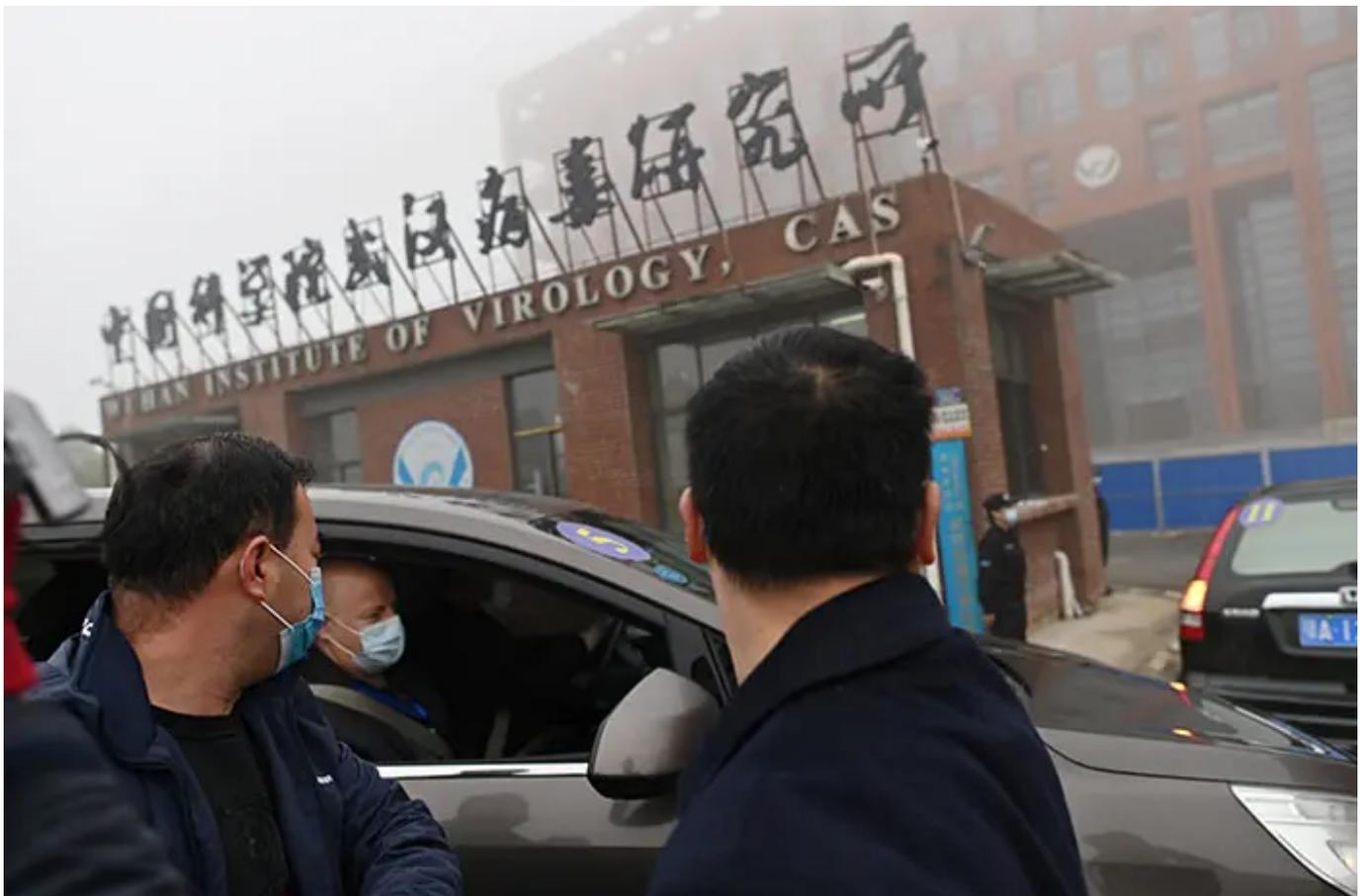




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The origin of COVID: Did people or nature open Pandora's box at Wuhan?

By Nicholas Wade | May 5, 2021



Members of the World Health Organization (WHO) team investigating the origins of the COVID-19 coronavirus arrive by car at the Wuhan Institute of Virology on February 3. (Photo by HECTOR RETAMAL/AFP via Getty Images)

The COVID-19 pandemic has disrupted lives the world over for more than a year. Its death toll will soon reach three million people. Yet the origin of pandemic remains

uncertain: The political agendas of governments and scientists have generated thick clouds of obfuscation, which the mainstream press seems helpless to dispel.

In what follows I will sort through the available scientific facts, which hold many clues as to what happened, and provide readers with the evidence to make their own judgments. I will then try to assess the complex issue of blame, which starts with, but extends far beyond, the government of China.

By the end of this article, you may have learned a lot about the molecular biology of viruses. I will try to keep this process as painless as possible. But the science cannot be avoided because for now, and probably for a long time hence, it offers the only sure thread through the maze.

The virus that caused the pandemic is known officially as SARS-CoV-2, but can be called SARS2 for short. As many people know, there are two main theories about its origin. One is that it jumped naturally from wildlife to people. The other is that the virus was under study in a lab, from which it escaped. It matters a great deal which is the case if we hope to prevent a second such occurrence.

I'll describe the two theories, explain why each is plausible, and then ask which provides the better explanation of the available facts. It's important to note that so far there is *no direct evidence* for either theory. Each depends on a set of reasonable conjectures but so far lacks proof. So I have only clues, not conclusions, to offer. But those clues point in a specific direction. And having inferred that direction, I'm going to delineate some of the strands in this tangled skein of disaster.

A tale of two theories. After the pandemic first broke out in December 2019, Chinese authorities reported that many cases had occurred in the wet market—a place selling wild animals for meat—in Wuhan. This reminded experts of the SARS1 epidemic of 2002, in which a bat virus had spread first to civets, an animal sold in wet markets, and from civets to people. A similar bat virus caused a second epidemic, known as MERS, in 2012. This time the intermediary host animal was camels.

The decoding of the virus's genome showed it belonged a viral family known as beta-coronaviruses, to which the SARS1 and MERS viruses also belong. The relationship supported the idea that, like them, it was a natural virus that had managed to jump from bats, via another animal host, to people. The wet market connection, the major point of similarity with the SARS1 and MERS epidemics, was soon broken: Chinese researchers found earlier cases in Wuhan with no link to the wet market. But that seemed not to matter when so much further evidence in support of natural emergence was expected shortly.

Wuhan, however, is home of the Wuhan Institute of Virology, a leading world center for research on coronaviruses. So the possibility that the SARS2 virus had escaped from the lab could not be ruled out. Two reasonable scenarios of origin were on the table.

From early on, public and media perceptions were shaped in favor of the natural emergence scenario by strong statements from two scientific groups. These statements were not at first examined as critically as they should have been.

“We stand together to strongly condemn conspiracy theories suggesting that COVID-19 does not have a natural origin,” a group of virologists and others wrote in the **Lancet** on February 19, 2020, when it was really far too soon for anyone to be sure what had happened. Scientists “overwhelmingly conclude that this coronavirus originated in wildlife,” they said, with a stirring rallying call for readers to stand with Chinese colleagues on the frontline of fighting the disease.

Contrary to the letter writers' assertion, the idea that the virus might have escaped from a lab invoked accident, not conspiracy. It surely needed to be explored, not rejected out of hand. A defining mark of good scientists is that they go to great pains to distinguish between what they know and what they don't know. By this criterion, the signatories of the Lancet letter were behaving as poor scientists: They were assuring the public of facts they could not know for sure were true.

It later turned out that the Lancet letter had been **organized and drafted** by Peter Daszak, president of the EcoHealth Alliance of New York. Daszak's organization funded coronavirus research at the Wuhan Institute of Virology. If the SARS2 virus had indeed escaped from research he funded, Daszak would be potentially culpable. This acute conflict of interest was not declared to the Lancet's readers. To the contrary, the letter concluded, “We declare no competing interests.”

Peter Daszak, a member of the World Health Organization (WHO) team investigating the origins of the COVID-19 coronavirus, talks on his cellphone at the Hilton Wuhan Optics Valley in Wuhan. (Photo by HECTOR RETAMAL/AFP via Getty Images)

Virologists like Daszak had much at stake in the assigning of blame for the pandemic. For 20 years, mostly beneath the public's attention, they had been playing a dangerous game. In their laboratories they routinely created viruses more dangerous than those that exist in nature. They argued that they could do so safely, and that by getting ahead of nature they could predict and prevent natural "spillovers," the cross-over of viruses from an animal host to people. If SARS2 had indeed escaped from such a laboratory experiment, a savage blowback could be expected, and the storm of public indignation would affect virologists everywhere, not just in

China. "It would shatter the scientific edifice top to bottom," an *MIT Technology Review* editor, Antonio Regalado, **said** in March 2020.

A second statement that had enormous influence in shaping public attitudes was a **letter** (in other words an opinion piece, not a scientific article) published on 17 March 2020 in the journal *Nature Medicine*. Its authors were a group of virologists led by Kristian G. Andersen of the Scripps Research Institute. "Our analyses clearly show that SARS-CoV-2 is not a laboratory construct or a purposefully manipulated virus," the five virologists declared in the second paragraph of their letter.

Unfortunately, this was another case of poor science, in the sense defined above. True, some older methods of cutting and pasting viral genomes retain tell-tale signs of manipulation. But newer methods, called "no-see-um" or "seamless" approaches, leave no defining marks. Nor do other methods for manipulating viruses such as serial passage, the repeated transfer of viruses from one culture of cells to another. If a virus has been manipulated, whether with a seamless method or by serial passage, there is no way of knowing that this is the case. Andersen and his colleagues were assuring their readers of something they could not know.

The discussion part of their letter begins, "It is improbable that SARS-CoV-2 emerged through laboratory manipulation of a related SARS-CoV-like coronavirus." But wait, didn't the lead say the virus had *clearly* not been manipulated? The authors' degree of certainty seemed to slip several notches when it came to laying out their reasoning.

The reason for the slippage is clear once the technical language has been penetrated. The two reasons the authors give for supposing manipulation to be improbable are decidedly inconclusive.

First, they say that the spike protein of SARS2 binds very well to its target, the human ACE2 receptor, but does so in a different way from that which physical calculations suggest would be the best fit. Therefore the virus must have arisen by natural selection, not manipulation.

If this argument seems hard to grasp, it's because it's so strained. The authors' basic assumption, not spelt out, is that anyone trying to make a bat virus bind to human cells could do so in only one way. First they would calculate the strongest possible fit between the human ACE2 receptor and the spike protein with which the virus latches onto it. They would then design the spike protein accordingly (by selecting the right string of amino acid units that compose it). Since the SARS2 spike protein is not of this calculated best design, the Andersen paper says, therefore it can't have been manipulated.

But this ignores the way that virologists do in fact get spike proteins to bind to chosen targets, which is not by calculation but by splicing in spike protein genes from other viruses or by serial passage. With serial passage, each time the virus's progeny are transferred to new cell cultures or animals, the more successful are selected until one emerges that makes a really tight bind to human cells. Natural selection has done all the heavy lifting. The Andersen paper's speculation about designing a viral spike protein through calculation has no bearing on whether or not the virus was manipulated by one of the other two methods.

The authors' second argument against manipulation is even more contrived. Although most living things use DNA as their hereditary material, a number of viruses use RNA, DNA's close chemical cousin. But RNA is difficult to manipulate, so researchers working on coronaviruses, which are RNA-based, will first convert the RNA genome to DNA. They manipulate the DNA version, whether by adding or altering genes, and then arrange for the manipulated DNA genome to be converted back into infectious RNA.

Only a certain number of these DNA backbones have been described in the scientific literature. Anyone manipulating the SARS2 virus "would probably" have used one of these known backbones, the Andersen group writes, and since SARS2 is not derived from any of them, therefore it was not manipulated. But the argument is conspicuously inconclusive. DNA backbones are quite easy to make, so it's obviously possible that SARS2 was manipulated using an unpublished DNA backbone.

And that's it. These are the two arguments made by the Andersen group in support of their declaration that the SARS2 virus was clearly not manipulated. And this conclusion, grounded in nothing but two inconclusive speculations, convinced the world's press that SARS2 could not have escaped from a lab. A technical critique of the Andersen letter takes it down in **harsher words**.

Science is supposedly a self-correcting community of experts who constantly check each other's work. So why didn't other virologists point out that the Andersen group's argument was full of absurdly large holes? Perhaps because in today's universities speech can be very costly. Careers can be destroyed for stepping out of line. Any virologist who challenges the community's declared view risks having his next grant application turned down by the panel of fellow virologists that advises the government grant distribution agency.

The Daszak and Andersen letters were really political, not scientific, statements, yet were amazingly effective. Articles in the mainstream press repeatedly stated that a

consensus of experts had ruled lab escape out of the question or extremely unlikely. Their authors relied for the most part on the Daszak and Andersen letters, failing to understand the yawning gaps in their arguments. Mainstream newspapers all have science journalists on their staff, as do the major networks, and these specialist reporters are supposed to be able to question scientists and check their assertions. But the Daszak and Andersen assertions went largely unchallenged.

Doubts about natural emergence. Natural emergence was the media's preferred theory until around February 2021 and the visit by a World Health Organization (WHO) commission to China. The commission's composition and access were heavily controlled by the Chinese authorities. Its members, who included the ubiquitous Daszak, kept asserting before, during, and after their visit that lab escape was extremely unlikely. But this was not quite the propaganda victory the Chinese authorities may have been hoping for. What became clear was that the Chinese had no evidence to offer the commission in support of the natural emergence theory.

This was surprising because both the SARS1 and MERS viruses had left copious traces in the environment. The intermediary host species of SARS1 was identified **within four months** of the epidemic's outbreak, and the host of MERS within nine months. Yet some 15 months after the SARS2 pandemic began, and after a presumably intensive search, Chinese researchers had failed to find either the original bat population, or the intermediate species to which SARS2 might have jumped, or any serological evidence that any Chinese population, including that of Wuhan, had ever been exposed to the virus prior to December 2019. Natural emergence remained a conjecture which, however plausible to begin with, had gained not a shred of supporting evidence in over a year.

And as long as that remains the case, it's logical to pay serious attention to the alternative conjecture, that SARS2 escaped from a lab.

Why would anyone want to create a novel virus capable of causing a pandemic? Ever since virologists gained the tools for manipulating a virus's genes, they have argued they could get ahead of a potential pandemic by exploring how close a given animal virus might be to making the jump to humans. And that justified lab experiments in enhancing the ability of dangerous animal viruses to infect people, virologists asserted.

With this rationale, they have recreated the 1918 flu virus, shown how the almost extinct polio virus can be synthesized from its published DNA sequence, and introduced a smallpox gene into a related virus.

These enhancements of viral capabilities are known blandly as gain-of-function experiments. With coronaviruses, there was particular interest in the spike proteins, which jut out all around the spherical surface of the virus and pretty much determine which species of animal it will target. In 2000 Dutch researchers, for instance, earned the gratitude of rodents everywhere by **genetically engineering** the spike protein of a mouse coronavirus so that it would attack only cats.

The spike proteins on the coronavirus's surface determine which animal it can infect. Image credit: CDC.gov

Virologists started studying bat coronaviruses in earnest after these turned out to be the source of both the SARS1 and MERS epidemics. In particular, researchers wanted to understand what changes needed to occur in a bat virus's spike proteins before it could infect people.

Researchers at the Wuhan Institute of Virology, led by China's leading expert on bat viruses, Shi Zheng-li or "Bat Lady," mounted frequent expeditions to the bat-infested caves of Yunnan in southern China and collected around a hundred different bat coronaviruses.

Shi then teamed up with Ralph S. Baric, an eminent coronavirus researcher at the University of North Carolina. **Their work** focused on enhancing the ability of bat viruses to attack humans so as to "examine the emergence potential (that is, the potential to infect humans) of circulating bat CoVs [coronaviruses]." In pursuit of this aim, in November 2015 they created a novel virus by taking the backbone of the SARS1 virus and replacing its spike protein with one from a bat virus (known as SHC014-CoV). This manufactured virus was able to infect the cells of the human airway, at least when tested against a lab culture of such cells.

The SHC014-CoV/SARS1 virus is known as a chimera because its genome contains genetic material from two strains of virus. If the SARS2 virus were to have been cooked up in Shi's lab, then its direct prototype would have been the SHC014-CoV/SARS1 chimera, the potential danger of which concerned many observers and prompted intense discussion.

"If the virus escaped, nobody could predict the trajectory," **said** Simon Wain-Hobson, a virologist at the Pasteur Institute in Paris.

Baric and Shi referred to the obvious risks in their paper but argued they should be weighed against the benefit of foreshadowing future spillovers. Scientific review panels, they wrote, "may deem similar studies building chimeric viruses based on circulating strains too risky to pursue." Given various restrictions being placed on gain-of function (GOF) research, matters had arrived in their view at "a crossroads of GOF research concerns; the potential to prepare for and mitigate future outbreaks must be weighed against the risk of creating more dangerous pathogens. In developing policies moving forward, it is important to consider the value of the data generated by these studies and whether these types of chimeric virus studies warrant further investigation versus the inherent risks involved."

That statement was made in 2015. From the hindsight of 2021, one can say that the value of gain-of-function studies in preventing the SARS2 epidemic was zero. The risk was catastrophic, if indeed the SARS2 virus was generated in a gain-of-function experiment.

Inside the Wuhan Institute of Virology. Baric had developed, and taught Shi, a general method for engineering bat coronaviruses to attack other species. The specific

targets were human cells grown in cultures and humanized mice. These laboratory mice, a cheap and ethical stand-in for human subjects, are genetically engineered to carry the human version of a protein called ACE2 that studs the surface of cells that line the airways.

Shi returned to her lab at the Wuhan Institute of Virology and resumed the work she had started on genetically engineering coronaviruses to attack human cells. How can we be so sure?

A May 20, 2020, photo of the Wuhan Institute of Virology in Wuhan, where research on bat coronaviruses was conducted. (Photo by Kyodo News via Getty Images)

Because, by a strange twist in the story, her work was funded by the National Institute of Allergy and Infectious Diseases (NIAID), a part of the US National Institutes of Health (NIH). And grant proposals that funded her work, which are a matter of public record, specify exactly what she planned to do with the money.

The grants were assigned to the prime contractor, Daszak of the EcoHealth Alliance, who subcontracted them to Shi. Here are extracts from the grants for fiscal years 2018 and 2019. (“CoV” stands for coronavirus and “S protein” refers to the virus’s spike protein.)

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

“We will use S protein sequence data, **infectious clone technology**, in vitro and in vivo infection experiments and analysis of receptor binding to test the hypothesis that % divergence thresholds in S protein sequences predict spillover potential.”

What this means, in non-technical language, is that Shi set out to create novel coronaviruses with the highest possible infectivity for human cells. Her plan was to take genes that coded for spike proteins possessing a variety of measured affinities for human cells, ranging from high to low. She would insert these spike genes one by one into the backbone of a number of viral genomes (“reverse genetics” and “infectious clone technology”), creating a series of chimeric viruses. These chimeric viruses would then be tested for their ability to attack human cell cultures (“in vitro”) and humanized mice (“in vivo”). And this information would help predict the likelihood of “spillover,” the jump of a coronavirus from bats to people.

The methodical approach was designed to find the best combination of coronavirus backbone and spike protein for infecting human cells. The approach could have generated SARS2-like viruses, and indeed may have created the SARS2 virus itself with the right combination of virus backbone and spike protein.

It cannot yet be stated that Shi did or did not generate SARS2 in her lab because her records have been sealed, but it seems she was certainly on the right track to have done so. “It is clear that the Wuhan Institute of Virology was systematically constructing novel chimeric coronaviruses and was assessing their ability to infect human cells and human-ACE2-expressing mice,” says Richard H. Ebright, a molecular biologist at Rutgers University and leading expert on biosafety.

“It is also clear,” Ebright said, “that, depending on the constant genomic contexts chosen for analysis, this work could have produced SARS-CoV-2 or a proximal progenitor of SARS-CoV-2.” “Genomic context” refers to the particular viral backbone used as the testbed for the spike protein.

The lab escape scenario for the origin of the SARS2 virus, as should by now be evident, is not mere hand-waving in the direction of the Wuhan Institute of Virology. It is a detailed proposal, based on the specific project being funded there by the NIAID.

Even if the grant required the work plan described above, how can we be sure that the plan was in fact carried out? For that we can rely on the word of Daszak, who has been much protesting for the last 15 months that lab escape was a ludicrous **conspiracy theory** invented by China-bashers.

On December 9, 2019, before the outbreak of the pandemic became generally known, Daszak gave an **interview** in which he talked in glowing terms of how researchers at the Wuhan Institute of Virology had been reprogramming the spike protein and generating chimeric coronaviruses capable of infecting humanized mice.

“And we have now found, you know, after 6 or 7 years of doing this, over 100 new SARS-related coronaviruses, very close to SARS,” Daszak says around minute 28 of the interview. “Some of them get into human cells in the lab, some of them can cause SARS disease in humanized mice models and are untreatable with therapeutic monoclonals and you can't vaccinate against them with a vaccine. So, these are a clear and present danger....

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“Interviewer: You say these are diverse coronaviruses and you can't vaccinate against them, and no anti-virals—so what do we do?

“Daszak: Well I think...coronaviruses—you can manipulate them in the lab pretty easily. Spike protein drives a lot of what happen with coronavirus, in zoonotic risk. So you can get the sequence, you can build the protein, and we work a lot with Ralph Baric at UNC to do this. Insert into the backbone of another virus and do some work in the lab. So you can get more predictive when you find a sequence. You've got this diversity. Now the logical progression for vaccines is, if you are going to develop a vaccine for SARS, people are going to use pandemic SARS, but let's insert some of these other things and get a better vaccine.” The insertions he referred to perhaps included an element called the furin cleavage site, discussed below, which greatly increases viral infectivity for human cells.

In disjointed style, Daszak is referring to the fact that once you have generated a novel coronavirus that can attack human cells, you can take the spike protein and make it the basis for a vaccine.

One can only imagine Daszak's reaction when he heard of the outbreak of the epidemic in Wuhan a few days later. He would have known better than anyone the

Wuhan Institute's goal of making bat coronaviruses infectious to humans, as well as the weaknesses in the institute's defense against their own researchers becoming infected.

But instead of providing public health authorities with the plentiful information at his disposal, he immediately launched a public relations campaign to persuade the world that the epidemic couldn't possibly have been caused by one of the institute's souped-up viruses. "The idea that this virus escaped from a lab is just pure baloney. It's simply not true," he declared in an April 2020 [interview](#).

The safety arrangements at the Wuhan Institute of Virology. Daszak was possibly unaware of, or perhaps he knew all too well, the [long history](#) of viruses escaping from even the best run laboratories. The smallpox virus escaped three times from labs in England in the 1960's and 1970's, causing 80 cases and 3 deaths. Dangerous viruses have leaked out of labs almost every year since. Coming to more recent times, the SARS1 virus has proved a true escape artist, leaking from laboratories in Singapore, Taiwan, and no less than four times from the Chinese National Institute of Virology in Beijing.

One reason for SARS1 being so hard to handle is that there were no vaccines available to protect laboratory workers. As Daszak mentioned in the December 19 interview quoted above, the Wuhan researchers too had been unable to develop vaccines against the coronaviruses they had designed to infect human cells. They would have been as defenseless against the SARS2 virus, if it were generated in their lab, as their Beijing colleagues were against SARS1.

A second reason for the severe danger of novel coronaviruses has to do with the required levels of lab safety. There are four degrees of safety, designated BSL1 to BSL4, with BSL4 being the most restrictive and designed for deadly pathogens like the Ebola virus.

The Wuhan Institute of Virology had a new BSL4 lab, but its state of readiness considerably alarmed the State Department inspectors who visited it from the Beijing embassy in 2018. "The new lab has a serious shortage of appropriately trained technicians and investigators needed to safely operate this high-containment laboratory," the inspectors wrote in a [cable](#) of January 19, 2018.

The real problem, however, was not the unsafe state of the Wuhan BSL4 lab but the fact that virologists worldwide don't like working in BSL4 conditions. You have to wear a space suit, do operations in closed cabinets, and accept that everything will

take twice as long. So the rules assigning each kind of virus to a given safety level were laxer than some might think was prudent.

Before 2020, the rules followed by virologists in China and elsewhere required that experiments with the SARS1 and MERS viruses be conducted in BSL3 conditions. But all other bat coronaviruses could be studied in BSL2, the next level down. BSL2 requires taking fairly minimal safety precautions, such as wearing lab coats and gloves, not sucking up liquids in a pipette, and putting up biohazard warning signs. Yet a gain-of-function experiment conducted in BSL2 might produce an agent more infectious than either SARS1 or MERS. And if it did, then lab workers would stand a high chance of infection, especially if unvaccinated.

Much of Shi's work on gain-of-function in coronaviruses was performed at the BSL2 safety level, as is stated in her publications and other documents. She has said in an [interview](#) with *Science* magazine that "[t]he coronavirus research in our laboratory is conducted in BSL-2 or BSL-3 laboratories."

"It is clear that some or all of this work was being performed using a biosafety standard—biosafety level 2, the biosafety level of a standard US dentist's office—that would pose an unacceptably high risk of infection of laboratory staff upon contact with a virus having the transmission properties of SARS-CoV-2," Ebright says.

"It also is clear," he adds, "that this work never should have been funded and never should have been performed."

This is a view he holds regardless of whether or not the SARS2 virus ever saw the inside of a lab.

Concern about safety conditions at the Wuhan lab was not, it seems, misplaced. According to a [fact sheet](#) issued by the State Department on January 15, 2021, "The U.S. government has reason to believe that several researchers inside the WIV became sick in autumn 2019, before the first identified case of the outbreak, with symptoms consistent with both COVID-19 and common seasonal illnesses."

David Asher, a fellow of the Hudson Institute and former consultant to the State Department, provided more detail about the incident at a [seminar](#). Knowledge of the incident came from a mix of public information and "some high end information collected by our intelligence community," he said. Three people working at a BSL3 lab at the institute fell sick within a week of each other with severe symptoms that required hospitalization. This was "the first known cluster that we're aware of, of

victims of what we believe to be COVID-19." Influenza could not completely be ruled out but seemed unlikely in the circumstances, he said.

Comparing the rival scenarios of SARS2 origin. The evidence above adds up to a serious case that the SARS2 virus could have been created in a lab, from which it then escaped. But the case, however substantial, falls short of proof. Proof would consist of evidence from the Wuhan Institute of Virology, or related labs in Wuhan, that SARS2 or a predecessor virus was under development there. For lack of access to such records, another approach is to take certain salient facts about the SARS2 virus and ask how well each is explained by the two rival scenarios of origin, those of natural emergence and lab escape. Here are four tests of the two hypotheses. A couple have some technical detail, but these are among the most persuasive for those who may care to follow the argument.

1) *The place of origin.* Start with geography. The two closest known relatives of the SARS2 virus were collected from bats living in caves in Yunnan, a province of southern China. If the SARS2 virus had first infected people living around the Yunnan caves, that would strongly support the idea that the virus had spilled over to people naturally. But this isn't what happened. The pandemic broke out 1,500 kilometers away, in Wuhan.

Beta-coronaviruses, the family of bat viruses to which SARS2 belongs, infect the horseshoe bat *Rhinolophus affinis*, which ranges across southern China. The bats' range is 50 kilometers, so it's unlikely that any made it to Wuhan. In any case, the first cases of the COVID-19 pandemic probably occurred in September, when **temperatures in Hubei province** are already cold enough to send bats into hibernation.

What if the bat viruses infected some intermediate host first? You would need a longstanding population of bats in frequent proximity with an intermediate host, which in turn must often cross paths with people. All these exchanges of virus must take place somewhere outside Wuhan, a busy metropolis which so far as is known is not a natural habitat of *Rhinolophus* bat colonies. The infected person (or animal) carrying this highly transmissible virus must have traveled to Wuhan without infecting anyone else. No one in his or her family got sick. If the person jumped on a train to Wuhan, no fellow passengers fell ill.

It's a stretch, in other words, to get the pandemic to break out naturally outside Wuhan and then, without leaving any trace, to make its first appearance there.

For the lab escape scenario, a Wuhan origin for the virus is a no-brainer. Wuhan is home to China's leading center of coronavirus research where, as noted above, researchers were genetically engineering bat coronaviruses to attack human cells. They were doing so under the minimal safety conditions of a BSL2 lab. If a virus with the unexpected infectiousness of SARS2 had been generated there, its escape would be no surprise.

2) Natural history and evolution. The initial location of the pandemic is a small part of a larger problem, that of its natural history. Viruses don't just make one time jumps from one species to another. The coronavirus spike protein, adapted to attack bat cells, needs repeated jumps to another species, most of which fail, before it gains a lucky mutation. Mutation—a change in one of its RNA units—causes a different amino acid unit to be incorporated into its spike protein and makes the spike protein better able to attack the cells of some other species.

Through several more such mutation-driven adjustments, the virus adapts to its new host, say some animal with which bats are in frequent contact. The whole process then resumes as the virus moves from this intermediate host to people.

In the case of SARS1, researchers have documented the successive changes in its spike protein as the virus evolved step by step into a dangerous pathogen. After it had gotten from bats into civets, there were six further changes in its spike protein before it became a mild pathogen in people. After a further 14 changes, the virus was much better adapted to humans, and with a further four, the **epidemic took off**.

But when you look for the fingerprints of a similar transition in SARS2, a strange surprise awaits. The virus has changed hardly at all, at least until recently. From its very first appearance, it was well adapted to human cells. Researchers led by Alina Chan of the Broad Institute compared SARS2 with late stage SARS1, which by then was well adapted to human cells, and found that the two viruses were similarly well adapted. "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," they **wrote**.

Even those who think lab origin unlikely agree that SARS2 genomes are remarkably uniform. Baric writes that "early strains identified in Wuhan, China, showed limited genetic diversity, which suggests that the virus may have been introduced from a single source."

A single source would of course be compatible with lab escape, less so with the massive variation and selection which is evolution's hallmark way of doing business.

The uniform structure of SARS2 genomes gives no hint of any passage through an intermediate animal host, and no such host has been identified in nature.

Proponents of natural emergence suggest that SARS2 incubated in a yet-to-be found human population before gaining its special properties. Or that it jumped to a host animal outside China.

All these conjectures are possible, but strained. Proponents of a lab leak have a simpler explanation. SARS2 was adapted to human cells from the start because it was grown in humanized mice or in lab cultures of human cells, just as described in Daszak's grant proposal. Its genome shows little diversity because the hallmark of lab cultures is uniformity.

Proponents of laboratory escape joke that of course the SARS2 virus infected an intermediary host species before spreading to people, and that they have identified it—a humanized mouse from the Wuhan Institute of Virology.

3) *The furin cleavage site.* The furin cleavage site is a minute part of the virus's anatomy but one that exerts great influence on its infectivity. It sits in the middle of the SARS2 spike protein. It also lies at the heart of the puzzle of where the virus came from.

The spike protein has two sub-units with different roles. The first, called S1, recognizes the virus's target, a protein called angiotensin converting enzyme-2 (or ACE2) which studs the surface of cells lining the human airways. The second, S2, helps the virus, once anchored to the cell, to fuse with the cell's membrane. After the virus's outer membrane has coalesced with that of the stricken cell, the viral genome is injected into the cell, hijacks its protein-making machinery and forces it to generate new viruses.

But this invasion cannot begin until the S1 and S2 subunits have been cut apart. And there, right at the S1/S2 junction, is the furin cleavage site that ensures the spike protein will be cleaved in exactly the right place.

The virus, a model of economic design, does not carry its own cleaver. It relies on the cell to do the cleaving for it. Human cells have a protein cutting tool on their surface known as furin. Furin will cut any protein chain that carries its signature target cutting site. This is the sequence of amino acid units proline-

arginine-arginine-alanine, or PRRA in the code that refers to each amino acid by a letter of the alphabet. PRRA is the amino acid sequence at the core of SARS2's furin cleavage site.

Viruses have all kinds of clever tricks, so why does the furin cleavage site stand out? Because of all known SARS-related beta-coronaviruses, only SARS2 possesses a furin cleavage site. All the other viruses have their S2 unit cleaved at a different site and by a different mechanism.

How then did SARS2 acquire its furin cleavage site? Either the site evolved naturally, or it was inserted by researchers at the S1/S2 junction in a gain-of-function experiment.

Consider natural origin first. Two ways viruses evolve are by mutation and by recombination. Mutation is the process of random change in DNA (or RNA for coronaviruses) that usually results in one amino acid in a protein chain being switched for another. Many of these changes harm the virus but natural selection retains the few that do something useful. Mutation is the process by which the SARS1 spike protein gradually switched its preferred target cells from those of bats to civets, and then to humans.

Mutation seems a less likely way for SARS2's furin cleavage site to be generated, even though it can't completely be ruled out. The site's four amino acid units are all together, and all at just the right place in the S1/S2 junction. Mutation is a random process triggered by copying errors (when new viral genomes are being generated) or by chemical decay of genomic units. So it typically affects single amino acids at different spots in a protein chain. A string of amino acids like that of the furin cleavage site is much more likely to be acquired all together through a quite different process known as recombination.

Recombination is an inadvertent swapping of genomic material that occurs when two viruses happen to invade the same cell, and their progeny are assembled with bits and pieces of RNA belonging to the other. Beta-coronaviruses will only combine with other beta-coronaviruses but can acquire, by recombination, almost any genetic element present in the collective genomic pool. What they cannot acquire is an element the pool does not possess. And no known SARS-related beta-coronavirus, the class to which SARS2 belongs, possesses a furin cleavage site.

Proponents of natural emergence say SARS2 could have picked up the site from some as yet unknown beta-coronavirus. But bat SARS-related beta-

coronaviruses evidently don't need a furin cleavage site to infect bat cells, so there's no great likelihood that any in fact possesses one, and indeed none has been found so far.

The proponents' next argument is that SARS2 acquired its furin cleavage site from people. A predecessor of SARS2 could have been circulating in the human population for months or years until at some point it acquired a furin cleavage site from human cells. It would then have been ready to break out as a pandemic.

If this is what happened, there should be traces in hospital surveillance records of the people infected by the slowly evolving virus. But none has so far come to light. According to the WHO [report on the origins of the virus](#), the sentinel hospitals in Hubei province, home of Wuhan, routinely monitor influenza-like illnesses and "no evidence to suggest substantial SARSCoV-2 transmission in the months preceding the outbreak in December was observed."

So it's hard to explain how the SARS2 virus picked up its furin cleavage site naturally, whether by mutation or recombination.

That leaves a gain-of-function experiment. For those who think SARS2 may have escaped from a lab, explaining the furin cleavage site is no problem at all. "Since 1992 the virology community has known that the one sure way to make a virus deadlier is to give it a furin cleavage site at the S1/S2 junction in the laboratory," [writes](#) Steven Quay, a biotech entrepreneur interested in the origins of SARS2. "At least 11 gain-of-function experiments, adding a furin site to make a virus more infective, are published in the open literature, including [by] Dr. Zhengli Shi, head of coronavirus research at the Wuhan Institute of Virology."

4) A question of codons. There's another aspect of the furin cleavage site that narrows the path for a natural emergence origin even further.

As everyone knows (or may at least recall from high school), the genetic code uses three units of DNA to specify each amino acid unit of a protein chain. When read in groups of 3, the 4 different kinds of DNA unit can specify $4 \times 4 \times 4$ or 64 different triplets, or codons as they are called. Since there are only 20 kinds of amino acid, there are more than enough codons to go around, allowing some amino acids to be specified by more than one codon. The amino acid arginine, for instance, can be designated by any of the six codons CGU, CGC, CGA, CGG, AGA or AGG, where A, U, G and C stand for the four different kinds of unit in RNA.

Here's where it gets interesting. Different organisms have different codon preferences. Human cells like to designate arginine with the codons CGT, CGC or CGG. But CGG is coronavirus's least popular codon for arginine. Keep that in mind when looking at how the amino acids in the furin cleavage site are encoded in the SARS2 genome.

Now the functional reason why SARS2 has a furin cleavage site, and its cousin viruses don't, can be seen by lining up (in a computer) the string of nearly 30,000 nucleotides in its genome with those of its cousin coronaviruses, of which the closest so far known is one called RaTG13. Compared with RaTG13, SARS2 has a 12-nucleotide insert right at the S1/S2 junction. The insert is the sequence T-CCT-CGG-CGG-GC. The CCT codes for proline, the two CGG's for two arginines, and the GC is the beginning of a GCA codon that codes for alanine.

There are several curious features about this insert but the oddest is that of the two side-by-side CGG codons. Only 5 percent of SARS2's arginine codons are CGG, and the double codon CGG-CGG has not been found in any other beta-coronavirus. So how did SARS2 acquire a pair of arginine codons that are favored by human cells but not by coronaviruses?

Proponents of natural emergence have an up-hill task to explain all the features of SARS2's furin cleavage site. They have to postulate a recombination event at a site on the virus's genome where recombinations are rare, and the insertion of a 12-nucleotide sequence with a double arginine codon unknown in the beta-coronavirus repertoire, at the only site in the genome that would significantly expand the virus's infectivity.

"Yes, but your wording makes this sound unlikely—viruses are specialists at unusual events," is the riposte of David L. Robertson, a virologist at the University of Glasgow who regards lab escape as a conspiracy theory. "Recombination is naturally very, very frequent in these viruses, there are recombination breakpoints in the spike protein and these codons appear unusual exactly because we've not sampled enough."

Robertson is correct that evolution is always producing results that may seem unlikely but in fact are not. Viruses can generate untold numbers of variants but we see only the one-in-a-billion that natural selection picks for survival. But this argument could be pushed too far. For instance, any result of a gain-of-function experiment could be explained as one that evolution would have arrived at in time. And the numbers game can be played the other way. For the furin cleavage

site to arise naturally in SARS2, a chain of events has to happen, each of which is quite unlikely for the reasons given above. A long chain with several improbable steps is unlikely to ever be completed.

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For the lab escape scenario, the double CGG codon is no surprise. The human-preferred codon is routinely used in labs. So anyone who wanted to insert a furin cleavage site into the virus's genome would synthesize the PRRA-making sequence in the lab and would be likely to use CGG codons to do so.

"When I first saw the furin cleavage site in the viral sequence, with its arginine codons, I said to my wife it was the smoking gun for the origin of the virus," said David Baltimore, an eminent virologist and former president of CalTech. "These features make a powerful challenge to the idea of a natural origin for SARS2," he said. [1]

A third scenario of origin. There's a variation on the natural emergence scenario that's worth considering. This is the idea that SARS2 jumped directly from bats to humans, without going through an intermediate host as SARS1 and MERS did. A leading advocate is the virologist David Robertson who notes that SARS2 can attack several other species besides humans. He believes the virus **evolved a generalist capability while still in bats**. Because the bats it infects are widely distributed in southern and central China, the virus had ample opportunity to jump to people, even though it seems to have done so on only one known occasion. Robertson's thesis explains why no one has so far found a trace of SARS2 in any intermediate host or in human populations surveilled before December 2019. It would also explain the puzzling fact that SARS2 has not changed since it first appeared in humans—it didn't need to because it could already attack human cells efficiently.

One problem with this idea, though, is that if SARS2 jumped from bats to people in a single leap and hasn't changed much since, it should still be good at infecting bats. And it seems it isn't.

"Tested bat species are poorly infected by SARS-CoV-2 and they are therefore unlikely to be the direct source for human infection," **write a scientific group** skeptical of natural emergence.

Still, Robertson may be onto something. The bat coronaviruses of the Yunnan caves can infect people directly. In April 2012 six miners clearing bat guano from the Mojiang mine contracted severe pneumonia with COVID-19-like symptoms and three

eventually died. A virus isolated from the Mojiang mine, called RaTG13, is still the closest known relative of SARS2. Much mystery surrounds the origin, reporting and strangely low affinity of RaTG13 for bat cells, as well as the nature of 8 similar viruses that Shi **reports** she collected at the same time but has not yet published despite their great relevance to the ancestry of SARS2. But all that is a story for another time. The point here is that bat viruses can infect people directly, though only in special conditions.

So who else, besides miners excavating bat guano, comes into particularly close contact with bat coronaviruses? Well, coronavirus researchers do. Shi says she and her group collected more than 1,300 bat samples during some eight visits to the Mojiang cave between 2012 and 2015, and there were doubtless many expeditions to other Yunnan caves.

Imagine the researchers making frequent trips from Wuhan to Yunnan and back, stirring up bat guano in dark caves and mines, and now you begin to see a possible missing link between the two places. Researchers could have gotten infected during their collecting trips, or while working with the new viruses at the Wuhan Institute of Virology. The virus that escaped from the lab would have been a natural virus, not one cooked up by gain of function.

The direct-from-bats thesis is a chimera between the natural emergence and lab escape scenarios. It's a possibility that can't be dismissed. But against it are the facts that 1) both SARS2 and RaTG13 seem to have only feeble affinity for bat cells, so one can't be fully confident that either ever saw the inside of a bat; and 2) the theory is no better than the natural emergence scenario at explaining how SARS2 gained its furin cleavage site, or why the furin cleavage site is determined by human-preferred arginine codons instead of by the bat-preferred codons.

Where we are so far. Neither the natural emergence nor the lab escape hypothesis can yet be ruled out. There is still no direct evidence for either. So no definitive conclusion can be reached.

That said, the available evidence leans more strongly in one direction than the other. Readers will form their own opinion. But it seems to me that proponents of lab escape can explain all the available facts about SARS2 considerably more easily than can those who favor natural emergence.

It's documented that researchers at the Wuhan Institute of Virology were doing gain-of-function experiments designed to make coronaviruses infect human cells and humanized mice. This is exactly the kind of experiment from which a SARS2-like virus

could have emerged. The researchers were not vaccinated against the viruses under study, and they were working in the minimal safety conditions of a BSL2 laboratory. So escape of a virus would not be at all surprising. In all of China, the pandemic broke out on the doorstep of the Wuhan institute. The virus was already well adapted to humans, as expected for a virus grown in humanized mice. It possessed an unusual enhancement, a furin cleavage site, which is not possessed by any other known SARS-related beta-coronavirus, and this site included a double arginine codon also unknown among beta-coronaviruses. What more evidence could you want, aside from the presently unobtainable lab records documenting SARS2's creation?

Proponents of natural emergence have a rather harder story to tell. The plausibility of their case rests on a single surmise, the expected parallel between the emergence of SARS2 and that of SARS1 and MERS. But none of the evidence expected in support of such a parallel history has yet emerged. No one has found the bat population that was the source of SARS2, if indeed it ever infected bats. No intermediate host has presented itself, despite an intensive search by Chinese authorities that included the testing of 80,000 animals. There is no evidence of the virus making multiple independent jumps from its intermediate host to people, as both the SARS1 and MERS viruses did. There is no evidence from hospital surveillance records of the epidemic gathering strength in the population as the virus evolved. There is no explanation of why a natural epidemic should break out in Wuhan and nowhere else. There is no good explanation of how the virus acquired its furin cleavage site, which no other SARS-related beta-coronavirus possesses, nor why the site is composed of human-preferred codons. The natural emergence theory battles a bristling array of implausibilities.

The records of the Wuhan Institute of Virology certainly hold much relevant information. But Chinese authorities seem unlikely to release them given the substantial chance that they incriminate the regime in the creation of the pandemic. Absent the efforts of some courageous Chinese whistle-blower, we may already have at hand just about all of the relevant information we are likely to get for a while.

So it's worth trying to assess responsibility for the pandemic, at least in a provisional way, because the paramount goal remains to prevent another one. Even those who aren't persuaded that lab escape is the more likely origin of the SARS2 virus may see reason for concern about the present state of regulation governing gain-of-function research. There are two obvious levels of responsibility: the first, for allowing virologists to perform gain-of-function experiments, offering minimal gain and vast risk; the second, if indeed SARS2 was generated in a lab, for allowing the virus to

escape and unleash a world-wide pandemic. Here are the players who seem most likely to deserve blame.

1. *Chinese virologists.* First and foremost, Chinese virologists are to blame for performing gain-of-function experiments in mostly BSL2-level safety conditions which were far too lax to contain a virus of unexpected infectiousness like SARS2. If the virus did indeed escape from their lab, they deserve the world's censure for a foreseeable accident that has already caused the deaths of three million people. True, Shi was trained by French virologists, worked closely with American virologists and was following international rules for the containment of coronaviruses. But she could and should have made her own assessment of the risks she was running. She and her colleagues bear the responsibility for their actions.

I have been using the Wuhan Institute of Virology as a shorthand for all virological activities in Wuhan. It's possible that SARS2 was generated in some other Wuhan lab, perhaps in an attempt to make a vaccine that worked against all coronaviruses. But until the role of other Chinese virologists is clarified, Shi is the public face of Chinese work on coronaviruses, and provisionally she and her colleagues will stand first in line for opprobrium.

2. *Chinese authorities.* China's central authorities did not generate SARS2, but they sure did their utmost to conceal the nature of the tragedy and China's responsibility for it. They suppressed all records at the Wuhan Institute of Virology and closed down its virus databases. They released a trickle of information, much of which may have been outright false or designed to misdirect and mislead. They did their best to manipulate the WHO's inquiry into the virus's origins, and led the commission's members on a fruitless run-around. So far they have proved far more interested in deflecting blame than in taking the steps necessary to prevent a second pandemic.

3. *The worldwide community of virologists.* Virologists around the world are a loose-knit professional community. They write articles in the same journals. They attend the same conferences. They have common interests in seeking funds from governments and in not being overburdened with safety regulations.

Virologists knew better than anyone the dangers of gain-of-function research. But the power to create new viruses, and the research funding obtainable by doing so, was too tempting. They pushed ahead with gain-of-function

experiments. They lobbied against the moratorium imposed on Federal funding for gain-of-function research in 2014, and it was raised in 2017.

The benefits of the research in preventing future epidemics have so far been nil, the risks vast. If research on the SARS1 and MERS viruses could only be done at the BSL3 safety level, it was surely illogical to allow any work with novel coronaviruses at the lesser level of BSL2. Whether or not SARS2 escaped from a lab, virologists around the world have been playing with fire.

Their behavior has long alarmed other biologists. In 2014 scientists calling themselves the Cambridge Working Group urged caution on creating new viruses. In prescient words, they specified the risk of creating a SARS2-like virus. "Accident risks with newly created 'potential pandemic pathogens' raise grave new concerns," they **wrote**. "Laboratory creation of highly transmissible, novel strains of dangerous viruses, especially but not limited to influenza, poses substantially increased risks. An accidental infection in such a setting could trigger outbreaks that would be difficult or impossible to control."

When molecular biologists discovered a technique for moving genes from one organism to another, they held a public conference at Asilomar in 1975 to discuss the possible risks. Despite much internal opposition, they drew up a list of stringent safety measures that could be relaxed in future—and duly were—when the possible hazards had been better assessed.

When the CRISPR technique for editing genes was invented, biologists convened a joint report by the US, UK and Chinese national academies of science to urge restraint on making heritable changes to the human genome. Biologists who invented gene drives have also been open about the dangers of their work and have sought to involve the public.

You might think the SARS2 pandemic would spur virologists to re-evaluate the benefits of gain-of-function research, even to engage the public in their deliberations. But no. Many virologists deride lab escape as a conspiracy theory, and others say nothing. They have barricaded themselves behind a Chinese wall of silence which so far is working well to allay, or at least postpone, journalists' curiosity and the public's wrath. Professions that cannot regulate themselves deserve to get regulated by others, and this would seem to be the future that virologists are choosing for themselves.

4. The US role in funding the Wuhan Institute of Virology.[2] From June 2014 to May 2019, Daszak's EcoHealth Alliance had a **grant** from the National Institute

of Allergy and Infectious Diseases (NIAID), part of the National Institutes of Health, to do gain-of-function research with coronaviruses at the Wuhan Institute of Virology. Whether or not SARS2 is the product of that research, it seems a questionable policy to farm out high-risk research to foreign labs using minimal safety precautions. And if the SARS2 virus did indeed escape from the Wuhan institute, then the NIH will find itself in the terrible position of having funded a disastrous experiment that led to the death of more than 3 million worldwide, including more than half a million of its own citizens.

The responsibility of the NIAID and NIH is even more acute because for the first three years of the grant to EcoHealth Alliance there was a moratorium on funding gain-of-function research. When the moratorium expired in 2017, it didn't just vanish but was replaced by a reporting system, the Potential Pandemic Pathogens Control and Oversight (P3CO) Framework, which required agencies to report for review any dangerous gain-of-function work they wished to fund.

The moratorium, referred to officially as a "pause," specifically barred funding any gain-of-function research that increased the pathogenicity of the flu, MERS or SARS viruses. It **defined gain-of-function** very simply and broadly as "research that improves the ability of a pathogen to cause disease."

But then a **footnote** on p.2 of the moratorium document states that "[a]n exception from the research pause may be obtained if the head of the USG funding agency determines that the research is urgently necessary to protect the public health or national security."

This seemed to mean that either the director of the NIAID, Anthony Fauci, or the director of the NIH, Francis Collins, or maybe both, would have invoked the exemption in order to keep the money flowing to Shi's gain-of-function research, and later to avoid notifying the federal reporting system of her research.

"Unfortunately, the NIAID Director and the NIH Director exploited this loophole to issue exemptions to projects subject to the Pause –preposterously asserting the exempted research was 'urgently necessary to protect public health or national security'—thereby nullifying the Pause," Dr. Richard Ebright said in an **interview** with Independent Science News.

But it's not so clear that the NIH thought it necessary to invoke any loopholes. Fauci told a Senate hearing on May 11 that "the NIH and NIAID categorically has

not funded gain-of-function research to be conducted in the Wuhan Institute of Virology.”

This was a surprising statement in view of all the evidence about Shi's experiments with enhancing coronaviruses and the language of the moratorium statute defining gain-of-function as “any research that improves the ability of a pathogen to cause disease.”

The explanation may be one of definition. Daszak's EcoHealth Alliance, for one, believes that the term gain-of-function applies only to enhancements of viruses that infect humans, not to animal viruses. “So gain-of-function research refers specifically to the manipulation of human viruses so as to be either more easily transmissible or to cause worse infection or be easier to spread,” an Alliance official told The Dispatch Fact Check.

If the NIH shares the EcoHealth Alliance view that “gain of function” applies only to human viruses, that would explain why Fauci could assure the Senate it had never funded such research at the Wuhan Institute of Virology. But the legal basis of such a definition is unclear, and it differs from that of the moratorium language which was presumably applicable.

Definitions aside, the bottom line is that the National Institutes of Health was supporting research of a kind that could have generated the SARS2 virus, in an unsupervised foreign lab that was doing work in BSL2 biosafety conditions.

In conclusion. If the case that SARS2 originated in a lab is so substantial, why isn't this more widely known? As may now be obvious, there are many people who have reason not to talk about it. The list is led, of course, by the Chinese authorities. But virologists in the United States and Europe have no great interest in igniting a public debate about the gain-of-function experiments that their community has been pursuing for years.

Nor have other scientists stepped forward to raise the issue. Government research funds are distributed on the advice of committees of scientific experts drawn from universities. Anyone who rocks the boat by raising awkward political issues runs the risk that their grant will not be renewed and their research career will be ended. Maybe good behavior is rewarded with the many perks that slosh around the distribution system. And if you thought that Andersen and Daszak might have blotted their reputation for scientific objectivity after their partisan attacks on the lab escape scenario, look at the second and third names on this [list of recipients](#) of an \$82

million grant announced by the National Institute of Allergy and Infectious Diseases in August 2020.

The US government shares a strange common interest with the Chinese authorities: Neither is keen on drawing attention to the fact that Shi's coronavirus work was funded by the US National Institutes of Health. One can imagine the behind-the-scenes conversation in which the Chinese government says, "If this research was so dangerous, why did you fund it, and on our territory too?" To which the US side might reply, "Looks like it was you who let it escape. But do we really need to have this discussion in public?"

Fauci is a longtime public servant who served with integrity under President Trump and has resumed leadership in the Biden Administration in handling the COVID-19 epidemic. Congress, no doubt understandably, may have little appetite for hauling him over the coals for the apparent lapse of judgment in funding gain-of-function research in Wuhan.

To these serried walls of silence must be added that of the mainstream media. To my knowledge, no major newspaper or television network has yet provided readers with an in-depth news story of the lab escape scenario, such as the one you have just read, although some have run brief editorials or opinion pieces. One might think that any plausible origin of a virus that has killed three million people would merit a serious investigation. Or that the wisdom of continuing gain-of-function research, regardless of the virus's origin, would be worth some probing. Or that the funding of gain-of-function research by the NIH and NIAID during a moratorium on such funding would bear investigation. What accounts for the media's apparent lack of curiosity?

The virologists' *omertà* is one reason. Science reporters, unlike political reporters, have little innate skepticism of their sources' motives; most see their role largely as purveying the wisdom of scientists to the unwashed masses. So when their sources won't help, these journalists are at a loss.

Another reason, perhaps, is the migration of much of the media toward the left of the political spectrum. Because President Trump said the virus had escaped from a Wuhan lab, editors gave the idea little credence. They joined the virologists in regarding lab escape as a dismissible conspiracy theory. During the Trump administration, they had no trouble in rejecting the position of the intelligence services that lab escape could not be ruled out. But when Avril Haines, President Biden's director of national intelligence, said the same thing, she too was largely

ignored. This is not to argue that editors should have endorsed the lab escape scenario, merely that they should have explored the possibility fully and fairly.

People round the world who have been pretty much confined to their homes for the last year might like a better answer than their media are giving them. Perhaps one will emerge in time. After all, the more months pass without the natural emergence theory gaining a shred of supporting evidence, the less plausible it may seem. Perhaps the international community of virologists will come to be seen as a false and self-interested guide. The common sense perception that a pandemic breaking out in Wuhan might have something to do with a Wuhan lab cooking up novel viruses of maximal danger in unsafe conditions could eventually displace the ideological insistence that whatever Trump said can't be true.

And then let the reckoning begin.

Notes

[1] This quotation was added to the article after initial publication.

[2] Section revised May 18, 2021

Acknowledgements

The first person to take a serious look at the origins of the SARS2 virus was Yuri Deigin, a biotech entrepreneur in Russia and Canada. In a long and brilliant **essay**, he dissected the molecular biology of the SARS2 virus and raised, without endorsing, the possibility that it had been manipulated. The essay, published on April 22, 2020, provided a roadmap for anyone seeking to understand the virus's origins. Deigin packed so much information and analysis into his essay that some have doubted it could be the work of a single individual and suggested some intelligence agency must have authored it. But the essay is written with greater lightness and humor than I suspect are ever found in CIA or KGB reports, and I see no reason to doubt that Deigin is its very capable sole author.

In Deigin's wake have followed several other skeptics of the virologists' orthodoxy. Nikolai Petrovsky calculated how tightly the SARS2 virus binds to the ACE2 receptors of various species and found to his surprise that it seemed **optimized for the human receptor**, leading him to infer the virus might have been generated in a laboratory. Alina Chan published a **paper** showing that SARS2 from its first appearance was very well adapted to human cells.

One of the very few establishment scientists to have questioned the virologists' absolute rejection of lab escape is Richard Ebright, who has long warned against the dangers of gain-of-function research. Another is David A. Relman of Stanford University. "Even though strong opinions abound, none of these scenarios can be confidently ruled in or ruled out with currently available facts," he **wrote**. Kudos too to Robert Redfield, former director of the Centers for Disease Control and Prevention, who **told CNN** on March 26, 2021 that the "most likely" cause of the epidemic was "from a laboratory," because he doubted that a bat virus could become an extreme human pathogen overnight, without taking time to evolve, as seemed to be the case with SARS2.

Steven Quay, a physician-researcher, has applied **statistical and bioinformatic tools** to ingenious explorations of the virus's origin, showing for instance how the hospitals receiving the early patients are clustered along the Wuhan **Nº2 subway line** which connects the Institute of Virology at one end with the international airport at the other, the perfect conveyor belt for distributing the virus from lab to globe.

In June 2020 Milton Leitenberg published an **early survey** of the evidence favoring lab escape from gain-of-function research at the Wuhan Institute of Virology.

Many others have contributed significant pieces of the puzzle. "Truth is the daughter," said Francis Bacon, "not of authority but time." The efforts of people such as those named above are what makes it so.

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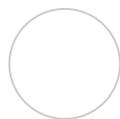


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Robert Schaefer ⌚ 4 months ago

Dear Mr. Wade, your comment that “no major newspaper or television network has yet provided readers with an in-depth news story of the lab escape scenario,” seems untrue given that CBS’s “60 Minutes” ran a segment on the lab hypothesis. Have you seen the segment, and if so, what are your opinions?

+ -101 — Reply



Gary ⌚ 4 months ago

Reply to [Robert Schaefer](#)

60 minutes!!!

You can't possibly be serious or you are simply still full on asleep....60 minutes long ago stopped being a trusted source.

+ 304 - Reply



Charles 4 months ago

Reply to [Gary](#)

But Gary, did you see the 60-Minute segment????

If not maybe you should before making your statement. If you did could you inform us of why it cannot be trusted? Honestly I want to know what you concluded and why. Can you do that?

+ -6 - Reply



Dedge 4 months ago

Reply to [Charles](#)

I agree with you. How can someone conclude that a program has no validity covering the same subject without having ever seen it?

+ -3 - Reply

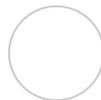


Dennis 4 months ago

Reply to [Charles](#)

I saw 60 minutes, and it doesn't come close to the kind of detailed examination that this article does.

+ 96 - Reply



Tom Krehbiel 4 months ago

Reply to [Dennis](#)

I'm sure that's true, Dennis. But it's rather unfair. There's no way a television show which has three segments consisting of perhaps 15 minutes apiece could be as in-depth as an article like this.

+ 8 - Reply



Oscar 2 months ago

Reply to [Dennis](#)

This article leaves out a lot of the technical details that go against its arguments. The crux of the problem with the lab origin theory is in the difficulty in replicating Covid-19 without cheating by reverse-engineering a virus after the fact.

+ -2 - Reply



Bruce Wing 4 months ago

Reply to [Robert Schaefer](#)

Fair comment. Maybe a better statement by the author would have been, "The overwhelming majority of the coverage on this subject has supported the contention

that the lab leak hypothesis is a hoax, but it does appear that some outlets are beginning to take the hypothesis more seriously.”

+ 50 — ➔ Reply

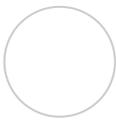


Phil ⌚ 3 months ago

🗨️ Reply to [Robert Schaefer](#)

Why does that even matter. The data and investigation he elucidates is of importance. The likely conclusion or at least conflicts of interest are what the article is about. Are we going to debate his grammar too? Find A misspelling or broken sentence and that debunks the article? Question the article and draw some conclusions people! Write your congressman, post this on social media. Demand answers! Our press is failing us either way.

+ 8 — ➔ Reply



Dan S ⌚ 4 months ago

To my knowledge, no major newspaper or television network has yet provided readers with an in-depth news story of the lab escape scenario, such as the one you have just read, although some have run brief editorials or opinion pieces.

There was this long piece from Nicolson Baker back in January covering much the same territory, though I don't know if that counts as major.

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

Usatoday might count as a major newspaper though.

<https://www.usatoday.com/in-depth/opinion/2021/03/22/why-covid-lab-leak-theory-wuhan-shouldnt-dismissed-column/4765985001/>

+ 47 — ➔ Reply



cosmictones ⌚ 4 months ago

🗨️ Reply to [Dan S](#)

He acknowledges there have been opinion pieces written on it (like the one in Usatoday). The syntax choice makes it unclear whether “brief” modifies both “editorials” and “opinion pieces” or just “editorials”. Oh well.

+ 30 — ➔ Reply



KW Sterling ⌚ 4 months ago

🗨️ Reply to [cosmictones](#)

He specifically uses the term “in-depth news story,” which would exclude opinion pieces.

+ 37 — ➔ Reply

EB ⌚ 4 months ago



| [Reply to cosmictones](#)

One huge problem in reporting is that the CCP bans foreign reporters from going in to the area, they might even kick you out all together if they catch you sniffing in the wrong area.

I have been reading about this for a year, but without proof from the scientific establishment, it was much harder.

For sure it is hard to believe anything coming out of Daszak and the other WHO, handpicked by China, investigators.

+ 38 - [Reply](#)



Plebius [🕒 4 months ago](#)

Fantastic to see this piece published here. Would love to hear a rebuttal from Daszak and the scientific community.

[✎](#) Last edited 4 months ago by Plebius

+ 431 - [Reply](#)



ralph [🕒 4 months ago](#)

Toward the end of the article it said that Trump made a comment regarding the escape of the virus. I think that Trump was the one who brought it when he came back from china.

+ -526 - [Reply](#)



KJ Potta [🕒 4 months ago](#)

| [Reply to ralph](#)

Stop with the nonsense!! Thats as bad as China blaming the US for sending the virus in with our military.

+ 132 - [Reply](#)



Leisureguy [🕒 4 months ago](#)

| [Reply to ralph](#)

If Trump had brought it back from China, the outbreak would have spread from Trump and those close to him. That is not how it in fact spread. Thus Trump did not bring it back from China.

+ 139 - [Reply](#)

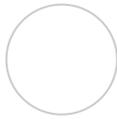


Marilyn [🕒 4 months ago](#)

| [Reply to ralph](#)

What a STUPID statement. Anyone with even half a brain knows the virus came from the lab and The CCP fast tracked the deadly virus to the world.

+ 1 - [Reply](#)



D. W. Orr ⌚ 4 months ago

Very well written and enlightening. The implications here are frightening. The Truth needs to be revealed. 3 million lives have been forsaken for what may be due to callous hubris.

+ 305 - ➔ Reply



Brandon Lerda ⌚ 3 months ago

| 🗨 Reply to [D. W. Orr](#)

Certainly many if not most of the lives lost in US were due to callous presidential hubris.+

+ -6 - ➔ Reply



Thomas ⌚ 4 months ago

Nicholson Baker published a long, well researched article in New York magazine on January 4, leaning toward lab leak.

+ 76 - ➔ Reply



Jacques Clouseau ⌚ 4 months ago

Good research and an excellent job putting it together, but I'm going to call your bluff and raise you a closed US bio lab. Speculative conspiracy theories cut both ways.

<https://www.the-scientist.com/news-opinion/cdc-shuts-down-army-labs-disease-research-66235>

+ -74 - ➔ Reply



PJBLOGGS ⌚ 4 months ago

| 🗨 Reply to [Jacques Clouseau](#)

According to Prof Francis Boyle of Law, Uni Illinois (drafted the US Congress law on bioweapons) – there is a paper trail of peer reviewed publications linking collaborative gain of function research on bat coronaviruses that involves biolabs at Uni Nth Carolina, Fort Detrick in Maryland, Winnipeg in Canada and the Wuhan Institute of Virology. These 4 labs worked on a SARS2 GOF Project. Dr Fauci was aware and involved too.

+ 69 - ➔ Reply



Lou Friend ⌚ 4 months ago

The lab escape hypothesis has been the dominant scenario presented in the US news since last March and repeated many times over. The Bayesian 'analysis' article was distributed throughout the web. I wasn't particularly impressed when he claimed the probabilities went from 98% zoonotic origin to 98% lab-created. Individual probabilities can be arbitrarily assigned to suit an agenda. The coronavirus was not that easily spread in its early stages since neither of the incidents with the miners and the many accidents at

Chapel Hill resulted in outbreaks. Both theories are plausible, while the lab release is much less probable due... [Read more »](#)

+ -168 - Reply



Jiri Severa 4 months ago

Reply to [Lou Friend](#)

This is silly patter, ignorant of most basic facts and Bayesian theory. Steven Quay's model started with a 99% zoonotic prior probability, because no similar-effect lab accident happened before. That said, though I hold Quay's work in high regard, I dislike his using a Bayesian model based on subjective estimates rather than actual measured values. I am a numbers guy who considers this a way of abusing numbers.

+ 69 - Reply



FMG 4 months ago

Reply to [Jiri Severa](#)

Being a numbers guy, you should know what it means to utilize "subjective estimates" as you label them. A prior probability distribution of a parameter that is to be estimated is not merely a subjective interpretation of a fact that we would like to quantify. In many practical applications of bayesian techniques, prior probabilities are estimates generated by previous work in the field. It is therefore often a misconception to believe that priors are made up distributions to conveniently generate "good" results. I could very much go into technical details about why using a prior, given large datasets, does not... [Read more »](#)

Last edited 4 months ago by FMG

+ 1 - Reply



Dan Eastwood 4 months ago

Reply to [Lou Friend](#)

I am a biostatistician and I examined parts of Quay's report. He is doing a series of Bayesian calculations based on questionable assumptions and conclusions. In one part, he examine the bias of study authors; while this ends up not changing the probability in this portion of the analysis, the implication is that biased authors somehow increase the likelihood the virus is of laboratory origin??? No. It might cast doubt on that source of information, but it is in no way confirmatory about the nature of the virus itself. Quay is also dropping the uncertainty in probability estimates at each... [Read more »](#)

+ 17 - Reply



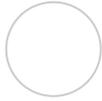
Jon 4 months ago

This essay is so full of holes. it's hard to know where to begin. Firstly, you try to discredit the idea that we would see telltale signs if it had been constructed, by arguing there are other methods that don't involve gene splicing, and then a few paragraphs later you

compare it to an experimental virus that is a chimera – i.e. gene-spliced. So which is it? You seem to want to argue both that a natural origin is unlikely, but that it also looks like it had one? One moment, you claim that it's not a perfect fit for... [Read more »](#)

 Last edited 4 months ago by Jon

+ -266 —  Reply



Marty  4 months ago

|  Reply to [Jon](#)

“One moment, you claim that it's not a perfect fit for ACE2, which indicates that it might have been done through serial passage, which mimics natural processes, but then later quote Petrovsky who was shocked at how optimised it was to ACE2 receptors. You can't have it both ways.” Errr... optimised doesn't have to mean it to have a maximal or minimal outcome.. “You dismiss a natural vector saying the bat caves are too far away, even in an article where you mention the wet markets, which could easily account for this.” Patient zero was before the emergence of the wetmarkets?... [Read more »](#)

+ 93 —  Reply



John Farmer  3 months ago

|  Reply to [Jon](#)

You need to reread the article. You can have a chimera and then show no traces of lab manipulation. Also, you should check your word play because you can have a 'not perfect' but still highly optimized ACE2 receptors which is shocking. And you me both know he dismissed the possibility of 100% natural vector with more facts than the bat caves are far away.

+ 13 —  Reply



Sally O'Brien  3 months ago

|  Reply to [Jon](#)

And a third origin worth considering is not even mentioned. The possibility that Covid19 is an evolved variant of one of the existing human corona viruses. Whatever happened to reports that the earliest samples of the virus were found in waste water in Europe?

It's far from certain that the novel corona virus arise in Wuhan. It has a higher chance of being detected there as there's an active virology lab there.

+ -9 —  Reply



Rich Seidner  4 months ago

There's no mention of the speed with which this family of viruses evolves over time. Early scientific reports suggested years between mutations.

I'm hoping that eventually, the sequence (no pun intended) of genetic variations will be identified.

+ 24 — ➔ Reply



nhz 4 months ago

Reply to [Rich Seidner](#)

This virus is evolving relatively slowly for a virus but new versions – with usually just a few point mutations – appear on a daily basis thanks to many millions of potential ‘incubators’. There are thousands of genetically different versions (‘strains’) by now, even though only a minority of detected cases are fully sequenced. There are websites where you can track the spread of certain variant strains across the globe. Most of these mutations probably have little or no influence on virus properties, but some strains might be more (or less) contagious or pathogenic – we simply don't know.

+ 29 — ➔ Reply



Tim Priest 4 months ago

Reply to [nhz](#)

"... some strains might be more (or less) contagious or pathogenic..."

Yes. Some are definitely more infectious, some may be associated with slightly more severe illness.

+ 8 — ➔ Reply



Lawrence 4 months ago

Reply to [Rich Seidner](#)

Per origination comments – FYI: Scientists first identified a human coronavirus in 1965. It caused a common cold. Later that decade, researchers found a group of similar human and animal viruses and named them after their crown-like appearance. Evolution and specie jumping is common. Just to sum up – SARS, MERS, H1N1, Bird Flu, Ebola, and SARS2 were all since 2002. So, every 3 years we have the potential for a full on global outbreak (pandemic). So, this article is well written (thank you Mr. Wade) but is at best interesting but lacks the call to action. Maybe it is... [Read more »](#)

+ 16 — ➔ Reply



Ray B 4 months ago

Reply to [Lawrence](#)

Lawrence, IF the Covid virus was created in the Wuhan lab & escaped, the fact the research was funded by US taxpayer grants is an important consideration, which should definitely not be swept under the carpet. This stinks of a cover-up by responsible persons in the DC swamp. The various strands of evidence outlined in the article, when pulled together, are compelling support for the pandemic having originated from a virus modified by researchers in the Wuhan lab. I believe that all

sensible people will hope this was the case, because it would mean the next, naturally occurring, pandemic will... [Read more »](#)

+ 94 — [Reply](#)



Billy Bloggins [🕒 4 months ago](#)

| [🗨️ Reply to Lawrence](#)

Ebola and H1N1 Influenza have been around much longer than “since 2002”, with the first Ebola outbreak occurring in the Democratic Republic of Congo in 1976. H1N1 was the pathogen responsible for the 1918-1919 “Spanish Flu” pandemic.

+ 24 — [Reply](#)



PJBLOGGS [🕒 4 months ago](#)

| [🗨️ Reply to Rich Seidner](#)

The paper by virologists from Australia & UK by Petrovsky et al notes that SARS2 spike protein is so much more adapted to humans than bats or any other animal known so far – that lab hypothesis has to need much more probable than zoonotic spread.

+ 28 — [Reply](#)



Tim Priest [🕒 4 months ago](#)

| [🗨️ Reply to PJBLOGGS](#)

Perhaps the appropriate conspiracy is one of silence about a period of undetected (or undeclared) human-human spread in China prior to the pandemic?

+ 22 — [Reply](#)



Dan B. [🕒 4 months ago](#)

A great article; comprehensive, well-written and with compellingly-documented arguments! It builds upon a few earlier posts that supported consideration for the lab-leak origin of SARS2 – such as Rowan Jacobson's Sept. 2020 piece in Boston Magazine (<https://www.bostonmagazine.com/news/2020/09/09/alina-chan-broad-institute-coronavirus/>) and his March 2021 piece in Newsweek (<https://www.newsweek.com/humans-not-animals-likely-took-covid-virus-wuhan-contrary-chinas-claims-1578861>). In addition, a similarly detailed article from July 2020 by Jonathan Latham and Allison Wilson is an interesting read that casts serious doubt on the “spillover” theory of SARS2 origin while proposing a novel take on the lab escape theory (<https://www.independentsciencenews.org/commentaries/a-proposed-origin-for-sars-cov-2-and-the-covid-19-pandemic/>).

+ 83 — [Reply](#)



HK [🕒 4 months ago](#)

There are a lot of conflicting information about the PCR test. I do not understand this test and I would like to know what sequence of the COVID-19 spike protein or any other components of the virus is used and if that component is specific to COVID-19 or not? Also, what proteins the mRNA of each of the COVID-19 vaccines, made by different companies, transcribe in our cells? Thank you.

+ 17 — ➔ Reply



nhz ⌚ 4 months ago

| ➔ Reply to [HK](#)

There are many different SARS-CoV-2 PCR tests and most of them target part(s) of the N gene which is the most conserved. Unfortunately the details of most commercial tests are not published and basically most of these tests are unvalidated. There are many issues with specificity and sensitivity of covid-19 PCR testing (risk of false positives and false negatives, need for sequencing confirmation of positives, choice of PCR primers/targets in relation to potential mutations, relevance of small amounts of detected virus RNA etc.). There are just two mRNA vaccines on the market now, Pfizer/BioNTech and Moderna. The basics of these... [Read more »](#)

+ 16 — ➔ Reply



Sciquest ⌚ 4 months ago

| ➔ Reply to [nhz](#)

It's important to point out that while PCR tests have limitations and were not developed for testing for SARS-CoV-2 specifically, they were a smart use of an existing technology that gave us detection capability that we had no other way to do.

+ 1 — ➔ Reply



John Walsh ⌚ 4 months ago

This NYT alumnus, not a scientist, puts forward a narrative much favored by the political Establishment that is driving us into conflict with China, a big part of which is to demonize the chosen enemy, But as with so much of this kind of thing, which is all over the mass media, it ends up with an attack on scientists. Hence the author writes: "Nor have other scientists stepped forward to raise the issue. Government research funds are distributed on the advice of committees of scientific experts drawn from universities. Anyone who rocks the boat by raising awkward political issues... [Read more »](#)

+ -197 — ➔ Reply

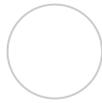


Roger Sweeny ⌚ 4 months ago

| ➔ Reply to [John Walsh](#)

If patriotism was once "the last refuge of a scoundrel", now it's "you're agreeing with Donald Trump." Hey, even a stopped clock is right twice a day

+ 64 — ➔ Reply



John V. Walsh 4 months ago

[Reply to Roger Sweeny](#)

Hi Roger, I agree with you that a stopped clock can be right twice a day. And in fact the NYT crew was horrified when Trump declared early on that he wanted to be a friend of Xi and even congratulated China at the outset of their handling of the pandemic. Such heresy is never to be forgiven however momentary it may be. The heresy was compounded when he said he wanted to "get along with Russia" and even had the unmitigated gall to invite Lavrov to the Oval Office and horrors have a summit at Helsinki with demon Putin.... [Read more »](#)

+ -71 - [Reply](#)



Angus 4 months ago

[Reply to John Walsh](#)

Scientists are human. They have biases and blind spots. They can fall sway to groupthink and orthodoxy that prevents even-handed appraisal of competing theories.

In your view, to point this out is to engage in unscientific discourse. I don't see it that way at all.

If we refuse to admit these possibilities, we're turning science from a truth-seeking process into a kind of secular priesthood.

+ 155 - [Reply](#)



Jae 4 months ago

[Reply to Angus](#)

Science is just the interpretation of what's around us. It's a study; it's not fact itself. I wish people would realize that. Thanks for your comment:)

+ 25 - [Reply](#)



Wisdom Seeker 4 months ago

[Reply to John Walsh](#)

I'm a professional scientist who has been professionally trained to recognize and avoid conflicts of interest. Daszak is not just "a working scientist". His own grant money funded – and thus he helped lead – the work at Wuhan which is in question. In any ethically functional scientific enterprise, everyone would recognize that Daszak has a conflict-of-interest of the highest level. Many have pointed it out, and that isn't a "smear", merely a recognition of the obvious. Daszak has every incentive to engage in cover-up rather than disinterested pursuit of the truth. Furthermore, Daszak's failure to disclose said conflict of... [Read more »](#)

+ 151 - [Reply](#)



Alexe 4 months ago

[Reply to John Walsh](#)

Similarly if Daszak, a working scientist, makes the case that the lab leak is wrong, he is accused of conflict of interest. Again that is not a scientific discussion but a smear. But Daszak is directly involved with the Wuhan institute and the one that directed funding to the gain of function research. Which if it is truly a lab leak situation, Daszak is completely screwed. His entire organization would be screwed in every way possible. Gain of function research would be screwed. How is that not a obvious conflict of interest? The author of this article has a degree... [Read more »](#)

 Last edited 4 months ago by Alexe

+ 92 -  Reply

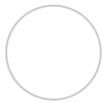


Blaise  4 months ago

|  Reply to [John Walsh](#)

Why then is the data not made available by the CCP? If there is no culpability then make the information known.

+ 9 -  Reply



Jason  9 days ago

|  Reply to [John Walsh](#)

This could have all been averted if China had been open from the beginning. The Chinese have prevented a proper investigation from ever possibly being conducted and has even openly engaged in punitive tariffs against countries merely wanting one. Plus the CPP spread conspiracy theories about the virus starting in the US with zero evidence.

+ -1 -  Reply



Pathcoin  4 months ago

This is an excellent review. It points to the fact that in this type of work detectives are required as the lead investigators, with scientists playing a secondary technical role. If we look at this from a detective point of view, our thought processes should follow MOM (means, opportunity, motive). Of the three, motive (escape vs purposeful release) is the most difficult to discern. If we look at the evidence from a journalistic point of view (who, what, when, where, how and why) we have a similar but slightly more detailed understanding. What-a highly infectious virus with unique coronavirus with... [Read more »](#)

+ 78 -  Reply



nhz  4 months ago

We should also look at WHO and its selection of Wuhan investigation team members, which includes several people who are potentially heavily compromised and have much at stake in case a lab origin is proven. Besides someone like Daszak also e.g. Marion Koopmans from the Netherlands who is heading (with Ron Fouchier) the Dutch lab that has been doing gain-of-function research for many years and was the source of the initial

controversy on the subject in the science community. Some other members seem to have been selected because they are only interested in finding natural origins. While the gain-of-function research... [Read more »](#)

+ 121 — ➔ Reply



Desmond Aubery ⌚ 4 months ago

Excellent, well-written, article. Kudos.

+ 76 — ➔ Reply



Jeff Id ⌚ 4 months ago

Thank you. Well written. I did not have an opinion on the origin until reading this. It is very clear now. The probability of natural evolution requires several difficult steps whereas artificially, the split site is well known in recent literature and an obvious 'gain of function' path.

I'm convinced.

+ 98 — ➔ Reply



Deguello ⌚ 4 months ago

| ➔ Reply to [Jeff Id](#)

Occam's Razor points directly at lab release.

+ 81 — ➔ Reply



Marty ⌚ 4 months ago

| ➔ Reply to [Deguello](#)

Exactly how? I think the author has thoroughly shown it's likely the opposite.

+ -46 — ➔ Reply



dbarr ⌚ 3 months ago

| ➔ Reply to [Marty](#)

The article points to a lab release.

+ 3 — ➔ Reply



Ray B ⌚ 4 months ago

| ➔ Reply to [Jeff Id](#)

Me too, Jeff. I have long thought it was the original virus taken from the Yunnan caves which accidentally escaped, but this article shows it was a human-modified version. Release was still definitely accidental, because only a total nutter would deliberately release a deadly virus on their own doorstep.

✎ Last edited 4 months ago by [Ray B](#)

+ 30 - ➔ Reply



James ⌚ 4 months ago

| ↻ Reply to [Ray B](#)

You mean a "total nutter" like an authoritarian central government who cares little for the lives of individual citizens, instead valuing the collective?

If you believe the numbers coming out of China, this was a minor public health blip in that nation compared to the rest of the globe. Why might that be? Either they are drastically lying about the true toll of the pandemic there, or they were prepared for this virus from the beginning.

+ 9 - ➔ Reply



Alex M ⌚ 4 months ago

Thank you for this very interesting article. Also thank you for evaluating the arguments for both theories and not just siding with one preferred theorie. While doing some further research about the topic 'furin cleavage sites', I've stumbled on this study arguing that they can (and have) actually occur(ed) naturally in coronaviruses. I'm not a scientist myself, so I lack the knowledge to digest all of its information, but it seems to disprove the claim that only SARS2 of all beta-coronaviruses possesses such a feature. One could criticize the credibility of this study (conflict of interest) since both scientists work... [Read more »](#)

+ 36 - ➔ Reply



David Priest ⌚ 4 months ago

| ↻ Reply to [Alex M](#)

You should definitely be skeptical of any scientist trying to discredit the lab origin, particularly those with links to Chinese institutions. I suggest checking out the heroic Chinese whistle-blower Dr. Li-Meng YAN (@DrLiMengYAN1).

+ 14 - ➔ Reply



Charles Forsberg ⌚ 4 months ago

In one sense it is irrelevant where the virus came from. We created an environment perfectly suited for air-borne global pandemics if the virus is infectious before people become sick. That global panemic-enabling environment has three components: (1) large cities with dense populations, (2) mass transit and (3) a global air transport industry. If a virus gets out, it creates a global pandemic before the people in the city where it started know it exists. The problem is similar to many American cities burning down in the 1800s (Chicago, Boston, etc.). The cities were made of wood so the only... [Read more »](#)

+ 68 - ➔ Reply

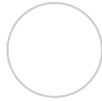
nhz ⌚ 4 months ago



Reply to [Charles Forsberg](#)

The environment we created sure is a big factor. But looking at the disease statistics a more effective and cheaper solution than massive engineering efforts (which makes people dependent on those engineering solutions) would be to do something about co-morbidities like obesity that seriously increase disease risk. Or providing a bit more fresh air and clean walking space for the average citizen (instead of locking people down in a small home). We also need to rethink the ever growing global transport streams and massive concentrations of people. For those who still believe in a natural origin for this pandemic, look... [Read more »](#)

+ 6 - Reply



Ray B 4 months ago

Reply to [nhz](#)

NHZ, massive engineering efforts aren't needed to improve the air where people gather enmasse.

It shouldn't be hard to install a UV treatment device on the air-con systems in office buildings, shopping malls, trains, & buses. Dentists use them to set the fillings in your teeth.

Installing virus-grade filters would be the less desirable option, as they require very regular maintenance to be effective, & are probably much larger than a UV machine.

+ 11 - Reply



A. K. Richter 4 months ago

Reply to [Charles Forsberg](#)

The environment is a huge factor for the spread, without a doubt, but this same global environment has existed for decades. Nearly a century. So one must ask themselves, 'Why doesn't this happen more often?'

Because as stated in the article, without the correct spike protein, jumping from species to species, specifically to humans, is a rare occurrence. Combine that with the need for a correct codon sequence, and it's rare that a disease as virulent as SARS2 just appears out of nowhere.

+ 15 - Reply



Jason 9 days ago

Reply to [Charles Forsberg](#)

It's irrelevant if the virus started with gain-of-function research?

If it's true, you think this says nothing about whether we should allow gain-of-function research to be carried out?

+ 0 - Reply

Michael McElfresh 4 months ago



I remain rather perplexed by the obsession with the origin of the virus and the need to speculate about something that will eventually be solved using real data. But right now, the answer to this question has no real bearing on the pandemic. The real question is how the first SARS killed so few people and the second SARS has killed so many people; except in countries like Australia, New Zealand, South Korea, Singapore, Hong Kong, and China. The latter countries stemmed the spread, greatly limiting the spread in their countries and presumably the rest of the world. The real... [Read more »](#)

+ -97 - ➔ Reply



nhz ⌚ 4 months ago

| ➔ Reply to [Michael McElfresh](#)

“how did this get loose and what can we do to get it under control.”

We need to know what went wrong and how to limit the damage of the virus, but for answering those questions you need to look into the origin (which isn't the same as blaming China or US). No way around it.

IMHO there are very good reasons NOT to leave this to the often compromised WHO “experts”.

+ 72 - ➔ Reply



Taxel ⌚ 4 months ago

| ➔ Reply to [nhz](#)

Define compromised? What do you mean “compromised”

+ -9 - ➔ Reply



Angus ⌚ 4 months ago

| ➔ Reply to [Michael McElfresh](#)

The question of SARS-CoV-2's origin has little bearing on the trajectory of the current pandemic. But it's hugely important when it comes to preventing future pandemics. If the research that supposedly protects us from zoonotic spillovers is in fact increasing the net pandemic risk (due to human error, accident, etc), then that research needs to be halted. At the very least, it should be limited and done only under tightly controlled conditions. This would require international agreement, and perhaps an auditing regime with actual teeth. One thing is for sure though: we will never sort this out if we leave... [Read more »](#)

+ 62 - ➔ Reply



Nicholas G ⌚ 4 months ago

| ➔ Reply to [Michael McElfresh](#)

The question does indeed have a bearing on the pandemic and potential future ones if the research conducted led to a release of the virus.

+ 15 - ➔ Reply

**NWJ** 4 months ago| Reply to [Michael McElfresh](#)

I disagree. Obsession with the source is exactly what is needed in order to come up with a preventative solution. The strategy is very different if the source is natural vs accidental lab release. As to your last statement, I would modify it to say "cover-up and lack of transparency breeds hostilities."

+ 32 - Reply

**michael888** 4 months ago| Reply to [Michael McElfresh](#)

The Asian countries stopped most Covid-19 entry at their borders. Singapore for example noted that the 2009 Swine flu came in and spread unimpeded (even with their ubiquitous masks); fortunately there were few deaths (this was NOT a lesson learned from SARS, which was mostly a hospital infection, though more deadly). Having a health check choke point at borders is simple 1950s Public Health protocol. Singapore has done an excellent job corralling, testing, quarantining and treating the infected, and their close contacts, that get by the cordon. Today they are dealing with a handful of 'community spread' cases that could... [Read more »](#)

+ 4 - Reply

**curious** 4 months ago| Reply to [Michael McElfresh](#)

Very true. Human had been fighting pandemics for thousands of years, and every single one of them was created by Mother Nature. And there has been no lack of conspiracy theories (often state sponsored), e.g. that AIDS was created in a CIA lab. In the case of AIDS, US government has never been asked, nor it has never offered a proof that AIDS was not lab made, but people generally believed that it was created by Mother Nature. Fast forward, there is this theory of lab leakage of coronavirus. Supposedly this human-affecting coronavirus somehow existed in the nature already, and... [Read more »](#)

+ -10 - Reply

**Vincent Gallagher** 4 months ago

Is this really the Bulletin of the Atomic Scientists? Lab escaped virus. Negative. This was refuted many moons ago. A phrase employed many moons ago, criticizing a particular 'train of thought' the author proposed, seems to apply: "pernicious conceits".

 Last edited 4 months ago by [Vincent Gallagher](#)

+ -231 - Reply

**Richard H Ebright** 4 months ago| Reply to [Vincent Gallagher](#)

This was never "refuted" and, indeed, not even credibly coherently rebutted..

+ 124 - Reply

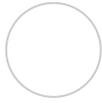


Lupe Rodriguez 4 months ago

Reply to [Vincent Gallagher](#)

This comment sounds extremely suspicious, as if it were made by a non-native speaker. It was refuted many moons ago? The article addresses the questionable issues in the "refutation"

+ 56 - Reply



Fiat Lux 4 months ago

Reply to [Vincent Gallagher](#)

Please provide the source(s) that refute the "escaped from a lab" theory. I am very interested in examining a coherent rebuttal to this article.

+ 68 - Reply



CHRIS WARDEN 4 months ago

Reply to [Vincent Gallagher](#)

How was it refuted?

Last edited 4 months ago by CHRIS WARDEN

+ 7 - Reply



Mary Gallagher 3 months ago

Reply to [Vincent Gallagher](#)

Now it's the National Academies saying the lab leak theory needs to be examined, along with other possibilities.

"In the case of SARS-CoV-2, there are multiple scenarios that could, in principle, explain its origin with varying degrees of plausibility based on our current understanding. These scenarios range from natural zoonotic spillover (when a virus spreads from non-human animals to humans) to those that are associated with laboratory work."

<https://www.nationalacademies.org/news/2021/06/let-scientific-evidence-determine-origin-of-sars-cov-2-urge-presidents-of-the-national-academies>

+ 0 - Reply



K Thacker MD 4 months ago

excellent article

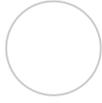
+ 57 - Reply

Bulldog84 4 months ago



Reading some of the snide comments on this obviously well-researched article, I find myself hoping that many of these commenters aren't scientists. If they are educated scientists, what a commentary on the sad state of science; then God help us all.

+ 91 - Reply



Marty 4 months ago

Reply to [Bulldog84](#)

I was thinking the same.. one thing this pandemic has shown us is the hubris of many scientists

+ 31 - Reply



Squatch 4 months ago

I'll sanitize my previous comment.

A very comprehensive overview. I thank the author.

Gain of function testing with pathogenic viruses should be viewed the same way as above ground nuclear bomb testing. Once released, there is no getting those atoms back in the packaging.

+ 72 - Reply



John S 4 months ago

There *is* a Chinese Whistleblower who has published two papers regarding the origin of the virus. Her Name is Dr. Li-Meng Yan. Of course, she has been ignored.

+ 102 - Reply

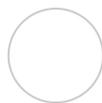


David Wright 4 months ago

Reply to [John S](#)

Dr. Yan compared the RaTG13 bat virus proposed by Shi as the ancestor of the SARS-COV-2 pandemic virus and found that the frequency of synonymous alleles between them was far greater than would be found if the SARS-COV-2 had evolved naturally. Her data driven conclusion was that either one or both of these viruses had to have been fabricated in a lab.

+ 51 - Reply



Kevin Olson 4 months ago

Reply to [David Wright](#)

Or, perhaps the RaTG13 sequence was a diversionary keyboard sequence/smokescreen which never was sequenced from a real virus, but was made out of whole cloth to provide a "wild progenitor" from which a lab escaped SARS-CoV-2 might have arguably derived. You know, something that looked to be close enough, from a galloping horse. Enough to throw us off the scent. I haven't to date seen any credible refutation of nerdhaspower's essay on the subject:

<https://nerdhaspower.weebly.com/ratg13-is-fake.html> It's been more than a year, I think. Plenty of time for someone to take a proper tilt at it. When I first heard of... [Read more »](#)

+ 10 —  Reply



KW  4 months ago

|  Reply to [John S](#)

Her work has been reviewed here

<https://rapidreviewscovid19.mitpress.mit.edu/pub/78we86rp/release/2>

+ 14 —  Reply



Dennis J Solomon  4 months ago

An excellent and timely article. Nearly 50 years ago one afternoon, I joined Salvador Luria to discuss the involving psychodynamics of viruses. Even then, a few decades after his L-D observations, we had learned that synthetic environments could channel 'random' mutations. By the late 1970s, these experiments were part of the entry-level biology lab course. Since SARS 2003, the SARS and MERV viruses have been cultured by at least 200 labs worldwide. Today, nearly every university and hospital lab has the skills to "select" more virulent, induced mutations. CRISPR is not necessary. Natural, Accidental or Intentional – Neither WHO nor... [Read more »](#)

+ 12 —  Reply



James  4 months ago

|  Reply to [Dennis J Solomon](#)

We need less tin-foil hat theories like this and more hard science, but until China actually grants independent investigators access to lab databases and records, we may never know the full story.

+ 7 —  Reply

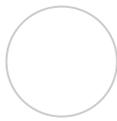


Jiri Severa  4 months ago

This is a fair synopsis of the "state of play". Nicholas Wade has most of it covered well but I do have few minor disagreements with it. E.g. I am not sure I would want to consider David Robertson's theory worthy of a paragraph, since it clearly explains nothing and substitutes – in the tired fashion of P. Daszak and K.Andersen – a self-validating narrative for evidence-based science. Weird things happen in nature, true, but if you want to argue for a bat-originating virus that binds much better to humans (within a couple of months) than to the original host,... [Read more »](#)

 Last edited 4 months ago by [Jiri Severa](#)

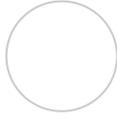
+ 29 —  Reply



BioMedTrilogy 4 months ago

The fact that the major coronavirus research center is in Wuhan and the pandemic started there will never go away.

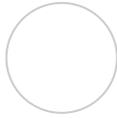
+ 35 - Reply



Lauri Bonn 4 months ago

Very thorough and extremely well written article until the last page where it seems that you minimalized Fauci's culpability and have given him a pass. That is truly disappointing.

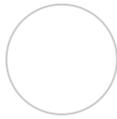
+ 50 - Reply



Mark Hoffman 4 months ago

Mr. Wade, thank you for your scholarly work here. This is the most comprehensive, succinct and yet understandable evaluation of the pros and cons of the virus origin theories – zoonotic vs. lab leak, that I have seen in the dozens, if not hundreds, of articles I have read regarding this virus. My hat is off to you for your effort and courage. I am passing this article on to others.

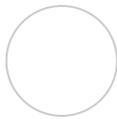
+ 62 - Reply



Allan Howard 4 months ago

When people are so quick to dismiss the lab escape scenario and label it a conspiracy theory, then you have to seriously question their motives. And it is of little consequence of course that the virus just happened to spring up in Wuhan of all places on the planet! Hmm..... Let's face it, there are numerous reasons why the PTB and the industry would deny and discredit the lab escape scenario and – if they know that to be the case – keep it from the public, who they know would be up in arms if they knew that it... [Read more »](#)

+ 25 - Reply



M. Bond 4 months ago

The origin of Covid 19 is easy to prove. If it didn't exist in the Wuhan Institute of Virology, it didn't come from there. If it did, it almost certainly came from there. The reason we don't know is because China "sealed" (destroyed?) the records. If Covid 19 was not present in the lab there is no reason to seal the records; China could end the discussion in a moment by unsealing the records. This article is very detailed and convincing, but the behavior of China proves it fairly conclusively as a simple matter of logic. Consider this: If Covid... [Read more »](#)

+ 144 - Reply

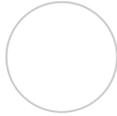


Dana Ludwig 4 months ago

Reply to [M. Bond](#)

Xenophobia and racial hate has a life of its own. I think China has no choice but to shut down data access. Remember Iraq's WMDs? Bush was re-elected even after the war started and the WMD's were not found and the war continued. Yet the US freely develops their own WMDs and freely conducts GOF viral research, and leaks viruses from their own labs. The rational answer is to negotiate international treaties to prohibit GOF research and research on pandemic-potential viruses before this happens again in some other country like the US.

+ -12 — ↪ Reply



anonymous reader ⌚ 4 months ago

Great writing. Best I've seen in a long time. Reminds me of the early 80's. Totally a wall of text and I had to break for chores and tasks but was glad to read the whole thing.

+ 54 — ↪ Reply



David Blackall ⌚ 4 months ago

I'm convinced that the Cov SARS 2 was everywhere before Wuhan China. There have been five serum studies showing the virus in population of Italy California Brazil and France, all with antibodies to the virus, like me way back in 2019. I was tested positive with coronavirus 229e the same thing.

The China conspiracy is to get the China mainland angry with us for war.

+ -64 — ↪ Reply



Wisdom Seeker ⌚ 4 months ago

↪ Reply to [David Blackall](#)

My understanding is that antibody tests have a significant (few percent) level of false positives. That is, they could test for any novel pathogen and find, by mistake, "matches" among various populations. So were the serum studies sufficiently specific that "false positives" have been conclusively ruled out? Can you provide citations?

+ 19 — ↪ Reply



Dave ⌚ 4 months ago

More HATE CHINA propaganda brought to you by the usual suspects.

+ -130 — ↪ Reply



Allan Howard ⌚ 4 months ago

↪ Reply to [Dave](#)

Perhaps you could quote some examples of this 'HATE CHINA propaganda' Dave?

No? Thought not!

+ 79 — ↪ Reply



Michael Lipkin 4 months ago

An excellent article. What happens next? We need to offer the Chinese immunity from prosecution in return for the total truth. The truth is valuable and if it is expensive then so be it.

+ 18 - Reply



Tim H 4 months ago

"It matters a great deal which is the case if we hope to prevent a second such occurrence."

Why? If both scenarios are plausible, then we need to work against both in order to prevent a reoccurrence.

Even if we discover conclusively that it was not an accidental laboratory escape this time, the fact that we couldn't rule it out for over a year means it's a mechanism we should seriously worry about – and vice versa.

+ 32 - Reply



Matha 4 months ago

Has the PRC government entombed the Wuhan Institute of Virology lab? Why not? Nothing left to escape?

+ 4 - Reply



Adriano Moccelin Lima 4 months ago

In August 2019, its deadly germ research operations were abruptly shutdown following serious safety violations, in particular relating to the disposal of dangerous materials.

Fort Detrick is the largest employer in Frederick County, Maryland.

NEW YORK TIMES

<https://www.nytimes.com/2019/08/05/health/germs-fort-detrick-biohazard.html>

CHINA: 2019 Military World Games opening ceremony in Wuhan

<https://youtu.be/vL46md51Nzw>

LIVE: Opening ceremony of 2019 Military World Games in Wuhan, China

<https://youtu.be/gCdAY-AOG-o?t=1240>

Last edited 4 months ago by Adriano Moccelin Lima

+ 0 - Reply



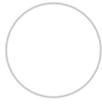
Becca Price 4 months ago

Fascinating article, and most persuasive. Can your data incorporate the findings that traces of SARS2 was found in the autumn of 2019 in various other places, including

France and California?

<https://phys.org/news/2021-05-host-sars-cov-coronaviruses.html?fbclid=IwAR1eMm5kUJetZjvftbuuqng5Uxg09IBRxdy8ScgWkFBSn9uXVJ1hLdulkc>

+ -7 - Reply



Wisdom Seeker 4 months ago

Reply to [Becca Price](#)

Link doesn't relate to claim made.

+ 10 - Reply



Kevin Olson 4 months ago

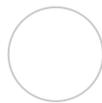
Reply to [Becca Price](#)

And apparently quite widely in Italy, especially in Lombardy and adjacent regions, as detected in samples collected as early as the beginning of September of 2019 for an entirely unrelated prospective lung cancer study:

<https://pubmed.ncbi.nlm.nih.gov/33176598/> (implying some people there were already infected at the end of August) It's not out of the question that this thing

escaped more than once, the first time(s) without anyone noticing. Or, like seasonal influenza, it could have been quietly circulating asymptotically until some triggering event (low Vitamin D levels?) precipitated the crisis. But, until the Chinese authorities are more forthcoming, it may be very... [Read more »](#)

+ 5 - Reply



Kam Berry 3 months ago

Reply to [Kevin Olson](#)

I'm not sure that the Italy case for pre-pandemic spread is conclusive.

<https://pubmed.ncbi.nlm.nih.gov/33207548/>

+ 1 - Reply



Lisa McFadden 4 months ago

Based on the peer reviewed literature, there are now six different theories explaining the origins of SARS-CoV-2. So right away, this writer disqualifies himself. Then he cites Steven Quay who has gotten zero citations for his theories that the virus was created in a lab. Lab origin is one of these six theories. It's a legit scientific theory. However, at this point, we can't prove any of the theories being proposed forward so we can speculate all we want, we just don't know. The Chinese have not been transparent with what happened at their labs and some of the other... [Read more »](#)

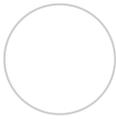
+ -11 - Reply



Jay Oh 4 months ago

Why call the lab escape possibility a conspiracy? The scientists surely did not intend for it to escape. The Chinese government neither. Gain of Function research was a global direction. Its an easy label. What is it is a tragedy. May we learn.

+ 25 — ➔ Reply



Stephen Bent ⌚ 4 months ago

Interesting arguments, I am still reserving judgment, but at least one of your arguments is misleading- I would point out that the furin site in SARS2 is suboptimal, and that MERS also contains an (even less optimal) furin cleavage site, so your assertion that "Because of all known SARS-related beta-coronaviruses, only SARS2 possesses a furin cleavage site" is only true if you carefully prune your phylogenetic tree or carefully circumscribe how efficient a furin cleavage site must be to count.

+ 18 — ➔ Reply



Bill Rhodes ⌚ 4 months ago

24,642,757 square miles of habitable land on planet earth, & this bug just happened to pop up within walking distance of a bio-lab, admittedly studying coronavirus in the months leading up to the plague.

If this is simply a coincidence, it's one for the record books.

+ 43 — ➔ Reply



curious ⌚ 4 months ago

↳ Reply to [Bill Rhodes](#)

You made a HUGE assumption that the covid19 first popped up in Wuhan. But the covid19 probably popped up elsewhere without being detected. It was discovered in Wuhan first as it is a big city with the capability to detect the covid19.

+ 0 — ➔ Reply



Michal Zapendowski ⌚ 4 months ago

From the moment I first heard that a lab studying coronaviruses was located in Wuhan – and the virus just happened to emerge there – it seemed like a huge coincidence. This article now has me convinced that the virus escaped from a Chinese coronavirus lab, at least until I see an equally convincing rebuttal

+ 20 — ➔ Reply



Tim Priest ⌚ 4 months ago

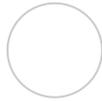
↳ Reply to [Michal Zapendowski](#)

Again, I reply. Why is there a virology lab in Wuhan? Because there is a history of novel viruses associated with bats from the area (China, remember, is a very large nation). I

would be much happier if Peter Daszak's responses were to be included with this account:

<https://www.nature.com/articles/d41586-020-02473-4>

+ -3 - Reply

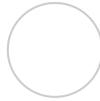


Jan Smit 4 months ago

Reply to [Tim Priest](#)

Strange that a valid remark is so heavily downvoted.

+ 4 - Reply



Mike Monge 3 months ago

Reply to [Jan Smit](#)

Go to the link and you will see that this is not really a "valid remark." It is an interview where Daszak complains about the NIH having the audacity to request samples from him, an attack against President Trump, and weaselly language about how the lab did not perform work on the new coronavirus. But if Wade is right, the lab was working on something which may have become SARS-2. So, nothing Daszak says can be considered a response to anything of which Wade has accused him.

+ 0 - Reply



Jax 4 months ago

Thanks to Nicholas Wade for this article. It's important that we non-scientists are kept informed particularly when it is in the interests of certain sections of the scientific community that we are kept as much in the dark as possible. My own belief that this virus is from the lab in Wuhan was formed by watching world-wide reactions to it, rather than listening to what was said about it. Governments world-wide reacted with horror and anxiety as soon as the pandemic was confirmed. Pandemic plans (which many governments have) were thrown out and panic seemed to be the... [Read more »](#)

+ 20 - Reply



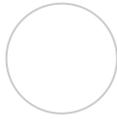
Aren 4 months ago

Reply to [Jax](#)

Given that USA NIAID significantly funded the gain-of-function research at Wuhan Virology Lab, I'm puzzled why they weren't able to get access to the research files and records of Dr Shi. Surely those research grants contain conditions about making results available to the grant donors ?

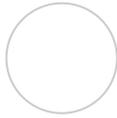
And particularly in this case, involving high-risk research into engineering viruses with potentially devastating impact on human society. Where was the oversight and accountability by the researchers ??

+ 14 - Reply

**Matham** 4 months ago

Very well researched. Hope others continue the investigation further and pressure builds up to ban gain of function research.

+ 10 — Reply

**PB** 4 months ago

Very informative article. However, the comment about bats going to hibernation in Hubei because of low temperatures in September is wrong. The cited source uses the following table which is clearly wrong:

<https://www.chinadiscovery.com/hubei-tours/weather.html#:~:text=With%20a%20sub%2Dtropical%20monsoonal,temperature%20reaching%200%20%C2%B0C.>

Just check the data given in the same website for “Weather Forecast for Major Cities in Hubei” and you will realize the inconsistency. On the same page we read: “The coldest month is January with average temperature of 1-5°C.” But the table shows temperatures for January ranging from -17 to -26 degrees Celsius.

+ 8 — Reply

**Larry Gilman** 4 months ago

| Reply to PB

The article is excellent but this criticism seems to me to be valid (albeit of a very minor point). The table of temperatures at the China Discovery site, reproduced in the cited source <https://zenodo.org/record/4477081#.YIGAG-hKhPY>, would give Wuhei province Scandinavian winters (-17 C [+1.4 F] max in January). This is geographically implausible. The temperatures for Wuhan airport at <https://www.timeanddate.com/weather/china/wuhan/climate> seem more realistic; these temperatures do go below the bat hibernation threshold, but only in Dec-Feb, not September. Having scrubbed this minor item, the case remains very strong that the lab-escape hypothesis cannot, to say the least, be dismissed out of hand.... [Read more](#) »

Last edited 4 months ago by Larry Gilman

+ 5 — Reply

**Robert** 4 months ago

Great article! It doesn't make any hasty conclusions but points out the evidence we have so far and the parties involved. The biggest reason that the lab leak is most likely is how China has reacted regarding the WIV...guilty written all over. The writer does mention this but wish he expanded on it more, like once this virus infections started, the CCP replaced the head of the lab with a military personnel and how one of the younger researchers at

the lab, probably patient zero, was scrubbed off their website soon after. It reads like a bad 2nd rate novel.... [Read more »](#)

+ 20 — Reply

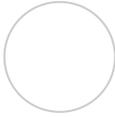


Larry Gilman ⌚ 4 months ago

| [Reply to Robert](#)

I'm not saying you're wrong, but it would be good to supply a source for the thing about the researcher being scrubbed from the website . . .

+ 3 — Reply



Dobby ⌚ 4 months ago

"There is no good explanation of how the virus acquired its furin cleavage site, which no other SARS-related beta-coronavirus possesses..." May want to read this

<https://www.sciencedirect.com/science/article/pii/S1873506120304165>

+ 13 — Reply



Bull ⌚ 3 months ago

| [Reply to Dobby](#)

Thanks, Dobby, for that link to the Wu and Zhao article. I suspect that, when Nicholas Wade used the phrase "SARS-related betacoronavirus", he was referring to the subgenus Sarbecovirus. Indeed, among the currently known Sarbecoviruses, SARS-CoV-2 is unique in having a furin cleavage site. But, as Wu and Zhao illustrate, furin cleavage sites are found in other subgenera of Betacoronavirus, like Merbecovirus, Embecovirus, and Hibecovirus. Perhaps Wade should have been more careful to avoid the misimpression that the furin cleavage site is rare within the Betacoronavirus genus. I imagine that Wade might respond to our comments by noting that:

1. Among... [Read more »](#)

+ 3 — Reply

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Nicholas Wade

Nicholas Wade is a science writer, editor, and author who has worked on the staff of *Nature*, *Science*, and, for many years, the *New York Times*.... [Read More](#)

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