INTRODUCTION

This is a noncommercial document prepared as an informal input to the U.S. Senate HELP Committee on the origins of the COVID-19 pandemic. Quotations from science journal articles are included under the [fair use concept of United States copyright law](https://www.copyright.gov/help/faq/faq-fairuse.html#:~:text=Under%20the%20fair%20use%20doctrine,news%20reporting%2C%20and%20scholarly%20reports). This is convenient for busy general readers who don’t want to have to wade through technical science journals but want to see scientific proof not just another blogger’s opinion.

Readers who are unfamiliar with the terminology of virus research should consult the last three pages of the ODNI report ([*The Potential Links Between the Wuhan Institute of Virology and the Origin of the COVID-19 Pandemic*](https://www.dni.gov/files/ODNI/documents/assessments/Report-on-Potential-Links-Between-the-Wuhan-Institute-of-Virology-and-the-Origins-of-COVID-19-20230623.pdf), 23 June 2023) for a clear explanation of biological terms that will occur in this discussion. It is a brief report (10 pages), clearly written and easily read, but it stops short of answering all questions.

My discussion here owes a heavy debt to Dr. Stephen Quay’s white paper, *Bayesian Analysis of SARS-CoV-2 Origin* and Jonathan Latham and Allison Wilson’s articles, especially “A Proposed Origin for SARS-CoV-2 and the COVID-19 Pandemic.”

Dr. Quay’s discussion may put off non-academic readers with its technical Bayesian math concepts, but the basic logic and biological science is there for those who take the trouble to read Quay’s excellent 193-page paper. My intent here is to simplify the scientific language, scrutinize Quay’s logic (which turns out to be impeccable), update the discussion with more recent articles, and add my own perspective. Having said that, Dr. Quay’s analysis *was* fully sufficient to establish an extremely high probability for the laboratory origin of the SARS-COV-2 virus and subsequent COVID-19 pandemic it produced.

My mind is still open to genuine new evidence (not artificially manufactured as part of a cover-up), but my working assumption is, basically, Jonathan Latham’s Mojiang Miner Passage Theory.[[1]](#footnote-1) The lack of an immediate progenitor and very close intermediate animal hosts for evolving early forms of the SARS-COV-2 virus (none have been found that sufficiently close the evolutionary distance) means we are not entitled to assume that the normal amount of time required for a natural (outside the lab) evolution of the virus was available.

In the beginning, the possible intermediate host animal was believed to be pangolin, of the *Manidae* family, commonly known as pangolins. These mammals are found in tropical areas of Asia and Africa. At present, different studies, including antibody detection, have not been able to demonstrate that this species could have been the intermediate host.[[2]](#footnote-2)

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Recent studies showed that SARS-CoV-2 was likely originated from bats, but its intermediate hosts are still largely unknown. In this study, we assembled the complete genome of a coronavirus identified in 3 sick Malayan pangolins. The molecular and phylogenetic analyses showed that this pangolin coronavirus (pangolin-CoV-2020) is genetically related to the SARS-CoV-2 as well as a group of bat coronaviruses but do not support the SARS-CoV-2 emerged directly from the pangolin-CoV-2020.[[3]](#footnote-3)

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From this analysis, it is evident that the viruses studied under the EcoHealth Alliance grant are very far distant from SARS-CoV-2. Included for comparison is RaTG13, one of the closest bat coronavirus relatives to SARS-CoV-2 collected by the Wuhan Institute of Virology and BANAL-52, one of several bat coronaviruses recently identified from bats living in caves in Laos. Although RaTG13 and BANAL-52 are 96-97% identical to SARS-CoV-2 at the nucleotide level (>900 nucleotide differences across the entire genome), the difference actually represents decades of evolutionary divergence from SARS-CoV-2. Experts in evolutionary biology and virology have made it clear that even the closest known relatives of SARS-CoV-2, which were not studied under the EcoHealth Alliance grant, are evolutionarily too distant from SARS-CoV-2 to have been the progenitor of the COVID-19 pandemic. Field studies continue the search for more proximate progenitors.[[4]](#footnote-4)

Given the evolutionary distance between the SARS-COV-2 genome and its closest relatives, plus the lack of time, both laboratory facilitation and frequent opportunities for human infection, re-infection, cross-infection, and coinfection would be necessary. The lab procedure known as serial passaging is a likely source for much of the fast development of SARS-COV-2 from its virus relatives being studied in Wuhan labs. Opportunities for frequent human infection, re-infection, cross infection, and coinfection were available at the Mojiang mines. The Mojiang miners’ illnesses were remarkably similar to COVID-19, and several of the miners’ blood samples tested positive for antibodies to SARS viruses.[[5]](#footnote-5)

Unless the intermediate host necessary for completing a natural zoonotic jump is identified, the dual-use gain-of-function research practice of viral serial passage should be considered a viable route by which the novel coronavirus arose. The practice of serial passage mimics a natural zoonotic jump, and offers explanations for SARS-CoV-2's distinctive spike-protein region and its unexpectedly high affinity for angiotensin converting enzyme (ACE2), as well as the notable polybasic furin cleavage site within it. Additional molecular clues raise further questions, all of which warrant full investigation into the novel coronavirus's origins and a re-examination of the risks and rewards of dual-use gain-of-function research.[[6]](#footnote-6)

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BtCoV/4991 and RaTG13 were collected from a mineshaft in Yunnan province, China, in 2012/2013 by researchers from the lab of Zheng-li Shi at the Wuhan Institute of Virology (WIV). Very shortly before, in the spring of 2012, six miners working in the mine had contracted a mysterious illness and three of them had died (Wu et al., 2014)….

All of this begs the question of why the Shi lab, which has no interest in fungi but a great interest in SARS-like bat coronaviruses, also searched the Mojiang mine for bat viruses on four separate occasions between August 2012 and July 2013, even though the mine is 1,000 Km from Wuhan (Ge et al., 2016).

These collecting trips began while some of the miners were still hospitalised….

Samples from the miners were later sent to the WIV in Wuhan and to Zhong Nanshan, further confirming that viral disease was strongly suspected. Some miners did test positive for coronavirus (the thesis is unclear on how many) ….

We suggest, first, that inside the miners RaTG13 (or a very similar virus) evolved into SARS-CoV-2, an unusually pathogenic coronavirus highly adapted to humans. Second, that the Shi lab used medical samples taken from the miners and sent to them by Kunming University Hospital for their research. It was this human-adapted virus, now known as SARS-CoV-2, that escaped from the WIV in 2019.[[7]](#footnote-7)

All the positive test results from the Wuhan market show the same genome of the original pandemic-causing SARS-COV-2 strain—no progenitor genomes. Animals sold for food at the Wuhan market were not infected with SARS-COV-2; positive test results came from human, not animal sources.

More compelling, the [China] CDC authors found that the samples collected from the market, which Pekar and Worobey claim are from infected animals, are admixed only with human genetic material and not with genetic material from raccoon dogs or other species potentially sold at the market. The only reasonable inference is that these positive samples did not derive from the faeces or urine or exhalations of a live non-human animal. Few results would better indicate that virus-positive market samples derive from infected humans as opposed to other species.[[8]](#footnote-8)

Blood tests of SARS-COV-2 patients show no prior versions of the virus that would indicate the virus had been making incremental mutational steps toward a high affinity for human biology. Prior versions of the virus that were still imperfectly adapted to humans would have been found if a natural evolution of the virus had occurred prior to an animal-to-human spillover event. But the available evidence indicates that SARS-COV-2 began its encounter with humans already highly matched to human biology.[[9]](#footnote-9)

It is not at all normal for a virus to enter a new host population without also evolving rapidly to adapt to it. Thus the first SARS coronavirus (SARS-CoV) acquired amino acid changes during its early spread in humans (Zhan et al., 2020). The alternative norm is for the virus to fail to adapt to its new host at all, such as has happened so far with every one of the many introductions into humans of the coronavirus MERS (Dudas et al., 2018).[[10]](#footnote-10)

It makes sense that random genetic mutations don’t produce a fully adapted germ that can directly transfer to a new host animal and thrive with no further modifications. Rather, when the accidental mutations hit first on a method for the germ to invade the new host, it invades but doesn’t live long because it is not well adapted to survive. If the accidental mutations hit on features that would help a germ survive in the new host first but there is no means to invade, to get past the animal’s front-line defenses, it does the germ no good. It never gets inside the new host. So, what typically happens with natural pandemics where a germ has successfully adapted to a new animal host is that the mutations that enable the germ to invade the host were achieved first. Then, the germ rapidly mutated inside the host to produce the additional adaptations required for the germ variant to thrive sufficiently to generate a full-blown infection and be passed to other humans.

This logic is confirmed in the history of virology. Science has found the same pattern in every *naturally produced* pandemic: invasion of humans by a new, slightly modified germ, *followed by a rapid series of (lucky) mutations* that make the additional changes required for the germ to survive and flourish in the human body and be easily passed on to other humans. When the germ doesn’t get so lucky with its mutations, and they rarely do, there is no pandemic.

In theory, early versions of SARS-COV-2 progenitor viruses might have partially evolved toward infectivity of humans by jumping between several animal species in a sequence that allowed the necessary mutations to be achieved incrementally before transferring to humans. But a series of possible animal hosts with the correct virus strain susceptibility for an incremental, multi-species chain of transfers has not been identified by science. And a group of likely candidate species has not been confirmed to have been infected by SARS-COV-2 precursor strains.

What we see with SARS-COV-2 is that the germ arrived at the Wuhan, China outbreak with the full package of mutations necessary for successful infection of humans. There is no biological record of the normal series of adaptive mutations occurring incrementally (although rapidly) among different patients (or animals). That means a lab origin of SARS-COV-2 is highly probable.

The odds against a single virus strain in a bat developing all the mutations needed to infect humans while retaining the ability to flourish in bats long enough to complete the job are astronomical. The changes needed to survive in humans make it very difficult for the virus to flourish in bats. Most SARS-COV-2 strains probably can’t infect bats at all, and the few that can will be out-competed by better adapted bat viruses and not survive.

So, where does all the intermediate adaptive mutation work get done to bridge the huge evolutionary distance between known bat viruses and SARS-CoV-2? There have been no confirmed human passage opportunities for the closest relatives of SARS-COV-2 other than in laboratory research and the bat virus infections experienced by the Mojiang (China) miners. There have been many opportunities for human encounters with bat corona viruses generally, but no documented opportunities outside research laboratories and associated field research locations for human encounters with bat coronaviruses that were genetically close enough to SARS-COV-2 to arguably be its near-to-immediate progenitors and be capable of infecting humans.

For instance, using different approaches, numerous researchers have concluded that the SARS-CoV-2 spike protein has a very high affinity for the human ACE2 receptor (Walls et al., 2020; Piplani et al., 2020; Shang and Ye et al., 2020; Wrapp et al., 2020). Such exceptional affinities, ten to twenty times as great as that of the original SARS virus, do not arise at random, making it very hard to explain in any other way than for the virus to have been strongly selected in the presence of a human ACE2 receptor (Piplani et al., 2020).[[11]](#footnote-11)

Where did coronaviruses have the opportunity to be in the presence of the human ACE2 receptor? Pangolins have a very similar ACE2 receptor, but they have been ruled out as the immediate progenitor of SARS-COV-2 for lack of evidence that pangolins were infected with SARS-COV-2 or a similar virus that could have made a jump to human infectivity. Other than in labs researching coronaviruses and the Mojiang miners, who seem to have contracted bat virus infections, there have been no documented frequent encounters between cells having the ACE2 receptor and coronaviruses genetically close to SARS-COV-2.

With SARS-COV-2 we see a virus achieving an ultra-enhanced human ACE2 match-up, a complex and difficult evolutionary change, without a visible evolutionary path for doing it. Decades, maybe even centuries of repeated passage of early, less adapted, forms of the virus through human systems would be required to achieve the full set of mutations required for efficient adaptation to human biology and preserve them through positive selection.

A few researchers have hypothesized that a weak version of SARS-COV-2 could have been circulating in humans undetected for forty years or so, providing more time for the necessary mutations to occur, but there is no evidence for that hypothesis. A recent *Science* article (2022), written by a host of established scientists, suggests that circulation of SARS-COV-2 progenitor viruses in humans did not occur before the COVID-19 pandemic began. A version of SARS-COV-2 circulating undetected in humans for forty years would have left a trail science would have discovered, but there is no scientific evidence that such an event occurred.

Understanding the circumstances that lead to pandemics is important for their prevention. We analyzed the genomic diversity of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) early in the coronavirus disease 2019 (COVID-19) pandemic. We show that SARS-CoV-2 genomic diversity before February 2020 likely comprised only two distinct viral lineages, denoted "A" and "B." Phylodynamic rooting methods, coupled with epidemic simulations, reveal that these lineages were the result of at least two separate cross-species transmission events into humans. The first zoonotic transmission likely involved lineage B viruses around 18 November 2019 (23 October to 8 December), and the separate introduction of lineage A likely occurred within weeks of this event. These findings indicate that it is unlikely that SARS-CoV-2 circulated widely in humans before November 2019 and define the narrow window between when SARS-CoV-2 first jumped into humans and when the first cases of COVID-19 were reported. As with other coronaviruses, SARS-CoV-2 emergence likely resulted from multiple zoonotic events.[[12]](#footnote-12)

Sounds like these authors have proved a “zoonotic” origin for the COVID-19 pandemic in the form of natural animal-to-human spillover events that occurred outside of research activities, but they are a long way from it. A theory that two animal-to-human virus spillovers occurred in nature in the absence of evidence for either spillover event and with no visible evolutionary pathway for the virus to have become infectious to humans is less probable than the virus escaping from a lab or research activity where adaptation of the virus to human biology had been intentionally or inadvertently facilitated.

Recombination of several coronavirus genetic lineages, including the two identified in the article quoted above, could have been accomplished knowingly or unknowingly faster and more easily in a laboratory than via natural evolution. Lab research offers a wide variety of animal passage options that could plausibly have spawned the two lineages. The lab release/escape theory, therefore, remains far more probable than the animal transfer theory, all things considered.

If we accept Pekar's work without question, to affirm the lab escape theory we must allow that two viral lineages escaped from labs, not just one. But that is no big deal. A single lab accident might have released two or more lineages that were being studied.

We shouldn’t accept Pekar’s work, however, because it employs circular reasoning to establish the Wuhan market as the place of origin for the COVID-19 pandemic. More thorough genetic analysis, Mutational Order Analysis (MOA),[[13]](#footnote-13) shows only a single lineage at the root of the pandemic, and a single “spillover” event, one that did not involve the virus strains found at the Wuhan market.

A single spillover event is a crucial observation because it strongly implies a lab leak (since scientists tend to work with pure cultures); whereas equivalent evidence for multiple and/or genetically diverse spillovers would have implied a natural source. MOA also shows that all lineage B viruses are descended from one lineage A virus….

Especially if one includes the new Gao et al. evidence, there are already powerful reasons to doubt both the market-zoonotic origin and a dual-spillover. These reasons are largely glossed over by the Pekar and Worobey preprints so they are worth outlining briefly:

*1) The market samples were probably taken late in the Wuhan outbreak.*

The first reason, and the simplest, is that the market samples were taken between Jan 1st and March 30th, 2020. Yet plentiful evidence, such as contemporaneous newspaper reports of an outbreak in Wuhan, implies that SARS-CoV-2 was circulating widely in Wuhan and beyond by January 1st. Such evidence makes it difficult to agree that the market samples, so hotly discussed, have any special relevance to the source of the pandemic virus itself.

For example, according to the WHO COVID origin investigation, there were 174 COVID-19 hospitalisations in Wuhan by December 31st 2019. Given the normal delay between infection and hospitalisation and the significant rate at which COVID-19 gives asymptomatic and mild cases, these hospitalisations likely represented only the tip of a large infectious outbreak in December.

Indeed, Ian Lipkin, an epidemiologist at Columbia University, told an interviewer he knew of an outbreak in Wuhan by December 15th, 2019. Lipkin has subsequently confirmed this statement. And in spring 2020, Peter Daszak, President of the EcoHealth Alliance, Marjorie Pollack, an epidemiologist who runs ProMED, and Public Health Professor Lawrence Gostin made similar statements to the LA Times. Further back still, according to ABC News, US security agencies were tracking a pneumonia outbreak in Wuhan in November.

Early wide spread of the virus in Wuhan is evidenced too by a detailed case study of a family from Guangdong who visited Wuhan between December 29th and January 4th, 2020. Five from a total of six family members contracted COVID-19 while in Wuhan, without them having visited any markets (Chan et al., 2020). Further afield, a significant body of genome sequence and antibody evidence suggests SARS-CoV-2 was in Europe and other countries in the fall of 2019, well before the Huanan market samples were taken (reviewed in Canuti et al., 2022).

If there were thousands of cases in the city of Wuhan by Jan 1st when the market was closed and 10,000 people per day usually visited it, how do samples taken then (or later) constitute credible evidence for a market origin? Quite likely, vendors and others at the market found to have COVID-19 infections were just typical for Wuhan in December 2019 (Courtier-Orgogoz and de Assis, 2022). Typical or not, the market samples were collected too late to distinguish a market origin from any other origin in or near Wuhan.

*2) Environmental samples collected at the market are of human origin and did not come from animals sold there.*

The aim of the Chinese CDC paper was to analyse the environmental samples (swabs from surfaces etc.) that they took in and around the Huanan market after Jan 1st, 2020 (Gao et al., 2022). They concluded that the market was only an amplifying event, in part because SARS-CoV-2-positive samples were associated with stalls belonging to multiple types of vendors, including those not selling animals (the Worobey preprint argues there is a correlation). More compelling, the CDC authors found that the samples collected from the market, which Pekar and Worobey claim are from infected animals, are admixed only with human genetic material and not with genetic material from raccoon dogs or other species potentially sold at the market. The only reasonable inference is that these positive samples did not derive from the faeces or urine or exhalations of a live non-human animal. Few results would better indicate that virus-positive market samples derive from infected humans as opposed to other species.

*3) Pekar and Worobey rely on circular reasoning to identify root viruses.*

The 2022 Pekar et al. preprint adapts the findings of a previous publication (Pekar et al., 2021) to generate the novel hypothesis of a split phylogeny that traces SARS-CoV-2 back to two independent spillovers, both occurring in the Huanan market. These two spillovers, they claim, are represented today by what are known as lineage A and lineage B viruses, which differ by only two mutations. However, the phylogenetic methods used for building evolutionary trees and thus identifying the root virus in both Pekar papers are highly problematic because they are vulnerable to uneven and biased sampling and unusual genetic phenomena, such as superspreading events (Liu et al., 2020). One key bias relevant here is that, for many early COVID-19 cases, contact with the Huanan market was a diagnostic requirement (Liu et al., 2020). This will tend to orient phylogenies towards the market. Further, Pekar et al. use a clock-based algorithm that uses sampling dates to infer the root virus. This method is designed to channel the choice of root virus towards those genomes sampled earliest. If the market was the early focus of sampling, which it was, then the Pekar method of inferring the root is based on two independent forms of circular reasoning. These biases were further amplified by the Pekar and Worobey authors, who themselves decided, based on scant evidence, which patient cases counted towards the dataset and sometimes what were their disease onset dates. The effect of this intervention was to add yet more circularity into the selection process for root viruses. To satisfactorily determine which viruses are closest to the true origin requires instead a different method, one that is explicitly independent of ascertainment biases and subjective decision-making (Liu et al., 2020).

*4) Pekar et al., lack the evidence for two spillover events.*

A key assertion of the Pekar preprint is its proposal that extant lineage A and lineage B viruses represent the descendants of two independent SARS-CoV-2 spillover events (Pekar et al., 2022). To succeed, this double spillover claim must explain why numerous genome sequences exist that are intermediate between lineage A and lineage B. To overcome this challenge, Pekar et al. propose that such intermediates are all either artifacts from sequencing errors or irrelevant to the origin question for other reasons. Sequencing errors are common enough, but Pekar et al. only demonstrate them convincingly in a minority of instances. For example, for most of their suggested sequence artifacts they rely on an unverifiable ‘personal communication’ from a single scientist (L. Chen) in China. To make a case for the irrelevance of others they have to suggest, for example, that two genomes sampled in February in Beijing are irrelevant–as if early sequences cannot have spread elsewhere or persisted. Ultimately, their bold suggestion that the phylogeny of SARS-CoV-2 is best explained by resolving it into two independent spillovers is very poorly supported by evidence.[[14]](#footnote-14)

Pekar, et al., did not discover any actual events of cross-species transmissions of SARS-COV-2 progenitor viruses. They only assumed that animal to human transfers likely occurred based upon what has happened with other coronaviruses and based upon purely theoretical models of their own construction. No SARS-COV-2 positive test results were obtained from animal sources at the Wuhan market.

Pekar’s theoretical models and methods don’t prove animal-to-human transfers occurred. Pekar’s findings only argue that, *if the animal-to-human transfers occurred*, they likely occurred within certain time windows. However, the models themselves have been questioned by Jonathan Latham, citing the more powerful and accurate MOA genetic tracing systems used by Kunar, et al., which establish earlier dates for SARS-CoV-2’s emergence (September-October 2019).

After four years of searching for animal species hosting close progenitor viruses of SARS-COV-2, researchers haven’t found any qualifying viruses in animals (including the A and B lineages mentioned by Pekar). Therefore, the only inference we are entitled to make is either that Pekar’s initial *assumption* that animal-to-human transfers occurred is wrong, or there is something wrong with the phylodynamic rooting methods and/or epidemic simulation models Pekar and his co-authors were using. If the inferred zoonotic transfer to humans of SARS-COV-2 or closely related progenitor viruses actually occurred, researchers should have found the progenitor viruses in one or more intermediate host animal species.

Many stored blood samples collected over several years **prior to the pandemic** have been examined for precursors of SARS-COV-2 with no results. The samples used in the study quoted above were taken **during** the pandemic. The Pekar article authors only **speculate** that animal hosts were the source of the viral lineages found in patients’ blood early in the pandemic, they have not produced the animals containing the viral lineages. We are therefore not entitled to assume that SARS-COV-2 evolved by a purely natural means minus any help from the laboratory. Even the original SARS outbreak of 2003 has not been definitively shown to have originated in a wild or farmed animal-to-human transfer. A wild (in nature outside of lab/research activities) zoonotic origin of the original SARS virus is merely held to be “likely.”

I disagree with the “likely” estimate for the animal-to-human spillover hypothesis for the origin of both the original SARS and COVID-19. (Camels have been shown to be likely spillover agents for MERS, though those findings could have been artificially produced by scientists motivated to do a cover-up.). This is not a conspiracy theory; it is simply a matter of the scientific evidence being insufficient to justify high-confidence conclusions.

However, when considering the last three main coronavirus epidemics, i.e. SARS, MERS and COVID-19, several requirements for the spillover model are not fulfilled. First of all, no epizootic necessary to reach the level of zoonotic pressure required for the spillover was ever recorded for either SARS, MERS or COVID-19.[[15]](#footnote-15)

Absent known animal-to-human transfer events, virus mutation research projects in labs/outdoor field research locations become the more likely source. Prior to the COVID-19 pandemic, passage of coronaviruses through human or mammalian cell lines was known to be occurring in one or more Chinese labs. Some of that research was authorized and funded by the United States National Institutes of Health (NIH) under a contract awarded to a U.S. company, EcoHealth Alliance, subcontracted in part to the Wuhan Institute of Virology (WIV) lab. (See <https://grantome.com/grant/NIH/R01-AI110964-06>.)[[16]](#footnote-16)

Perhaps most critically, U.S. funding is directly tied to research at the Wuhan Institute of Virology via the U.S. Agency for International Development and the National Institutes of Health, including funding for research on a close cousin virus 96 percent similar to SARS-CoV-2.[[17]](#footnote-17)

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The [23 June, 2023 ODNI] report, [*The Potential Links Between the Wuhan Institute of Virology and the Origin of the COVID-19 Pandemic*](https://www.dni.gov/files/ODNI/documents/assessments/Report-on-Potential-Links-Between-the-Wuhan-Institute-of-Virology-and-the-Origins-of-COVID-19-20230623.pdf), disclosed a lot of information that has previously been reported about the virological research center in Wuhan, the city where the first cases of COVID-19 were detected in late 2019. Some biosafety standards and equipment at the facility were found to be lacking, including appropriate precautions for working with SARS-like coronaviruses and aging infrastructure. Workers at the lab had been ill at around the time the pandemic started. The lab held an incredibly large collection of bat samples, conducted genetic engineering experiments on coronaviruses, and conducted experimentation on making hybrid coronaviruses. Also previously reported, the lab had links to the Chinese military—reportedly for public health work.[[18]](#footnote-18)

In “[Did the SARS-CoV-2 virus arise from a bat coronavirus research program in a Chinese laboratory? Very possibly](https://thebulletin.org/2020/06/did-the-sars-cov-2-virus-arise-from-a-bat-coronavirus-research-program-in-a-chinese-laboratory-very-possibly/),” [Milton Leitenberg](https://thebulletin.org/biography/milton-leitenberg/), a biowarfare expert, tells us that…

Documentary evidence indicates that the novel-bat-virus projects at Wuhan CDC and the Wuhan Institute of Virology used personal protective equipment and biosafety standards that would pose high risk of accidental infection of a lab worker upon contact with a virus having the transmission properties of the outbreak virus.

A substantial amount of bat virus research took place in Wuhan China circa 2009-2018. That research could have resulted in the witting or unwitting production of one or more close progenitor viruses to SARS-COV-2, which then infected lab workers and/or Mojiang miners.

The WIV is just a few miles from the market and, according to its US funders and the people who work there, it specialises in the collection and study and enhancement of SARS-related coronaviruses (Latinne et al., 2020). For decades, a major goal of its research has been to identify or create ones primed for human spillover (e.g. Li et al., 2019).[[19]](#footnote-19)

Blood samples from the ill Mojiang miners were sent to the Wuhan Institue of Virology and a lot of bat virus sampling work was done at the Mojiang mines not long after receipt of the blood samples. One or more cycles of reinfection and additional mutations may have combined to produce the viral genome of SARS-COV-2.[[20]](#footnote-20)

Though never mentioned by Ge et al., the ‘abandoned’ mine (which subsequently became known as the Mojiang mine) where BtCoV/4991 was found had recently been the site of a mystery disease outbreak. In April 2012, just two and a half months before the first WIV sampling trip, six miners had become sick and three of them had died. Indeed, the mine outbreak was presumably why the WIV researchers were sampling there (and the Zhou et al. addendum later confirmed this).

The nature of the 2012 disease outbreak became much clearer with the discovery (by an anonymous Twitter user called @TheSeeker268) of a 2013 Chinese Master’s thesis. This thesis is titled “The Analysis of Six Patients with Severe Pneumonia Caused by Unknown Viruses.” Its abstract specifically mentions a possible outbreak of SARS-like coronaviruses….

According to the Master’s thesis, the miners had been shovelling bat guano. This implied that the mystery disease probably originated from bats. That, along with various test results and consultations led the author to conclude that the most likely cause of the outbreak was a coronavirus. But perhaps most startling of all the findings to emerge from the translation was that the symptoms of the miners closely resembled those of COVID-19 (Rahalkar and Bahulikar, 2020b).[[21]](#footnote-21)

Was RaTG13, the closest known viral genome to SARS-COV-2, a key step in a research-fostered evolutionary cycle that produced the SARS-COV-2 viruse that caused the pandemic? Maybe, maybe not. Some experts have questioned whether RaTG13 is a natural genome or even real beyond an artificially contrived computer printout.

Experts agree that RaTG13 could not have been the direct progenitor of COVID-19. The differences between the two viruses are spread across the genome, and evolution from one to the other could require decades. Other viruses circulating in Southeast Asia have since been shown to have slightly more similar genomes, though phylogenetic analyses still place RaTG13 as the closest relative. However, its existence has fueled speculation about whether a closer relative could be among the unpublished viruses under study at the WIV.

Their [WIV] research papers and grant proposals show that they were interested in bat coronaviruses with features shared by SARS-CoV-2, like a furin cleavage site and the ability to infect human cells through a receptor called ACE2....

A University of California Davis letter to Sen. Dianne Feinstein, D-Calif., goes further, suggesting that USAID may have been involved with its [RaTG13] discovery.

“In China alone, we sampled >10,000 bats and ~2,000 other mammals, using PREDICT protocols to discover 52 novel SARS related-CoV’s [coronaviruses], including the closest relative of the Wuhan nCoV [SARS-CoV-2],” reads the letter.

The letter also reports “supplemental funding from NIH” to Shi Zhengli.

PREDICT was USAID’s $200 million, 10 year virus-hunting program, which had the aim of predicting zoonotic diseases and also coincided with a boom in U.S. biodefense efforts after 9/11.[[22]](#footnote-22)

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The research that NIH approved under the grant to EcoHealth Alliance with a subaward to the Wuhan Institute of Virology in Wuhan, China sought to understand how animal coronaviruses, especially bat coronaviruses, evolve naturally in the environment and have the potential to become transmissible to the human population. This research included studying viral diversity in bat reservoirs, surveying people who work in live animal markets or other occupations with high exposure to wildlife for evidence of bat coronavirus infection and analyzing data to predict which newly discovered viruses pose the greatest threat to human health.[[23]](#footnote-23)

Frequent opportunities for infection, re-infection, cross-infection, and coinfection with possible progenitor bat coronaviruses had already occurred among the Mojiang miners circa 2012. Scientists from WIV took samples from bats in those mines and investigated the miners’ illnesses. Cross-contamination could have occurred via lab researchers, who were infected or contaminated with mutated viruses from the lab, coming into contact with bats and miners infected with other virus mutations. Frequent cross-contamination opportunities leading to human infections would facilitate the accelerated evolution of human-adapted bat viruses via genetic recombination and the natural equivalent of serial passaging.

Wuhan labs and Mojiang mines are the only two plausible sources for the otherwise missing opportunities for early progenitor viruses to move *rapidly* towards the high-human-affinity SARS-COV-2 genome via selective mutation in the presence of human or human-like ACE2 receptors. African Green monkey VERO cell lines and humanized tissues in mice are regularly used in laboratory research. Both offer frequent opportunities for bat viruses to move closer to human infectivity.

I am not picking on China; I am only following the logic, evidence, and mathematical probabilities. The initial SARS-COV-2 outbreak *was* in Wuhan. Chinese researchers interacting with the Mojiang miners, or interacting with virus-infected bats in the mines or markets, intentionally or unintentionally provided opportunities for a lab-altered virus to be introduced into an interactive mix of viruses, bats, and humans—perhaps repeatedly.

A *lot* of bat virus research was done in Yunnan province (where the Mojiang mines are located).[[24]](#footnote-24) The real possibility of multiple interactive virus exposures as described above means that any future discovery of a bat infected with SARS-COV-2 (or a 99.9% genetically similar progenitor virus) in Yunnan province must be considered suspect due to the possibility of cross-contamination from the laboratory-miner-field-researcher interactive milieu. Given China’s confirmed efforts to cover-up and obstruct the initial investigation into the origins of the COVID-19 pandemic, an intentionally fabricated viral genome (such as RaTG13 has been reputed to be) is also a possibility that must be considered prior to validating any new findings.

Putting Quay’s work together with Latham and Wilson’s yields the most explanatory model of an event scenario that could have produced the COVID-19 pandemic. Milton Lietenberg’s throwing his scientific weight behind the possibility of a lab leak being the cause of the pandemic has gone a long way toward establishing the legitimacy of the lab leak hypothesis. Other scientists and science writers such as Ariel Fernández, Bernd Kiana, Nicholas Wade, Katherine Eban, Rossana Segreto, Yuri Deigin, Karl Sirotkin, and Dan Sirotkin have contributed substantially to the case for a laboratory origin.

Students of this subject also owe a significant debt to Lynn Klotz, who has provided the lion’s share of lab safety data concerning accidental release of germs from biological research labs, and to research scientists and investigative journalists like Nicholas Wade, Filippa Lentzos and Matt Field from the *Bulletin of Atomic Scientists*, Emily Kopp and Karolina Corin from *U.S. Right to Know*, Sharon Lerner, Mara Hvistendahl, and Maia Hibbett from *The Intercept*, Alison Young and Nick Penzenstadler writing for USA Today, and Amy Maxmen and Smriti Mallapaty writing for *Nature*.

The bottom line is that, while there is no direct evidence for either a natural animal-to-human spillover theory (zoonosis) or the laboratory release/escape theory, the lab origin theory scores much higher based on indirect evidence and logic. Scientists have looked into the zoonosis theory for four years and counting and could find no direct evidence for the natural evolution plus animal-to-human spillover origin of SARS-COV-2/COVID-19. However, investigators were not allowed to perform a proper forensic investigation in Chinese labs to find evidence for the lab release theory. Process of elimination suggests the evidence is (or *was*) there for the lab release theory.

For casual Internet visitors, if you only have time to read a few articles, read Milton Leitenberg’s “[Did the SARS-CoV-2 virus arise from a bat coronavirus research program in a Chinese laboratory? Very possibly](https://thebulletin.org/2020/06/did-the-sars-cov-2-virus-arise-from-a-bat-coronavirus-research-program-in-a-chinese-laboratory-very-possibly/)” as well as the 2015 *USA Today* journalistic masterpiece by Alison Young and Nick Penzenstadler, “[Inside America's Secretive Biolabs](http://www.usatoday.com/story/news/2015/05/28/biolabs-pathogens-location-incidents/26587505/).” The authors reveal many incidents of dangerous laboratory mistakes and interview science experts who establish that a huge amount of research on dangerous germs goes on around the world in largely safe, but *not perfectly safe*, laboratories. If you can squeeze out a few more minutes read Jonathan Latham and Allison Wilson’s two articles, “[A Proposed Origin for SARS-CoV-2 and the COVID-19 Pandemic](https://www.independentsciencenews.org/commentaries/a-proposed-origin-for-sars-cov-2-and-the-covid-19-pandemic/), and “[A Chinese PhD Thesis Sheds Important New Light on the Origin of COVID-19](https://www.independentsciencenews.org/commentaries/a-chinese-phd-thesis-sheds-important-new-light-on-the-origin-of-the-covid-19-coronavirus/).”

**For the HELP Committee members:**

This “white paper” (still a partially complete work in progress) should be of help in countering critics of the newly released Senate subcommittee report on the origins of COVID-19 (such as Angela Rasmussen, who was cited in the DHS newsletter 22 April 2023, see [COVID-19, Covid-19 origins, China | Homeland Security Newswire](https://www.homelandsecuritynewswire.com/dr20230422-senate-republicans-release-covid-origins-report).) Many of the articles in the bibliography below will serve to strengthen the scientific arguments of the Senate HELP Committee “Muddy Waters” report.

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Respectfully submitted.

Rick Harrison, M.Sgt., USAF (Retired)

2639 E. 2nd Street, Apt. 4

Bloomington, IN 47401

rdharrison75@gmail.com

812-361-4807

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**The COVID-19 Pandemic (SARS-COV-2 Virus)—Did It Come from a Lab?**

Why bother to question the natural evolution/zoonosis (animal spillover) theory when animals appear to have been the source of similar virus pandemics in the past? With the earlier SARS and MERS viral epidemics (2003 forward), strongly implicated (but not fully proved) intermediate animal hosts for the evolving viruses were found within four to ten months of the outbreak of the diseases.[[25]](#footnote-25) This didn’t happen with COVID-19.[[26]](#footnote-26) Intermediate animal hosts of closely related progenitors of the SARS-COV-2 virus required to support the natural animal origin (zoonotic) theory have still not been found after *four years* of looking. “Chinese researchers have failed to find a bat population as the source of SARS-CoV-2, or an intermediate host to which SARS-CoV-2 might have jumped despite an intensive search.…”[[27]](#footnote-27)

“The so-called progenitor virus should be 99.9 percent the same as the pandemic virus, Linfa Wang, the director of the emerging infectious diseases program at Duke-NUS Medical School in Singapore told the *Science* panel.”[[28]](#footnote-28) Similar genomes to SARS-COV-2 were found in bats and pangolins, but they *are not close enough*; “…a progenitor virus that shares >99% identity with SARS-CoV-2 remains unknown.”[[29]](#footnote-29) The bat virus found in Wuhan is only 96% identical to SARS-COV-2. It does not have the ability to directly infect humans.

SARS-CoV-2 which recently affected the human population worldwide is suspected to have originated from bats. It was found to be closely related to the Sarbecoviruses MN996532\_raTG13 and RmYN02 from the Chinese horseshoe bats Rhinolophus affinis and Rhinolophus malayanus, respectively (Zhou et al., 2020a; Zhou et al., 2020b) There is no evidence of direct transmission of Sarbecoviruses from bats to humans yet (Afelt et al., 2018a). The only direct Sarbecovirus infections of humans have been linked to laboratory accidents during the SARS epidemic.[[30]](#footnote-30)

Further evolution of those close-but-not-close-enough bat virus genomes via multiple intermediate hosts would be necessary for a jump to humans. In a *Nature* article in 2017, David Cyranoski informed us that the original SARS (SARS-COV-1) was confidently seen as a leap to humans from bats because Chinese scientists found all the genetic building blocks of SARS in a single population of horseshoe bats. This has not been done for SARS-COV-2.[[31]](#footnote-31) (Scientists did not, however, confirm the presence of the full intact SARS virus genome in a bat or the transfer of the virus from a bat to a human. It remains possible that the original SARS pandemic was caused by a lab release/escape.)

The genetic patterns of SARS-CoV-2 don’t match up well to science’s expectations of a natural evolution event. “Although experimental studies have shown that recombinational exchanges occur at random along the coronaviral genome, in nature, they are vastly overrepresented in regions controlling viral interaction with host cells.”[[32]](#footnote-32) Positive selection would preserve useful mutations in such areas, yes, but for random mutations to get that much work done in those areas there would have to be evidence of equal mutation frequency across the entire virus genome. That is not the mutational pattern found in SARS-COV-2.

SARS-COV-2 mutations that differentiate it from its nearest known relatives are not averaged out across the genome; they are concentrated in the areas that give the virus the ability to enter human cells and get past human immune defenses. Having an abnormally large number of mutations focused on key, functionally critical areas where the difficulty factor for success is high suggests an intelligently guided effort to build a virus that can get past the human body’s defenses, not a random act of natural evolution.

Defenders of the zoonosis (animal-to-human spillover) theory of the origin of SARS-CoV-2 argue that positive selection could explain that pattern. In theory, it could. But a random process would take decades longer than a well-designed laboratory project to achieve so many functionally focused mutations. A random evolutionary process would have left a decades- or centuries-long trail of gradual wandering alterations that incrementally grew closer and closer to the highly adapted SARS-COV-2 viral genome. It would also have left a larger smattering of random mutations across the entire genome, mutations that had no relevance to human infectivity. That trail of a random, incremental genome evolution for the SARS-COV-2 virus doesn’t seem to be out there.

Advances in genetic science have made it possible for labs to modify genomes without leaving traces of human intervention. RNA/DNA sequence and biochemical analyses, therefore, won't always be able to detect the lab origin of a virus genome. Only a forensic investigation of what actually occurred in the lab can answer the question of whether a new virus genome arose via natural zoonosis or laboratory-encouraged alterations (direct or indirect).

Laboratory “serial passage” of viruses through human, humanized, or closely related mammalian cell cultures can indirectly encourage the creation of a new, more dangerous, virus that is better adapted to humans. Direct genetic engineering techniques can do the same thing. We are therefore not entitled to assume random natural evolution of the SARS-CoV-2 virus without supporting evidence. In this case, science can’t find the trail of random evolution in nature. However, we do know that many labs were working diligently to produce all the possible genetic variations that coronavirus genomes would allow.

There is so far no scientifically validated evidence that directly supports a natural origin….

The article then provides arguments against the laboratory engineering hypothesis, which are not conclusive for the following reasons. First, it assumes that the optimisation of the receptor binding domain for human ACE2 requires prior knowledge of the adaptive mutations, whereas selection in cell culture or animal models would lead to the same effect. Second, the absence of traces of reverse-engineering systems does not preclude genome editing, which is performed with so-called seamless techniques. Finally, the absence of a previously known backbone is not a proof, since researchers can work for several years on viruses before publishing their full genome (this was the case for RaTG13, the closest known virus, which was collected in 2013 and published in 2020)…. However, the pangolin hypothesis has since been abandoned, so the whole reasoning should be re-evaluated. Although considerable evidence supports the natural origins of other outbreaks (eg, Nipah, MERS, and the 2002–04 SARS outbreak) direct evidence for a natural origin for SARS-CoV-2 is missing.…

A research-related origin is plausible….

…a research-related origin (which might have occurred at sampling sites, during transportation or within the laboratory, and might have involved natural, selected, or engineered viruses).[[33]](#footnote-33)

Contrary to what propaganda articles sponsored by special interests will tell you, the laboratory origin theory of the COVID-19 pandemic is very much alive and well. Here is a quote from the U.S. House of Representatives *Second Interim Report on the Origins of the COVID-19 Pandemic*, citing the Lancet Commission on Lessons for the Future from the COVID-19 Pandemic.

A recent publication by the Lancet COVID-19 Commission similarly acknowledged that either a natural spillover event or research-related activities may have caused the pandemic, stating: “three research-associated hypotheses are still plausible: infection in the field, infection with a natural virus in the laboratory, and infection with a manipulated virus in the laboratory.”…

“Advances in biotechnology in the past two decades have made it possible to create new and highly dangerous pathogens through genetic manipulation – for example, creating new chimeric viruses by combining the genetic material of more than one viral pathogen, or mutant viruses through the deliberative insertion of a furin cleavage site. The bioengineering of SARS-CoV-like viruses for the study and testing of potential drugs and vaccines advanced substantially after the outbreak of severe acute respiratory syndrome [SARS] in the 2000s. Laboratory experiments included the creation of novel viruses (e.g., so-called consensus viruses that average the genetic code across a set of natural viruses), the mutation of viruses (such as through the insertion of a furin cleavage site), the creation of chimeric viruses, and the serial passaging of viruses through cell cultures to test their transmissibility, virulence, immunogenicity, and host tropism. Research that can increase the transmissibility and virulence of pathogens is called gain-of-function research of concern, although which specific experiments should fall into this category is contested by scientists. As laboratory technologies have rapidly advanced, many scientists have warned of the increasing risks of undersupervised and under-regulated genetic manipulation of SARS-CoV-like viruses and other potential pandemic pathogens.”[[34]](#footnote-34)

Even before one entertains suspicions of foul play by greedy scientists in pursuit of big research money or favors from Communist agents trying to dominate the world with biowarfare, the mathematical odds of an eventual accidental release of a dangerous germ from a scientific research lab are enormous. “Accidental viral infections among workers of hospitals or research laboratories are an emerging threat due to reasons among which stand out the growing volume of dangerous virus research done including with biohazard class 3 or 4 agents....”[[35]](#footnote-35)

The risk associated with the accidental laboratory escape of potential pandemic pathogens is under the magnifying lens of research and policy making communities. The recent debate on the genetic manipulation of highly virulent influenza viruses has made clear the necessity for quantitative risk/benefit assessment before starting research projects involving biosafety level (BSL) 3 and 4 agents. According to data collected in 2010 and 2011, the number of BSL 4 laboratories worldwide is 38, mostly concentrated in the US and Europe.

The official number of BSL 3 facilities worldwide is unknown, since most laboratories where research on infectious diseases is carried out and many hospital laboratories operate at safety level 3. Their number, however, is of the order of several thousands: there were 1,362 in the US alone in 2008.[[36]](#footnote-36)

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Inside America's secretive biolabs

Alison Young and Nick Penzenstadler, USA TODAY

Vials of bioterror bacteria have gone missing. Lab mice infected with deadly viruses have escaped, and wild rodents have been found making nests with research waste. Cattle infected in a university's vaccine experiments were repeatedly sent to slaughter and their meat sold for human consumption. Gear meant to protect lab workers from lethal viruses such as Ebola and bird flu has failed, repeatedly.

A USA TODAY Network investigation reveals that hundreds of lab mistakes, safety violations and near-miss incidents have occurred in biological laboratories coast to coast in recent years, putting scientists, their colleagues and sometimes even the public at risk.

Oversight of biological research labs is fragmented, often secretive and largely self-policing, the investigation found. And even when research facilities commit the most egregious safety or security breaches — as more than 100 labs have — federal regulators keep their names secret.[[37]](#footnote-37)

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A further important oversight by the Andersen authors concerns the history of lab outbreaks of viral pathogens. They write: “there are documented instances of laboratory escapes of SARS-CoV.” This is a rather matter-of-fact allusion to the fact that since 2003 there have been six documented outbreaks of SARS from labs, not all in China, with some leading to fatalities (Furmanski, 2014).

Andersen et al might have also have noted that two major human pandemics are widely accepted to have been caused by lab outbreaks of viral pathogens, H1N1 in 1977 and Venezuelan Equine Encephalitis (summarised in Furmanski, 2014). Andersen could even have noted that literally hundreds of lab accidents with viruses have resulted in near-misses or very localised outbreaks (summarised by Lynn Klotz and Sam Husseini and also Weiss et al., 2015).[[38]](#footnote-38)

The COVID-19 pandemic has been an enormous tragedy of catastrophic proportions. Estimates of the death toll range from 6 million to 40 million. In “Should we discount the laboratory origin of COVID-19?” Rossana Segreto, Yuri Deigin, and Kevin McCairn, et al., remind us that identifying the true origin of SARS-CoV-2 is essential to prevent future outbreaks. The search for SARS-CoV-2′s origin should therefore include an open and unbiased inquiry. In a *Proceedings of the National Academies of Science* article published ten months after the pandemic began, Stanford University’s David Relman argues this point very persuasively.

SARS-CoV-2 is a betacoronavirus whose apparent closest relatives, RaTG13 and RmYN02, are reported to have been collected from bats in 2013 and 2019, respectively, in Yunnan Province, China. COVID-19 was first reported in December 2019 more than 1,000 miles away in Wuhan City, Hubei Province, China. Beyond these facts, the “origin story” is missing many key details, including a plausible and suitably detailed recent evolutionary history of the virus, the identity and provenance of its most recent ancestors, and surprisingly, the place, time, and mechanism of transmission of the first human infection. Even though a definitive answer may not be forthcoming, and even though an objective analysis requires addressing some uncomfortable possibilities, it is crucial that we pursue this question. Preventing the next pandemic depends on understanding the origins of this one.

Some have argued that a deliberate engineering scenario is unlikely because one would not have had the insight a priori to design the current pandemic virus. This argument fails to acknowledge the possibility that two or more as yet undisclosed ancestors (i.e., more proximal ancestors than RaTG13 and RmYN02) had already been discovered and were being studied in a laboratory—for example, one with the SARS-CoV-2 backbone and spike protein receptor-binding domain, and the other with the SARS-CoV-2 polybasic furin cleavage site. It would have been a logical next step to wonder about the properties of a recombinant virus and then create it in the laboratory.[[39]](#footnote-39)

Assumptions that natural evolution and zoonosis, not a laboratory, produced COVID-19 remain a very long way from meeting the standard of scientific evidence required for accepted theories. There is no clear evidence for zoonotic transfer of the virus from bats or other intermediate animal species to humans.[[40]](#footnote-40) There is no contiguous and convincing evolutionary history.

What we do know is that there have been a lot of genetic modifications of related viruses going on in laboratories since the original SARS outbreak in 2003. Here are excerpts from four articles from 2003, 2007, 2008, and 2015 respectively.

We sequenced complete SARS-CoV genomes taken from primary human tissues (SIN3408, SIN3725V, SIN3765V), cultured isolates (SIN848, SIN846, SIN842, SIN845, SIN847, SIN849, SIN850, SIN852, SIN3408L), and five consecutive Vero cell passages (SIN2774\_P1, SIN2774\_P2, SIN2774\_P3, SIN2774\_P4, SIN2774\_P5) arising from SIN2774 isolate. These represented individual patient samples, serial in vitro passages in cell culture, and paired human and cell culture isolates.[[41]](#footnote-41)

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“We adapted the SARS-CoV (Urbani strain) by serial passage in the respiratory tract of young BALB/c mice. Fifteen passages resulted in a virus (MA15) that is lethal for mice following intranasal inoculation. Lethality is preceded by rapid and high titer viral replication in lungs, viremia, and dissemination of virus to extrapulmonary sites accompanied by lymphopenia, neutrophilia, and pathological changes in the lungs.”[[42]](#footnote-42)

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Recombinant severe acute respiratory virus (SARS-CoV) variants...have been generated. All these viruses were rescued in monkey (Vero E6) cells and were also infectious for human (Huh-7, Huh7.5.1 and CaCo-2) cell lines and for transgenic (Tg) mice expressing the SARS-CoV receptor human angiotensin converting enzyme-2 (hACE-2)....[[43]](#footnote-43)

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The emergence of severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome (MERS)-CoV underscores the threat of cross-species transmission events leading to outbreaks in humans. Here we examine the disease potential of a SARS-like virus, SHC014-CoV, which is currently circulating in Chinese horseshoe bat populations. Using the SARS-CoV reverse genetics system, we generated and characterized a chimeric virus expressing the spike of bat coronavirus SHC014 in a mouse-adapted SARS-CoV backbone. The results indicate that group 2b viruses encoding the SHC014 spike in a wild-type backbone can efficiently use multiple orthologs of the SARS receptor human angiotensin converting enzyme II (ACE2), replicate efficiently in primary human airway cells and achieve in vitro titers equivalent to epidemic strains of SARS-CoV. Additionally, in vivo experiments demonstrate replication of the chimeric virus in mouse lung with notable pathogenesis.[[44]](#footnote-44)

To demonstrate that the origin of SARS-CoV-2/COVID-19 is a legitimately open question in science (as well as politics) consider this excerpt from Erwan Sallard, Jose Halloy, Didier Casane, Etienne Decroly, and Jacques van Helden’s article, “Tracing the origins of SARS-COV-2 in coronavirus phylogenies: a review,” published in the science journal, *Environmental Chemistry Letters*.

The data currently available are not sufficient to firmly assert whether SARS-CoV2 results from a zoonotic emergence or from an accidental escape of a laboratory strain....

**Genetic manipulations of viruses and gain‑of‑function experiments**

The issue of the natural or synthetic origin of SARS-CoV-2 deserves to be examined in more detail on the basis of available evidence. Hypotheses must be examined knowing which types of genetic manipulations are currently carried out in laboratories. Indeed, the manipulation of genomes of potentially pathogenic viruses is a common practice, which aims at understanding the mechanisms of replication and emergence of these viruses, and at developing new antiviral or vaccine strategies. Due to the risks of unexpected species cross-contamination of a new host (especially humans) and accidental dissemination of artificial recombinant viruses, these investigations are conducted in high-security laboratories (BSL3 or BSL4) subject to strict control and transparency procedures….

The risk of accidental escape of new potentially pandemic pathogens is increased by the proliferation of high biosafety laboratories (BSL-3 and BSL-4) in densely populated areas (Van Boeckel et al. 2013). In addition, experiments on viruses such as avian influenza viruses or SARS from chiropterans, that are currently unable to infect humans, are allowed in BSL-3 laboratories: It increases the risk of accidents because selection or mutagenesis can confer an epidemic potential to these viruses (Enserink 2003; Normile 2004; Henkel et al. 2012)....[[45]](#footnote-45)

The debate about the advisability of genetically modifying dangerous germs and intentionally cultivating them in laboratories has been going on since the mid 1970s. Here, in a quote from a 2014 article by a group of U.S. CDC-affiliated scientists, we see that the purpose of manipulating such dangerous germs in the lab is actually to develop protection against them.

Pandemic risk assessment that utilizes sequence data can take place only after critical genetic signatures are identified through laboratory research into the consequences for relevant biological properties (or phenotypes). These critical genetic features include those that based on previous experimental validation are predicted to confer virulence and/or have the ability to transmit efficiently in mammals....

Laboratories worldwide have employed reverse genetics to study the mechanisms by which HPAI H5N1 and other zoonotic influenza viruses evolve and how these mechanisms influence host receptor specificity, antigenic variation, replication, pathogenesis, drug susceptibility, and transmission. Besides being used to create vaccine viruses for the development of live, attenuated and inactivated prepandemic H5N1 influenza vaccines, reverse-genetics methodologies also have been used for many years to study the phenotypic consequences of particular mutations, including genetic changes that confer a gain of function (GOF)….

Results from more than 15 years of H5N1 GOF studies were compiled to assist researchers at institutions worldwide in their risk assessment of naturally occurring influenza viruses to facilitate an early response in the face of emerging zoonotic influenza virus threats.[[46]](#footnote-46)

Sounds good. But genetic alteration of viruses in labs to make them more dangerous risks creating the pandemic the research is meant to prevent, mitigate, or minimize *before* vaccines and antiviral drugs are developed and ready.

There are some biochemical options that *nature* rarely explores. Nature might take an additional one or more centuries to spontaneously generate a dangerous germ we intentionally produce in a lab. In that time science would have significantly advanced in general terms to where our vaccine and antiviral drug capabilities would protect the public faster and more effectively against the new super-germ when it finally emerged *naturally*. Some super-germs, newly made more dangerous in labs, would have a low probability of being produced by natural evolution at all.

Can labs really do things nature isn’t likely to eventually do via random mutation, even over centuries? Maybe. There are limits to the kinds of changes that naturally occur in living systems.

Five antigenic sites in the virus surface hemagglutinin protein, which together comprise 131 amino acid positions, are thought to determine the full scope of antigenic drift of influenza A virus. Koel et al. (p. 976) show that major antigenic change can be caused by single amino acid substitutions. These single substitutions substantially skew the way the immune system “sees” the virus. All substitutions of importance are located next to the receptor-binding site in the hemagglutinin. Because there are few positions of importance for antigenic drift, there are strict biophysical limitations to the substitutions at these positions, which restricts the number of new antigenic drift variants at any point in time. Thus, the evolution of influenza virus may be more predictable than previously thought.[[47]](#footnote-47)

This single example of physical limiting factors to spontaneous mutations doesn’t prove there are dangerous germ designs nature would not stumble upon but which laboratories could nonetheless force into existence, but it suggests there might be. My point is that risk-benefit analyses need to be done for newly proposed research to determine if such is the case for proposed research projects. The problem, of course, is that scientists and research corporations get paid for doing the projects, not for rejecting them as too dangerous. Foxes can’t be used to guard the hen house. By default the risk-benefit analysis must be done by government, but the government can be a fox too. Our foreign enemies force us to stay current in dangerous germ research in order to have vaccines and medications ready in case of a biowarfare attack. It’s not an easy problem to solve.

The bottom line on the question of beating Mother Nature to the creation of new dangerous germs is that each case is different and should be closely evaluated for risks and benefits. Features already present in biological systems, placed within the context of the laws of chemistry and physics, make some spontaneous natural developments in viral genomes more likely than others. Some might take thousands of years to evolve, if they ever did—unless. Unless scientists intentionally rebuild a virus genome to get past preexistent barriers in nature. And germ modification in labs is not restricted to the original root strain of a pandemic. In theory, new variations can be engineered in the middle of a pandemic, though on the surface that would obviously seem unwise.

Flipping through the SARS-COV-2 news stories of the past few years, one readily sees new variants of concern regularly springing from SARS-COV-2, variants that more effectively invade our bodies and get past the human immune system. Natural evolution does tend to work that way, but both the [Omicron and Pirola variants contain an abnormally large number of mutations](https://www.msn.com/en-us/health/medical/new-pirola-variant-of-covid-is-spreading-fast-has-experts-concerned/ar-AA1g6t57?ocid=iehp&cvid=e57be780059c4508b63d5b3856fce421&ei=24) for a single naturally occurring variant.[[48]](#footnote-48)

Overall, the speed and regularity of these difficult to achieve evolutionary developments seems to run contrary to probability expectations. A high probability of laboratory modification exists where *complex* and *functionally focused* genome changes have occurred in an *unusually short time*. While viruses, which are not truly alive, are the simplest of “organisms,” human biology is extremely complex. It is a needle-threading exercise for new virus designs to get past human defenses. Biological evolution always goes in the direction of more efficient design, but it is a slow process. Some of the SARS-COV-2 variations seem to have changed too much too fast.

So, in addition to the question of the origin of the first SARS-COV-2 genome, there is the question of whether one or more of the recent SARS-COV-2 variants came from a lab. “Synthetic biology” is a new term in science, and it means exactly that: artificially modified living or, in the case of viruses, nearly living, systems. Synthetic *living* biological systems can now be built nearly but *not fully* from scratch. Science can’t breathe life into something that isn’t already alive. However, viruses can be built from scratch. Science can now not only alter the genomic systems of living things, but produce, at least for the simplest “organisms” such as viruses, new basic genome “backbones” or “chassis” to which various genes can be added. Modifying a virus variant is easier than creating a new species.

Viruses are merely reactive biochemical structures that, when introduced into living organisms, can induce replication of the virus genome by living cells. In common speech we say that antiviral drugs “kill” viruses, but technically the viruses are only “deactivated” (a word preferred by most research scientists), not “killed,” because the viruses were never genuinely alive.

Note that the authors of the quote below say that (existing) cells can be “streamlined” and “augmented,” not “created.” It is easy to read too much into science articles that celebrate progress.

The essence of life is still a mystery to science. Science *cannot create or build new life from non-living elements*. So, when you see the word “design” in the quote below and other articles on synthetic biology, think “modify,” not “create.” Science has its limits, but it now has impressive capabilities as well.

One of the goals of synthetic biology is the development of robust chassis cells for their application in medicine, agriculture, and the food, chemical and environmental industries. These cells can be streamlined by removing undesirable features and can be augmented with desirable functionalities to design an optimized organism. In a direct analogy with a car chassis, they provide the frame for different modules or “plug‐in” regulatory networks, metabolic pathways, or safety elements. In an effort to ensure a safe microbial chassis upfront, safety measures are implemented as genetic safeguards to limit risks such as unwanted cellular proliferation or horizontal gene transfer.[[49]](#footnote-49)

The stated goal of synthetic biology and gain-of-function projects in applications such as the food industry is to optimize, improve, and protect, but scientists admit there are risks even there. In the realm of virus biology, the risks are higher and the ability to build-in safety minimal. In the context of genetically engineering viruses, one needs to substitute “dangerous germ escape” for “unwanted cellular proliferation,” and substitute “accidental supergerm creation” for “[unwanted] horizontal gene transfer.” The risks are exponentially greater in genetically altering viruses that in genetically altering agricultural food products. Viruses are inherently dangerous.

Our fear of viruses has prompted us to try to produce new dangerous viruses before Mother Nature produces them so we can have vaccines and antiviral drugs ready when Mother Nature eventually turns them loose on the general population. “In considering the threat of bioterrorism or accidental release of genetically engineered viruses, it is worth remembering that nature is the ultimate bioterrorist.”[[50]](#footnote-50) The authors of this quote stop short of claiming that Mother Nature is capable of producing anything a gain-of-function, synthetic biology, or biowarfare lab project can create. Other science journal articles seem to assume that Mother Nature can do and eventually will do anything humans can do in laboratories. That assumption is no longer self-evident.

Scientists make a good case that the necessary protective advancements in vaccine and antiviral drug science won’t occur without dangerous research. But, is it wise to take enormous risks in creating new escape-prone supergerms to assist the production of vaccines against them if Mother Nature is not likely to produce the same germ until hundreds or thousands of years down the road when science will be so far advanced that the germ will no longer be a catastrophic threat? Clearly not, but science won’t always be able to predict the odds of Mother Nature creating a specific new virus, or even know what the viable genetic modification options for a virus are until the they explore the possibilities physically in a lab. Risk of new virus creation comes with that exploration.

With *huge* amounts of money involved in cutting edge germ research, the decision to explore the creation of dangerous new germs tends to get pushed towards a green light. The threat of future biowarfare use of new supergerms by an enemy or terrorist also lends weight to the argument to do the dangerous research. We want to prepare our vaccines and antiviral drug defenses in advance of such threats. That can’t be done without the dangerous research. Mother Nature may not be in a hurry to produce supergerms, but our foreign enemies probably are. The question of how much risk is warranted in a specific research project can be difficult to answer.

SARS-CoV-2, the germ that produced the COVID-19 pandemic, is different enough from other coronaviruses, with several critical mutations concentrated in the immune defeating and host access areas of the genome, that Mother Nature wasn’t likely to produce it naturally for quite some time (probably much longer than the forty years or so typically cited). That means that our civilian and government research labs would not be pressed to rush into artificially creating SARS-CoV-2 based on a *wise* risk-benefit trade-off analysis in relation to *staying ahead of Mother Nature alone*.

However, new capabilities of science in synthetic biology allow our foreign enemies to get to new dangerous germ designs a lot faster than Mother Nature. Mother Nature may be the “ultimate bioterrorist,” but only in the sense that she relentlessly explores all possibilities in genome variation—albeit very slowly. Mother Nature may be relentless, but she is not the fastest kid on the block. Human laboratories are faster.

As the latest U.S. Intelligence assessment indicates, the U.S. government knew there was some involvement of the Chinese military (People’s Liberation Army) in the activities of the Wuhan Institute of Virology. Perhaps that was enough to prompt a basic concern sufficient to convince the United States and other nations to “cover the bases” in regard to future biowarfare use of highly virulent coronaviruses such as SARS-COV-2. So the U.S. government made the decision, wise or unwise, to provide funding for research into the worst-case variants of the SARS-COV family of viruses, the goal being to arrive at effective vaccines and antiviral drugs ahead of the biowarfare threat. The concern in this case isn’t so much should the research have been done, but how safely was it done.

There will always be a human temptation to grab the big money accruing to the first bioscience corporation to achieve an effective vaccine or antiviral drug. That temptation may prompt bioscience companies to drive their researchers too hard and ask them to work too fast—and not ask too many questions. Is that what happened with the COVID-19 pandemic? Maybe, maybe not.

Eco-Health Alliance is a *non-profit* corporation. In theory, they are not positioned to get huge windfall profits. However, if a project is the first to achieve breakthrough results, there is nothing stopping primary researchers and management staff at a nonprofit research organization from taking their accumulated knowledge and expertise to a regular for-profit bioscience corporation, vaccine manufacturer, or pharmaceutical company in return for large bonuses and increased salaries. The other U.S.-sponsored research activities in the coronavirus arena were also “non-profit” activities (government agencies, USAID, NIH, universities with government funding, and national research laboratories).

Despite full collaboration between government and private research labs, it still took roughly a year and a half to get SARS-COV-2 vaccines out to the bulk of the U.S. public, with over 2 million doses arriving at distribution points in twelve months. Millions fell ill and died in the meantime. Fortunately, the U.S. government quickly shared whatever relevant scientific knowledge it had with the large vaccine producers, Moderna and Pfizer. This resulted in the rapid production of very effective vaccines that clearly saved millions of lives (including mine). It was a magnificent and heroic effort, but, on the surface, the situation *seems* to argue that the strategy of intentionally producing super germs in the lab to get ahead of pandemics caused by those germs doesn’t always work.

On the other hand, there are situational elements that argue the other way. In defense of the U.S. government-funded research, the prior SARS and MERS virus outbreaks dating from 2003 clearly showed the lethal potential of coronaviruses and generated an expectation that further dangerous mutations would occur in the near future. The whole enterprise of biodefense against newly evolved germs invokes unavoidable intelligent guesses and rationally justifiable gambles. Full certainty about biocontainment of research germs, foreign enemies’ biowarfare research timelines, or Mother Nature’s evolutionary time tables is never going to be available.

With complex questions in microbiology and genetics, it is often the case that scientists don’t know what they don’t know. Not all possible mutations and their effects can be predicted in advance. Probative research must be done to generate mutations and see what the effect is. The obvious problem in doing this with potentially lethal viruses is that new dangerous germs will at times be produced in the lab—and not fully contained. If the newly created germ escapes the lab before vaccines are ready, the research has created the problem it was trying to solve.

Given that no laws preclude private researchers from doing a project the U.S. government has denied government contractors due to safety concerns, and that other nations and bioresearch corporations outside the United States are free to do research regardless of more cautious U.S. laws and regulations, dangerous germ research is almost certainly going to happen *somewhere* regardless of U.S. government risk-benefit conclusions. Once a foreign or private dangerous germ research project is successful (and avoids problems caused by germ escapes), the research company can, and probably will, sell the results to the U.S. government for BIG money because the project’s achievements advance the future safety of U.S. citizens. Therefore, one might argue that we may as well do the research ourselves where it is less expensive than buying it from a third party (who might also sell to our enemies) and where we have more direct control over safety and security.

If we rush out and stop all dangerous germ research, Mother Nature, our foreign enemies, or bioterrorists may get there first. If we rush into pushing the production of new dangerous germs that would be otherwise difficult to achieve by Mother Nature, we may ourselves produce a pandemic. The bottom line seems to be that our foreign enemies or bioterrorists will eventually be capable of doing the same research, then throwing the new germs at us as bioweapons when we have no vaccines and antiviral medicines ready to defend against them.

Reliable accounts of WWII indicate that Nazi Germany was not far from achieving the atomic bomb. If we had lost that weapon of mass destruction (WMD) arms race, where would the world be now? Many potential biowarfare agent germs are considered WMD-class weapons. I think we can now see why.

At a minimum, some dangerous germ research will have to be done to develop vaccines and antiviral drugs in time to stop future pandemics that are known to be high probability outcomes from Mother Nature alone. And the case for defending against future biowarfare is not trivial; there is a real threat.

So the wiser course seems to be to do the dangerous new germ research to be able to defend against our foreign enemies and Mother Nature. The real issue is whether safety will be maximized when the dangerous research is done. Here we encounter two more “Catch-22s”: the natural difficulty level of containing highly contagious germs and the exorbitant impact of big money.

The natural difficulty level of containing highly contagious viruses means a fully safe lab is almost impossibly expensive to create and operate. The money motive means that private research corporations, who are in the research business for money, will, like all other businesses, look for ways to cut corners on expenses to maximize profits and work as fast as possible to beat the competition.

The U.S. government contracting system is set up to award government contracts to the *lowest* bidder where other elements seem to be equal (such as safety history). To win the contract, a scientific research corporation, even a non-profit one, must bid low. Competing contractors will be tempted to say (they may even make themselves believe it) that they can ensure safety for less money than their competitors—and for less money than the safety task truly requires. Grants to nonprofit organizations are in fixed amounts. Unexpected costs inevitably arise in large operations and inflation forces nonprofits to try to do more with less. This all militates towards there being inadequate money available to contain highly contagious germs.

For a little more background to the dangerous germ research problem, consider the following excerpts from Marc Lipsitch, Joshua B. Plotkin, Lone Simonsen, and Barry Bloom’s, “Evolution, safety, and highly pathogenic influenza viruses,” and Diane DiEuliis and James Giordano’s, “The need for modernization of biosecurity in the post-COVID world.”

Experience with influenza has shown that predictions of virus phenotype or fitness from nucleotide sequence are imperfect, and that predicting the timing and course of evolution is extremely difficult. Such uncertainty means that the risk of experiments with mammalian-transmissible, possibly highly virulent influenza viruses remains high even if some aspects of their laboratory biology are reassuring; it also implies limitations on the ability of laboratory observations to guide interpretation of surveillance of strains in the field. Given these considerations, we propose that future experiments with virulent pathogens whose accidental or deliberate release could lead to extensive spread in human populations should be limited by explicit risk-benefit considerations, in the United States and worldwide.

In response to two sets of experiments on mammalian-transmissible, modified influenza A/H5N1 viruses the US Department of Health and Human Services has promulgated a new Policy on Dual Use Research of Concern. This policy, and other statements from US and international bodies identify the need for risk mitigation in future studies of mammalian-transmissible variants of highly pathogenic influenza virus and certain other infectious agents, raising an important new question: how should funders, regulators and researchers evaluate what future experiments should be done with such viruses?[[51]](#footnote-51)

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At present, there are two hypotheses about the emergence of SARS-CoV-2; the first is that it was due to a naturally occurring zoonotic jump, and the second contends that it spread due to an accidental dispersion of a laboratory-acquired infection in Wuhan, China. While the pandemic’s actual origins remain occluded, it is useful to examine the latter possibility as a paradigm for evaluating biosecurity policy in the post-COVID world. While the pandemic may not have emerged from a research lab, this is possible with research on dangerous pathogens and prompts questions for biosecurity.[[52]](#footnote-52)

In addition to working the question(s) of the origin of COVID-19 (and some of its variants), government officials, scientists, and public-interest-minded citizens need to address the question of biosecurity generally. Some experts have pointed out that legitimate biosecurity concerns can lead to burdensome government interference in research. The result of badly designed and implemented security procedures can be obstructive overkill and large sums of wasted money that would be better spent directly researching deadly natural diseases. (See N. Wurtz, M. P. Grobusch, and D. Raoult, “Negative impact of laws regarding biosecurity and bioterrorism on real diseases.”)

Research on highly pathogenic microorganisms in biosafety level 3 and 4 laboratories is very important for human public health, as it provides opportunities for the development of vaccines and novel therapeutics as well as diagnostic methods to prevent epidemics. However, in recent years, after the anthrax and World Trade Center attacks in 2001 in the USA, the threat of bioterrorism has grown for both the public and the authorities. As a result, technical and physical containment measures and biosafety and biosecurity practices have been implemented in laboratories handling these dangerous pathogens. Working with selected biological agents and toxins is now highly regulated, owing to their potential to pose a threat to public health and safety, despite the fact that the anthrax attack was found to be the result of a lack of security at a US Army laboratory. Thus, these added regulations have been associated with a large amount of fruitless investment. Herein, we describe the limitations of research in these facilities, and the multiple consequences of the increased regulations. These limitations have seriously negatively impacted on the number of collaborations, the size of research projects, and, more generally, scientific research on microbial pathogens. Clearly, the actual number of known victims and fatalities caused by the intentional use of microorganisms has been negligible as compared with those caused by naturally acquired human infections.[[53]](#footnote-53)

If we forbid all dangerous research, newly evolved pathogenic germs will catch us unprepared with no vaccines or therapeutic drugs to stop them. We would be prudent to similarly stay ahead of potential biowarfare agent development by our enemies by having vaccines and therapeutic drugs prepared in advance or at least in the process of development. In the race to stay ahead we can’t afford politically motivated “whitewash” and “show and tell” facsimile safety measures that slow down research and waste money while not increasing safety—but we do need *real* safety measures.

While it is true that real safety measures also slow down research and make it more expensive, if we rush through dangerous research minus real safety measures the highly contagious new germs escape our labs with the effect that we have attacked ourselves with the germs we were trying to defend against. This is a genuine dilemma for which there is no perfect solution, only prudent trade-off judgments and wise risk-benefit calculations. Some risky work needs to be done, but with strict discipline by researchers and high integrity among project administrators. We certainly don’t want to contract the work out to the nation that is our number one national security threat.

Independent government oversight and real-time quality control, not self-policing by laboratories and scientific research contractor corporations, is the answer. Business-oriented contractors won’t want to spend a large portion of their profits policing themselves, and government labs won’t be inclined to admit their own mistakes. We have been letting the fox guard the henhouse.

The U.S. National Institutes of Health (NIH) during Dr. Anthony Fauci’s nearly four-decade tenure as Director of the National Institute of Allergy and Infectious Diseases (NIAID) seems to have gone out of its way to give the foxes gainful employment. In his article, “Research on highly pathogenic H5N1 influenza virus: the way forward,” Fauci tells us...

The voluntary moratorium on gain-of-function research related to the transmissibility of highly pathogenic H5N1 influenza virus should continue, pending the resolution of critical policy questions concerning the rationale for performing such experiments and how best to report their results. The potential benefits and risks of these experiments must be discussed and understood by multiple stakeholders, including the general public, and all decisions regarding such research must be made in a transparent manner.[[54]](#footnote-54)

Sounds right, and, in concept, it is right. But there are a couple of troubling points.

First, the moratorium on dangerous H5N1 flu research was **voluntary**. What that means is that well-intended, conscientious scientists would not violate it. But those are not the scientists we have to worry about. Greedy and ambitious scientists who put public safety a distant second place behind their personal ambitions are the ones we need to worry about. A voluntary moratorium only gives overly ambitious scientists a chance to get ahead of competitors who have sufficient moral integrity to respect the moratorium. Similarly, past policies that banned dangerous gain-of-function germ experiments by government agencies but allowed private research firms to do them put the prerogative to do reckless experiments into exactly the wrong hands: those motivated by money.

Second, Fauci's NIH/NIAID later awarded a [coronavirus research contract](https://grantome.com/grant/NIH/R01-AI110964-06) (2014-2019) to Peter Daszak’s EcoHealth Alliance, which then subcontracted the dangerous research on coronaviruses to **China**—the nation now classified by U.S. defense and intelligence agencies as the leading national security threat to the United States. Both actions fell short of a prudently protective standard for guarding the public against dangerous germ releases.

The editors of *Scientific American* remind us in, “Why the U.S. Needs a Formal Reckoning on the COVID Pandemic,” that the United States needs answers about the origins and implications of the COVID-19 pandemic. “After Pearl Harbor, 9/11 and other major tragedies, the U.S. has examined itself to see how to prevent the next catastrophe. We need to do the same for the COVID pandemic.”[[55]](#footnote-55)

That “formal reckoning” has not yet been completed (or it hasn’t been released to the public), so, in the public arena at least, the jury is still out on the question of COVID-19’s origin. In my view the lab release theory is well ahead on points. In Rossana Segreto, Yuri Deigin, and Kevin McCairn’s article, “Should we discount the laboratory origin of COVID-19?” we are shown a number of reasons the zoonosis (animal origin) theory doesn’t explain the COVID-19 pandemic as well as the lab release theory. Those reasons include…

low rate of evolution in the early phase of transmission

lack of evidence for recombination events

high pre-existing binding to human angiotensin-converting enzyme 2 (ACE2)

a novel furin cleavage site (FCS) insert

a flat ganglioside-binding domain (GBD) of the spike protein which conflicts with host evasion survival patterns exhibited by other coronaviruses

high human and mouse peptide mimicry[[56]](#footnote-56)

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Low rate of virus evolution in the early phase of human transmission during the COVID-19 outbreak means the SARS-COV-2 virus was already optimized to infect humans. For that to be true the virus must have previously had opportunities to evolve inside humans or by passage through human/humanized cell lines. But there are no *known* situations where that could have occurred in the wild (outside a laboratory or research station) other than the Mojiang mines, which seem to have been a research station.

The *preexisting* close matchup of the SARS-COV-2 virus to the human ACE2 receptor suggests optimization of this feature occurred before the earliest (publicly) identified human case of SARS-COV-2 infection. The abrupt appearance of both a new furin cleavage site and a novel flat ganglioside-binding domain (GBD) of the spike protein not present in other members of SARS-COV-2’s close virus relatives supports the argument that a normal gradual evolution of SARS-COV-2 in nature did not occur. High human and mouse peptide mimicry suggests lab exposure to the human and mouse cell lines that are common features of virus research projects.

All three of the major new SARS-COV-2 features (ACE2 receptor matchup, furin cleavage site, and flat ganglioside-binding domain (GBD) modification of the spike protein) are focused on areas critical to optimized infection of humans. There is no natural trail of the required genetic recombination events in wild coronavirus populations to indicate a normal incremental evolutionary construction of any of these key features. That suggests that the complex genetic alterations necessary for the SARS-COV-2 virus were produced in a lab with the support of field research, not by natural evolution. Unfortunately, scientific investigators were denied access to Wuhan labs where the evidence for lab modification might have been found.

Segreto, Deigin, and McCairn gave us good reasons to suspect a laboratory origin of SARS-COV-2. Here are some other good reasons.

SARS-CoV-2 has a pair of arginine codons that are routinely used in labs. If the emergence were natural, it would require 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. This sequence of events is extremely unlikely, and adding a furin cleavage site is known to make a virus more deadly.[[57]](#footnote-57)

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It is noteworthy that the laboratory workhorse of coronavirus research is the VERO cell, isolated from a female African Green monkey in 1962, and containing an ACE2 receptor that is 100% homologous to the human ACE2 in the 25 critical amino acids for infectivity.

This in silico work was confirmed in the laboratory with respect to rhesus macaques. Within weeks of the identification of SARS-CoV-2, the Wuhan laboratory had demonstrated that the pandemic virus would infect and produce a pneumonia in rhesus macaques.[[58]](#footnote-58)

An enormous amount of coronavirus research has been done over the past twenty years. Lab release theory debunkers leave out the fact that most coronavirus research uses VERO cells from African Green monkeys, thus providing the close passage opportunities to the ACE2 receptor that an evolving coronavirus needs to move towards human infectivity.

Here, we used a combined transcriptomics and proteomics approach to produce a correlated transcriptome and proteome map of SARS-CoV-2 in the African Green monkey kidney cell line Vero E6. This cell line is routinely used to propagate viruses from clinical samples as well as to generate stocks of virus for academic research, drug susceptibility testing and vaccine challenge studies.[[59]](#footnote-59)

African Green monkeys’ 100% matchup to the genetic structure of the SARS-COV-2 ACE2 spike protein means that, *if we assume nature is likely to evolve a SARS-COV-2 type supergerm at all*, it is just a matter of time before frequent laboratory passage of coronaviruses in VERO cells generates the precise ACE2 matchup and optimized spike protein configuration we see in SARS-COV-2. The accelerated “evolution” produced by laboratory passage experiments means the labs have an excellent chance of getting to the most dangerous forms of germs, including coronaviruses, before Mother Nature. The lab release theory of the origin of SARS-COV-2/COVID-19 then begins with a reasonably high probability, provided only that we know dangerous gain-of-function genetic research projects have been done with coronaviruses.

Those kinds of research projects are well documented. In fact, genetic recombination lab experiments with viruses, including gain-of-function research resulting in increased human infectivity of SARS-like viruses, have become fairly common. A lot of serial passaging work has been done on coronaviruses in the world’s laboratories, including Wuhan.

There have been three publications, in 2015, 2016 and 2017, describing the WIV gain of function research. The WIV, having learned both basic and traceless infectious-clone technology from joint research with a laboratory at the University of North Carolina (UNC) in 2015, initiated construction of novel chimeric coronaviruses without UNC immediately thereafter. WIV’s first publication on the use of basic infectious-clone technology to construct novel chimeric coronaviruses at WIV appeared in 2016. WIV’s first publication on the use of traceless, signature-free infectious-clone technology also appeared in 2016.[[60]](#footnote-60)

Processing bat viruses through monkey kidney cell lines (passaging), even for routine research purposes, increases the opportunities for viruses to mutate in ways that move them a step closer to human infectivity. The same is true of using mice to process virus cell lines.

As we detailed in our previous article, in their search for SARS-like viruses with zoonotic spillover potential, researchers at the WIV have passaged live bat viruses in monkey and human cells (Wang et al., 2019). They have also performed many recombinant experiments with diverse bat coronaviruses (Ge et al., 2013; Menachery et al., 2015; Hu et al., 2017). Such experiments have generated international concern over the possible creation of potential pandemic viruses (Lipsitch, 2018). As we showed too, the Shi lab had also won a grant to extend that work to whole live animals. They planned “virus infection experiments across a range of cell cultures from different species and humanized mice” with recombinant bat coronaviruses. Yet Andersen et al did not discuss this research at all, except to say: “Basic research involving passage of bat SARS-CoV-like coronaviruses in cell culture and/or animal models has been ongoing for many years in biosafety level 2 laboratories across the world.”[[61]](#footnote-61)

There is, therefore, every reason to suspect that the SARS-COV-2 virus originated in a Wuhan lab or elsewhere in the Chinese research system. In separate articles, Fox News writers Brie Stimson and Greg Norman inform us that it now turns out, four years later, that after all the denials, researchers at the Wuhan lab appear to have been the first to fall ill.[[62]](#footnote-62) David Asher, the U.S. State Departments primary COVID-19 investigator said the same thing.

David Asher, who led State Department inquiries into Covid-19's origins, told *The Mail on Sunday* that three scientists are believed to have become ill with the mysterious respiratory condition in the second week of November, 2019.[[63]](#footnote-63)

But the key thing that was declassified that the first known cluster that we're aware of, of victims of we believe to be COVID-19. There is a possibility it was influenza, but I'm very doubtful that three people in highly protected circumstances in a level three laboratory working on coronaviruses would all get sick with influenza that put them in a hospital or in severe conditions all in the same week, and it didn't have anything [to do] with the coronavirus. That's highly hard to believe.[[64]](#footnote-64)

Pandemics arising from animal viruses transferred naturally to humans tend to involve multiple jumps from several animal species to humans, and/or from the same animal species to humans multiple times. This allows complex genetic adaptation to a new species to occur incrementally in stages. A direct transfer between an animal species to humans in one step is highly improbable.

Animal spillover germ releases also tend to breakout in multiple locations.[[65]](#footnote-65) Zoonotic viral pandemics normally begin with several somewhat different strains of the virus that are not yet sufficiently adapted to humans to cause a pandemic. They evolve independently in animals and humans to the point where they can more effectively infect humans and cause serious illness. Each of the early strains show significant genetic differences. Historically, tracing viral genomes from the blood of pandemic patients backwards has led to several patients who were “patient 0s,” the first patient to be found infected with a unique strain of the same emerging pandemic virus. However, Dr. Stephen Quay tells us that, contrary to the typical expectation of multiple early strains and several “patient 0s,” there seems to have been only *a single index case* of COVID-19.[[66]](#footnote-66)

In the usual pandemic scenario, the multiple evolving strains of an emerging, pandemic-capable, human virus leave evidence in the blood of infected humans in the form of antibodies to the various strains of the emerging virus (called the “seroconversion” factor). No evidence of antibodies to early, still evolving, SARS-COV-2 strains were found in the blood of patients taken before the pandemic started. This indicates COVID-19 was not a standard zoonosis event, making the laboratory origin hypothesis the most probable explanation.[[67]](#footnote-67)

The fact that all the SARS-COV-2/COVID-19 patient infections that were traced backwards led to a single patient 0 (or three patient 0s at the same lab) and a single strain of the virus[[68]](#footnote-68) (with *possibly* two lineages having no evolutionary source identified outside the lab) means two things: 1) the SARS-COV-2 virus was already fully adapted to humans when it emerged at Wuhan, and 2) the virus had no prior access to the public (other than in labs and at the Mojiang mines). Both suggest that development of the germ’s pandemic capability occurred (intentionally or inadvertently) within the protected environment of a lab and/or tightly controlled field research activity.

At this point it should be clear that the lab origin theory for SARS-COV-2/COVID-19 is not a conspiracy theory; it is the best supported scientific theory we have on COVID-19’s origin. There is nothing surprising about a laboratory origin of a new type of virus. Escaped germs and laboratory acquired infections are well-documented in the scientific literature. And they are frequent enough to pose significant risks to public safety.[[69]](#footnote-69)

No matter how SARS-CoV-2 arose, virology has a long and troubling history of risky sample collecting, contamination incidents, research accidents, and lab escapes. At least once, in the case of H1N1 flu, the consequence was a global pandemic (Nakajima et al., 1978).[[70]](#footnote-70)

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And in October, U.S. officials halted new federal funding for 18 projects that tweak the influenza, SARS, or MERS viruses to make them more pathogenic or likely to spread among mammals. Federal officials and outside experts are now reviewing the risks and benefits of such "gain-of-function" studies to decide whether they should be allowed to resume.[[71]](#footnote-71)

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The Asian region has a two-decade record of a little less than one laboratory-acquired infection per year. After the first SARS-CoV-1 epidemic was ended, SARS-CoV-1 jumped four more times into the human population, all from laboratories, with two in China. The last smallpox death in the entire world was a secretary who worked two floors above a research lab in England and contracted it through the ventilation system. The head of that laboratory committed suicide over his anguish for causing her death.[[72]](#footnote-72)

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Laboratory accidents and the escape of highly dangerous pathogens from laboratories are frequent occurrences worldwide. The accidental infection of researchers in the highest containment biosafety facilities—labelled BSL-2, BSL-3 and BSL-4—occurs worldwide, as do accidental releases by other means.... Releases via infection of researchers took place in the highest containment facilities in the United States—at the Centers for Disease Control and Prevention (CDC) in Atlanta and at the US Army Medical Research Institute of Infectious Diseases (USAMRIID)—but in all cases only the researcher became ill, and there was no further transmission of the pathogen....

Between 2009 and 2015, the FSAP recorded 749 incidents in seven categories—not solely releases or researcher infections—from 276 facilities....

It takes only one superspreading graduate student or maintenance worker to start a pandemic.

It is known that a very large percentage of the individuals infected with the SARS-CoV-2 virus show no symptoms and do not become clinically ill, which would facilitate an unrecognized infection of one or more laboratory researchers....[[73]](#footnote-73)

Matt Field, writing for the *Bulletin of Atomic Scientists*, tells us there were “309 lab acquired infections and 16 pathogen lab escapes between 2000 and 2021.”[[74]](#footnote-74) So, the threat of a germ escaping from a lab is quite real.

Compounding the problem is that researchers are busily trying to produce new and more dangerous germs. The stated purpose is to get vaccines and antiviral drugs ready for the time Mother Nature sets the same germs loose on the world by means of natural evolution or aggressor nations use them for biowarfare. World governments and scientific institutions are aware of the problem. But there seems to be no perfect solution to it.

The U.S. government placed a moratorium on gain-of-function research in 2014. This was lifted on 19 December 2017 and a new policy allowing limited gain-of-function research with an NIH (National Institutes of Health) waiver was instituted under the Obama administration. See the [National Institutes of Health website announcement of the policy change](https://grants.nih.gov/grants/guide/notice-files/NOT-OD-17-071.html).[[75]](#footnote-75)

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. At least eleven gain-of-function experiments, adding a furin site to make a virus more infective, are published in the open literature, including Dr. Zhengli Shi, head of coronavirus research at the WIV. This has caused a flurry of Chinese papers since the pandemic began trying to show a natural furin site in a related virus (this one example was later shown to be an error in interpretation) or to show that furin sites from distant cousins of CoV-2 might be the source through a process called recombination, where two different viruses infect the same host and then make a mistake in copying their genetic material, and swap sequences.

These convoluted, hypothetical methods each fail, however. It turns out that it is Daszak himself who has shown that the subgenera of coronaviruses that have furin sites are found in different bat hosts, which live in different regions of China, than the sarbecovirus subgenera of which CoV-2 is a member.[[76]](#footnote-76)

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The term Gain-of-Function (GoF) describes the gain of new functions by organisms through genetic changes, which can naturally occur or by experimental genetic modifications. Gain-of-Function research on viruses is enhancing transmissibility, virus replication, virulence, host range, immune evasion or drug and vaccine resistance to get insights into the viral mechanisms, to create and analyze animal models, to accelerate drug and vaccine development and to improve pandemic preparedness. A subset is the GoF research of concern (GOFROC) on enhanced potentially pandemic pathogens (ePPPs) that could be harmful for humans. A related issue is the military use of research as dual-use research of concern (DURC). Influenza and coronaviruses are main research targets, because they cause pandemics by airborne infections.[[77]](#footnote-77)

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The U.S. government is responding to a resurgence in concerns about GOF studies, which have deeply split the scientific community. Three years ago, two separate research teams revealed that they had made a version of the H5N1 avian influenza strain that spread between ferrets. Many scientists worried that if the potent new lab strain were accidentally or deliberately released, it could result in a deadly pandemic. Proponents argued that such studies will help public health researchers detect an impending flu pandemic and prepare vaccines.[[78]](#footnote-78)

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Genomic analyses show that SARS-CoV-2 is a chimera, with most of its sequence identical to that of the bat CoV RaTG13, except for the receptor binding domain (RBD), which is almost identical to that of a pangolin (Manis javanica) CoV and has been optimized to bind the ACE2 receptor in human cells. Such gain-of-function chimeras can in principle arise via natural recombination, but that would be unlikely in this case. The natural recombination would require that the viruses from bat and pangolin infected the same cell in the same organism simultaneously, a rather improbable event considering the low population density of pangolins, the dearth of CoV-infected specimens in their natural populations, and the fact that CoV RaTG13 does not have significant affinity for the pangolin ACE2, and therefore is unlikely to penetrate the infected pangolin cell.

Gain-of-function recombinations of coronaviruses have been ongoing in the laboratory for more than a decade. As early as 2007, the group headed by Zheng-li Shi from the Wuhan Institute of Virology (WIV) created a series of “bat-man” CoV chimeric spike proteins, to enable CoVs to jump from one species to another and model “spillover effects” that could trigger a pandemic. Shi’s goal was to turn the bat CoVs into huACE2-binding molecules, that is, to design promoters of human infection….

An indicator that the NIH-funded research had gone too far arose when the tinkered CoV-RaTG13 became endowed at the spike protein with a “detonator”, that is, a cleavage site recognized and activated by the host-cell enzyme furin…. This site has not been identified in other CoVs from the same lineage. The way this cleavage site is incorporated attests to the artificial origin of SARS-CoV-2.

Strikingly, the two adjacent arginines are coded by two consecutive CGG codons. Only about 5% of arginines in SARS-CoV-2 or RaTG13 are coded by CGG. This implies that the CGGCGG in the inset would have an estimated 0.25% probability to “naturally” occur as an encoder of the RR motif. Other suspicious aspects pertain to the way in which the encoding cassette was inserted to create the cleavage site….

Clues from molecular biology uphold the artificial origin of SARS-CoV-2, reinforcing the recent investigation by journalist Nicholas Wade. The gain-of function insertions of human adapted pangolin CoV RBD and furin-associated cleavage site are likely the result of genetic manipulations conducted in a laboratory. Such manipulations may have been carried out without leaving a trace. A thorough investigation of the research records at WIV is needed, notwithstanding the recent deletion of their internet database.[[79]](#footnote-79)

Recombinational lab experiments with viruses, including gain-of-function lab operations resulting in human infectivity of SARS-like viruses, have been done many times over the past 20 years.[[80]](#footnote-80) Some of those experiments actually involved inserting a furin cleavage site into a spike protein, the very features that make SARS-COV-2 so dangerous to humans.

Whether SARS-CoV-2 is one of these manipulated viruses is difficult to ascertain from merely examining the virus itself. “SARS-CoV-2 is thought to derive from a bat SARS-CoV-related coronavirus with a furin cleavage site that enhances the capacity of the virus to infect human cells.” No other coronaviruses in SARS-CoV-2’s subgenus have been observed with a furin cleavage site, although they are found naturally in numerous families of coronaviruses. “Since 2006 … furin cleavage sites have also been the subject of laboratory manipulation, including their insertion into coronavirus spike proteins.”[[81]](#footnote-81)

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An experiment that created a hybrid version of a bat coronavirus — one related to the virus that causes SARS (severe acute respiratory syndrome) — has triggered renewed debate over whether engineering lab variants of viruses with possible pandemic potential is worth the risks.

In an article published in *Nature Medicine* on 9 November, scientists investigated a virus called SHC014, which is found in horseshoe bats in China. The researchers created a chimaeric virus, made up of a surface protein of SHC014 and the backbone of a SARS virus that had been adapted to grow in mice and to mimic human disease. The chimaera infected human airway cells — proving that the surface protein of SHC014 has the necessary structure to bind to a key receptor on the cells and to infect them. It also caused disease in mice, but did not kill them.

Although almost all coronaviruses isolated from bats have not been able to bind to the key human receptor, SHC014 is not the first that can do so. In 2013, researchers reported this ability for the first time in a different coronavirus isolated from the same bat population.[[82]](#footnote-82)

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The emergence of severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome (MERS)-CoV underscores the threat of cross-species transmission events leading to outbreaks in humans. Here we examine the disease potential of a SARS-like virus, SHC014-CoV, which is currently circulating in Chinese horseshoe bat populations. Using the SARS-CoV reverse genetics system, we generated and characterized a chimeric virus expressing the spike of bat coronavirus SHC014 in a mouse-adapted SARS-CoV backbone. The results indicate that group 2b viruses encoding the SHC014 spike in a wild-type backbone can efficiently use multiple orthologs of the SARS receptor human angiotensin converting enzyme II (ACE2), replicate efficiently in primary human airway cells and achieve in vitro titers equivalent to epidemic strains of SARS-CoV. Additionally, in vivo experiments demonstrate replication of the chimeric virus in mouse lung with notable pathogenesis.[[83]](#footnote-83)

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The experiments referenced above where labs were culturing bat coronaviruses and intentionally encouraging or inadvertently facilitating genetic changes in the viruses that moved them toward increased human pathogenesis by repeatedly passaging viruses through monkey, mouse, or humanized animal cell lines are not the only experiments of the kind that have been done. There are quite a few others. And there are field research activities to consider.

In 2012, Chinese miners at the Mojiang mines had frequent exposures to bat viruses. The miner’s frequent, recurring exposure to bat viruses may have had the same effect as many laboratory “passage” experiments. Even so, some laboratory assistance would be necessary to make achievement of all the necessary mutations required to produce the highly infectious set of properties seen in SARS-COV-2 a high probability outcome. The possibility of a SARS-CoV-2 germ escape from a laboratory/field research activity should therefore be considered the leading candidate for the origin of the COVID-19 pandemic.[[84]](#footnote-84) The Mojiang miner passage theory of Jonathan Latham was the first theory of this kind to be offered and remains the most likely alternative.

There is a sort of metalogic in the evolutionary dynamics of viruses that argues as much for a lab release as for an animal-to-human spillover origin of the COVID-19 pandemic. Consider this 2009-vintage quote from prominent scientists David M. Morens, Jeffery K. Taubenberger, and Anthony S. Fauci.

If there is good news, it is that successive pandemics and pandemic-like events generally appear to be decreasing in severity over time. This diminution is surely due in part to advances in medicine and public health, but it may also reflect viral evolutionary “choices” that favor optimal transmissibility with minimal pathogenicity — a virus that kills its hosts or sends them to bed is not optimally transmissible.[[85]](#footnote-85)

SARS-COV-2 only scores a 50% matchup to this trend. It is highly transmissible, but it is lethal to the elderly and those with preexisting health problems. It sends a lot of normal people to bed for extended periods. Long COVID can do that repeatedly. And SARS-COV-2 mutates frequently enough to threaten finding the right combinations to be more disabling, and more lethal, over time. Left unmitigated by vaccines and antiviral drugs, it might well have burned itself out completely by thinning the human population density to a point where transmissibility decreased dramatically. Such a genome does not constitute an optimal evolutionary change for a virus. It *does* constitute a moderately effective biowarfare weapon.

Both SARS and MERS were arguably more lethal and more severely disabling in terms of forcing isolation of the patient. The MERS fatality rate is higher than SARS-COV-2. I personally experienced a very severe, life-threatening illness with both SARS outbreaks, much more severe than with SARS-COV-2. SARS-1 forced me to isolate by confining me to bed with clear symptoms of hyper-contagion (violent coughing). SARS-COV-2 did not do that in my case, even before the vaccines came out. SARS-COV-2 can also produce symptom-free periods which help spread the illness.

So, natural evolution *may* have moved SARS and MERS toward a partially “kinder, gentler,” more transmissible form of virus via their relative SARS-COV-2 in order to optimize transmissibility. With only eight years to make the genetic changes to move the original SARS (2012) to SARS-COV-2 (2020) however, it is not likely that SARS-COV-2 evolved from the original SARS virus via natural spontaneous evolution.

In any case, SARS-COV-2 isn’t kind and gentle enough for optimized transmissibility. Heavy physical activity aggravates the severity of COVID-19, necessitating an unusual rest and recovery period, which, again, would keep the patient from optimally spreading the germ. There is no direct evidence that SARS-COV-2 was intentionally designed to be a biowarfare agent. However, precluding intense physical activity is a goal of biowarfare agents. SARS-COV-2 could have easily been discovered to be a potentially useful biowarfare weapon after the virus emerged from routine (but dangerous) civilian coronavirus research projects.

The phenomenon of long COVID, with the virus infecting a wide variety of bodily organs and tissues, in some ways gives the virus increased survivability because it is hard for the immune system to clear the virus from so many areas simultaneously, perhaps especially deep muscle tissue and the brain. Having a very long-term infection keeps the virus in circulation better than a short-term infection. The net result of long COVID isn’t fully in favor of virus survivability, however. People or animals with long COVID don’t compete well with the healthy, they circulate in public less often due to low energy and can manage fewer social activities. In the long run, they may not survive the illness at all.

Long COVID is compatible with the goals of natural evolution, but still a long way from optimally transmissible. And, again, there wasn’t enough time for a natural evolution of SARS-COV-2 from the original SARS virus or any other know virus relative. Long COVID therefore doesn’t rule out a lab origin.

Clearly, the government has not ruled out the lab release theory. It has recently proposed significant changes to federal regulations governing research with risky viruses.

An expert panel on Friday endorsed a sweeping set of proposed changes to the federal government’s program for regulating experiments that involve tinkering with risky viruses and other pathogens. The move sets the stage for a closely watched decision by the Biden administration about its approach to protecting against lab disasters that could kick off a pandemic.

The experts unanimously approved draft recommendations that, among other things, ask health officials to extend their oversight to less dangerous pathogens, including ones similar to the coronavirus. They also recommended an end to exemptions for research related to vaccine development and surveillance of emerging viruses.

‘We have a lot of oversight on paper, but not really a lot of oversight,’ said Dr. Kenneth Bernard, a retired rear admiral and a member of the expert panel….[[86]](#footnote-86)

Genome analyses are not the only considerations relevant to evaluating arguments for or against the lab release and zoonotic theories of the origin of SARS-COV-2. Some relevant considerations lie outside genetics and microbiology entirely. Geography, event timelines, patterns of global spread, attempted cover-ups, obstruction of scientific investigation, and books and articles so clearly biased as to qualify as disinformation are all relevant factors. Why bother to attempt a cover-up of the natural evolution of a virus? Attempts at cover-up imply a lab origin. Political and international security considerations might also enter into the question.

The pandemic originating in Wuhan makes prefect sense. The Wuhan Institute of Virology was very close to the market where the largest early cluster, if not the index case, occurred.

Wuhan is also home to the world’s leading research centre for bat coronaviruses. There are two virology labs in the city, both have either collected bat coronaviruses or researched them in the recent past. The Shi lab, which collected BtCoV/4991 and RaTG13, recently received grants to evaluate by experiment the potential for pandemic pathogenicity of the novel bat coronaviruses they collected from the wild.[[87]](#footnote-87)

The two closest known (presumed to be) wild virus relatives of SARS-CoV-2 are RaTG13 and RmYN02. Chinese scientists say they were discovered in Yunnan province, near Mojiang, *far* to the south, approximately 800-1000 miles from Wuhan. There were markets in other cities as close as approximately 150 miles to Yunnan province that would have been much more likely sites for a zoonosis cross-species transfer and wild virus outbreak than the city of Wuhan. Thus, a germ escape from the WIV or [another lab in the Wuhan area](https://theintercept.com/2021/09/06/new-details-emerge-about-coronavirus-research-at-chinese-lab/) is strongly implicated.

The point of origin for a virus is not necessarily the point of origin of a pandemic caused by the virus. Collection of biological samples from bats for virus research was being done in Yunnan province. While the pandemic clearly began in Wuhan, the virus, *or its progenitors* (closest relatives) could have originated somewhere else, possibly in the Mojiang mines in Yunnan province where all the bats “hang out.”

If tightly controlled scientific research is being done at the point of origin in a field activity for *moderately* contagious viruses, an outbreak won’t usually occur there because strict field safety precautions are employed to protect scientists from infection, and the total interactive exposure time is short. Open air further reduces the chance of accidental infection—again, for *moderately* contagious germs. However, if biological samples and/or infected animals are moved back to a laboratory for many years of follow-on research, the risk of accidental release increases over time despite the safety precautions employed at the lab. *Thousands* of mistakes have been reported at research laboratories over the years.

SARS-COV-2 is well beyond moderately contagious. It has demonstrated itself capable of producing a heavy viral burden in the open air of heavily populated areas with much human activity (shopping centers, for example)—more so for confined enclosed spaces like caves where bat samples were collected and ill miners did extended work shoveling bat guano. If SARS-COV-2 originated in a Mojiang mine someone would almost certainly be infected before the collected virus samples got to the WIV in Wuhan. Mojiang miners did become seriously ill with a COVID-19-like illness, but that was more than six years before the COVID-19 outbreak. The fact that a separate pandemic (other than the ongoing SARS-1 and MERS epidemics) did not result from the 2012 Mojiang mine incident indicates the miners were ill with a (near or remote) progenitor virus, one not as aggressively contagious as SARS-COV-2—perhaps the original SARS (SARS-COV-1) or a variant.

The caves and mines of Mojiang where the virus research was conducted may have been far enough from the closest village to preclude infections in the village, But a *hyper-contagious* virus, such as SARS-COV-2, is going to infect someone in the field research activity or escape into the public domain while researchers are in transit from Yunnan Province to Wuhan (an approximately 1,000-mile trip). SARS-COV-2 viruses would attach to researchers’ clothing and to equipment surfaces where they would endure for several days. It is difficult to decontaminate clothing and surfaces before airborne viruses get into the air. And it is a fairly extreme precaution to douse clothing and equipment with harsh chemicals while still in the field location. Doing that means you already know you are dealing with a hyper-contagious virus.

More stringent safety precautions are taken in the labs than at the field collection sites. The purpose of dangerous virus research is to get ahead of mother nature. To the extent that such research is successful, laboratories will always precede Mother Nature in producing the most dangerous viruses. Therefore, the final, hyper-contagious genome of SARS-COV-2, was almost certainly produced, directly or indirectly, in a Wuhan lab. Otherwise, the outbreak would have occurred hundreds of miles to the south in Yunnan province or along the transit route researchers drove from Yunnan to Wuhan (unless they flew, which might produce exposures at the airports).

In the article, “Climate change and other risk drivers of animal health and zoonotic disease emergencies: The need for a multidisciplinary and multisectoral approach to disaster risk management,” C. Wannous reminds us that climate change is increasing the chances of human-animal interface.[[88]](#footnote-88) Climate change and population growth may have pushed humans and bats closer together in Yunnan province, giving evolving viruses the exposures to humans needed to develop human infectivity.

That is all too true, but the mathematical probabilities still favor an outbreak of a virus as***hyper-contagious***as SARS-COV-2 ***near its point of origin***, not 1,000 miles away. Significant progress towards the SARS-COV-2 genome might have occurred via the bat-to-human interactions in the Mojiang mines, but the final steps to make an emerging ***hyper-contagious***coronavirus optimized for humans probably took place in a lab in Wuhan.

One or more reasonably close progenitors of SARS-COV-2 were probably collected from the Mojiang mine bats and/or miners by researchers in Wuhan. The next evolutionary step towards SARS-COV-2 was probably encouraged in a Wuhan lab via serial passaging of the viruses through human cell lines or cells close to human such as monkey and mouse.

Scientists at the Wuhan labs did not necessarily know what the result would be from their work; but they were **trying to produce the most dangerous forms** of coronaviruses so vaccines and antiviral drugs could be developed to protect against them. The SARS-COV-2 virus is apparently what they got. There were at least two virus labs in Wuhan that, in theory, could have processed bat virus samples from the Mojiang mines. The Wuhan Center for Disease Control and Prevention is located there as well as the WIV.

Both have conducted large projects on novel bat viruses and maintained large research collections of novel bat viruses, and at least the WIV possessed the virus that is the most closely related known virus in the world to the outbreak virus, bat virus RaTG13. This virus was isolated in 2013 and had its genome published on January 23, 2020. Seven more years of bat coronavirus collection followed the 2013 RaTG13 isolation.

One component of the novel-bat-virus project at the Wuhan Institute of Virology involved infection of laboratory animals with bat viruses. Therefore, the possibility of a lab accident includes scenarios with direct transmission of a bat virus to a lab worker, scenarios with transmission of a bat virus to a laboratory animal and then to a lab worker, and scenarios involving improper disposal of laboratory animals or laboratory waste.[[89]](#footnote-89)

So, it is entirely possible that a newly emerged SARS-COV-2 virus somehow escaped past tight biosecurity containment measures, with tragic results. That hasn’t been proved, but it is by far the most probable scenario.

Other possibilities? While the chance that SARS-COV-2 was an intentional creation or accidental biproduct of biowarfare germ research is relatively small compared to a civilian research laboratory escape, it is not zero.

Some of the genetic alterations achieved by SARS-COV-2 have been described as difficult for naturally occurring random mutations to achieve. Should that difficulty level eventually be proved, it would mean that the dangerous coronavirus research projects were never good risk-benefit tradeoffs for vaccine protection against naturally occurring pandemics because we were not in a race with Mother Nature. Only staying ahead of biowarfare threats would have justified doing such dangerous research in a situation where Mother Nature could be shown to be out of the race.

However, we don’t presently know the total difficulty level of achieving the SARS-COV-2 genome via random mutations alone. Scientists cannot be blamed for making a risk-benefit judgment based upon information available at the time, but the concept does have relevance for future risk/benefit tradeoff decisions.

The fact that a hard-to-naturally-evolve virus genome structure did in fact emerge argues for at least partial *direct* engineering of the SARS-COV-2 genome, although in most cases serial passage work in labs (*indirect* engineering) could eventually accomplish the same modifications as direct genetic engineering.

Naturally occurring respiratory viruses don't normally attack all the body's organs and systems as SARS-COV-2 does (described in the article by Iroegbu, et al.)[[90]](#footnote-90) A situation where biowarfare researchers monitor civilian virus research that intentionally produces dangerous viruses for the purpose of getting vaccines and antiviral drugs ready to defeat them only makes sense. Biowarfare scientists in aggressive nations evaluate new germ creations in the civilian labs and keep for their own use those germs deemed to be effective as biowarfare agents. Scientists in non-aggressive nations, like the United States, must also monitor the same germs to prepare vaccines and antiviral drugs not only against the chance Mother Nature will spawn a pandemic with the germs, but against the risk of foreign enemies or bioterrorists using the germs as biowarfare weapons.

Highly contagious and heavily disabling viruses make reasonably good biowarfare agents—assuming the country using them is itself vaccinated against them and has effective antiviral drugs on hand. In terms of disabling effects, SARS-COV-2 is a good candidate for a moderately useful biowarfare agent. It doesn’t incapacitate people instantaneously, but it can incapacitate in a few weeks while tracking back through an enemy’s forces all the way to their home country, temporarily reducing battlefield effectiveness and damaging the nation’s economy. Long-COVID drags out the effect, magnifying the damage. SARS-COV-2 isn’t a perfect germ weapon, but neither are any of the world’s other biowarfare agents perfect weapons.

According to the U.S. House of Representatives *Second Interim Report on the Origins of the COVID-19 Pandemic*, China has had an offensive biowarfare program and the military organization responsible did have ties to the Wuhan Institute of Virology.

The declassified Updated Assessment failed to mention the long history of coronavirus collaboration between scientists from the Chinese People’s Liberation Army (PLA) Fifth Institute of the Academy of Military Medical Sciences and scientists at the Wuhan Institute of Virology. It also failed to mention the Fifth Institute’s acknowledged role in China’s biological weapons program. The PLA’s Academy of Military Medical Science (AMMS) was founded in 1951 and functions as China’s military medical research organization. It is comprised of 11 institutes, one of which is the Institute of Microbiology and Epidemiology, also known as the Fifth Institute. In the 1990s, China officially declared the Fifth Institute as part of its defensive biological weapons program under the Biological and Toxin Weapons Convention Confidence Building Measures. In 2005, the U.S. State Department publicly stated the U.S. assessment that China also operates an offensive biological weapons program, specifically identifying two Chinese entities as likely involved, one of which is the Fifth Institute.[[91]](#footnote-91)

What I am saying here is not that we were attacked by biowarfare germs. China itself seems to have been hit too hard for that to be true. What I am saying is that China’s biowarfare research establishment may have been evaluating SARS-COV-2 for use in future biowarfare. That increases the number of labs and research staff involved in handling the germs, thereby increasing the chance of an accidental release.

In some cases, there might be less government oversight in a biowarfare lab than a civilian research lab—though in other cases possibly more. Certainly, there would be less *international* oversight in biowarfare labs, at least in biowarfare labs of aggressor nations. There might also be lower safety standards in biowarfare labs due to emphasis on bioweapons production on a demanding timeline required by national security planning objectives. Rushing scientists doing dangerous virus research obviously increases safety problems.

If virus research labs are as safe as the three NIH scientists say they are in the quote that follows on the next page, an intentional release of SARS-COV-2 becomes as probable as an accidental one! If labs are fully safe and the intermediate animal hosts for progenitor viruses of SARS-COV-2 required for natural evolution are not out there, there is only one alternative left: intentional release. But statistics on laboratory acquired infections and accidental germ escapes from labs tell us that labs are not fully safe.

Actually, there are other alternatives, also related to biowarfare research. An unintended release of germs could be caused by a preemptive air attack or a commando raid on a germ warfare lab. Germ and chemical warfare agent releases were rumored to have occurred during explosions at the Iraqi Army base at Khamisiyah in the first Gulf War in 1991. A nonproliferation operation intended to interdict an illegal germ warfare agent transfer between nations could also cause an unintended release if a physical struggle occurred between germ couriers and a nonproliferation field operations team. However, there have been no indications of air raids or commando attacks in China, and we know that germ labs are *not* fully safe.

The following quote lays out the key elements of the debate over dangerous lab research, concluding that dangerous research should continue, but carefully. I agree the research needs to be done—*very* carefully—but done to stay ahead of aggressor nations’ biowarfare programs as much as to stay ahead of Mother Nature. And they should be done on home turf, inside the United States.

**Biosafety and biosecurity concerns**

As novel pathogens emerge, scientists must be able to continue to work with them safely and appropriately in teams using the talents of many highly trained researchers. Numerous layers of robust biosafety and biosecurity protection and oversight are in place to safeguard the scientists and the public alike, including rigorous safety training, biocontainment practices, regulations and oversight, select agent rules, background investigations and biosurety oversight. The H5N1 studies under discussion were both performed in high containment laboratories with rigorous and appropriate oversight and biosecurity measures, as is the case for all such research in the US….

In considering the threat of bioterrorism or accidental release of genetically engineered viruses, it is worth remembering that nature is the ultimate bioterrorist. Indeed, H5N1 mutations, including some of those made in the two studies under discussion, occur spontaneously in nature, probably at a high rate, although they have not yet led to a pandemic. Given the relative rarity of pandemics caused by newly emerging influenza viruses, their explosive transmissibility may result from unique and virus-specific mutational changes that arise at very low frequency. For past pandemics, we have had limited ability to detect such changes by surveillance or by animal model experimentation. Thus, our best hope in preventing and controlling the microbial agents that continually challenge us is to increase fundamental knowledge about the mechanisms by which they emerge, spread and cause disease, so that we can develop countermeasures such as enhanced surveillance, better diagnostics, vaccines and drug therapies. In moving forward we need to be safety conscious and to have consensus safety measures and policies in place, while at the same time using all available tools to seek broad understanding about the complex relationships between viruses and hosts. It is only this knowledge that stands between us and the devastation of future influenza pandemics. In reconsidering the proper balance between progress and safety, the critical importance of advancing scientific knowledge needs to be kept front and centre.[[92]](#footnote-92)

Whatever the actual level of safety in the worlds high-security biocontainment labs may be, and wherever one prefers to make the trade-off between avoiding lab-released germs and protecting against future natural pandemics via dangerous research, dangerous germ escapes are an implicit danger of advancing biotechnology. Science and government acknowledge the theoretical possibility of an intentional or accidental germ release as seen in the quotes below.

In “From biodefence to biosecurity: The Obama administration's strategy for countering biological threats,” (the third quote below) Gregory D. Koblentz confirmed that the United States government viewed the threat of bioterrorism, biowarfare, and pandemics as absolutely real. In the fourth quote, Reynolds Salerno (International Biological Threat Reduction, Global Security Programs, Sandia National Laboratories) and Lauren Hickok confirm that bioterrorism is a real and increasing threat. The threat of biowarfare and bioterrorism is no longer just conspiracy theory stuff. It has become part of our world.

There is an increasing concern within both the scientific and security communities that the ongoing revolution in biology has great potential to be misused in offensive biological weapons programs. In light of the 11 September tragedy, we can no longer afford to be complacent about the possibility of biological terrorism. Here we review the major relevant trends in genomics research and development, and discuss how these capabilities might be misused in the design of new bioweapons. We also discuss how the breakthroughs that have come from the genomics revolution may be used to enhance detection, protection and treatment so that biological warfare agents are never used.[[93]](#footnote-93)

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Advances in biological research likely will permit development of a new class of advanced biological warfare (ABW) agents engineered to elicit novel effects. In addition, biotechnology will have applications supporting ABW weaponization, dissemination, and delivery. Such new agents and delivery systems would provide a variety of new use options, expanding the BW paradigm. Although ABW agents will not replace threats posed by traditional biological agents such as Bacillus anthracis (anthrax) and Variola (smallpox), they will necessitate novel approaches to counterproliferation, detection, medical countermeasures, and attribution.[[94]](#footnote-94)

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The Seventh Review Conference of the Biological Weapons Convention (BWC), the first international treaty to outlaw an entire class of weapons, was held in Geneva in December 2011. On 7 December, Secretary of State Hillary Clinton became the highest-ranking US government official to address a BWC meeting. Secretary Clinton told the assembled delegation that ‘we view the risk of bioweapons attack as both a serious national security challenge and a foreign policy priority’. At the same time, she warned that a large-scale disease outbreak ‘could cripple an already fragile global economy’. Secretary Clinton's speech reflected a new understanding that the range of biological threats to international security has expanded from state-sponsored biological warfare programmes to include biological terrorism, dual-use research and naturally occurring infectious diseases such as pandemics.[[95]](#footnote-95)

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The anthrax attacks of 2001 demonstrated that bioterrorism poses a significant threat to U.S. national security. This threat is increasing as a result of the rapid expansion in scale and technical capabilities of the global biotechnology industry, which is broadening the availability of materials, technologies, and expertise needed to produce a biological weapon and is lowering the barriers to biological weapons terrorism and proliferation. At the same time, there has been a rise of sophisticated yet loosely networked transnational terrorist groups that have shown an interest in bioterrorism. The United States must confront this convergence. Although the U.S. government pursues many different biodefense programs to bolster its ability to detect and respond to a bioterrorist attack, these efforts must be augmented with preventive measures to meet today's international challenges. U.S. Homeland Security Presidential Directive 10 of April 2004 defines "Prevention and Protection" as one of the four essential pillars of the U.S. response to the bioterrorist threat.[[96]](#footnote-96)

In their article, “Unusual Features of the SARS-CoV-2 Genome Suggesting Sophisticated Laboratory Modification,” Li-Meng Yan (Rule of Law Society & Rule of Law Foundation, New York) and Adrian David Cheok (iUniversity in Tokyo) offer a scientific case for direct laboratory manipulation of coronavirus genomes having been one element contributing to the origin of the SARS-CoV-2 virus and associated COVID-19 pandemic.

Nonetheless, SARS-CoV-2 shows biological characteristics that are inconsistent with a naturally occurring, zoonotic virus. In this report, we describe the genomic, structural, medical, and literature evidence, which, when considered together, strongly contradicts the natural origin theory. The evidence shows that SARS-CoV-2 should be a laboratory product created by using bat coronaviruses ZC45 and/or ZXC21 as a template and/or backbone. Building upon the evidence, we further postulate a synthetic route for SARS-CoV-2, demonstrating that the laboratory-creation of this coronavirus is convenient and can be accomplished in approximately six months….

The existing scientific publications supporting a natural origin theory rely heavily on a single piece of evidence—a previously discovered bat coronavirus named RaTG13, which shares a 96% nucleotide sequence identity with SARS-CoV-2. However, the existence of RaTG13 in nature and the truthfulness of its reported sequence are being widely questioned….

Consistent with this notion, genomic, structural, and literature evidence also suggest a non-natural origin of SARS-CoV-2. In addition, abundant literature indicates that gain-of-function research has long advanced to the stage where viral genomes can be precisely engineered and manipulated to enable the creation of novel coronaviruses possessing unique properties….

i. The genomic sequence of SARS-CoV-2 is suspiciously similar to that of a bat coronavirus discovered by military laboratories in the Third Military Medical University (Chongqing, China) and the Research Institute for Medicine of Nanjing Command (Nanjing, China).

ii. The receptor-binding motif (RBM) within the Spike protein of SARS-CoV-2, which determines the host specificity of the virus, resembles that of SARS-CoV from the 2003 epidemic in a suspicious manner. Genomic evidence suggests that the RBM has been genetically manipulated.

iii. SARS-CoV-2 contains a unique furin-cleavage site in its Spike protein, which is known to greatly enhance viral infectivity and cell tropism. Yet, this cleavage site is completely absent in this particular class of coronaviruses found in nature. In addition, rare codons associated with this additional sequence suggest the strong possibility that this furin cleavage site is not the product of natural evolution and could have been inserted into the SARS-CoV-2 genome artificially by techniques other than simple serial passage or multi-strain recombination events inside co-infected tissue cultures or animals….

1. If it was a laboratory product, the most critical element in its creation, the backbone/template virus (ZC45/ZXC21), is owned by military research laboratories.

2. The genome sequence of SARS-CoV-2 has likely undergone genetic engineering, through which the virus has gained the ability to target humans with enhanced virulence and infectivity.

3. The characteristics and pathogenic effects of SARSCoV-2 are unprecedented. The virus is highly transmissible, onset-hidden, multi-organ targeting, sequelae-unclear, lethal, and associated with various symptoms and complications.

4. SARS-CoV-2 caused a world-wide pandemic, taking millions of lives and shutting down the global economy. It has a destructive power like no other.

…several coronaviruses [genomes] recently published (RaTG13, RmYN02, and several pangolin coronaviruses) are highly suspicious and likely fraudulent.[[97]](#footnote-97)

Evidence for direct or indirect laboratory manipulation of viruses as a possible source of the COVID-19 pandemic has been given by other researchers, including Jonathan Latham, Allison Wilson, Rossana Segreto, and Yuri Deigin.[[98]](#footnote-98) The High-Risk Research & Dangerous “Gain-of-Function” Projects section of the bibliography below lists many articles that discuss such genetic modification work. The articles provide additional relevant references.

In our previous article we briefly discussed how the pandemic might have been caused either by a virus collection accident, or through viral passaging, or through genetic engineering and a subsequent lab escape. The genetic engineering possibility deserves attention and is extensively assessed in an important preprint (Segreto and Deigin, 2020).[[99]](#footnote-99)

The Chinese military, the Peoples Liberation Army (PLA), does seem to have had its fingers in the coronavirus research pie. Freedom of Information Act documents obtained from the U.S. State Department by the U.S. Right to Know public interest group indicate that the cooperation between the PLA and Wuhan Institute of Virology was “robust.”

The cables may represent some of the research that informs a 2021 statement from the State Department that “the WIV has engaged in classified research, including laboratory animal experiments, on behalf of the Chinese military since at least 2017.”

But while some information can be gleaned through the cable’s headings, the rest of the content is fully redacted.

One heading suggests “robust cooperation between WIV and PLA AMMS,” likely a reference to the Academy of Military Medical Sciences….

The cables challenge the certainty expressed by the lab’s Western collaborators, including EcoHealth Alliance President Peter Daszak, that all of the lab’s novel viruses have already been made public, thus the lab could not have been secretly working on the progenitor to SARS-CoV-2. The Wuhan Institute of Virology hosted a coronavirus database that was made inaccessible to the public in September 2019 and ultimately taken offline.

“There is no possible way that people outside China, including all of the scientists arguing against the research related origin hypothesis, know for certain that a precursor virus was not held within the repository of the WIV,” Metzl said.[[100]](#footnote-100)

An article in the *New York Post* in 2021 (Lee Brown, “US-Linked Chinese Military Scientist Filed Patent for COVID Vaccine Just after Contagion Emerged”) linked the Wuhan virus lab with China’s military. And the [newly released report (23 June 2023) from U.S. Intelligence](https://www.dni.gov/files/ODNI/documents/assessments/Report-on-Potential-Links-Between-the-Wuhan-Institute-of-Virology-and-the-Origins-of-COVID-19-20230623.pdf) indicates there were links between the Chinese military and the Wuhan virology lab.

The close working relationship between the pair supports declassified US intelligence released in January that said the Wuhan lab was conducting “secret military activity,” *The Australian* said.

“Despite the WIV presenting itself as a civilian institution, the United States has determined that the WIV has collaborated on publications and secret projects with China’s military,” the intelligence stated….

They researched genetically manipulating coronaviruses soon before the pandemic hit, funded in part by the NIH, where Fauci runs the National Institute of Allergy and Infectious Diseases, the report said, citing a research paper submitted to the *Journal of Virology* in November 2019….

The revelation appeared in a report by the paper’s award-winning investigations writer Sharri Markson as part of her research for an upcoming book, “What Really Happened in Wuhan[[101]](#footnote-101)

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The [23 June 2023 ODNI] report, [*The Potential Links Between the Wuhan Institute of Virology and the Origin of the COVID-19 Pandemic*](https://www.dni.gov/files/ODNI/documents/assessments/Report-on-Potential-Links-Between-the-Wuhan-Institute-of-Virology-and-the-Origins-of-COVID-19-20230623.pdf), disclosed a lot of information that has previously been reported about the virological research center in Wuhan, the city where the first cases of COVID-19 were detected in late 2019. Some biosafety standards and equipment at the facility were found to be lacking, including appropriate precautions for working with SARS-like coronaviruses and aging infrastructure. Workers at the lab had been ill at around the time the pandemic started. The lab held an incredibly large collection of bat samples, conducted genetic engineering experiments on coronaviruses, and conducted experimentation on making hybrid coronaviruses. Also previously reported, the lab had links to the Chinese military—reportedly for public health work.[[102]](#footnote-102)

**Indications of Cover-up**

While there are no indications of an intent by China or any other country to make a biowarfare attack via the COVID-19 pandemic, there is insufficient information to absolutely rule an attack out. I am certainly not going to guarantee you it didn’t happen, but it would seem to have been a rather clumsy attack. Since COVID-19 has afflicted all nations, regardless of who your prime suspect might be, the attack, if there was one, didn’t spare the nation originating the attack. So, an accidental germ release is the more probable theory.

There *are* indications that *something* was covered up. A frontline doctor interviewed by a Chinese news reporter revealed there was a [huge outbreak in Wuhan in January 2020 that was heavily suppressed by the Chinese authorities](https://usrtk.org/covid-19-origins/wuhan-doctor-early-covid-cases-suppressed/?mc_cid=179989ed2a&mc_eid=5597d51fd9). A copy of that interview, partially redacted, was recovered by the U.S. Right to Know organization under a Freedom of Information Act lawsuit against the U.S. State Department.[[103]](#footnote-103)

Chinese government obstruction of the WHO investigation of COVID-19’s origins is [well documented](https://www.nbcnews.com/news/world/who-official-says-agency-not-invited-take-part-china-s-n1197516).[[104]](#footnote-104) COVID-19 samples were destroyed contrary to standard medical research practice.[[105]](#footnote-105) China has been credibly accused of hoarding medical protective equipment months before admitting the COVID-19 outbreak.

Suppression of information and individuals by Chinese authorities. A publication by two Chinese university academics discussed both the WHCDC and the WIV and concluded that “the killer coronavirus probably originated from a laboratory in Wuhan”; the publication was removed from the internet by Chinese government officials. The paper had been posted on Research Gate but was blocked after 24 hours. After being placed on an archive file by internet users, it was again blocked after a week, and the two Chinese authors were pressured to retract the paper. However, it is still available on Web archives.

The Chinese government closed the laboratory in Shanghai that first published the genome of COVID-19 on January 10, explaining that it had been shuttered for “rectification”; the closure happened on January 11. The government then permitted the same genome to be published by Shi on January 12. Chinese citizens who reported on the coronavirus were censured and, in some cases, “disappeared.” These have included businessman Fang Bin, lawyer Chen Qiushi, former state TV reporter Li Zehua and, most recently, Zhang Zhan, a lawyer. They are reportedly being held in extrajudicial detention centers for speaking out about China’s response to the pandemic. They are usually accused of “picking quarrels and provoking trouble.”

Another aspect of Chinese government secrecy involved in the SARS-CoV-2 pandemic relates to official reporting by Chinese government officials on the severity of the outbreak in China and on levels of mortality. The number of cases and deaths are suspected of being undercounted by at least an order of magnitude, and possibly two, meaning that the reported figures could be as little as one percent of the actual totals. In the last week of April 2020, Caixin, one of the most reliable publications in China, reported that a serological study had been carried out in Wuhan on 11,000 inhabitants. Extrapolating from its results, which showed that five to six percent of the sample of 11,000 persons carried antibodies for SARS-CoV-2, Caixin estimated that 500,000 people in the city had been infected, or 10 times the level of official Chinese government reporting. The publication was quickly deleted by Chinese government censors.

The Chinese government has also attempted to obscure the origins of the pandemic with disinformation. On March 13, Chinese Foreign Ministry spokesperson Zhao Lijian suggested that the United States might have introduced the coronavirus to Wuhan. A month later, Zhao Lijian again posted Russian coronavirus and biowarfare-related disinformation, this time followed by online posts from Chinese ambassadors in 13 countries spread across the world. This was unprecedented diplomatic behavior for China, but not an accident. It was a concerted, deliberate, and preposterous disinformation campaign, repeated in May by CGTN, the China Global Television Network, which reposted the disinformation to the social media sites Weibo, Facebook, and Twitter.[[106]](#footnote-106)

Also, and significantly, according to a recent report by United States Senator Marco Rubio (on the Select Committee on Intelligence and the Committee on Foreign Relations), the Chinese seem to have been working on a SARS-COV-2 vaccine months before they made the first report of the virus to the world.

Scientists agree that China has been less than fully forthcoming on relevant scientific data.

The fact that, years after the collection campaign in 2011/2012, new viruses could be isolated from the stored fecal samples can be interpreted as an indication that other previously undiscovered sub-strains are stored in the samples at the Wuhan Institute for Virology, possibly also those that have an even stronger sequence similarity to SARS-CoV-2 than those already analyzed.[[107]](#footnote-107)

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It is telling that when Dr. Shi introduced the world to CoV-2 for the first time in January 2020 she showed hundreds of gene sequences of this novel virus but stopped just short of showing the furin site, the one she is purported to have introduced, seemingly not wanting to call attention to her handywork….

She could have perhaps saved many lives just by telling the world that she saw a furin site in the virus sequence….

Dr. Shi has denied the virus came from her lab, but she has created such a record of multiple examples of obfuscation, half-truths, contrived specimens, genetic sequences taken from thin air but published in premier journals and US NIH databases, etc. that her veracity is deeply damaged.

Perhaps her words and actions on December 30, 2019 show the truth. Her very first response when told there was an unknown outbreak in Wuhan and to return back quickly from a meeting she was attending in Shanghai was to say, “Could this have come from our lab?”

“I wondered if [the municipal health authority] got it wrong,” she says. “I had never expected this kind of thing to happen in Wuhan, in central China.” Her studies had shown that the southern, subtropical provinces of Guangdong, Guangxi and Yunnan have the greatest risk of coronaviruses jumping to humans from animals—particularly bats, a known reservoir….

Her other action on December 30 was to alter WIV computer databases of novel coronaviruses used by the world’s virologists for research to make it more difficult to search for which coronaviruses she had in her building. In short, the day she was asked to address the pandemic in Wuhan, she chose to spend time to make unavailable to her fellow scientists of the world her decades of coronavirus work.[[108]](#footnote-108)

There are other indications of cover-up.

The notion that CoV-2 was a laboratory creation, designed for maximum virulence, that escaped the laboratory accidentally has additional rings of evidence. From President Xi announcing in February new laws about laboratory security, to abundant evidence that the WIV was closed in October with few personnel inside, to the top military medical research doctor, General Chen Wei, being placed in charge of the WIV, to many more clues, it is clear an event occurred in Wuhan sometime in late 2019 that is most consistent with a laboratory escape.[[109]](#footnote-109)

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The first work in which the nucleotide sequence of SARSCoV-2 was described and compared with other viruses, was published by Zhengli Shi and coworkers very soon after the outbreak of the wave of infections in Wuhan. It was submitted to *Nature* on January 20, accepted 9 days later on January 29 and published online on February 3, 2020; it appeared in one of the journal's issues on March 12, 2020 (5). This is a short period of time for an extensive paper with 29 authors from 4 Chinese institutions, starting with the identification of the first patient by the end of December 2019 to virus isolation, sequencing, data aquisition, writing, approval by all authors, submission, reviewing and revision.[[110]](#footnote-110)

The Chinese may not be the only ones trying to hide the truth. Conflict of interest of some of the authors and scientists insisting on the zoonosis theory of COVID-19’s origins has been established, and the leading article supporting the zoonosis theory has been shown to be bad, or at least premature, science. ABC News reported that a fairly senior CIA officer went to Congress in 2023 with claims that the panel of seven science experts the CIA convened to investigate the origins of COVID-19 were offered significant monetary bonuses by the most senior member on the team to change their opinion from the lab-leak theory to fully uncertain. (Note: This does not mean the attempt to alter panel member opinions was officially approved by the agency. It may merely be a situation where the senior team member or one or more other persons had been compromised by outside influence.)

The Central Intelligence Agency (CIA) confirms to ABC News it is “looking into” accusations that several members of an agency team tasked with COVID-19 pandemic analysis were paid off “significant” hush money in order to buy a shift in their position about where the virus came from -- but the agency emphasized it does not pay its analysts to reach particular conclusions.

“At [the] CIA we are committed to the highest standards of analytic rigor, integrity and objectivity. We do not pay analysts to reach specific conclusions,” CIA spokesperson Tammy Kupperman Thorp said in a statement to ABC News. “We take these allegations extremely seriously and are looking into them. We will keep our Congressional oversight committees appropriately informed.”[[111]](#footnote-111)

Apparently, the Chinese were not the only ones engaged in covering up the truth. Jonathan Latham's article, “The Great Raccoon Dog Mystery,” exposes activities at science conferences that seem to have been undertaken to keep the lab leak theory from getting serious attention. Those incidents involved scientists from the United States and Europe. While those scientists may have incorrectly classified Latham as a conspiracy theory advocate and were afraid he would turn the conference into a media circus, it seems more likely that they were trying to preclude the lab leak theory of COVID-19's origin from being assigned the high level of credibility it deserves based on a fair scientific assessment. Latham’s points were scientifically valid and he is a biologist with a PhD in virology. Latham makes a strong case that scientists at the conferences were attempting to hide the fact that researchers intentionally avoided doing experiments that could weaken the zoonosis theory of COVID-19’s origin and strengthen the lab release theory.

It is not clear whether the scientists who *appeared* (they are innocent until proved guilty) to be involved in cover-up activities were acting at the official behest of U.S. and European governments or for private or special interest reasons. My guess is that the driving motive came from private/special interests, though the scientists might have tried to use legitimate government concerns to cover their actions. The problem is that those actions went too far; they compromised the integrity of science and thwarted an enormous public interest in understanding the origins of the COVID-19 pandemic.

Yes, the integrity of science is sometimes sacrificed for big money or ideological reasons (for example, to advance the atheist-Communist worldview) See my book, *Darwin’s New Clothes*. Debunkers of the lab release theory argue that because RaTG13 is the closest known genome to SARS-COV-2 the pandemic began with a jump of SARS-COV-2 or a close progenitor from bats to an intermediate animal to humans. But RaTG13 doesn't even appear to be a legitimate virus genome. It seems to have been artificially contrived. Rigorous peer-review checks that are the hallmark of scientific integrity seem to have been dispensed with for theories on COVID-19’s origin that let laboratories off the hook.

Dr. Steven Quay concluded the bat Cov genome RaTG13, thought by proponents of the animal origin theory to be the precursor of the SARS-CoV-2 virus, was almost certainly not obtained from an authentic fecal swab from an *Rhinolophus affinis* (Horseshoe) bat as claimed by Chinese virus researchers, giving it a probability of less than one chance in 13 million of being authentic.

Other researchers have noted that RaTG13 seems to have been an artificial patchwork of RNA segments from various sources, not a natural genome. A normal scientific peer review process would have caught the many anomalies prior to publication of the article announcing the discovery of RaTG13, raising the possibility of a cover-up of the true origins of SARS-COV-2.[[112]](#footnote-112)

In any case, the size of the genetic difference between RaTG13 and SARS-CoV-2 is large enough to suggest a laboratory origin, especially in the absence of known intermediate animal progenitors. Premature dismissal of the lab release alternative therefore suggests a coverup. There was altogether too much of a rush to jump to the zoonosis conclusion. Dismissing the lab origin theory out of hand should not have occurred without the standard evidence to prove an animal origin and prior to a full forensic investigation into related laboratory activities.

Dangerous gain-of-function research with potentially pandemic causing germs was known to be in progress at Wuhan prior to the outbreak of COVID-19. The U.S. State Department lead investigator into the origins of COVID-19, David Asher, made that revelation to a British newspaper in 2021: “'They were engaged in a shocking range of dangerous experiments into highly pathogenic, man-made versions of Covid-like viruses in Wuhan.”[[113]](#footnote-113) Asher also indicated that a substantial amount of information related to the origins of COVID-19 remained classified.[[114]](#footnote-114)

A leaked research proposal, ostensibly from EcoHealth Alliance to DARPA (Defense Advanced Research Projects Agency), outlines a research project aiming to produce exactly those changes we see in SARS-CoV-2![[115]](#footnote-115)

A grant proposal written by the U.S.-based nonprofit the EcoHealth Alliance and submitted in 2018 to the Defense Advanced Research Projects Agency, or DARPA, provides evidence that the group was working — or at least planning to work — on several risky areas of research. Among the scientific tasks the group described in its proposal, which was rejected by DARPA, was the creation of full-length infectious clones of bat SARS-related coronaviruses and the insertion of a tiny part of the virus known as a “proteolytic cleavage site” into bat coronaviruses. Of particular interest was a type of cleavage site able to interact with furin, an enzyme expressed in human cells....

Richard Ebright, a molecular biologist at Rutgers University who has espoused the possibility that SARS-CoV-2 may have originated in a lab, agreed. “The relevance of this is that SARS Cov-2, the pandemic virus, is the only virus in its entire genus of SARS-related coronaviruses that contains a fully functional cleavage site at the S1, S2 junction,” said Ebright, referring to the place where two subunits of the spike protein meet. “And here is a proposal from the beginning of 2018, proposing explicitly to engineer that sequence at that position in chimeric lab-generated coronaviruses.”[[116]](#footnote-116)

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The DEFUSE grant proposal was led by EcoHealth Alliance President Peter Daszak.

Now, drafts and notes uncovered through the Freedom of Information Act reveal fresh details about the intended research.

Specifically, the scientists sought to insert furin cleavage sites at the S1/S2 junction of the spike protein; to assemble synthetic viruses in six segments; to identify coronaviruses up to 25 percent different from SARS; and to select for receptor binding domains adept at infecting human receptors.

The genome of SARS-CoV-2, the virus that causes COVID-19, matches the viruses described in the research proposal.[[117]](#footnote-117)

On the surface, it looks like someone, perhaps on the Chinese side of things, went ahead with that research proposal (or one very much like it), although DARPA rejected it. Obviously, things didn’t turn out all that well.

**Summary & Conclusion**

Zoonosis theory advocates must demonstrate that early intermediate forms of the SARS-COV-2 virus had an opportunity to cross-species transfer to humans. That has not been done. Investigators have **not** shown that animals were present at the Wuhan Market that were infected with SARS-COV-2 or close relatives. The Director of China’s CDC, Gao Fu, stated that test results indicate that wildlife at the Wuhan market were not infected with COVID-19.[[118]](#footnote-118) Bats **weren't sold** at the Wuhan Market, and the pangolin's sold there were **not infected**. Scientists have also challenged the frequent claim that bats pose an extraordinary threat of disease crossover to humans.

While bats are often referred to as reservoirs of viral pathogens, a meta-analysis of the literature reveals many cases in which there is not enough evidence to claim so…. We conclude, that with the exception of a few viruses, bats pose little zoonotic danger to humans and that they operate a highly efficient anti-inflammatory response that we should strive to understand.

Although the coronavirus isolated from bats in Wuhan (China) was found to be 96% genetically identical to the beta coronavirus that started the current pandemic, this degree of similarity accounts for a temporal distance of several to many years between the two, when taking the mutation rate of the virus into account (Boni et al., 2020; Ruiz-Aravena et al., 2022). Notably, the receptor-binding domain (RBD) of the bat virus cannot bind to human cells, indicating that it is not the direct source of the pandemic…. Although there is some evidence that the potential ancestral COVID-19 virus had originated in bats (Shereen et al., 2020), to date, two years after the pandemic first struck, we still do not know the direct source of the human pathogenic COVID-19 variant…. Our findings suggest that in many cases the confidence regarding the bats’ role as reservoir animals is not sufficiently supported. Although we do not claim that bats are never the origin of human pathogens, we suggest that their role has been consistently exaggerated and often without the necessary scientific basis.[[119]](#footnote-119)

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“It is possible that the virus was passed directly from bats to humans because there are bat coronaviruses that can bind to human angiotensin-converting enzyme 2 and thereby infect humans without adaptation. Bats known to harbour these viruses are present across east Asia, including in central China.”[[120]](#footnote-120) This alternative helps keep the zoonosis theory alive in the face of so much opposing evidence, but it is a *purely theoretically* possible.[[121]](#footnote-121) There is no hard data supporting a direct transfer from bats to humans.

The bat viruses found by researchers to have the ability to jump directly to humans *did not have the properties of SARS-COV-2*.[[122]](#footnote-122) Bats have not been found that were actually infected with SARS-COV-2 or infected with a virus close enough to SARS-COV-2 to permit completing the transformation into SARS-CoV-2 via rapid mutations helped by positive selection after making a direct leap to humans. Bats have a very low affinity to SARS-COV-2 infection. In pure theory direct transfer of the virus from bats to human sounds good, but, based on what science actually knows, it is very unlikely.

We must remember that positive selection events can be encouraged in the lab through “serial passage” of viruses through human cell cultures or humanized cells in animal organs, tissues, and cell lines. Positive selection events for genetically difficult virus mutations are more likely to originate in laboratories via repeated encouragement using cell-passage techniques. The mutations can also be artificially forced via direct engineering

Passaging is a standard virological technique for adapting viruses to new species, tissues, or cell types. It is normally done by deliberately infecting a new host species or a new host cell type with a high dose of virus. This initial viral infection would ordinarily die out because the host’s immune system vanquishes the ill-adapted virus. But, in passaging, before it does die out a sample is extracted and transferred to a new identical tissue, where viral infection restarts. Done iteratively, this technique (called “serial passaging” or just “passaging”) intensively selects for viruses adapted to the new host or cell type (Herfst et al., 2012).[[123]](#footnote-123)

In serial passaging, a slightly adapted virus is repeatedly saved from extinction by human intervention, then given another chance to adapt a little further towards human infectivity by reinjecting it into other cells from mice, monkeys, or humans. This rescue and reintroduction cycle is repeated over and over until the virus is well adapted to the human cell type. Mother Nature, on the other hand, *rarely* has a chance to save an ill-adapted virus before it becomes extinct. The phrase “intensively selects” in the quote from Latham and Wilson above does not mean intensive *natural* selection; it is *artificially orchestrated* selection, closely managed by scientists in a lab.

This seems to be what occurred during the origination of SARS-COV-2. The normal sequence of gradual genome change in nature through a long series of progenitor virus relatives of SARS-COV-2 cannot be demonstrated. So, when the critics of the lab release theory of the origins of COVID-19 say the virus could have evolved by jumping directly from bats to humans and then surviving in humans by a rapid series of positive selection events they are misleading citizens looking for the best, most probable explanation. That scenario is *theoretically* possible but statistically *very* improbable. The odds heavily favor a laboratory origin.

Dr. Steven Quay tells us (citing Damas, et al.[[124]](#footnote-124)) that bat species score low on the genetic affinities required for susceptibility to SARS-COV-2 infection. It is unlikely that bats will even be infected by SARS-COV-2 or a closely related progenitor virus. Therefore, a direct jump of SARS-COV-2 from bats to humans almost certainly did not occur.

A surprising finding from the ACE2 in silico surveillance work was the very poor predicted affinity of the ACE2 receptors in both bats and pangolins. Of 37 bat species studied, 8 scored low and 29 scored very low. As expected by these predictions, cell lines derived from big brown bat (Eptesicus fuscus), Lander’s horseshoe bat (Rhinolophus landeri), and Daubenton’s bat (Myotis daubentonii) could not be infected with SARS-CoV-2.[[125]](#footnote-125)

**Dangers of Gain of Function Research**

Inappropriately named gain-of-function influenza research seeks to confer airborne transmission on avian influenza A viruses that otherwise cause only dead-end infections in humans. A recent study has succeeded in doing this with a highly pathogenic ostrich H7N1 virus in a ferret model without loss of virulence. If transposable to humans, this would constitute a novel virus with a case fatality rate ~30 greater than that of Spanish flu. A commentary from three distinguished virologists considered the benefits of this work to outweigh potential risks. I beg to disagree with conclusions in both papers, for the underlying science is not as strong as it appears.[[126]](#footnote-126)

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**Was the WIV doing experiments that might release PPPs?**

Since 2004, shortly after the original SARS outbreak, researchers from the WIV have been collecting bat coronaviruses in an intensive search for SARS-like pathogens (Li et al., 2005). Since the original collecting trip, many more have been conducted (Ge et al., 2013; Ge et al., 2016; Hu et al., 2017; Zhou et al., 2018)….

In 2013 the Shi lab reported isolating an infectious clone of a bat coronavirus that they called WIV-1 (Ge et al., 2013). WIV-1 was obtained by introducing a bat coronavirus into monkey cells, passaging it, and then testing its infectivity in human (HeLa) cell lines engineered to express the human ACE2 receptor (Ge et al., 2013)….

In this particular set of experiments the researchers combined “the spike of bat coronavirus SHC014 in a mouse-adapted SARS-CoV backbone” into a single engineered live virus. The spike was supplied by the Shi lab. They put this bat/human/mouse virus into cultured human airway cells and also into live mice. The researchers observed “notable pathogenesis” in the infected mice (Menachery et al. 2015)….

The overarching purpose of such work was to see whether an enhanced pathogen could emerge from the wild by creating one in the lab.…

Given the research and collection history of the Shi lab at WIV it is therefore entirely plausible that a bat SARS-like coronavirus ancestor of Sars-CoV-2 was trained up on the human ACE2 receptor by passaging it in cells expressing that receptor.[[127]](#footnote-127)

Have we done all we could to sort out the COVID-19 pandemic mystery? Have we learned the lessons of trusting contract researchers to not cut corners to increase profits and allowing projects that do not provide adequate oversight and security to prevent clandestine biowarfare skimming off legitimate medical research to support Communist military programs?

Proactive security measures are obviously required for dangerous germ research. But citizen whistleblowing and investigative reporting are (understandably) much more difficult in classified research projects, especially those occurring in foreign countries. It is therefore difficult for citizens to sanity check dangerous U.S. government germ research projects.

This may, in part, be an irresolvable problem. Legitimately classified high-security research can’t be subjected to public scrutiny. So, personnel reliability screenings must be very thorough and kept fully up to date. Physical safety and security measures and real-time quality control oversight must be in place in all dangerous germ research activities. We already knew that (and, presumably, have been doing it)—but in the case of COVID-19 it wasn’t enough.

The real problem in the U.S. and Western cultures is the “I wanna be a millionaire club.” When the contract kick-back and espionage bribe amounts get high enough, somebody will inevitably take the money and compromise a critical program. We have good safety procedures and guidelines—in theory, and on paper. But when dangerous germ research is placed within a business context, corners can be cut to save overhead expenses and increase profits. When it is placed in the context of an international germ warfare arms race, espionage tactics such as bribes and blackmail, and even sabotage can come into play, introducing new risks.

Non-profit scientific research organizations such as EcoHealth Alliance will tend to be more strapped for operating funds than profit-seeking businesses. Ironically, the problem in the case of COVID-19 may be that not enough money was invested in the project. Given what we now know of the near impossibility of containing pandemic level germs, the amount of the contract awarded to EcoHealth Alliance to research emerging coronaviruses, among which can be presumed to be germs with *pandemic-threat capability* (and *potential bioterror/biowarfare agents*) seems ridiculously *low*.

Was this a case of underbidding to get a contract, or a situation where a favor was done by awarding a contract to a friend and keeping the cost low so as not to get too much attention? Did biowarfare research departments of foreign nations find a way to piggy-back off EcoHealth Alliance’s research project in Wuhan?

The most ridiculous aspect of all was the U.S. NIH funding research on deadly pandemic level pathogens *in laboratories in Communist China*. Placing dangerous research activities in the hands of our #1 foreign adversary flagrantly invited abuse of the process.

Our culture needs to change from profit *uber alles* (and personal power-building, favor-trading, and deal-making) to what’s best for the country, the free world, and the public interest. We need to return to an old-fashioned concept of public service—and proactive quality control.

Quality control checking to prevent profit-and-foreign-interest-driven abuses (**before** a major problem arises) seems to be lacking. We say the right words, publish the right guidelines, then we let major health contractors go out and police themselves, doing things their own way, forgetting that science research contractors are (usually) businesses seeking to maximize profit, and the non-profit contractors have less money to work with, making them susceptible to cutting corners on safety or possibly at greater risk of taking bribes from our foreign enemies.

Elected and appointed officials need to focus more on providing authentic government functions, such as oversight and quality control of dangerous research, and spend less time on the hyper-politicized culture wars. In the high-threat environment of a sizzling hot “cold war,” we can’t afford to be distracted by politics so much that we fail to perform the essential services of government regarding protection of the public.

Both parties, Republicans as well as Democrats, need to start incrementally scaling back the culture-war politicization of everything, while watching that the opposing party doesn’t cheat and genuinely meets them halfway. When that happens, there may be some time left over to focus on the legitimate tasks of government, including problem solving in the biosecurity arena.

Control strategies for influenza and other emerging diseases are not adequately developed; the Fineberg Report on the evaluation of WHO’s response to the 2009 H1N1 pandemic emphasized that “the world is ill prepared to respond to a severe influenza pandemic or to any similarly global, sustained and threatening public health emergency.” The urgent need for general guidance in this matter is reminiscent of the dilemma addressed at the Asilomar conference on recombinant DNA molecules in 1975....

It is noteworthy that in the United States there were 395 biosecurity breaches involving select agents and 7 laboratory-acquired infections during 2003 to 2009. These incidents, which occurred in both BL3 and BL4 laboratories, highlight the potential risks and the need to fully consider improved biosecurity and the immunization of staff with regularly updated H5N1 vaccines.[[128]](#footnote-128)

**SARS-COV-2 Bibliography**

**SARS-COV-2 Origins—General Information/Need for an Investigation\***

\*Note: The article by Xiao, Jun Li, et al. “Emergence of SARS-COV-2 through recombination and strong purifying selection,” emphasizes a key point about the apparently rapid and focused evolution of the SARS-CoV-2 virus to become capable of infecting humans. Intermediate host animals have not been found which would normally be required to accomplish the jump from animal to human (multiple steps of small genome changes). It remains possible that the requisite strong purifying selection was accomplished by laboratory manipulation (multiple passage of the virus through human or human-like cell lines, including in mice that had been genetically altered to have human-like cells.) This article, therefore, does not constitute a definitive argument for the zoonosis (animal transfer) theory of SARS-COV-2’s origin. Laboratory manipulation of the virus remains equally plausible, and some would say, more plausible. Going the other way, articles like the Becker, et al., article that describe laboratory manipulation of SARS-like viruses do not prove that SARS-COV-2 originated in a laboratory. However, they do establish the possibility of lab origin by showing that laboratory modification of viruses has been going on for many years.

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**SARS-COV-2 Origins—Lab Leak Theory\***

\*Note: The article by Steven C. Quay, MD, PhD, “Bayesian Analysis of SARS-CoV-2 Origin,” is the closest thing we have to date to a definitive answer on the origin of the SARS-CoV-2 virus and resulting COVID-19 pandemic. Dr. Quay’s analysis shows a lab release origin scores 98.8% probability compared to the natural zoonotic, animal transfer origin at 1.2%. The [Root Claim website](https://www.rootclaim.com/analysis/What-is-the-source-of-COVID-19-SARS-CoV-2) has a slightly different analysis, but is also heavily weighted toward a lab release origin. Rootclaim doesn’t fully rule out a biowarfare agent release as Quay does. I think that is a somewhat more defensible position as it is still too early to rule anything out. Root Claim gives the lab release theory 89%, two forms of the zoonosis origin a combined 6.4%, and a biowarfare lab germ (intentionally or unintentionally released) 4.5% probability. The article by Shu Yuan, Si-Cong Jiang, and Zi-Lin Li, “Analysis of possible intermediate hosts of the new coronavirus SARS-CoV-2,” reveals that the pattern of the outbreak does not match what typically happens with animal origin virus pandemics: too little genetic variation in the SARS-COV-2 viruses found, no original or intermediate animal hosts of the SARS-COV-2 virus found, and a single point of origin of the pandemic at Wuhan, China, versus multiple areas of the original outbreak that would be expected in a typical animal origin pandemic. Not all these articles strongly support the lab origin theory. For example, the following quote from an article by Yujia Alina Chan and Shing Hei Zhan, “The Emergence of the Spike Furin Cleavage Site in SARS-CoV-2,” makes only a single point arguing that the artificial origin of SARS-COV-2 is hard to rule out.

Even so, the knowledge that scientists had a workflow for identifying novel cleavage sites in diverse SARSr-CoVs and experimentally characterizing these cleavage sites in SARSr-CoVs—likely in a manner that makes the resulting recombinant SARSr-CoV practically indistinguishable from a rare SARSr-CoV with a naturally emerging FCS—makes it challenging to rule out an artificial origin of the SARS-CoV-2 S1/S2 FCS (Daszak 2018; Lerner and Hibbett 2021).

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**Cover-up/Conflict of Interest**

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**High-Risk Research & Dangerous “Gain-of-Function” Projects\***

\*Viktor Muller’s article, “A plea for caution: huge risks associated with lab-bred flu,” gives an excellent example of the risks and benefits of high-risk germ modification research. His editorial concerns the deadly H5N1 flu, but the same types of pros and cons apply to intentionally modifying other dangerous germs. If you are not familiar with the term “gain-of-function,” it refers to genetic manipulation of germs, direct or indirect, that can increase the transmissibility and virulence of the germs.

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\*Note: Readers should keep in mind that many germs that originate in nature need not be further developed in laboratories to be dangerous enough to be used as biowarfare weapons. All (publicly known) historical cases of biowarfare involved the use of germs produced by nature. Those germs were fully natural—not modified in laboratories. So, the mere fact that a germ has not been modified in a laboratory does not mean it could not be used as a biowarfare weapon.

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(Note: This U.S. government document ascribes substantial biological warfare and epidemic defense and research functions to China’s People’s Liberation Army. It does not indicate the presence of offensive biological warfare functions, but, as a Communist nation, I think it is a reasonable presumption that China does have an offensive biological weapons program as a well-kept secret. It would be foolish to assume otherwise. RH)

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**Zoonosis Hypothesis (Animal to Human Crossover) & Related Science\***

\*Note: With the exception of the article by Anderson, Rambaut, and Lipkin et al., “The proximal origin of SARS-CoV-2,” the authors of these articles do not argue definitively for the zoonosis (animal transfer to humans) theory of the origins of COVID-19—nor do they argue against it. They are presenting objective scientific data that has to do with viruses in animals that have the potential to transfer to humans. Some, such as the Roujian, Lu, Xiang Zhao, and Juan Li, et al. article, do say that the virus, SARS-COV-2, **might** have originated in bats and used another animal as an intermediate host to facilitate transfer to humans. No definite conclusions are drawn with respect to origins of SARS-CoV-2. Critical commentaries of the Anderson, Rambaut, and Lipkin, et al., article, “The proximal origin of SARS-CoV-2,” have largely shown it to be bad science, at least in the sense of premature. The Jonathan E. Pekar, Andrew Magee, and Edyth Parker, et al., article, “The molecular epidemiology of multiple zoonotic origins of SARS-CoV-2,” seems to be a follow-on attempt by some of the same authors (Anderson, Rambaut, and Holmes) to make a stronger case for the zoonotic origin of SARS-CoV-2/COVID-19 than the evidence can presently support.

I have included a few articles in this section that pertain to the SARS-COV-1 or SARS-related viruses because they clarified some interesting points on SARS and related viruses’ *supposed* zoonotic origin. (which has not been proved beyond reasonable doubt).

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**Evolution, Structure, and Mutation of SARS-COV-2 & Related Viruses**

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**Other Pandemic Germs (SARS-COV-1, MERS, Influenza Strains, etc.)**

SARS-COV-2 is not the last threat we will see of pandemic germs. Oddly, influenza viruses, with which we are all so familiar, pose a potential serious future threat of mutating into a pandemic capable germ. Consider the following NIH press statement on the National Science Advisory Board for Biosecurity (NSABB Review) of H5N1 Research.

Tuesday, December 20, 2011

<https://www.nih.gov/news-events/news-releases/press-statement-nsabb-review-h5n1-research>.

The U.S. government remains concerned about the threat of influenza, for the risks it poses seasonally, as well as its potential to cause a pandemic. Our domestic and global influenza surveillance efforts have become increasingly capable, along with expanded vaccine manufacturing capacity and assistance to other countries in their efforts to detect and respond to a pandemic. To enhance the detection of and response to influenza outbreaks, the U.S. government supports a broad range of domestic and global preparedness and response efforts that include research on better diagnostics, vaccines, and therapeutics.

Currently, H5N1 avian influenza virus — the strain commonly referred to as "bird flu" — rarely infects humans and does not spread easily from person to person. However, many scientists and public health officials are concerned that the virus could evolve in nature into a form that is transmissible among humans — an event that could potentially make this deadly virus an extremely serious global public health threat. Thus research on factors that can affect the transmissibility of the H5N1 virus is critically important to international efforts to prepare and prevent threats to public health.

While the public health benefits of such research can be important, certain information obtained through such studies has the potential to be misused for harmful purposes. The National Science Advisory Board for Biosecurity (NSABB) — an independent expert committee that advises the Department of Health and Human Services (HHS) and other Federal departments and agencies on matters of biosecurity — completed a review of two unpublished manuscripts describing NIH-funded research on the transmissibility of H5N1. These manuscripts — which describe laboratory experiments that resulted in viruses with enhanced transmissibility in mammals – concluded that the H5N1 virus has greater potential than previously believed to gain a dangerous capacity to be transmitted among mammals, including perhaps humans, and describe some of the genetic changes that appear to correlate with this potential.....

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