b)(6)@state.gov>
Paulopol, Andreea I (b)(6)@state.gov>;
Gross, Laura J (b)(6)@state.gov>;
To: (b)(6)@state.gov>;
Gibbs, Jeffrey (b)(6)@state.gov>;
(b)(6)@state.gov>
CC: (b)(6)@state.gov>
Subject: Re: Please read/Review: DRAFT 2021 China BWC compliance 12.10.2020
Date: Fri, 11 Dec 2020 00:13:33 +0000

Thank you. I will defer to Jeff (b)(5)
(b)(5)

From: Paulopol, Andreea I (b)(6)@state.gov>
Sent: Thursday, December 10, 2020 6:31 PM
To: Gross, Laura J (b)(6)@state.gov>; (b)(6)@state.gov>; Gibbs, Jeffrey J (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>
Cc: (b)(6)@state.gov>
Subject: Please read/Review: DRAFT 2021 China BWC compliance 12.10.2020

Welcome your feedback by 10am tomorrow, please.

Once we agree on text, I'll add citations and so on.

Many thanks,
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

SENSITIVE BUT UNCLASSIFIED

SENSITIVE BUT UNCLASSIFIED

SENSITIVE BUT UNCLASSIFIED

(b)(6)

From: "Stilwell, David R" (b)(6)@state.gov>
To: (b)(6)@state.gov>
CC: Feith, David <(b)(6)@state.gov>;
(b)(6)@state.gov>
Subject: RE: New York Mag: The Lab Leak Hypothesis
Date: Wed, 6 Jan 2021 01:31:25 +0000

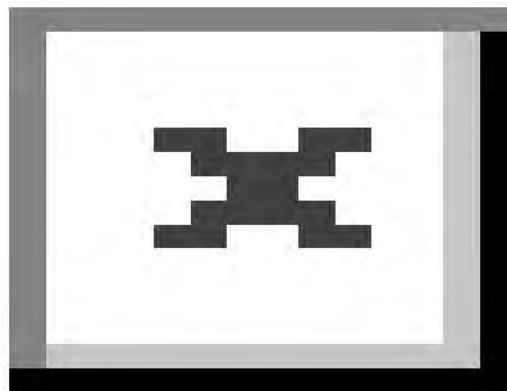
Having spent a lifetime in the world of USAF heavy equipment operators I'm used to posers, loud-mouths, and ego's. But I always imagined the laboratories and classrooms of the scientific world to be filled with kind, gentle, introverted, objective people who avoided drama and sought the truth. Then I read the attached.

(b)(5)

Alina Chan offers some useful insights on the sensitivities in an article from Sep '20.

Best

Dave



From: (b)(6)@state.gov>
Sent: Tuesday, January 5, 2021 9:33 AM
To: Feith, David <(b)(6)@state.gov>; (b)(6)@state.gov>
Cc: Stilwell, David R <(b)(6)@state.gov>
Subject: RE: New York Mag: The Lab Leak Hypothesis

It's a good read, though Angela Rasmussen (Georgetown virologist) shredded it rather savagely yesterday and thinks he misunderstands a lot of the science he's trying to describe.

At the end of the day, there's no question but that it's possible all of this was the result of a lab accident. The challenge after that is to assess the relative probability of such an event as opposed to natural emergence, factoring in the available evidence, and to figure out whether it's actually possible to know for certain – pinning down outbreak origins is historically a pretty iffy business.

From: Feith, David <(b)(6)@state.gov>
Sent: Monday, January 4, 2021 2:22 PM
To: (b)(6)@state.gov>; (b)(6)@state.gov>
Cc: Stilwell, David R <(b)(6)@state.gov>
Subject: FW: New York Mag: The Lab Leak Hypothesis

From: Feith, David <(b)(6)@state.gov>
Sent: Monday, January 4, 2021 2:20 PM
To: EAP-FO-Principals-DL <EAP-FO-Principals-DL@state.gov>; DL NSC Asia (DL.Asia@whmo.mil) <DL.Asia@whmo.mil>; (b)(6)@who.eop.gov; Ruggiero, Anthony J. EOP/NSC (b)(6)
Subject: New York Mag: The Lab Leak Hypothesis

This looks awfully interesting. The story the New Yorker wouldn't tell...

<https://nymag.com/intelligencer/article/coronavirus-lab-escape-theory.html>

The Lab-Leak Hypothesis

The Lab Leak Hypothesis

For decades, scientists have been hot-wiring viruses in hopes of

preventing a pandemic, not causing one. But what if ...?

By *Nicholson Baker*

I.

Flask Monsters

What happened was fairly simple, I've come to believe. It was an accident. A virus spent some time in a laboratory, and eventually it got out. SARS-CoV-2, the virus that causes COVID-19, began its existence inside a bat, then it learned how to infect people in a claustrophobic mine shaft, and then it was made more infectious in one or more laboratories, perhaps as part of a scientist's well-intentioned but risky effort to create a broad-spectrum vaccine. SARS-2 was not designed as a biological weapon. But it was, I think, designed. Many thoughtful people dismiss this notion, and they may be right. They sincerely believe that the coronavirus arose naturally, "zoonotically," from animals, without having been previously studied, or hybridized, or sluiced through cell cultures, or otherwise worked on by trained professionals. They hold that a bat, carrying a coronavirus, infected some other creature, perhaps a pangolin, and that the pangolin may have already been sick with a different coronavirus disease, and out of the conjunction and commingling of those two diseases within the pangolin, a new disease, highly infectious to humans, evolved. Or they hypothesize that two coronaviruses recombined in a bat, and this new virus spread to other bats, and then the bats infected a person directly — in a rural setting, perhaps — and that this person caused a simmering undetected outbreak of respiratory disease, which over a period of months or years evolved to become virulent and highly transmissible but was not noticed until it appeared in Wuhan.

There is no direct evidence for these zoonotic possibilities, just as there is no direct evidence for an experimental mishap — no written confession, no incriminating notebook, no official accident report. Certainty craves detail, and detail requires an investigation. It has been a full year, 80 million people have been infected, and, surprisingly, no public investigation has taken place. We still know very little about the origins of this disease.

Nevertheless, I think it's worth offering some historical context for our yearlong medical nightmare. We need to hear from the people who for years have contended that certain types of virus experimentation might lead to a disastrous pandemic like this one. And we need to stop hunting for new exotic diseases in the wild, shipping them back to laboratories, and hot-wiring their genomes to prove how dangerous to human life they might become.

Over the past few decades, scientists have developed ingenious methods of evolutionary acceleration and recombination, and they've learned how to trick viruses, coronaviruses in particular, those spiky hairballs of protein we now know so well, into moving quickly from one species of animal to another or from one type of cell culture to another. They've made machines that mix and mingle the viral code for bat diseases with the code for human diseases — diseases like SARS, severe acute respiratory syndrome, for example, which arose in China in 2003, and MERS, Middle East respiratory syndrome, which broke out a decade later and has to do with bats and camels. Some of the experiments — “gain of function” experiments — aimed to create new, more virulent, or more infectious strains of diseases in an effort to predict and therefore defend against threats that might conceivably arise in nature. The term *gain of function* is itself a euphemism; the Obama White House more accurately described this work as “experiments that may be reasonably anticipated to confer attributes to influenza, MERS, or SARS viruses such that the virus would have enhanced pathogenicity and/or transmissibility in mammals via the respiratory route.” The virologists who carried out these experiments have accomplished amazing feats of genetic transmutation, no question, and there have been very few publicized accidents over the years. But there have been some.

And we were warned, repeatedly. The intentional creation of new microbes that combine virulence with heightened transmissibility “poses extraordinary risks to the public,” wrote infectious-disease experts Marc Lipsitch and Thomas Inglesby in 2014. “A rigorous and transparent risk-assessment process for this work has not yet been established.” That's still true today. In 2012, in *Bulletin of the Atomic Scientists*, Lynn Klotz warned that there was an 80 percent chance, given how many laboratories were then handling virulent viro-varietals, that a leak of a potential pandemic pathogen would occur sometime in the next 12 years.

A lab accident — a dropped flask, a needle prick, a mouse bite, an illegibly labeled bottle — is apolitical. Proposing that something unfortunate happened during a scientific experiment in Wuhan — where COVID-19 was first diagnosed and where there are three high-security virology labs, one of which

held in its freezers the most comprehensive inventory of sampled bat viruses in the world — isn't a conspiracy theory. It's just a theory. It merits attention, I believe, alongside other reasoned attempts to explain the source of our current catastrophe.

II.

“A Reasonable Chance”

From early 2020, the world was brooding over the origins of COVID-19. People were reading research papers, talking about what kinds of live animals were or were not sold at the Wuhan seafood market — wondering where the new virus had come from.

Meanwhile, things got strange all over the world. The Chinese government shut down transportation and built hospitals at high speed. There were video clips of people who'd suddenly dropped unconscious in the street. A doctor on YouTube told us how we were supposed to scrub down our produce when we got back from the supermarket. A scientist named Shi Zhengli of the Wuhan Institute of Virology published a paper saying that the novel coronavirus was 96 percent identical to a bat virus, RaTG13, found in Yunnan province in southern China. On March 13, I wrote in my journal that there seemed to be something oddly artificial about the disease: “It's too airborne — too catching — it's something that has been selected for infectivity. That's what I suspect. No way to know so no reason to waste time thinking about it.”

This was just a note to self — at the time, I hadn't interviewed scientists about SARS-2 or read their research papers. But I did know something about pathogens and laboratory accidents; I published a book last year, *Baseless*, that talks about some of them. The book is named after a Pentagon program, Project Baseless, whose goal, as of 1951, was to achieve “an Air Force-wide combat capability in biological and chemical warfare at the earliest possible date.”

A vast treasure was spent by the U.S. on the amplification and aerial delivery of diseases — some well known, others obscure and stealthy. America's biological-weapons program in the '50s had A1-priority status, as high as nuclear weapons. In preparation for a total war with a numerically superior communist foe, scientists bred germs to be resistant to antibiotics and other drug therapies, and they infected lab animals with them, using a technique

called “serial passaging,” in order to make the germs more virulent and more catching.

And along the way, there were laboratory accidents. By 1960, hundreds of American scientists and technicians had been hospitalized, victims of the diseases they were trying to weaponize. Charles Armstrong, of the National Institutes of Health, one of the consulting founders of the American germ-warfare program, investigated Q fever three times, and all three times, scientists and staffers got sick. In the anthrax pilot plant at Camp Detrick, Maryland, in 1951, a microbiologist, attempting to perfect the “foaming process” of high-volume production, developed a fever and died. In 1964, veterinary worker Albert Nickel fell ill after being bitten by a lab animal. His wife wasn’t told that he had Machupo virus, or Bolivian hemorrhagic fever. “I watched him die through a little window to his quarantine room at the Detrick infirmary,” she said.

In 1977, a worldwide epidemic of influenza A began in Russia and China; it was eventually traced to a sample of an American strain of flu preserved in a laboratory freezer since 1950. In 1978, a hybrid strain of smallpox killed a medical photographer at a lab in Birmingham, England; in 2007, live foot-and-mouth disease leaked from a faulty drainpipe at the Institute for Animal Health in Surrey. In the U.S., “more than 1,100 laboratory incidents involving bacteria, viruses and toxins that pose significant or bioterror risks to people and agriculture were reported to federal regulators during 2008 through 2012,” reported *USA Today* in an exposé published in 2014.

In 2015, the Department of Defense discovered that workers at a germ-warfare testing center in Utah had mistakenly sent close to 200 shipments of live anthrax to laboratories throughout the United States and also to Australia, Germany, Japan, South Korea, and several other countries over the past 12 years. In 2019, laboratories at Fort Detrick — where “defensive” research involves the creation of potential pathogens to defend against — were shut down for several months by the Centers for Disease Control and Prevention for “breaches of containment.” They reopened in December 2019.

High-containment laboratories have a whispered history of near misses. Scientists are people, and people have clumsy moments and poke themselves and get bitten by the enraged animals they are trying to nasally inoculate. Machines can create invisible aerosols, and cell solutions can become contaminated. Waste systems don’t always work properly. Things can go wrong in a hundred different ways.

Hold that human fallibility in your mind. And then consider the cautious words of Alina Chan, a scientist who works at the Broad Institute of MIT and Harvard. “There is a reasonable chance that what we are dealing with is the result of a lab accident,” Chan told me in July of last year. There was also, she added, a reasonable chance that the disease had evolved naturally — both were scientific possibilities. “I don’t know if we will ever find a smoking gun, especially if it was a lab accident. The stakes are so high now. It would be terrifying to be blamed for millions of cases of COVID-19 and possibly up to a million deaths by year end, if the pandemic continues to grow out of control. The Chinese government has also restricted their own scholars and scientists from looking into the origins of SARS-CoV-2. At this rate, the origin of SARS-CoV-2 may just be buried by the passage of time.”

I asked Jonathan A. King, a molecular biologist and biosafety advocate from MIT, whether he’d thought *lab accident* when he first heard about the epidemic. “Absolutely, absolutely,” King answered. Other scientists he knew were concerned as well. But scientists, he said, in general were cautious about speaking out. There were “very intense, very subtle pressures” on them not to push on issues of laboratory biohazards. Collecting lots of bat viruses, and passaging those viruses repeatedly through cell cultures, and making bat-human viral hybrids, King believes, “generates new threats and desperately needs to be reined in.”

“All possibilities should be on the table, including a lab leak,” a scientist from the NIH, Philip Murphy — chief of the Laboratory of Molecular Immunology — wrote me recently. Nikolai Petrovsky, a professor of endocrinology at Flinders University College of Medicine in Adelaide, Australia, said in an email, “There are indeed many unexplained features of this virus that are hard if not impossible to explain based on a completely natural origin.” Richard Ebright, a molecular biologist at Rutgers University, wrote that he’d been concerned for some years about the Wuhan laboratory and about the work being done there to create “chimeric” (i.e., hybrid) SARS-related bat coronaviruses “with enhanced human infectivity.” Ebright said, “In this context, the news of a novel coronavirus in Wuhan ***screamed*** lab release.”

III.

“No Credible Evidence”

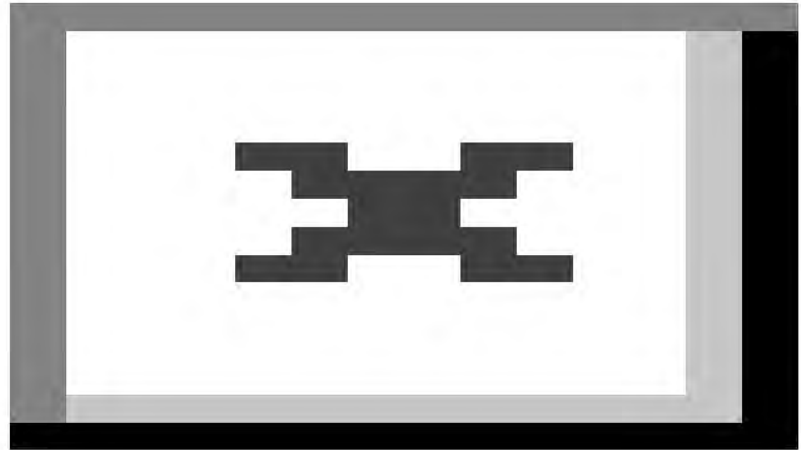
The new disease, as soon as it appeared, was intercepted — stolen and politicized by people with ulterior motives. The basic and extremely

interesting scientific question of what happened was sucked up into an ideological sharknado.

Some Americans boycotted Chinese restaurants; others bullied and harassed Asian Americans. Steve Bannon, broadcasting from his living room, in a YouTube series called *War Room*, said that the Chinese Communist Party had made a biological weapon and intentionally released it. He called it the “CCP virus.” And his billionaire friend and backer, Miles Guo, a devoted Trump supporter, told a right-wing website that the communists’ goal was to “use the virus to infect selective people in Hong Kong, so that the Chinese Communist Party could use it as an excuse to impose martial law there and ultimately crush the Hong Kong pro-democracy movement. But it backfired terribly.”

In *The Lancet*, in February, a powerful counterstatement appeared, signed by 27 scientists. “We stand together to strongly condemn conspiracy theories suggesting that COVID-19 does not have a natural origin,” the statement said. “Scientists from multiple countries have published and analyzed genomes of the causative agent, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), and they overwhelmingly conclude that this coronavirus originated in wildlife, as have so many other emerging pathogens.”

The behind-the-scenes organizer of this *Lancet* statement, Peter Daszak, is a zoologist and bat-virus sample collector and the head of a New York nonprofit called EcoHealth Alliance — a group that (as veteran science journalist Fred Gutler explained later in *Newsweek*) has channeled money from the National Institutes of Health to Shi Zhengli’s laboratory in Wuhan, allowing the lab to carry on recombinant research into diseases of bats and humans. “We have a choice whether to stand up and support colleagues who are being attacked and threatened daily by conspiracy theorists or to just turn a blind eye,” Daszak said in February in *Science* magazine.



How Did It Get Out? 1. The Tongguan Mine Shaft in Mojiang, Yunnan, where, in 2013, fragments of RaTG13, the closest known relative of SARSCoV-2, were recovered and transported to the Wuhan Institute of Virology; **2. The Wuhan Institute of Virology**, where Shi Zhengli's team brought the RaTG13 sample, sequenced its genome, then took it out of the freezer several times in recent years; **3. The Wuhan Center for Disease Control and Prevention**, which first reported signs of the novel coronavirus in hospital patients; **4. The Huanan Seafood Wholesale Market**, an early suspected origin of the pandemic, where the first major outbreak occurred. Illustration: Map by Jason Lee

Vincent Racaniello, a professor at Columbia and a co-host of a podcast called *This Week in Virology*, said on February 9 that the idea of an accident in Wuhan was “complete bunk.” The coronavirus was 96 percent similar to a bat virus found in 2013, Racaniello said. “It’s not a man-made virus. It wasn’t released from a lab.”

Racaniello’s dismissal was seconded by a group of scientists from Ohio State, the University of Pennsylvania, and the University of North Carolina, who put out a paper in *Emerging Microbes and Infections* to quiet the “speculations, rumors, and conspiracy theories that SARS-CoV-2 is of laboratory origin.” There was “currently no credible evidence” that SARS-2 leaked from a lab, these scientists said, using a somewhat different argument from Racaniello’s. “Some people have alleged that the human SARS-CoV-2 was leaked directly from a laboratory in Wuhan where a bat CoV (RaTG13) was recently

reported,” they said. But RaTG13 could not be the source because it differed from the human SARS-2 virus by more than a thousand nucleotides. One of the paper’s authors, Susan Weiss, told the Raleigh *News & Observer*, “The conspiracy theory is ridiculous.”

The most influential natural-origin paper, “The Proximal Origin of SARS-CoV-2,” by a group of biologists that included Kristian Andersen of Scripps Research, appeared online in a preliminary version in mid-February.

“We do not believe any type of laboratory-based scenario is plausible,” the scientists said. Why? Because molecular-modeling software predicted that if you wanted to optimize an existing bat virus so that it would replicate well in human cells, you would arrange things a different way than how the SARS-2 virus actually does it — even though the SARS-2 virus does an extraordinarily good job of replicating in human cells. The laboratory-based scenario was implausible, the paper said, because, although it was true that the virus could conceivably have developed its unusual genetic features in a laboratory, a stronger and “more parsimonious” explanation was that the features came about through some kind of natural mutation or recombination. “What we think,” explained one of the authors, Robert F. Garry of Tulane University, on YouTube, “is that this virus is a recombinant. It probably came from a bat virus, plus perhaps one of these viruses from the pangolin.” Journalists, for the most part, echoed the authoritative pronouncements of Daszak, Racaniello, Weiss, Andersen, and other prominent natural-originists. “The balance of the scientific evidence strongly supports the conclusion that the new coronavirus emerged from nature — be it the Wuhan market or somewhere else,” said the Washington *Post*’s “Fact Checker” column. “Dr. Fauci Again Dismisses Wuhan Lab As Source of Coronavirus,” said *CBS News*, posting a video interview of Anthony Fauci by *National Geographic*. “If you look at the evolution of the virus in bats, and what’s out there now,” Fauci said, “it’s very, very strongly leaning toward ‘This could not have been artificially or deliberately manipulated’ — the way the mutations have naturally evolved.”

Everyone took sides; everyone thought of the new disease as one more episode in an ongoing partisan struggle. Think of Mike Pompeo, that landmass of Cold War truculence; think of Donald Trump himself. They stood at their microphones saying, in a winking, I-know-something-you-don’t-know sort of way, that this disease escaped from a Chinese laboratory. Whatever they were saying must be wrong. It became impermissible, almost taboo, to admit that, of course, SARS-2 could have come from a lab accident. “The administration’s claim that the virus spread from a Wuhan lab has made the notion politically

toxic, even among scientists who say it could have happened,” wrote science journalist Mara Hvistendahl in the Intercept.

IV.

“Is It a Complete Coincidence?”

Even so, in January and February of 2020, there were thoughtful people who were speaking up, formulating their perplexities.

One person was Sam Hussein, who works for Consortium News. He went to a CDC press conference at the National Press Club on February 11, 2020. By then, 42,000 people had gotten sick in China and more than a thousand had died. But there were only 13 confirmed cases in the U.S. Halfway through the Q&A period, Hussein went to the microphone and asked the CDC’s representative, Anne Schuchat, where the virus had come from. His head was spinning, he told me later.

“Obviously the main concern is how to stop the virus,” Hussein said; nonetheless, he wanted to know more about its source. “Is it the CDC’s contention,” he asked, “that there’s absolutely no relation to the BSL-4 lab in Wuhan? It’s my understanding that this is the only place in China with a BSL-4 lab. We in the United States have, I think, two dozen or so, and there have been problems and incidents.” (A BSL-4 laboratory is a maximum-security biosafety-level-four facility, used to house research on the most dangerous known pathogens. *New York* has confirmed there are at least 11 BSL-4 facilities currently operating in the U.S.) Hussein hastened to say that he wasn’t implying that what happened in Wuhan was in any way intentional. “I’m just asking, Is it a complete coincidence that this outbreak happened in the one city in China with a BSL-4 lab?”

Schuchat thanked Hussein for his questions and comments. Everything she’d seen was quite consistent with a natural, zoonotic origin for the disease, she said.

That same month, a group of French scientists from Aix-Marseille University posted a paper describing their investigation of a small insertion in the genome of the new SARS-2 virus. The virus’s spike protein contained a sequence of amino acids that formed what Etienne Decroly and colleagues called a “peculiar furin-like cleavage site” — a chemically sensitive region on the lobster claw of the spike protein that would react in the presence of an enzyme called furin, which is a type of protein found everywhere within the

human body, but especially in the lungs. When the spike senses human furin, it shudders, chemically speaking, and the enzyme opens the protein, commencing the tiny morbid ballet whereby the virus burns a hole in a host cell's outer membrane and finds its way inside.

The code for this particular molecular feature — not found in SARS or any SARS-like bat viruses, but present in a slightly different form in the more lethal MERS virus — is easy to remember because it's a roar: "R-R-A-R." The letter code stands for amino acids: arginine, arginine, alanine, and arginine. Its presence, so Decroly and his colleagues observed, may heighten the "pathogenicity" — that is, the god-awfulness — of a disease.

Botao Xiao, a professor at the South China University of Technology, posted a short paper on a preprint server titled "The Possible Origins of 2019-nCoV Coronavirus." Two laboratories, the Wuhan Center for Disease Control and Prevention (WHCDC) and the Wuhan Institute of Virology, were not far from the seafood market, which was where the disease was said to have originated, Xiao wrote — in fact, the WHCDC was only a few hundred yards away from the market — whereas the horseshoe bats that hosted the disease were hundreds of miles to the south. (No bats were sold in the market, he pointed out.) It was unlikely, he wrote, that a bat would have flown to a densely populated metropolitan area of 15 million people. "The killer coronavirus probably originated from a laboratory in Wuhan," Xiao believed. He urged the relocation of "biohazardous laboratories" away from densely populated places. His article disappeared from the server.

And late in the month, a professor at National Taiwan University, Fang Chitai, gave a lecture on the coronavirus in which he described the anomalous R-R-A-R furin cleavage site. The virus was "unlikely to have four amino acids added all at once," Fang said — natural mutations were smaller and more haphazard, he argued. "From an academic point of view, it is indeed possible that the amino acids were added to COVID-19 in the lab by humans." When the *Taiwan News* published an article about Fang's talk, Fang disavowed his own comments, and the video copy of the talk disappeared from the website of the Taiwan Public Health Association. "It has been taken down for a certain reason," the association explained. "Thank you for your understanding."

“A Serious Shortage of Appropriately Trained Technicians”

In the spring, I did some reading on coronavirus history. Beginning in the 1970s, dogs, cows, and pigs were diagnosed with coronavirus infections; dog shows were canceled in 1978 after 25 collies died in Louisville, Kentucky. New varieties of coronaviruses didn't start killing humans, though, until 2003 — that's when restaurant chefs, food handlers, and people who lived near a live-animal market got sick in Guangzhou, in southern China, where the shredded meat of a short-legged raccoonlike creature, the palm civet, was served in a regional dish called “dragon-tiger-phoenix soup.” The new disease, SARS, spread alarmingly in hospitals, and it reached 30 countries and territories. More than 800 people died; the civet-borne virus was eventually traced to horseshoe bats.

Later, smaller outbreaks of SARS in Taiwan, Singapore, and China's National Institute of Virology in Beijing were all caused by laboratory accidents. Of the Beijing Virology Institute, the World Health Organization's safety investigators wrote, in May 2004, that they had “serious concerns about biosafety procedures.” By one account, a SARS storage room in the Beijing lab was so crowded that the refrigerator holding live virus was moved out to the hallway. “Scientists still do not fully understand exactly where or how SARS emerged 18 months ago,” wrote *Washington Post* reporter David Brown in June 2004. “But it is clear now that the most threatening source of the deadly virus today may be places they know intimately — their own laboratories.”

I'm just asking, Is it a complete coincidence that this outbreak happened in the one city in China with a BSL-4 lab?

MERS arose in 2012, possibly spread by camels that had contracted the disease from bats or bat guano, then passed it to human drinkers of raw camel milk and butchers of camel meat. It was an acute sickness, with a high fatality rate, mostly confined to Saudi Arabia. Like SARS, MERS ebbed quickly — it all but disappeared outside the Middle East, except for an outbreak in 2015 at the Samsung Medical Center in South Korea, where a single case of MERS led to more than 180 infections, many involving hospital workers.

In January 2015, the brand-new BSL-4 lab in Wuhan, built by a French contractor, celebrated its opening, but full safety certification came slowly. According to State Department cables from 2018 leaked to the *Washington Post*, the new BSL-4 lab had some start-up problems, including “a serious shortage of appropriately trained technicians and investigators needed to safely operate this high-containment laboratory.” The staff had gotten some training at a BSL-4 lab in Galveston, Texas, but they were doing potentially dangerous work with SARS-like viruses, the memo said, and they needed more help from the U.S.

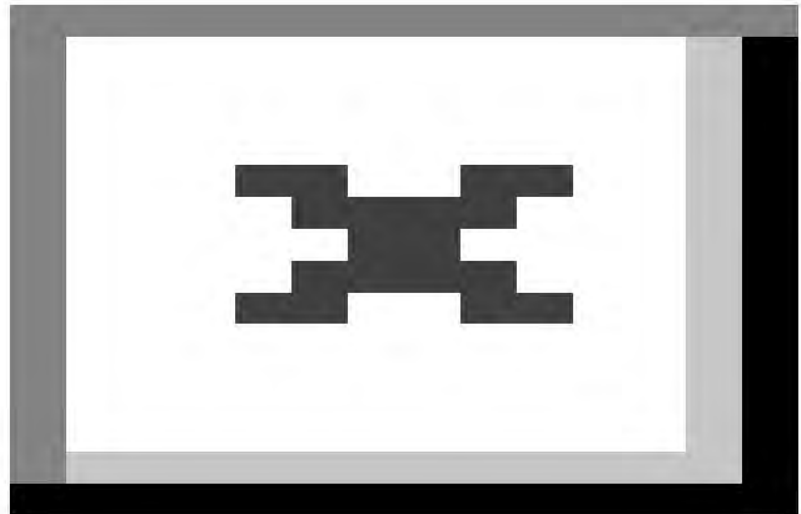
In November or December of 2019, the novel coronavirus began to spread. Chinese scientists initially named it “Wuhan seafood market pneumonia virus,” but soon that idea went away. The market, closed and decontaminated by Chinese officials on January 1, 2020, was an amplifying hub, not the source of the outbreak, according to several studies by Chinese scientists. Forty-five percent of the earliest SARS-2 patients had no link with the market.

VI.

Emergence

Now let’s take a step back. AIDS, fatal and terrifying and politically charged, brought on a new era in government-guided vaccine research, under the guidance of Anthony Fauci. A virologist at Rockefeller University, Stephen S. Morse, began giving talks on “emerging viruses” — other plagues that might be in the process of coming out of nature’s woodwork. In 1992, Richard Preston wrote a horrific account of one emergent virus, Ebola, in *The New Yorker*, which became a best-selling book in 1994; Laurie Garrett’s *The Coming Plague: Newly Emerging Diseases in a World Out of Balance* appeared that same year and was also a best seller. The idea seemed to be everywhere: We were on the verge of a wave of zoonotic, emergent plagues.

This new, useful term, *emerging*, began to glow in the research papers of some coronavirologists, who were out of the spotlight, working on common colds and livestock diseases. The term was useful because it was fluid. An emerging disease could be real and terrifying, as AIDS was — something that had just arrived on the medical scene and was confounding our efforts to combat it — or it could be a disease that hadn’t arrived, and might never arrive, but could be shown in a laboratory to be waiting in the wings, just a few mutations away from a human epidemic. It was real and unreal at the same time — a quality that was helpful when applying for research grants.



Where Did It Come From? This chart measures the genetic similarity of known viruses to the novel coronavirus (which appears in yellow). By far the closest is the bat virus RaTG13, which appears in blue, and which was recovered in 2013 and brought to the Wuhan Institute of Virology. The first SARS, marked in red, is a much more distant relative. Graphic: Zhou, P., Yang, XL., Wang, XG. et al. A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature* 579, 270–273 (2020)

Take, for instance, this paper from 1995: “High Recombination and Mutation Rates in Mouse Hepatitis Viruses Suggest That Coronaviruses May Be Potentially Important Emerging Viruses.” It was written by Dr. Ralph Baric and his bench scientist, Boyd Yount, at the University of North Carolina. Baric, a gravelly voiced former swim champion, described in this early paper how his lab was able to train a coronavirus, MHV, which causes hepatitis in mice, to jump species, so that it could reliably infect BHK (baby-hamster kidney) cell cultures. They did it using serial passaging: repeatedly dosing a mixed solution of mouse cells and hamster cells with mouse-hepatitis virus, while each time decreasing the number of mouse cells and upping the concentration of hamster cells. At first, predictably, the mouse-hepatitis virus couldn’t do much with the hamster cells, which were left almost free of infection, floating in

their world of fetal-calf serum. But by the end of the experiment, after dozens of passages through cell cultures, the virus had mutated: It had mastered the trick of parasitizing an unfamiliar rodent. A scourge of mice was transformed into a scourge of hamsters. And there was more: "It is clear that MHV can rapidly alter its species specificity and infect rats and primates," Baric said. "The resulting virus variants are associated with demyelinating diseases in these alternative species." (A demyelinating disease is a disease that damages nerve sheaths.) With steady prodding from laboratory science, along with some rhetorical exaggeration, a lowly mouse ailment was morphed into an emergent threat that might potentially cause nerve damage in primates. That is, nerve damage in us.

A few years later, in a further round of "interspecies transfer" experimentation, Baric's scientists introduced their mouse coronavirus into flasks that held a suspension of African-green-monkey cells, human cells, and pig-testicle cells. Then, in 2002, they announced something even more impressive: They'd found a way to create a full-length infectious clone of the entire mouse-hepatitis genome. Their "infectious construct" replicated itself just like the real thing, they wrote.

Not only that, but they'd figured out how to perform their assembly seamlessly, without any signs of human handiwork. Nobody would know if the virus had been fabricated in a laboratory or grown in nature. Baric called this the "no-see'm method," and he asserted that it had "broad and largely unappreciated molecular biology applications." The method was named, he wrote, after a "very small biting insect that is occasionally found on North Carolina beaches."

In 2006, Baric, Yount, and two other scientists were granted a patent for their invisible method of fabricating a full-length infectious clone using the seamless, no-see'm method. But this time, it wasn't a clone of the mouse-hepatitis virus — it was a clone of the entire deadly human SARS virus, the one that had emerged from Chinese bats, via civets, in 2002. The Baric Lab came to be known by some scientists as "the Wild Wild West." In 2007, Baric said that we had entered "the golden age of coronavirus genetics."

"I would be afraid to look in their freezers," one virologist told me.

Baric and Shi Zhengli of the Wuhan Institute of Virology, the two top experts on the genetic interplay between bat and human coronaviruses, began collaborating in 2015.

VII.

“I Had Not Slept a Wink”

Early in the pandemic, *Scientific American* profiled Shi Zhengli, known in China as the “bat woman.” Shi trapped hundreds of bats in nets at the mouths of caves in southern China, sampled their saliva and their blood, swabbed their anuses, and gathered up their fecal pellets. Several times, she visited and sampled bats in a mine in Mojiang, in southern China, where, in 2012, six men set to work shoveling bat guano were sickened by a severe lung disease, three of them fatally. Shi’s team took the samples back to Wuhan and analyzed whatever fragments of bat virus she could find. In some cases, when she found a sequence that seemed particularly significant, she experimented with it in order to understand how it might potentially infect humans. Some of her work was funded by the National Institutes of Health and some of it by the U.S. Defense Threat Reduction Agency of the Department of Defense via Peter Daszak’s EcoHealth Alliance.

As Shi explained to *Scientific American*, late in December 2019, she heard from the director of the Wuhan Institute that there was an outbreak of a new disease in the city. Medical samples taken from hospital patients arrived at her lab for analysis. Shi determined that the new virus was related to SARS but even more closely related to a bat disease that her own team had found on a virus-hunting trip: the now-famous RaTG13. Shi was surprised that the outbreak was local, she said: “I had never expected this kind of thing to happen in Wuhan, in central China.” The bat hiding places that she’d been visiting were, after all, as far away as Orlando, Florida, is from New York City. Could this new virus, she wondered, have come from her own laboratory? She checked her records and found no exact matches. “That really took a load off my mind,” she said. “I had not slept a wink for days.”

If one of the first thoughts that goes through the head of a lab director at the Wuhan Institute of Virology is that the new coronavirus could have come from her lab, then we are obliged to entertain the scientific possibility that it could indeed have come from her lab. Right then, there should have been a comprehensive, pockets-inside-out, fully public investigation of the Virology Institute, along with the other important virus labs in Wuhan, including the one close by the seafood market, headquarters of the Wuhan CDC. There should have been interviews with scientists, interviews with biosafety teams, close parsings of laboratory notebooks, freezer and plumbing and decontamination systems checks — everything. It didn’t happen. The Wuhan

Institute of Virology closed down its databases of viral genomes, and the Chinese Ministry of Education sent out a directive: "Any paper that traces the origin of the virus must be strictly and tightly managed."

Shi made some WeChat posts early in 2020. "The novel 2019 coronavirus is nature punishing the human race for keeping uncivilized living habits," she wrote. "I, Shi Zhengli, swear on my life that it has nothing to do with our laboratory." She advised those who believed rumors, and gave credence to unreliable scientific papers, to "shut their stinking mouths."

VIII.

“ ‘Bug to Drug’ in 24 Hours”

It wasn't only AIDS that changed the way the NIH funded research. The War on Terror also influenced which diseases got the most attention. In the late '90s, under Bill Clinton and then George W. Bush, biodefense specialists became interested — again — in anthrax. The Defense Threat Reduction Agency built a small anthrax factory in Nevada, using simulants, to demonstrate how easy it would be for a terrorist to build a small anthrax factory. And in the first year of the Bush presidency, the Defense Intelligence Agency wrote up plans to create a vaccine-resistant form of anthrax using state-of-the-art gene-splicery. A front-page article describing these initiatives, "U.S. Germ Warfare Research Pushes Treaty Limits," appeared in the New York *Times* on September 4, 2001, one week before 9/11. "Pentagon Says Projects Are Defense, Is Pressing Ahead," was the subtitle.

After the 9/11 attacks, and the mysterious anthrax mailings that began a week later (which said, "TAKE PENACILIN [sic] NOW / DEATH TO AMERICA / DEATH TO ISRAEL / ALLAH IS GREAT"), the desire for biopreparedness became all consuming. Now there were emerging biothreats from humans as well as from the evolving natural world. Fauci's anti-terror budget went from \$53 million in 2001 to \$1.7 billion in 2003. Setting aside his work toward an AIDS vaccine, which was taking longer than he'd foreseen, Fauci said he would be going all out to defend against a suite of known Cold War agents, all of which had been bred and perfected in American weapons programs many years before — brucellosis, anthrax, tularemia, and plague, for instance. "We are making this the highest priority," Fauci said. "We are really marshaling all available resources."

I would be afraid to look in their freezers.

Vaccine development had to progress much faster, Fauci believed; he wanted to set up “vaccine systems” and “vaccine platforms,” which could be quickly tailored to defend against a particular emergent strain some terrorist with an advanced biochemistry degree might have thrown together in a laboratory. “Our goal within the next 20 years is ‘bug to drug’ in 24 hours,” Fauci said. “This would specifically meet the challenge of genetically engineered bioagents.” The first Project BioShield contract Fauci awarded was to VaxGen, a California pharmaceutical company, for \$878 million worth of shots of anthrax vaccine.

By 2005, so much money was going toward biothreat reduction and preparedness that more than 750 scientists sent a protest letter to the NIH. Their claim was that grants to study canonical biowar diseases — anthrax, plague, brucellosis, and tularemia, all exceptionally rare in the U.S. — had increased by a factor of 15 since 2001, whereas funds for the study of widespread “normal” diseases, of high public-health importance, had decreased.

Fauci was firm in his reply: “The United States through its leaders made the decision that this money was going to be spent on biodefense,” he said. “We disagree with the notion that biodefense concerns are of ‘low public-health significance.’”

In 2010, by one count, there were 249 BSL-3 laboratories and seven BSL-4 laboratories in the U.S., and more than 11,000 scientists and staffers were authorized to handle the ultralethal germs on the government’s select pathogen list. And yet the sole bioterrorist in living memory who actually killed American citizens, according to the FBI — the man who sent the anthrax letters — turned out to be one of the government’s own researchers. Bruce Ivins, an eccentric, suicidal laboratory scientist from Ohio who worked in vaccine development at Fort Detrick, allegedly wanted to boost the fear level so as to persuade the government to buy more of the patented, genetically engineered anthrax VaxGen vaccine, of which he was a co-inventor. (See David Willman’s fascinating biography of Ivins, *Mirage Man*.) Fauci’s staff at NIH funded Ivins’s vaccine laboratory and gave \$100 million to VaxGen to accelerate vaccine production. (The NIH’s \$878 million contract with VaxGen, however, was quietly canceled in 2006; Ivins, who was never charged, killed himself in 2008.)

“The whole incident amounted to a snake eating its own tail,” wrote Wendy Orent in an August 2008 piece titled “Our Own Worst Bioenemy” in the Los Angeles *Times*. “No ingenious biowarrior from Al Qaeda sent the lethal

envelopes through the U.S. postal system. An American scientist did.” What confirmed Ivins’s guilt, according to the FBI, was that there was a genetic match between the anthrax used in the killings and the strain held at Fort Detrick.

IX.

“Weapons of Mass Disruption”

After SARS appeared in 2003, Ralph Baric’s laboratory moved up the NIH funding ladder. SARS was a “dual use” organism — a security threat and a zoonotic threat at the same time. In 2006, Baric wrote a long, fairly creepy paper on the threat of “weaponizable” viruses. Synthetic biology had made possible new kinds of viral “weapons of mass disruption,” he wrote, involving, for example, “rapid production of numerous candidate bioweapons that can be simultaneously released,” a scattershot terror tactic Baric called the “‘survival of the fittest’ approach.”

Baric hoped to find a SARS vaccine, but he couldn’t; he kept looking for it, year after year, supported by the NIH, long after the disease itself had been contained. It wasn’t really gone, Baric believed. Like other epidemics that pop up and then disappear, as he told a university audience some years later, “they don’t go extinct. They are waiting to return.” What do you do if you run a well-funded laboratory, an NIH “center of excellence,” and your emergent virus is no longer actually making people sick? You start squeezing it and twisting it into different shapes. Making it stand on its hind legs and quack like a duck, or a bat. Or breathe like a person.

Baric’s safety record is good — although there was a minor mouse-bite incident in 2016, uncovered by ProPublica — and his motives are beyond reproach: “Safe, universal, vaccine platforms are needed that can be tailored to new pathogens as they emerge, quickly tested for safety, and then strategically used to control new disease outbreaks in human populations,” he wrote in a paper on public health. But the pioneering work he did over the past 15 years — generating tiny eager single-stranded flask monsters and pitting them against human cells, or bat cells, or gene-spliced somewhat-human cells, or monkey cells, or humanized mice — was not without risk, and it may have led others astray.

In 2006, for instance, Baric and his colleagues, hoping to come up with a “vaccine strategy” for SARS, produced noninfectious virus replicon particles (or VRPs) using the Venezuelan-equine-encephalitis virus (another American

germ-warfare agent), which they fitted with various SARS spike proteins. Then, wearing Tyvek suits and two pairs of gloves each, and working in a biological safety cabinet in a BSL-3-certified laboratory, they cloned and grew recombinant versions of the original SARS virus in an incubator in a medium that held African-green-monkey cells. When they had grown enough virus, the scientists swapped out one kind of spike protein for a carefully chosen mutant, and they challenged their prototype vaccine with it in mice.

The scientists also tried their infectious SARS clones in something called an air-liquid interface, using a relatively new type of cell culture developed by Raymond Pickles of the University of North Carolina's Cystic Fibrosis Center. Pickles had perfected a method of emulating the traits of human airway tissue by cultivating cells taken from lung-disease patients — nurturing the culture over four to six weeks in such a way that the cells differentiated and developed a crop of tiny moving hairs, or cilia, on top and goblet cells within that produced real human mucus. In fact, before infecting these HAE (human airway epithelial) cells with a virus, the lab worker must sometimes rinse off some of the accumulated mucus, as if helping the lab-grown tissue to clear its throat. So Baric was exposing and adapting his engineered viruses to an extraordinarily true-to-life environment — the juicy, sticky, hairy inner surface of our breathing apparatus.

SARS-2 seems almost perfectly calibrated to grab and ransack our breathing cells and choke the life out of them. “By the time SARS-CoV-2 was first detected in late 2019, it was already pre-adapted to human transmission,” Alina Chan and her co-authors have written, whereas SARS, when it first appeared in 2003, underwent “numerous adaptive mutations” before settling down. Perhaps viral nature hit a bull’s-eye of airborne infectivity, with almost no mutational drift, no period of accommodation and adjustment, or perhaps some lab worker somewhere, inspired by Baric’s work with human airway tissue, took a spike protein that was specially groomed to colonize and thrive deep in the ciliated, mucosal tunnels of our inner core and cloned it onto some existing viral bat backbone. It could have happened in Wuhan, but — because anyone can now “print out” a fully infectious clone of any sequenced disease — it could also have happened at Fort Detrick, or in Texas, or in Italy, or in Rotterdam, or in Wisconsin, or in some other citadel of coronaviral inquiry. No conspiracy — just scientific ambition, and the urge to take exciting risks and make new things, and the fear of terrorism, and the fear of getting sick. Plus a whole lot of government money.

“Risky Areas for Spillover”

Project Bioshield began to fade by the end of the Bush administration, although the expensive high-containment laboratories, controversial preservers and incubators of past and future epidemics, remain. By 2010, some BioShield projects had dissolved into Obama’s Predict program, which paid for laboratories and staff in 60 “risky areas for spillover” around the world. Jonna Mazet, a veterinary scientist from the University of California, Davis, was in charge of Predict, which was a component of USAID’s “Emerging Pandemic Threats” program. Her far-flung teams collected samples from 164,000 animals and humans and claimed to have found “almost 1,200 potentially zoonotic viruses, among them 160 novel coronaviruses, including multiple SARS- and MERS-like coronaviruses.” The fruits of Predict’s exotic harvest were studied and circulated in laboratories worldwide, and their genetic sequences became part of GenBank, the NIH’s genome database, where any curious RNA wrangler anywhere could quickly synthesize snippets of code and test out a new disease on human cells.

Baric, Jonna Mazet, and Peter Daszak of EcoHealth worked together for years — and Daszak also routed Predict money to Shi Zhengli’s bat-surveillance team in Wuhan through his nonprofit, mingling it with NIH money and money from the U.S. Defense Threat Reduction Agency. In 2013, Mazet announced that Shi Zhengli’s virus hunters, with Predict’s support, had, for the first time, isolated and cultured a live SARS-like virus from bats and demonstrated that this virus could bind to the human ACE2, or “angiotensin-converting enzyme 2,” receptor, which Baric’s laboratory had determined to be the sine qua non of human infectivity. “This work shows that these viruses can directly infect humans and validates our assumption that we should be searching for viruses of pandemic potential before they spill over to people,” Mazet said.

Daszak, for his part, seems to have viewed his bat quests as part of an epic, quasi-religious death match. In a paper from 2008, Daszak and a co-author described Bruegel’s painting *The Fall of the Rebel Angels* and compared it to the contemporary human biological condition. The fallen angels could be seen as pathogenic organisms that had descended “through an evolutionary (not spiritual) pathway that takes them to a netherworld where they can feed only on our genes, our cells, our flesh,” Daszak wrote. “Will we succumb to the multitudinous horde? Are we to be cast downward into chthonic chaos represented here by the heaped up gibbering phantasmagory against which we rail and struggle?”

XI.

“Lab-Made?”

There are, in fact, some helpful points of agreement between zoonoticists — those who believe in a natural origin of the SARS-2 virus — and those who believe that it probably came from a laboratory. Both sides agree, when pressed, that a lab origin can’t be conclusively ruled out and a natural origin can’t be ruled out either — because nature, after all, is capable of improbable, teleological-seeming achievements. Both sides also agree, for the most part, that the spillover event that began the human outbreak probably happened only once, or a few times, quite recently, and not many times over a longer period. They agree that bat virus RaTG13 (named for the *Rinolophus affinis* bat, from Tongguan, in 2013) is the closest match to the human virus that has yet been found, and that although the two viruses are very similar, the spike protein of the bat virus lacks the features the human spike protein possesses that enable it to work efficiently with human tissue.

Zoonoticists hold that SARS-2’s crucial features — the furin cleavage site and the ACE2 receptor — are the result of a recombinant event involving a bat coronavirus (perhaps RaTG13 or a virus closely related to it) and another, unknown virus. Early on, researchers proposed that it could be a snake sold at the seafood market — a Chinese cobra or a banded krait —but no: Snakes don’t typically carry coronaviruses. Then there was a thought that the disease came from sick smuggled pangolins, because there existed a certain pangolin coronavirus that was, inexplicably, almost identical in its spike protein to the human coronavirus — but then, no: There turned out to be questions about the reliability of the genetic information in that diseased-pangolin data set, on top of which there were no pangolins for sale at the Wuhan market. Then a group from China’s government veterinary laboratory at Harbin tried infecting beagles, pigs, chickens, ducks, ferrets, and cats with SARS-2 to see if they could be carriers. (Cats and ferrets got sick; pigs, ducks, and most dogs did not.)

In September, some scientists at the University of Michigan, led by Yang Zhang, reported that they had created a “computational pipeline” to screen nearly a hundred possible intermediate hosts, including the Sumatran orangutan, the Western gorilla, the Olive baboon, the crab-eating macaque, and the bonobo. All these primates were “permissive” to the SARS-2 coronavirus and should undergo “further experimental investigation,” the scientists proposed.

Despite this wide-ranging effort, there is at the moment no animal host that zoonoticists can point to as the missing link. There's also no single, agreed-upon hypothesis to explain how the disease may have traveled from the bat reservoirs of Yunnan all the way to Wuhan, seven hours by train, without leaving any sick people behind and without infecting anyone along the way.

The zoonoticists say that we shouldn't find it troubling that virologists have been inserting and deleting furin cleavage sites and ACE2-receptor-binding domains in experimental viral spike proteins for years: The fact that virologists have been doing these things in laboratories, in advance of the pandemic, is to be taken as a sign of their prescience, not of their folly. But I keep returning to the basic, puzzling fact: This patchwork pathogen, which allegedly has evolved without human meddling, first came to notice in the only city in the world with a laboratory that was paid for years by the U.S. government to perform experiments on certain obscure and heretofore unpublicized strains of bat viruses — which bat viruses then turned out to be, out of all the organisms on the planet, the ones that are most closely related to the disease. What are the odds?

In July, I discovered a number of volunteer analysts who were doing a new kind of forensic, samizdat science, hunched over the letter code of the SARS-2 genome like scholars deciphering the cuneiform impressions in Linear B tablets. There were the anonymous authors of Project Evidence, on GitHub, who “disavow all racism and violent attacks, including those which are aimed at Asian or Chinese people,” and there was Yuri Deigin, a biotech entrepreneur from Canada, who wrote a massive, lucid paper on Medium, “Lab-Made?,” which illumined the mysteries of the spike protein. Jonathan Latham of the Bioscience Resource Project, with his co-author Allison Wilson, wrote two important papers: one a calm, unsparing overview of laboratory accidents and rash research and the other a close look at the small outbreak of an unexplained viral pneumonia in a bat-infested copper mine in 2012. I corresponded with Alina Chan (now the subject of a nicely turned piece in *Boston* magazine by Rowan Jacobsen) and with the pseudonymous Billy Bostickson, a tireless researcher whose Twitter photo is a cartoon of an injured experimental monkey, and Monali Rahalkar, of the Agharkar Research Institute in Pune, India, who wrote a paper with her husband, Rahul Bahulikar, that also sheds light on the story of the bat-guano-shoveling men whose virus was remarkably like SARS-2, except that it was not nearly as catching. I talked to Rossana Segreto, a molecular biologist at the University of Innsbruck, whose paper, “Is Considering a Genetic-Manipulation Origin for SARS-CoV-2 a Conspiracy Theory That Must Be Censored?,” co-authored with Yuri Deigin, was finally published in November under a milder title; it argued

that SARS-2's most notable features, the furin site and the human ACE2-binding domain, were unlikely to have arisen simultaneously and "might be the result of lab manipulation techniques such as site directed mutagenesis." Segreto is also the person who first established that a bat-virus fragment named BtCoV/4991, identified in 2013, was 100 percent identical to the closest known cousin to SARS-CoV-2, the bat virus RaTG13, thereby proving that the virus closest to the SARS-2-pandemic virus was linked back not to a bat cave but to a mine shaft, and that this same virus had been stored and worked on in the Wuhan Institute for years. This made possible the first big investigative piece on SARS-2's origins, in the *Times* of London, in July: "Nobody can deny the bravery of scientists who risked their lives harvesting the highly infectious virus," the *Times* authors write. "But did their courageous detective work lead inadvertently to a global disaster?"

XII.

"A New, Non-Natural Risk"

In 2011, a tall, confident Dutch scientist, Ron Fouchier, using grant money from Fauci's group at NIH, created a mutant form of highly pathogenic avian influenza, H5N1, and passaged it ten times through ferrets in order to prove that he could "force" (his word) this potentially fatal disease to infect mammals, including humans, "via aerosols or respiratory droplets." Fouchier said his findings indicated that these avian influenza viruses, thus forced, "pose a risk of becoming pandemic in humans."

This experiment was too much for some scientists: Why, out of a desire to prove that something extremely infectious could happen, would you make it happen? And why would the U.S. government feel compelled to pay for it to happen? Late in 2011, Marc Lipsitch of the Harvard School of Public Health got together with several other dismayed onlookers to ring the gong for caution. On January 8, 2012, the *New York Times* published a scorcher of an editorial, "An Engineered Doomsday." "We cannot say there would be no benefits at all from studying the virus," the *Times* said. "But the consequences, should the virus escape, are too devastating to risk."

These gain-of-function experiments were an important part of the NIH's approach to vaccine development, and Anthony Fauci was reluctant to stop funding them. He and Francis Collins, director of the National Institutes of Health, along with Gary Nabel, NIAID director of vaccine research, published an opinion piece in the *Washington Post* in which they contended that the ferret flu experiments, and others like them, were "a risk worth taking."

“Important information and insights can come from generating a potentially dangerous virus in the laboratory,” they wrote; the work can “help delineate the principles of virus transmission between species.” The work was safe because the viruses were stored in a high-security lab, they believed, and the work was necessary because nature was always coming up with new threats. “Nature is the worst bioterrorist,” Fauci told a reporter. “We know that through history.”

Soon afterward, there followed some distressing screwups in secure federal laboratories involving live anthrax, live smallpox, and live avian influenza. These got attention in the science press. Then Lipsitch’s activists (calling themselves the Cambridge Working Group) sent around a strong statement on the perils of research with “Potential Pandemic Pathogens,” signed by more than a hundred scientists. The work might “trigger outbreaks that would be difficult or impossible to control,” the signers said. Fauci reconsidered, and the White House in 2014 announced that there would be a “pause” in the funding of new influenza, SARS, and MERS gain-of-function research.

Baric, in North Carolina, was not happy. He had a number of gain-of-function experiments with pathogenic viruses in progress. “It took me ten seconds to realize that most of them were going to be affected,” he told NPR. Baric and a former colleague from Vanderbilt University wrote a long letter to an NIH review board expressing their “profound concerns.” “This decision will significantly inhibit our capacity to respond quickly and effectively to future outbreaks of SARS-like or MERS-like coronaviruses, which continue to circulate in bat populations and camels,” they wrote. The funding ban was itself dangerous, they argued. “Emerging coronaviruses in nature do not observe a mandated pause.”

Hoping to smooth over controversy by showing due diligence, the National Science Advisory Board for Biosecurity, founded in the BioShield era under President Bush, paid a consulting firm, Gryphon Scientific, to write a report on gain-of-function research, which by now was simply referred to as GoF. In chapter six of this thousand-page dissertation, published in April 2016, the consultants take up the question of coronaviruses. “Increasing the transmissibility of the coronaviruses could significantly increase the chance of a global pandemic due to a laboratory accident,” they wrote.

The Cambridge Working Group continued to write letters of protest and plead for restraint and sanity. Steven Salzberg, a professor of biomedical engineering at Johns Hopkins, said, “We have enough problems simply keeping up with the current flu outbreaks — and now with Ebola — without

scientists creating incredibly deadly new viruses that might accidentally escape their labs.” David Relman of Stanford Medical School said, “It is unethical to place so many members of the public at risk and then consult only scientists — or, even worse, just a small subset of scientists — and exclude others from the decision-making and oversight process.” Richard Ebright wrote that creating and evaluating new threats very seldom increases security: “Doing so in biology — where the number of potential threats is nearly infinite, and where the asymmetry between the ease of creating threats and the difficulty of addressing threats is nearly absolute — is especially counterproductive.” Lynn Klotz wrote, “Awful as a pandemic brought on by the escape of a variant H5N1 virus might be, it is SARS that now presents the greatest risk. The worry is less about recurrence of a natural SARS outbreak than of yet another escape from a laboratory researching it to help protect against a natural outbreak.” Marc Lipsitch argued that gain-of-function experiments can mislead, “resulting in worse not better decisions,” and that the entire gain-of-function debate as overseen by the NIH was heavily weighted in favor of scientific insiders and “distinctly unwelcoming of public participation.”

Nariyoshi Shinomiya, a professor of physiology and nano-medicine at the National Defense Medical College in Japan, offered this warning: “Similar to nuclear or chemical weapons there is no going back once we get a thing in our hands.”

But in the end, Baric was allowed to proceed with his experiments, and the research papers that resulted, showered with money, became a sort of *Anarchist’s Cookbook* for the rest of the scientific world. In November 2015, Baric and colleagues published a collaboration paper with Shi Zhengli titled “A SARS-like Cluster of Circulating Bat Coronaviruses Shows Potential for Human Emergence.” Into a human SARS virus that they had adapted so that it would work in mice, Baric and Shi et al. inserted the spike protein of a bat virus, SHC014, discovered by Shi in southern China. They dabbed the mice nasally with virus and waited, looking for signs of sickness: “hunching, ruffled fur.” They also infected human airway cells with the mouse-adapted bat-spike-in-a-human-virus backbone. In both mice and human airway cells, the chimeric virus caused a “robust infection.”

This proved, Baric and Shi believed, that you did not need civets or other intermediate hosts in order for bats to cause an epidemic in humans and that therefore all the SARS-like viruses circulating in bat populations “may pose a future threat.” Peter Daszak, who had used Predict funds to pay Shi for her work on the paper, was impressed by this conclusion; the findings, he said,

“move this virus from a candidate emerging pathogen to a clear and present danger.”

Richard Ebright was trenchantly unenthusiastic. “The only impact of this work,” he said, “is the creation, in a lab, of a new, non-natural risk.”

Early in 2016, Baric and Shi again collaborated. Shi sent Baric a fresh bat virus spike protein, and Baric inserted it into the backbone of a human SARS virus and then used that infectious clone to attack human airway cells. “The virus readily and efficiently replicated in cultured human airway tissues, suggesting an ability to potentially jump directly to humans,” reported the UNC’s website. This time, they also used the bat-human hybrid virus to infect transgenic humanized mice that grew human ACE2 protein. The mice, young and old, lost weight and died, proving, again, that this particular bat virus was potentially “poised to emerge in human populations.” It was “an ongoing threat,” Baric wrote. But was it? Civets and camels that are exposed to a lot of bat-guano dust may be an ongoing threat and a manageable one. But the bats themselves just want to hang in their caves and not be bothered by frowning sightseers in spacesuits who want to poke Q-tips in their bottoms. This 2016 “poised for human emergence” paper was supported by eight different NIH grants. In 2015, Baric’s lab received \$8.3 million from the NIH; in 2016, it received \$10.5 million.

Gain-of-function research came roaring back under Trump and Fauci. “The National Institutes of Health will again fund research that makes viruses more dangerous,” said an article in *Nature* in December 2017. Carrie Wolinetz of the NIH’s office of science policy defended the decision. “These experiments will help us get ahead of viruses that are already out there and pose a real and present danger to human health,” she told *The Lancet*. The NIH, Wolinetz said, was committed to a leadership role with gain-of-function research internationally. “If we are pursuing this research in an active way, we will be much better positioned to develop protection and countermeasures should something bad happen in another country.”

A reporter asked Marc Lipsitch what he thought of the resumption of NIH funding. Gain-of-function experiments “have done almost nothing to improve our preparedness for pandemics,” he said, “yet they risked creating an accidental pandemic.”

“Proximity Is a Problem”

In April, four months into the coronavirus emergency, a deputy director at the NIH wrote an email to EcoHealth Alliance. “You are instructed to cease providing any funds to Wuhan Institute of Virology,” it said. In response, Daszak and the chief scientific officer of New England Biolabs (a company that sells seamless gene-splicing products to laboratories, among other things) got 77 Nobel Prize winners to sign a statement saying that the cancellation deprived the “nation and the world of highly regarded science that could help control one of the greatest health crises in modern history and those that may arise in the future.” Later, as a condition of further funding, the NIH wrote to say it wanted Daszak to arrange an outside inspection of the Wuhan lab and to procure from Wuhan’s scientists a sample of whatever they’d used to sequence the SARS-2 virus. Daszak was outraged (“I am not trained as a private detective”), and again he fought back. He was reluctant to give up his own secrets, too. “Conspiracy-theory outlets and politically motivated organizations have made Freedom of Information Act requests on our grants and all of our letters and emails to the NIH,” he told *Nature*. “We don’t think it’s fair that we should have to reveal everything we do.”

But Daszak has survived — even prospered. Recently, *The Lancet* made him the lead investigator in its inquiry into the origins of the pandemic, and the World Health Organization named him to its ten-person origins investigation. (“We’re still close enough to the origin to really find out more details about where it has come from,” Daszak told *Nature*.)

The NIH has also set up an ambitious new international program, called CREID, which stands for Centers for Research in Emerging Infectious Diseases, and it has put Daszak’s EcoHealth in charge of trapping animals and looking for obscure bat viruses in Singapore, Malaysia, and Thailand. Baric is one of Daszak’s partners in CREID. The virus hunting and collecting, which Richard Ebright likens to “looking for a gas leak with a lighted match,” will continue and widen with U.S. funding. “We’re going to work in remote parts of Malaysia and Thailand to get to the front line of where the next pandemic is going to start,” Daszak told NPR.

In May, an interviewer from the People’s Pharmacy website asked Baric if he had any thoughts on whether the coronavirus began with a natural bat-to-human transfer. “Or was there something a little bit more, perhaps, insidious involved?”

“Well, of course the answers to those questions are in China,” Baric replied. “Exactly how they work in that facility is something that would be very difficult for a Westerner to know,” he said. “The main problems that the Institute of Virology has is that the outbreak occurred in close proximity to that Institute. That Institute has in essence the best collection of virologists in the world that have gone out and sought out, and isolated, and sampled bat species throughout Southeast Asia. So they have a very large collection of viruses in their laboratory. And so it’s — you know — proximity is a problem. It’s a problem.”

Over the course of the fall, and especially after the election muffled Donald Trump’s influence over the country’s public-health apparatus, that proximity problem — and the uncomfortable questions of origins it raised — began to grow somewhat more discussable. The BBC, *Le Monde*, and Italy’s RAI have all recently taken seriously the scientific possibility of a lab leak. In late October, the World Health Organization convened the first meeting of its second inquiry into the origins of the disease. The WHO’s effort is perhaps the world’s best chance to satisfy its curiosity about goings-on at the Wuhan Institute of Virology and at the Wuhan CDC’s virus lab near the Wuhan seafood market. But, as the *New York Times* has reported, the WHO’s information gathering has been hindered by Chinese secretiveness since February, when an initial investigative team sent to Beijing was told its members’ access to scientists would be restricted and that it couldn’t visit the seafood market, then considered a hub of the pandemic.

When a BBC video team tried to inspect the Yunnan mine shaft, they found the road to the mine blocked by a strategically parked truck that had “broken down” shortly before they arrived. Reporter John Sudworth asked Daszak, one of the ten members of the second WHO investigative team, whether he would push for access to the Wuhan Institute of Virology. “That’s not my job to do that,” Daszak replied.

In November, David Relman, the Stanford microbiologist, one of the most thoughtful of the voices warning against gain-of-function research, published a paper in *Proceedings of the National Academy of Sciences* on the urgent need to unravel the origins of COVID-19. “If SARS-CoV-2 escaped from a lab to cause the pandemic,” he wrote, “it will become critical to understand the chain of events and prevent this from happening again.” Conflicts of interest by researchers and administrators will need to be addressed, Relman wrote; to reach the truth, the investigation must be transparent, international, and, as much as possible, unpolitical. “A more complete understanding of the

origins of COVID-19 clearly serves the interests of every person in every country on this planet.”

“The world is sitting on a precedent-setting decision right now,” wrote Alina Chan on December 8. “It is unclear if SARS2 is 100 percent natural or emerged due to lab/research activities. If we walk away from this, demonstrating that we cannot effectively investigate its origins, it will pave the way for future COVIDS.”

Just before this issue of *New York* went to press, I reached Ralph Baric by phone and asked him where he now believed SARS-2 came from. (Anthony Fauci, Shi Zhengli, and Peter Daszak didn’t respond to emails, and Kristian Andersen said he was busy with other things.) Baric said he still thought the virus came from bats in southern China, perhaps directly, or possibly via an intermediate host, although the smuggled pangolins, in his view, were a red herring. The disease evolved in humans over time without being noticed, he suspected, becoming gradually more infectious, and eventually a person carried it to Wuhan “and the pandemic took off.” Then he said, “Can you rule out a laboratory escape? The answer in this case is probably not.”

XIV.

Transmission

So how did we actually get this disease?

Here’s what I think happened. In April 2012, in a copper mine in Mojiang, China, three men were given an awful job — they were told to shovel bat guano out of a mine shaft. They went to work and shoveled guano for seven hours a day in the confined, insufficiently ventilated space of the mine shaft, and by the end of the week, they were sick with a viral pneumonia of unknown etiology. Three more, younger shovelers were hired to replace the ones who were out sick.

The viral load in their lungs was so huge, because of all the guano dust, that their lungs became a kind of accelerated laboratory passaging experiment, as Jonathan Latham and Allison Wilson have written, forcing the virus to switch its allegiance from bats to humans. SARS experts were consulted, and the disease was judged to be SARS-like but not SARS. It was something new. (Shi Zhengli told *Scientific American* that the guano shovelers had died of a fungal disease, but, as Monali Rahalkar pointed out, they were treated with antivirals,

and their symptoms were consistent with viral pneumonia with attendant secondary fungal infections.)

Although it was a severe disease, and in the end three of the shovelers died, there was no resultant epidemic. It was actually a case of industrial overexposure to an infectious substance — what we might call a massive OSHA violation. The bat disease that the men encountered wasn't necessarily all that dangerous except in an environment of immunosuppressive overload.

Peter Daszak and Shi Zhengli were interested, of course, because this unidentified coronavirus disease involved bats and people. Of the fragmentary bits of virus Shi retrieved from the mine shaft, one was SARS-like, and Shi sequenced it and called it BtCoV/4991 and published a paper about it. Several times — in 2016 and 2018 and 2019 — this most interesting sample, a portion of what we now know as RaTG13, was taken out of the freezers in Shi's lab and worked on in undisclosed ways. (Peter Daszak claims that these samples have disintegrated and can't be validated or studied.) Samples of the nameless human disease also traveled back to the Wuhan Institute of Virology — few specifics about these valuable specimens have been released by Chinese sources, however.

This is the period in the story that demands a very close investigation, when chimeric assemblages may have been created and serially passaged, using BtCoV/4991, a.k.a. RaTG13, and other bat viruses, perhaps along with forms of the human virus. It's when Shi and Baric both published papers that were about what happened when you hot-swapped mutant spike proteins between bat viruses and human viruses.

The link, via the renamed sample BtCoV/4991, to the copper mine is of exceptional importance because of the one huge difference between the unnamed guano shovelers' virus and the SARS-2 virus that is now ravaging, for example, California: transmissibility. Airborne human-to-human transmissibility — the kind of thing that gain-of-functioneers like Ron Fouchier and Ralph Baric were aiming at, in order to demonstrate what Baric called "lurking threats" — is COVID-19's crucial distinguishing feature. If six men had gotten extremely sick with COVID-19 back in 2012 in southern China, doctors and nurses in the hospital where they lay dying would likely have gotten sick as well. There might have been hundreds or thousands of cases. Instead, only the shovelers themselves, who had breathed a heavy concentration of guano dust for days, got it.

The existence of bat virus RaTG13 is therefore not necessarily evidence of a natural bat origin. In fact, it seems to me to imply the opposite: New functional components may have been overlaid onto or inserted into the RaTG13 genome, new Tinkertoy intermolecular manipulations, especially to its spike protein, which have the effect of making it unprecedentedly infectious in human airways.

This is where the uniquely peculiar furin insert and/or the human-tuned ACE2-receptor-binding domain may come in — although it's also possible that either of these elements could have evolved as part of some multistep zoonotic process. But in the climate of gonzo laboratory experimentation, at a time when all sorts of tweaked variants and amped-up substitutions were being tested on cell cultures and in the lungs of humanized mice and other experimental animals, isn't it possible that somebody in Wuhan took the virus that had been isolated from human samples, or the RaTG13 bat virus sequence, or both (or other viruses from that same mine shaft that Shi Zhengli has recently mentioned in passing), and used them to create a challenge disease for vaccine research — a chopped-and-channeled version of RaTG13 or the miners' virus that included elements that would make it thrive and even rampage in people? And then what if, during an experiment one afternoon, this new, virulent, human-infecting, furin-ready virus got out?

For more than 15 years, coronavirologists strove to prove that the threat of SARS was ever present and must be defended against, and they proved it by showing how they could doctor the viruses they stored in order to force them to jump species and go directly from bats to humans. More and more bat viruses came in from the field teams, and they were sequenced and synthesized and "rewired," to use a term that Baric likes. In this international potluck supper of genetic cookery, hundreds of new variant diseases were invented and stored. And then one day, perhaps, somebody messed up. It's at least a reasonable, "parsimonious" explanation of what might have happened.

This may be the great scientific meta-experiment of the 21st century. Could a world full of scientists do all kinds of reckless recombinant things with viral diseases for many years and successfully avoid a serious outbreak? The hypothesis was that, yes, it was doable. The risk was worth taking. There would be no pandemic.

I hope the vaccine works.

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David Feith
Deputy Assistant Secretary
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(b)(6)

(b)(6) @state.gov

(b)(6)

From: "Stilwell, David R"
To: Feith, David (b)(6)@state.gov>
Subject: RE: New York Mag: The Lab Leak Hypothesis
Date: Mon, 4 Jan 2021 20:16:41 +0000

Way ahead of you; sent 20 minutes ago. Also sent a copy to (b)(6)

China is going to use this: In 1977, a worldwide epidemic of influenza A began in Russia and China; it was eventually traced to a sample of an American strain of flu preserved in a laboratory freezer since 1950.

From: Feith, David (b)(6)@state.gov>
Sent: Monday, January 4, 2021 3:14 PM
To: Stilwell, David R (b)(6)@state.gov>
Subject: FW: New York Mag: The Lab Leak Hypothesis

Pass to (b)(6) before 4pm call?

From: Feith, David (b)(6)@state.gov>
Sent: Monday, January 4, 2021 2:20 PM
To: EAP-FO-Principals-DL <EAP-FO-Principals-DL@state.gov>; DL NSC Asia (DL.Asia@whmo.mil) <DL.Asia@whmo.mil>; MPottinger (b)(6) Ruggiero, Anthony J. (b)(6)
(b)(6)
Subject: New York Mag: The Lab Leak Hypothesis

This looks awfully interesting. The story the New Yorker wouldn't tell...

<https://nymag.com/intelligencer/article/coronavirus-lab-escape-theory.html>

Jan 4, 2021, 6:00 A.M.

The Lab-Leak Hypothesis

The Lab Leak Hypothesis

For decades, scientists have been hot-wiring viruses in hopes of

preventing a pandemic, not causing one. But what if ...?

By *Nicholson Baker*

I.

Flask Monsters

What happened was fairly simple, I've come to believe. It was an accident. A virus spent some time in a laboratory, and eventually it got out. SARS-CoV-2, the virus that causes COVID-19, began its existence inside a bat, then it learned how to infect people in a claustrophobic mine shaft, and then it was made more infectious in one or more laboratories, perhaps as part of a scientist's well-intentioned but risky effort to create a broad-spectrum vaccine. SARS-2 was not designed as a biological weapon. But it was, I think, designed. Many thoughtful people dismiss this notion, and they may be right. They sincerely believe that the coronavirus arose naturally, "zoonotically," from animals, without having been previously studied, or hybridized, or sluiced through cell cultures, or otherwise worked on by trained professionals. They hold that a bat, carrying a coronavirus, infected some other creature, perhaps a pangolin, and that the pangolin may have already been sick with a different coronavirus disease, and out of the conjunction and commingling of those two diseases within the pangolin, a new disease, highly infectious to humans, evolved. Or they hypothesize that two coronaviruses recombined in a bat, and this new virus spread to other bats, and then the bats infected a person directly — in a rural setting, perhaps — and that this person caused a simmering undetected outbreak of respiratory disease, which over a period of months or years evolved to become virulent and highly transmissible but was not noticed until it appeared in Wuhan.

There is no direct evidence for these zoonotic possibilities, just as there is no direct evidence for an experimental mishap — no written confession, no incriminating notebook, no official accident report. Certainty craves detail, and detail requires an investigation. It has been a full year, 80 million people have been infected, and, surprisingly, no public investigation has taken place. We still know very little about the origins of this disease.

Nevertheless, I think it's worth offering some historical context for our yearlong medical nightmare. We need to hear from the people who for years have contended that certain types of virus experimentation might lead to a disastrous pandemic like this one. And we need to stop hunting for new exotic diseases in the wild, shipping them back to laboratories, and hot-wiring their genomes to prove how dangerous to human life they might become.

Over the past few decades, scientists have developed ingenious methods of evolutionary acceleration and recombination, and they've learned how to trick viruses, coronaviruses in particular, those spiky hairballs of protein we now know so well, into moving quickly from one species of animal to another or from one type of cell culture to another. They've made machines that mix and mingle the viral code for bat diseases with the code for human diseases — diseases like SARS, severe acute respiratory syndrome, for example, which arose in China in 2003, and MERS, Middle East respiratory syndrome, which broke out a decade later and has to do with bats and camels. Some of the experiments — “gain of function” experiments — aimed to create new, more virulent, or more infectious strains of diseases in an effort to predict and therefore defend against threats that might conceivably arise in nature. The term *gain of function* is itself a euphemism; the Obama White House more accurately described this work as “experiments that may be reasonably anticipated to confer attributes to influenza, MERS, or SARS viruses such that the virus would have enhanced pathogenicity and/or transmissibility in mammals via the respiratory route.” The virologists who carried out these experiments have accomplished amazing feats of genetic transmutation, no question, and there have been very few publicized accidents over the years. But there have been some.

And we were warned, repeatedly. The intentional creation of new microbes that combine virulence with heightened transmissibility “poses extraordinary risks to the public,” wrote infectious-disease experts Marc Lipsitch and Thomas Inglesby in 2014. “A rigorous and transparent risk-assessment process for this work has not yet been established.” That's still true today. In 2012, in *Bulletin of the Atomic Scientists*, Lynn Klotz warned that there was an 80 percent chance, given how many laboratories were then handling virulent viro-varietals, that a leak of a potential pandemic pathogen would occur sometime in the next 12 years.

A lab accident — a dropped flask, a needle prick, a mouse bite, an illegibly labeled bottle — is apolitical. Proposing that something unfortunate happened during a scientific experiment in Wuhan — where COVID-19 was first diagnosed and where there are three high-security virology labs, one of which

held in its freezers the most comprehensive inventory of sampled bat viruses in the world — isn't a conspiracy theory. It's just a theory. It merits attention, I believe, alongside other reasoned attempts to explain the source of our current catastrophe.

II.

“A Reasonable Chance”

From early 2020, the world was brooding over the origins of COVID-19. People were reading research papers, talking about what kinds of live animals were or were not sold at the Wuhan seafood market — wondering where the new virus had come from.

Meanwhile, things got strange all over the world. The Chinese government shut down transportation and built hospitals at high speed. There were video clips of people who'd suddenly dropped unconscious in the street. A doctor on YouTube told us how we were supposed to scrub down our produce when we got back from the supermarket. A scientist named Shi Zhengli of the Wuhan Institute of Virology published a paper saying that the novel coronavirus was 96 percent identical to a bat virus, RaTG13, found in Yunnan province in southern China. On March 13, I wrote in my journal that there seemed to be something oddly artificial about the disease: “It's too airborne — too catching — it's something that has been selected for infectivity. That's what I suspect. No way to know so no reason to waste time thinking about it.”

This was just a note to self — at the time, I hadn't interviewed scientists about SARS-2 or read their research papers. But I did know something about pathogens and laboratory accidents; I published a book last year, *Baseless*, that talks about some of them. The book is named after a Pentagon program, Project Baseless, whose goal, as of 1951, was to achieve “an Air Force-wide combat capability in biological and chemical warfare at the earliest possible date.”

A vast treasure was spent by the U.S. on the amplification and aerial delivery of diseases — some well known, others obscure and stealthy. America's biological-weapons program in the '50s had A1-priority status, as high as nuclear weapons. In preparation for a total war with a numerically superior communist foe, scientists bred germs to be resistant to antibiotics and other drug therapies, and they infected lab animals with them, using a technique

called “serial passaging,” in order to make the germs more virulent and more catching.

And along the way, there were laboratory accidents. By 1960, hundreds of American scientists and technicians had been hospitalized, victims of the diseases they were trying to weaponize. Charles Armstrong, of the National Institutes of Health, one of the consulting founders of the American germ-warfare program, investigated Q fever three times, and all three times, scientists and staffers got sick. In the anthrax pilot plant at Camp Detrick, Maryland, in 1951, a microbiologist, attempting to perfect the “foaming process” of high-volume production, developed a fever and died. In 1964, veterinary worker Albert Nickel fell ill after being bitten by a lab animal. His wife wasn’t told that he had Machupo virus, or Bolivian hemorrhagic fever. “I watched him die through a little window to his quarantine room at the Detrick infirmary,” she said.

In 1977, a worldwide epidemic of influenza A began in Russia and China; it was eventually traced to a sample of an American strain of flu preserved in a laboratory freezer since 1950. In 1978, a hybrid strain of smallpox killed a medical photographer at a lab in Birmingham, England; in 2007, live foot-and-mouth disease leaked from a faulty drainpipe at the Institute for Animal Health in Surrey. In the U.S., “more than 1,100 laboratory incidents involving bacteria, viruses and toxins that pose significant or bioterror risks to people and agriculture were reported to federal regulators during 2008 through 2012,” reported *USA Today* in an exposé published in 2014.

In 2015, the Department of Defense discovered that workers at a germ-warfare testing center in Utah had mistakenly sent close to 200 shipments of live anthrax to laboratories throughout the United States and also to Australia, Germany, Japan, South Korea, and several other countries over the past 12 years. In 2019, laboratories at Fort Detrick — where “defensive” research involves the creation of potential pathogens to defend against — were shut down for several months by the Centers for Disease Control and Prevention for “breaches of containment.” They reopened in December 2019.

High-containment laboratories have a whispered history of near misses. Scientists are people, and people have clumsy moments and poke themselves and get bitten by the enraged animals they are trying to nasally inoculate. Machines can create invisible aerosols, and cell solutions can become contaminated. Waste systems don’t always work properly. Things can go wrong in a hundred different ways.

Hold that human fallibility in your mind. And then consider the cautious words of Alina Chan, a scientist who works at the Broad Institute of MIT and Harvard. “There is a reasonable chance that what we are dealing with is the result of a lab accident,” Chan told me in July of last year. There was also, she added, a reasonable chance that the disease had evolved naturally — both were scientific possibilities. “I don’t know if we will ever find a smoking gun, especially if it was a lab accident. The stakes are so high now. It would be terrifying to be blamed for millions of cases of COVID-19 and possibly up to a million deaths by year end, if the pandemic continues to grow out of control. The Chinese government has also restricted their own scholars and scientists from looking into the origins of SARS-CoV-2. At this rate, the origin of SARS-CoV-2 may just be buried by the passage of time.”

I asked Jonathan A. King, a molecular biologist and biosafety advocate from MIT, whether he’d thought *lab accident* when he first heard about the epidemic. “Absolutely, absolutely,” King answered. Other scientists he knew were concerned as well. But scientists, he said, in general were cautious about speaking out. There were “very intense, very subtle pressures” on them not to push on issues of laboratory biohazards. Collecting lots of bat viruses, and passaging those viruses repeatedly through cell cultures, and making bat-human viral hybrids, King believes, “generates new threats and desperately needs to be reined in.”

“All possibilities should be on the table, including a lab leak,” a scientist from the NIH, Philip Murphy — chief of the Laboratory of Molecular Immunology — wrote me recently. Nikolai Petrovsky, a professor of endocrinology at Flinders University College of Medicine in Adelaide, Australia, said in an email, “There are indeed many unexplained features of this virus that are hard if not impossible to explain based on a completely natural origin.” Richard Ebright, a molecular biologist at Rutgers University, wrote that he’d been concerned for some years about the Wuhan laboratory and about the work being done there to create “chimeric” (i.e., hybrid) SARS-related bat coronaviruses “with enhanced human infectivity.” Ebright said, “In this context, the news of a novel coronavirus in Wuhan ***screamed*** lab release.”

III.

“No Credible Evidence”

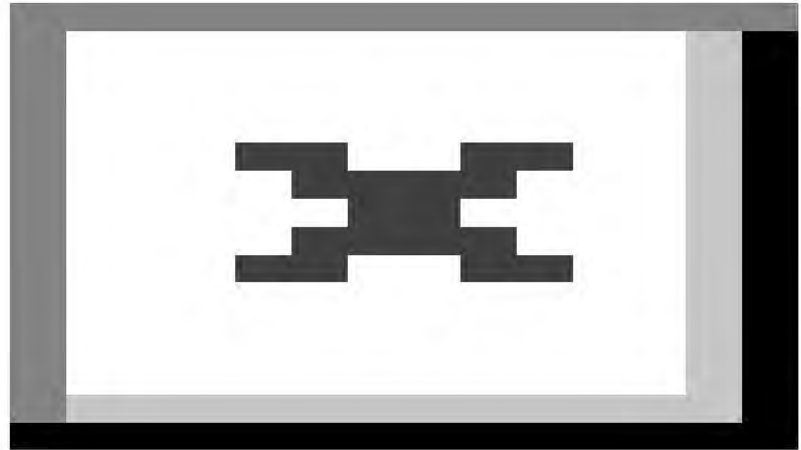
The new disease, as soon as it appeared, was intercepted — stolen and politicized by people with ulterior motives. The basic and extremely

interesting scientific question of what happened was sucked up into an ideological sharknado.

Some Americans boycotted Chinese restaurants; others bullied and harassed Asian Americans. Steve Bannon, broadcasting from his living room, in a YouTube series called *War Room*, said that the Chinese Communist Party had made a biological weapon and intentionally released it. He called it the “CCP virus.” And his billionaire friend and backer, Miles Guo, a devoted Trump supporter, told a right-wing website that the communists’ goal was to “use the virus to infect selective people in Hong Kong, so that the Chinese Communist Party could use it as an excuse to impose martial law there and ultimately crush the Hong Kong pro-democracy movement. But it backfired terribly.”

In *The Lancet*, in February, a powerful counterstatement appeared, signed by 27 scientists. “We stand together to strongly condemn conspiracy theories suggesting that COVID-19 does not have a natural origin,” the statement said. “Scientists from multiple countries have published and analyzed genomes of the causative agent, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), and they overwhelmingly conclude that this coronavirus originated in wildlife, as have so many other emerging pathogens.”

The behind-the-scenes organizer of this *Lancet* statement, Peter Daszak, is a zoologist and bat-virus sample collector and the head of a New York nonprofit called EcoHealth Alliance — a group that (as veteran science journalist Fred Gutierl explained later in *Newsweek*) has channeled money from the National Institutes of Health to Shi Zhengli’s laboratory in Wuhan, allowing the lab to carry on recombinant research into diseases of bats and humans. “We have a choice whether to stand up and support colleagues who are being attacked and threatened daily by conspiracy theorists or to just turn a blind eye,” Daszak said in February in *Science* magazine.



How Did It Get Out? 1. The Tongguan Mine Shaft in Mojiang, Yunnan, where, in 2013, fragments of RaTG13, the closest known relative of SARSCoV-2, were recovered and transported to the Wuhan Institute of Virology; **2. The Wuhan Institute of Virology**, where Shi Zhengli's team brought the RaTG13 sample, sequenced its genome, then took it out of the freezer several times in recent years; **3. The Wuhan Center for Disease Control and Prevention**, which first reported signs of the novel coronavirus in hospital patients; **4. The Huanan Seafood Wholesale Market**, an early suspected origin of the pandemic, where the first major outbreak occurred. Illustration: Map by Jason Lee

Vincent Racaniello, a professor at Columbia and a co-host of a podcast called *This Week in Virology*, said on February 9 that the idea of an accident in Wuhan was “complete bunk.” The coronavirus was 96 percent similar to a bat virus found in 2013, Racaniello said. “It’s not a man-made virus. It wasn’t released from a lab.”

Racaniello’s dismissal was seconded by a group of scientists from Ohio State, the University of Pennsylvania, and the University of North Carolina, who put out a paper in *Emerging Microbes and Infections* to quiet the “speculations, rumors, and conspiracy theories that SARS-CoV-2 is of laboratory origin.” There was “currently no credible evidence” that SARS-2 leaked from a lab, these scientists said, using a somewhat different argument from Racaniello’s. “Some people have alleged that the human SARS-CoV-2 was leaked directly from a laboratory in Wuhan where a bat CoV (RaTG13) was recently

reported,” they said. But RaTG13 could not be the source because it differed from the human SARS-2 virus by more than a thousand nucleotides. One of the paper’s authors, Susan Weiss, told the Raleigh *News & Observer*, “The conspiracy theory is ridiculous.”

The most influential natural-origin paper, “The Proximal Origin of SARS-CoV-2,” by a group of biologists that included Kristian Andersen of Scripps Research, appeared online in a preliminary version in mid-February.

“We do not believe any type of laboratory-based scenario is plausible,” the scientists said. Why? Because molecular-modeling software predicted that if you wanted to optimize an existing bat virus so that it would replicate well in human cells, you would arrange things a different way than how the SARS-2 virus actually does it — even though the SARS-2 virus does an extraordinarily good job of replicating in human cells. The laboratory-based scenario was implausible, the paper said, because, although it was true that the virus could conceivably have developed its unusual genetic features in a laboratory, a stronger and “more parsimonious” explanation was that the features came about through some kind of natural mutation or recombination. “What we think,” explained one of the authors, Robert F. Garry of Tulane University, on YouTube, “is that this virus is a recombinant. It probably came from a bat virus, plus perhaps one of these viruses from the pangolin.” Journalists, for the most part, echoed the authoritative pronouncements of Daszak, Racaniello, Weiss, Andersen, and other prominent natural-originists. “The balance of the scientific evidence strongly supports the conclusion that the new coronavirus emerged from nature — be it the Wuhan market or somewhere else,” said the Washington *Post*’s “Fact Checker” column. “Dr. Fauci Again Dismisses Wuhan Lab As Source of Coronavirus,” said *CBS News*, posting a video interview of Anthony Fauci by *National Geographic*. “If you look at the evolution of the virus in bats, and what’s out there now,” Fauci said, “it’s very, very strongly leaning toward ‘This could not have been artificially or deliberately manipulated’ — the way the mutations have naturally evolved.”

Everyone took sides; everyone thought of the new disease as one more episode in an ongoing partisan struggle. Think of Mike Pompeo, that landmass of Cold War truculence; think of Donald Trump himself. They stood at their microphones saying, in a winking, I-know-something-you-don’t-know sort of way, that this disease escaped from a Chinese laboratory. Whatever they were saying must be wrong. It became impermissible, almost taboo, to admit that, of course, SARS-2 could have come from a lab accident. “The administration’s claim that the virus spread from a Wuhan lab has made the notion politically

toxic, even among scientists who say it could have happened,” wrote science journalist Mara Hvistendahl in the Intercept.

IV.

“Is It a Complete Coincidence?”

Even so, in January and February of 2020, there were thoughtful people who were speaking up, formulating their perplexities.

One person was Sam Hussein, who works for Consortium News. He went to a CDC press conference at the National Press Club on February 11, 2020. By then, 42,000 people had gotten sick in China and more than a thousand had died. But there were only 13 confirmed cases in the U.S. Halfway through the Q&A period, Hussein went to the microphone and asked the CDC’s representative, Anne Schuchat, where the virus had come from. His head was spinning, he told me later.

“Obviously the main concern is how to stop the virus,” Hussein said; nonetheless, he wanted to know more about its source. “Is it the CDC’s contention,” he asked, “that there’s absolutely no relation to the BSL-4 lab in Wuhan? It’s my understanding that this is the only place in China with a BSL-4 lab. We in the United States have, I think, two dozen or so, and there have been problems and incidents.” (A BSL-4 laboratory is a maximum-security biosafety-level-four facility, used to house research on the most dangerous known pathogens. *New York* has confirmed there are at least 11 BSL-4 facilities currently operating in the U.S.) Hussein hastened to say that he wasn’t implying that what happened in Wuhan was in any way intentional. “I’m just asking, Is it a complete coincidence that this outbreak happened in the one city in China with a BSL-4 lab?”

Schuchat thanked Hussein for his questions and comments. Everything she’d seen was quite consistent with a natural, zoonotic origin for the disease, she said.

That same month, a group of French scientists from Aix-Marseille University posted a paper describing their investigation of a small insertion in the genome of the new SARS-2 virus. The virus’s spike protein contained a sequence of amino acids that formed what Etienne Decroly and colleagues called a “peculiar furin-like cleavage site” — a chemically sensitive region on the lobster claw of the spike protein that would react in the presence of an enzyme called furin, which is a type of protein found everywhere within the

human body, but especially in the lungs. When the spike senses human furin, it shudders, chemically speaking, and the enzyme opens the protein, commencing the tiny morbid ballet whereby the virus burns a hole in a host cell's outer membrane and finds its way inside.

The code for this particular molecular feature — not found in SARS or any SARS-like bat viruses, but present in a slightly different form in the more lethal MERS virus — is easy to remember because it's a roar: "R-R-A-R." The letter code stands for amino acids: arginine, arginine, alanine, and arginine. Its presence, so Decroly and his colleagues observed, may heighten the "pathogenicity" — that is, the god-awfulness — of a disease.

Botao Xiao, a professor at the South China University of Technology, posted a short paper on a preprint server titled "The Possible Origins of 2019-nCoV Coronavirus." Two laboratories, the Wuhan Center for Disease Control and Prevention (WHCDC) and the Wuhan Institute of Virology, were not far from the seafood market, which was where the disease was said to have originated, Xiao wrote — in fact, the WHCDC was only a few hundred yards away from the market — whereas the horseshoe bats that hosted the disease were hundreds of miles to the south. (No bats were sold in the market, he pointed out.) It was unlikely, he wrote, that a bat would have flown to a densely populated metropolitan area of 15 million people. "The killer coronavirus probably originated from a laboratory in Wuhan," Xiao believed. He urged the relocation of "biohazardous laboratories" away from densely populated places. His article disappeared from the server.

And late in the month, a professor at National Taiwan University, Fang Chitai, gave a lecture on the coronavirus in which he described the anomalous R-R-A-R furin cleavage site. The virus was "unlikely to have four amino acids added all at once," Fang said — natural mutations were smaller and more haphazard, he argued. "From an academic point of view, it is indeed possible that the amino acids were added to COVID-19 in the lab by humans." When the *Taiwan News* published an article about Fang's talk, Fang disavowed his own comments, and the video copy of the talk disappeared from the website of the Taiwan Public Health Association. "It has been taken down for a certain reason," the association explained. "Thank you for your understanding."

“A Serious Shortage of Appropriately Trained Technicians”

In the spring, I did some reading on coronavirus history. Beginning in the 1970s, dogs, cows, and pigs were diagnosed with coronavirus infections; dog shows were canceled in 1978 after 25 collies died in Louisville, Kentucky. New varieties of coronaviruses didn't start killing humans, though, until 2003 — that's when restaurant chefs, food handlers, and people who lived near a live-animal market got sick in Guangzhou, in southern China, where the shredded meat of a short-legged raccoonlike creature, the palm civet, was served in a regional dish called “dragon-tiger-phoenix soup.” The new disease, SARS, spread alarmingly in hospitals, and it reached 30 countries and territories. More than 800 people died; the civet-borne virus was eventually traced to horseshoe bats.

Later, smaller outbreaks of SARS in Taiwan, Singapore, and China's National Institute of Virology in Beijing were all caused by laboratory accidents. Of the Beijing Virology Institute, the World Health Organization's safety investigators wrote, in May 2004, that they had “serious concerns about biosafety procedures.” By one account, a SARS storage room in the Beijing lab was so crowded that the refrigerator holding live virus was moved out to the hallway. “Scientists still do not fully understand exactly where or how SARS emerged 18 months ago,” wrote *Washington Post* reporter David Brown in June 2004. “But it is clear now that the most threatening source of the deadly virus today may be places they know intimately — their own laboratories.”

I'm just asking, Is it a complete coincidence that this outbreak happened in the one city in China with a BSL-4 lab?

MERS arose in 2012, possibly spread by camels that had contracted the disease from bats or bat guano, then passed it to human drinkers of raw camel milk and butchers of camel meat. It was an acute sickness, with a high fatality rate, mostly confined to Saudi Arabia. Like SARS, MERS ebbed quickly — it all but disappeared outside the Middle East, except for an outbreak in 2015 at the Samsung Medical Center in South Korea, where a single case of MERS led to more than 180 infections, many involving hospital workers.

In January 2015, the brand-new BSL-4 lab in Wuhan, built by a French contractor, celebrated its opening, but full safety certification came slowly. According to State Department cables from 2018 leaked to the *Washington Post*, the new BSL-4 lab had some start-up problems, including “a serious shortage of appropriately trained technicians and investigators needed to safely operate this high-containment laboratory.” The staff had gotten some training at a BSL-4 lab in Galveston, Texas, but they were doing potentially dangerous work with SARS-like viruses, the memo said, and they needed more help from the U.S.

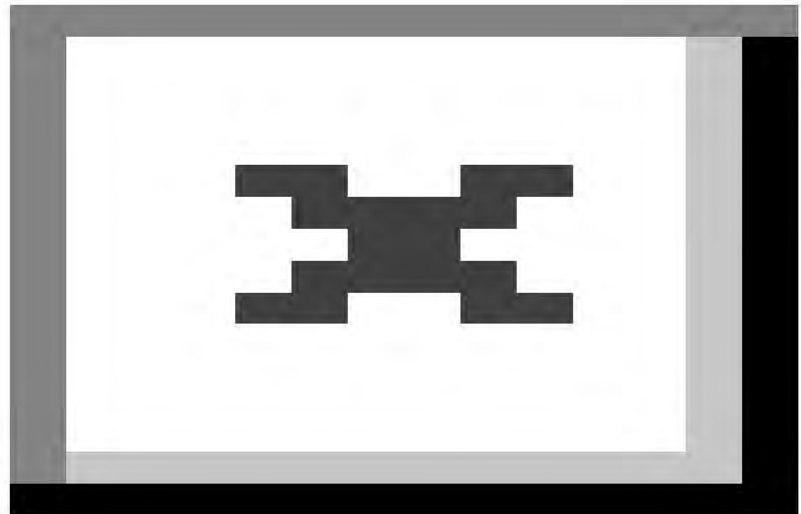
In November or December of 2019, the novel coronavirus began to spread. Chinese scientists initially named it “Wuhan seafood market pneumonia virus,” but soon that idea went away. The market, closed and decontaminated by Chinese officials on January 1, 2020, was an amplifying hub, not the source of the outbreak, according to several studies by Chinese scientists. Forty-five percent of the earliest SARS-2 patients had no link with the market.

VI.

Emergence

Now let’s take a step back. AIDS, fatal and terrifying and politically charged, brought on a new era in government-guided vaccine research, under the guidance of Anthony Fauci. A virologist at Rockefeller University, Stephen S. Morse, began giving talks on “emerging viruses” — other plagues that might be in the process of coming out of nature’s woodwork. In 1992, Richard Preston wrote a horrific account of one emergent virus, Ebola, in *The New Yorker*, which became a best-selling book in 1994; Laurie Garrett’s *The Coming Plague: Newly Emerging Diseases in a World Out of Balance* appeared that same year and was also a best seller. The idea seemed to be everywhere: We were on the verge of a wave of zoonotic, emergent plagues.

This new, useful term, *emerging*, began to glow in the research papers of some coronavirologists, who were out of the spotlight, working on common colds and livestock diseases. The term was useful because it was fluid. An emerging disease could be real and terrifying, as AIDS was — something that had just arrived on the medical scene and was confounding our efforts to combat it — or it could be a disease that hadn’t arrived, and might never arrive, but could be shown in a laboratory to be waiting in the wings, just a few mutations away from a human epidemic. It was real and unreal at the same time — a quality that was helpful when applying for research grants.



Where Did It Come From? This chart measures the genetic similarity of known viruses to the novel coronavirus (which appears in yellow). By far the closest is the bat virus RaTG13, which appears in blue, and which was recovered in 2013 and brought to the Wuhan Institute of Virology. The first SARS, marked in red, is a much more distant relative. Graphic: Zhou, P., Yang, XL., Wang, XG. et al. A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature* 579, 270–273 (2020)

Take, for instance, this paper from 1995: “High Recombination and Mutation Rates in Mouse Hepatitis Viruses Suggest That Coronaviruses May Be Potentially Important Emerging Viruses.” It was written by Dr. Ralph Baric and his bench scientist, Boyd Yount, at the University of North Carolina. Baric, a gravelly voiced former swim champion, described in this early paper how his lab was able to train a coronavirus, MHV, which causes hepatitis in mice, to jump species, so that it could reliably infect BHK (baby-hamster kidney) cell cultures. They did it using serial passaging: repeatedly dosing a mixed solution of mouse cells and hamster cells with mouse-hepatitis virus, while each time decreasing the number of mouse cells and upping the concentration of hamster cells. At first, predictably, the mouse-hepatitis virus couldn’t do much with the hamster cells, which were left almost free of infection, floating in

their world of fetal-calf serum. But by the end of the experiment, after dozens of passages through cell cultures, the virus had mutated: It had mastered the trick of parasitizing an unfamiliar rodent. A scourge of mice was transformed into a scourge of hamsters. And there was more: "It is clear that MHV can rapidly alter its species specificity and infect rats and primates," Baric said. "The resulting virus variants are associated with demyelinating diseases in these alternative species." (A demyelinating disease is a disease that damages nerve sheaths.) With steady prodding from laboratory science, along with some rhetorical exaggeration, a lowly mouse ailment was morphed into an emergent threat that might potentially cause nerve damage in primates. That is, nerve damage in us.

A few years later, in a further round of "interspecies transfer" experimentation, Baric's scientists introduced their mouse coronavirus into flasks that held a suspension of African-green-monkey cells, human cells, and pig-testicle cells. Then, in 2002, they announced something even more impressive: They'd found a way to create a full-length infectious clone of the entire mouse-hepatitis genome. Their "infectious construct" replicated itself just like the real thing, they wrote.

Not only that, but they'd figured out how to perform their assembly seamlessly, without any signs of human handiwork. Nobody would know if the virus had been fabricated in a laboratory or grown in nature. Baric called this the "no-see'm method," and he asserted that it had "broad and largely unappreciated molecular biology applications." The method was named, he wrote, after a "very small biting insect that is occasionally found on North Carolina beaches."

In 2006, Baric, Yount, and two other scientists were granted a patent for their invisible method of fabricating a full-length infectious clone using the seamless, no-see'm method. But this time, it wasn't a clone of the mouse-hepatitis virus — it was a clone of the entire deadly human SARS virus, the one that had emerged from Chinese bats, via civets, in 2002. The Baric Lab came to be known by some scientists as "the Wild Wild West." In 2007, Baric said that we had entered "the golden age of coronavirus genetics."

"I would be afraid to look in their freezers," one virologist told me.

Baric and Shi Zhengli of the Wuhan Institute of Virology, the two top experts on the genetic interplay between bat and human coronaviruses, began collaborating in 2015.

VII.

“I Had Not Slept a Wink”

Early in the pandemic, *Scientific American* profiled Shi Zhengli, known in China as the “bat woman.” Shi trapped hundreds of bats in nets at the mouths of caves in southern China, sampled their saliva and their blood, swabbed their anuses, and gathered up their fecal pellets. Several times, she visited and sampled bats in a mine in Mojiang, in southern China, where, in 2012, six men set to work shoveling bat guano were sickened by a severe lung disease, three of them fatally. Shi’s team took the samples back to Wuhan and analyzed whatever fragments of bat virus she could find. In some cases, when she found a sequence that seemed particularly significant, she experimented with it in order to understand how it might potentially infect humans. Some of her work was funded by the National Institutes of Health and some of it by the U.S. Defense Threat Reduction Agency of the Department of Defense via Peter Daszak’s EcoHealth Alliance.

As Shi explained to *Scientific American*, late in December 2019, she heard from the director of the Wuhan Institute that there was an outbreak of a new disease in the city. Medical samples taken from hospital patients arrived at her lab for analysis. Shi determined that the new virus was related to SARS but even more closely related to a bat disease that her own team had found on a virus-hunting trip: the now-famous RaTG13. Shi was surprised that the outbreak was local, she said: “I had never expected this kind of thing to happen in Wuhan, in central China.” The bat hiding places that she’d been visiting were, after all, as far away as Orlando, Florida, is from New York City. Could this new virus, she wondered, have come from her own laboratory? She checked her records and found no exact matches. “That really took a load off my mind,” she said. “I had not slept a wink for days.”

If one of the first thoughts that goes through the head of a lab director at the Wuhan Institute of Virology is that the new coronavirus could have come from her lab, then we are obliged to entertain the scientific possibility that it could indeed have come from her lab. Right then, there should have been a comprehensive, pockets-inside-out, fully public investigation of the Virology Institute, along with the other important virus labs in Wuhan, including the one close by the seafood market, headquarters of the Wuhan CDC. There should have been interviews with scientists, interviews with biosafety teams, close parsings of laboratory notebooks, freezer and plumbing and decontamination systems checks — everything. It didn’t happen. The Wuhan

Institute of Virology closed down its databases of viral genomes, and the Chinese Ministry of Education sent out a directive: “Any paper that traces the origin of the virus must be strictly and tightly managed.”

Shi made some WeChat posts early in 2020. “The novel 2019 coronavirus is nature punishing the human race for keeping uncivilized living habits,” she wrote. “I, Shi Zhengli, swear on my life that it has nothing to do with our laboratory.” She advised those who believed rumors, and gave credence to unreliable scientific papers, to “shut their stinking mouths.”

VIII.

“ ‘Bug to Drug’ in 24 Hours”

It wasn’t only AIDS that changed the way the NIH funded research. The War on Terror also influenced which diseases got the most attention. In the late ’90s, under Bill Clinton and then George W. Bush, biodefense specialists became interested — again — in anthrax. The Defense Threat Reduction Agency built a small anthrax factory in Nevada, using simulants, to demonstrate how easy it would be for a terrorist to build a small anthrax factory. And in the first year of the Bush presidency, the Defense Intelligence Agency wrote up plans to create a vaccine-resistant form of anthrax using state-of-the-art gene-splicery. A front-page article describing these initiatives, “U.S. Germ Warfare Research Pushes Treaty Limits,” appeared in the *New York Times* on September 4, 2001, one week before 9/11. “Pentagon Says Projects Are Defense, Is Pressing Ahead,” was the subtitle.

After the 9/11 attacks, and the mysterious anthrax mailings that began a week later (which said, “TAKE PENACILIN [sic] NOW / DEATH TO AMERICA / DEATH TO ISRAEL / ALLAH IS GREAT”), the desire for biopreparedness became all consuming. Now there were emerging biothreats from humans as well as from the evolving natural world. Fauci’s anti-terror budget went from \$53 million in 2001 to \$1.7 billion in 2003. Setting aside his work toward an AIDS vaccine, which was taking longer than he’d foreseen, Fauci said he would be going all out to defend against a suite of known Cold War agents, all of which had been bred and perfected in American weapons programs many years before — brucellosis, anthrax, tularemia, and plague, for instance. “We are making this the highest priority,” Fauci said. “We are really marshaling all available resources.”

I would be afraid to look in their freezers.

Vaccine development had to progress much faster, Fauci believed; he wanted to set up “vaccine systems” and “vaccine platforms,” which could be quickly tailored to defend against a particular emergent strain some terrorist with an advanced biochemistry degree might have thrown together in a laboratory. “Our goal within the next 20 years is ‘bug to drug’ in 24 hours,” Fauci said. “This would specifically meet the challenge of genetically engineered bioagents.” The first Project BioShield contract Fauci awarded was to VaxGen, a California pharmaceutical company, for \$878 million worth of shots of anthrax vaccine.

By 2005, so much money was going toward biothreat reduction and preparedness that more than 750 scientists sent a protest letter to the NIH. Their claim was that grants to study canonical biowar diseases — anthrax, plague, brucellosis, and tularemia, all exceptionally rare in the U.S. — had increased by a factor of 15 since 2001, whereas funds for the study of widespread “normal” diseases, of high public-health importance, had decreased.

Fauci was firm in his reply: “The United States through its leaders made the decision that this money was going to be spent on biodefense,” he said. “We disagree with the notion that biodefense concerns are of ‘low public-health significance.’”

In 2010, by one count, there were 249 BSL-3 laboratories and seven BSL-4 laboratories in the U.S., and more than 11,000 scientists and staffers were authorized to handle the ultralethal germs on the government’s select pathogen list. And yet the sole bioterrorist in living memory who actually killed American citizens, according to the FBI — the man who sent the anthrax letters — turned out to be one of the government’s own researchers. Bruce Ivins, an eccentric, suicidal laboratory scientist from Ohio who worked in vaccine development at Fort Detrick, allegedly wanted to boost the fear level so as to persuade the government to buy more of the patented, genetically engineered anthrax VaxGen vaccine, of which he was a co-inventor. (See David Willman’s fascinating biography of Ivins, *Mirage Man*.) Fauci’s staff at NIH funded Ivins’s vaccine laboratory and gave \$100 million to VaxGen to accelerate vaccine production. (The NIH’s \$878 million contract with VaxGen, however, was quietly canceled in 2006; Ivins, who was never charged, killed himself in 2008.)

“The whole incident amounted to a snake eating its own tail,” wrote Wendy Orent in an August 2008 piece titled “Our Own Worst Bioenemy” in the *Los Angeles Times*. “No ingenious biowarrior from Al Qaeda sent the lethal

envelopes through the U.S. postal system. An American scientist did.” What confirmed Ivins’s guilt, according to the FBI, was that there was a genetic match between the anthrax used in the killings and the strain held at Fort Detrick.

IX.

“Weapons of Mass Disruption”

After SARS appeared in 2003, Ralph Baric’s laboratory moved up the NIH funding ladder. SARS was a “dual use” organism — a security threat and a zoonotic threat at the same time. In 2006, Baric wrote a long, fairly creepy paper on the threat of “weaponizable” viruses. Synthetic biology had made possible new kinds of viral “weapons of mass disruption,” he wrote, involving, for example, “rapid production of numerous candidate bioweapons that can be simultaneously released,” a scattershot terror tactic Baric called the “‘survival of the fittest’ approach.”

Baric hoped to find a SARS vaccine, but he couldn’t; he kept looking for it, year after year, supported by the NIH, long after the disease itself had been contained. It wasn’t really gone, Baric believed. Like other epidemics that pop up and then disappear, as he told a university audience some years later, “they don’t go extinct. They are waiting to return.” What do you do if you run a well-funded laboratory, an NIH “center of excellence,” and your emergent virus is no longer actually making people sick? You start squeezing it and twisting it into different shapes. Making it stand on its hind legs and quack like a duck, or a bat. Or breathe like a person.

Baric’s safety record is good — although there was a minor mouse-bite incident in 2016, uncovered by ProPublica — and his motives are beyond reproach: “Safe, universal, vaccine platforms are needed that can be tailored to new pathogens as they emerge, quickly tested for safety, and then strategically used to control new disease outbreaks in human populations,” he wrote in a paper on public health. But the pioneering work he did over the past 15 years — generating tiny eager single-stranded flask monsters and pitting them against human cells, or bat cells, or gene-spliced somewhat-human cells, or monkey cells, or humanized mice — was not without risk, and it may have led others astray.

In 2006, for instance, Baric and his colleagues, hoping to come up with a “vaccine strategy” for SARS, produced noninfectious virus replicon particles (or VRPs) using the Venezuelan-equine-encephalitis virus (another American

germ-warfare agent), which they fitted with various SARS spike proteins. Then, wearing Tyvek suits and two pairs of gloves each, and working in a biological safety cabinet in a BSL-3-certified laboratory, they cloned and grew recombinant versions of the original SARS virus in an incubator in a medium that held African-green-monkey cells. When they had grown enough virus, the scientists swapped out one kind of spike protein for a carefully chosen mutant, and they challenged their prototype vaccine with it in mice.

The scientists also tried their infectious SARS clones in something called an air-liquid interface, using a relatively new type of cell culture developed by Raymond Pickles of the University of North Carolina's Cystic Fibrosis Center. Pickles had perfected a method of emulating the traits of human airway tissue by cultivating cells taken from lung-disease patients — nurturing the culture over four to six weeks in such a way that the cells differentiated and developed a crop of tiny moving hairs, or cilia, on top and goblet cells within that produced real human mucus. In fact, before infecting these HAE (human airway epithelial) cells with a virus, the lab worker must sometimes rinse off some of the accumulated mucus, as if helping the lab-grown tissue to clear its throat. So Baric was exposing and adapting his engineered viruses to an extraordinarily true-to-life environment — the juicy, sticky, hairy inner surface of our breathing apparatus.

SARS-2 seems almost perfectly calibrated to grab and ransack our breathing cells and choke the life out of them. “By the time SARS-CoV-2 was first detected in late 2019, it was already pre-adapted to human transmission,” Alina Chan and her co-authors have written, whereas SARS, when it first appeared in 2003, underwent “numerous adaptive mutations” before settling down. Perhaps viral nature hit a bull’s-eye of airborne infectivity, with almost no mutational drift, no period of accommodation and adjustment, or perhaps some lab worker somewhere, inspired by Baric’s work with human airway tissue, took a spike protein that was specially groomed to colonize and thrive deep in the ciliated, mucosal tunnels of our inner core and cloned it onto some existing viral bat backbone. It could have happened in Wuhan, but — because anyone can now “print out” a fully infectious clone of any sequenced disease — it could also have happened at Fort Detrick, or in Texas, or in Italy, or in Rotterdam, or in Wisconsin, or in some other citadel of coronaviral inquiry. No conspiracy — just scientific ambition, and the urge to take exciting risks and make new things, and the fear of terrorism, and the fear of getting sick. Plus a whole lot of government money.

“Risky Areas for Spillover”

Project Bioshield began to fade by the end of the Bush administration, although the expensive high-containment laboratories, controversial preservers and incubators of past and future epidemics, remain. By 2010, some BioShield projects had dissolved into Obama’s Predict program, which paid for laboratories and staff in 60 “risky areas for spillover” around the world. Jonna Mazet, a veterinary scientist from the University of California, Davis, was in charge of Predict, which was a component of USAID’s “Emerging Pandemic Threats” program. Her far-flung teams collected samples from 164,000 animals and humans and claimed to have found “almost 1,200 potentially zoonotic viruses, among them 160 novel coronaviruses, including multiple SARS- and MERS-like coronaviruses.” The fruits of Predict’s exotic harvest were studied and circulated in laboratories worldwide, and their genetic sequences became part of GenBank, the NIH’s genome database, where any curious RNA wrangler anywhere could quickly synthesize snippets of code and test out a new disease on human cells.

Baric, Jonna Mazet, and Peter Daszak of EcoHealth worked together for years — and Daszak also routed Predict money to Shi Zhengli’s bat-surveillance team in Wuhan through his nonprofit, mingling it with NIH money and money from the U.S. Defense Threat Reduction Agency. In 2013, Mazet announced that Shi Zhengli’s virus hunters, with Predict’s support, had, for the first time, isolated and cultured a live SARS-like virus from bats and demonstrated that this virus could bind to the human ACE2, or “angiotensin-converting enzyme 2,” receptor, which Baric’s laboratory had determined to be the sine qua non of human infectivity. “This work shows that these viruses can directly infect humans and validates our assumption that we should be searching for viruses of pandemic potential before they spill over to people,” Mazet said.

Daszak, for his part, seems to have viewed his bat quests as part of an epic, quasi-religious death match. In a paper from 2008, Daszak and a co-author described Bruegel’s painting *The Fall of the Rebel Angels* and compared it to the contemporary human biological condition. The fallen angels could be seen as pathogenic organisms that had descended “through an evolutionary (not spiritual) pathway that takes them to a netherworld where they can feed only on our genes, our cells, our flesh,” Daszak wrote. “Will we succumb to the multitudinous horde? Are we to be cast downward into chthonic chaos represented here by the heaped up gibbering phantasmagory against which we rail and struggle?”

XI.

“Lab-Made?”

There are, in fact, some helpful points of agreement between zoonoticists — those who believe in a natural origin of the SARS-2 virus — and those who believe that it probably came from a laboratory. Both sides agree, when pressed, that a lab origin can’t be conclusively ruled out and a natural origin can’t be ruled out either — because nature, after all, is capable of improbable, teleological-seeming achievements. Both sides also agree, for the most part, that the spillover event that began the human outbreak probably happened only once, or a few times, quite recently, and not many times over a longer period. They agree that bat virus RaTG13 (named for the *Rinolophus affinis* bat, from Tongguan, in 2013) is the closest match to the human virus that has yet been found, and that although the two viruses are very similar, the spike protein of the bat virus lacks the features the human spike protein possesses that enable it to work efficiently with human tissue.

Zoonoticists hold that SARS-2’s crucial features — the furin cleavage site and the ACE2 receptor — are the result of a recombinant event involving a bat coronavirus (perhaps RaTG13 or a virus closely related to it) and another, unknown virus. Early on, researchers proposed that it could be a snake sold at the seafood market — a Chinese cobra or a banded krait —but no: Snakes don’t typically carry coronaviruses. Then there was a thought that the disease came from sick smuggled pangolins, because there existed a certain pangolin coronavirus that was, inexplicably, almost identical in its spike protein to the human coronavirus — but then, no: There turned out to be questions about the reliability of the genetic information in that diseased-pangolin data set, on top of which there were no pangolins for sale at the Wuhan market. Then a group from China’s government veterinary laboratory at Harbin tried infecting beagles, pigs, chickens, ducks, ferrets, and cats with SARS-2 to see if they could be carriers. (Cats and ferrets got sick; pigs, ducks, and most dogs did not.)

In September, some scientists at the University of Michigan, led by Yang Zhang, reported that they had created a “computational pipeline” to screen nearly a hundred possible intermediate hosts, including the Sumatran orangutan, the Western gorilla, the Olive baboon, the crab-eating macaque, and the bonobo. All these primates were “permissive” to the SARS-2 coronavirus and should undergo “further experimental investigation,” the scientists proposed.

Despite this wide-ranging effort, there is at the moment no animal host that zoonoticists can point to as the missing link. There's also no single, agreed-upon hypothesis to explain how the disease may have traveled from the bat reservoirs of Yunnan all the way to Wuhan, seven hours by train, without leaving any sick people behind and without infecting anyone along the way.

The zoonoticists say that we shouldn't find it troubling that virologists have been inserting and deleting furin cleavage sites and ACE2-receptor-binding domains in experimental viral spike proteins for years: The fact that virologists have been doing these things in laboratories, in advance of the pandemic, is to be taken as a sign of their prescience, not of their folly. But I keep returning to the basic, puzzling fact: This patchwork pathogen, which allegedly has evolved without human meddling, first came to notice in the only city in the world with a laboratory that was paid for years by the U.S. government to perform experiments on certain obscure and heretofore unpublicized strains of bat viruses — which bat viruses then turned out to be, out of all the organisms on the planet, the ones that are most closely related to the disease. What are the odds?

In July, I discovered a number of volunteer analysts who were doing a new kind of forensic, samizdat science, hunched over the letter code of the SARS-2 genome like scholars deciphering the cuneiform impressions in Linear B tablets. There were the anonymous authors of Project Evidence, on GitHub, who “disavow all racism and violent attacks, including those which are aimed at Asian or Chinese people,” and there was Yuri Deigin, a biotech entrepreneur from Canada, who wrote a massive, lucid paper on Medium, “Lab-Made?,” which illumined the mysteries of the spike protein. Jonathan Latham of the Bioscience Resource Project, with his co-author Allison Wilson, wrote two important papers: one a calm, unsparing overview of laboratory accidents and rash research and the other a close look at the small outbreak of an unexplained viral pneumonia in a bat-infested copper mine in 2012. I corresponded with Alina Chan (now the subject of a nicely turned piece in *Boston* magazine by Rowan Jacobsen) and with the pseudonymous Billy Bostickson, a tireless researcher whose Twitter photo is a cartoon of an injured experimental monkey, and Monali Rahalkar, of the Agharkar Research Institute in Pune, India, who wrote a paper with her husband, Rahul Bahulikar, that also sheds light on the story of the bat-guano-shoveling men whose virus was remarkably like SARS-2, except that it was not nearly as catching. I talked to Rossana Segreto, a molecular biologist at the University of Innsbruck, whose paper, “Is Considering a Genetic-Manipulation Origin for SARS-CoV-2 a Conspiracy Theory That Must Be Censored?,” co-authored with Yuri Deigin, was finally published in November under a milder title; it argued

that SARS-2's most notable features, the furin site and the human ACE2-binding domain, were unlikely to have arisen simultaneously and "might be the result of lab manipulation techniques such as site directed mutagenesis." Segreto is also the person who first established that a bat-virus fragment named BtCoV/4991, identified in 2013, was 100 percent identical to the closest known cousin to SARS-CoV-2, the bat virus RaTG13, thereby proving that the virus closest to the SARS-2-pandemic virus was linked back not to a bat cave but to a mine shaft, and that this same virus had been stored and worked on in the Wuhan Institute for years. This made possible the first big investigative piece on SARS-2's origins, in the *Times* of London, in July: "Nobody can deny the bravery of scientists who risked their lives harvesting the highly infectious virus," the *Times* authors write. "But did their courageous detective work lead inadvertently to a global disaster?"

XII.

"A New, Non-Natural Risk"

In 2011, a tall, confident Dutch scientist, Ron Fouchier, using grant money from Fauci's group at NIH, created a mutant form of highly pathogenic avian influenza, H5N1, and passaged it ten times through ferrets in order to prove that he could "force" (his word) this potentially fatal disease to infect mammals, including humans, "via aerosols or respiratory droplets." Fouchier said his findings indicated that these avian influenza viruses, thus forced, "pose a risk of becoming pandemic in humans."

This experiment was too much for some scientists: Why, out of a desire to prove that something extremely infectious could happen, would you make it happen? And why would the U.S. government feel compelled to pay for it to happen? Late in 2011, Marc Lipsitch of the Harvard School of Public Health got together with several other dismayed onlookers to ring the gong for caution. On January 8, 2012, the *New York Times* published a scorcher of an editorial, "An Engineered Doomsday." "We cannot say there would be no benefits at all from studying the virus," the *Times* said. "But the consequences, should the virus escape, are too devastating to risk."

These gain-of-function experiments were an important part of the NIH's approach to vaccine development, and Anthony Fauci was reluctant to stop funding them. He and Francis Collins, director of the National Institutes of Health, along with Gary Nabel, NIAID director of vaccine research, published an opinion piece in the *Washington Post* in which they contended that the ferret flu experiments, and others like them, were "a risk worth taking."

“Important information and insights can come from generating a potentially dangerous virus in the laboratory,” they wrote; the work can “help delineate the principles of virus transmission between species.” The work was safe because the viruses were stored in a high-security lab, they believed, and the work was necessary because nature was always coming up with new threats. “Nature is the worst bioterrorist,” Fauci told a reporter. “We know that through history.”

Soon afterward, there followed some distressing screwups in secure federal laboratories involving live anthrax, live smallpox, and live avian influenza. These got attention in the science press. Then Lipsitch’s activists (calling themselves the Cambridge Working Group) sent around a strong statement on the perils of research with “Potential Pandemic Pathogens,” signed by more than a hundred scientists. The work might “trigger outbreaks that would be difficult or impossible to control,” the signers said. Fauci reconsidered, and the White House in 2014 announced that there would be a “pause” in the funding of new influenza, SARS, and MERS gain-of-function research.

Baric, in North Carolina, was not happy. He had a number of gain-of-function experiments with pathogenic viruses in progress. “It took me ten seconds to realize that most of them were going to be affected,” he told NPR. Baric and a former colleague from Vanderbilt University wrote a long letter to an NIH review board expressing their “profound concerns.” “This decision will significantly inhibit our capacity to respond quickly and effectively to future outbreaks of SARS-like or MERS-like coronaviruses, which continue to circulate in bat populations and camels,” they wrote. The funding ban was itself dangerous, they argued. “Emerging coronaviruses in nature do not observe a mandated pause.”

Hoping to smooth over controversy by showing due diligence, the National Science Advisory Board for Biosecurity, founded in the BioShield era under President Bush, paid a consulting firm, Gryphon Scientific, to write a report on gain-of-function research, which by now was simply referred to as GoF. In chapter six of this thousand-page dissertation, published in April 2016, the consultants take up the question of coronaviruses. “Increasing the transmissibility of the coronaviruses could significantly increase the chance of a global pandemic due to a laboratory accident,” they wrote.

The Cambridge Working Group continued to write letters of protest and plead for restraint and sanity. Steven Salzberg, a professor of biomedical engineering at Johns Hopkins, said, “We have enough problems simply keeping up with the current flu outbreaks — and now with Ebola — without

scientists creating incredibly deadly new viruses that might accidentally escape their labs.” David Relman of Stanford Medical School said, “It is unethical to place so many members of the public at risk and then consult only scientists — or, even worse, just a small subset of scientists — and exclude others from the decision-making and oversight process.” Richard Ebright wrote that creating and evaluating new threats very seldom increases security: “Doing so in biology — where the number of potential threats is nearly infinite, and where the asymmetry between the ease of creating threats and the difficulty of addressing threats is nearly absolute — is especially counterproductive.” Lynn Klotz wrote, “Awful as a pandemic brought on by the escape of a variant H5N1 virus might be, it is SARS that now presents the greatest risk. The worry is less about recurrence of a natural SARS outbreak than of yet another escape from a laboratory researching it to help protect against a natural outbreak.” Marc Lipsitch argued that gain-of-function experiments can mislead, “resulting in worse not better decisions,” and that the entire gain-of-function debate as overseen by the NIH was heavily weighted in favor of scientific insiders and “distinctly unwelcoming of public participation.”

Nariyoshi Shinomiya, a professor of physiology and nano-medicine at the National Defense Medical College in Japan, offered this warning: “Similar to nuclear or chemical weapons there is no going back once we get a thing in our hands.”

But in the end, Baric was allowed to proceed with his experiments, and the research papers that resulted, showered with money, became a sort of *Anarchist’s Cookbook* for the rest of the scientific world. In November 2015, Baric and colleagues published a collaboration paper with Shi Zhengli titled “A SARS-like Cluster of Circulating Bat Coronaviruses Shows Potential for Human Emergence.” Into a human SARS virus that they had adapted so that it would work in mice, Baric and Shi et al. inserted the spike protein of a bat virus, SHC014, discovered by Shi in southern China. They dabbed the mice nasally with virus and waited, looking for signs of sickness: “hunching, ruffled fur.” They also infected human airway cells with the mouse-adapted bat-spike-in-a-human-virus backbone. In both mice and human airway cells, the chimeric virus caused a “robust infection.”

This proved, Baric and Shi believed, that you did not need civets or other intermediate hosts in order for bats to cause an epidemic in humans and that therefore all the SARS-like viruses circulating in bat populations “may pose a future threat.” Peter Daszak, who had used Predict funds to pay Shi for her work on the paper, was impressed by this conclusion; the findings, he said,

“move this virus from a candidate emerging pathogen to a clear and present danger.”

Richard Ebright was trenchantly unenthusiastic. “The only impact of this work,” he said, “is the creation, in a lab, of a new, non-natural risk.”

Early in 2016, Baric and Shi again collaborated. Shi sent Baric a fresh bat virus spike protein, and Baric inserted it into the backbone of a human SARS virus and then used that infectious clone to attack human airway cells. “The virus readily and efficiently replicated in cultured human airway tissues, suggesting an ability to potentially jump directly to humans,” reported the UNC’s website. This time, they also used the bat-human hybrid virus to infect transgenic humanized mice that grew human ACE2 protein. The mice, young and old, lost weight and died, proving, again, that this particular bat virus was potentially “poised to emerge in human populations.” It was “an ongoing threat,” Baric wrote. But was it? Civets and camels that are exposed to a lot of bat-guano dust may be an ongoing threat and a manageable one. But the bats themselves just want to hang in their caves and not be bothered by frowning sightseers in spacesuits who want to poke Q-tips in their bottoms. This 2016 “poised for human emergence” paper was supported by eight different NIH grants. In 2015, Baric’s lab received \$8.3 million from the NIH; in 2016, it received \$10.5 million.

Gain-of-function research came roaring back under Trump and Fauci. “The National Institutes of Health will again fund research that makes viruses more dangerous,” said an article in *Nature* in December 2017. Carrie Wolinetz of the NIH’s office of science policy defended the decision. “These experiments will help us get ahead of viruses that are already out there and pose a real and present danger to human health,” she told *The Lancet*. The NIH, Wolinetz said, was committed to a leadership role with gain-of-function research internationally. “If we are pursuing this research in an active way, we will be much better positioned to develop protection and countermeasures should something bad happen in another country.”

A reporter asked Marc Lipsitch what he thought of the resumption of NIH funding. Gain-of-function experiments “have done almost nothing to improve our preparedness for pandemics,” he said, “yet they risked creating an accidental pandemic.”

“Proximity Is a Problem”

In April, four months into the coronavirus emergency, a deputy director at the NIH wrote an email to EcoHealth Alliance. “You are instructed to cease providing any funds to Wuhan Institute of Virology,” it said. In response, Daszak and the chief scientific officer of New England Biolabs (a company that sells seamless gene-splicing products to laboratories, among other things) got 77 Nobel Prize winners to sign a statement saying that the cancellation deprived the “nation and the world of highly regarded science that could help control one of the greatest health crises in modern history and those that may arise in the future.” Later, as a condition of further funding, the NIH wrote to say it wanted Daszak to arrange an outside inspection of the Wuhan lab and to procure from Wuhan’s scientists a sample of whatever they’d used to sequence the SARS-2 virus. Daszak was outraged (“I am not trained as a private detective”), and again he fought back. He was reluctant to give up his own secrets, too. “Conspiracy-theory outlets and politically motivated organizations have made Freedom of Information Act requests on our grants and all of our letters and emails to the NIH,” he told *Nature*. “We don’t think it’s fair that we should have to reveal everything we do.”

But Daszak has survived — even prospered. Recently, *The Lancet* made him the lead investigator in its inquiry into the origins of the pandemic, and the World Health Organization named him to its ten-person origins investigation. (“We’re still close enough to the origin to really find out more details about where it has come from,” Daszak told *Nature*.)

The NIH has also set up an ambitious new international program, called CREID, which stands for Centers for Research in Emerging Infectious Diseases, and it has put Daszak’s EcoHealth in charge of trapping animals and looking for obscure bat viruses in Singapore, Malaysia, and Thailand. Baric is one of Daszak’s partners in CREID. The virus hunting and collecting, which Richard Ebright likens to “looking for a gas leak with a lighted match,” will continue and widen with U.S. funding. “We’re going to work in remote parts of Malaysia and Thailand to get to the front line of where the next pandemic is going to start,” Daszak told NPR.

In May, an interviewer from the People’s Pharmacy website asked Baric if he had any thoughts on whether the coronavirus began with a natural bat-to-human transfer. “Or was there something a little bit more, perhaps, insidious involved?”

“Well, of course the answers to those questions are in China,” Baric replied. “Exactly how they work in that facility is something that would be very difficult for a Westerner to know,” he said. “The main problems that the Institute of Virology has is that the outbreak occurred in close proximity to that Institute. That Institute has in essence the best collection of virologists in the world that have gone out and sought out, and isolated, and sampled bat species throughout Southeast Asia. So they have a very large collection of viruses in their laboratory. And so it’s — you know — proximity is a problem. It’s a problem.”

Over the course of the fall, and especially after the election muffled Donald Trump’s influence over the country’s public-health apparatus, that proximity problem — and the uncomfortable questions of origins it raised — began to grow somewhat more discussable. The BBC, *Le Monde*, and Italy’s RAI have all recently taken seriously the scientific possibility of a lab leak. In late October, the World Health Organization convened the first meeting of its second inquiry into the origins of the disease. The WHO’s effort is perhaps the world’s best chance to satisfy its curiosity about goings-on at the Wuhan Institute of Virology and at the Wuhan CDC’s virus lab near the Wuhan seafood market. But, as the *New York Times* has reported, the WHO’s information gathering has been hindered by Chinese secretiveness since February, when an initial investigative team sent to Beijing was told its members’ access to scientists would be restricted and that it couldn’t visit the seafood market, then considered a hub of the pandemic.

When a BBC video team tried to inspect the Yunnan mine shaft, they found the road to the mine blocked by a strategically parked truck that had “broken down” shortly before they arrived. Reporter John Sudworth asked Daszak, one of the ten members of the second WHO investigative team, whether he would push for access to the Wuhan Institute of Virology. “That’s not my job to do that,” Daszak replied.

In November, David Relman, the Stanford microbiologist, one of the most thoughtful of the voices warning against gain-of-function research, published a paper in *Proceedings of the National Academy of Sciences* on the urgent need to unravel the origins of COVID-19. “If SARS-CoV-2 escaped from a lab to cause the pandemic,” he wrote, “it will become critical to understand the chain of events and prevent this from happening again.” Conflicts of interest by researchers and administrators will need to be addressed, Relman wrote; to reach the truth, the investigation must be transparent, international, and, as much as possible, unpolitical. “A more complete understanding of the

origins of COVID-19 clearly serves the interests of every person in every country on this planet.”

“The world is sitting on a precedent-setting decision right now,” wrote Alina Chan on December 8. “It is unclear if SARS2 is 100 percent natural or emerged due to lab/research activities. If we walk away from this, demonstrating that we cannot effectively investigate its origins, it will pave the way for future COVIDS.”

Just before this issue of *New York* went to press, I reached Ralph Baric by phone and asked him where he now believed SARS-2 came from. (Anthony Fauci, Shi Zhengli, and Peter Daszak didn’t respond to emails, and Kristian Andersen said he was busy with other things.) Baric said he still thought the virus came from bats in southern China, perhaps directly, or possibly via an intermediate host, although the smuggled pangolins, in his view, were a red herring. The disease evolved in humans over time without being noticed, he suspected, becoming gradually more infectious, and eventually a person carried it to Wuhan “and the pandemic took off.” Then he said, “Can you rule out a laboratory escape? The answer in this case is probably not.”

XIV.

Transmission

So how did we actually get this disease?

Here’s what I think happened. In April 2012, in a copper mine in Mojiang, China, three men were given an awful job — they were told to shovel bat guano out of a mine shaft. They went to work and shoveled guano for seven hours a day in the confined, insufficiently ventilated space of the mine shaft, and by the end of the week, they were sick with a viral pneumonia of unknown etiology. Three more, younger shovelers were hired to replace the ones who were out sick.

The viral load in their lungs was so huge, because of all the guano dust, that their lungs became a kind of accelerated laboratory passaging experiment, as Jonathan Latham and Allison Wilson have written, forcing the virus to switch its allegiance from bats to humans. SARS experts were consulted, and the disease was judged to be SARS-like but not SARS. It was something new. (Shi Zhengli told *Scientific American* that the guano shovelers had died of a fungal disease, but, as Monali Rahalkar pointed out, they were treated with antivirals,

and their symptoms were consistent with viral pneumonia with attendant secondary fungal infections.)

Although it was a severe disease, and in the end three of the shovelers died, there was no resultant epidemic. It was actually a case of industrial overexposure to an infectious substance — what we might call a massive OSHA violation. The bat disease that the men encountered wasn't necessarily all that dangerous except in an environment of immunosuppressive overload.

Peter Daszak and Shi Zhengli were interested, of course, because this unidentified coronavirus disease involved bats and people. Of the fragmentary bits of virus Shi retrieved from the mine shaft, one was SARS-like, and Shi sequenced it and called it BtCoV/4991 and published a paper about it. Several times — in 2016 and 2018 and 2019 — this most interesting sample, a portion of what we now know as RaTG13, was taken out of the freezers in Shi's lab and worked on in undisclosed ways. (Peter Daszak claims that these samples have disintegrated and can't be validated or studied.) Samples of the nameless human disease also traveled back to the Wuhan Institute of Virology — few specifics about these valuable specimens have been released by Chinese sources, however.

This is the period in the story that demands a very close investigation, when chimeric assemblages may have been created and serially passaged, using BtCoV/4991, a.k.a. RaTG13, and other bat viruses, perhaps along with forms of the human virus. It's when Shi and Baric both published papers that were about what happened when you hot-swapped mutant spike proteins between bat viruses and human viruses.

The link, via the renamed sample BtCoV/4991, to the copper mine is of exceptional importance because of the one huge difference between the unnamed guano shovelers' virus and the SARS-2 virus that is now ravaging, for example, California: transmissibility. Airborne human-to-human transmissibility — the kind of thing that gain-of-functioneers like Ron Fouchier and Ralph Baric were aiming at, in order to demonstrate what Baric called "lurking threats" — is COVID-19's crucial distinguishing feature. If six men had gotten extremely sick with COVID-19 back in 2012 in southern China, doctors and nurses in the hospital where they lay dying would likely have gotten sick as well. There might have been hundreds or thousands of cases. Instead, only the shovelers themselves, who had breathed a heavy concentration of guano dust for days, got it.

The existence of bat virus RaTG13 is therefore not necessarily evidence of a natural bat origin. In fact, it seems to me to imply the opposite: New functional components may have been overlaid onto or inserted into the RaTG13 genome, new Tinkertoy intermolecular manipulations, especially to its spike protein, which have the effect of making it unprecedentedly infectious in human airways.

This is where the uniquely peculiar furin insert and/or the human-tuned ACE2-receptor-binding domain may come in — although it's also possible that either of these elements could have evolved as part of some multistep zoonotic process. But in the climate of gonzo laboratory experimentation, at a time when all sorts of tweaked variants and amped-up substitutions were being tested on cell cultures and in the lungs of humanized mice and other experimental animals, isn't it possible that somebody in Wuhan took the virus that had been isolated from human samples, or the RaTG13 bat virus sequence, or both (or other viruses from that same mine shaft that Shi Zhengli has recently mentioned in passing), and used them to create a challenge disease for vaccine research — a chopped-and-channeled version of RaTG13 or the miners' virus that included elements that would make it thrive and even rampage in people? And then what if, during an experiment one afternoon, this new, virulent, human-infecting, furin-ready virus got out?

For more than 15 years, coronavirologists strove to prove that the threat of SARS was ever present and must be defended against, and they proved it by showing how they could doctor the viruses they stored in order to force them to jump species and go directly from bats to humans. More and more bat viruses came in from the field teams, and they were sequenced and synthesized and "rewired," to use a term that Baric likes. In this international potluck supper of genetic cookery, hundreds of new variant diseases were invented and stored. And then one day, perhaps, somebody messed up. It's at least a reasonable, "parsimonious" explanation of what might have happened.

This may be the great scientific meta-experiment of the 21st century. Could a world full of scientists do all kinds of reckless recombinant things with viral diseases for many years and successfully avoid a serious outbreak? The hypothesis was that, yes, it was doable. The risk was worth taking. There would be no pandemic.

I hope the vaccine works.

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Paulopol, Andreea I (b)(6)@state.gov>;
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To: Gibbs, Jeffrey J (b)(6)@state.gov>;
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DiNanno, Thomas G (b)(6)@state.gov>;
Gross, Laura J (b)(6)@state.gov>
CC: (b)(6)@state.gov>;
(b)(6)@state.gov>;
(b)(6)@state.gov>
Subject: RE: Mike's summary of post cables/Nature Medicine re COVID19
Date: Mon, 14 Dec 2020 16:20:27 +0000

.... Rutger's **Ebright**, a longtime opponent of gain of function research, says that the **Andersen** analysis (on "Natural Medicine", April 2020) fails to rule out animal-passage as an origin of SARS-CoV-2. "The reasoning is unsound," he wrote in an email to *Newsweek*. "They favor the possibility 'that the virus mutated in an animal host such as a pangolins' yet, simultaneously, they disfavor the possibility that the virus mutated in 'animal passage.' Because the two possibilities are identical, apart from location, one can't logically favor one and disfavor the other."

- See BY **FRED GUTERL**, **NAVEED JAMALI** AND **TOM O'CONNOR** ON
4/27/20 AT 3:34 PM EDT
[HTTPS://WWW.NEWSWEEK.COM/CONTROVERSIAL-WUHAN-LAB-EXPERIMENTS-THAT-MAY-HAVE-STARTED-CORONAVIRUS-PANDEMIC-1500503](https://www.newsweek.com/controversial-wuhan-lab-experiments-that-may-have-started-coronavirus-pandemic-1500503)

From: Paulopol, Andreea I (b)(6)@state.gov>
Sent: Monday, December 14, 2020 11:04 AM
To: (b)(6)@state.gov>; Gibbs, Jeffrey J (b)(6)@state.gov>; (b)(6)
(b)(6) Pease, Michael (b)(6) DiNanno, Thomas G
(b)(6) Gross, Laura J (b)(6)
Cc: (b)(6) (b)(6)
Subject: RE: Mike's summary of post cables/Nature Medicine re COVID19

I understand that some folks here may not be interested in the science, but the attached article from Nature Medicine may be worth reviewing.

Also, <https://sciencebusiness.net/covid-19/international-news/china-was-slammed-initial-covid-19-secrecy-its-scientists-led-way>

China was slammed for initial COVID-19 secrecy, but its scientists led the way in tackling the virus

"The Chinese have been leading the way in publishing open-access evidence on case management, genomics and numerous areas of public health and epidemiology, which has been vital in informing the response in more or less every country."

From: (b)(6)@state.gov>
Sent: Sunday, December 13, 2020 6:30 PM
To: Gibbs, Jeffrey J <(b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>; DiNanno, Thomas G <(b)(6)@state.gov>; Paulopol, Andreea I <(b)(6)@state.gov>; Gross, Laura J <(b)(6)@state.gov>
Cc: (b)(6)@state.gov>; (b)(6)@state.gov>
Subject: Re: Mike's summary of post cables

Many of you may have read this article but it remains important as reminder of several inconvenient facts. Don't underestimate cognitive dissonance and wishful disbelief in science and government. The level of groupthink on the COVID19 origins issue is ridiculous. I personally pray it came straight out of Mother Nature but, thus far, have found no objective scientific analysis to explain it. So where did it come from—how, who, and why? The VCAWG should be a straight forward evidence based discussion, not supposition, imposition, or borderline superstition level theories.

<https://www.bostonmagazine.com/news/2020/09/09/alina-chan-broad-institute-coronavirus/>

RESEARCH

Could COVID-19 Have Escaped from a Lab?

The world's preeminent scientists say a theory from the Broad Institute's Alina Chan is too wild to be believed. But when the theory is about the possibility of COVID being man-made, is this science or censorship?

by ROWAN JACOBSEN, 9/9/2020, 9:29 a.m.

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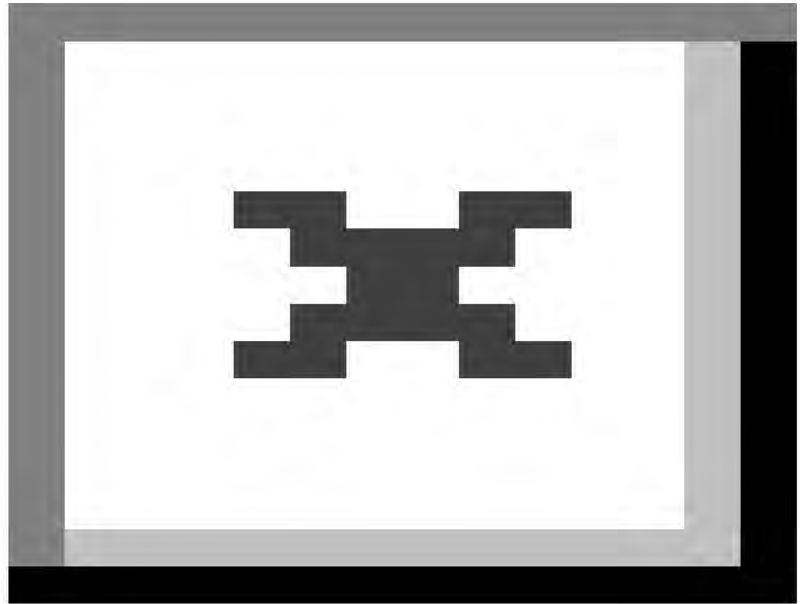


Illustration by Benjamin Purvis

In January, as she watched the news about a novel virus spreading out of control in China, Alina Chan braced for a shutdown. The molecular biologist at the Broad Institute of Harvard and MIT started stockpiling medicine and supplies. By the time March rolled around and a quarantine seemed imminent, she'd bought hundreds of dollars' worth of fillets from her favorite fishmonger in Cambridge and packed them into her freezer. Then she began to ramp down her

projects in the lab, isolating her experimental cells from their cultures and freezing them in small tubes.

As prepared as she was for the shutdown, though, she found herself unprepared for the frustration of being frozen out of work. She paced the walls of her tiny apartment feeling bored and useless. Chan has been a puzzle demon since childhood, which was precisely what she loved about her work—the chance to solve fiendishly difficult problems about how viruses operate and how, through gene therapy, they could be repurposed to help cure devastating genetic diseases. Staring out her window at the eerily quiet streets of her Inman Square neighborhood, she groaned at the thought that it could be months before she was at it again. Her mind wandered back to 2003, when she was a teenager growing up in Singapore and the first SARS virus, a close relative of this coronavirus, appeared in Asia. It hadn't been anything like this. That one had been relatively easy to corral. *How had this virus come out of nowhere and shut down the planet? Why was it so different?* she asked herself.

ADVERTISING

Then it hit her: The world's greatest puzzle was staring her in the face. Stuck at home, all she had to work with was her brain and her laptop. Maybe they were enough. Chan fired up the kettle for the first of what would become hundreds of cups of tea, stacked four boxes on her kitchen counter to raise her laptop to the proper height, pulled back her long dark hair, and began reading all of the scientific literature she could find on the coronavirus.

It wasn't long before she came across an article about the remarkable stability of the virus, whose genome had barely changed from the earliest human cases, despite trillions of replications. This perplexed Chan. Like many emerging infectious diseases, COVID-19 was thought to be zoonotic—it originated in animals, then somehow found its way into people. At the time, the Chinese government and most scientists insisted the jump had happened at Wuhan's seafood market, but that didn't make sense to Chan. If the virus had leapt from animals to humans in the market, it should have immediately started evolving to life inside its new human hosts. But it hadn't.

On a hunch, she decided to look at the literature on the 2003 SARS virus, which had jumped from civets to people. *Bingo*. A few papers mentioned its rapid evolution in its first months of existence. Chan felt the familiar surge of puzzle endorphins. The new virus really wasn't behaving like it should. Chan knew that delving further into this puzzle would require some deep genetic analysis, and she knew just the person for the task. She opened Google Chat and fired off a message to Shing Hei Zhan. He was an old friend from her days at the University of British Columbia and, more important, he was a computational god.

"Do you want to partner on a very unusual paper?" she wrote.

Sure, he replied.

One thing Chan noticed about the original SARS was that the virus in the first human cases was subtly different—a few dozen letters of genetic code—from the one in the civets. That meant it had immediately morphed. She asked Zhan to pull up the genomes for the coronaviruses that had

been found on surfaces in the Wuhan seafood market. Were they at all different from the earliest documented cases in humans?

Zhan ran the analysis. Nope, they were 100 percent the same. Definitely from humans, not animals. The seafood-market theory, which Chinese health officials and the World Health Organization espoused in the early days of the pandemic, was wrong. Chan's puzzle detectors pulsed again. "Shing," she messaged Zhan, "this paper is going to be insane."

In the coming weeks, as the spring sun chased shadows across her kitchen floor, Chan stood at her counter and pounded out her paper, barely pausing to eat or sleep. It was clear that the first SARS evolved rapidly during its first three months of existence, constantly fine-tuning its ability to infect humans, and settling down only during the later stages of the epidemic. In contrast, the new virus looked a lot more like late-stage SARS. "It's almost as if we're missing the early phase," Chan marveled to Zhan. Or, as she put it in their paper, as if "it was already well adapted for human transmission."

That was a profoundly provocative line. Chan was implying that the virus was already familiar with human physiology when it had its coming-out party in Wuhan in late 2019. If so, there were three possible explanations.

Perhaps it was just staggeringly bad luck: The mutations had all occurred in an earlier host species, and just happened to be the perfect genetic arrangement for an invasion of humanity. But that made no sense. Those mutations would have been disadvantageous in the old host.

Maybe the virus had been circulating undetected in humans for months, working out the kinks, and nobody had noticed. Also unlikely. China's health officials would not have missed it, and even if they had, they'd be able to go back now through stored samples to find the trail of earlier versions. And they weren't coming up with anything.

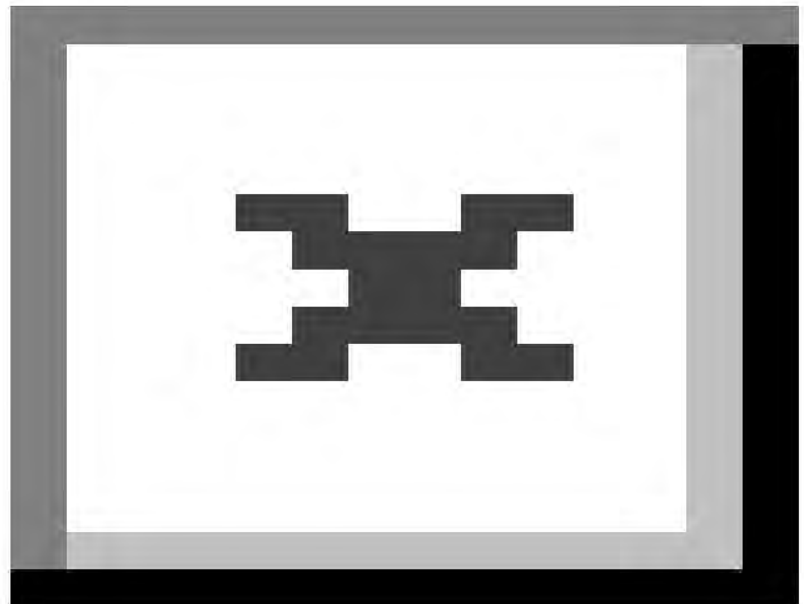
That left a third possibility: The missing phase had happened in a lab, where the virus had been trained on human cells. Chan knew this was the third rail of potential explanations. At the time, conspiracy theorists were spinning bioweapon fantasies, and Chan was loath to give them any ammunition. But she also didn't want to play politics by withholding her findings. Chan is in her early thirties, still at the start of her career, and an absolute idealist about the purity of the scientific process. Facts were facts.

Or at least they used to be. Since the start of the pandemic, the Trump administration has been criticized for playing fast and loose with facts—denying, exaggerating, or spinning them to suit the president's political needs. As a result, many scientists have learned to censor themselves for fear that their words will be misrepresented. Still, Chan thought, if she were to sit on scientific research just to avoid providing ammunition to conspiracy theorists or Trump, would she be any better than them?

Chan knew she had to move forward and make her findings public. In the final draft of her paper, she torpedoed the seafood-market theory, then laid out a case that the virus seemed curiously well adapted to humans. She mentioned all three possible explanations, carefully wording the third to emphasize that if the novel coronavirus did come from a lab, it would have been the result of an accident in the course of legitimate research.

On May 2, Chan uploaded the paper to a site where as-yet-unpublished biology papers known as “preprints” are shared for open peer review. She tweeted out the news and waited. On May 16, the *Daily Mail*, a British tabloid, picked up her research. The very next day, *Newsweek* ran a story with the headline “Scientists Shouldn’t Rule Out Lab as Source of Coronavirus, New Study Says.”

And that, Chan says, is when “shit exploded everywhere.”



Alina Chan, a molecular biologist at the Broad Institute, says we can't rule out the possibility that the novel coronavirus originated in a lab—even though she knows it's a politically radioactive thing to say. / Photo by Mona Miri

Chan had come to my attention a week before the *Newsweek* story was published through her smart and straightforward tweets, which I found refreshing at a time when most scientists were avoiding any serious discussion about the possibility that COVID-19 had escaped from a biolab.

I'd written a lot about genetic engineering and so-called gain-of-function research—the fascinating, if scary, line of science in which scientists alter viruses to make them more transmissible or lethal as a way of assessing how close those viruses are to causing pandemics. I also knew that deadly pathogens escape from biolabs with surprising frequency. Most of these accidents end up being harmless, but many researchers have been infected, and people have died as a result.

For years, concerned scientists have warned that this type of pathogen research was going to trigger a pandemic. Foremost among them was Harvard epidemiologist Marc Lipsitch, who founded the Cambridge Working Group in 2014 to lobby against these experiments. In a series of policy papers, op-eds, and scientific forums, he pointed out that accidents involving deadly pathogens occurred more than twice a week in U.S. labs, and estimated that just 10 labs performing gain-of-function research over a 10-year period would run a nearly 20 percent risk of an accidental release. In 2018, he argued that such a release could “lead to global spread of a virulent virus, a biosafety incident on a scale never before seen.”

Thanks in part to the Cambridge Working Group, the federal government briefly instituted a moratorium on such research. By 2017, however, the ban was lifted and U.S. labs were at it again. Today, in the United States and across the globe, there are dozens of labs conducting experiments on a daily basis with the deadliest known pathogens. One of them is the Wuhan Institute of Virology. For more than a decade, its scientists have been discovering coronaviruses in bats in southern China and bringing them back to their lab in Wuhan. There, they mix genes from different strains of these novel viruses to test their infectivity in human cells and lab animals.

When word spread in January that a novel coronavirus had caused an outbreak in Wuhan—which is a thousand miles from where the bats that carry this lineage of viruses are naturally found—many experts were quietly alarmed. There was no proof that the lab was the source of the virus, but the pieces fit.

Despite the evidence, the scientific community quickly dismissed the idea. Peter Daszak, president of EcoHealth Alliance, which has funded the work of the Wuhan Institute of Virology and other labs searching for new viruses, called the notion “preposterous,” and many other experts echoed that sentiment.

That wasn't necessarily what every scientist thought in private, though. “They can't speak directly,” one scientist told me confidentially, referring to the virology community's fear of having their comments sensationalized in today's politically charged environment. “Many virologists don't want to be hated by everyone in the field.”

There are other potential reasons for the pushback. There's long been a sense that if the public and politicians really knew about the dangerous pathogen research being conducted in many laboratories, they'd be outraged. Denying the possibility of a catastrophic incident like this, then, could be seen as a form of career preservation. “For the substantial subset of virologists who perform gain-of-function research,” Richard Ebright, a Rutgers microbiologist and another founding member of the Cambridge Working Group, told me, “avoiding restrictions on research funding, avoiding implementation of appropriate biosafety standards, and avoiding

implementation of appropriate research oversight are powerful motivators.” Antonio Regalado, biomedicine editor of *MIT Technology Review*, put it more bluntly. If it turned out COVID-19 came from a lab, he tweeted, “it would shatter the scientific edifice top to bottom.”

That’s a pretty good incentive to simply dismiss the whole hypothesis, but it quickly amounted to a global gaslighting of the media—and, by proxy, the public. An unhealthy absolutism set in: Either you insisted that any questions about lab involvement were absurd, or you were a tool of the Trump administration and its desperation to blame China for the virus. I was used to social media pundits ignoring inconvenient or politically toxic facts, but I’d never expected to see that from some of our best scientists.

Which is why Chan stood out on Twitter, daring to speak truth to power. “It is very difficult to do research when one hypothesis has been negatively cast as a conspiracy theory,” she wrote. Then she offered some earnest advice to researchers, suggesting that most viral research should be done with neutered viruses that have had their replicating machinery removed in advance, so that even if they escaped confinement, they would be incapable of making copies of themselves. “When these precautions are not followed, risk of lab escape is exponentially higher,” she explained, adding, “I hope the pandemic motivates local ethics and biosafety committees to think carefully about how they can reduce risk.” She elaborated on this in another tweet several days later: “I’d also—personally—prefer if high biosafety level labs were not located in the most populous cities on earth.”

How Safe Are Boston’s Biolabs?

As one of the world centers of biotech, the Hub is peppered with academic and corporate labs doing research on pathogens. Foremost among them is Boston University’s National Emerging Infectious Diseases Laboratories (NEIDL), the only lab in the city designated as BSL-4 (the highest level of biosafety and the same level as the Wuhan Institute of Virology). It is one of just a dozen or so in the United States equipped to work with live versions of the world’s most dangerous viruses, including Ebola and Marburg. Researchers there began doing so in 2018 after a decade of controversy: Many locals objected to the risks of siting such a facility in the center of a major metropolitan area.

The good news? Before opening, NEIDL undertook one of the most thorough risk assessments in history, learning from the mistakes of other facilities. Even Lynn Klotz, a senior science fellow at the Washington, DC–based Center for Arms Control and Non-Proliferation, who advised local groups that opposed NEIDL, told the medical website *Contagion* that the lab likely has the best possible security protocols and measures in place.

But the reality, Klotz added, is that most lab accidents are caused by human error, and there is only so much that can be done through good design and protocols to proactively prevent such mistakes. (Or to guard against an intentional release by a disgruntled researcher, as allegedly happened in the anthrax attacks of 2001.) Rutgers molecular biologist Richard Ebright, a longtime critic of potentially dangerous pathogen research, says the risks introduced by NEIDL are not low enough and “definitely not” worth the negligible benefits.

Still, risk is relative. Klotz has estimated the chance of a pathogen escape from a BSL-4 lab at 0.3 percent per year, and NEIDL is probably significantly safer than the typical BSL-4 lab. And if catching a deadly pathogen is your fear, well, currently you run a good risk of finding one in your own neighborhood. Until that gets cleared up, the city’s biolabs are probably among the safer spaces in town.

Chan had started using her Twitter account this intensely only a few days earlier, as a form of outreach for her paper. The social platform has become the way many scientists find out about one another’s work, and studies have shown that attention on Twitter translates to increased citations for a paper in scientific literature. But it’s a famously raw forum. Many scientists are

not prepared for the digital storms that roil the Twitterverse, and they don't handle it well. Chan dreaded it at first, but quickly took to Twitter like a digital native. "Having Twitter elevates your work," she says. "And I think it's really fun to talk to nonscientists about that work."

After reading her tweets, I reviewed her preprint, which I found mind-blowing, and wrote her to say so. She thanked me and joked that she worried it might be "career suicide."

It wasn't long before it began to look like she might be right.

Speaking her mind, it turns out—even in the face of censure—was nothing new for Chan, who is Canadian but was raised in Singapore, one of the more repressive regimes on earth. Her parents, both computer science professionals, encouraged free thinking and earnest inquiry in their daughter, but the local school system did not. Instead, it was a pressure-cooker of a system that rewarded students for falling in line, and moved quickly to silence rebels.

That was a bad fit for Chan. "You have to bow to teachers," she says. "Sometimes teachers from other classes would show up and ask me to bow to them. And I would say, 'No, you're not my teacher.' Back then they believed in corporal punishment. A teacher could just take a big stick and beat you in front of the class. I got whacked so many times."

Still, Chan rebelled in small ways, skipping school and hanging out at the arcade. She also lost interest in her studies. "I just really didn't like school. And I didn't like all the extracurriculars they pack you with in Singapore," she says. That changed when a teacher recruited her for math Olympiads, in which teams of students compete to solve devilishly hard arithmetic puzzles. "I really loved it," she says. "You just sit in a room and think about problems."

Chan might well have pursued a career in math, but then she came up against teams from China in Olympiad competitions. "They would just wipe everyone else off the board," she says. "They were machines. They'd been trained in math since they could walk. They'd hit the buzzer before you could even comprehend the question. I thought, *I'm not going to survive in this field.*"

Chan decided to pursue biology instead, studying at the University of British Columbia. "I liked viruses from the time I was a teen," she says. "I remember the first time I learned about HIV. I thought it was a puzzle and a challenge." That instinct took her to Harvard Medical School as a postdoc, where the puzzle became how to build virus-like biomolecules to accomplish tasks inside cells, and then to Ben Deverman's lab at the Broad Institute. "When I see an interesting question, I want to spend 100 percent of my time working on it," she says. "I get really fixated on answering scientific questions."

Deverman, for his part, says he wasn't actively looking to expand his team when Chan came along, but when "opportunities to hire extraordinary people fall in my lap," he takes them. "Alina brings a ton of value to the lab," he explains, adding that she has an ability to pivot between different topics and cut to the chase. Nowhere was that more on display than with her coronavirus work, which Deverman was able to closely observe. In fact, Chan ran so many ideas past him that he eventually became a coauthor. "She is insightful, determined, and has the rare ability to explain complex scientific findings to other scientists and to the public," he says.

Those skills would prove highly useful when word got out about her coronavirus paper.

If Chan had spent a lifetime learning how to pursue scientific questions, she spent most of the shutdown learning what happens when the answers you come up with are politically radioactive. After the *Newsweek* story ran, conservative-leaning publications seized on her paper as conclusive evidence that the virus had come from a lab. “Everyone focused on the one line,” Chan laments. “The tabloids just zoomed in on it.” Meanwhile, conspiracists took it as hard evidence of their wild theories that there had been an intentional leak.

Chan spent several exhausting days putting out online fires with the many people who had misconstrued her findings. “I was so naive,” she tells me with a quick, self-deprecating laugh. “I just thought, *Shouldn’t the world be thinking about this fairly?* I really have to kick myself now.”

Even more troubling, though, were the reactions from other scientists. As soon as her paper got picked up by the media, luminaries in the field sought to censure her. Jonathan Eisen, a well-known professor at UC Davis, criticized the study in *Newsweek* and on his influential Twitter account, writing, “Personally, I do not find the analysis in this new paper remotely convincing.” In a long thread, he argued that comparing the new virus to SARS was not enough to show that it was preadapted to humans. He wanted to see comparisons to the initial leap of other viruses from animals to humans.

Moments later, Daszak piled on. The NIH had recently cut its grant to his organization, EcoHealth Alliance, after the Trump administration learned that some of it had gone to fund the Wuhan Institute of Virology’s work. Daszak was working hard to get it restored and trying to stamp out any suggestion of a lab connection. He didn’t hold back on Chan. “This is sloppy research,” he tweeted, calling it “a poorly designed phylogenetic study with too many inferences and not enough data, riding on a wave of conspiracy to drive a higher impact.” Peppering his tweets with exclamation points, he attacked the wording of the paper, arguing that one experiment it cited was impossible, and told Chan she didn’t understand her own data. Afterward, a Daszak supporter followed up his thread with a GIF of a mike drop.

It was an old and familiar dynamic: threatened silverback male attempts to bully a junior female member of the tribe. As a postdoc, Chan was in a vulnerable position. The world of science is still a bit medieval in its power structure, with a handful of institutions and individuals deciding who gets published, who gets positions, who gets grants. There’s little room for rebels.

What happened next was neither old nor familiar: Chan didn’t back down. “Sorry to disrupt mike drop,” she tweeted, providing a link to a paper in the prestigious journal *Nature* that “does that exact experiment you thought was impossible.” Politely but firmly, she justified each point Daszak had attacked, showing him his mistakes. In the end, Daszak was reduced to arguing that she had used the word “isolate” incorrectly. In a coup de grâce, Chan pointed out that actually the word had come from online data provided by GenBank, the NIH’s genetic sequence database. She offered to change it to whatever made sense. At that point, Daszak stopped replying. He insists, however, that Chan is overinterpreting her findings.

With Eisen, Chan readily agreed to test her hypothesis by finding other examples of viruses infecting new hosts. Within days, a perfect opportunity came along when news broke that the coronavirus had jumped from humans to minks at European fur farms. Sure enough, the mink

version began to rapidly mutate. “You actually see the rapid evolution happening,” Chan said. “Just in the first few weeks, the changes are quite drastic.”

Chan also pointed out to Eisen that the whole goal of a website such as bioRxiv (pronounced “bioarchive”)—where she posted the paper—is to elicit feedback that will make papers better before publication. Good point, he replied. Eventually he conceded that there was “a lot of interesting analysis in the paper” and agreed to work with Chan on the next draft.

The Twitter duels with her powerful colleagues didn’t rattle Chan. “I thought Jonathan was very reasonable,” she says. “I really appreciated his expertise, even if he disagreed with me. I like that kind of feedback. It helped to make our paper better.”

With Daszak, Chan is more circumspect. “Some people have trouble keeping their emotions in check,” she says. “Whenever I saw his comments, I’d just think, *Is there something I can learn here? Is there something he’s right about that I should be fixing?*” Ultimately, she decided, there was not.

By late May, both journalists and armchair detectives interested in the mystery of the coronavirus were discovering Chan as a kind of Holmes to our Watson. She crunched information at twice our speed, zeroing in on small details we’d overlooked, and became a go-to for anyone looking for spin-free explications of the latest science on COVID-19. It was thrilling to see her reasoning in real time, a reminder of why I’ve always loved science, with its pursuit of patterns that sometimes leads to exciting revelations. The website CNET featured her in a story about “a league of scientists-turned-detectives” who were using genetic sequencing technologies to uncover COVID-19’s origins. After it came out, Chan added “scientist-turned-detective” to her Twitter bio.

She’s lived up to her new nom de tweet. As the search for the source of the virus continued, several scientific teams published papers identifying a closely related coronavirus in pangolins—anteater-like animals that are heavily trafficked in Asia for their meat and scales. The number of different studies made it seem as though this virus was ubiquitous in pangolins. Many scientists eagerly embraced the notion that the animals might have been the intermediate hosts that had passed the novel coronavirus to humans. It fit their preexisting theories about wet markets, and it would have meant no lab had been involved.

As Chan read the pangolin papers, she grew suspicious. The first one was by a team that had analyzed a group of the animals intercepted by anti-smuggling authorities in southern China. They found the closely related virus in a few of them, and published the genomes for that virus. Some of the other papers, though, were strangely ambiguous about where their data was coming from, or how their genomes had been constructed. Had they really taken samples from actual pangolins?

Once again, Chan messaged Shing Hei Zhan. “Shing, something’s weird here,” she wrote. Zhan pulled up the raw data from the papers and compared the genomes they had published. Individual copies of a virus coming from different animals should have small differences, just as individuals of a species have genetic differences. Yet the genomes in all of the pangolin papers were perfect matches—the authors were all simply using the first group’s data set. Far from being ubiquitous,

the virus had been found only in a few pangolins who were held together, and it was unclear where they had caught it. The animals might have even caught it from their own smuggler.

Remarkably, one group of authors in *Nature* even appeared to use the same genetic sequences from the other paper as if it were confirmation of their own discovery. “These sequences appear to be from the same virus (Pangolin-CoV) that we identified in the present study.”

Chan called them out on Twitter: “Of course it’s the same Pangolin-CoV, you used the same dataset!” For context, she later added, “Imagine if clinical trials were playing fast and loose with their patient data; renaming patients, throwing them into different datasets without clarification, possibly even describing the same patient multiple times across different studies unintentionally.”

She and Zhan posted a new preprint on bioRxiv dismantling the pangolin papers. Confirmation came in June when the results of a study of hundreds of pangolins in the wildlife trade were announced: Not a single pangolin had any sign of a coronavirus. Chan took a victory lap on Twitter: “Supports our hypothesis all this time.” The pangolin theory collapsed.

Chan then turned her Holmesian powers on bigger game: Daszak and the Wuhan Institute of Virology. Daszak had been pleading his case everywhere from *60 Minutes* to the *New York Times* and has been successful in rallying sympathy to his cause, even getting 77 Nobel laureates to sign a letter calling for the NIH to restore EcoHealth Alliance’s funding.

In several long and detailed “tweetorials,” Chan began to cast a cloud of suspicion on the WIV’s work. She pointed out that scientists there had discovered a virus that is more than 96 percent identical to the COVID-19 coronavirus in 2013 in a mineshaft soon after three miners working there had died from a COVID-like illness. The WIV didn’t share these findings until 2020, even though the goal of such work, Chan pointed out, was supposedly to identify viruses with the potential to cause human illnesses and warn the world about them.

Even though that virus had killed three miners, Daszak said it wasn’t considered a priority to study at the time. “We were looking for SARS-related virus, and this one was 20 percent different. We thought it was interesting, but not high risk. So we didn’t do anything about it and put it in the freezer,” he told a reporter from *Wired*. It was only in 2020, he maintained, that they started looking into it once they realized its similarity to COVID-19. But Chan pointed to an online database showing that the WIV had been genetically sequencing the mine virus in 2017 and 2018, analyzing it in a way they had done in the past with other viruses in preparation for running experiments with them. Diplomatic yet deadpan, she wrote, “I think Daszak was misinformed.”

For good measure, almost in passing, Chan pointed out a detail no one else had noticed: COVID-19 contains an uncommon genetic sequence that has been used by genetic engineers in the past to insert genes into coronaviruses without leaving a trace, and it falls at the exact point that would allow experimenters to swap out different genetic parts to change the infectivity. That same sequence can occur naturally in a coronavirus, so this was not irrefutable proof of an unnatural origin, Chan explained, “only an observation.” Still, it was enough for one Twitter user to muse,

"If capital punishment were as painful as what Alina Chan is doing to Daszak/WIV regarding their story, it would be illegal."

Daszak says that indeed he had been misinformed and was unaware that that virus found in the mine shaft had been sequenced before 2020. He also says that a great lab, with great scientists, is now being picked apart to search for suspicious behavior to support a preconceived theory. "If you believe, deep down, something fishy went on, then what you do is you go through all the evidence and you try to look for things that support that belief," he says, adding, "That is not how you find the truth."

Many of the points in Chan's tweetorials had also been made by others, but she was the first reputable scientist to put it all together. That same week, London's *Sunday Times* and the BBC ran stories following the same trail of breadcrumbs that Chan had laid out to suggest that there had been a coverup at the WIV. The story soon circulated around the world. In the meantime, the WIV has steadfastly denied any viral leak. Lab director Yanyi Wang went on Chinese television and described such charges as "pure fabrication," and went on to explain that the bat coronavirus from 2013 was so different than COVID that it could not have evolved into it this quickly and that the lab only sequenced it and didn't obtain a live virus from it.

To this day, there is no definitive evidence as to whether the virus occurred naturally or had its origins in a lab, but the hypothesis that the Wuhan facility was the source is increasingly mainstream and the science behind it can no longer be ignored. And Chan is largely to thank for that.

In late spring, Chan walked through the tall glass doors of the Broad Institute for the first time in months. As she made her way across the gleaming marble foyer, her sneaker squeaks echoed in the silence. It was like the zombie apocalypse version of the Broad; all the bright lights but none of the people. It felt all the weirder that she was wearing her gym clothes to work.

A few days earlier, the Broad had begun letting researchers back into their labs to restart their projects. All computer work still needed to be done remotely, but bench scientists such as Chan could pop in just long enough to move along their cell cultures, provided they got tested for the virus every four days.

In her lab, Chan donned her white lab coat and took inventory, throwing out months of expired reagents and ordering new materials. Then she rescued a few samples from the freezer, took her seat at one of the tissue-culture hoods—stainless steel, air-controlled cabinets in which cell engineers do their work—and began reviving some of her old experiments.

She had mixed emotions about being back. It felt good to free her gene-therapy projects from their stasis, and she was even more excited about the new project she and Deverman were working on: an online tool that allows vaccine developers to track changes in the virus's genome by time, location, and other characteristics. "It came out of my personal frustration at not being able to get answers fast," she says.

On the other hand, she missed being all-consuming by her detective work. "I wanted to stop after the pangolin preprint," she says, "but this mystery keeps drawing me back in." So while she

waits for her cell cultures to grow, she's been sleuthing on the side—only this time she has more company: Increasingly, scientists have been quietly contacting her to share their own theories and papers about COVID-19's origins, forming something of a growing underground resistance. "There's a lot of curiosity," she says. "People are starting to think more deeply about it." And they have to, she says, if we are going to prevent future outbreaks: "It's really important to find out where this came from so it doesn't happen again."

That is what keeps Chan up at night—the possibility of new outbreaks in humans from the same source. If the virus emerged naturally from a bat cave, there could well be other strains in existence ready to spill over. If they are closely related, whatever vaccines we develop might work on them, too. But that might not be the case with manipulated viruses from a laboratory. "Someone could have been sampling viruses from different caves for a decade and just playing mix-and-match in the lab, and those viruses could be so different from one another that none of our vaccines will work on them," she says. Either way, "We need to find where this came from, and close it down."

Whatever important information she finds, we can be sure Chan will share it with the world. Far from being shaken by the controversy her paper stirred, she is more committed than ever to holding a line that could all too easily be overrun. "Scientists shouldn't be censoring themselves," she says. "We're obliged to put all the data out there. We shouldn't be deciding that it's better if the public doesn't know about this or that. If we start doing that, we lose credibility, and eventually we lose the public's trust. And that's not good for science." In fact, it would cause an epidemic of doubt, and that wouldn't be good for any of us.

From: Gibbs, Jeffrey J. (b)(6) @state.gov>
Sent: Sunday, December 13, 2020 2:42 PM
To: (b)(6) @state.gov>; (b)(6) @state.gov>; DiNanno, Thomas G (b)(6) @state.gov>; Paulopol, Andreea I. (b)(6) @state.gov>; (b)(6) @state.gov>; Gross, Laura J. (b)(6) @state.gov>
Cc: (b)(6) @state.gov>; (b)(6) @state.gov>
Subject: Re: Mike's summary of post cables

Great. Points 2, 4, and 5 are key (b)(5)

(b)(5)

Jeff Gibbs

Senior Adviser AVC
SSD/AVC

(b)(6)

From: (b)(6) @state.gov>
Sent: Saturday, December 12, 2020 12:43 PM

To: (b)(6)@state.gov; DiNanno, Thomas G (b)(6)@state.gov; Paulopol, Andreea I (b)(6)@state.gov; (b)(6)@state.gov; (b)(6)@state.gov; (b)(6)@state.gov
Cc: (b)(6)@state.gov; (b)(6)@state.gov; Gibbs, Jeffrey J (b)(6)@state.gov; (b)(6)@state.gov
Subject: (b)(6) summary of post cables

Thanks, (b)(6)

(b)(5)

(BTW, Bullets 1, 4, and 5 (especially 5) have been widely reported on Taiwan TV.)

From: (b)(6)@state.gov
Sent: Saturday, December 12, 2020 11:46 AM
To: DiNanno, Thomas G (b)(6)@state.gov; Paulopol, Andreea I (b)(6)@state.gov; (b)(6)@state.gov; Gross, Laura J (b)(6)@state.gov
Cc: (b)(6)@state.gov; (b)(6)@state.gov; (b)(6)@state.gov; (b)(6)@state.gov; Gibbs, Jeffrey J (b)(6)@state.gov
Subject: Re: response from CDC/NIH

I have found over 90 Embassy Beijing cables dealing with COVID-19 from 7 Jan to present. As luck would have it, we had consulate personnel on the scene in Wuhan. I have harvested about half of the cables -- I am almost up to March. So far, these cables document:

- Gross corruption and ineptitude by the local government officials (some of whom were later fired). Arguably, these officials enabled COVID-19 to go from outbreak to epidemic to pandemic.
- Frequent requests from USG via multiple channels to try to assist, scientifically collaborate, and more importantly, attempt to obtain critical data on the epidemiological and medical aspects of the outbreak as it was spreading throughout China and to other countries.
- Private PPE and other donations from the US.
- Consistent stonewalling by the PRC as the epidemic grows into a global pandemic.
- The WHO publicly saying what the PRC wanted, and privately/unofficially/candidly complaining about the utter lack of transparency and cooperation.

- Note: On multiple occasions WHO leaders publicly praised the PRC leadership for adhering to international health standards and aggressively attacking the virus.

(b)(6)

(b)(6)



From: (b)(6)@state.gov>
To: David Asher (b)(6)@hudson.org>;
Gibbs, Jeffrey J (b)(6)@state.gov>
(b)(6)@state.gov>;
CC: (b)(6)@state.gov>;
(b)(6)@state.gov>;
(b)(6)@state.gov>
Subject: Re: METZL - Origins of SARS-CoV-2
Date: Mon, 25 Jan 2021 00:53:35 +0000

Sounds great!! We need to write up this plan and present it to (b)(6) and then (b)(6)

Sent from Workspace ONE Boxer

On January 24, 2021 at 6:42:49 PM EST, David Asher (b)(6)@hudson.org wrote:

ChiComms are kicking our ass.

<https://www.nytimes.com/2021/01/22/business/china-covid-19-beijing.html?referringSource=articleShare>

(b)(5)

<https://twitter.com/andyweberncb/status/1350269832617472004?s=21>

<https://www.armscontrol.org/act/2021-01/features/pandemic-shows-need-biological-readiness>

David L. Asher, Ph.D

Senior Fellow

Hudson Institute

1201 Pennsylvania Avenue, NW

Fourth Floor

Washington, DC 20004

o. | c. (b)(6)

<https://www.hudson.org/experts/1299-david-asher>

On Jan 24, 2021, at 14:25, (b)(6)@state.gov wrote:

He seems like he might be a good addition to our expert panel. Seems to have a balanced view.

(b)(6)

Senior Adviser AVC
SSD/AVC

c: (b)(6)
From: David Asher (b)(6)@hudson.org>
Sent: Sunday, January 24, 2021 2:15 PM
To: Gibbs, Jeffrey J (b)(6)@state.gov>
Cc: (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>
(b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>
Subject: Re: METZL - Origins of SARS-CoV-2

We can do a call with Jamie. Old colleague and friend. Total genius. He also is quite close to Biden, who was his boss on the Hill.

David L. Asher, Ph.D
Senior Fellow
Hudson Institute
1201 Pennsylvania Avenue, NW
Fourth Floor
Washington, DC 20004
o. | c: (b)(6)
<https://www.hudson.org/experts/1299-david-asher>

On Jan 24, 2021, at 13:31, Gibbs, Jeffrey J (b)(6)@state.gov> wrote:

The best summary I have seen so far. This piece is very comprehensive.

Jeff Gibbs

Senior Adviser AVC
SSD/AVC

c: (b)(6)
From: David Asher (b)(6)@hudson.org>
Sent: Saturday, January 23, 2021 8:33 PM
To: (b)(6)@state.gov>
Cc: (b)(6)@state.gov>; Gibbs, Jeffrey J (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>
Subject: Re: METZL - Origins of SARS-CoV-2

Jamie is an old colleague and friend. Super smart. Very close to President Biden. I will see if he retains a clearance since he could help convince the powers that be that our research is not some politically slanted BS.

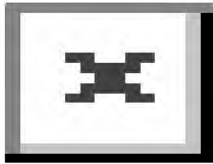
David L. Asher, Ph.D
Senior Fellow
Hudson Institute
1201 Pennsylvania Avenue, NW

Fourth Floor
Washington, DC 20004
o. | c. (b)(6)

<https://www.hudson.org/experts/1299-david-asher>

On Jan 23, 2021, at 6:43 PM, (b)(6)@state.gov wrote:

<https://jamiemetzl.com/origins-of-sars-cov-2/>



Origins of SARS-CoV-2 | Jamie Metzl

NOTE: This post was originally published on April 16, 2020 and has been updated regularly. A number of people have reached out to me questioning my assertion that "the most likely starting point of the coronavirus crisis is an accidental leak from one of the Chinese virology institutes in W ...

jamiemetzl.com

NOTE: This post was originally published on April 16, 2020 and has been updated regularly.

A number of people have reached out to me questioning my assertion that "the most likely starting point of the coronavirus crisis is an accidental leak from one of the Chinese virology institutes in Wuhan" (see [this CNN interview](#), [this Newsweek editorial](#), [this WSJ editorial](#), and [this The Hill editorial](#)). As referenced in [this Forbes profile](#), I have been making this claim consistently since January 2020 and will continue to do so until this issue gets the attention it deserves. We owe everyone who has died from COVID-19, all the people who have lost their loved ones and livelihoods, and future generations a thorough, unbiased, and unrestricted investigation of how the tragedy began and has unfolded.

Let me be clear, I do not believe this was likely a genome edited virus (although [this paper](#) suggests how it could have been and we should not discount this possibility), just that it had very likely been isolated and cultured in one of the Wuhan labs (the Wuhan CDC or, more likely, the Wuhan Institute of Virology, WIV). I also want to be clear that this is only highly informed inference based on publicly available information and my application of Occam's razor (and mathematical probabilities). I have no definitive way of proving this thesis but the evidence is, in my view, extremely convincing. If forced to place odds on the confidence of my hypothesis, I would say there's an 85% chance the pandemic started with an accidental leak from the Wuhan Institute of Virology or Wuhan CDC and a 15% chance it began in some other way (in fairness, [here](#) is an article making the case for a zoonotic jump "in the wild"). If China keeps preventing a full and unrestricted international forensic investigation into the origins of the pandemic, I believe it is fair to deny Beijing the benefit of the doubt.

The purpose of this post is to present the evidence and my views so that readers can come to their own conclusions. If there is additional evidence I am missing, please let me know. I do not have a political agenda other than finding out why so many people around the world are dead from COVID-19 and how we can learn the lessons from this catastrophe to prevent the next ones. What we need, and should all be calling for regardless of our nationalities or political persuasions, is a full and unrestricted international forensic investigation into the origins of COVID-19 with full access to all relevant data, lab records, biological samples, and people in China and beyond. Getting to the bottom of this essential question should be an unrestricted and unbiased data-driven pursuit. While access to essential information is being denied, we are forced to be more speculative than we otherwise would be.

Because there is a lot of material to get through below, let me just summarize what I believe to be the most likely scenario.

- In 2012, six miners working in a bat-infested copper mine in southern China (Yunnan province) were infected with a bat coronavirus. All of them developed symptoms exactly like COVID-19 symptoms. Three of them died.
- Viral samples taken from the Yunnan miner were taken to the Wuhan Institute of Virology, the only level 4 biosecurity lab in China that was also studying bat coronaviruses.
- The WIV carried out gain of function research, almost certainly on these and a range of related and other samples (which is different than genetically engineering the viruses). Chimeric viruses were likely developed in this process. There has never been a full and public accounting for what viruses are in the WIV sample set and database, and key elements of the database have been taken off line or deleted.
- Given the close relationship of the Chinese Peoples' Liberation Army (PLA) in the development and constriction of the Wuhan Institute of Virology, it is fair to assume a connection between the PLA and the WIV.
- In late 2019 the SARS-CoV-2 virus appeared in Wuhan. The closest known relative of this virus is the RaTG13 virus sampled from the Yunnan mine where the miners had been infected.
- The difference between the RaTG13 virus and SARS-CoV-2 could potentially be explained by the gain of function research pushing the development of chimeric viruses.
- It is also plausible that SARS-CoV-2 could have been among the viruses held in or derived from a different virus in the WIV repository.
- In the earliest known stage of the outbreak, the virus was already very well-adapted to human cells.
- In the critical first weeks after the outbreak, Wuhan authorities worked aggressively to silence the whistleblowers and destroy evidence that could prove incriminating.
- When Beijing authorities got involved a bit later, they likely faced a choice of implicating the Wuhan authorities, and, in effect, taking blame for what was quickly emerging as a major global problem, or turning into the curve and going all in for the coverup. I believe they likely chose the second option.

- The Chinese government then massively lobbied the WHO to prevent the WHO from declaring COVID-19 as an international emergency and prevented WHO investigators from entering China for nearly a month.
- In late January 2020, PLA Major General Chen Wei was put in charge of containment efforts in Wuhan. This role included supervision of the WIV, which had previously been considered a civilian institution. General Chen is China's top biological weapons expert. Allegations that the PLA was conducting covert dual civilian-military research research on bat coronaviruses at WIV have not been proven.
- The Chinese authorities have gone to great lengths to destroy evidence and silence anyone in China who might be in a position to provide evidence on the origins of COVID-19.
- Although nothing can be fully conclusive in light of Chinese obfuscation, the continued absence of any meaningful evidence of a zoonotic chain of transmission and mutation in the wild and the accretion of other evidence is pointing increasingly, in my view, toward an accidental lab leak as the most likely origin of COVID-19. Given the extent to which China would benefit from discovering evidence of a transmission in the wild, we can assume Chinese authorities are doing all they can to find this kind of evidence without success. This failure would explain why Chinese officials have recently begun, with little credible evidence, asserting that the outbreak started in India or Bangladesh.
- In light of all of this, only a full and unrestricted international forensic investigation into the origins of the pandemic, with complete access to all samples, lab records, scientists, health officials, etc. will suffice.
- Ensuring the most thorough and highest quality investigation exploring all possible hypothesis is and should be in all of our interest, including that of the Chinese government and people.

I want to be clear that I am a progressive who believes in asking tough questions and seeking the truth. I in no way seek to support or align myself with any activities that may be considered unfair, dishonest, nationalistic, racist, bigoted, or biased in any way. I also believe that whatever the original reasons for the outbreak, the reason why so many more Americans have died from COVID-19 than most anyone else is the catastrophic failure of the Trump administration to respond effectively.

As I argued in my Newsweek piece:

Just as we wouldn't imagine having a plane crash and not immediately trying to figure out what happened, we can't let the COVID-19 crisis unfold without urgently understanding how our systems have so spectacularly failed. There are plenty of fingers to point, and we must thoughtfully point them now, at all of us, for our own good. For all we know, a new and even worse pandemic could begin even before we have overcome this one... Until we get to the bottom of all these failures and work to fix them, we remain dangerously susceptible to the next pandemic... Whatever the origins of the outbreak, including the possibility of an accidental leak from the Chinese virology lab in Wuhan, China's dangerous and ongoing information suppression activities are the foundations of this

crisis. We have to find out fast where and how this outbreak began... The WHO could have raised hell when China denied access to WHO experts for those critical early weeks, did not need to initially parrot Chinese propaganda and could certainly have sounded the alarm earlier. We have to ask how we can help the WHO do better... The United States had all the information it needed by January to mount a massive response, but Trump actively undermined the findings of his own intelligence and health officials. Worse, he passed misinformation to the American people that potentially led to many thousands of deaths. We've got to ask why this happened... Until we get to the bottom of all these failures and work to fix them, we remain dangerously susceptible to the next pandemic... We are all on the same plane with a shared interest in not letting it crash... Let's work together to safely land the plane.

Although I do not necessarily ascribe to all of the assertions made in each of these documents, my sources include:

- This [Nature Medicine](#) study
- This [Bulletin of the Atomic Scientists](#) article
- This [Epoch Times](#) documentary (which should be viewed with significant caution due to its propagandistic tone)
- This [Lancet](#) piece
- This [Washington Post](#) article
- This [The Diplomat](#) editorial
- The [Nature](#) article
- This [Project Evidence](#) site
- This [Cell](#) study
- This [Science Direct](#) study
- This [New York Times](#) report
- This [Newsweek](#) article
- This [Washington Post](#) article
- This [Daily Telegraph](#) story
- This [Guardian](#) article
- This [Bloomberg](#) article
- This [Asia Times](#) story
- This [NBC News](#) story
- This [New Yorker](#) piece
- This [NPR](#) report
- This [E-PAI \(Electronically Available Public Information\)](#) report
- This [BioRxiv](#) pre-publication research paper
- This [Atlantic](#) piece
- This [National Review](#) article
- This [Associated Press](#) story
- This [Nerd Has Power](#) post
- This [Nature](#) article

- This [Telegraph](#) piece
- This [QRB Discovery](#) manuscript
- This [Bulletin of the Atomic Scientists](#) editorial
- This [Bulletin of the Atomic Scientists](#) article
- This [Independent Science News](#) piece
- This [Daniel Lucey](#) blog post
- This [Science](#) article
- This [Independent Science News](#) piece
- This [Wiley](#) preprint essay
- This [Wiley](#) preprint letter
- This [Cell Host & Microbe](#) paper
- This [Frontiers in Public Health](#) article
- This [Unherd](#) post
- This [New York Times](#) story
- This [BioEssays](#) paper
- This [BioEssays](#) paper
- This [PNAS](#) opinion piece
- This [New York Times](#) article
- This [Daily Mail](#) article
- This [Associated Press](#) article
- This [Quantitative Biology](#) paper
- This [New York](#) magazine article
- This [Nature Medicine](#) editorial
- This [France Culture](#) article
- This [Wall Street Journal](#) editorial

I am extremely open to other perspectives and welcome any additional information. If you have anything you believe relevant, I would be grateful for you to pass it along. I am not wedded to any particular outcome other than getting to the deepest possible understanding of what went wrong and how we can fix it.

As I [have already stated publicly](#), "Even if the coronavirus is an accidental leak from a Wuhan lab, we are all one interconnected humanity who must work together to get through this crisis." It is my view that Chinese researchers at these institutes were studying these viruses with the best intentions of developing surveillance systems, treatments, and vaccines for the good of humanity. Countries make mistakes, even terrible and deadly ones. I was in the White House when the US bombed the Chinese embassy in Belgrade. We believed it was an accident but many Chinese people thought it was a deliberate act. I understood why.

Moments like these are inherently difficult and we should all do our very best to find the answers to our most important questions in the most honest, careful, and considered manner possible.

We must also be doing everything we can to build the surveillance, response, treatment, vaccine development, and public health capacities we need to make all of us safe. COVID-19 has been a terrible catastrophe, but there could very well be much worse facing us in the future.

In this spirit, I have compiled this summary of the available evidence. Because China is still restricting access to the relevant data and people, the case remains speculative by necessity.

- Beginning on December 10, 2019, increasing numbers of people, many of who had visited the Huanan Seafood Market in Wuhan, fell ill due to a new disease.
- The novel coronavirus outbreak did not originate in the seafood market (Lancet). (This was clear early on but Chinese officials held to this story until late May 2020, when the evidence against this claim became wholly indefensible, more below.)
- The Huanan Seafood Market didn't have bats for sale, and most bats species in Wuhan would be hibernating at the time of outbreak. It was reported that 34% of cases had no contact with the market, and 'No epidemiological link was found between the first patient and later cases.' (Lancet)
- According to a DIA report, "about 33 percent of the original 41 identified cases did not have direct exposure" to the market. That, along with what's known of the laboratory's work in past few years, raised reasonable suspicion that the pandemic may have been caused by a lab error, not the wet market. (Newsweek)
- A Broad Institute study asserts that genetic examination of four samples containing the virus from the seafood market to those taken from the Wuhan patient are '99.9 per cent' identical. This suggests it came from infected visitors or vendors, indicating 'Sars-CoV-2 had been imported into the market by humans'. The authors found no evidence 'of cross-species transmission' at the market.
- This market is less than 9 miles away from The Wuhan Institute of Virology (WIV), Chinese Academy of Sciences, which:
 - Developed chimeric SARS-like coronaviruses
 - Conducted 'dangerous' gain-of-function research on the SARS-CoV-1 virus, some of which had been funded by the US government (Asia Times)
 - Established a 96.2% match with SARS-CoV-2 and a virus they sampled from a cave over 1,000 miles away from Wuhan
 - Injected live piglets with bat coronaviruses as recently as July 2019
 - Published a paper on a close descendant of SARS-CoV-1, MERS-CoV, in November 2019
 - Was hiring researchers to work on bat coronaviruses as recently as November 2019
- United States embassy and consular officials who visited the Wuhan Institute of Virology in January 2018 were deeply concerned. Their cable sent to the State Department noted:
 - "the new lab has a serious shortage of appropriately trained technicians and investigators needed to safely operate this high-containment laboratory"
 - "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.” (Washington Post)

- (For more on laboratory safety in China, see [this link](#).)
- The market is also less than 3 miles away from the Wuhan Centre for Disease Control, which:
 - Was accused of being the source of the outbreak from a now-withdrawn academic paper from a notable Chinese scholar at the South China University of China
 - Once kept horseshoe bats, a known reservoir of SARS-CoV-1, within its labs
 - Once performed surgery on live animals within its labs
 - Had a researcher who quarantined on two separate occasions; once upon coming into contact with bat blood after being ‘attacked’ and another time when he was urinated upon in a cave while wearing inadequate personal protection
 - Had previously done bat virus research funded by the US NIH (in a grant to EcoHealth Alliance)
 - possessed the virus that is the most closely related known virus in the world to the outbreak virus, bat virus RaTG13. This virus was isolated in 2013 and had its genome published on January 23, 2020. Seven more years of bat coronavirus collection followed the 2013 RaTG13 isolation. One component of the novel-bat-virus project at the Wuhan Institute of Virology involved infection of laboratory animals with bat viruses. Therefore, the possibility of a lab accident includes scenarios with direct transmission of a bat virus to a lab worker, scenarios with transmission of a bat virus to a laboratory animal and then to a lab worker, and scenarios involving improper disposal of laboratory animals or laboratory waste. (Bulletin of the Atomic Scientists)
 - began its gain of function research program for bat coronaviruses in 2015. Using a natural virus, institute researchers made “substitutions in its RNA coding to make it more transmissible. They took a piece of the original SARS virus and inserted a snippet from a SARS-like bat coronavirus, resulting in a virus that is capable of infecting human cells.” (Bulletin of the Atomic Scientists)
- Even before this outbreak, China had a very poor safety record at many of its biosecurity facilities.
- In the years since the SARS outbreak, many instances of mishaps involving the accidental release of pathogens have taken place in labs throughout the world. Hundreds of breaches have occurred in the U.S., including a 2014 release of anthrax from a U.S. government lab that exposed 84 people. The SARS virus escaped from a Beijing lab in 2004, causing eleven infections and one death. An accidental release is not complicated and doesn’t require malicious intent. All it takes is for a lab worker to get sick, go home for the night, and unwittingly spread the virus to others. (Newsweek)
- Although it does not appear likely this virus was engineered (Nature Medicine), trying to determine the exact pattern and genomic ancestry of the virus is difficult, particularly as

many of the recombinant regions may be small and are likely to change as more viruses related to SARS-CoV-2 are sampled. (Cell)

- Using the current standard genetic engineering technology, many alterations of several bases in the RNA genome would be undetectable, including construction of a chimeric coronavirus encoding an unpublished spike protein in an unpublished genome. (Independent Science News)
- After months of speculation and with the market origin story indefensible, the Chinese Centers for Disease Control and Prevention finally admitted only in late May 2020 that it has ruled the site out as the origin point of the outbreak. According to Gao Fu, the director of the Chinese CDC, "It now turns out that the market is one of the victims."
- Nikolai Petrovsky and colleagues at Flinders University in Australia have found that SARS-CoV-2 has a higher affinity for human receptors than for any other animal species they tested, including pangolins and horseshoe bats. He suggests that this could have happened if the virus was being cultured in human cells, adding that "We can't exclude the possibility that this came from a laboratory experiment." (Wall Street Journal)
- According to the WHO, "the virus has been remarkable stable since it was first reported in Wuhan, with sequences well conserved in different countries, suggesting that the virus was well adapted to human transmission from the moment it was first detected."
- This Quantitative Biology paper by Nikola Petrovsky et al makes the very strong case that that the SARS-CoV-2 virus was already pre-adapted to humans by the time it appeared in late 2020.
- Similarly, Sirotkin and Sirotkin assert in their Wiley preprint essay: "Unless the intermediate host necessary for completing a natural zoonotic jump is identified, the dual-use gain-of-function research practice of viral serial passage should be considered a viable route by which the novel coronavirus arose. The practice of serial passage mimics a natural zoonotic jump, and offers explanations for SARS-CoV-2's distinctive spike-protein region and its unexpectedly high affinity for angiotensin converting enzyme (ACE2), as well as the notable polybasic furin cleavage site within it. Additional molecular clues raise further questions, all of which warrant full investigation into the novel coronavirus's origins and a re-examination of the risks and rewards of dual-use gain-of-function research.
- The two known coronaviruses genetically closest to SARS-CoV-2, RaTG13 and RmYN02, were discovered in bats in Yunnan, China. The genome of RaTG13 is 96.2% similar to SARS-CoV-2. That of RmYN02 is 93.3 % similar. Given that the SARS-CoV-2 genome is made up of 30,000 nucleotides (aka letters), the genetic distance between RaTG13 and SARS-CoV-2 is a significant 1,200 nucleotides. Under normal circumstances in wild, this would suggest that the two viruses diverged decades ago. But an essential question is whether gain of function research could have massively sped up this evolutionary rate, including by inducing the development of chimeric viruses well adapted to human cells. This type of research could have been done using the tools of genome editing (which I believe is highly unlikely in this case) or by exposing different viruses to human cells or humanized mouse or other animal cells in a laboratory.

- Stanford's David Relman states: "SARS-CoV-2 is a betacoronavirus whose apparent closest relatives, RaTG13 and RmYN02, are reported to have been collected from bats in 2013 and 2019, respectively, in Yunnan Province, China. COVID-19 was first reported in December 2019 more than 1,000 miles away in Wuhan City, Hubei Province, China. Beyond these facts, the "origin story" is missing many key details, including a plausible and suitably detailed recent evolutionary history of the virus, the identity and provenance of its most recent ancestors, and surprisingly, the place, time, and mechanism of transmission of the first human infection... Some have argued that a deliberate engineering scenario is unlikely because one would not have had the insight a priori to design the current pandemic virus. This argument fails to acknowledge the possibility that two or more as yet undisclosed ancestors (i.e., more proximal ancestors than RaTG13 and RmYN02) had already been discovered and were being studied in a laboratory—for example, one with the SARS-CoV-2 backbone and spike protein receptor binding domain, and the other with the SARS-CoV-2 polybasic furin cleavage site. It would have been a logical next step to wonder about the properties of a recombinant virus and then create it in the laboratory... there is probably more than one recent ancestral lineage that contributes to SARS-CoV-2 because its genome shows evidence of recombination between different parental viruses. In nature, recombination is common among coronaviruses. But it's also common in some research laboratories where recombinant engineering is used to study those viruses."
- (Alina Chan, a junior scientist at the Broad Institute demonstrates how shoddy much of the pangolin research has been in this important Twitter thread.)
- The Brufsky et al Wiley pre-print letter lays out the underlying science which seems to explain why the gain of function research at the WIV is the most likely origin of the pandemic. To be fair, the conclusion these authors draw is extremely cautious: "These unique features of SARS-CoV-2 raise several questions concerning the proximal origin of the virus that require further discussion." They do not list the question but the implication is clear enough.
- The analysis by Boni, Robertson, and their colleagues made those researchers believe that despite the genetic closeness, RaTG13 and SARS-CoV-2 split up quite a long time ago, possibly in 1969. This analysis, however, does not account for the ability of gain of function research to speed up the evolutionary timeline and potentially push the "natural" formation of chimeric viruses.
- It could also be possible that SARS-CoV-2 might be the result of gain of function research on another virus in the Wuhan Institute of Virology repository. Quoting a private communication from a scientist I trust (who chose to remain anonymous out of personal safety concerns), "the issue is that there is this internal database at the WIV that even other Chinese scientists can't access. Even the first team to point out the similarity of SARS2 to the 4991 sequence — they had no idea that 4991 aka RaTG13 had been fully genome sequenced. What other viruses are in this database? Was the pangolin CoV RBD also in this database by mid 2019?"
- In an August 12, 2020 BioEssays paper, Sirotkin and Sirotkin assert that the WIV is sitting on somewhere in the neighborhood of 2,000 undisclosed wild viruses, and Dr. Shi

herself disclosed that 9 previously undisclosed betacoronaviruses that had been held in a WIV lab repository. The database issues are further explored in in this thread as well as in this thread.)

- All the Wuhan Institute of Virology virus databases were taken down early in 2020 and remain offline. There are estimated to be at least 100 unpublished sequences of bat betacoronaviruses in these databases which need to be sequenced by international scientists. Based on information and links provided here, these databases include:
 - WIV Database 1: <http://batvirus.whiov.ac.cn/> (Archive seems to be unavailable)
 - WIV SQL online Database 2: <http://csdata.org/p/308/>,
Archived: <https://web.archive.org/web/20200507214518/http://csdata.org/p/308/> and: <http://archive.is/HLuio>
 - WIV Database 3: <http://www.viruses.nsd.cn/vri.jsp>,
Archived: <https://web.archive.org/web/20200125203943/http://www.viruses.nsd.cn/vri.jsp>, Discussion of significance here: Guoke Faji 2019/236 and the SARS-CoV-2 Outbreak <http://archive.is/uHqSw#selection-29.0-29.47>
 - WIV Database 4: <http://www.viruses.nsd.cn/chinavpi>,
Archived: <https://web.archive.org/web/20200404100024/http://www.viruses.nsd.cn/chinavpi>, Referenced in a paper by Zhiming Yuan of the Key Laboratory of Special Pathogens and Biosafety, Wuhan Institute of Virology, (+86-27-87197242, Email: yzm@wh.iov.cn), "*Investigation of Viral Pathogen Profiles in Some Natural Hosts and Vectors in China*",
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6178075/>
 - WIV Database 5: http://www.wfcc.info/ccinfo/collection/col_by_country/c/86/,
Archived: https://web.archive.org/web/20200515223251/http://www.wfcc.info/ccinfo/collection/col_by_country/c/86/ which in turn links to: http://wfcc.info/ccinfo/collection/by_id/613, Archived: https://web.archive.org/web/20200108181714/http://wfcc.info/ccinfo/collection/by_id/613 links to: <http://www.virus.org.cn/> (404 for the database in question),
Archived: <https://web.archive.org/web/20191230091754/http://www.virus.org.cn/>, And an archived description of the WIV database: https://web.archive.org/web/20200117011358/http://www.whiov.ac.cn/xwdt105286/zxw/201804/t20180423_5000795.html
- Sirotkin and Sirotkin also state: "Unless the intermediate host necessary for completing a natural zoonotic jump is identified, the dual-use gain-of-function research practice of viral serial passage should be considered a viable route by which the novel coronavirus arose."
 - "The long-standing practice of serial passage is a form of gain-of-function research that forces zoonosis between species, and requires the same molecular adaptations necessary for a natural zoonotic jump to occur within a laboratory, leaving the same genetic signatures behind as a natural jump but occurring in a much shorter period of time... serial passage through a live animal host simply forces the same molecular processes that occur in nature to happen during a zoonotic jump, and in vitro passage through cell culture mimics many elements

of this process—and neither necessarily leaves any distinguishing genetic traces.”

- “A coronavirus that targets the ACE2 receptor like SARS-CoV-2 was first isolated from a wild bat in 2013 by a team out of Wuhan. This research was funded in part by EcoHealth Alliance, and set the stage for the manipulation of bat-borne coronavirus genomes that target this receptor and can become airborne. Many more viruses have been collected in Wuhan over the years, and one research expedition captured as many as 400 wild viruses, which were added to a private repository that has since grown to over 1500 strains of virus, meaning that the Wuhan Center for Disease Control and Prevention has a massive catalogue of largely undisclosed viruses to draw from for experiments... But for whatever reason, the Wuhan Institute of Virology has refused to release the lab notebooks of its researchers, which are ubiquitous in even the simplest laboratories and are expected to be meticulously detailed given the sensitive and delicate work that takes place in BSL-4 research labs intent on documenting their intellectual property, despite the fact that these notebooks would likely be enough to exonerate the lab from having any role in the creation of SARS-CoV-2.”
- “The prospect that serial passage through lab animals or on commercial farms may have played a role in the creation of SARS-CoV-2 is also raised by an April 2020 preprint, which appears to have been retracted after Chinese authorities implemented the censorship of any papers relating to the origins of the novel coronavirus.” (For the last point, see [this link](#).)
- “These data do not support the idea that SARS-CoV-2 was circulating in humans prior to the outbreak began in Wuhan in the early winter or fall of 2019, making a zoonotic jump even more unlikely since natural jumps leave wide serological footprints in their new host populations as early variants of a prospective virus make limited and unsuccessful jumps into individuals of the new host species, a trial-and-error that must occur before mutations that allow adaptation to a new host species are selected.”
- In a BioEssays paper, issued November 17, 2020, authors Deigin and Segreto assert: “Severe acute respiratory syndrome-coronavirus (SARS-CoV)-2’s origin is still controversial. Genomic analyses show SARS-CoV-2 likely to be chimeric, most of its sequence closest to bat CoV RaTG13, whereas its receptor binding domain (RBD) is almost identical to that of a pangolin CoV. Chimeric viruses can arise *via* natural recombination or human intervention. The furin cleavage site in the spike protein of SARS-CoV-2 confers to the virus the ability to cross species and tissue barriers, but was previously unseen in other SARS-like CoVs. Might genetic manipulations have been performed in order to evaluate pangolins as possible intermediate hosts for bat-derived CoVs that were originally unable to bind to human receptors? Both cleavage site and specific RBD could result from site-directed mutagenesis, a procedure that does not leave a trace. Considering the devastating impact of SARS-CoV-2 and importance of preventing future pandemics, researchers have a responsibility to carry out a thorough analysis of all possible SARS-CoV-2 origins.” At very least, this paper credibly raises a

serious hypothesis worthy of far deeper exploration. Some key points made in the paper include:

- “the two main SARS-CoV-2 features, (1) the presence of a furin cleavage site missing in other CoVs of the same group and (2) an receptor binding domain (RBD) optimized to bind to human cells might be the result of lab manipulation techniques such as site-directed mutagenesis.”
- “In order to evaluate the emergence potential of novel CoVs, researchers have created a number of chimeric CoVs, consisting of bat CoV backbones, normally unable to infect human cells, whose spike proteins were replaced by those from CoVs compatible with human ACE2. These chimeras were meant to simulate recombination events that might occur in nature... Synthetically generating diverse panels of potential pre-emergent CoVs was declared a goal of active grants for the EcoHealth Alliance, which funded some of such research at WIV, in collaboration with laboratories in the USA and other international partners.”
- “Due to the broad-spectrum of research conducted over almost 20 years on bat SARS-CoVs justified by their potential to spill over from animal to human, a possible synthetic origin by laboratory engineering of SARS-CoV-2 cannot be excluded... SARS-CoV-2 could have been synthesized by combining a backbone similar to RaTG13 with the RBD of CoV similar to the one recently isolated from pangolins.”
- “Another open question is the reason for modification and subsequent deletion of WIV’s own viral database.”
- China has taken a series of steps since the beginning of this crisis which seem consistent with a coverup. Although the coverup began with local and provincial Wuhan authorities, it later involved decisions made by the Chinese leadership at the highest level. These steps include:
 - On December 31, Chinese authorities started censoring news of the virus from search engines, deleting terms including “SARS variation,” “Wuhan Seafood market” and “Wuhan Unknown Pneumonia.” (Daily Telegraph)
 - Officials closed the market the day after notifying the WHO and sent in teams with strong disinfectants. Samples from animals were taken but, four months later, the results have not been shared with foreign scientists. The actions led to claims that they were deliberately wiping away crucial traces. (Daily Telegraph)
 - Many China scholars noted that it was quite unusual for Chinese government authorities to identify Wuhan’s Huanan South China Seafood Market so quickly as the source of the outbreak. They thought this behavior so uncharacteristic that it raised suspicions in their minds.
 - The Hubei health commission ordered genomics companies to stop testing for the new virus and to destroy all samples.
 - On January 1, an employee of a genomics company in Wuhan received a phone call from an official at the Hubei Provincial Health Commission, ordering the company to stop testing samples from Wuhan related to the new disease and to destroy all existing samples. (Caixin Global)

- On January 1, Wuhan Institute of Virology's director general, Yanyi Wang, messaged her colleagues, saying the National Health Commission told her the lab's COVID-19 data shall not be published on social media and shall not be disclosed to the media. And on January 3, the commission sent this document, never posted online, but saved by researchers, telling labs to destroy COVID-19 samples or send them to the depository institutions designated by the state. (Bulletin of the Atomic Scientists)
- On January 3, China's National Health Commission (NHC) ordered institutions not to publish any information related to the unknown disease and ordered labs to transfer any samples they had to designated testing institutions or destroy them. (Caixin Global)
- Even with full sequences decoded by three state labs independently, Chinese health officials remained silent. (AP)
- China sat on releasing the genetic map, or genome, of the virus for more than a week after three different government labs had fully decoded the information. Tight controls on information and competition within the Chinese public health system were to blame, according to dozens of interviews and internal documents. (AP)
- WHO officials complained in internal meetings that they were making repeated requests to the Chinese authorities for more data, especially to find out if the virus could spread efficiently between humans, but to no avail. "We have informally and formally been requesting more epidemiological information," WHO's China representative Galea said. "But when asked for specifics, we could get nothing." (AP)
- Beijing did not notify the World Health Organization of the outbreak for at least four days after Wuhan officials were notified. A WHO investigation team was not allowed to visit Wuhan until three weeks after that, and the team was not given full and unrestricted access even during this preliminary field visit
- The Chinese government closed the laboratory in Shanghai that first published the genome of COVID-19 on January 10, explaining that it had been shuttered for "rectification." Chinese citizens who reported on the coronavirus were censured and, in some cases, "disappeared." These have included businessman Fang Bin, lawyer Chen Qiushi, former state TV reporter Li Zehua and, most recently, Zhang Zhan, a lawyer. They are reportedly being held in extrajudicial detention centers for speaking out about China's response to the pandemic. (Bulletin of the Atomic Scientists)
- Chinese government labs only released the genome after another lab published it ahead of authorities on a virologist website on Jan. 11. Even then, China stalled for at least two weeks more on providing WHO with detailed data on patients and cases, according to recordings of internal meetings held by the U.N. health agency through January — all at a time when the outbreak arguably might have been dramatically slowed. (AP)
- Although international law obliges countries to report information to WHO that could have an impact on public health, the U.N. agency has no enforcement

powers and cannot independently investigate epidemics within countries. Instead, it must rely on the cooperation of member states. According to WHO's chief of emergencies, Dr. Michael Ryan, this type of obfuscation and interference "would not happen in Congo and did not happen in Congo and other places." (AP)

- Not only did China block the WHO investigation team from going to Wuhan for nearly a month, it also severely curtailed its activities after that.
- On Jan. 14, the head of China's National Health Commission said in a confidential teleconference with provincial health officials that the situation was "severe and complex," that "clustered cases suggest that human-to-human transmission is possible," and that "the risk of transmission and spread is high." The Commission issued a 63-page document on response procedures that same day that was labeled "internal" and "not to be publicly disclosed." The next day, the head of China's disease control emergency center, announced on state television that "the risk of sustained human-to-human transmission is low." This same message was delivered to the World Health Organization. (Washington Post)
- Between the day the full genome was first decoded by a government lab on Jan. 2 and the day WHO declared a global emergency on Jan. 30, the outbreak spread by a factor of 100 to 200 times, according to retrospective infection data from the Chinese Center for Disease Control and Prevention. (AP) Chinese officials actively lobbied the WHO to prevent the emergency declaration, which almost certainly slowed the international response,
- Offers from the United States to send medical experts to Wuhan in early January were rejected by the central government. (Diplomat)
- This Chinese preprint paper was released in February 2020 and then mysteriously retracted. In it, two Chinese experts assert that, "Somebody was entangled with the evolution of 2019-nCoV coronavirus. In addition to origins of natural recombination and intermediate host, the killer coronavirus probably originated from a laboratory in Wuhan... Regulations may be taken to relocate these laboratories far away from city center and other densely populated places."
- Although WIV officials have commented publicly about social media posting alleging that one of their prior researchers may be "patient zero," the WIV has not provided any information about that person
- A WIV researcher who publicly accused the director of the Institute of selling infected lab animals to vendors on Weibo (with pictures of herself and her employee ID included) later claimed she was 'hacked' and disavowed her prior allegation
- In contrast to its earlier (and inaccurate) assertion that the outbreak originated in the Wuhan seafood market, a Ministry of Foreign Affairs spokesperson on March 12 accused the United States Army of intentionally bringing SARS-CoV-2 to Wuhan

- Beijing disinfected the Wuhan market before a full international investigation could be conducted and 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. (Washington Post)
- On Feb. 14, Chinese President Xi Jinping called for a new biosecurity law to be accelerated. On Wednesday, The Chinese government has placed severe restrictions requiring approval before any research institution publishes anything on the origin of the novel coronavirus. (Washington Post)
- This was followed immediately by a China Ministry of Science & Technology announcement of new guidelines for laboratories, especially in handling viruses. Almost at the same time, the Chinese newspaper Global Times published an article on “chronic inadequate management issues at laboratories, including problems of biological wastes.”
- Labs analyzing the pathogen were instructed to destroy samples, a health center that had published the virus’s genome sequence was temporarily shut down the following day, and doctors were prevented from submitting case information to the country’s infectious disease tracking network. (Diplomat)
- Reports of health care workers falling ill, an early indicator of human-to-human transmission, were suppressed. More indirectly, state media coverage of doctors being penalized reportedly had a chilling effect on other medical professionals who might have sounded the alarm. (Diplomat)
- In an official document marked “internal document, please keep confidential” reported out by CNN, Hubei provincial officials listed 5,918 new cases for Feb. 10, more than twice what was reported publicly for all of China on that day. On March 7, the total death toll in Hubei was listed in the report at 3,456 but publicly stated as 2,986. According to the Washington Post, “the Hubei documents add weight to the conclusion that China deliberately hid the true dimensions of the disaster.”
- In March 2020, Beijing announced the expulsion of American journalists working for The New York Times, The Wall Street Journal and The Washington Post, the media organizations who have exposed some of the most significant misdeeds and coverups by the Chinese government over recent decades
- In April 2020, with the outbreak in full swing, the WIV deleted a press release detailing the January 2019 U.S. State Department visit
- The Chinese government has now banned any researcher from publishing anything on the origins of this crisis without prior approval of the Ministry of Science and Technology (Nature)
- On April 24, the New York Times reported that Beijing has successfully pressured European Union officials to water down references to China in an EU report. The original language had stated, “China has continued to run a global disinformation

campaign to deflect blame for the outbreak of the pandemic and improve its international image... Both overt and covert tactics have been observed.”

- It appears there may have been a sudden drop in cellphone usage at WIV in early October followed by a cellphone blackout, suggesting the possibility of an accident inside WIV on October 6 followed by a traffic closure. Without further detail about sourcing, however, this information remains speculative. (E-PAI report)
- Zhang Zan, a Chinese citizen journalist arrested by Chinese authorities in May for asking tough questions about the origin of the pandemic and accused, absurdly, of “picking quarrels and provoking troubles,” was sentenced to four years in prison on December 28, 2020. According to Quartz: Three other citizen journalists—Chen Qiushi, Fang Bin, and Li Zehua—all disappeared in February as soon as their coverage of Wuhan during the pandemic started to gain traction online. Li Zehua resurfaced in April, saying he had been taken by police on suspicion of disturbing public order but was later released as the authorities did not press charges. Meanwhile, Chen and Fang’s whereabouts still aren’t known, though Chen is reportedly staying under home surveillance at his parents’ house.
- On November 25, 2020, Kyodo News reported that “Chinese authorities warned doctors, who responded to the novel coronavirus in the early stage of the outbreak in Wuhan, that they could be punished for espionage if they revealed what went on during the period.”
- Also in November, 2020, the Chinese government launched a concerted propaganda campaign claiming, without meaningful evidence, that the pandemic began in the Indian subcontinent.
- This December 19, 2020 New York Times article outlines in stunning detail the extent to which China actively and aggressively suppressed information about the pandemic, silenced whistleblowers and people raising essential questions, the manipulated outgoing information in order to hoard essential supplies from abroad. This history, in the context of COVID-19 and many other “sensitive” issues, suggests that an international investigation into the origins of COVID-19 that relies primarily on data gathered and information provided by the Chinese authorities, as the WHO investigation appears to do, can not be considered legitimate.
- According to a December 30, 2020 AP article, “More than a year since the first known person was infected with the coronavirus, an AP investigation shows the Chinese government is strictly controlling all research into its origins, clamping down on some while actively promoting fringe theories that it could have come from outside China. The government is handing out hundreds of thousands of dollars in grants to scientists researching the virus’ origins in southern China and affiliated with the military, the AP has found. But it is monitoring their findings and mandating that the publication of any data or research must be approved by a new task force managed by China’s cabinet, under direct orders from President Xi Jinping, according to internal documents obtained by the AP. A rare leak from

within the government, the dozens of pages of unpublished documents confirm what many have long suspected: The clampdown comes from the top."

○ Here is a link to the official Chinese regulation.

- On April 18, 2020, Director of the Wuhan Institute of Virology of the Chinese Academy of Sciences said in an interview that "there is no way this virus came from us."
- In early May, the World Health Organization's representative in China, Gauden Galea, publicly complained that China had refused repeated requests to permit the WHO to participate in whatever investigations the Chinese government was undertaking itself. He said that the WHO had not been given access to laboratory logs at the WIV or the Wuhan Chinese Center for Disease Control and Prevention. (Bulletin of the Atomic Scientists)
- On May 3, US Secretary of State Mike Pompeo said "There is a significant amount of evidence that this came from that laboratory in Wuhan." China's Global Times, run by the ruling Communist Party's official People's Daily, said in an editorial responding to this interview that "The Trump administration continues to engage in unprecedented propaganda warfare while trying to impede global efforts in fighting the COVID-19 pandemic."
- On May 4, the Guardian claimed its sources insisted a "15-page dossier" highlighted by the Australian Daily Telegraph accusing China of a deadly cover up was not culled from intelligence from the Five Eyes Network, an alliance between the UK, US, Australia, New Zealand and Canada.
- Bloomberg reported on May 5 that a majority of the 17 agencies that provide and analyze intelligence for the U.S. government believe the pandemic started after the virus was leaked from the Wuhan lab, but based mostly on circumstantial evidence.
- The U.S. Department of Homeland Security and Britain's National Cyber Security Center recently issued a statement saying hackers are "actively targeting organisations ... that include healthcare bodies, pharmaceutical companies, academia, medical research organisations, and local government." This was widely construed as suggesting that state-sponsored Chinese hackers were attempting to steal COVID-19 research. (NPR)
- On May 19, the World Health Assembly agreed to an "impartial, independent and comprehensive evaluation" of the international response to COVID-19. China did not object to the resolution but Chinese president Xi Jinping said the investigation should only take place after the pandemic is contained. This is not likely to happen any time soon.
- Investigating the range of possible spillover sites—from the wet market, to an accidental lab or fieldwork infection, or an unnoticed lab leak—requires a forensic investigation. Obtaining case histories, epidemiological data, and viral samples from different times and places, including the earliest possible samples from infected individuals and samples from wildlife, is paramount... A forensic investigation would additionally involve auditing and sampling viral collections at relevant labs that had been studying coronaviruses, examining the types of experiments carried out and the viruses used, and reviewing the safety and security practices in place... A COVID-19 origins investigation will need to be

negotiated and begun rapidly before relevant data diminishes or disappears entirely as time passes. (Bulletin of the Atomic Scientists)

- Determining whether WIV had anything to do with the virus will require a forensic investigation, say several scientists. Investigators would be looking for viruses that matched the genetic sequence of SARS-CoV-2 and, if they found one, any evidence that it could have escaped. To do that, authorities would need to take samples from the lab, interview staff, review lab books and records of safety incidents, and see what types of experiment researchers had been doing. An independent investigation at the WIV facility is probably the only way to convincingly rule out the lab as a possible source of the outbreak, but such a probe is still being blocked by the Chinese authorities. (Nature) This is outrageous.
- On June 7, China issued a white paper called, "China's Actions to Fight the Covid-19 Epidemic." This document asserted: "China's action composes the heroic paean to the people's lives above all else, highlighting the responsibility of a great power to life, the people, history and the international community. China has always adhered to the concept of a community of a shared future for mankind. It has always worked hand in hand with other countries and fought side by side, making unremitting efforts to fight for an early global epidemic prevention and control." Some observers noted this narrative did not reflect an accurate assessment of the historical record of the COVID-19 pandemic or Chinese history more generally. It is estimated that 47 million people died senselessly under former Chinese Leader Mao Tse Tung.
- On July 10, the WHO announced that a two-member advance team of experts has left for China to organize an investigation into the origins of the novel coronavirus. It is unlikely this team will have the authority to conduct the type of full forensic investigation that is required.
- In fact, the WHO has agreed with the Chinese government that investigations into the first patients in China and the market's role in the outbreak will be led by Chinese scientists, with WHO experts able to review and "augment, rather than duplicate," studies undertaken by China officials. The exact language from the WHO Terms of Reference document states that "Some of the abovementioned work may already be partially done or documented by the time the international team initiates its work, and the study will therefore build on existing information and augment, rather than duplicate, ongoing or existing efforts." It also asserts that "The final composition of the international team should be agreed by both China and WHO." In light of all the evidence of active efforts by the Chinese government to destroy evidence, deny access to key records, and silence relevant domestic (and even international) voices, this level of deference to Beijing falls well below the standard of even basic accountability. As I have written elsewhere, it would be wrong to blame the WHO for this given the designed weakness of its mandate, the result of efforts by many states over decades to defend state sovereignty at the expense of our common good as humans sharing the same planet (sorry to throw in more idealism here, but I invite you to join OneShared.World if you are interested in addressing our world's dangerous collective action problem).

- Here is an annotated version of the WHO Terms of Reference with comments provided by Giles Demaneuf. It is abundantly clear that the Chinese government aggressively negotiated compromises, structural limitations, and borderline falsehoods into the document. I have great faith in the personal integrity of many of the ten people chosen to represent the international community in this investigation, but they will almost certainly not be able to fulfill their obligation to humanity and future generations if they follow the terms of reference to the letter. It is my hope they will demand the most thorough investigation of all possible hypotheses, demand full access to all relevant people and materials, demonstrate full transparency, and speak publicly and forcefully, in their collective and/or personal capacities, if they don't have full access to everything and everyone they need.
- On July 15, Chinese virologist Shi Zhengli, the noted WIV bat virus specialist, sent written comments to Science magazine refuting allegations of a leak. Nothing in her comments in any way reduces the pressing need for a full and unrestricted international investigation into the origins of the pandemic.
- In my July 29, 2020 Washington Post editorial, I write: "The closest known relative to SARS-CoV-2 is a virus sampled by Chinese researchers from six miners infected while working in a bat-infested cave in southern China in 2012. These miners developed symptoms we now associate with Covid-19. Half of them died. These viral samples were then taken to the Wuhan Institute of Virology—the only facility in China that's a biosafety Level 4 laboratory, the highest possible safety designation. The Level 4 designation is reserved for facilities dealing with the most dangerous pathogens. Wuhan is more than 1,000 miles north of Yunnan province, where the cave is located. If the virus jumped to humans through a series of human-animal encounters in the wild or in wet markets, as Beijing has claimed, we would likely have seen evidence of people being infected elsewhere in China before the Wuhan outbreak. We have not. The alternative explanation, a lab escape, is far more plausible. We know the Wuhan Institute of Virology was using controversial 'gain of function' techniques to make viruses more virulent for research purposes. A confidential 2018 State Department cable released this month highlighting the lab's alarming safety record should heighten our concern. Suggesting that an outbreak of a deadly bat coronavirus coincidentally occurred near the only level 4 virology institute in all of China—which happened to be studying the closest known relative of that exact virus—strains credulity."
- Understanding the link between the Chinese miners exposed in the Yunnan cave in 2012 and the potential outbreak in Wuhan in late 2019 is essential. Anyone with a serious interest in getting to the bottom of the origins questions should be required to read the July 15 Latham and Wilson Independent Science News paper in full. It states: "We suggest, first, that inside the miners RaTG13 (or a very similar virus) evolved into SARS-CoV-2, an unusually pathogenic coronavirus highly adapted to humans. Second, that the Shi lab used medical samples taken from the miners and sent to them by Kunming University Hospital for their research. It was this human-adapted virus, now known as SARS-CoV-2, that escaped from the WIV in 2019." This Frontiers in Public Health article raises similar questions.

- It is impossible to overstate the implications of the SARS-CoV-2 virus being so well adapted to humans from the outset. Zhan and Chan in their May 2 paper state that “by the time SARS-CoV-2 was first detected in late 2019, it was already pre-adapted to human transmission to an extent similar to late epidemic SARS-CoV. However, no precursors or branches of evolution stemming from a less human-adapted SARS-CoV-2-like virus have been detected... In comparison to the SARS-CoV epidemic, the SARS-CoV-2 epidemic appears to be missing an early phase during which the virus would be expected to accumulate adaptive mutations for human transmission. However, if this were the origin story of SARS-CoV-2, there is a surprising absence of precursors or branches emerging from a less recent, less adapted common ancestor among humans and animals.” The Latham and Wilson July 15 paper provides by far the best explanation: this virus that escaped from the lab had likely come from a human sample (one of the miners).
- In my Washington Post editorial, I say: “Not getting to the bottom of this crisis would be the height of absurdity. Too much is at stake. To ensure everyone’s safety, the WHO and outside investigators must be empowered to explore all relevant questions about the origins of the pandemic without limits. This comprehensive forensic investigation must include full access to all of the scientists, biological samples, laboratory records and other materials from the Wuhan virology institutes and other relevant Chinese organizations. Denying that access should be considered an admission of guilt by Beijing.”
- In my August 17 editorial in *The Hill*, I state that “Congress should immediately establish a bipartisan national commission, modeled on the 9/11 Commission, to prepare a full, complete account of four essential failures and what we can do to address them.” These four failures are ones made by China, the WHO, the US government, and all of us in not preparing for the full panoply of global existential threats. “Some may feel that establishing such a commission while the pandemic still rages would be like launching the 9/11 commission while the Twin Towers were still falling. But would it not have been better to do exactly that, rather than blindly charge into two wars without deep analysis and a long-term strategy? Getting to the bottom of our current crisis is not just an intellectual exercise. The COVID-19 pandemic is far from over but there are no guarantees that an even worse pandemic, possibly supercharged by a synthetic pathogen, might be just around the corner.”
- In September 2020, the Lancet released the first statement of its COVID-19 commission. The statement asserts: “The origins of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) are yet to be definitively determined, but evidence to date supports the view that SARS-CoV-2 is a naturally occurring virus rather than the result of laboratory creation and release. Research into the origins of SARS-CoV-2 should proceed expeditiously, scientifically, and objectively, unhindered by geopolitical agendas and misinformation.” It makes little sense for an investigation commission to claim an initial finding before a full investigation has been carried out. It would be far more credible to state that the commission would explore all possible hypothesis to help get to the bottom of the origins issue. Further, by contrasting “a naturally occurring virus rather than the result of laboratory creation and release,” the commission completely

disregards the possibility of gain of function work followed by a lab leak, the exact scenario that could potentially compromise commission chair, Peter Daszak.

- Selecting Peter Daszak to lead the Lancet commission is also questionable. As I wrote in my message to Lancet editor, Richard Horton: "Peter's organization worked closely with the Wuhan Institute of virology and supported gain of function research on bat coronaviruses. If the pandemic stems from an accidental leak of one of these viruses, Peter would potentially be implicated. I am not at all suggesting that he did anything wrong, just that one of the possible origin stories includes him. Because so much is riding on this investigation, I think it essential that we make sure the commission itself represents a balance of perspectives, while excluding conspiracy theorists and people with political axes to grind... Putting together a commission that is both impartial and balanced and seen as being impartial and balanced will be critical for everything that follows." ([Here is a Twitter link](#) to Peter describing in his own words the process for manipulating the spike proteins of coronaviruses in a lab.)
- In November, 2020, The WHO released the names of the 10 scientists selected in coordination with the Chinese government to visit Wuhan to assess the origins of the pandemic. Surprisingly, Peter Daszak was on this list. As I mentioned in a 11/27 tweet, "I have great respect for Peter but his clear conflict of interest and [prior] funding relationship with WIV should preclude him from these types of roles." I also tweeted that the key to making this a legitimate process will be "ensuring full & unrestricted access to all samples, records, scientists, etc. as part of a deep forensic investigation with no political interference" and the ability to "interview any scientist in China in conditions of complete privacy & security." I have deep reservations about the leading role the Chinese government will play in this investigation on its own failure, which already includes significant oversight of which scientists are selected as investigators and the ability to have Chinese government and government-related scientists doing the primary investigations (would we let the DRC negotiate these kinds of terms as Ebola raged?). Doing a serious investigation will absolutely require significant whistleblower protections for any Chinese scientists who may wish to come forward. This should include an anonymous and safe digital portal and significant protective safeguards including the possibility of asylum.
- This open letter to the WHO COVID-19 international investigations team outlines essential questions which must be addressed by the WHO investigation. A question not included in the petition but which I believe must be asked is: "What was and is the relationship between the Chinese People's Liberation Army and the Wuhan Institute of Virology? Was the PLA engaged in any research at the WIV and did the PLA store any viral samples in the facility prior to the outbreak?"
- On January 6, 2021, after the Chinese government failed to provide visa's for members of the WHO COVID-19 expert committee, foreign ministry spokesperson Hua Chunying stated: "on the issue of COVID-19 origin-tracing, China has always been open, transparent and responsible and taken the lead in carrying out scientific cooperation in tracing the origin with WHO with the purpose of promoting international research on origin-tracing. In February and July last year, when China was faced with daunting domestic epidemic prevention and control tasks, China invited WHO experts to China

twice to carry out cooperation on origin-tracing and formulate the China part of a global scientific cooperation plan on origin-tracing. In October last year, the Chinese side reached agreement on the members of the international expert group. Since then, the experts of the two sides have maintained frequent interactions. Four video meetings were held on October 30, December 3, December 10 and December 18 respectively. With a scientific attitude, Chinese experts shared the outcomes of China's origin-tracing efforts in a science-based and candid manner, and the cooperation between the two sides has made positive progress. Recently, in a positive and constructive attitude, China has maintained close communication with WHO on the expert panel's trip to China for cooperation on origin-tracing. At present, the global pandemic situation remains very serious, and China is also making all-out efforts to prevent and control the epidemic. Chinese health and epidemic prevention departments and experts are devoting themselves to intense anti-epidemic work. Having all this said, in order to support international COVID-19 cooperation, China has overcome difficulties, accelerated preparatory work at home and tried its best to create favorable conditions for the international expert team's visit to China. WHO knows that clearly. The issue of origin-tracing is very complicated. In order to ensure the smooth progress of the work of the international expert group in China, necessary procedures need to be fulfilled and relevant specific arrangements need to be made. At present, the two sides are in negotiating on this." This (technical term, baloney) answer begs the question that has been clear from the earliest days of the pandemic — what is China trying to hide?

- Nature Medicine published on January 13, 2021, an opinion piece by Angela Rasmussen seeking to debunk what she called "often contradictory and sometimes outright ridiculous conspiracy theories that spread faster than the virus itself." As a foundation of her argument, she asserted that "A favorite version of the laboratory-origin stories relies on the fact that SARS-CoV-2 was engineered for gain-of-function studies that were also previously performed with bat SARS-like coronaviruses to understand cross-species transmission risk (*Nat. Med.* **21**, 1508–1513; 2015). The irony is that those gain-of-function studies provided valuable information about the biology of SARS-CoV-2. Gain-of-function research is also subject to intense scrutiny and governmental oversight, precisely because of the high risk involved in conducting it safely; thus, it is extremely unlikely that gain-of-function research on hard-to-obtain coronaviruses (such as bat SARS-like coronaviruses) could occur under the radar." By definition, therefore, this argument would fail if it were shown that animal pathogen research was being carried out at WIV in secret and "under the radar."
- On January 15, 2021, the US State Department issued a Fact Sheet in which the following assertion was made: "Despite the WIV presenting itself as a civilian institution, the United States has determined that the WIV has collaborated on publications and secret projects with China's military. The WIV has engaged in classified research, including laboratory animal experiments, on behalf of the Chinese military since at least 2017." This claim was vetted with all relevant US government agencies and appears credible. In my Twitter response to this assertion I call for additional evidence of this claim to be released and for Five Eyes intelligence services to issue a joint statement assessing this claim.

- It has always been, and remains, my position, that we need to actively examine all possible origin hypothesis. This certainly includes both zoonotic jump and an accidental lab leak. Any credible investigation into the origins of COVID-19 must actively explore both of these hypotheses.

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- [xi jinping](#)
- [Yunnan](#)

24 Comments

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- [Dennis](#) April 16, 2020 at 3:03 pm

Keep on keeping on (b)(6) We're here for the truth. I'm sure your going to dig it up somehow?.... balanced but true.???

[Reply](#)

- [Emily](#) April 20, 2020 at 1:00 pm

Thank you

Reply

- The triple truth ruth May 19, 2020 at 1:55 am

The problem with speculation concerning the possibility of an accident is that we still end up in the same place A TWO to THREE YEAR PANDEMIC that can go either way—deadlier or benign. As it is it will be hard enough for the rest of the world to get back to the task at hand rebuilding the global economy. I remember past futurists and they all ended up talking what ended up being garbage crystal eyeballing. Anything that makes this worse is exactly the sort of stupidity that got us all here. No one is looking good. Even New Zealand will sooner or later have to deal with the economic consequences. Enough with the blaming and scapegoating. IT'S THE RNA, STUPID and the stupid too.

Reply

- KLC November 24, 2020 at 8:22 am

As the author lays out clearly at the beginning of the article the point is to fully investigate the origin of this outbreak so as to implement measures that are most likely to prevent future pandemic outbreaks. It's not about blaming – it's about fact-finding and improving safety. No one with an egregious conflict of interest such as Peter Daszak should be a party to the forensic investigation of the WIV lab(s) that needs to be conducted.

Reply

- HY April 20, 2020 at 7:14 pm

Just FYI, that wet market in Wuhan did sell a lot wild animals in addition to seafood. It even had a wild animal restaurant inside. Apparently not many seafood on the menu.

Reply

- Nova Vieho May 14, 2020 at 1:49 pm

There are identical wet markets in every small and large city all over China with it's vast 1.3 billion population. Certainly Guandong and Yunan where the suspects are from host countless such markets, and are ~1000 miles away from Wuhan. Everyone please I appeal to your commonsense and try not to believe that somehow this bat virus "choose" Wuhan all places in China to jump to humans, which would be an insane coincidence with no comparison in history.

Reply

- Aaron April 21, 2020 at 1:28 am

I have an article proving that they were studying Corona type viruses derived from bats at the wuhan lab.

If you are interested email me at

(b)(6)@riderzlaw.com

Reply

- Davina Rhine April 21, 2020 at 9:46 pm

Thank you sharing your insight and review methodology. If you haven't you may want to look at Curtards published paper that came out early April. It was detailed and thorough. Curtard made the observation that he had only seen this combination of strains experiently. The link to the full paper is in pubmed. Thank you for asking the difficult questions which it seems for whatever reason the majority in postions of influence, media, institutions or policy arent asking at best or worst censoring those who are. This applies to questions not only of origin but of treatments and management including public policy decisions. Unfortunately the general public en masse are also getting angry about these questions being raised which is baffling; you cant make robust and critical decisions that affect many without vigirous review of all the data, science and scenarios especially from the perspective of cost benefit analysis and therapeutic management.

Reply

- Alex Hallatt April 23, 2020 at 6:02 pm

This is in that Nature Medicine paper you reference first:

"Theories of SARS-CoV-2 origins

It is improbable that SARS-CoV-2 emerged through laboratory manipulation of a related SARS-CoV-like coronavirus. As noted above, the RBD of SARS-CoV-2 is optimized for binding to human ACE2 with an efficient solution different from those previously predicted^{7,11}. Furthermore, if genetic manipulation had been performed, one of the several reverse-genetic systems available for betacoronaviruses would probably have been used¹⁹. However, the genetic data irrefutably show that SARS-CoV-2 is not derived from any previously used virus backbone²⁰. Instead, we propose two scenarios that can plausibly explain the origin of SARS-CoV-2: (i) natural selection in an animal host before zoonotic transfer; and (ii) natural selection in humans following zoonotic transfer. We also discuss whether selection during passage could have given rise to SARS-CoV-2."

Reply

- Derek May 9, 2020 at 12:29 am

No one is asserting that this virus was manipulated with genome editing tools or even that it was grown via in vitro culture (evidence of immunoevasive adaptations make it most likely to have evolved in a host); but there is evidence that these labs were collecting wild type viruses and doing animal passage gain

of function experiments, both of which could have brought this strain to Wuhan before an accidental release.

Reply

- Davina Rhine April 24, 2020 at 2:11 am

I referenced a paper looking at the covid19 strains earlier. In error I listed the scientist name as Curtard. Its Coutard. You can access it here:

<https://www.sciencedirect.com/science/article/pii/S0166354220300528>

Reply

- Melinda Correll April 29, 2020 at 1:04 pm

Thank you so much for putting together this excellent summary. I've been following this closely since the beginning and you brought out some points that I was not aware of. We have the freedom to speak out and if we don't speak out we might find some day in the near future that we can no longer. So thank you and keep on keepin on.

Reply

- Steven Atukwase May 3, 2020 at 6:47 am

As some one with some knowledge in zoology, i think that it would be necessary for the habitat of the alleged animals ie bats that could have been the source of COVID-19 virus to be thoroughly scanned in minute detail to confirm or dismiss that hypothesis. Because if the virus was from bats that were taken from a natural ecosystem, then there must be other bats over the habitat which carry those pathogens. There is no way that only one animal (one bat) could have contracted and spread the virus because they normally live in large groups., there should be others which have it. If it is discovered that there are no other bats carrying the virus then this is likely to help question the validity of that hypothesis. With the natural occurrence of the virus eliminated, that would leave the scientists to highly suspect the artificial (lab) hypothesis.

At the same time there is need to ask: If infected bats were experimented on, didn't other people e.g hunters at a different location or traders at a different market get into contact with bats from the same source and get infected? The assumption here is that the habitat was not restricted, but freely accessed. If it was restricted then the controller should be contacted for information.

The inquiry into the origin of COVID-19 is essential to prevent the resurgence of the disease after some time so it should be highly encouraged.

Mr Jamie Metzl, thank you for the interest to conduct that research as it will contribute to preventing the likely resurfacing of that virus.

Reply

- Diane May 1, 2020 at 2:21 pm

Hi Jamie, keep up your good work. At the moment we don't know why China behaved the way it did. This makes for conspiratorial thinking. While we have the freedoms to question China's behaviour and motives we should. If our conspiratorial ideas turn out to wrong at least we shall be sure of this. Keep up the investigating,
Diane

Reply

- Jon R May 3, 2020 at 4:39 pm

I used to manage a BSL-3 virology lab. I agree the most likely explanation is a laboratory accident. If this had occurred anywhere else in China I would have believed otherwise. As stated in the article these accidents happen, for instance, a very uncommon but highly lethal infection is monkey B virus which has killed researchers in the past:

<https://www.cdc.gov/herpesvirus/cause.html>

A comment that has troubled me coming out of the Chinese government was along the lines of how their authoritarian government was superior for fighting pandemic outbreaks. This was likely a reaction to some White House comment, but China is definitely a student of history and one has to wonder what steps they would take to finally become the biggest power in the world and have the Renminbi become the world's reserve currency. The later would require an enormous debt event, which we are now facing.

Reply

- Hazel Henderson May 11, 2020 at 4:45 pm

Thank you for this very useful summary. I co- wrote an article in March, 2020 with physicist Fritjof Capra, as a global systems -oriented futurist scenario , pointing to feedback loops from natural ecosystems to our unsustainable industrial lifestyles which not only make pandemics more likely, but also relate to all the crises in natural systems resulting from fossilized sectors emissions of greenhouse gases and other pollutants..This article " Pandemics :Lessons Looking Back from 2050 " is at <http://www.ethicalmarkets.com> , which is a global alternative media Certified B.Corporation I founded and have personally funded with my book royalties and our global TV series since 2004. We take no advertising and have 30,000 professional users .We would be happy to serve pro bono as one of your " media partners".I just signed up for your Newsletter .

Reply

- Gordon Guo May 14, 2020 at 2:04 pm

Thank you so much Jamie for helping everyone to focus on the "on the record" facts, common sense, and logic.
As someone with a strong connection to China, I can say that there are identical wet

markets in every small, medium, and large city all over China with it's vast 1.3 billion population. Certainly Guangdong and Yunnan province where the suspects bats are from, 1000 miles from Wuhan, have countless such markets. Everyone please I appeal to your commonsense and try not to believe that somehow this bat virus "choose" Wuhan near the WIV of all places in all of China to jump to humans, which would be an unbelievable coincidence with no comparison in history.

On more thing that is little mentioned. is that this prolific "bat woman" coronavirus research program based out of the WIV regularly treks to bat cave in Yunnan and elsewhere to collect virus samples. So the accident itself does not necessarily have to have happened inside the WIV. Despite the requirement for full hazmat suits and virus deactivation at collection, humans make mistakes and they could have accidentally infected themselves and brought it back to Wuhan where they work and live.

A final point is that the WIV is a very new lab, only commissioned 2-3 years ago as the flagship lab in China, widely praised by state media in print and even video documentaries. It's China's first attempt at the top BSL4 security. Again, common sense: new lab, new practices = higher likelihood of accidents.

Reply

- Mook Lan Fa May 17, 2020 at 5:59 am

I didn't want to believe you at first because it's the same theory that Chump is pushing but science is science and we must get to the bottom of this! 🐼 I believe you now because you don't have a dog in the hunt and you said:

- There weren't any bats for sale;
- They would've been hibernating during that time;
- The virus was a 96.4% match;
- China has a history of poor security; and
- Although you didn't say this, I believe this theory now because Pompous said that he had significant evidence that he couldn't share with a smug look on his face. It's like he's got the smoking gun document and he's going to release it right before the election...

Anyway, what I don't understand is why you don't think the virus hasn't been genetically manipulated? I'm not a scientist, but as a layman, I have been following COVID-19 closely, and I've noticed that it has attacked in sequence:

- 1) The elderly;
- 2) Those with comorbidities;
- 3) Those with latent comorbidities — almost like it's accelerating whatever is going to kill you when you grow old;
- 4) People of color;
- 5) Now children; and
- 6) Possibly hiding and coming out later.

It's acting like a bioweapon?

Reply

- dMay 22, 2020 at 7:16 am

Hi Jamie, it's a great summary and analysis, thanks.

I'd as well add here a link to the withdrawn paper of dr. Xiao, cited as well in

<https://project-evidence.github.io/>

https://chanworld.org/wp-content/uploads/wpforo/default_attachments/1581810860-447056518-Originsof2019-NCov-XiaoB-Res.pdf

I think that this is really important for these reasons:

– I think it's the first (only?) Chinese scientist paper which tries to explain the outbreak.

Some statements are actually also pretty serious and wild like

"the killer coronavirus probably originated from a laboratory in Wuhan."

and

"In summary, somebody was entangled with the evolution of 2019-nCoV coronavirus"

– dr Xiao also hypothesized two possible ways in which the contamination might have occurred:

1) from the WHCDC to the market:

"Surgery was performed on the caged animals and the tissue samples were collected for DNA and RNA extraction and sequencing

The tissue samples and contaminated trashes were source of pathogens. They were only ~280 meters from the seafood market."

2) in another hypothesis he links a possible contamination between the WHCDC (WIV) and the adjacent Union hospital:

"The WHCDC was also adjacent to the Union Hospital where the first group of doctors were infected during this epidemic.

It is plausible that the virus leaked around and some of them contaminated the initial patients in this epidemic, though solid proofs are needed in future study. "

– and then he goes on explaining the chimeric researches performed at the WHCDC(or WIV) and why a lab accident is likely.

"The second laboratory was 12 kilometers from the seafood market and belonged to Wuhan Institute of Virology, Chinese Academy of Sciences.

This laboratory reported that the Chinese horseshoe bats were natural reservoirs for the severe acute respiratory syndrome coronavirus (SARS-CoV) which caused the 2002-3 pandemic

. The principle investigator participated in a project which generated a chimeric virus using

the SARS-CoV reverse genetics system, and reported the potential for human

emergence

. A direct speculation was that SARS-CoV or its derivative might leak from the laboratory."

p.s.

typo: the market is 280 meters away from the WDC not 3 miles

"The market is also less than 3 miles away from the Wuhan Centre"

Reply

- Werner August 4, 2020 at 4:30 am

Typo: "It ((is)) my view that Chinese researchers at these institutes were studying these viruses with the best intentions of developing surveillance systems, treatments, and vaccines for the good of humanity. "

Reply

- green August 28, 2020 at 9:52 pm

"47 million people died senselessly under former Chinese Leader Mao Tse Tung" —it is a lie.

Reply

- Betty October 16, 2020 at 10:02 pm

why does the scientific community ignore these facts? You do not have to be a corona virologist to figure this sequence of events out! It is basic detective work: the viral sequence is the equivalent of finger prints.

Reply

- Frank November 24, 2020 at 3:48 am

Jamie: Your collection of information looks like a collection of partial conspiracy theories, not one compact coherent theory of how SARS-CoV-2 came to infect humans. It seems designed to appeal to our biases and emotions, not our reason. Some particulars:

The Chinese government would be behaving exactly the same way no matter how this pandemic began: The Chinese release information that places the Communist government in a good light or that punishes individuals and organizations the government wants to blame. Any information that reflects badly on the government is suppressed. It doesn't matter if the pandemic began with the transfer of the virus to people or wild animals eaten by people in bat-infested Southern China (the logical location) or the escape of the virus from a lab in Wuhan, the Chinese government would not permit an international investigation of the origins of the pandemic. They destroyed all of the samples from the Hunan Seafood (wild animal) Market, so no one could discover what role this market played a role in the pandemic – a danger that had been

recognized from the first SARS outbreak and should have been eliminated. Some, but not all, of the December 2019 cases were linked to this wild animal market, but the earliest known case today dates apparently dates back to at least November 17, so the first transmission to humans could have occurred in this market in November or October. Alternatively, If the virus escaped from a lab, it wouldn't have made any difference if that virus evolved naturally, was the product of gain of function experiments or was produced for more nefarious purposes. We can't logically draw any reliable conclusions from China's behavior, because totalitarian governments suppress information whenever it is in their best interest. China would not want an international team discovering or confirming ANY of these possible origins.

Since SARS-CoV-2 can be transmitted by asymptomatic or mildly symptomatic infected patients, we can't be sure that the pandemic originated in Wuhan, a location where bats aren't a major problem. Two cases of COVID were identified in France in late December in 2019. Somehow, before even being identified, the virus had traveled halfway around the world, was transmitted between humans at least once in France, and the trail apparently ended. We now know the virus had infected a number of Americans in Washington (state), California, and probably elsewhere by late January without being detected – even though doctors knew what to look for by then. Given that no one was alerted to the new disease until late December 2019 and given that asymptomatic or mildly symptomatic infected patients can transmit the virus to others, Patient Zero could have been infected ALMOST ANYWHERE AND TRAVELED TO WUHAN UNDETECTED. The disease could have been transmitted between humans a number of times in less densely populated areas without leaving a detectable trail.. What probably made Wuhan special and the "origin" of the pandemic is that it may have the site of the first super-spreader events that converted the infection into an epidemic.

The viruses from the first three SARS-CoV-2 patients were genetically different, so the disease pre-dated them. Analysis of all known variants suggests that the common ancestor to known strains existed in November 2019, or possibly October. The Chinese reported a suspected infection on November 17 in the vicinity of Wuhan. The South China Morning Post obtained a report showing the government has identified hundreds or suspected cases in December in the vicinity of Wuhan. The virus likely evolved in the logical location, bat-infected Southern China, and then traveled north to Wuhan undetected in a human or wild animal. We know that all of the December cases in Wuhan were not linked to wild animal market, but the November cases might have originated there.

Of course, it is suspicious that Wuhan contained two institutions where dangerous viruses were studied, especially a new BSL 4 institution. However, Wuhan was ALSO the site of the Hunan Seafood Market, the largest wild animal market in Central China. Wuhan is bigger than New York City, where the US pandemic first exploded. Wuhan had the sophisticated medical system needed to detect a new disease and the high population density to permit rapid growth of the pandemic.. There are probably

institutes of virology half of Chinese large cities where the pandemic could have begun. There are 9 BSL 4 facilities in the US, all but one near or in a major city. There is nothing suspicious about the presence of a virology institute in the Chinese city where the pandemic began. The fact that research was being done on SARS-like viruses is also not surprising given the outbreak of SARS-CoV-1 in China two decades earlier.. News reports that US visitors to that new lab were concerned about safety were totally misrepresented; the US personnel who visited the institute reported it was being under-utilized, because a nervous Chinese government was unwilling to sanction work with dangerous viruses the facility was designed to handle and because of a shortage of trained staff. However they noted that the latter problems was being addressed by training some staff at laboratories outside the US.

"Gain of function" experiments are performed in laboratories to rapidly simulate the evolutionary process by which viruses acquire the ability to efficiently replicate in different types of cell. Such mutated viruses are studied as models of viruses that might evolve naturally and cause pandemics. Since SARS-CoV-2 was not closely related to any known SARS-like virus and appears to have arisen from recombination (not mutation) of sequences from several different coronaviruses (most likely in bats), it probably is NOT the product of a gain of function experiment. Nor does it appear to have been genetically engineered. US funding agencies stopped gain-of-function experiments for several years (including experiments in Wuhan) while experts debated whether the information gained was worth the CUMULATIVE risk of running such experiments in dozens of labs over decades. The calculated cumulative risk was small and the risk from any one laboratory in any month (Wuhan in November 2019) was microscopic. EVERY VIRAL PANDEMIC BEFORE COVID BEGAN WHEN A VIRUS THAT REPLICATED IN A SPECIES IN CLOSE CONTACT WITH HUMANS MUTATED AND ACQUIRED THE ABILITY TO REPLICATE TO THE HIGH LEVELS IN HUMANS NEEDED FOR EFFECTIVE TRANSMISSION: Swine influenza, avian influenza. HIV (from a monkey virus that causes immunosuppression), SARS-CoV-1 (pangolins), MERS (camels), measles (cattle), smallpox (rodents), chickenpox, Hepatitis (birds?) etc. It is possible – BUT CERTAINLY NOT LIKELY ENOUGH TO WARRANT SUPPORTING CONSPIRACY THEORIES – that COVID is the first man-made pandemic. No evidence that this pandemic didn't evolve like every other pandemic in history.

Reply

- David December 12, 2020 at 2:04 pm

It's a question that may never be conclusively answered: Was the SARS-CoV-2 virus inside one of the Wuhan labs (Wuhan Institute of Virology, Wuhan CDC) before the beginning of the COVID-19 pandemic?

At the start of the outbreak, Shi Zhengli, head of the WIV's centre for emerging infectious diseases, thought it was possible that the virus had come from the WIV. She admitted she was worried and said she lost sleep thinking about it. She spoke of her

relief when she checked and found no record of the virus in her lab's records. A lab-leak hypothesis is clearly not far-fetched if Shi Zhengli herself thought it was possible and was worried sick by the idea.

It's worth re-reading Shi Zhengli's quotes from Scientific American's profile of her in March 2020: "If coronaviruses were the culprit, she remembers thinking, 'Could they have come from our lab?' ... she frantically went through her own lab's records from the past few years to check for any mishandling of experimental materials, especially during disposal. Shi breathed a sigh of relief when the results came back: none of the sequences matched those of the viruses her team had sampled from bat caves. 'That really took a load off my mind,' she says. 'I had not slept a wink for days.'"

If you accept Shi Zhengli's reassurances that there was no record of the virus in her lab, the matter is closed as far as the WIV goes. But there is good reason to be sceptical.

For one thing, Shi Zhengli would not have been the one to decide whether to disclose to the world that the virus was stored in her lab. The Chinese state alone would have made that decision. And if the virus was in the lab, it is almost certain that the Chinese state would have covered it up. This is a government that recently detained up to one million Uyghurs in concentration camps and then denied the fact despite being confronted with irrefutable evidence.

And then there's the issue of the WIV virus database being deleted. Whether or not there's anything incriminating in the virus database, the decision to delete comes across as though they're hiding something. Surely the Chinese authorities must understand that their recent behaviour and their history of cover-ups makes the lab-leak hypothesis more believable.

If the virus was inside either of the labs, it does not seem likely that it will be uncovered by the WHO's investigation into the origins of the virus. Indeed, if the virus was in the labs, it may take years or decades for the facts to emerge. In time, scientists, journalists, and others will perhaps uncover conclusive evidence. Or a whistleblower in China may get the word out. Or, as happens from time to time with authoritarian regimes, future Chinese leaders may reveal the truth if they think it's in their interests to discredit their predecessors.

For now, anyone interested in the virus's origins will remain in one of three camps: 1. Convinced of natural zoonosis 2. Convinced of a lab leak 3. Undecided and awaiting more evidence.

Reply

(b)(6)

(b)(6)

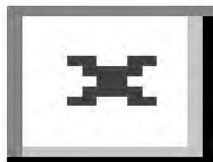


From: "Gibbs, Jeffrey J" (b)(6)@state.gov>
(b)(6)@state.gov>;
(b)(6)@state.gov>;
(b)(6)@state.gov>;
To: (b)(6)@state.gov>;
DiNanno, Thomas G (b)(6)@state.gov>;
Feith, David (b)(6)@state.gov>;
(b)(6)@state.gov>
Subject: Re: Initial analysis of Baric emails: May/June US-China VTC's on COVID-19 (SBU)
Date: Mon, 28 Dec 2020 17:09:09 +0000

This article raises some interesting questions that may be applicable to Covid-19 origin and the detection of genetic engineering.

<https://www.independentsciencenews.org/news/researchers-are-substantially->

[undercounting-editing-errors/](#)



Researchers Are Substantially Undercounting Gene-Editing Errors, Concludes a New Paper - Independent Science News

by Jonathan Latham, PhD. The standard gene-editing tool, CRISPR-Cas9, frequently produces a type of DNA mutation that ordinary genetic analysis misses, claims new research published in the journal Science Advances. In describing these findings the researchers called such oversights "serious pitfalls" of gene editing (Skryabin et al., 2020). In all, the new results suggest that gene-editing ...

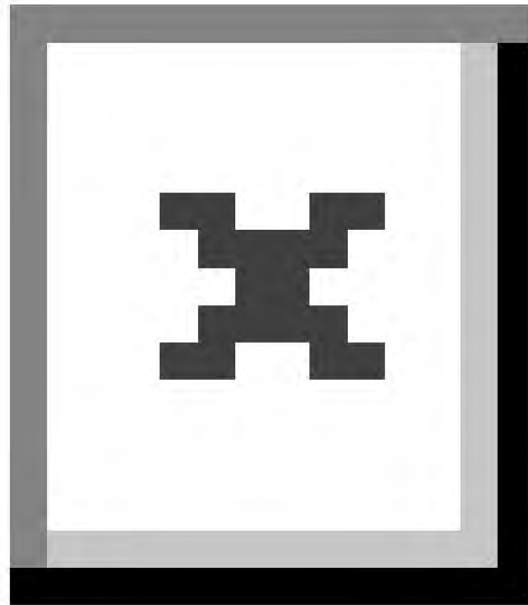
Researchers Are Substantially Undercounting Gene-Editing Errors, Concludes a New Paper

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by Jonathan Latham, PhD

The standard gene-editing tool, CRISPR-Cas9, frequently produces a type of DNA mutation that ordinary genetic analysis misses, claims new research published in the journal *Science Advances*. In describing these findings the researchers called such oversights “serious pitfalls” of gene editing ([Skryabin et al., 2020](#)). In all, the new results suggest that gene-editing is more error-prone than thought and, further, that identifying and discarding defective and unwanted outcomes is not as easy as generally supposed.

Derived originally from the bacterium *streptococcus pyogenes*, CRISPR-Cas9 is a DNA cutting and targeting system. CRISPR stands for clustered regularly interspaced short palindromic repeats and refers to the RNA molecule that is the targeting component of the system. This CRISPR RNA is sometimes also referred to as the guide RNA. The Cas9 component is a nuclease, that is, an enzyme that cuts DNA. Thus, in the editing process, the Cas9 enzyme is guided to the intended cut site by the CRISPR RNA. The whole assembly is often just called CRISPR.



CRISPR Enzyme on DNA (Photo: MIT News)

Other gene-editing methods exist (e.g. Zn Finger, TALENs). However, because of the flexibility of its RNA targeting mechanism, CRISPR in particular has been the subject of enormous excitement in the biotech and agricultural research sectors.

CRISPR has mostly been used to create genetic mutations or to insert foreign DNA at desired locations in a genome. Nevertheless, other applications, like gene drives, have also been mooted. Despite the excitement, as Friends of the Earth has summarised, just a tiny handful of commercial gene-edited products can be found on the market.

For many uses, however, gene-editing with CRISPR is insufficiently precise and a great deal of research is currently oriented towards fixing this defect.

Much of CRISPR's lack of precision derives from the fact that, though it is called 'editing', CRISPR and related techniques are cutting enzymes only. They have no DNA repair function. This means that when repairs are made to the DNA at the cut site (and the cut *must* be repaired for the cell to survive) they are largely out of the control of the experimenter. Ten independent editing events will therefore give ten different mutations at the same location in the genome.

Thus, at a very basic level, each mutation created at the target site is likely to be unique. Even to the extent, as we reported, that DNA from other species may end up being unexpectedly incorporated into the edited genome.

To add to this uncertainty, different genome locations, different cell types, different species, and different versions of CRISPR, can all influence the kinds of genetic alteration found at the target site.

In some applications—primarily basic research—lack of precision of this kind is not necessarily a major problem. In crop breeding, for example, cells or organisms containing undesirable alterations or off-target mutations can, in theory, be detected and discarded.

But in many applications, primarily in medicine and commercial products, only more-or-less-complete precision is acceptable, for reasons of safety. Inaccurate editing of human cells in an early gene therapy trial once resulted in 2 of 11 treated children developing leukaemia due to off-target effects and led to the trial being shut down.

The question of whether researchers and/or developers of edited organisms could or would adequately detect and discard undesirable mutations is a live concern. Recombinetics is a commercial company that, in 2016, created a hornless cow it claimed was the intended result of a precise gene edit. But FDA researchers who examined the company's own DNA sequence data were subsequently able to show that both of the independently edited calves contained, at the site of the edit, entire antibiotic resistance genes (Norris et al., 2020).

By the time FDA was able to show this, however, offspring of the calves were already incorporated into a Brazilian breeding program. This breeding program has now been abandoned.

The new research, published on Feb 12th, directly addresses whether CRISPR researchers can, in fact, detect aberrant edits.

The German and Chinese researchers edited mouse oocytes (i.e. embryos) with the added step (compared to simple cutting) of adding a stretch of DNA (the donor DNA) which they hoped would become integrated at the cut site.

What they unexpectedly found, however, is that, at a high proportion of target sites, complex insertions of the desired DNA occurred. Rather than simply integrating single copies of the donor DNA into the cut site, DNA integrations were commonly head-to-tail arrangements of multiple copies. As the paper states:

"Overall, we conclude that the repetitive head-to-tail integration of the donor DNA template is a common by-product of the CRISPR-Cas9-mediated HDR-based genome editing process,

regardless of the donor DNA template size, sequence composition, or strandedness of the template (dsDNA or ssDNA).” [editor’s note: ds=double stranded; ss=single stranded]

By ‘common’ the researchers meant that, in one experiment, among 34 edited mice, six contained head-to-tail insertions. In other experiments 30 of 49 mice contained head-to-tail insertions.

In other words, complex and aberrant DNA insertions were common findings. Importantly, they occurred in multiple experiments, meaning this seems to be true regardless of what DNA was inserted or which stretch of the genome it was inserted into. This in itself is a very significant finding.

Even more notable, however, was that these complex genetic rearrangements were rarely detected by standard analytical methods. The authors called this finding “disturbing”.

They wrote:

“conventionally applied PCR analysis, in most cases, failed to identify these multiple integration events, which led to a high rate of falsely claimed precisely edited alleles.”

Undetected, such aberrant events “would undermine the validity of studies” according to the authors.

In experimental settings this is undoubtedly true. But for the general public a more important implication exists. With companies and biohackers hoping to bring genome-edited products rapidly (and without regulatory scrutiny) to the market, this research represents a significant cautionary tale; especially since the authors speculate that their results probably apply equally to other editing methods, such as TALENs and Zn Finger nucleases.

References

Boris V. Skryabin, Delf-Magnus Kummerfeld, Leonid Gubar, Birte Seeger, Helena Kaiser et al. (2020) Pervasive head-to-tail insertions of DNA templates mask desired CRISPR-Cas9–mediated genome editing events. *Science Advances* 6 eaax2941 DOI: 10.1126/sciadv.aax2941

If this article was useful to you please consider sharing it with your networks.

Jeff Gibbs

Senior Adviser AVC

SSD/AVC

(b)(6)

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

Sent: Monday, December 28, 2020 8:06 AM

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

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

Gibbs, Jeffrey J (b)(6)@state.gov>; (b)(6)@state.gov>

Subject: RE: Initial analysis of Baric emails: May/June US-China VTC's on COVID-19 (SBU)

I'm in the office.



(b)(6)

Chief of Staff
Bureau of Arms Control, Verification and Compliance
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OpenNet: (b)(6)@state.gov

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

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

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

Sent: Sunday, December 27, 2020 9:55 PM

To: (b)(6)@state.gov>; (b)(6)@state.gov>; DiNanno, Thomas G
(b)(6)@state.gov>; Feith, David (b)(6)@state.gov>; Gibbs, Jeffrey J (b)(6)@state.gov>;

(b)(6)@state.gov>

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

Subject: Re: Initial analysis of Baric emails: May/June US-China VTC's on COVID-19 (SBU)

(b)(6) If you happen to go in tomorrow, I recommend you work with (b)(6) and David F on a short fuse "Coliseum request." (b)(5)

(b)(5)

(b)(5)

(b)(6)

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

Sent: Sunday, December 27, 2020 9:37 PM

To: (b)(6)@state.gov; (b)(6)@state.gov; DiNanno, Thomas G (b)(6)@state.gov; Feith, David (b)(6)@state.gov; Gibbs, Jeffrey J (b)(6)@state.gov; (b)(6)@state.gov
Cc: (b)(6)@state.gov
Subject: Re: Initial analysis of Baric emails: May/June US-China VTC's on COVID-19

Awesome context, as always (b)(5)

(b)(5)

From: (b)(6)@state.gov
Sent: Sunday, December 27, 2020 8:54 PM
To: (b)(6)@state.gov; (b)(6)@state.gov; DiNanno, Thomas G (b)(6)@state.gov; Feith, David (b)(6)@state.gov; (b)(6)@state.gov; (b)(6)@state.gov
Cc: (b)(6)@state.gov; (b)(6)@state.gov
Subject: Re: Initial analysis of Baric emails: May/June US-China VTC's on COVID-19

Under **WIV's Microbial Resources and Bioinformatics Research Center**, there are 6 groups:

1. Virus Resources and Biotechnology Subject Group (病毒资源与生物技术学科组),
2. Applied Microbiology and Genetic Engineering Subject Group (应用微生物与基因工程学科组),
3. System Virology Group (系统病毒学学科组),
4. Insect Virus Genetic Engineering Group (昆虫病毒基因工程学科组),
5. Molecular Virology and Bioengineering Technology Group (分子病毒学及生物工程技术学科组),
6. **Arbovirus Vector Control Subject Group** (虫媒病毒媒介控制学科组, headed by **Yuan Zhi-Ming**)

To carry out arbovirus detection and biological control of vector mosquitoes.

Focuses on the rapid detection of dengue virus, Japanese encephalitis virus and West Nile virus and the interaction between the virus and the host, mosquito pathogenic microorganisms and their genetic resources, microbial genomics and comparative genomics, and mosquito toxin protein characteristics and the mode of action, the genetic improvement of mosquito-killing bacteria and the construction of engineered strains, the development of new bacterial mosquito-killing preparations and the assessment of the environmental safety of wild-type and recombinant microorganisms, etc., develop new biological control technologies, and establish and perfect biological control Integrated control system for mosquitoes based on arboviruses.

From: (b)(6)@state.gov>
Sent: Sunday, December 27, 2020 7:13 PM
To: (b)(6)@state.gov>; DiNanno, Thomas G (b)(6)@state.gov>; Feith, David (b)(6)@state.gov>; Gibbs, Jeffrey J (b)(6)@state.gov>; (b)(6)@state.gov>
Cc: (b)(6)@state.gov>; (b)(6)@state.gov>
Subject: Re: Initial analysis of Baric emails: May/June US-China VTC's on COVID-19

Please run

, Director WIV Lev 4 Lab, to ground ASAP (b)(6) Can you look into this person? Thanks very much!

From: (b)(6)@state.gov>
Sent: Sunday, December 27, 2020 12:46 PM
To: DiNanno, Thomas G (b)(6)@state.gov>; Feith, David (b)(6)@state.gov>; Gibbs, Jeffrey J (b)(6)@state.gov>; (b)(6)@state.gov>
Cc: (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>
Subject: Initial analysis of Baric emails: May/June US-China VTC's on COVID-19

Reference my last note below, attached is the relevant raw OCR'd text recovered from Baric's emails documenting his participation in a series of two US National Academy of Science – Chinese Academy of Science VTCs in May and one in June on the subject of COVID-19.

Initial summary of findings:

- Context: These brief verbal exchanges occurred months after the PRC had successfully conquered the pandemic and prevented any meaningful exchange of data and scientific collaboration, meanwhile most of the rest of the world is still trying unsuccessfully to deal with the pandemic.
- Dates of the three two-hour VTCs: 11 and 13 May, 9 June.
- Purpose: *"to discuss what has been learned thus far from the pandemic, how to mitigate its impact, and preventing future pandemics."* (Note: subject of SARS-CoV-2's origin was off the table from the very beginning of the planning sessions, so was anything else that might be deemed "political")
- Unstated purpose: to allow the PRC to maintain the façade of cooperation while preventing any meaningful exchange of data and any inquiry into COVID-19's origin that might be unfavorable to the regime, and some of the VTC participants.
- CAS allowed the US to use the Zoom record feature to produce a transcript of the call. In return the US approved the following PRC press release. Here's an approved draft of the PRC version of events:

○

Scientists from China and US Share Experience in COVID-19 Prevention and Control

About 30 scientists from China and the United States held an online dialogue to share their experience in COVID-19 prevention and control and opinions on the prevention of future pandemic on May 12th and 14th (Beijing time). The virtual dialogue was jointly organized by the Chinese Academy of Sciences (CAS), the National Academy of Sciences (NAS) and the National Academy of Medicine (NAM). Participants shared their experience in fighting against COVID-19 and exchanged views on such topics as clinical issues related to treatment and management of patients, and limiting the spread of COVID-19 and steps towards restarting society.

COVID-19, an infectious disease caused by the most recently discovered coronavirus, has so far spread to 216 countries, areas and territories, with over 4.5 million confirmed cases and claiming 300 thousand deaths globally, according to the World Health Organization. "The pandemic will not really be controlled in any country, until it is ultimately controlled in every country. So it's in our mutual interest to do our best to learn as rapidly and as effectively as we can from one another," said Dr. Harvey Fineberg, President of the Gordon and Betty Moore Foundation, one participant of the dialogue.

Experts taking part in the dialogue agreed that it is of great importance to have a discussion to promote exchanges between the scientific communities of the two countries. "It's an extension of a dialogue that's been going between scientists in China and the U.S. We are very happy to be able to continue this dialogue in this time when actually all the work we are doing becomes very important," said Diane Griffin, Vice President of NAS, in the dialogue. Dr. George F. Gao, convener from the Chinese side, Director-General of the Chinese Center for Disease Prevention and Control, said, "This is a great dialogue. We hope that both sides could continue to organize dialogues like this, and contribute to the global efforts in fighting against the COVID-19 pandemic from the scientific perspective."

- Notable participants included Baric, Daszak, Shi and Yuan (WIV leaders)
- The agenda items listed below speak volumes IMHO given:
 - This is the first such exchange we are aware of, six months into a devastating pandemic and the US is still struggling with these questions
 - Discussion of such critical and sweeping issues is limited to a 6-hour exchange between a couple dozen US and PRC personnel
 - The PRC has continued to prevent direct access to raw data and collaboration between scientists.
 - The only alternative has been to wait for PRC-government sanctioned academic papers and misleading press releases to emerge.

- Issues discussed:

Day 1

Introductory remarks and group introductions

- o China situational overview

- o U.S. situational overview

Clinical Issues Related to Treatment and Management of Patients

Clinical manifestations of COVID-19 disease:

- o What range of clinical, end-organ, organ, and other body system manifestations of disease has been documented in China

Influence of Patient Characteristics:

- o How did patient age, gender, general health condition, or other characteristics influence the efficacy of drugs, NPIs, or best practices?

- o How was this determined?

Protection of Medical Personnel:

- o What measures have proven most effective in [text not recovered by OCR]

Drug Treatments:

- o What has been the Chinese experience with developing drug treatments or using existing drugs in treatment of patients, from prophylaxis to pre-symptomatic patients to patients with severe symptoms?

Non-pharmaceutical Interventions:

- o Were effective non-pharmaceutical interventions (NPIs) for patient care identified?

- o Were there other best practices for management of COVID-19 patients that emerged from the pandemic experience?

Immune plasma:

- o What is China's experience in using immune plasma or other antibody-based therapies in the treatment of COVID-19 patients or prevention of further spread of disease?

Lessons Learned:

- o Were other lessons learned from China's pandemic experience that should be applied to future staffing and equipping of hospitals or other patient care facilities?

Future Collaboration:

- o What are the most fruitful areas of future scientific collaborations between our countries in this area?

Day 2

Viral shedding:

- o What is the degree of shedding among pre-symptomatic/asymptomatic individuals?

- o Do recovered patients continue to shed infectious virus? If yes, for how long?

- o Has post-infection viral shedding been demonstrated to result in new infections?

- o Has an explanation regarding pathogenesis leading to apparent recrudescence of disease in previously positive, then negative patients been arrived at?

Immune response:

- o How is immune response being measured? Is it via binding assays versus neutralization tests, use of antibody assays in diagnosis of acute disease and as an indicator of protection?

- o Was there standardization of your testing tools?

- o Immunity: After recovery, do patients have immunity? How protective is this immunity?

o Is there indication of persistence of such immunity?

Vaccines:

o Has the Chinese research community made progress in the development of COVID-19 vaccines?

Exposure routes:

o Has progress been made in understanding the routes of exposure to COVID-19 air, water, and surfaces, both indoors and outdoors?

Contact with Animals:

o Would increased surveillance of or interventions to reduce contact with pets, wild, or livestock animal species help limit the future spread of COVID-19 or other coronaviruses?

Halting Spread:

o What measures have proven most effective in halting viral spread in China?

Preventing a Fall Resurgence:

o What steps should be taken in anticipation of a fall resurgence in transmission?

Reestablishing Normality:

o What lessons has China learned about returning society and the economy to a "normal" state?

Future Collaboration:

o What are the most fruitful areas of future scientific collaborations between our countries in this area?

Day 3 (June 9)

Immune Response and Immunotherapy

o Use of antibody assays in diagnosis of acute disease and as an indicator of protection

o How is immune response being measured?

o Was there standardization of testing tools?

o What is the overall situation of serologic investigation in the US?

o What can be said about the characterization of the

Innate immune responses?

humoral immune response?

cellular immune response?

o What is China's experience in using immune plasma or other antibody-based therapies for COVID-19 patients and for prevention of infection?

o Is the use of immune plasma effective?

o Have there been any complications?

o What has been China's experience with human monoclonal antibodies for treatment and prevention?

o Do a majority of the monoclonal antibodies isolated from patient B cells produce neutralizing antibodies?

o What immunopathologies are evident in the patients with COVID-19?

o Are there any biomarkers in patients who develop systemic inflammation?

o What is the most effective treatment for patients who develop a cytokine storm?

Immunity

o After recovery, what types of antiviral immune responses are present?

o Do these immune responses protect from re-infection?

- o What is known about the durability of neutralizing antibody and longevity of protective immunity?
- o Did recovery from SARS provide any protection from infection with SARS-CoV-2?
- o Progress in the development of vaccine in the U.S. especially mRNA vaccine?
- Reactivation or Reinfection of Recovered Patients, Fall resurgence
- o Has reactivation of latent virus or re-infection been seen among survivors?
- o Is reactivation/reinfection a concern with respect to a fall resurgence?
- o What steps should be taken in anticipation of a fall resurgence in transmission?
- o What is the COVID-19 prevention and control strategy in the US for the second half of this year?
- o When do you expect COVID-19 vaccine to be available in the U.S.?

- Chinese Participants included

- Zhu Chen: Dr. Zhu Chen is president of the Red Cross Society of China, CAS member. He was previously minister of the National Health Commission of China. (Only available on the 14th)
- George F. Gao: Dr. George F. Gao is Director-General of CCDC, a professor at the CAS Institute of Microbiology, CAS member.
- Dongfeng Gu: Dr. Dongfeng Gu is vice president of Southern University of Science and Technology, CAS member.
- Hualiang Jiang: Dr. Hualiang Jiang is currently a professor at CAS Shanghai Institute of Materia Medica (SIMM), CAS member. He was previous director of SIMM, and now he is the chairman of the Scientific Committee of the institute. His research focuses on drug discovery and development. (Only available on the 12th)
- Lanjuan Li: Dr. Lanjuan Li is a physician and professor in infectious diseases, a member of the Chinese Academy of Engineering. She is currently director of the State Key Laboratory for Diagnosis and Treatment of Infectious Diseases. (Only available on the 12th)
- Zhengli Shi: Dr. Zhengli Shi is a professor at CAS Wuhan Institute of Virology.
- Chen Wang: Dr. Chen Wang is vice president and a member of the Chinese Academy of Engineering, and president of the Chinese Academy of Medical Sciences. (Only available on the 14th)
- Guiqiang Wang: Dr. Guiqiang Wang is a professor at the Peking University First Hospital and is president of the Society of Infectious Diseases, Chinese Medical Association. (Only available on the 12th)
- Haiming Wei: Dr. Haiming Wei is a professor at the University of Science and Technology of China.
- Zhiming Yuan: Dr. Zhiming Yuan is a professor at CAS Wuhan Institute of Virology, Director of Wuhan P4 lab.

- Yongqing Zhang: Dr. Yongqing Zhang is Deputy Director-General of CAS Bureau of Frontier Sciences and Education, a professor at CAS Institute of Genetics and Developmental Biology. (Only available on the 12th)
- Guoping Zhao: Dr. Guoping Zhao is a professor at CAS Shanghai Institutes for Biological Sciences, CAS member.
- Qi Zhou: Dr. Qi Zhou is Deputy Secretary-General of CAS, Director of CAS Institute of Zoology, CAS member. (Only available on the 12th)
- US Participants included
 - Ralph Baric: Dr. Ralph Baric, PhD, is a Professor in the Department of Epidemiology at the University of North Carolina's School of Public Health.
 - Peter Daszak: Dr. Peter Daszak, PhD, is president of EcoHealth Alliance, a nonprofit non-governmental organization that supports various programs on global health.
 - Victor Dzau: Dr. Victor Dzau, MD, is currently president of the U.S. National Academy of Medicine of the U.S. National Academy of Sciences, Engineering and Medicine. He was previously the president and CEO of Duke University Medical Center.
 - David Franz: Dr. David R. Franz, DVM, PhD, is currently retired, but served in the U.S. Army Medical Research and Materiel Command for 23 of 27 years on active duty and as Commander of the U.S. Army Medical Research Institute of Infectious Diseases (USAMRIID).
 - Harvey Fineberg: Dr. Harvey Fineberg, MD, is currently president of the Gordon and Betty Moore Foundation, immediately prior to which he was President of the Institute of Medicine (now the National Academy of Medicine).
 - Diane Griffin: Dr. Diane Griffin, MD, PhD, is University Distinguished Service Professor in the W. Harry Feinstone Department of Molecular Microbiology and Immunology at Johns Hopkins Bloomberg School of Public Health and the current vice-president of the U.S. National Academy of Sciences.
 - Peggy Hamburg: Dr. Margaret (Peggy) Hamburg, MD, is an American physician and public health administrator. She served as the 21st Commissioner of the U.S. Food and Drug Administration from May 2009 to April 2015 and is currently foreign secretary for the U.S. National Academy of Medicine.
 - James Le Duc: Dr. James Le Duc, PhD, is the director of the Galveston National Laboratory, professor, Microbiology and Immunology and the John Sealy Distinguished Chair in Tropical and Emerging Virology, University of Texas Medical Branch, Galveston Texas.
 - Stanley Perlman: Dr. Stanley Perlman, MD, PhD, is Professor of Microbiology and Immunology and of Pediatrics at the University of Iowa Health Care.
 - David Relman: Dr. David Relman, MD, PhD is a microbiologist and the Thomas C. and Joan M. Merigan Professor in Medicine and in Microbiology & Immunology at the Stanford University School of Medicine.
 - Linda Saif: Dr. Linda J. Saif, PhD, is Distinguished University Professor, Department of Veterinary Preventive Medicine, Food Animal Health Research Program, Ohio Agricultural Research and Development Center of the Ohio State University.

- Pei-Yong Shi: Dr. Pei-Yong Shi, PhD, is I.H. Kempner Professor of Human Genetics, University of Texas Medical Branch, Galveston Texas.

From: Pease, Michael

Sent: Saturday, December 26, 2020 5:17 PM

To: DiNanno, Thomas G. (b)(6)@state.gov>; Feith, David (b)(6)@state.gov>; Gibbs, Jeffrey J (b)(6)@state.gov>; (b)(6)@state.gov>

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

Subject: Baric UNC FOIA Emails Update

First, the bad news: UNC's or Baric's lawyers did what most lawyers do when responding to FOIA requests - i.e., they purposefully converted all emails to low resolution image files. This makes it very hard to convert them back to usable text. Consequently we get a higher percentage of misidentified letters, numbers and symbols (aka "noise") during the OCR process.

Now for the good news: The techs at Sayari did a great job of OCRing the huge set of PDF image files, although there is still a significant amount of noise in the text to contend with. From the resulting 89 raw text files (76MB) I was able to isolate at least 2,141 emails within about 200 threads spanning dates from October 2017 through 30 July 2020.

Of note, as highlighted below:

- Baric was involved in hundreds of "Red Dawn" emails about the pandemic involving USG officials starting around 22 January.
- It appears that there may have been at least three virtual meetings involving Baric with Chinese scientists in May and June (will take a look at those emails).
- Baric may have been working with DTRA in early 2019.
- Baric may have been a source for INR regarding the origins of COVID-19 (7 emails between 23 and 25 March - will take a look at those emails).

More to follow.

Here is a summary table of unique subject lines/threads harvested from the text files:

Thread Subject Text	Emails	Days	Earliest Thread Email	Latest Thread Email	Found In
Collaborative coronavirus discussion invitation	1	1	1/10/2017	1/10/2017	1-1-1000.txt
nice work !!!!!!!	2	1	2/15/2017	2/15/2017	1-1-1000.txt
Zika in SE Asia	1	1	4/19/2017	4/19/2017	1-1-1000.txt
Nido2017 invited speakers	1	1	4/25/2017	4/25/2017	1-1-1000.txt
Professorship Virology, Berlin	1	1	5/10/2017	5/10/2017	1-1-1000.txt

Nido2017 Oral Presentation	1	1	5/26/2017	5/26/2017	1-1-1000.txt
Nido2017 Group Photo	1	1	6/7/2017	6/7/2017	1-1-1000.txt
Nido2017 Gala Dinner	1	1	6/8/2017	6/8/2017	1-1-1000.txt
Nido2017 Gala Dinner at the Grand Hall	1	1	6/8/2017	6/8/2017	1-1-1000.txt
Thank you for attending Nido2017	1	1	6/15/2017	6/15/2017	1-1-1000.txt
CETR Program Information	1	1	6/23/2017	6/23/2017	1-1-1000.txt
Nido2017 Photo Gallery	1	1	7/3/2017	7/3/2017	1-1-1000.txt
IDEA team photo	1	1	7/13/2017	7/13/2017	1-1-1000.txt
NBIC Biosurveillance Presentation Series	9	6	7/13/2017	7/18/2017	1-1-1000.txt
NBIC Biosurveillance Presentation Series info for presenters	2	2	7/18/2017	7/19/2017	1-1-1000.txt
Talk	2	1	7/19/2017	7/19/2017	1-1-1000.txt
Virology Special Issue Presubmission Deadline is Aug 18, 2017	1	1	8/14/2017	8/14/2017	1-1-1000.txt
CEPI invitation to vaccine R&D pipeline and cost tracking survey against epidemic infectious diseases	1	1	9/27/2017	9/27/2017	1-1-1000.txt
NAS GNL invitation to participate in a meeting of U.S. and Chinese experts, Jan 16-18 2018	1	1	11/2/2017	11/2/2017	1-1-1000.txt
NAS mtg in Galveston	2	2	11/10/2017	11/11/2017	1-1-1000.txt
RFA-AI-17-042: Centers of Excellence for Translational Research (CETR)	1	1	12/1/2017	12/1/2017	1-1-1000.txt
Flight arrangements to Galveston for NAS/Chinese Academy meeting Jan. 16-18	7	3	12/18/2017	12/20/2017	1-1-1000.txt
Happy Holidays from Virologica Sinica!	1	1	12/22/2017	12/22/2017	1-1-1000.txt
US-China meeting in Galveston	2	3	1/3/2018	1/5/2018	1-1-1000.txt
Agenda and travel info for upcoming Galveston, Texas meeting	1	1	1/12/2018	1/12/2018	1-1-1000.txt
Two tenure track assistant professor positions at Duke-NUS EID	1	1	1/17/2018	1/17/2018	1-1-1000.txt
Thank You!	2	1	1/19/2018	1/19/2018	1-1-1000.txt
EcoHealth Alliance - W9	1	1	1/24/2018	1/24/2018	1-1-1000.txt
Nice meeting you in Galveston and invitation to Wuhan meeting in October 2018	2	1	2/7/2018	2/7/2018	1-1-1000.txt
Ralph's upcoming visit	1	1	2/23/2018	2/23/2018	1-1-1000.txt
trip to new york	2	1	3/6/2018	3/6/2018	1-1-1000.txt
"Baric Dinner" has been canceled.	1	1	3/6/2018	3/6/2018	1-1-1000.txt
"Baric Dinner" has been canceled.	1	1	3/6/2018	3/6/2018	1-1-1000.txt
[RESCHEDULED] Call with Peter - now on 3/15	1	1	3/12/2018	3/12/2018	1-1-1000.txt
dual use safety language	1	1	3/23/2018	3/23/2018	1-1-1000.txt

Visit to UNC	1	1	3/28/2018	3/28/2018	1-1-1000.txt
Invitation Letter for the 8th International Symposium on Emergin Viral Diseases	5	140	4/14/2018	8/31/2018	1-1-1000.txt
visit	1	1	4/23/2018	4/23/2018	1-1-1000.txt
Information for ICEID 2018 Plenary and Panel Speakers	1	1	8/10/2018	8/10/2018	1-1-1000.txt
Thank you for speaking at ICEID	2	1	8/30/2018	8/30/2018	1-1-1000.txt
Abstract for Wuhan meeting	1	1	9/24/2018	9/24/2018	1-1-1000.txt
International Symposium on Emerging Viral Diseases, Wuhan	4	10	9/30/2018	10/9/2018	1-1-1000.txt
Final Program of the 8th International Symposium on Emerging Viral Diseases	1	1	10/15/2018	10/15/2018	1-1-1000.txt
NASEM bio meetings in Harbin, China in Jan 2019?	4	4	11/13/2018	11/16/2018	1-1-1000.txt
Visa information for NAS January trip to Harbin, China	1	1	11/28/2018	11/28/2018	1-1-1000.txt
NASEM bio meetings in Harbin, China in Jan 2019 - update and conference call	1	1	12/11/2018	12/11/2018	1-1-1000.txt
NASEM bio meetings in Harbin, China in Jan 2019 - conference call on 12/18 at 2 PM ET	1	1	12/14/2018	12/14/2018	1-1-1000.txt
NASEM bio meetings in Harbin, China in Jan 2019 - conference call on 12/18 at 2 PM ET docs	2	1	12/17/2018	12/17/2018	1-1-1000.txt
NASEM bio meetings in Harbin, China in Jan 2019 - travel memo and final agenda	1	1	1/3/2019	1/3/2019	1-1-1000.txt
new call from DTRA	1	1	1/3/2019	1/3/2019	1-1-1000.txt
National Academies Travel Reimbursement: Harbin 2019 meeting	1	1	1/11/2019	1/11/2019	1-1-1000.txt
postdoctoral position available at the Virus Ecology Unit, Rocky mountain Laboratories, NIAID	1	1	1/14/2019	1/14/2019	1-1-1000.txt
National Academies Travel Reimbursement: Harbin 2019 meeting - docs and photos	1	1	1/17/2019	1/17/2019	1-1-1000.txt
Ralph's visit to Columbia	3	1	3/20/2019	3/20/2019	1-1-1000.txt
new coronavirus from Wuhan	6	2	1/9/2020	1/10/2020	1-1-1000.txt
Rg novel coronavirus	2	12	1/10/2020	1/21/2020	1-1-1000.txt
Wuhan outbreak	5	9	1/20/2020	1/28/2020	1-1-1000.txt
{EXTERNAL} 2019-nCoV	1	1	1/22/2020	1/22/2020	1-1-1000.txt
2019-nCoV	10	8	1/22/2020	1/29/2020	1-1-1000.txt
2019-nCov	2	4	1/23/2020	1/26/2020	1-1-1000.txt
Wolverines 2019-nCoV Call	1	1	1/26/2020	1/26/2020	1-1-1000.txt

Red Dawn Call Listening Session 2019-nCoV Call	139	20	1/26/2020	2/14/2020	1-1-1000.txt 1-1001-2000.txt 1-2001-3000.txt 1-3001-4000.txt 1-4001-5000.txt 9-6001-7000.txt
2019-nCoV	18	3	1/28/2020	1/30/2020	1-1-1000.txt
Red Dawn: Wolverines 2019-nCoV Call is open	3	1	1/29/2020	1/29/2020	1-1-1000.txt
deadline question re: Virology paper/for publication in San Jose Mercury News/Bay Area News Group	1	1	1/30/2020	1/30/2020	1-1-1000.txt
Red Dawn Call Listening Session 2019-nCoV Call,	3	1	2/2/2020	2/2/2020	1-1-1000.txt
Red Dawn Call Listening Session 2019-nCoV Call	12	9	2/2/2020	2/10/2020	1-1-1000.txt 1-1001-2000.txt 1-2001-3000.txt
Reminder - Invitation to the Global Research and Innovation Forum: Towards a Roadmap for the 2019 Novel Coronavirus	1	1	2/3/2020	2/3/2020	1-1-1000.txt
2019-nCoV in kids--the dog that didn't bark	1	1	2/3/2020	2/3/2020	1-1-1000.txt
Reminder - Invitation to the Global Research and Innovation Forum: Towards a Roadmap for the 2019 Novel	1	1	2/3/2020	2/3/2020	1-1-1000.txt
{EXTERNAL} Red Dawn Call Listening Session 2019-nCoV Call	1	1	2/4/2020	2/4/2020	1-1001-2000.txt
URGENT: Please review by NOON if at all possible...	10	1	2/4/2020	2/4/2020	1-1-1000.txt 1-1001-2000.txt
Link to documents on prioritisation of vaccines documents	1	1	2/5/2020	2/5/2020	1-1001-2000.txt
please use -	1	1	2/5/2020	2/5/2020	1-1001-2000.txt
Thanks and News about the letter	1	1	2/7/2020	2/7/2020	1-1001-2000.txt
nCoV-2019	4	1	2/8/2020	2/8/2020	1-1001-2000.txt
nCoV-2019	3	1	2/8/2020	2/8/2020	1-1001-2000.txt

ACE/ACE2	1	1	2/10/2020	2/10/2020	1-2001-3000.txt
Red Dawn COVID-2019	5	1	2/13/2020	2/13/2020	1-3001-4000.txt
Isolation and Quarantine for HCWs	25	2	2/14/2020	2/15/2020	1-4001-5000.txt
Isolation and Quarantine for HCWS	4	2	2/14/2020	2/15/2020	1-4001-5000.txt
Flash!!! Red Dawn Call Saturday Air Evacuation--What Time works??	15	1	2/15/2020	2/15/2020	1-4001-5000.txt
Flash!! Red Dawn Call Air Evacuation Risk Mitigation Measures	2	1	2/15/2020	2/15/2020	1-4001-5000.txt
Flash!! Red Dawn Call Detection Kits, Disease Characterization	1	1	2/15/2020	2/15/2020	1-5001-5508.txt
Red Dawn Breaking, COVID-19	11	3	2/16/2020	2/18/2020	1-5001-5508.txt 2-2001-3000.txt
Red Dawn Breaking, COVID-19 Collaborative, Feb 16	15	7	2/16/2020	2/22/2020	1-5001-5508.txt 2-1-1000.txt 2-2001-3000.txt
Red Dawn Breaking, COVID-19 Collaborative, Feb 16 start	137	9	2/16/2020	2/24/2020	1-4001-5000.txt 1-5001-5508.txt 2-1-1000.txt 2-1001-2000.txt 2-2001-3000.txt
Time to chat about coronavirus?	3	2	2/17/2020	2/18/2020	1-4001-5000.txt
Red Dawn Breaking, COVID-19 Collaborative, Feb 16 start --- Rapid testing vs Safe and compliant quarantine -	1	1	2/21/2020	2/21/2020	2-1-1000.txt
Red Dawn Breaking, COVID-19 Collaborative, Feb 16 start -- asymptomatic vs symptomatic, flu vs COVID-19	1	1	2/24/2020	2/24/2020	2-2001-3000.txt
Red Dawn Breaking Bad, Start	2	2	2/24/2020	2/25/2020	2-3001-4000.txt

Red Dawn Breaking Bad, Start Feb 24	121	7	2/24/2020	3/1/2020	2-2001-3000.txt 2-3001-4000.txt 2-4001-5000.txt 2-5001-6000.txt
Red Dawn Rising Start Feb 29	124	5	2/29/2020	3/4/2020	2-5001-6000.txt 2-6001-6093.txt 3-1-1000.txt
Restricted Wolverine Call Sunday Evening (today) at 8 PM EST	2	1	3/1/2020	3/1/2020	3-1-1000.txt
Updated Travel Policy and Meeting Guidelines in Response to Coronavirus	1	1	3/3/2020	3/3/2020	3-1-1000.txt
Red Dawn Rising Start Feb 29 -- Evidence of how NPI works --	1	1	3/4/2020	3/4/2020	3-1-1000.txt
Red	2	1	3/5/2020	3/5/2020	2-2001-3000.txt 3-5001-6000.txt
Red Dawn Raging Start March	6	8	3/5/2020	3/12/2020	3-5001-6000.txt 4-8001-9000.txt
Red Dawn Raging Start	16	9	3/5/2020	3/13/2020	3-5001-6000.txt 4-1-1000.txt 4-1001-2000.txt 4-13001-14000.txt 4-2001-3000.txt 4-3001-4000.txt 6-1-1000.txt 7-10001-11000.txt 7-8001-9000.txt

					3-1-1000.txt
					3-1001-2000.txt
					3-2001-3000.txt
					3-3001-4000.txt
					3-4001-5000.txt
					3-5001-6000.txt
					3-6001-6626.txt
					4-1-1000.txt
					4-10001-11000.txt
					4-1001-2000.txt
					4-11001-12000.txt
					4-12001-13000.txt
					4-13001-14000.txt
Red Dawn Raging Start March 4	204	12	3/5/2020	3/16/2020	4-2001-3000.txt
					4-3001-4000.txt
					4-4001-5000.txt
					4-5001-6000.txt
					4-6001-7000.txt
					4-7001-8000.txt
					4-8001-9000.txt
					4-9001-10000.txt
					5-1-1000.txt
					5-1001-2000.txt
					5-2001-3000.txt
					5-4001-5000.txt
					5-5001-

					6000.txt 5-6001- 7000.txt 6-1-1000.txt 7-1-1000.txt 7-12001- 12178.txt
Dean Nelson and other admin at CVM were in/are still in Wash DC	1	1	3/6/2020	3/6/2020	3-1001- 2000.txt
[EXTERNAL] Red Dawn Raging Start March 4	15	5	3/8/2020	3/12/2020	3-1001- 2000.txt 3-2001- 3000.txt 3-3001- 4000.txt 3-4001- 5000.txt 4-3001- 4000.txt

[EXTERNAL] Red Dawn Raging Start March 4	45	9	3/8/2020	3/16/2020	3-1001-2000.txt 3-2001-3000.txt 3-3001-4000.txt 3-4001-5000.txt 4-2001-3000.txt 6-1001-2000.txt 6-3001-4000.txt 7-10001-11000.txt 7-1001-2000.txt 7-3001-4000.txt 7-4001-5000.txt 7-6001-7000.txt 7-8001-9000.txt
[EXTERNAL] Red Dawn Raging Start	2	1	3/9/2020	3/9/2020	3-3001-4000.txt
Red Dawn Raging, Start March 4	4	1	3/10/2020	3/10/2020	3-4001-5000.txt
[EXT] Red Dawn Raging Start March 4	2	1	3/12/2020	3/12/2020	4-1-1000.txt
Epidemiologist needed	1	1	3/13/2020	3/13/2020	4-6001-7000.txt
Singapore's measures to contain COVID-19	11	2	3/15/2020	3/16/2020	5-4001-5000.txt 7-8001-9000.txt
Impact of Social Distancing Practices	1	1	3/16/2020	3/16/2020	7-12001-12178.txt
Red Dawn Responding, Start 16	2	2	3/16/2020	3/17/2020	8-1-1000.txt
[EXTERNAL] Red Dawn	4	5	3/16/2020	3/20/2020	7-10001-11000.txt 9-1-1000.txt 9-1001-2000.txt

Red Dawn Responding, Start 16 March	91	15	3/16/2020	3/30/2020	10-4001-5000.txt 7-12001-12178.txt 8-1-1000.txt 8-1001-1670.txt 9-1-1000.txt 9-1001-2000.txt 9-2001-3000.txt 9-4001-5000.txt 9-5001-6000.txt
Social Distancing	1	1	3/17/2020	3/17/2020	8-1-1000.txt
No reinfection and titer data in COVID Plasma	4	1	3/18/2020	3/18/2020	8-1-1000.txt
COVID Plasma	1	1	3/18/2020	3/18/2020	8-1-1000.txt
CONFIRMED - COVID-19 Conversations Webinar Series Advisory Group Meeting	1	1	3/18/2020	3/18/2020	8-1-1000.txt
Has everyone seen this?	2	1	3/19/2020	3/19/2020	8-1001-1670.txt
NPI New Statistical Analysis Study	1	1	3/19/2020	3/19/2020	8-1001-1670.txt
The psychological impact of quarantine and how to reduce it	3	1	3/19/2020	3/19/2020	9-1-1000.txt
[EXTERNAL] Red Dawn Reflux,	1	1	3/19/2020	3/19/2020	9-1-1000.txt
Have you seen this article on hydroxychloroquine and azithromycin tx	2	1	3/19/2020	3/19/2020	8-1001-1670.txt
[EXTERNAL] Red Dawn Reflux, Start	2	1	3/19/2020	3/19/2020	9-1-1000.txt 9-1001-2000.txt
[EXTERNAL] Red Dawn Reflux,	5	2	3/19/2020	3/20/2020	9-1001-2000.txt 9-2001-3000.txt
[EXTERNAL] Red Dawn Reflux, Start 2020 0319, 10:35	5	2	3/19/2020	3/20/2020	9-1-1000.txt 9-1001-2000.txt
[EXTERNAL] Red Dawn Reflux, Start 2020	6	2	3/19/2020	3/20/2020	9-1-1000.txt 9-1001-2000.txt

[EXTERNAL] Red Dawn Reflux, Start 2020 0319,	5	2	3/19/2020	3/20/2020	9-1-1000.txt 9-2001-3000.txt
[EXTERNAL] Red Dawn Reflux, Start 2020 0319, 10:35 EDT	69	4	3/19/2020	3/22/2020	8-1001-1670.txt 9-1-1000.txt 9-1001-2000.txt
Red Dawn Reflux, Start 2020 0319, 10:35 EDT	11	5	3/19/2020	3/23/2020	8-1001-1670.txt 9-1001-2000.txt 9-2001-3000.txt
[EXTERNAL] Red Dawn Reflux, Start 2020 0319, 10:35 EDT	12	5	3/19/2020	3/23/2020	9-1-1000.txt 9-1001-2000.txt 9-2001-3000.txt
[EXTERNAL] Red	2	1	3/20/2020	3/20/2020	9-1-1000.txt 9-1001-2000.txt
Update & action items - NAM-APHA COVID-19 Webinar Series	8	2	3/21/2020	3/22/2020	9-1-1000.txt 9-1001-2000.txt
Webinar topic	1	1	3/22/2020	3/22/2020	9-1001-2000.txt
Red Dawn Suppression, Start Mar 23, 10:00	1	1	3/23/2020	3/23/2020	9-2001-3000.txt
Red Dawn Suppression, Start Mar	2	1	3/23/2020	3/23/2020	9-2001-3000.txt
BWIRP Files	4	1	3/23/2020	3/23/2020	9-2001-3000.txt
The Science of Social Distancing: A free webinar from NAM and APHA	4	2	3/23/2020	3/24/2020	9-2001-3000.txt
Inquiry on Interest and Availability to Participate in INR Analytic Exchange on Scientific Evidence on Origins of Novel	7	3	3/23/2020	3/25/2020	9-2001-3000.txt 9-3001-4000.txt
Red Dawn Suppression, Start Mar 23, 10:00 EDT	83	5	3/23/2020	3/27/2020	9-1001-2000.txt 9-2001-3000.txt 9-3001-4000.txt 9-4001-

					5000.txt 9-5001- 6000.txt
FDA announcement	1	1	3/24/2020	3/24/2020	9-2001- 3000.txt
*** China Data Dr. Michael Joyner***	1	1	3/25/2020	3/25/2020	9-2001- 3000.txt
*** China Data Dr. Michael Joyner**	1	1	3/25/2020	3/25/2020	9-2001- 3000.txt
[EXTERNAL] ***China Data Dr. Michael Joyner***	2	1	3/25/2020	3/25/2020	9-2001- 3000.txt
China Data Dr. Michael Joyner	2	1	3/25/2020	3/25/2020	9-2001- 3000.txt
China Data Dr. Michael Joyner	2	1	3/25/2020	3/25/2020	9-2001- 3000.txt
Reuse of N95 Masks	5	2	3/25/2020	3/26/2020	9-3001- 4000.txt
Red Dawn Pondering, Start Mar 27, 15:45	42	16	3/27/2020	4/11/2020	9-5001- 6000.txt 9-6001- 7000.txt
CONFIRMED: Second advisory call for COVID-19 webinar series	1	1	3/28/2020	3/28/2020	9-5001- 6000.txt
[EXTERNAL] Red Dawn Pondering, Start Mar 27, 15:45	2	1	3/29/2020	3/29/2020	9-5001- 6000.txt
Red Dawn Pondering, Start Mar 27,	2	1	3/29/2020	3/29/2020	9-5001- 6000.txt
Masks	10	4	3/29/2020	4/1/2020	9-5001- 6000.txt
updates - NAM-APHA webinar series	1	1	3/31/2020	3/31/2020	9-5001- 6000.txt
Red Dawn Rooster, Start April 2, 17:00	29	6	4/2/2020	4/7/2020	9-5001- 6000.txt 9-6001- 7000.txt
Red Dawn Rolling, Start April 6, 15:00	35	6	4/6/2020	4/11/2020	9-6001- 7000.txt
Advisory Group Call: NAM-APHA COVID-19 Webinar Series	7	87	4/6/2020	7/1/2020	10-5001- 6000.txt 10-6001- 7000.txt
Health, Safety & Store Updates â€” The Latest	2	4	4/7/2020	4/10/2020	9-6001-

from Kroger					7000.txt
Health, Safety & Store Updates - The Latest from Kroger	2	4	4/7/2020	4/10/2020	9-6001-7000.txt
NAM-APHA COVID-19 Webinar Series Update	2	1	4/9/2020	4/9/2020	9-6001-7000.txt
Red Dawn	3	32	4/12/2020	5/13/2020	10-5001-6000.txt 4-12001-13000.txt 9-6001-7000.txt
Red Dawn Breaking Debacle - How can we help those at risk?	1	1	4/13/2020	4/13/2020	9-6001-7000.txt
Red Dawn Setting, Begin 13 April 08:00	60	23	4/13/2020	5/5/2020	10-1-1000.txt 10-1001-2000.txt 10-2001-3000.txt 9-10001-11000.txt 9-13001-14000.txt 9-15001-16000.txt 9-6001-7000.txt 9-7001-8000.txt 9-8001-9000.txt 9-9001-10000.txt

Red Dawn Setting, Begin 13April 08:00	176	24	4/13/2020	5/6/2020	10-1-1000.txt 10-1001-2000.txt 10-2001-3000.txt 10-3001-4000.txt 9-10001-11000.txt 9-11001-12000.txt 9-12001-13000.txt 9-13001-14000.txt 9-14001-15000.txt 9-15001-16000.txt 9-16001-16505.txt 9-6001-7000.txt 9-7001-8000.txt 9-8001-9000.txt 9-9001-10000.txt
Update on Health Data Security	1	1	4/14/2020	4/14/2020	9-7001-8000.txt
Red Dawn Setting, Begin 13 April	4	2	4/14/2020	4/15/2020	9-7001-8000.txt 9-8001-9000.txt
Red Dawn Setting, Begin	8	13	4/14/2020	4/26/2020	10-1-1000.txt 9-11001-12000.txt 9-12001-13000.txt 9-8001-9000.txt
talk on the phone?	7	3	4/16/2020	4/18/2020	9-7001-8000.txt 9-8001-

					9000.txt
Red Dawn Setting, Begin 13April	3	3	4/20/2020	4/22/2020	10-1-1000.txt
Drug repurposing screen paper	2	1	4/22/2020	4/22/2020	9-10001-11000.txt
questions from leadership group	1	1	4/22/2020	4/22/2020	9-10001-11000.txt
interesting paper	4	1	4/22/2020	4/22/2020	9-10001-11000.txt
New paper	2	1	4/23/2020	4/23/2020	9-10001-11000.txt
background for NAM-APHA advisory group call tomorrow	4	15	4/23/2020	5/7/2020	10-3001-4000.txt 9-11001-12000.txt 9-13001-14000.txt
NIAID COVID strategic plan	1	1	4/24/2020	4/24/2020	9-10001-11000.txt
2020 April 25 Daily COVID-19 LST Report (Red Dawn Setting, Begin 13April 08:00]	1	1	4/26/2020	4/26/2020	9-12001-13000.txt
Register Now! Webinar on Can old drugs take down a new coronavirus? The state of COVID-19 drug repurposing efforts	1	1	4/27/2020	4/27/2020	9-12001-13000.txt
Register Now! Webinar on Can old drugs take down a new coronavirus? The state of COVID-19 drug repurposing	2	1	4/27/2020	4/27/2020	9-12001-13000.txt
Direct observation of repeated infections with endemic coronaviruses	13	2	4/28/2020	4/29/2020	9-13001-14000.txt
apropos "warp speed" vaccine development	1	1	4/30/2020	4/30/2020	9-14001-15000.txt
Just in: Compilation of RECS	1	1	4/30/2020	4/30/2020	9-14001-15000.txt
INVITIVION: virtual U.S. China dialogue meeting on COVID-19	1	1	5/3/2020	5/3/2020	10-1-1000.txt
Paul H. Lambert recommends as speaker in the webeninar: IABS webinar on COVID, MAY 27: upfdate Information, with	1	1	5/4/2020	5/4/2020	10-1001-2000.txt
lecture on COVID-19 animal models by Emmie de Wit, NIAID, on May 6 at 3:00 p.m.	2	1	5/4/2020	5/4/2020	10-1001-2000.txt
Paul H. Lambert recommends as speaker in the webeninar: IABS webinar on COVID, MAY 27: upfdate Information,	2	2	5/4/2020	5/5/2020	10-1001-2000.txt

Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7	11	7	5/4/2020	5/10/2020	10-1001-2000.txt 10-3001-4000.txt
Red Dawn Posturing, Begin May 5, 12:50 EDT	84	49	5/5/2020	6/22/2020	10-2001-3000.txt 10-3001-4000.txt 10-4001-5000.txt 10-5001-6000.txt
Paper of interest	3	1	5/6/2020	5/6/2020	10-3001-4000.txt
webinar on extreme weather and COVID-19	9	8	5/8/2020	5/15/2020	10-3001-4000.txt 10-4001-5000.txt
Re. List of Chinese participants - Virtual U.S. China dialogue meeting on COVID-19: planning discussion on May 7	1	1	5/11/2020	5/11/2020	10-3001-4000.txt
Virtual U.S. China dialogue meeting on COVID-19: ZOOM link for first call	1	1	5/11/2020	5/11/2020	10-3001-4000.txt
Virtual U.S. China dialogue meeting on COVID-19: final docs, Zoom link (and back up phone number)	4	1	5/11/2020	5/11/2020	10-3001-4000.txt
Virtual U.S. China dialogue meeting on COVID-19: final docs	1	1	5/12/2020	5/12/2020	10-3001-4000.txt
Virtual U.S. China dialogue meeting on COVID-19: Zoom link for Wednesday May 13 call 9pm et	9	3	5/12/2020	5/14/2020	10-3001-4000.txt
Red Dawn Posturing, Begin May 5, 12:50	2	2	5/13/2020	5/14/2020	10-4001-5000.txt
Red Dawn Posturing, Begin May 5,	2	2	5/13/2020	5/14/2020	10-5001-6000.txt
CCPP19: Early safety preprint posted on medRxiv	1	1	5/14/2020	5/14/2020	10-3001-4000.txt
[EXTERNAL] Your preprint 10.1101/2020.05.12.20099879 has posted on medRxiv	1	1	5/14/2020	5/14/2020	10-3001-4000.txt
Follow up Meeting to Discuss Results of the Virtual U.S. China dialogue meeting on COVID-19	6	5	5/14/2020	5/18/2020	10-4001-5000.txt
Nice interview with Cat Lutz	4	1	5/15/2020	5/15/2020	10-4001-5000.txt
SARS-COV-2 NHP Research Publications	1	1	5/20/2020	5/20/2020	10-4001-5000.txt

SARS-CoV-2 NHP Research Publications	3	1	5/20/2020	5/20/2020	10-4001-5000.txt
3rd Virtual U.S. China dialogue meeting on COVID-19	3	3	5/20/2020	5/22/2020	10-4001-5000.txt
background for tomorrow's NAM-APHA advisory group call	2	1	5/21/2020	5/21/2020	10-4001-5000.txt
Reaching out to Red Dawn team members	2	1	5/25/2020	5/25/2020	10-4001-5000.txt
3rd Virtual U.S. China dialogue meeting on COVID-19 Tuesday, June 9, 9-11PM ET	11	10	6/1/2020	6/10/2020	10-4001-5000.txt
ZOOM link 3rd Virtual U.S. China dialogue meeting, Tuesday, June 9, 9-11PM ET	4	6	6/4/2020	6/9/2020	10-4001-5000.txt
[SUSPICIOUS MESSAGE] Agenda & background for NAM-APHA advisory group call at 2 pm	1	1	6/5/2020	6/5/2020	10-4001-5000.txt
Agenda & background for NAM-APHA advisory group call at 2 pm	2	1	6/5/2020	6/5/2020	10-4001-5000.txt
June 10 Daily COVID-19 LST Report	2	2	6/10/2020	6/11/2020	10-5001-6000.txt
Join us for a Conversation with California's COVID-19 Testing Task Force Leaders on Friday, June 26th	1	1	6/22/2020	6/22/2020	10-5001-6000.txt
Red Dawn Posturing, Update on California Testing Task Force Webinar Friday 26 June, 4-	1	1	6/23/2020	6/23/2020	10-5001-6000.txt
Red Dawn Posturing, Update on California Testing Task Force Webinar Friday 26 June, 4-5 PM EDT	3	3	6/23/2020	6/25/2020	10-5001-6000.txt
Red Dawn Posturing	3	6	6/25/2020	6/30/2020	10-5001-6000.txt
Red Dawn Rhapsodizing Begin July 2, 2020	61	25	7/2/2020	7/26/2020	10-6001-7000.txt 10-7001-7245.txt
Op-Ed - Treat COVID19 as though it were airborne - until we prove that it is not	5	2	7/14/2020	7/15/2020	10-6001-7000.txt
July 20 Daily COVID-19 LST Report	2	2	7/20/2020	7/21/2020	10-6001-7000.txt
COVID-19 Conversations: K-12 School Reopening Webinar - Draft Agenda	2	3	7/21/2020	7/23/2020	10-6001-7000.txt
[EXTERNAL] Your preprint 10.1101/2020.07.29.20162917 has posted on medRxiv	2	1	7/30/2020	7/30/2020	10-7001-7245.txt
Preprint 10.1101/2020.07.29.20162917 has posted on medRxiv	1	1	7/30/2020	7/30/2020	10-7001-7245.txt

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

From: David Asher (b)(6)@hudson.org>
To: Gibbs, Jeffrey J (b)(6)@state.gov>
(b)(6)@state.gov>;
(b)(6)@state.gov>;
CC: (b)(6)@state.gov>;
(b)(6)@state.gov>;
(b)(6)@state.gov>
Subject: Re: METZL - Origins of SARS-CoV-2
Date: Mon, 25 Jan 2021 02:00:40 +0000

Begin forwarded message:

From: Jamie Metzl (b)(6)@gmail.com>
Date: January 24, 2021 at 8:46:03 PM EST
To: David Asher (b)(6)@hudson.org>
Subject: From Jamie

(b)(6) – thanks so much for reaching out and for the great and important work you have been doing. This has all been an uphill climb but I certainly believe that the lab leak hypothesis is starting to get much more active consideration. It would be my pleasure to catch up and to join you for a Hudson event.

With warm regards,
Jamie

jamiemetzl.com
hackingdarwin.com
OneShared.World

David L. Asher, Ph.D
Senior Fellow
Hudson Institute
1201 Pennsylvania Avenue, NW
Fourth Floor
Washington, DC 20004
o. | c. (b)(6)
<https://www.hudson.org/experts/1299-david-asher>

On Jan 24, 2021, at 2:25 PM, Gibbs, Jeffrey J (b)(6)@state.gov> wrote:

He seems like he might be a good addition to our expert panel. Seems to have a balanced view.

Jeff Gibbs
Senior Adviser AVC
SSD/AVC

C: (b)(6)
From: David Asher (b)(6)@hudson.org>
Sent: Sunday, January 24, 2021 2:15 PM
To: (b)(6)@state.gov>
Cc: (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>
Subject: Re: METZL - Origins of SARS-CoV-2

We can do a call with Jamie. Old colleague and friend. Total genius. He also is quite close to Biden, who was his boss on the Hill.

David L. Asher, Ph.D
Senior Fellow
Hudson Institute
1201 Pennsylvania Avenue, NW
Fourth Floor
Washington, DC 20004
o. | c (b)(6)
<https://www.hudson.org/experts/1299-david-asher>

On Jan 24, 2021, at 13:31, (b)(6)@state.gov> wrote:

The best summary I have seen so far. This piece is very comprehensive.

(b)(6)
Senior Adviser AVC
SSD/AVC
C: (b)(6)
From: David Asher (b)(6)@hudson.org>
Sent: Saturday, January 23, 2021 8:33 PM
To: (b)(6)@state.gov>
Cc: (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>; (b)(6)@state.gov>
Subject: Re: METZL - Origins of SARS-CoV-2

Jamie is an old colleague and friend. Super smart. Very close to President Biden. I will see if he retains a clearance since he could help convince the powers that be that our research is not some politically slanted BS.

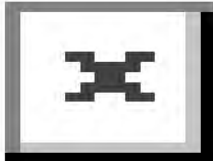
David L. Asher, Ph.D
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1201 Pennsylvania Avenue, NW
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Washington, DC 20004

o. | c. (b)(6)

<https://www.hudson.org/experts/1299-david-asher>

On Jan 23, 2021, at 6:43 PM, (b)(6)@state.gov wrote:

<https://jamiemetzl.com/origins-of-sars-cov-2/>



Origins of SARS-CoV-2 | Jamie Metzl

NOTE: This post was originally published on April 16, 2020 and has been updated regularly. A number of people have reached out to me questioning my assertion that "the most likely starting point of the coronavirus crisis is an accidental leak from one of the Chinese virology institutes in W ...

jamiemetzl.com

NOTE: This post was originally published on April 16, 2020 and has been updated regularly.

A number of people have reached out to me questioning my assertion that "the most likely starting point of the coronavirus crisis is an accidental leak from one of the Chinese virology institutes in Wuhan" (see this CNN interview, this Newsweek editorial, this WSJ editorial, and this The Hill editorial). As referenced in this Forbes profile, I have been making this claim consistently since January 2020 and will continue to do so until this issue gets the attention it deserves. We owe everyone who has died from COVID-19, all the people who have lost their loved ones and livelihoods, and future generations a thorough, unbiased, and unrestricted investigation of how the tragedy began and has unfolded.

Let me be clear, I do not believe this was likely a genome edited virus (although this paper suggests how it could have been and we should not discount this possibility), just that it had very likely been isolated and cultured in one of the Wuhan labs (the Wuhan CDC or, more likely, the Wuhan Institute of Virology, WIV). I also want to be clear that this is only highly informed inference based on publicly available information and my application of Occam's razor (and mathematical probabilities). I have no definitive way of proving this thesis but the evidence is, in my view, extremely convincing. If forced to place odds on the confidence of my hypothesis, I would say there's an 85% chance the pandemic started with an accidental leak from the Wuhan Institute of Virology or Wuhan CDC and a 15% chance it began in some other way (in fairness, here is an article making the case for a zoonotic jump "in the wild"). If China keeps preventing a full and unrestricted international forensic investigation into the origins of the pandemic, I believe it is fair to deny Beijing the benefit of the doubt.

The purpose of this post is to present the evidence and my views so that readers can come to their own conclusions. If there is additional evidence I am missing, please let me know. I do not have a political agenda other than finding out why so many people around the world are dead from COVID-19 and how we can learn the lessons from this catastrophe to prevent the next ones. What we need, and should all be calling for regardless of our nationalities or political persuasions, is a full and unrestricted international forensic investigation into the origins of COVID-19 with full access to all relevant data, lab records, biological samples, and people in China and beyond. Getting to the bottom of this essential question should be an unrestricted and unbiased data-driven pursuit. While access to essential information is being denied, we are forced to be more speculative than we otherwise would be.

Because there is a lot of material to get through below, let me just summarize what I believe to be the most likely scenario.

- In 2012, six miners working in a bat-infested copper mine in southern China (Yunnan province) were infected with a bat coronavirus. All of them developed symptoms exactly like COVID-19 symptoms. Three of them died.
- Viral samples taken from the Yunnan miner were taken to the Wuhan Institute of Virology, the only level 4 biosecurity lab in China that was also studying bat coronaviruses.
- The WIV carried out gain of function research, almost certainly on these and a range of related and other samples (which is different than genetically engineering the viruses). Chimeric viruses were likely developed in this process. There has never been a full and public accounting for what viruses are in the WIV sample set and database, and key elements of the database have been taken off line or deleted.
- Given the close relationship of the Chinese Peoples' Liberation Army (PLA) in the development and constriction of the Wuhan Institute of Virology, it is fair to assume a connection between the PLA and the WIV.
- In late 2019 the SARS-CoV-2 virus appeared in Wuhan. The closest known relative of this virus is the RaTG13 virus sampled from the Yunnan mine where the miners had been infected.
- The difference between the RaTG13 virus and SARS-CoV-2 could potentially be explained by the gain of function research pushing the development of chimeric viruses.
- It is also plausible that SARS-CoV-2 could have been among the viruses held in or derived from a different virus in the WIV repository.
- In the earliest known stage of the outbreak, the virus was already very well-adapted to human cells.
- In the critical first weeks after the outbreak, Wuhan authorities worked aggressively to silence the whistleblowers and destroy evidence that could prove incriminating.
- When Beijing authorities got involved a bit later, they likely faced a choice of implicating the Wuhan authorities, and, in effect, taking blame for what was quickly emerging as a major global problem, or turning into the curve and going all in for the coverup. I believe they likely chose the second option.

- The Chinese government then massively lobbied the WHO to prevent the WHO from declaring COVID-19 as an international emergency and prevented WHO investigators from entering China for nearly a month.
- In late January 2020, PLA Major General Chen Wei was put in charge of containment efforts in Wuhan. This role included supervision of the WIV, which had previously been considered a civilian institution. General Chen is China's top biological weapons expert. Allegations that the PLA was conducting covert dual civilian-military research research on bat coronaviruses at WIV have not been proven.
- The Chinese authorities have gone to great lengths to destroy evidence and silence anyone in China who might be in a position to provide evidence on the origins of COVID-19.
- Although nothing can be fully conclusive in light of Chinese obfuscation, the continued absence of any meaningful evidence of a zoonotic chain of transmission and mutation in the wild and the accretion of other evidence is pointing increasingly, in my view, toward an accidental lab leak as the most likely origin of COVID-19. Given the extent to which China would benefit from discovering evidence of a transmission in the wild, we can assume Chinese authorities are doing all they can to find this kind of evidence without success. This failure would explain why Chinese officials have recently begun, with little credible evidence, asserting that the outbreak started in India or Bangladesh.
- In light of all of this, only a full and unrestricted international forensic investigation into the origins of the pandemic, with complete access to all samples, lab records, scientists, health officials, etc. will suffice.
- Ensuring the most thorough and highest quality investigation exploring all possible hypothesis is and should be in all of our interest, including that of the Chinese government and people.

I want to be clear that I am a progressive who believes in asking tough questions and seeking the truth. I in no way seek to support or align myself with any activities that may be considered unfair, dishonest, nationalistic, racist, bigoted, or biased in any way. I also believe that whatever the original reasons for the outbreak, the reason why so many more Americans have died from COVID-19 than most anyone else is the catastrophic failure of the Trump administration to respond effectively.

As I argued in my Newsweek piece:

Just as we wouldn't imagine having a plane crash and not immediately trying to figure out what happened, we can't let the COVID-19 crisis unfold without urgently understanding how our systems have so spectacularly failed. There are plenty of fingers to point, and we must thoughtfully point them now, at all of us, for our own good. For all we know, a new and even worse pandemic could begin even before we have overcome this one... Until we get to the bottom of all these failures and work to fix them, we remain dangerously susceptible to the next pandemic... Whatever the origins of the outbreak, including the possibility of an accidental leak from the Chinese virology lab in Wuhan, China's dangerous and ongoing information suppression activities are the foundations of this

crisis. We have to find out fast where and how this outbreak began... The WHO could have raised hell when China denied access to WHO experts for those critical early weeks, did not need to initially parrot Chinese propaganda and could certainly have sounded the alarm earlier. We have to ask how we can help the WHO do better... The United States had all the information it needed by January to mount a massive response, but Trump actively undermined the findings of his own intelligence and health officials. Worse, he passed misinformation to the American people that potentially led to many thousands of deaths. We've got to ask why this happened... Until we get to the bottom of all these failures and work to fix them, we remain dangerously susceptible to the next pandemic... We are all on the same plane with a shared interest in not letting it crash... Let's work together to safely land the plane.

Although I do not necessarily ascribe to all of the assertions made in each of these documents, my sources include:

- This [Nature Medicine](#) study
- This [Bulletin of the Atomic Scientists](#) article
- This [Epoch Times](#) documentary (which should be viewed with significant caution due to its propagandistic tone)
- This [Lancet](#) piece
- This [Washington Post](#) article
- This [The Diplomat](#) editorial
- The [Nature](#) article
- This [Project Evidence](#) site
- This [Cell](#) study
- This [Science Direct](#) study
- This [New York Times](#) report
- This [Newsweek](#) article
- This [Washington Post](#) article
- This [Daily Telegraph](#) story
- This [Guardian](#) article
- This [Bloomberg](#) article
- This [Asia Times](#) story
- This [NBC News](#) story
- This [New Yorker](#) piece
- This [NPR](#) report
- This [E-PAI \(Electronically Available Public Information\)](#) report
- This [BioRxiv](#) pre-publication research paper
- This [Atlantic](#) piece
- This [National Review](#) article
- This [Associated Press](#) story
- This [Nerd Has Power](#) post
- This [Nature](#) article

- This [Telegraph](#) piece
- This [QRB Discovery](#) manuscript
- This [Bulletin of the Atomic Scientists](#) editorial
- This [Bulletin of the Atomic Scientists](#) article
- This [Independent Science News](#) piece
- This [Daniel Lucey](#) blog post
- This [Science](#) article
- This [Independent Science News](#) piece
- This [Wiley](#) preprint essay
- This [Wiley](#) preprint letter
- This [Cell Host & Microbe](#) paper
- This [Frontiers in Public Health](#) article
- This [Unherd](#) post
- This [New York Times](#) story
- This [BioEssays](#) paper
- This [BioEssays](#) paper
- This [PNAS](#) opinion piece
- This [New York Times](#) article
- This [Daily Mail](#) article
- This [Associated Press](#) article
- This [Quantitative Biology](#) paper
- This [New York](#) magazine article
- This [Nature Medicine](#) editorial
- This [France Culture](#) article
- This [Wall Street Journal](#) editorial

I am extremely open to other perspectives and welcome any additional information. If you have anything you believe relevant, I would be grateful for you to pass it along. I am not wedded to any particular outcome other than getting to the deepest possible understanding of what went wrong and how we can fix it.

As I [have already stated publicly](#), "Even if the coronavirus is an accidental leak from a Wuhan lab, we are all one interconnected humanity who must work together to get through this crisis." It is my view that Chinese researchers at these institutes were studying these viruses with the best intentions of developing surveillance systems, treatments, and vaccines for the good of humanity. Countries make mistakes, even terrible and deadly ones. I was in the White House when the US bombed the Chinese embassy in Belgrade. We believed it was an accident but many Chinese people thought it was a deliberate act. I understood why.

Moments like these are inherently difficult and we should all do our very best to find the answers to our most important questions in the most honest, careful, and considered manner possible.

We must also be doing everything we can to build the surveillance, response, treatment, vaccine development, and public health capacities we need to make all of us safe. COVID-19 has been a terrible catastrophe, but there could very well be much worse facing us in the future.

In this spirit, I have compiled this summary of the available evidence. Because China is still restricting access to the relevant data and people, the case remains speculative by necessity.

- Beginning on December 10, 2019, increasing numbers of people, many of who had visited the Huanan Seafood Market in Wuhan, fell ill due to a new disease.
- The novel coronavirus outbreak did not originate in the seafood market (Lancet). (This was clear early on but Chinese officials held to this story until late May 2020, when the evidence against this claim became wholly indefensible, more below.)
- The Huanan Seafood Market didn't have bats for sale, and most bats species in Wuhan would be hibernating at the time of outbreak. It was reported that 34% of cases had no contact with the market, and 'No epidemiological link was found between the first patient and later cases.' (Lancet)
- According to a DIA report, "about 33 percent of the original 41 identified cases did not have direct exposure" to the market. That, along with what's known of the laboratory's work in past few years, raised reasonable suspicion that the pandemic may have been caused by a lab error, not the wet market. (Newsweek)
- A Broad Institute study asserts that genetic examination of four samples containing the virus from the seafood market to those taken from the Wuhan patient are '99.9 per cent' identical. This suggests it came from infected visitors or vendors, indicating 'Sars-CoV-2 had been imported into the market by humans'. The authors found no evidence 'of cross-species transmission' at the market.
- This market is less than 9 miles away from The Wuhan Institute of Virology (WIV), Chinese Academy of Sciences, which:
 - Developed chimeric SARS-like coronaviruses
 - Conducted 'dangerous' gain-of-function research on the SARS-CoV-1 virus, some of which had been funded by the US government (Asia Times)
 - Established a 96.2% match with SARS-CoV-2 and a virus they sampled from a cave over 1,000 miles away from Wuhan
 - Injected live piglets with bat coronaviruses as recently as July 2019
 - Published a paper on a close descendant of SARS-CoV-1, MERS-CoV, in November 2019
 - Was hiring researchers to work on bat coronaviruses as recently as November 2019
- United States embassy and consular officials who visited the Wuhan Institute of Virology in January 2018 were deeply concerned. Their cable sent to the State Department noted:
 - "the new lab has a serious shortage of appropriately trained technicians and investigators needed to safely operate this high-containment laboratory"
 - "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.” (Washington Post)

- (For more on laboratory safety in China, see [this link](#).)
- The market is also less than 3 miles away from the Wuhan Centre for Disease Control, which:
 - Was accused of being the source of the outbreak from a now-withdrawn academic paper from a notable Chinese scholar at the South China University of China
 - Once kept horseshoe bats, a known reservoir of SARS-CoV-1, within its labs
 - Once performed surgery on live animals within its labs
 - Had a researcher who quarantined on two separate occasions; once upon coming into contact with bat blood after being ‘attacked’ and another time when he was urinated upon in a cave while wearing inadequate personal protection
 - Had previously done bat virus research funded by the US NIH (in a grant to EcoHealth Alliance)
 - possessed the virus that is the most closely related known virus in the world to the outbreak virus, bat virus RaTG13. This virus was isolated in 2013 and had its genome published on January 23, 2020. Seven more years of bat coronavirus collection followed the 2013 RaTG13 isolation. One component of the novel-bat-virus project at the Wuhan Institute of Virology involved infection of laboratory animals with bat viruses. Therefore, the possibility of a lab accident includes scenarios with direct transmission of a bat virus to a lab worker, scenarios with transmission of a bat virus to a laboratory animal and then to a lab worker, and scenarios involving improper disposal of laboratory animals or laboratory waste. (Bulletin of the Atomic Scientists)
 - began its gain of function research program for bat coronaviruses in 2015. Using a natural virus, institute researchers made “substitutions in its RNA coding to make it more transmissible. They took a piece of the original SARS virus and inserted a snippet from a SARS-like bat coronavirus, resulting in a virus that is capable of infecting human cells.” (Bulletin of the Atomic Scientists)
- Even before this outbreak, China had a very poor safety record at many of its biosecurity facilities.
- In the years since the SARS outbreak, many instances of mishaps involving the accidental release of pathogens have taken place in labs throughout the world. Hundreds of breaches have occurred in the U.S., including a 2014 release of anthrax from a U.S. government lab that exposed 84 people. The SARS virus escaped from a Beijing lab in 2004, causing eleven infections and one death. An accidental release is not complicated and doesn’t require malicious intent. All it takes is for a lab worker to get sick, go home for the night, and unwittingly spread the virus to others. (Newsweek)
- Although it does not appear likely this virus was engineered (Nature Medicine), trying to determine the exact pattern and genomic ancestry of the virus is difficult, particularly as

many of the recombinant regions may be small and are likely to change as more viruses related to SARS-CoV-2 are sampled. (Cell)

- Using the current standard genetic engineering technology, many alterations of several bases in the RNA genome would be undetectable, including construction of a chimeric coronavirus encoding an unpublished spike protein in an unpublished genome. (Independent Science News)
- After months of speculation and with the market origin story indefensible, the Chinese Centers for Disease Control and Prevention finally admitted only in late May 2020 that it has ruled the site out as the origin point of the outbreak. According to Gao Fu, the director of the Chinese CDC, "It now turns out that the market is one of the victims."
- Nikolai Petrovsky and colleagues at Flinders University in Australia have found that SARS-CoV-2 has a higher affinity for human receptors than for any other animal species they tested, including pangolins and horseshoe bats. He suggests that this could have happened if the virus was being cultured in human cells, adding that "We can't exclude the possibility that this came from a laboratory experiment." (Wall Street Journal)
- According to the WHO, "the virus has been remarkable stable since it was first reported in Wuhan, with sequences well conserved in different countries, suggesting that the virus was well adapted to human transmission from the moment it was first detected."
- This Quantitative Biology paper by Nikola Petrovsky et al makes the very strong case that that the SARS-CoV-2 virus was already pre-adapted to humans by the time it appeared in late 2020.
- Similarly, Sirotkin and Sirotkin assert in their Wiley preprint essay: "Unless the intermediate host necessary for completing a natural zoonotic jump is identified, the dual-use gain-of-function research practice of viral serial passage should be considered a viable route by which the novel coronavirus arose. The practice of serial passage mimics a natural zoonotic jump, and offers explanations for SARS-CoV-2's distinctive spike-protein region and its unexpectedly high affinity for angiotensin converting enzyme (ACE2), as well as the notable polybasic furin cleavage site within it. Additional molecular clues raise further questions, all of which warrant full investigation into the novel coronavirus's origins and a re-examination of the risks and rewards of dual-use gain-of-function research.
- The two known coronaviruses genetically closest to SARS-CoV-2, RaTG13 and RmYN02, were discovered in bats in Yunnan, China. The genome of RaTG13 is 96.2% similar to SARS-CoV-2. That of RmYN02 is 93.3 % similar. Given that the SARS-CoV-2 genome is made up of 30,000 nucleotides (aka letters), the genetic distance between RaTG13 and SARS-CoV-2 is a significant 1,200 nucleotides. Under normal circumstances in wild, this would suggest that the two viruses diverged decades ago. But an essential question is whether gain of function research could have massively sped up this evolutionary rate, including by inducing the development of chimeric viruses well adapted to human cells. This type of research could have been done using the tools of genome editing (which I believe is highly unlikely in this case) or by exposing different viruses to human cells or humanized mouse or other animal cells in a laboratory.

- Stanford's David Relman states: "SARS-CoV-2 is a betacoronavirus whose apparent closest relatives, RaTG13 and RmYN02, are reported to have been collected from bats in 2013 and 2019, respectively, in Yunnan Province, China. COVID-19 was first reported in December 2019 more than 1,000 miles away in Wuhan City, Hubei Province, China. Beyond these facts, the "origin story" is missing many key details, including a plausible and suitably detailed recent evolutionary history of the virus, the identity and provenance of its most recent ancestors, and surprisingly, the place, time, and mechanism of transmission of the first human infection... Some have argued that a deliberate engineering scenario is unlikely because one would not have had the insight a priori to design the current pandemic virus. This argument fails to acknowledge the possibility that two or more as yet undisclosed ancestors (i.e., more proximal ancestors than RaTG13 and RmYN02) had already been discovered and were being studied in a laboratory—for example, one with the SARS-CoV-2 backbone and spike protein receptor binding domain, and the other with the SARS-CoV-2 polybasic furin cleavage site. It would have been a logical next step to wonder about the properties of a recombinant virus and then create it in the laboratory... there is probably more than one recent ancestral lineage that contributes to SARS-CoV-2 because its genome shows evidence of recombination between different parental viruses. In nature, recombination is common among coronaviruses. But it's also common in some research laboratories where recombinant engineering is used to study those viruses."
- (Alina Chan, a junior scientist at the Broad Institute demonstrates how shoddy much of the pangolin research has been in this important Twitter thread.)
- The Brufsky et al Wiley pre-print letter lays out the underlying science which seems to explain why the gain of function research at the WIV is the most likely origin of the pandemic. To be fair, the conclusion these authors draw is extremely cautious: "These unique features of SARS-CoV-2 raise several questions concerning the proximal origin of the virus that require further discussion." They do not list the question but the implication is clear enough.
- The analysis by Boni, Robertson, and their colleagues made those researchers believe that despite the genetic closeness, RaTG13 and SARS-CoV-2 split up quite a long time ago, possibly in 1969. This analysis, however, does not account for the ability of gain of function research to speed up the evolutionary timeline and potentially push the "natural" formation of chimeric viruses.
- It could also be possible that SARS-CoV-2 might be the result of gain of function research on another virus in the Wuhan Institute of Virology repository. Quoting a private communication from a scientist I trust (who chose to remain anonymous out of personal safety concerns), "the issue is that there is this internal database at the WIV that even other Chinese scientists can't access. Even the first team to point out the similarity of SARS2 to the 4991 sequence — they had no idea that 4991 aka RaTG13 had been fully genome sequenced. What other viruses are in this database? Was the pangolin CoV RBD also in this database by mid 2019?"
- In an August 12, 2020 BioEssays paper, Sirotkin and Sirotkin assert that the WIV is sitting on somewhere in the neighborhood of 2,000 undisclosed wild viruses, and Dr. Shi

herself disclosed that 9 previously undisclosed betacoronaviruses that had been held in a WIV lab repository. The database issues are further explored in in this thread as well as in this thread.)

- All the Wuhan Institute of Virology virus databases were taken down early in 2020 and remain offline. There are estimated to be at least 100 unpublished sequences of bat betacoronaviruses in these databases which need to be sequenced by international scientists. Based on information and links provided here, these databases include:
 - WIV Database 1: <http://batvirus.whiov.ac.cn/> (Archive seems to be unavailable)
 - WIV SQL online Database 2: <http://csdata.org/p/308/>,
Archived: <https://web.archive.org/web/20200507214518/http://csdata.org/p/308/> and: <http://archive.is/HLuio>
 - WIV Database 3: <http://www.viruses.nsd.cn/vri.jsp>,
Archived: <https://web.archive.org/web/20200125203943/http://www.viruses.nsd.cn/vri.jsp>, Discussion of significance here: Guoke Faji 2019/236 and the SARS-CoV-2 Outbreak <http://archive.is/uHqSw#selection-29.0-29.47>
 - WIV Database 4: <http://www.viruses.nsd.cn/chinavpi>,
Archived: <https://web.archive.org/web/20200404100024/http://www.viruses.nsd.cn/chinavpi>, Referenced in a paper by Zhiming Yuan of the Key Laboratory of Special Pathogens and Biosafety, Wuhan Institute of Virology, (+86-27-87197242, Email: yzm@wh.iov.cn), "*Investigation of Viral Pathogen Profiles in Some Natural Hosts and Vectors in China*",
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6178075/>
 - WIV Database 5: http://www.wfcc.info/ccinfo/collection/col_by_country/c/86/,
Archived: https://web.archive.org/web/20200515223251/http://www.wfcc.info/ccinfo/collection/col_by_country/c/86/ which in turn links to: http://wfcc.info/ccinfo/collection/by_id/613, Archived: https://web.archive.org/web/20200108181714/http://wfcc.info/ccinfo/collection/by_id/613 links to: <http://www.virus.org.cn/> (404 for the database in question),
Archived: <https://web.archive.org/web/20191230091754/http://www.virus.org.cn/>, And an archived description of the WIV database: https://web.archive.org/web/20200117011358/http://www.whiov.ac.cn/xwdt105286/zhxw/201804/t20180423_5000795.html
- Sirotkin and Sirotkin also state: "Unless the intermediate host necessary for completing a natural zoonotic jump is identified, the dual-use gain-of-function research practice of viral serial passage should be considered a viable route by which the novel coronavirus arose."
 - "The long-standing practice of serial passage is a form of gain-of-function research that forces zoonosis between species, and requires the same molecular adaptations necessary for a natural zoonotic jump to occur within a laboratory, leaving the same genetic signatures behind as a natural jump but occurring in a much shorter period of time... serial passage through a live animal host simply forces the same molecular processes that occur in nature to happen during a zoonotic jump, and in vitro passage through cell culture mimics many elements

of this process—and neither necessarily leaves any distinguishing genetic traces.”

- “A coronavirus that targets the ACE2 receptor like SARS-CoV-2 was first isolated from a wild bat in 2013 by a team out of Wuhan. This research was funded in part by EcoHealth Alliance, and set the stage for the manipulation of bat-borne coronavirus genomes that target this receptor and can become airborne. Many more viruses have been collected in Wuhan over the years, and one research expedition captured as many as 400 wild viruses, which were added to a private repository that has since grown to over 1500 strains of virus, meaning that the Wuhan Center for Disease Control and Prevention has a massive catalogue of largely undisclosed viruses to draw from for experiments... But for whatever reason, the Wuhan Institute of Virology has refused to release the lab notebooks of its researchers, which are ubiquitous in even the simplest laboratories and are expected to be meticulously detailed given the sensitive and delicate work that takes place in BSL-4 research labs intent on documenting their intellectual property, despite the fact that these notebooks would likely be enough to exonerate the lab from having any role in the creation of SARS-CoV-2.”
- “The prospect that serial passage through lab animals or on commercial farms may have played a role in the creation of SARS-CoV-2 is also raised by an April 2020 preprint, which appears to have been retracted after Chinese authorities implemented the censorship of any papers relating to the origins of the novel coronavirus.” (For the last point, see [this link](#).)
- “These data do not support the idea that SARS-CoV-2 was circulating in humans prior to the outbreak began in Wuhan in the early winter or fall of 2019, making a zoonotic jump even more unlikely since natural jumps leave wide serological footprints in their new host populations as early variants of a prospective virus make limited and unsuccessful jumps into individuals of the new host species, a trial-and-error that must occur before mutations that allow adaptation to a new host species are selected.”
- In a BioEssays paper, issued November 17, 2020, authors Deigin and Segreto assert: “Severe acute respiratory syndrome-coronavirus (SARS-CoV)-2’s origin is still controversial. Genomic analyses show SARS-CoV-2 likely to be chimeric, most of its sequence closest to bat CoV RaTG13, whereas its receptor binding domain (RBD) is almost identical to that of a pangolin CoV. Chimeric viruses can arise *via* natural recombination or human intervention. The furin cleavage site in the spike protein of SARS-CoV-2 confers to the virus the ability to cross species and tissue barriers, but was previously unseen in other SARS-like CoVs. Might genetic manipulations have been performed in order to evaluate pangolins as possible intermediate hosts for bat-derived CoVs that were originally unable to bind to human receptors? Both cleavage site and specific RBD could result from site-directed mutagenesis, a procedure that does not leave a trace. Considering the devastating impact of SARS-CoV-2 and importance of preventing future pandemics, researchers have a responsibility to carry out a thorough analysis of all possible SARS-CoV-2 origins.” At very least, this paper credibly raises a

serious hypothesis worthy of far deeper exploration. Some key points made in the paper include:

- “the two main SARS-CoV-2 features, (1) the presence of a furin cleavage site missing in other CoVs of the same group and (2) an receptor binding domain (RBD) optimized to bind to human cells might be the result of lab manipulation techniques such as site-directed mutagenesis.”
- “In order to evaluate the emergence potential of novel CoVs, researchers have created a number of chimeric CoVs, consisting of bat CoV backbones, normally unable to infect human cells, whose spike proteins were replaced by those from CoVs compatible with human ACE2. These chimeras were meant to simulate recombination events that might occur in nature... Synthetically generating diverse panels of potential pre-emergent CoVs was declared a goal of active grants for the EcoHealth Alliance, which funded some of such research at WIV, in collaboration with laboratories in the USA and other international partners.”
- “Due to the broad-spectrum of research conducted over almost 20 years on bat SARS-CoVs justified by their potential to spill over from animal to human, a possible synthetic origin by laboratory engineering of SARS-CoV-2 cannot be excluded... SARS-CoV-2 could have been synthesized by combining a backbone similar to RaTG13 with the RBD of CoV similar to the one recently isolated from pangolins.”
- “Another open question is the reason for modification and subsequent deletion of WIV’s own viral database.”
- China has taken a series of steps since the beginning of this crisis which seem consistent with a coverup. Although the coverup began with local and provincial Wuhan authorities, it later involved decisions made by the Chinese leadership at the highest level. These steps include:
 - On December 31, Chinese authorities started censoring news of the virus from search engines, deleting terms including “SARS variation,” “Wuhan Seafood market” and “Wuhan Unknown Pneumonia.” (Daily Telegraph)
 - Officials closed the market the day after notifying the WHO and sent in teams with strong disinfectants. Samples from animals were taken but, four months later, the results have not been shared with foreign scientists. The actions led to claims that they were deliberately wiping away crucial traces. (Daily Telegraph)
 - Many China scholars noted that it was quite unusual for Chinese government authorities to identify Wuhan’s Huanan South China Seafood Market so quickly as the source of the outbreak. They thought this behavior so uncharacteristic that it raised suspicions in their minds.
 - The Hubei health commission ordered genomics companies to stop testing for the new virus and to destroy all samples.
 - On January 1, an employee of a genomics company in Wuhan received a phone call from an official at the Hubei Provincial Health Commission, ordering the company to stop testing samples from Wuhan related to the new disease and to destroy all existing samples. (Caixin Global)

- On January 1, Wuhan Institute of Virology's director general, Yanyi Wang, messaged her colleagues, saying the National Health Commission told her the lab's COVID-19 data shall not be published on social media and shall not be disclosed to the media. And on January 3, the commission sent this document, never posted online, but saved by researchers, telling labs to destroy COVID-19 samples or send them to the depository institutions designated by the state. (Bulletin of the Atomic Scientists)
- On January 3, China's National Health Commission (NHC) ordered institutions not to publish any information related to the unknown disease and ordered labs to transfer any samples they had to designated testing institutions or destroy them. (Caixin Global)
- Even with full sequences decoded by three state labs independently, Chinese health officials remained silent. (AP)
- China sat on releasing the genetic map, or genome, of the virus for more than a week after three different government labs had fully decoded the information. Tight controls on information and competition within the Chinese public health system were to blame, according to dozens of interviews and internal documents. (AP)
- WHO officials complained in internal meetings that they were making repeated requests to the Chinese authorities for more data, especially to find out if the virus could spread efficiently between humans, but to no avail. "We have informally and formally been requesting more epidemiological information," WHO's China representative Galea said. "But when asked for specifics, we could get nothing." (AP)
- Beijing did not notify the World Health Organization of the outbreak for at least four days after Wuhan officials were notified. A WHO investigation team was not allowed to visit Wuhan until three weeks after that, and the team was not given full and unrestricted access even during this preliminary field visit
- The Chinese government closed the laboratory in Shanghai that first published the genome of COVID-19 on January 10, explaining that it had been shuttered for "rectification." Chinese citizens who reported on the coronavirus were censured and, in some cases, "disappeared." These have included businessman Fang Bin, lawyer Chen Qiushi, former state TV reporter Li Zehua and, most recently, Zhang Zhan, a lawyer. They are reportedly being held in extrajudicial detention centers for speaking out about China's response to the pandemic. (Bulletin of the Atomic Scientists)
- Chinese government labs only released the genome after another lab published it ahead of authorities on a virologist website on Jan. 11. Even then, China stalled for at least two weeks more on providing WHO with detailed data on patients and cases, according to recordings of internal meetings held by the U.N. health agency through January — all at a time when the outbreak arguably might have been dramatically slowed. (AP)
- Although international law obliges countries to report information to WHO that could have an impact on public health, the U.N. agency has no enforcement

powers and cannot independently investigate epidemics within countries. Instead, it must rely on the cooperation of member states. According to WHO's chief of emergencies, Dr. Michael Ryan, this type of obfuscation and interference "would not happen in Congo and did not happen in Congo and other places." (AP)

- Not only did China block the WHO investigation team from going to Wuhan for nearly a month, it also severely curtailed its activities after that.
- On Jan. 14, the head of China's National Health Commission said in a confidential teleconference with provincial health officials that the situation was "severe and complex," that "clustered cases suggest that human-to-human transmission is possible," and that "the risk of transmission and spread is high." The Commission issued a 63-page document on response procedures that same day that was labeled "internal" and "not to be publicly disclosed." The next day, the head of China's disease control emergency center, announced on state television that "the risk of sustained human-to-human transmission is low." This same message was delivered to the World Health Organization. (Washington Post)
- Between the day the full genome was first decoded by a government lab on Jan. 2 and the day WHO declared a global emergency on Jan. 30, the outbreak spread by a factor of 100 to 200 times, according to retrospective infection data from the Chinese Center for Disease Control and Prevention. (AP) Chinese officials actively lobbied the WHO to prevent the emergency declaration, which almost certainly slowed the international response,
- Offers from the United States to send medical experts to Wuhan in early January were rejected by the central government. (Diplomat)
- This Chinese preprint paper was released in February 2020 and then mysteriously retracted. In it, two Chinese experts assert that, "Somebody was entangled with the evolution of 2019-nCoV coronavirus. In addition to origins of natural recombination and intermediate host, the killer coronavirus probably originated from a laboratory in Wuhan... Regulations may be taken to relocate these laboratories far away from city center and other densely populated places."
- Although WIV officials have commented publicly about social media posting alleging that one of their prior researchers may be "patient zero," the WIV has not provided any information about that person
- A WIV researcher who publicly accused the director of the Institute of selling infected lab animals to vendors on Weibo (with pictures of herself and her employee ID included) later claimed she was 'hacked' and disavowed her prior allegation
- In contrast to its earlier (and inaccurate) assertion that the outbreak originated in the Wuhan seafood market, a Ministry of foreign Affairs spokesperson on March 12 accused the United States Army of intentionally bringing SARS-CoV-2 to Wuhan

- Beijing disinfected the Wuhan market before a full international investigation could be conducted and 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. (Washington Post)
- On Feb. 14, Chinese President Xi Jinping called for a new biosecurity law to be accelerated. On Wednesday, The Chinese government has placed severe restrictions requiring approval before any research institution publishes anything on the origin of the novel coronavirus. (Washington Post)
- This was followed immediately by a China Ministry of Science & Technology announcement of new guidelines for laboratories, especially in handling viruses. Almost at the same time, the Chinese newspaper Global Times published an article on “chronic inadequate management issues at laboratories, including problems of biological wastes.”
- Labs analyzing the pathogen were instructed to destroy samples, a health center that had published the virus’s genome sequence was temporarily shut down the following day, and doctors were prevented from submitting case information to the country’s infectious disease tracking network. (Diplomat)
- Reports of health care workers falling ill, an early indicator of human-to-human transmission, were suppressed. More indirectly, state media coverage of doctors being penalized reportedly had a chilling effect on other medical professionals who might have sounded the alarm. (Diplomat)
- In an official document marked “internal document, please keep confidential” reported out by CNN, Hubei provincial officials listed 5,918 new cases for Feb. 10, more than twice what was reported publicly for all of China on that day. On March 7, the total death toll in Hubei was listed in the report at 3,456 but publicly stated as 2,986. According to the Washington Post, “the Hubei documents add weight to the conclusion that China deliberately hid the true dimensions of the disaster.”
- In March 2020, Beijing announced the expulsion of American journalists working for The New York Times, The Wall Street Journal and The Washington Post, the media organizations who have exposed some of the most significant misdeeds and coverups by the Chinese government over recent decades
- In April 2020, with the outbreak in full swing, the WIV deleted a press release detailing the January 2019 U.S. State Department visit
- The Chinese government has now banned any researcher from publishing anything on the origins of this crisis without prior approval of the Ministry of Science and Technology (Nature)
- On April 24, the New York Times reported that Beijing has successfully pressured European Union officials to water down references to China in an EU report. The original language had stated, “China has continued to run a global disinformation

campaign to deflect blame for the outbreak of the pandemic and improve its international image... Both overt and covert tactics have been observed.”

- It appears there may have been a sudden drop in cellphone usage at WIV in early October followed by a cellphone blackout, suggesting the possibility of an accident inside WIV on October 6 followed by a traffic closure. Without further detail about sourcing, however, this information remains speculative. (E-PAI report)
- Zhang Zan, a Chinese citizen journalist arrested by Chinese authorities in May for asking tough questions about the origin of the pandemic and accused, absurdly, of “picking quarrels and provoking troubles,” was sentenced to four years in prison on December 28, 2020. According to Quartz: Three other citizen journalists—Chen Qiushi, Fang Bin, and Li Zehua—all disappeared in February as soon as their coverage of Wuhan during the pandemic started to gain traction online. Li Zehua resurfaced in April, saying he had been taken by police on suspicion of disturbing public order but was later released as the authorities did not press charges. Meanwhile, Chen and Fang’s whereabouts still aren’t known, though Chen is reportedly staying under home surveillance at his parents’ house.
- On November 25, 2020, Kyodo News reported that “Chinese authorities warned doctors, who responded to the novel coronavirus in the early stage of the outbreak in Wuhan, that they could be punished for espionage if they revealed what went on during the period.”
- Also in November, 2020, the Chinese government launched a concerted propaganda campaign claiming, without meaningful evidence, that the pandemic began in the Indian subcontinent.
- This December 19, 2020 New York Times article outlines in stunning detail the extent to which China actively and aggressively suppressed information about the pandemic, silenced whistleblowers and people raising essential questions, the manipulated outgoing information in order to hoard essential supplies from abroad. This history, in the context of COVID-19 and many other “sensitive” issues, suggests that an international investigation into the origins of COVID-19 that relies primarily on data gathered and information provided by the Chinese authorities, as the WHO investigation appears to do, can not be considered legitimate.
- According to a December 30, 2020 AP article, “More than a year since the first known person was infected with the coronavirus, an AP investigation shows the Chinese government is strictly controlling all research into its origins, clamping down on some while actively promoting fringe theories that it could have come from outside China. The government is handing out hundreds of thousands of dollars in grants to scientists researching the virus’ origins in southern China and affiliated with the military, the AP has found. But it is monitoring their findings and mandating that the publication of any data or research must be approved by a new task force managed by China’s cabinet, under direct orders from President Xi Jinping, according to internal documents obtained by the AP. A rare leak from

within the government, the dozens of pages of unpublished documents confirm what many have long suspected: The clampdown comes from the top."

○ Here is a link to the official Chinese regulation.

- On April 18, 2020, Director of the Wuhan Institute of Virology of the Chinese Academy of Sciences said in an interview that "there is no way this virus came from us."
- In early May, the World Health Organization's representative in China, Gauden Galea, publicly complained that China had refused repeated requests to permit the WHO to participate in whatever investigations the Chinese government was undertaking itself. He said that the WHO had not been given access to laboratory logs at the WIV or the Wuhan Chinese Center for Disease Control and Prevention. (Bulletin of the Atomic Scientists)
- On May 3, US Secretary of State Mike Pompeo said "There is a significant amount of evidence that this came from that laboratory in Wuhan." China's Global Times, run by the ruling Communist Party's official People's Daily, said in an editorial responding to this interview that "The Trump administration continues to engage in unprecedented propaganda warfare while trying to impede global efforts in fighting the COVID-19 pandemic."
- On May 4, the Guardian claimed its sources insisted a "15-page dossier" highlighted by the Australian Daily Telegraph accusing China of a deadly cover up was not culled from intelligence from the Five Eyes Network, an alliance between the UK, US, Australia, New Zealand and Canada.
- Bloomberg reported on May 5 that a majority of the 17 agencies that provide and analyze intelligence for the U.S. government believe the pandemic started after the virus was leaked from the Wuhan lab, but based mostly on circumstantial evidence.
- The U.S. Department of Homeland Security and Britain's National Cyber Security Center recently issued a statement saying hackers are "actively targeting organisations ... that include healthcare bodies, pharmaceutical companies, academia, medical research organisations, and local government." This was widely construed as suggesting that state-sponsored Chinese hackers were attempting to steal COVID-19 research. (NPR)
- On May 19, the World Health Assembly agreed to an "impartial, independent and comprehensive evaluation" of the international response to COVID-19. China did not object to the resolution but Chinese president Xi Jinping said the investigation should only take place after the pandemic is contained. This is not likely to happen any time soon.
- Investigating the range of possible spillover sites—from the wet market, to an accidental lab or fieldwork infection, or an unnoticed lab leak—requires a forensic investigation. Obtaining case histories, epidemiological data, and viral samples from different times and places, including the earliest possible samples from infected individuals and samples from wildlife, is paramount... A forensic investigation would additionally involve auditing and sampling viral collections at relevant labs that had been studying coronaviruses, examining the types of experiments carried out and the viruses used, and reviewing the safety and security practices in place... A COVID-19 origins investigation will need to be

negotiated and begun rapidly before relevant data diminishes or disappears entirely as time passes. (Bulletin of the Atomic Scientists)

- Determining whether WIV had anything to do with the virus will require a forensic investigation, say several scientists. Investigators would be looking for viruses that matched the genetic sequence of SARS-CoV-2 and, if they found one, any evidence that it could have escaped. To do that, authorities would need to take samples from the lab, interview staff, review lab books and records of safety incidents, and see what types of experiment researchers had been doing. An independent investigation at the WIV facility is probably the only way to convincingly rule out the lab as a possible source of the outbreak, but such a probe is still being blocked by the Chinese authorities. (Nature) This is outrageous.
- On June 7, China issued a white paper called, "China's Actions to Fight the Covid-19 Epidemic." This document asserted: "China's action composes the heroic paean to the people's lives above all else, highlighting the responsibility of a great power to life, the people, history and the international community. China has always adhered to the concept of a community of a shared future for mankind. It has always worked hand in hand with other countries and fought side by side, making unremitting efforts to fight for an early global epidemic prevention and control." Some observers noted this narrative did not reflect an accurate assessment of the historical record of the COVID-19 pandemic or Chinese history more generally. It is estimated that 47 million people died senselessly under former Chinese Leader Mao Tse Tung.
- On July 10, the WHO announced that a two-member advance team of experts has left for China to organize an investigation into the origins of the novel coronavirus. It is unlikely this team will have the authority to conduct the type of full forensic investigation that is required.
- In fact, the WHO has agreed with the Chinese government that investigations into the first patients in China and the market's role in the outbreak will be led by Chinese scientists, with WHO experts able to review and "augment, rather than duplicate," studies undertaken by China officials. The exact language from the WHO Terms of Reference document states that "Some of the abovementioned work may already be partially done or documented by the time the international team initiates its work, and the study will therefore build on existing information and augment, rather than duplicate, ongoing or existing efforts." It also asserts that "The final composition of the international team should be agreed by both China and WHO." In light of all the evidence of active efforts by the Chinese government to destroy evidence, deny access to key records, and silence relevant domestic (and even international) voices, this level of deference to Beijing falls well below the standard of even basic accountability. As I have written elsewhere, it would be wrong to blame the WHO for this given the designed weakness of its mandate, the result of efforts by many states over decades to defend state sovereignty at the expense of our common good as humans sharing the same planet (sorry to throw in more idealism here, but I invite you to join OneShared.World if you are interested in addressing our world's dangerous collective action problem).

- Here is an annotated version of the WHO Terms of Reference with comments provided by Giles Demaneuf. It is abundantly clear that the Chinese government aggressively negotiated compromises, structural limitations, and borderline falsehoods into the document. I have great faith in the personal integrity of many of the ten people chosen to represent the international community in this investigation, but they will almost certainly not be able to fulfill their obligation to humanity and future generations if they follow the terms of reference to the letter. It is my hope they will demand the most thorough investigation of all possible hypotheses, demand full access to all relevant people and materials, demonstrate full transparency, and speak publicly and forcefully, in their collective and/or personal capacities, if they don't have full access to everything and everyone they need.
- On July 15, Chinese virologist Shi Zhengli, the noted WIV bat virus specialist, sent written comments to Science magazine refuting allegations of a leak. Nothing in her comments in any way reduces the pressing need for a full and unrestricted international investigation into the origins of the pandemic.
- In my July 29, 2020 Washington Post editorial, I write: "The closest known relative to SARS-CoV-2 is a virus sampled by Chinese researchers from six miners infected while working in a bat-infested cave in southern China in 2012. These miners developed symptoms we now associate with Covid-19. Half of them died. These viral samples were then taken to the Wuhan Institute of Virology—the only facility in China that's a biosafety Level 4 laboratory, the highest possible safety designation. The Level 4 designation is reserved for facilities dealing with the most dangerous pathogens. Wuhan is more than 1,000 miles north of Yunnan province, where the cave is located. If the virus jumped to humans through a series of human-animal encounters in the wild or in wet markets, as Beijing has claimed, we would likely have seen evidence of people being infected elsewhere in China before the Wuhan outbreak. We have not. The alternative explanation, a lab escape, is far more plausible. We know the Wuhan Institute of Virology was using controversial 'gain of function' techniques to make viruses more virulent for research purposes. A confidential 2018 State Department cable released this month highlighting the lab's alarming safety record should heighten our concern. Suggesting that an outbreak of a deadly bat coronavirus coincidentally occurred near the only level 4 virology institute in all of China—which happened to be studying the closest known relative of that exact virus—strains credulity."
- Understanding the link between the Chinese miners exposed in the Yunnan cave in 2012 and the potential outbreak in Wuhan in late 2019 is essential. Anyone with a serious interest in getting to the bottom of the origins questions should be required to read the July 15 Latham and Wilson Independent Science News paper in full. It states: "We suggest, first, that inside the miners RaTG13 (or a very similar virus) evolved into SARS-CoV-2, an unusually pathogenic coronavirus highly adapted to humans. Second, that the Shi lab used medical samples taken from the miners and sent to them by Kunming University Hospital for their research. It was this human-adapted virus, now known as SARS-CoV-2, that escaped from the WIV in 2019." This Frontiers in Public Health article raises similar questions.

- It is impossible to overstate the implications of the SARS-CoV-2 virus being so well adapted to humans from the outset. Zhan and Chan in their May 2 paper state that “by the time SARS-CoV-2 was first detected in late 2019, it was already pre-adapted to human transmission to an extent similar to late epidemic SARS-CoV. However, no precursors or branches of evolution stemming from a less human-adapted SARS-CoV-2-like virus have been detected... In comparison to the SARS-CoV epidemic, the SARS-CoV-2 epidemic appears to be missing an early phase during which the virus would be expected to accumulate adaptive mutations for human transmission. However, if this were the origin story of SARS-CoV-2, there is a surprising absence of precursors or branches emerging from a less recent, less adapted common ancestor among humans and animals.” The Latham and Wilson July 15 paper provides by far the best explanation: this virus that escaped from the lab had likely come from a human sample (one of the miners).
- In my Washington Post editorial, I say: “Not getting to the bottom of this crisis would be the height of absurdity. Too much is at stake. To ensure everyone’s safety, the WHO and outside investigators must be empowered to explore all relevant questions about the origins of the pandemic without limits. This comprehensive forensic investigation must include full access to all of the scientists, biological samples, laboratory records and other materials from the Wuhan virology institutes and other relevant Chinese organizations. Denying that access should be considered an admission of guilt by Beijing.”
- In my August 17 editorial in *The Hill*, I state that “Congress should immediately establish a bipartisan national commission, modeled on the 9/11 Commission, to prepare a full, complete account of four essential failures and what we can do to address them.” These four failures are ones made by China, the WHO, the US government, and all of us in not preparing for the full panoply of global existential threats. “Some may feel that establishing such a commission while the pandemic still rages would be like launching the 9/11 commission while the Twin Towers were still falling. But would it not have been better to do exactly that, rather than blindly charge into two wars without deep analysis and a long-term strategy? Getting to the bottom of our current crisis is not just an intellectual exercise. The COVID-19 pandemic is far from over but there are no guarantees that an even worse pandemic, possibly supercharged by a synthetic pathogen, might be just around the corner.”
- In September 2020, the Lancet released the first statement of its COVID-19 commission. The statement asserts: “The origins of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) are yet to be definitively determined, but evidence to date supports the view that SARS-CoV-2 is a naturally occurring virus rather than the result of laboratory creation and release. Research into the origins of SARS-CoV-2 should proceed expeditiously, scientifically, and objectively, unhindered by geopolitical agendas and misinformation.” It makes little sense for an investigation commission to claim an initial finding before a full investigation has been carried out. It would be far more credible to state that the commission would explore all possible hypothesis to help get to the bottom of the origins issue. Further, by contrasting “a naturally occurring virus rather than the result of laboratory creation and release,” the commission completely

disregards the possibility of gain of function work followed by a lab leak, the exact scenario that could potentially compromise commission chair, Peter Daszak.

- Selecting Peter Daszak to lead the Lancet commission is also questionable. As I wrote in my message to Lancet editor, Richard Horton: "Peter's organization worked closely with the Wuhan Institute of virology and supported gain of function research on bat coronaviruses. If the pandemic stems from an accidental leak of one of these viruses, Peter would potentially be implicated. I am not at all suggesting that he did anything wrong, just that one of the possible origin stories includes him. Because so much is riding on this investigation, I think it essential that we make sure the commission itself represents a balance of perspectives, while excluding conspiracy theorists and people with political axes to grind... Putting together a commission that is both impartial and balanced and seen as being impartial and balanced will be critical for everything that follows." ([Here is a Twitter link](#) to Peter describing in his own words the process for manipulating the spike proteins of coronaviruses in a lab.)
- In November, 2020, The WHO released the names of the 10 scientists selected in coordination with the Chinese government to visit Wuhan to assess the origins of the pandemic. Surprisingly, Peter Daszak was on this list. As I mentioned in a 11/27 tweet, "I have great respect for Peter but his clear conflict of interest and [prior] funding relationship with WIV should preclude him from these types of roles." I also tweeted that the key to making this a legitimate process will be "ensuring full & unrestricted access to all samples, records, scientists, etc. as part of a deep forensic investigation with no political interference" and the ability to "interview any scientist in China in conditions of complete privacy & security." I have deep reservations about the leading role the Chinese government will play in this investigation on its own failure, which already includes significant oversight of which scientists are selected as investigators and the ability to have Chinese government and government-related scientists doing the primary investigations (would we let the DRC negotiate these kinds of terms as Ebola raged?). Doing a serious investigation will absolutely require significant whistleblower protections for any Chinese scientists who may wish to come forward. This should include an anonymous and safe digital portal and significant protective safeguards including the possibility of asylum.
- This open letter to the WHO COVID-19 international investigations team outlines essential questions which must be addressed by the WHO investigation. A question not included in the petition but which I believe must be asked is: "What was and is the relationship between the Chinese People's Liberation Army and the Wuhan Institute of Virology? Was the PLA engaged in any research at the WIV and did the PLA store any viral samples in the facility prior to the outbreak?"
- On January 6, 2021, after the Chinese government failed to provide visa's for members of the WHO COVID-19 expert committee, foreign ministry spokesperson Hua Chunying stated: "on the issue of COVID-19 origin-tracing, China has always been open, transparent and responsible and taken the lead in carrying out scientific cooperation in tracing the origin with WHO with the purpose of promoting international research on origin-tracing. In February and July last year, when China was faced with daunting domestic epidemic prevention and control tasks, China invited WHO experts to China

twice to carry out cooperation on origin-tracing and formulate the China part of a global scientific cooperation plan on origin-tracing. In October last year, the Chinese side reached agreement on the members of the international expert group. Since then, the experts of the two sides have maintained frequent interactions. Four video meetings were held on October 30, December 3, December 10 and December 18 respectively. With a scientific attitude, Chinese experts shared the outcomes of China's origin-tracing efforts in a science-based and candid manner, and the cooperation between the two sides has made positive progress. Recently, in a positive and constructive attitude, China has maintained close communication with WHO on the expert panel's trip to China for cooperation on origin-tracing. At present, the global pandemic situation remains very serious, and China is also making all-out efforts to prevent and control the epidemic. Chinese health and epidemic prevention departments and experts are devoting themselves to intense anti-epidemic work. Having all this said, in order to support international COVID-19 cooperation, China has overcome difficulties, accelerated preparatory work at home and tried its best to create favorable conditions for the international expert team's visit to China. WHO knows that clearly. The issue of origin-tracing is very complicated. In order to ensure the smooth progress of the work of the international expert group in China, necessary procedures need to be fulfilled and relevant specific arrangements need to be made. At present, the two sides are in negotiating on this." This (technical term, baloney) answer begs the question that has been clear from the earliest days of the pandemic — what is China trying to hide?

- Nature Medicine published on January 13, 2021, an opinion piece by Angela Rasmussen seeking to debunk what she called "often contradictory and sometimes outright ridiculous conspiracy theories that spread faster than the virus itself." As a foundation of her argument, she asserted that "A favorite version of the laboratory-origin stories relies on the fact that SARS-CoV-2 was engineered for gain-of-function studies that were also previously performed with bat SARS-like coronaviruses to understand cross-species transmission risk (*Nat. Med.* **21**, 1508–1513; 2015). The irony is that those gain-of-function studies provided valuable information about the biology of SARS-CoV-2. Gain-of-function research is also subject to intense scrutiny and governmental oversight, precisely because of the high risk involved in conducting it safely; thus, it is extremely unlikely that gain-of-function research on hard-to-obtain coronaviruses (such as bat SARS-like coronaviruses) could occur under the radar." By definition, therefore, this argument would fail if it were shown that animal pathogen research was being carried out at WIV in secret and "under the radar."
- On January 15, 2021, the US State Department issued a Fact Sheet in which the following assertion was made: "Despite the WIV presenting itself as a civilian institution, the United States has determined that the WIV has collaborated on publications and secret projects with China's military. The WIV has engaged in classified research, including laboratory animal experiments, on behalf of the Chinese military since at least 2017." This claim was vetted with all relevant US government agencies and appears credible. In my Twitter response to this assertion I call for additional evidence of this claim to be released and for Five Eyes intelligence services to issue a joint statement assessing this claim.

- It has always been, and remains, my position, that we need to actively examine all possible origin hypothesis. This certainly includes both zoonotic jump and an accidental lab leak. Any credible investigation into the origins of COVID-19 must actively explore both of these hypotheses.
- [belgrade](#)
- [Biden](#)
- [Broad Institute](#)
- [Chen Wei](#)
- [china](#)
- [coronavirus](#)
- [covid19](#)
- [crisis](#)
- [Daszak](#)
- [epoch times](#)
- [nature medicine](#)
- [pandemic](#)
- [PLA](#)
- [RaTG13](#)
- [SARS-CoV-2](#)
- [sars-cov2](#)
- [trump](#)
- [united states](#)
- [whistleblower](#)
- [World Health Organization](#)
- [Wuhan](#)
- [Wuhan Institute of Virology](#)
- [xi jinping](#)
- [Yunnan](#)

24 Comments

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- [Dennis](#)[April 16, 2020 at 3:03 pm](#)

Keep on keeping on Jaime! We're here for the truth. I'm sure your going to dig it up somehow?.... balanced but true.???

[Reply](#)

- [Emily](#)[April 20, 2020 at 1:00 pm](#)

Thank you

Reply

- The triple truth ruth May 19, 2020 at 1:55 am

The problem with speculation concerning the possibility of an accident is that we still end up in the same place A TWO to THREE YEAR PANDEMIC that can go either way—deadlier or benign. As it is it will be hard enough for the rest of the world to get back to the task at hand rebuilding the global economy. I remember past futurists and they all ended up talking what ended up being garbage crystal eyeballing. Anything that makes this worse is exactly the sort of stupidity that got us all here. No one is looking good. Even New Zealand will sooner or later have to deal with the economic consequences. Enough with the blaming and scapegoating. IT'S THE RNA, STUPID and the stupid too.

Reply

- KLC November 24, 2020 at 8:22 am

As the author lays out clearly at the beginning of the article the point is to fully investigate the origin of this outbreak so as to implement measures that are most likely to prevent future pandemic outbreaks. It's not about blaming – it's about fact-finding and improving safety. No one with an egregious conflict of interest such as Peter Daszak should be a party to the forensic investigation of the WIV lab(s) that needs to be conducted.

Reply

- HY April 20, 2020 at 7:14 pm

Just FYI, that wet market in Wuhan did sell a lot wild animals in addition to seafood. It even had a wild animal restaurant inside. Apparently not many seafood on the menu.

Reply

- Nova Vieho May 14, 2020 at 1:49 pm

There are identical wet markets in every small and large city all over China with it's vast 1.3 billion population. Certainly Guandong and Yunan where the suspects are from host countless such markets, and are ~1000 miles away from Wuhan. Everyone please I appeal to your commonsense and try not to believe that somehow this bat virus "choose" Wuhan all places in China to jump to humans, which would be an insane coincidence with no comparison in history.

Reply

- Aaron April 21, 2020 at 1:28 am

I have an article proving that they were studying Corona type viruses derived from bats at the wuhan lab.

If you are interested email me at
aaron@riderzlaw.com

Reply

- Davina Rhine April 21, 2020 at 9:46 pm

Thank you sharing your insight and review methodology. If you haven't you may want to look at Curtards published paper that came out early April. It was detailed and thorough. Curtard made the observation that he had only seen this combination of strains experiently. The link to the full paper is in pubmed. Thank you for asking the difficult questions which it seems for whatever reason the majority in postions of influence, media, institutions or policy arent asking at best or worst censoring those who are. This applies to questions not only of origin but of treatments and management including public policy decisions. Unfortunately the general public en masse are also getting angry about these questions being raised which is baffling; you cant make robust and critical decisions that affect many without vigirous review of all the data, science and scenarios especially from the perspective of cost benefit analysis and therapeutic management.

Reply

- Alex Hallatt April 23, 2020 at 6:02 pm

This is in that Nature Medicine paper you reference first:

"Theories of SARS-CoV-2 origins

It is improbable that SARS-CoV-2 emerged through laboratory manipulation of a related SARS-CoV-like coronavirus. As noted above, the RBD of SARS-CoV-2 is optimized for binding to human ACE2 with an efficient solution different from those previously predicted^{7,11}. Furthermore, if genetic manipulation had been performed, one of the several reverse-genetic systems available for betacoronaviruses would probably have been used¹⁹. However, the genetic data irrefutably show that SARS-CoV-2 is not derived from any previously used virus backbone²⁰. Instead, we propose two scenarios that can plausibly explain the origin of SARS-CoV-2: (i) natural selection in an animal host before zoonotic transfer; and (ii) natural selection in humans following zoonotic transfer. We also discuss whether selection during passage could have given rise to SARS-CoV-2."

Reply

- Derek May 9, 2020 at 12:29 am

No one is asserting that this virus was manipulated with genome editing tools or even that it was grown via in vitro culture (evidence of immunoevasive adaptations make it most likely to have evolved in a host); but there is evidence that these labs were collecting wild type viruses and doing animal passage gain

of function experiments, both of which could have brought this strain to Wuhan before an accidental release.

Reply

- Davina Rhine April 24, 2020 at 2:11 am

I referenced a paper looking at the covid19 strains earlier. In error I listed the scientist name as Curtard. Its Coutard. You can access it here:

<https://www.sciencedirect.com/science/article/pii/S0166354220300528>

Reply

- Melinda Correll April 29, 2020 at 1:04 pm

Thank you so much for putting together this excellent summary. I've been following this closely since the beginning and you brought out some points that I was not aware of. We have the freedom to speak out and if we don't speak out we might find some day in the near future that we can no longer. So thank you and keep on keepin on.

Reply

- Steven Atukwase May 3, 2020 at 6:47 am

As some one with some knowledge in zoology, i think that it would be necessary for the habitat of the alleged animals ie bats that could have been the source of COVID-19 virus to be thoroughly scanned in minute detail to confirm or dismiss that hypothesis. Because if the virus was from bats that were taken from a natural ecosystem, then there must be other bats over the habitat which carry those pathogens. There is no way that only one animal (one bat) could have contracted and spread the virus because they normally live in large groups., there should be others which have it. If it is discovered that there are no other bats carrying the virus then this is likely to help question the validity of that hypothesis. With the natural occurrence of the virus eliminated, that would leave the scientists to highly suspect the artificial (lab) hypothesis.

At the same time there is need to ask: If infected bats were experimented on, didn't other people e.g hunters at a different location or traders at a different market get into contact with bats from the same source and get infected? The assumption here is that the habitat was not restricted, but freely accessed. If it was restricted then the controller should be contacted for information.

The inquiry into the origin of COVID-19 is essential to prevent the resurgence of the disease after some time so it should be highly encouraged.

Mr Jamie Metzl, thank you for the interest to conduct that research as it will contribute to preventing the likely resurfacing of that virus.

Reply

- Diane May 1, 2020 at 2:21 pm

Hi Jamie, keep up your good work. At the moment we don't know why China behaved the way it did. This makes for conspiratorial thinking. While we have the freedoms to question China's behaviour and motives we should. If our conspiratorial ideas turn out to wrong at least we shall be sure of this. Keep up the investigating,
Diane

Reply

- Jon R May 3, 2020 at 4:39 pm

I used to manage a BSL-3 virology lab. I agree the most likely explanation is a laboratory accident. If this had occurred anywhere else in China I would have believed otherwise. As stated in the article these accidents happen, for instance, a very uncommon but highly lethal infection is monkey B virus which has killed researchers in the past:

<https://www.cdc.gov/herpesvirus/cause.html>

A comment that has troubled me coming out of the Chinese government was along the lines of how their authoritarian government was superior for fighting pandemic outbreaks. This was likely a reaction to some White House comment, but China is definitely a student of history and one has to wonder what steps they would take to finally become the biggest power in the world and have the Renminbi become the world's reserve currency. The later would require an enormous debt event, which we are now facing.

Reply

- Hazel Henderson May 11, 2020 at 4:45 pm

Thank you for this very useful summary. I co- wrote an article in March, 2020 with physicist Fritjof Capra, as a global systems -oriented futurist scenario , pointing to feedback loops from natural ecosystems to our unsustainable industrial lifestyles which not only make pandemics more likely, but also relate to all the crises in natural systems resulting from fossilized sectors emissions of greenhouse gases and other pollutants..This article " Pandemics :Lessons Looking Back from 2050 " is at <http://www.ethicalmarkets.com> , which is a global alternative media Certified B.Corporation I founded and have personally funded with my book royalties and our global TV series since 2004. We take no advertising and have 30,000 professional users .We would be happy to serve pro bono as one of your " media partners".I just signed up for your Newsletter .

Reply

- Gordon Guo May 14, 2020 at 2:04 pm

Thank you so much Jamie for helping everyone to focus on the "on the record" facts, common sense, and logic.

As someone with a strong connection to China, I can say that there are identical wet

markets in every small, medium, and large city all over China with it's vast 1.3 billion population. Certainly Guangdong and Yunnan province where the suspects bats are from, 1000 miles from Wuhan, have countless such markets. Everyone please I appeal to your commonsense and try not to believe that somehow this bat virus "choose" Wuhan near the WIV of all places in all of China to jump to humans, which would be an unbelievable coincidence with no comparison in history.

On more thing that is little mentioned. is that this prolific "bat woman" coronavirus research program based out of the WIV regularly treks to bat cave in Yunnan and elsewhere to collect virus samples. So the accident itself does not necessarily have to have happened inside the WIV. Despite the requirement for full hazmat suits and virus deactivation at collection, humans make mistakes and they could have accidentally infected themselves and brought it back to Wuhan where they work and live.

A final point is that the WIV is a very new lab, only commissioned 2-3 years ago as the flagship lab in China, widely praised by state media in print and even video documentaries. It's China's first attempt at the top BSL4 security. Again, common sense: new lab, new practices = higher likelihood of accidents.

Reply

- Mook Lan Fa May 17, 2020 at 5:59 am

I didn't want to believe you at first because it's the same theory that Chump is pushing but science is science and we must get to the bottom of this! 🐼 I believe you now because you don't have a dog in the hunt and you said:

- There weren't any bats for sale;
- They would've been hibernating during that time;
- The virus was a 96.4% match;
- China has a history of poor security; and
- Although you didn't say this, I believe this theory now because Pompous said that he had significant evidence that he couldn't share with a smug look on his face. It's like he's got the smoking gun document and he's going to release it right before the election...

Anyway, what I don't understand is why you don't think the virus hasn't been genetically manipulated? I'm not a scientist, but as a layman, I have been following COVID-19 closely, and I've noticed that it has attacked in sequence:

- 1) The elderly;
- 2) Those with comorbidities;
- 3) Those with latent comorbidities — almost like it's accelerating whatever is going to kill you when you grow old;
- 4) People of color;
- 5) Now children; and
- 6) Possibly hiding and coming out later.

It's acting like a bioweapon?

Reply

- dMay 22, 2020 at 7:16 am

Hi Jamie, it's a great summary and analysis, thanks.

I'd as well add here a link to the withdrawn paper of dr. Xiao, cited as well in

<https://project-evidence.github.io/>

https://chanworld.org/wp-content/uploads/wpforo/default_attachments/1581810860-447056518-Originsof2019-NCov-XiaoB-Res.pdf

I think that this is really important for these reasons:

– I think it's the first (only?) Chinese scientist paper which tries to explain the outbreak.

Some statements are actually also pretty serious and wild like

"the killer coronavirus probably originated from a laboratory in Wuhan."

and

"In summary, somebody was entangled with the evolution of 2019-nCoV coronavirus"

– dr Xiao also hypothesized two possible ways in which the contamination might have occurred:

1) from the WHCDC to the market:

"Surgery was performed on the caged animals and the tissue samples were collected for DNA and RNA extraction and sequencing

The tissue samples and contaminated trashes were source of pathogens. They were only ~280 meters from the seafood market."

2) in another hypothesis he links a possible contamination between the WHCDC (WIV) and the adjacent Union hospital:

"The WHCDC was also adjacent to the Union Hospital where the first group of doctors were infected during this epidemic.

It is plausible that the virus leaked around and some of them contaminated the initial patients in this epidemic, though solid proofs are needed in future study. "

– and then he goes on explaining the chimeric researches performed at the WHCDC(or WIV) and why a lab accident is likely.

"The second laboratory was 12 kilometers from the seafood market and belonged to Wuhan Institute of Virology, Chinese Academy of Sciences.

This laboratory reported that the Chinese horseshoe bats were natural reservoirs for the severe acute respiratory syndrome coronavirus (SARS-CoV) which caused the 2002-3 pandemic

. The principle investigator participated in a project which generated a chimeric virus using

the SARS-CoV reverse genetics system, and reported the potential for human

emergence

. A direct speculation was that SARS-CoV or its derivative might leak from the laboratory."

p.s.

typo: the market is 280 meters away from the WDC not 3 miles

"The market is also less than 3 miles away from the Wuhan Centre"

Reply

- Werner August 4, 2020 at 4:30 am

Typo: "It ((is)) my view that Chinese researchers at these institutes were studying these viruses with the best intentions of developing surveillance systems, treatments, and vaccines for the good of humanity. "

Reply

- green August 28, 2020 at 9:52 pm

"47 million people died senselessly under former Chinese Leader Mao Tse Tung" —it is a lie.

Reply

- Betty October 16, 2020 at 10:02 pm

why does the scientific community ignore these facts? You do not have to be a corona virologist to figure this sequence of events out! It is basic detective work: the viral sequence is the equivalent of finger prints.

Reply

- Frank November 24, 2020 at 3:48 am

Jamie: Your collection of information looks like a collection of partial conspiracy theories, not one compact coherent theory of how SARS-CoV-2 came to infect humans. It seems designed to appeal to our biases and emotions, not our reason. Some particulars:

The Chinese government would be behaving exactly the same way no matter how this pandemic began: The Chinese release information that places the Communist government in a good light or that punishes individuals and organizations the government wants to blame. Any information that reflects badly on the government is suppressed. It doesn't matter if the pandemic began with the transfer of the virus to people or wild animals eaten by people in bat-infested Southern China (the logical location) or the escape of the virus from a lab in Wuhan, the Chinese government would not permit an international investigation of the origins of the pandemic. They destroyed all of the samples from the Hunan Seafood (wild animal) Market, so no one could discover what role this market played a role in the pandemic – a danger that had been

recognized from the first SARS outbreak and should have been eliminated. Some, but not all, of the December 2019 cases were linked to this wild animal market, but the earliest known case today dates apparently back to at least November 17, so the first transmission to humans could have occurred in this market in November or October. Alternatively, If the virus escaped from a lab, it wouldn't have made any difference if that virus evolved naturally, was the product of gain of function experiments or was produced for more nefarious purposes. We can't logically draw any reliable conclusions from China's behavior, because totalitarian governments suppress information whenever it is in their best interest. China would not want an international team discovering or confirming ANY of these possible origins.

Since SARS-CoV-2 can be transmitted by asymptomatic or mildly symptomatic infected patients, we can't be sure that the pandemic originated in Wuhan, a location where bats aren't a major problem. Two cases of COVID were identified in France in late December in 2019. Somehow, before even being identified, the virus had traveled halfway around the world, was transmitted between humans at least once in France, and the trail apparently ended. We now know the virus had infected a number of Americans in Washington (state), California, and probably elsewhere by late January without being detected – even though doctors knew what to look for by then. Given that no one was alerted to the new disease until late December 2019 and given that asymptomatic or mildly symptomatic infected patients can transmit the virus to others, Patient Zero could have been infected ALMOST ANYWHERE AND TRAVELED TO WUHAN UNDETECTED. The disease could have been transmitted between humans a number of times in less densely populated areas without leaving a detectable trail.. What probably made Wuhan special and the "origin" of the pandemic is that it may have the site of the first super-spreader events that converted the infection into an epidemic.

The viruses from the first three SARS-CoV-2 patients were genetically different, so the disease pre-dated them. Analysis of all known variants suggests that the common ancestor to known strains existed in November 2019, or possibly October. The Chinese reported a suspected infection on November 17 in the vicinity of Wuhan. The South China Morning Post obtained a report showing the government has identified hundreds or suspected cases in December in the vicinity of Wuhan. The virus likely evolved in the logical location, bat-infected Southern China, and then traveled north to Wuhan undetected in a human or wild animal. We know that all of the December cases in Wuhan were not linked to wild animal market, but the November cases might have originated there.

Of course, it is suspicious that Wuhan contained two institutions where dangerous viruses were studied, especially a new BSL 4 institution. However, Wuhan was ALSO the site of the Hunan Seafood Market, the largest wild animal market in Central China. Wuhan is bigger than New York City, where the US pandemic first exploded. Wuhan had the sophisticated medical system needed to detect a new disease and the high population density to permit rapid growth of the pandemic.. There are probably

institutes of virology half of Chinese large cities where the pandemic could have begun. There are 9 BSL 4 facilities in the US, all but one near or in a major city. There is nothing suspicious about the presence of a virology institute in the Chinese city where the pandemic began. The fact that research was being done on SARS-like viruses is also not surprising given the outbreak of SARS-CoV-1 in China two decades earlier.. News reports that US visitors to that new lab were concerned about safety were totally misrepresented; the US personnel who visited the institute reported it was being under-utilized, because a nervous Chinese government was unwilling to sanction work with dangerous viruses the facility was designed to handle and because of a shortage of trained staff. However they noted that the latter problems was being addressed by training some staff at laboratories outside the US.

"Gain of function" experiments are performed in laboratories to rapidly simulate the evolutionary process by which viruses acquire the ability to efficiently replicate in different types of cell. Such mutated viruses are studied as models of viruses that might evolve naturally and cause pandemics. Since SARS-CoV-2 was not closely related to any known SARS-like virus and appears to have arisen from recombination (not mutation) of sequences from several different coronaviruses (most likely in bats), it probably is NOT the product of a gain of function experiment. Nor does it appear to have been genetically engineered. US funding agencies stopped gain-of-function experiments for several years (including experiments in Wuhan) while experts debated whether the information gained was worth the CUMULATIVE risk of running such experiments in dozens of labs over decades. The calculated cumulative risk was small and the risk from any one laboratory in any month (Wuhan in November 2019) was microscopic. EVERY VIRAL PANDEMIC BEFORE COVID BEGAN WHEN A VIRUS THAT REPLICATED IN A SPECIES IN CLOSE CONTACT WITH HUMANS MUTATED AND ACQUIRED THE ABILITY TO REPLICATE TO THE HIGH LEVELS IN HUMANS NEEDED FOR EFFECTIVE TRANSMISSION: Swine influenza, avian influenza. HIV (from a monkey virus that causes immunosuppression), SARS-CoV-1 (pangolins), MERS (camels), measles (cattle), smallpox (rodents), chickenpox, Hepatitis (birds?) etc. It is possible – BUT CERTAINLY NOT LIKELY ENOUGH TO WARRANT SUPPORTING CONSPIRACY THEORIES – that COVID is the first man-made pandemic. No evidence that this pandemic didn't evolve like every other pandemic in history.

Reply

- David December 12, 2020 at 2:04 pm

It's a question that may never be conclusively answered: Was the SARS-CoV-2 virus inside one of the Wuhan labs (Wuhan Institute of Virology, Wuhan CDC) before the beginning of the COVID-19 pandemic?

At the start of the outbreak, Shi Zhengli, head of the WIV's centre for emerging infectious diseases, thought it was possible that the virus had come from the WIV. She admitted she was worried and said she lost sleep thinking about it. She spoke of her

relief when she checked and found no record of the virus in her lab's records. A lab-leak hypothesis is clearly not far-fetched if Shi Zhengli herself thought it was possible and was worried sick by the idea.

It's worth re-reading Shi Zhengli's quotes from Scientific American's profile of her in March 2020: "If coronaviruses were the culprit, she remembers thinking, 'Could they have come from our lab?' ... she frantically went through her own lab's records from the past few years to check for any mishandling of experimental materials, especially during disposal. Shi breathed a sigh of relief when the results came back: none of the sequences matched those of the viruses her team had sampled from bat caves. 'That really took a load off my mind,' she says. 'I had not slept a wink for days.'"

If you accept Shi Zhengli's reassurances that there was no record of the virus in her lab, the matter is closed as far as the WIV goes. But there is good reason to be sceptical.

For one thing, Shi Zhengli would not have been the one to decide whether to disclose to the world that the virus was stored in her lab. The Chinese state alone would have made that decision. And if the virus was in the lab, it is almost certain that the Chinese state would have covered it up. This is a government that recently detained up to one million Uyghurs in concentration camps and then denied the fact despite being confronted with irrefutable evidence.

And then there's the issue of the WIV virus database being deleted. Whether or not there's anything incriminating in the virus database, the decision to delete comes across as though they're hiding something. Surely the Chinese authorities must understand that their recent behaviour and their history of cover-ups makes the lab-leak hypothesis more believable.

If the virus was inside either of the labs, it does not seem likely that it will be uncovered by the WHO's investigation into the origins of the virus. Indeed, if the virus was in the labs, it may take years or decades for the facts to emerge. In time, scientists, journalists, and others will perhaps uncover conclusive evidence. Or a whistleblower in China may get the word out. Or, as happens from time to time with authoritarian regimes, future Chinese leaders may reveal the truth if they think it's in their interests to discredit their predecessors.

For now, anyone interested in the virus's origins will remain in one of three camps: 1. Convinced of natural zoonosis 2. Convinced of a lab leak 3. Undecided and awaiting more evidence.

Reply

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