

Abstract

Right through 2020 anyone suggesting any hypothesis other than Zoonotic origin for Covid 19 was labeled a conspiracy theorist. Three papers contributed to this. February 3, 2020 paper by Dr Shi et al, '*A pneumonia outbreak associated with a new coronavirus of probable bat origin*', February 19, 2020 Lancet paper "*Statement in support of the scientists, public health professionals, and medical professionals of China combating COVID-19*" and March 17, 2020 article in *Nature Medicine* "*The proximal origin of SARS-CoV-2*". by Andersen et al. First concerns were raised by a fact sheet issued by Department of State, USA on January 15, 2021. The three papers were then refuted scientifically by *Bayesian Analysis of SARS-CoV-2 Origin*, dated January 29, 2021, by Dr. Steven C. Quay. The theory of lab leak gained strength with The Bulletin of Atomic Scientists article "*The origin of COVID: Did people or nature open Pandora's box at Wuhan?*" by Nicholas Wade on May 5, 2021. This was followed by "*The Quest for the Coronavirus Progenitor Integrating Intelligence and Science*" by Lt. Col. (res.) Dr. Dany Shoham on May 11, 2021. On May 14, 2021, a group of 18 scientists called for investigation into origins of Covid 19 by an open letter published in the *Science*. Finally on May 27, 2021, President Biden directed the US Intelligence Community to determine whether Covid 19 emerged from human-animal contact or via a laboratory accident and give him a report in 90 days.

In the meanwhile a terrible tragedy was unfolding in India. By end of 2020, it seemed India had held its own against the pandemic. A State election (Bihar – November 2020) was conducted without any major incident. In January 2021, India launched its own vaccination program and felt confident enough to hold massive religious functions and multitude of local and state level elections. But it had let its guard down in a critical area. It was not monitoring the mutations of Covid 19. Unknown to India, the Delta variant – now considered a Global cause for concern, had taken roots and led to the most devastating wave of the pandemic so far seen in any country. By middle of May 2021, India seemed to be a flailing if not failed state, as patients could not get beds in hospitals and even when they did, basics such as a regular supply of oxygen was not available. This was a far cry from the country that had held its own in an eyeball to eyeball confrontation against China less than a year ago after bloody border clashes that left scores of soldiers on either side dead in June 2020. Till 2020 India appeared to be the only economic rival to China in its quest to replace the dominant global economy USA,. By mid 2021, Indian economy was in shambles, its reputation torn to shreds and worst of all, the morale of its citizens was at its nadir.

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An arrogant Communist Party of China in act of savagery, mocked India as in a social media post. it contrasted its own scientific achievement against the plight of Indians dying due to the pandemic. It showed the best and worst of China. It was put out by Communist Party of China but was deleted after outrage from Chinese people themselves.

Lighting a fire in China VS lighting a fire in India



The barbaric social media post on Weibo by an handle associated with the Communist Party's Central Political and Legal Affairs Commission -a Chinese Law Enforcement Agency on May 1, 2021 showed an image of a rocket launch in China, along with another image of the cremation ceremonies of India's Covid-19 victims when India was recording 400,000 Covid 19 cases a day

This paper points out that lost in the debate of the origin of Covid 19 – natural origin and lab leak is that there is a third and far more sinister possibility – that Covid 19 is a Bio weapon. Rootclaim – a platform that claims to integrate all available evidence, assesses it for credibility and uses probabilistic models to reach conclusions about the likelihood of competing hypotheses. Its conclusions are claimed to represent the best available understanding of the complexity and uncertainty in the world, assigns the Bio weapon theory a probability of 3.5%. This by itself warrants a serious investigation into an event that has killed millions and disrupted life of almost every single human being on the planet.

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The paper argues that the probability of Covid 19 being a Bio weapon at 3.5% is grossly understated. At the very least the probability is 25% more than the 16% starting point of Rootclaim or 20%. Evidence with respect to Natural Origin theory and the Lab Leak theory lies within the Republic of China and therefore requires cooperation of the Chinese Government. On the other hand all the data and evidence for determination of whether or not Delta variant is of Natural origin or is a Synthetic Pathogen, lies in India, where it was first found. Thus such an investigation is independent of cooperation or otherwise of Chinese Communist Party. If Delta variant is indeed a Synthetic Pathogen, both Lab Leak Theory AND Bio Weapon theory stand proven not only in the eyes of the World but most importantly in the hearts and minds of millions of decent Chinese women and men.

Investigation into the origin of Delta variant – Natural Mutation or Synthetic Pathogen, is therefore the need of the hour.

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1 Background

There is mounting evidence about the lab origin of Covid 19 – which was dismissed as a Conspiracy Theory by so called eminent scientists in 2020. The Lab Leak Theory is now a serious hypothesis. Bio Weapon theory is still beyond the pale. It should not be. Not after the Delta variant delivered a knockout punch to India's ambitions of being a serious rival to China in its own backyard – Asia, at the very least for the foreseeable future.

2 Problems with Covid 19 having Natural Origin Theory

The primary source for the Author in stating that there are serious problems with the theory of Covid having natural origin are:

- a) Fact Sheet issued by Department of State, United States on January 15, 2021,

<https://fb.usembassy.gov/fact-sheet-activity-wuhan-institute-of-virology/>

- b) *Bayesian Analysis of SARS-CoV-2 Origin*, dated January 29, 2021, Steven C. Quay, MD, Ph.D, Covid 19

- c) Blog of Jamie Metzel '*The Origin of SARS-Cov-2*', first published on April 16, 2020 and regularly updated thereafter / <https://jamiemetzl.com/origins-of-sars-cov-2>

- d) The Bulletin of Atomic Scientists "*The origin of COVID: Did people or nature open Pandora's box at Wuhan?*" by Nicholas Wade | May 5, 2021

[https://thebulletin.org/2021/05/the-origin-of-covid-did-people-or-nature-open-pandoras-box-at-wuhan/?utm_source=Newsletter&utm_medium=Email&utm_campaign=ThursdayNewsletter05062021&utm_content=DisruptiveTechnologies OriginCovid_05052021](https://thebulletin.org/2021/05/the-origin-of-covid-did-people-or-nature-open-pandoras-box-at-wuhan/?utm_source=Newsletter&utm_medium=Email&utm_campaign=ThursdayNewsletter05062021&utm_content=DisruptiveTechnologiesOriginCovid_05052021)

- e) *The Quest for the Coronavirus Progenitor: Integrating Intelligence and Science*," by Lt. Col. (res.) Dr. Dany Shoham, BESA Center Perspectives Paper No. 2,021, May 11, 2021

<https://besacenter.org/the-quest-for-the-coronavirus-progenitor-integrating-intelligence-and-science/>

3 Critique of the Accepted Wisdom of 2020 by Dr Quay

Dr Quay has offered a detailed critique of the three papers that had the World accept Natural Origin of Covid 19 theory until May 26, 2021 With public awareness of a possible lab incident origin for the pandemic skyrocketing, President Biden issued this statement asserting: *“I have now asked the Intelligence Community to redouble their efforts to collect and analyze information that could bring us closer to a definitive conclusion, and to report back to me in 90 days.”*

Paper 1: The February 3, 2020 paper by WIV scientist Dr. Shi et al. entitled: “A pneumonia outbreak associated with a new coronavirus of probable bat origin.”

The basis for the hypothesis that SARS-CoV-2 probably evolved from bats initially came from this paper from Dr. Zheng-Li Shi’s laboratory at the Wuhan Institute of Virology (WIV). In that paper the Wuhan laboratory made two claims:

1), “a bat fecal sample collected from Tongguan town, Mojiang county in Yunnan province in 2013” contained a coronavirus, originally designated “Rhinolophus bat coronavirus BtCoV/499133” in 2016 but renamed in their paper, RaTG13; and

Whereas Dr Quay states that

“Based on using the mean and standard deviation of the nine authentic bat fecal specimens from the Wuhan laboratory, the probability that RaTG13 came from a true fecal sample but had the composition reported by the Wuhan laboratory is one in thirteen million;

2), the genomes of RaTG13 and SARS-CoV-2 had an overall identity of 96.2%, making it the closest match to SARS-CoV-2 of any coronavirus identified at that time. RaTG13 remains the closest match to SARS-CoV-2 at the current time.

Dr Quay states:- *The pattern of synonymous to non-synonymous (S/NS) sequence differences between RaTG13 and SARS-CoV-2 in a 2201 nucleotide region flanking the S1/S2 junction of the Spike Protein records 112 synonymous mutation differences with only three non-synonymous changes. Based on the S/NS mutational frequencies elsewhere in these two genomes and generally in other coronaviruses **the probability that***

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this mutation pattern arose naturally is approximately one in ten million. A similar pattern of unnatural S/SN substitutions was seen in a 10,818 nt region of the pp1ab gene. This pp1ab gene pattern has a probability of occurring naturally of less than one in 100 billion. A total of four regions of the RaTG13 genome, coding for 7,938 nt and about one-quarter of the entire genome, contain over 200 synonymous mutations without a single non-synonymous mutation. This has a probability of one in 10-17. A possible explanation, the absolute criticality of the specific amino acid sequence in the regions which might make a non-synonymous change non-infective, is ruled out by the rapid appearance of an abundance of non-synonymous mutations in these very regions when examining the over 80,000 human SARS-CoV-2 specimens sequenced to date. An alternative hypothesis, that this arose by codon substitution is examined. It is demonstrated, by example from a published codon-optimized SARS-Cov-2 Spike Protein experiment, that the anomalous S/SN pattern is precisely the pattern which is produced, by design, when synthetic biology is used and represents a signature of laboratory construction.

Based on the findings concerning the RaTG13 data, including anomalies and inconsistent statements about RaTG13, its origin, renaming, and sequencing timing; the finding that the specimen it is purported to have come from; is not bat feces and has a signature of cell culture contamination; the unexplained method-dependent 5% sequence difference for RaTG13; and the S/SN mutation pattern reported, which to my knowledge has never been seen in nature, it can be concluded that **RaTG13 is not a pristine biological entity but shows evidence of genetic manipulation in the laboratory.**”

He concludes - Until a satisfactory explanation of the findings in this paper have been offered by the Wuhan laboratory, all hypotheses of the proximal origin of the entry of SARS-CoV-2 into the human population should now include the likelihood that the seminal paper contains contrived data. For example, the hypothesis that SARS-CoV-2 was the subject of laboratory research and at some point escaped the laboratory should be included in the narrative of the origin of SARS-CoV-2 research.

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Paper 2: The February 19, 2020 Lancet paper entitled: “Statement in support of the scientists, public health professionals, and medical professionals of China combating COVID-19.”

The paper has been seriously criticized as a Political rather than a Scientific statement since there was very little actual data available at the time to permit reaching such a definitive conclusion either in favour of Natural Origin or Lab leak theory. Dr Quay has offered detailed arguments showing lack of evidence to support definitive conclusions. In November 2020 the Watchdog group, US Right-to-Know, reported the following with respect to the *Lancet* article:

“Emails obtained by U.S. Right to Know show that a statement in The Lancet authored by 27 prominent public health scientists condemning “conspiracy theories suggesting that COVID-19 does not have a natural origin” was organized by employees of Eco Health Alliance, a non-profit group that has received millions of dollars of U.S. taxpayer funding to genetically manipulate coronaviruses with scientists at the Wuhan Institute of Virology... The emails obtained via public records requests show that EcoHealth Alliance President Peter Daszak drafted the Lancet statement, and that he intended it to “not be identifiable as coming from any one organization or person” but rather to be seen as “simply a letter from leading scientists”. Daszak wrote that he wanted “to avoid the appearance of a political statement.”

A separate, worrisome article entitled, “Peter Daszak’s Eco Health Alliance Has Hidden Almost \$40 Million In Pentagon Funding And Militarized Pandemic Science,60” seems to indicate a serious conflict of interest with respect to Dr. Daszak’s participation in any investigations on the origin of SARS-CoV-2.

Paper 3: The March 17, 2020 article in *Nature Medicine* entitled “The proximal origin of SARS-CoV-2” by Andersen et al.

The claims made in the Paper and Response thereto by Dr Quay make an illuminating reading.

Paper Claim 1

“While the analyses above suggest that SARS-CoV-2 may bind human ACE2 with high affinity, computational analyses **predict that the interaction is not ideal** and that the RBD sequence is different from those

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shown in SARS-CoV to be optimal for receptor binding. Thus, the high-affinity binding of the SARS-CoV-2 spike protein to human ACE2 is **most likely the result of natural selection on a human or human-like ACE2** that permits another optimal binding solution to arise. **This is strong evidence that SARS-CoV-2 is not the product of purposeful manipulation.** [emphasis added.]

Response

A later analysis of over 3800 possible substitutions of amino acids in a 200 amino acid receptor binding region, much larger than the small, selective region referred to in this paper, shows that CoV-2 is 99.5% optimized for binding to the ACE-2 receptor. This near perfect binding has never been seen before in a recent interspecies transmission jump.

Paper Claim 2

“Polybasic cleavage sites have not been observed in related ‘lineage B’ betacoronaviruses, although other human betacoronaviruses, including HKU1 (lineage A), have those sites and predicted O-linked glycans. Given the level of genetic variation in the spike, **it is likely that SARS-CoV-2-like viruses with partial or full polybasic cleavage sites will be discovered in other species.**” [emphasis added.]

Response

As of the writing of this manuscript no other lineage B (sarbecovirus) has been found to have a furin site. In addition, the furin site of CoV-2 has the unusual -CGG-CGG- codon dimer, which has never been seen in an analysis of 58 other sarbecoviruses, that is, 580,000 codons. Since recombination between subgenera of beta coronaviruses is rare, or unknown, there is no source for the CGG-CGG dimer via a natural recombination event.

Paper Claim 3

The acquisition of polybasic cleavage sites by HA has also been observed after repeated passage in cell culture or through animals.”

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Response

It is curious why the above statement did not lead to a hypothesis somewhere in the article about a similar mechanism on CoV-2, a clear indication of a laboratory origin.

Paper Claim 4

It is improbable that SARS-CoV-2 emerged through laboratory manipulation of a related SARS-CoV-like coronavirus.”

Response

This conclusory statement is unsupported by evidence.

Paper Claim 5

Furthermore, if genetic manipulation had been performed, one of the several reverse-genetic systems available for beta corona viruses would **probably have been used**. However, the genetic data irrefutably show that SARS-CoV-2 is not derived from any previously used virus backbone.” [emphasis added.]

Response

There is no explanation for why a prior backbone would necessarily be used. All synthetic biology chimera corona viruses created in the past as published in prior papers have each used a unique backbone with no particular pattern in backbone selection. Each backbone was selected for the particular needs of those current experiments. This non-repeating prior pattern of reverse-genetic systems makes the above statement untenable. And with 16,000+ reported corona virus specimens at the WIV it entirely reasonable a non-published virus could have been used

Claim of Paper 6

“Natural selection in an animal host before Zoonotic transfer. For a precursor virus to acquire both the polybasic cleavage site and mutations in the spike protein suitable for binding to human ACE2, **an animal host would probably have to have a high population density (to allow natural selection to proceed efficiently)** and an ACE2-encoding gene that is similar to the human ortholog.” [emphasis added.]

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Response

The paragraph discusses the pangolin as the possible intermediate host but at the time of this manuscript the corona virus data from pangolins has been discredited. This author agrees with statement that selection of the two unique features of CoV-2 require a high population density of the animal host. Of course, in the laboratory the animal hosts for either *in vitro* cell culture experiments or in animal experiments are a single species at high density.

Paper Claim 7

Natural selection in humans following Zoonotic transfer. “It is possible that a progenitor of SARS-CoV-2 jumped into humans, acquiring the genomic features described above through adaptation during **undetected human-to-human transmission**. Once acquired, these adaptations would enable the pandemic to take off and produce a sufficiently large cluster of cases to trigger the surveillance system that detected it.” [emphasis added.]

“Studies of banked human samples could provide information on whether such cryptic spread has occurred. Further serological studies should be conducted to determine the extent of prior human exposure to SARS-CoV-2.”

Response

As will be shown in later sections, this prior undetected human-to-human transmission would be evident in archived specimens from before the fall of 2019. In both SARS-CoV-1 and MERS, this prior sero conversion averaged about 0.6% with almost 5% among workers exposed to the intermediate hosts. At the time of the writing of this manuscript, in limited sampling of archived specimens there has been no sero conversion detected. The author believes there are thousands of archived specimens from Wuhan taken in the fall of 2019 and these should be immediately examined for evidence of sero conversion. Since finding sero conversion among these specimens would be strong evidence for a Zoonotic origin and not a laboratory accident, the absence of any information from China on this important evidence is hard to understand.

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Paper Claim 8

Selection during passage. “Basic research involving passage of bat SARS-CoV-like corona viruses in cell culture and/or animal models has been ongoing for many years in bio safety level 2 laboratories across the world, and there are documented instances of laboratory escapes of SARS-CoV. **We must therefore examine the possibility of an inadvertent laboratory release of SARS-CoV-2.**”

“In theory, it is possible that SARS-CoV-2 acquired RBD mutations during adaptation to passage in cell culture, as has been observed in studies of SARS-CoV.” New polybasic cleavage sites have been observed only after prolonged passage of low-pathogenicity avian influenza virus in vitro or in vivo. Furthermore, a hypothetical generation of SARS-CoV-2 by cell culture or animal passage would have required prior isolation of a progenitor virus with very high genetic similarity, **which has not been described.** Subsequent generation of a polybasic cleavage site would have then required repeated passage in cell culture or animals with ACE2 receptors similar to those of humans, **but such work has also not previously been described.** [emphasis added.]

Response

The authors correctly describe a method for CoV-2 to have been generated in the laboratory and then dismiss it because the work has not been published previously. As active scientists themselves, the authors must know how disingenuous this sounds. Almost by definition elite scientists, like Dr. Shi of the WIV, work in secret until the publication of any given line of research. As they say, the absence of evidence cannot be used as evidence of its absence. A peer-reviewed paper entitled, *“Might SARS-CoV-2 Have Arisen via Serial Passage through an Animal Host or Cell Culture? A potential explanation for much of the novel coronavirus’ distinctive genome,”* provides a compelling argument that serial passage in the laboratory might indeed have been the manner in which CoV-2 acquired many of its devastating traits.

Paper Claim 9

Although the **evidence shows that SARS-CoV-2 is not a purposefully manipulated virus**, it is currently impossible to prove or disprove the other theories of its origin described here. However, **since we observed all notable SARS-CoV-2 features, including the optimized RBD and**

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polybasic cleavage site, in related corona viruses in nature, we do not believe that any type of laboratory-based scenario is plausible.”
[emphasis added.]

Response

This author could identify no prior evidence in the paper to warrant saying it is not a purposefully manipulated virus. There is also no evidence that would point to a purposely manipulated virus. The evidence in the paper shows that no prior Zoonotic interspecies transmission has ever had an RBD as optimized as the CoV-2 RBD for the human ACE2. The evidence also shows that there is no natural source for the polybasic cleavage site (PCS). No other member of the subgenera to which CoV-2 belongs has a PCS. Since these are the only coronaviruses from which recombination could supply a polybasic cleavage site, **the data in this paper refutes the natural origin.** The belief statement concerning a laboratory-based scenario would be closer to the evidence if it was professed with, “despite evidence which is consistent with a laboratory-based scenario.”

Conclusions of Dr Quay

Three high visibility papers were published between January and May 2021 which purported to settle the question of the origin of SARS-CoV-2 as a Zoonotic transmission and not a laboratory accident. The analysis above concludes that these papers are not persuasive.

4 Mainstreaming of Lab Origin Theory

In his seminal paper, - **Bayesian Analysis of SARS-CoV-2 Origin, dated January 29, 2021, Dr Quay**, started with Zoonotic origin having a probability of 98.8% with Lab Leak Theory having a probability of 1.2%.

He took as many as 25 filters to make changes in the probability of each of the Theories and finally came to the startling conclusion that took the probability of Lab Leak theory to 99.8% reducing natural origin probability to just 0.2%..

As Dr Quay notes a 99.8% probability is considered beyond Reasonable Doubt even in a criminal trial

The conclusions of Dr Quay are tabulated below

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S.No.	Evidence	Zoonotic Origin	Lab Origin
		Probability in %	
	Initial State	98.8	1.2
1	International committees to determine CoV-2 origin may not be impartial	98.8%	
2	Three key zoonotic papers: pros and cons	98.8%	
3	SARS-like infections among employees of the Wuhan Institute of Virology in the Fall of 2019 reported by US Government		No Change
4	Location of first cases near Wuhan Institute of Virology	95.1	4.9
5	Lack of evidence of seroconversion in Wuhan and Shanghai	80.9	19.1
6	Lack of posterior diversity	30.8	69.2
7	Opportunity: The Wuhan Institute of Virology has publicly disclosed that by 2017 it had developed the techniques to collect novel coronaviruses, systematically modify the receptor binding domain to improve binding or alter zoonotic tropism and transmission, insert a furin site to permit human cell infection, make chimera and synthetic viruses, perform experiments in humanized mice, and optimize the ORF8 gene to increase human cell death.		No Change
8	Lack of furin cleavage sites in any other sarbecovirus	4.7	95.3
9	Rare usage of -CGG- single codons & no CGG-CGG pairs	0.5%	99.5
10	Rare usage of -CGG- single codons & no CGG-CGG pairs	0.5%	99.8
11	Spike Protein receptor binding region (200 amino acids) optimized for humans		
12	Whole genome analysis shows pre-adaption of CoV-2		
13	The finding of CoV-2 in Barcelona wastewater in early 2019 was an artifact		
14	Shi and the WHO comment early on that CoV-2 seemed to begin with a single patient		
15	Mammalian biodiversity between Yunnan and Hubei is significantly different, limiting a potential common intermediate host		
16	The ancestor of CoV-2 can only obtain a furin site from other subgenera viruses but recombination is limited/non-existent between subgenera		
17	Canvas of 410 animals shows humans and primates are the best, bats are the worst, for ACE2-Spike Protein interaction		
18	Canvas of 410 animals shows humans and primates are the best, bats are the worst, for ACE2-Spike Protein interaction		
19	A government requested review of samples collected from a mineshaft may have caused the COVID-19 pandemic		
20	The Hunan Seafood Market and farmed animals in Hubei province are not the source of CoV-2.	0.2%	
21	Line 2 of the Wuhan Metro System is the likely conduit of the pandemic and is the closest subway line to the WIV0.2		S.No. 11-28 confirm the probability levels reached at S. No 10
22	Feral and domestic cats are not the intermediate host		
23	Extraordinary pre-adaption for the use of human tRNA is observed		
24	Evidence of lax operations and disregard of laboratory safety protocols and regulations in China		
25	Previous SARS-CoV-1 laboratory accidents		
26	Shi and Daszak use Wuhan residents as negative control for zoonotic coronavirus exposure	0.2%	
27	RaTG13 could be CoV-2 precursor using the synthetic biology 'No See 'Em' technique		
28	Location, location, location: Based on the distance between known SARS-CoV-1 laboratory-acquired infections and the hospital of admission of the infected personnel, the WIV is within the expected hospital catchment for a CoV-2 LA10.2		
	Conclusion	0.2	99.8

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Dr Quay has offered detailed reasons for each of the factors he has taken into consideration. Details can be read by accessing the paper from i

<https://zenodo.org/record/4477081#.YNb1UOgzblU>

The evidence under S. No 6 to 10 were explained in simple language In a podcast of June 6th, 2021 Hudson event titled Uncovering the Origins of COVID-19: A Scientific Discussion, the transcript of which can be found on

<https://www.hudson.org/research/17021-transcript-uncovering-the-origins-of-covid-19-a-scientific-discussion>

Dr Quay's explanation is best read in his own words

"Six Undisputed Facts.

As a reminder of what we're going to talk about today, what is a Zoonosis, it's important to remember it has three elements. There's always an animal and then a microbe that's infecting that animal, and then the microbe jumps to humans. So those three elements of a host animal, a microbe and human are common to all Zoonosis.....

So today we're going to talk about six facts, four that relate to whether the zoonosis began in the community or was laboratory acquired. And to that address the question of, was this an unmodified natural virus that escaped from the laboratory or had it been genetically manipulated?

.....And the laboratories that I'm talking about for this exercise are really three, although the Wuhan Institute of Virology is the dominant one. But the Wuhan CDC, which is very close to a market is in contention and a place called the Wuhan Institute of Biologic Products, a vaccine manufacturer is also in the mix.

So the first challenge for a natural origin is what I call the location problem. The first patient is 1500 kilometers from the closest ancestral host in nature, but only 3.4 kilometers from the closest ancestral host in a refrigerator of the Wuhan Institute of Virology.....

So what do community-acquired Zoonosis and laboratory-acquired zoonosis have in common? Well, remember they both begin with an animal or tissues from an animal. So in the laboratory, you might have

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*animal cells growing in a Petri dish and they get infected with a virus, and then a staff member gets infected. So, that's what they have in common. What they have in distinction and will be the focus of today's presentation is really these three things that can be summarized nicely for the **community-acquired zoonosis as diversity** and for the **laboratory-acquired zoonosis, a singularity**.*

So when you think of those three elements we spoke of before that the animals with a community-acquired infection, there are many animals, high levels of population infection. The virus is very genetically variant because it's been in the animals for weeks, months, years, there's a lot of genetic variability and there are many pre-epidemic infections in the human community, which we'll talk about in just a minute.

The laboratory-acquired zoonosis, on the other hand is a singularity. It is one animal or one test tube with animal cells. It's one genetically pure virus, because in the lab, we always work with pure viruses, otherwise it's too complicated. And there's no pre-epidemic infection in the community, of course, it's one lab worker walking out one day, asymptotically infected and then starting the process.

*So let's talk about this term, what's called **Seroconversion Evidence**. So one of the hallmarks of a community-acquired infection is this practice, abortive infection where it jumps from animals to humans, but it doesn't have all the mutations it needs to support human to human spread. So what you get is multiple humans that have this infection, it burns up, they may not even know they have it. But the way to identify it is once an epidemic has occurred, you go back into the geographic region of the starting point. You go into the refrigerators of hospitals and blood banks. You pull samples out and you test them for the virus, from the epidemic because you now have an assay for that.*

The beauty is that you do not need to know where the host is because you're relying on the antibodies. You're relying on evidence of infection in the community before it comes about. Again with SARS-1 the civet cat was the intermediate host and it was jumping to humans repeatedly, but burning out because it didn't have all the mutations it needed. On November 16th, 2002, it got that last mutation it needed, to not only jump into humans, but to support human to human transfer.

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In a lab escape model, of course you have a pure culture of a virus exiting the laboratory with a single human, maybe asymptotically, walking into a subway and spreading the virus, and so you won't find it in the community at all.

So the first fact I want to speak about that everyone agrees on is that there is no pre-epidemic infections. COVID-19 wasn't smoldering in the community before the pandemic began as was observed with previous coronavirus epidemics. So the WHO report in March states, a total of 9,522 stored samples from patients with influenza-like disease in Wuhan or the surrounding area in late 2019, were tested for SARS-CoV-2 with an established assay. They were all negative So based on similar testing for the two previous coronavirus epidemic, SARS and MERS, a middle Eastern virus in camel's to humans, you would have expected 1 to 4%. So just remembering the numbers here, that's 100 to 400 patients with stored samples, where you should find the virus, and there were zero. So running the math on this, the probability that a community-acquired zoonosis like the previous, would have this resolved, is literally less than one in a million. In fact, Dr. Shi and Dr. Daszak, these are key play players in this whole process, Dr. Shi is the Head of the Wuhan Institute of Virology. She's worked for over a decade with Dr. Daszak, the President of EcoHealth Alliance. In 2018, they published a very interesting paper on serologic evidence of bat to human viruses in Yunnan, Southern China, where we think SARS-CoV-2 came from, and for this study, they actually used a control group from Wuhan. They wrote in their paper, "As a control, we collected 240 specimens from blood donors in Wuhan, 1,000 kilometers away, where inhabitants have a much lower likelihood of being infected." And of course in their study, zero of those patients were infected. About 2.7% in the southern province actually had evidence of coronavirus infections. So with respect to no pre-epidemic infections, it's a singularity.

Fact two, is that there are no animal hosts exists. Neither the COVID virus or any close relative has yet been found in nature, unlike prior natural zoonoses. So this is quite incredible because this surveillance exercise that China did over the last year is unprecedented in biology, largest effort ever done to find something in nature. More than 80,000 wildlife, livestock and poultry samples from Wuhan, from Hubei, the province it's in, from all of China, all 31 provinces were tested, and there were no positive results for either SARS-CoV-2 antibodies, meaning an animal that had an infection or the virus itself, which is an extremely sensitive test.

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In May 2020, Dr. Anderson and other virologists published a seminal paper, it's been downloaded over a million times, in which they predicted based on the properties of the virus, that, "The animal hosts would probably have to have a high population density in order to achieve the outcome that happened." And of course, we know running the math again on this, that the prevalence in the population has to be less than 0.004% to get these results. And again, a reminder the Wuhan Institute of Virology testing SARS-1 or MERS, the other two coronavirus infections, over 90% of the animals in the markets were positive.

So again, the probability that SARS-CoV-2 is a wild origin with this result, is again, less than one in a million. *In fact, just a reminder, SARS-CoV-1 in 2003, it took us four months to identify the civet cat shown here on the left, as the intermediate host. With MERS, it took a little bit longer, nine months to find the camel as the intermediate host, and we're now at 18 months, and we do not have an intermediate host. So it's one animal and probably because they didn't look at any animals in the laboratory is one of the foundational reasons it was missed.*

Fact three is that SARS-CoV-2 started genetically pure like the synthetic vaccine. *So we've all had experience, we've now given tens of millions of vaccines in the United States. And every vaccine is genetically identical with every other one. That's a man-made genetic product, that's the hallmark. And in fact, COVID coronavirus had little genetic diversity at the outset, again, unlike prior natural zoonoses. So some of the most prominent virologists and names in the world here have all commented on this unusual property. Dr. Baric probably the preeminent synthetic biologist in coronaviruses in the world wrote, "That early strains showed limited genetic diversity, suggesting that it may have been introduced as a single source." **Dr. Shi herself, this is very interesting, she put a draft of a paper on January 23rd up on the internet, and she wrote, "The almost identical sequences of this virus in different patients imply a probable recent introduction in humans."** Sometime after that, and before it finally got finalized February 3rd, she realized the implication of that, because **that sentence is no longer in her paper.***

Way back in April 2020 before the investigation and everything, the WHO said, "All published at genetic sequences isolated, suggest a single point introduction in the human population around the time the virus was first reported in humans, in Wuhan in December 2019." And Dr. Rambaut and Holmes, the two virologists who came up with the classification system for the SARS-CoV-2 coronaviruses wrote, "That

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because of early sampling and genome sequencing, we know that we have the root sequence is identified and because many of the genomes from the earlier sample cases are genetically identical, and it's also probably identical to the most recent common ancestor, we have a lot of information and they said, "This occurrence is different to previous viruses and epidemics, where there is a great deal of genetic diversity in the virus."

Here's a little example of how this kind of work is done. So because the mutations are two relative. So every mutation in a virus and infection, when it gets passed on, is on top of the previous ones. What you have on the left is an experiment where 10 patients are sequenced and there's 10 mutations. And you look at a pattern to see who gave the infection to whom. And what you see is that mutation one is in all of the 10 patients, but mutation two is not in patient A. And then you see oh, my gosh, mutation three is not in patient B. You run this through a computer algorithm and you get this pattern here, which is genetic evidence that patient A gave the virus to patient B, C, D, et cetera.

*We see there's over 1.9 million sequences here, and everyone can be traced back to a first genetic index patient. **The first patient with the most ancestral genome. So let's see who that patient is. Well, it turns out it's a 39 year old man with a bronchial lavage specimen. That's a deep specimen from the lungs that was collected on January 5th. He was not part of any market. He was not exposed. He stayed at a hospital near the market. But it's quite telling that he was in the hospital. He was in the General Hospital of the Central Theater Command of the People's Liberation Army of China, about three kilometers from the Wuhan Institute of Virology.....***

*So once you know this process, where... So you have clade A, which is that index patient. Once you know how this got from bats to intermediate host in the laboratory or the world, to clade A. And then two mutations here is shown, gets you to the next clade and the next clade. You can rank order all 176 million cases. Why is this important? Because if you find a source or if you identify, hypothesize maybe this began in a market, then the simple thing is to test, "Well, is it clade A in that market or did the virus come into the market?" So fact four is a very important fact. Again, there's no disagreement. This is from the WHO report, all the markets, where there is genetic information about this virus are all downstream from that first patient at the PLA hospital. So they're all either clade B or what we call clade A.1, where it's in clade A, but it has an additional mutation from that PLA. **So the WHO report itself documents that this could not have***

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begun in the markets with the data that we currently have. It also allows you to test other hypotheses. So here's one, testing the environmental specimens. If it began in the market in some way, they should have been clade A, correct? Well, the WHO report, again, shows that they are all clade B. So that hypothesis is not supported. Hypothesis two, if it began in a market, you should expect all the animals to test positive. Again, after 336 tests, no animal tests positive. And finally, if it began in a market, then the patients in the market should be clade A. They should not be clade B. So busy slide, I get it. But these four patients over here, that I'm circling next to the PLA hospital, those are the four clade A patients. Zero of those four, have any relationship to the markets. These orange boxes are the 11 early patients with an association to the market. 11 out of 11 of those are clade B.

So really the Chinese CDC had in May of 2020, said it as succinctly as anyone can, that the virus went into the market, it did not come out of the market.....

*An additional frustration is that the WHO report actually censored early non-market related cases. On the left is a Lancet paper in January, February 2020, where you see color coded that three of the first four patients had no relationship to a market. So the blue is not market-related, whatever that brown color is market related. And we knew early on that three of the four cases were not related to a market. This same data in the WHO report on the right, actually censors those early non-market cases. So their chart of the same data now begins later than the beginning of the Lancet paper and their first three patients all begin from the market. This is not science. This is obfuscation. **So with respect to the three predictions we had on laboratory-acquired zoonosis, they are all met.***

Let's now turn to the two undisputed facts about whether the virus was a natural virus, or whether it was gain-of-function research.

Fact five is the fact that we all agree on. That COVID's powerful infectious trigger isn't found anywhere in the related viral group in nature, but it's been repeatedly inserted into viruses by laboratories in the past, including the Wuhan Institute of Virology.

So this is a chart showing 58 viruses that are closely related to SARS-CoV-2. And what I mean closely-related, is this is a sampling of all of the virus that had a common ancestor, most recent common ancestor, MRCA about a thousand years ago. So this is basically the last

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millennials diversity in this class of coronaviruses that SARS-CoV-2 resides in. And this sequence of amino acids S-P-R-R-A, shown here, is not found in any of these viruses. So for the last 1,000 years, these viruses in nature have been existing and doing all their things, recombining, but without ever generating a furin cleavage site.

I call this the immaculate insertion, because it has two aspects of uniqueness. One is that what I've just described, it is the only spike protein in this class of coronaviruses that has a furin insertion site. There's no other sites. And the one way that these things can be acquired is by recombining with a virus from the same class that has something different. So one poor bat gets two viruses. The viruses start exchanging genetic material, and you come out with this hybrid virus. But you can't acquire something that doesn't exist in the population. And at the protein level, it doesn't exist. There's lots of codes, genetic codes for furin sites.

*So now we look at the code and we come up with what we talked about in our Wall Street Journal op-ed, which is the CGG-CGG double codon This is a language. If genetic material is a language for telling protein factories how to make proteins from genetic material, these are two words that these coronaviruses never use. They've never put CGG-CGG together in codons, anywhere in the world. **So it's a double uniqueness. The first has probability of one in greater than 100,000. The second, one in 500,000.** And yet, we know that laboratories have been inserting furin cleavage sites since 1992. Every case that they do it, it's always a gain-of-function. It's the surest way to guarantee you're going to gain a function. And I show here a map of the labs, locations of the labs, because this is a worldwide activity. It's not just China and it's not been recent. Again, it started in 1992.*

*So one of the things that a furin cleavage site does, is it permits immediate cell surface fusion. So again, a very complicated slide, but this little picture on the left here is SARS-CoV-1, which has to go through this complicated process to get into a cell. It takes time and it's also inefficient. On the right side, you see that the SARS 2 interacts with the membrane and bingo, the genetic materials inside. This allows not only expanded species tropism, but more importantly, and probably more lethally, it expands the cellular tropism, the different cells in the body that this virus can infect. **So with a furin cleavage site, you can get into the lungs, but you can't get into the heart, the brain and the endothelium.** And this is really telling, because these are the areas where the most severe infections and where the lethal infections are coming from.*

So with this information, why did Dr. Shi, the head of the Wuhan Institute of Virology, not feature this furin site in her seminal paper? If the site came from nature, an innocent virologist would have been highly motivated to describe the first example of a furin cleavage site in this class of coronaviruses in a thousand years of evolution. This busy slide, I apologize, but this is from her paper, on the left. She stops at position 675. Now, if she'd gone just six positions further, she would have disclosed the furin cleavage site, she did not.

A little while later, a French Canadian team highlighted this when they were the first to describe the furin cleavage site. And remarkably in that paper, they called it a gain-of-function to this virus for efficient spreading in human populations. And in their title, they say, "This cleavage site is absent in any coronaviruses from this same clade."

*Now, if I had wanted to describe to you what experiments were probably going on when someone got infected, I could have done it, I could have come up with a hypothetical description, but in fact, **this published paper from Dr. Baric in North Carolina and Dr. Shi and her colleagues at the Wuhan Institute of Virology, published in early 2020 is exactly the experiments I would describe being the foundation for a lab-leak hypothesis.** So this paper is entitled The Pathogenesis of SARS-CoV-2 in Transgenic Mice Expressing Human Angiotensin-Converting Enzyme 2, the ACE2 enzyme" So I've been doing laboratory research for 30 years, I've kind of gone through this paper and they had to hit everything right on the nail and had to have begin no later than January 28th to get this study done in time to publish it. But this is exactly the kind of work that probably was going on in earlier 2019.*

Fact six is that the virus is highly adapted for infection of humans from the start, unlike prior natural zoonoses. And growth in humanized mice would allow this lab adaption, like in that previous paper. I call this the pre-adaption trifecta, because whether you look at the entire genome, just the spike protein or the factory equipment that the virus uses in the body, it's all pre-adapted. At the whole genome level, this paper by Dr. Alina Chan and colleagues from the Broad Institute shows that **in SARS 1, there were two phases. There was an early phase, where it hadn't perfected human-to-human transfer. And then a later phase, a consolidation phase, where human transfer was going on. And SARS 2, of course shows only this later phase.**

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If you look at just the spike protein, you get this incredible set of experiments from a group in San Francisco. They basically said, “Okay, there’s 200 sequences in the spike protein that are important for binding. There’s 20 different amino acids. There are already 20 there, but let’s create all 3,800 other possible spike proteins and test every single one of them in the laboratory for affinity, for binding to ACE2.” So these are two charts that have all 3,800 experiments.

So the brown is where it made it worse. The white is where it was indifferent, and only these little blue squares is where it improved it. And only 0.5% of changes in these 3,800 amino acids made an improvement. Remarkably, nature did this experiment itself because the UK strain, which is this mutation right here in blue, it’s N501Y. In the fall of 2020, it was a rapidly expanding case. It proves this research, and it also establishes the validity of this process.

One of the last pieces of evidence, the State Department has said that they have evidence that three cases of SARS-like infections occurred in the fall of 2019. China, the Wuhan Institute of Virology and WHO have all said, “This did not occur.” Myself and DRASTIC, our colleague, Gilles Demaneuf did a statistical analysis of whether this was possible based on the incidents of COVID in Wuhan in the first half of 2020. And our analysis shows that there’s a one in trillion chance that no one at this institution had SARS-CoV-2.

So the prediction with respect to lab versus community was met in all three cases. Two findings that are associated with gain-of-function, the furin site and serial passage pre-adaption are our met. And so, in my opinion, without a public debate on whether gain-of-function experiments should continue without a change in current regulations, the next pandemic is right now being created somewhere in the world, where this dangerous work is being done.

Dr Quay has ended on a chilling note He is clear that the Covid 19 is of lab origin and that it resulted from a Gain of Function research. If that is so why should anyone NOT investigate whether or not Covid 19 is indeed a bio weapon?

5 The Quest for the Coronavirus Progenitor: Integrating Intelligence and Science by Lt. Col. (res.) Dr. Dany Shoham, BESA Center Perspectives Paper No. 2,021, May 11, 2021

The Executive Summary of this very interesting paper bears reproduction

“The integration of intelligence and science will be the key to uncovering the genomic origin and direct source of the virus that sparked the COVID-19 pandemic. Both the Fact Sheet issued by the US Department of State and recent elaborations by closely involved US officials clearly illustrate that such integration is vital. Intelligence is critical, as China continues to refuse to provide complete information for an inquiry into the possibility of an unnatural contagion scenario.

As a consequence of the unconvincing findings of the China-led WHO investigation on the emanation of COVID-19, the quest for the SARS-CoV-2 , primal strain, the virus that gave rise to the pandemic, has been amplified. That quest, posed initially as an intelligence challenge in January 2020, **made a quantum leap in January 2021, when the US Department of State issued a Fact Sheet largely based on intelligence.**

The document states, *inter alia*, that “The previously undisclosed information in this Fact Sheet, combined with open-source reporting, highlights three elements about COVID-19’s origin that deserve greater scrutiny”:

5.1. Illnesses inside the Wuhan Institute of Virology (WIV):

The US government has reason to believe that several researchers inside the WIV became sick in autumn 2019, before the first identified case of the outbreak, with symptoms consistent with both COVID-19 and common seasonal illnesses. This raises questions about the credibility of WIV senior researcher Shi Zhengli’s public claim that there was “zero infection” among the WIV’s staff and students of SARS-CoV-2 or SARS-related viruses.

Accidental infections in labs have caused several previous virus outbreaks in China and elsewhere, including a 2004 SARS outbreak in Beijing that infected nine people, killing one. The CCP has prevented independent journalists, investigators, and global health authorities from interviewing researchers at the WIV, including those who were ill in the fall of 2019. Any credible inquiry into the origin of the virus must include interviews with these researchers and a full accounting of their previously unreported illness.

5.2. Research at the WIV:

Starting in at least 2016, and with no indication of a stop prior to the COVID-19 outbreak, WIV researchers conducted experiments involving RaTG13, the bat coronavirus identified by the WIV in January 2020 as its closest sample to SARS-CoV-2 (96.2% similar).

The WIV became a focal point for international coronavirus research after the 2003 SARS outbreak and has since studied animals including mice, bats, and pangolins.

The WIV has a published record of conducting “gain-of-function” research to engineer chimeric viruses. But the WIV has not been transparent or consistent about its record of studying viruses most similar to the COVID-19 virus, including RaTG13, which it sampled from a cave in Yunnan Province in 2013 after several miners [who had entered the cave] died of a SARS-like illness.

WHO investigators must have access to the records of the WIV’s work on bat and other coronaviruses before the COVID-19 outbreak. As part of a thorough inquiry, they must have a full accounting of why the WIV altered and then removed online records of its work with RaTG13 and other viruses

5.3 Secret military activity at the WIV

Secrecy and non-disclosure are standard practice for Beijing. For many years the US has publicly raised concerns about China’s past biological weapons work, which Beijing has neither documented nor demonstrably eliminated, despite its clear obligations under the Biological Weapons Convention. Despite the WIV presenting itself as a civilian institution, the US has determined that the WIV has collaborated on publications and secret projects with China’s military. The WIV has engaged in classified research, including laboratory animal experiments, on behalf of the Chinese military since at least 2017. The report continues, “Today’s revelations just scratch the surface of what is still hidden about COVID-19’s origin in China. Any credible investigation into the origin of COVID-19 demands complete, transparent access to the research labs in Wuhan, including their facilities, samples, personnel, and records.”

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The proximity of first reported Covid 19 cases to such a lab as the Wuhan Institute of Virology

- Where there have been unreported infections AND,
- Which is carrying out dangerous research that can cause such a pandemic as what we are witnessing today AND
- Which has secret military nexus, AND
- Is located in the city which first witnessed outbreak of Covid 19 AND
- Is now free from the pandemic even as the world continues to suffer from it.

Bio weapon becomes a valid theory to investigate

6 Bio Weapon Theory

Dr Quay has this to say about the Bio Weapon Theory

“Lab-made Bio-Weapon Hypothesis

But was SARS-CoV-2 more than just a gain-of-function experiment that escaped a laboratory? Could it have been one part of a two-part novel virus-vaccine bio weapons program?

General Chen Wei has been involved in vaccine research since joining the People’s Liberation Army after college. In a 2017 internal speech at the AMMS (Academy of Military Medical Sciences) she said: “只要有矛.才能研究盾.” which translates roughly as, “you need to have an arrow to study a shield.” I believe a Rubicon has been crossed by the world with this pandemic and framing the proper understanding of how we got here, and the proper response will be the critical next steps.

Evidence of adenovirus vaccine sequences in early patients would suggest both that SARS-CoV-2 was created in a laboratory and that there was sufficient priority set on this project to create a specific vaccine for the chimera coronavirus.

When Oppenheimer saw the application of Einstein's physics in the embodiment of the atomic bomb, he is said to have quoted a line from the Hindu scripture, the Bhagavad Gita, which reads: 'Now I am become Death, the destroyer of worlds.'

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The contribution of physics' research to human killing would total less than 300,000 people in two ten-square mile zones in Japan, and the horrors of those events led the world to regulate the raw materials of such bombs and to sanction sovereign nations who attempted to violate the rules.

This had followed the contribution of chemistry to human killing in the form of chemical warfare during World War I, in which 100,000 were killed, and led the nations of the world to an historic agreement to never use chemical warfare again. It is now only 'rogue' operators who violate the norms civilized nations have agreed to.

It seems to be biology's turn to show its dark arts. If it is generally understood that biology/biotechnology has been harnessed to create a pandemic that has killed more people than physics and chemistry research combined, and to be a weapon where no place on earth is safe from its effects (SARS-CoV-2 has been detected in the deepest Amazon jungles and at research stations in Antarctica), there needs to be developed a new set of regulations, rules, etc. to both honor the 1.8 million innocent people who died from COVID-19 and to protect the world so this never happens again. It is also urgent to gather further data to support or refute

if this was a Chinese bio weapons program, as the consequences of that would be significant.”

There is no direct evidence of whether the release was accidental, or deliberate but circumstantial evidence makes it is highly likely it was accidental”

Dr Quay goes on to add that –“*The US government uses the following definitions: “Gain-of-function (GOF) studies, or research that improves the ability of a pathogen to cause disease, help define the fundamental nature of human-pathogen interactions, thereby enabling assessment of the pandemic potential of emerging infectious agents, informing public health and preparedness efforts, and furthering medical countermeasure development.*

Gain-of-function studies may entail biosafety and biosecurity risks; therefore, the risks and benefits of gain-of function research must be evaluated, both in the context of recent U.S. biosafety incidents and to keep pace with new technological developments, in order to determine which types of studies should go forward and under what conditions.”

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“Dual use research of concern (DURC) is life sciences research that, based on current understanding, can be reasonably anticipated to provide knowledge, information, products, or technologies that could be directly misapplied to pose a significant threat with broad potential consequences to public health and safety, agricultural crops, and other plants, animals, the environment, materiel, or national security. ”

For this analysis, the assumption is made that GOF and DURC are largely the same processes and techniques in the laboratory and thus can only be distinguished by direct, documentary evidence of the intent of the research from administrators in the facilities conducting the work.

In the absence of any such documentary evidence that bio weapon research was being conducted or that SARS-CoV-2 is a bio weapon and to take the least inflammatory posture, the initial state for the above prior analysis will be recalculated by eliminating the hypothesis, and its accompanying probability, that SARS-CoV-2 was created as a bio weapon.”

7 Problems with Position of Dr Quay on Bio Weapon Theory

Basically Dr Quay’s logic for eliminating Bio Weapon theory is three fold.

- 7.1 *Circumstantial evidence makes it is highly likely it was accidental*
- 7.2 *Absence of any such documentary evidence that bio weapon research was being conducted.*
- 7.3 ***To take the least inflammatory posture,***

None of the three arguments make any scientific sense. Circumstantial evidence that a Bio Weapon could not have been released in Wuhan finds support from Jamie Metzel and Professor Muller as well. But there are some serious issues with this premise.

Problem 1 Covid 19 as a Bio weapon could have been transported out of Wuhan Institute of Virology for use elsewhere in the world and accidentally leaked during transportation.

Problem 2 Why would Chinese Government ever release documentary evidence that it was engaged in development of Covid 19 as a Bio weapon???

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Problem 3 Least Inflammatory Posture – This is out and out a political argument and has no basis in science. In any case, Dr Quay is patently wrong here. Least Inflammatory Posture is Zoonotic Origin – so why then consider Lab Origin theory at all?

In addition to these three problems Biggest Problem is His Own Position on Most Curious Evidence, – which he did NOT factor in his analysis is as under:

“The most significant evidence provided herein is the finding from RNA-Seq performed by the Wuhan Institute of Virology (WIV) of lavage patient samples collected on December 30, 2019.³ These ICU patients were the subject of the seminal paper, entitled, “A pneumonia outbreak associated with a new coronavirus of probable bat origin,” from Dr. Zhengli Shi and colleagues that first characterized SARS-CoV-2.⁴ This author has confirmed that the RNA-Seq of all five patients contained SARS-CoV-2 sequences.

Surprisingly the specimens also contained the adenovirus “pShuttle” vector, developed by Chinese scientists in 2005 for SARS-CoV-1.⁵ Two immunogens were identified, the Spike Protein gene of SARS-CoV-2 and the synthetic construct H7N9 HA gene.⁶ Hundreds of perfectly homologous (150/150) raw reads suggest this is not an artefact. Reads that cross the vector-immunogen junction are identified.

While adenovirus is a common infection the wildtype viruses have low homology to the vaccine vector sequence, by design, to avoid rejection of the vaccine due to prior exposure to wild type adenoviruses.

Two patients from the same hospital who had bronchial lavage on the same day but had their specimens sent to the Hubei CDC did not have adenovirus vaccine sequences.

Three explanations come to mind from this evidence:

1. These represent sample preparation artifacts at the WIV, such as sample spillover on the sequencer.
2. These patients were admitted with an unknown infection, were not responding to the treatment protocols for a infection of unknown origin, and they were vaccinated with an experimental vaccine in a desperate but compassionate therapeutic “Hail Mary.”

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3. A clinical trial of a combination influenza/SARS-CoV-2 vaccine was being conducted and an accidental release into Wuhan occurred.

Only WIV scientists and Chinese authorities can answer these questions. Until the evidence of the adenovirus sequences has been confirmed by other scientists, this author will not include this evidence in the Bayesian analysis.

Obviously if a vaccine containing the Spike Protein of SARS-CoV-2 was being administered to patients in Wuhan in December 2019 the question of laboratory origin is a settled matter. The remaining analysis is being conducted without the adenovirus vaccine evidence.”

8 Probability of Covid 19 being a Bio Weapon – The RootClaim View

The only known analysis of the Bio Weapon theory can be found on <https://www.rootclaim.com/analysis/What-is-the-source-of-COVID-19-SARS-CoV-2>.

Rootclaim claims to outperforms human reasoning by correcting for the biases and flaws of human intuition. The platform integrates all available evidence, assesses it for credibility and uses probabilistic models to reach conclusions about the likelihood of competing hypotheses. Its conclusions are said to represent the best available understanding of the complexity and uncertainty in our world a platform that

It started with a 16% probability of Covid 19 as a Bio Weapon but reduced to 3.5% after running through 10 filters

Why would anyone investigating death of as many as 4 million people, worldwide and an economic loss running into Trillions of Dollars, want to completely ignore a 3.5% possibility of a particular theory?

A near absence of any discussion on this does not augur well for scientific temper and smacks of self censorship for political reasons.

But first of all – let us see what Rootclaim has to say about Covid 19 being a Bio Weapon

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Bio Weapon Probability

	Start	16%
1	Contagion and Mortality	1.5%
2	Oubreak Location: Wuhan	0.5%
3	Virus Sources near Wuhan	0.3%
4	Chimera	2.4%
5	Furin Cleavage	8%
6	Well Adopted	9%
7	WIV Lab Procedures	6%
8	WIV Disassociation	3.2%
9	Chinese Response	2.2%
10	Missing Evidence	3.5%

Unfortunately, none of the sources that the Author could access had any specific comments to offer on the rationale given for reduction of probability of Covid 19 being a bio weapon and hence he has tried to do it himself by offering Counter View wherever necessary. He has not attempted to quantify his revised estimate except to suggest that the revised probability should be far more than 3.5%

9 Author's Analysis of Rootclaim Projection of Probability

9.1 Contagion and Mortality

View

COVID-19 is more contagious than the typical flu, but not as fatal as recent viruses like MERS or SARS. Overall, it is not particularly well-suited as a traditional bioweapon, and COVID-19 broke out during a relatively peaceful time. This indicates that, if it was used as a bioweapon, it would probably not be released as a method of killing people but for a different purpose such as disrupting the world economy.

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Relevant Factors:

- It is a relatively peaceful time in human history.
- Biological weapons have been used primarily during wars or terrorist attacks.
- Contagious with a long incubation period:

Comparisons to a bio weapon:

- COVID-19 is relatively contagious (more so than the flu), and has a long incubation period without showing symptoms
 - This initially seems like a perfect stealth virus that would make it easy to infect an entire population.
 - These characteristics mean that it cannot be targeted to a location without running the risk of infecting additional populations.
 - Previous bio weapons used materials which could be confined to a specific geographical area of exposure, like anthrax, which is not a contagious disease
 - The 0.5-2% fatality rate of COVID-19 is not as dangerous as other recent diseases like SARS (11% fatality rate, see Abstract), MERS (35% fatality rate, see "Key facts"), or Ebola (50% fatality rate, see "Key facts")
 - This indicates that, if released as a bio weapon, its purpose was not to kill large portions of the population.
 - This differs from other usages of bio weapons as a method of killing as detailed in the starting point
 - In peaceful times such as these, it is conceivable that such an attack could be targeted towards the global economy, or some other purpose.

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Probabilistic Estimates:

Since COVID-19 broke out during a relatively peaceful time, the likelihood of it being a bio weapon is reduced by 5x.

The characteristics of COVID-19 are not similar to traditional bio weapons, narrowing the scope of the "bio weapon" hypothesis to a new type of economic warfare and reducing the likelihood of it having been deliberately released as a bio weapon by an additional 2x, for a total reduction of 10x.

Counter View

This factor has been used to make the single most reduction in the probability of Covid 19 being a Bio weapon. On a detailed analysis, it appears that this very factor should significantly enhance the probability of its being a Bio – weapon.

The View itself offers three cogent reason why Covid 19 **should** be considered a Bio Weapon

Reason 1

“If it was used as a bio weapon, it would probably not be released as a method of killing people but for a different purpose such as disrupting the world economy

Counter Reason 1

The reality is that China is the **ONLY** major economy (i.e. exceeding GDP of One Trillion Dollars) to record the positive growth in 2020 - the year of the pandemic.

Reason 2

In peaceful times such as these, it is conceivable that such an attack could be targeted towards the global economy. The characteristics of COVID-19 are not similar to traditional bio weapons, narrowing the scope of the "bio weapon" hypothesis to a new type of economic warfare

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Counter Reason 2

These are NOT peaceful times between China and India, the only country that seemed to be standing in the way of China's hegemony over Asia, before the pandemic struck and Delta variant ravaged India. .

2020 was the most violent time at the Line of Actual Control between India and China in over four decades. Beginning on 5 May 2020, Chinese and Indian troops engaged in aggressive melee, face-offs and skirmishes at locations along the Sino-Indian border, including near the disputed Pangong Lake in Ladakh and the Tibet Autonomous Region, and near the border between Sikkim and the Tibet Autonomous Region. Additional clashes also took place at locations in eastern Ladakh along the Line of Actual Control (LAC).

In late May 2020, Chinese forces objected to Indian road construction in the Galwan river valley..According to Indian sources, melee fighting on 15/16 June 2020 resulted in the deaths of 20 Indian soldiers and casualties of many Chinese soldiers..Media reports stated that soldiers were taken captive on both sides and released in the coming few days while official sources on both sides went on to deny this. Partial disengagement from Galwan, Hot Springs and Gogra occurred in June–July 2020 while complete disengagement from Pangong Lake north and south bank took place in February 2021..Part of the disengagement deal at Pangong Lake was the withdrawal of Indian troops from positions they had occupied between 29 August to 3 September in the Chushul sector overlooking Chinese fixtures at Spanggur Gap and Spanggur Tso..As on 31 March 2021, there has been no change in the posture of the IAF or PLAAF since the Galwan clash. **On 7 September, for the first time in 45 years, shots were fired along the LAC, with both sides blaming each other for the firing.**

Source: https://en.wikipedia.org/wiki/2020%E2%80%932021_China_%E2%80%93India_skirmishes

Reason 3

The 0.5-2% fatality rate of COVID-19 is not as dangerous as other recent diseases like SARS (11% fatality rate, see Abstract), MERS (35% fatality rate, see "Key facts"), or Ebola (50% fatality rate, see "Key facts")

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Counter Reason 3

An economic warfare implies that the Economy of the aggressor would benefit at the cost of the economy of the victims. The warfare would be meaningless if the warfare were to result in a total collapse of world economy. Indeed that would have been the case. if Covid 19 had the fatality rate of Ebola i.e. 50%. As on date i.e. June 25, 2021, the total cases in the world are 180,787,428. At fatality rate of 50% - more than 90 million people would have been dead leaving global economy comatose for years if not decades.

Thus low fatality rate would actually boost the case for use of Covid 19 as a part of economic warfare NOT detract from it

The Rootclaim analysis ignores that the damage inflicted by Covid 19 is compatible with that by a strategic biological warfare

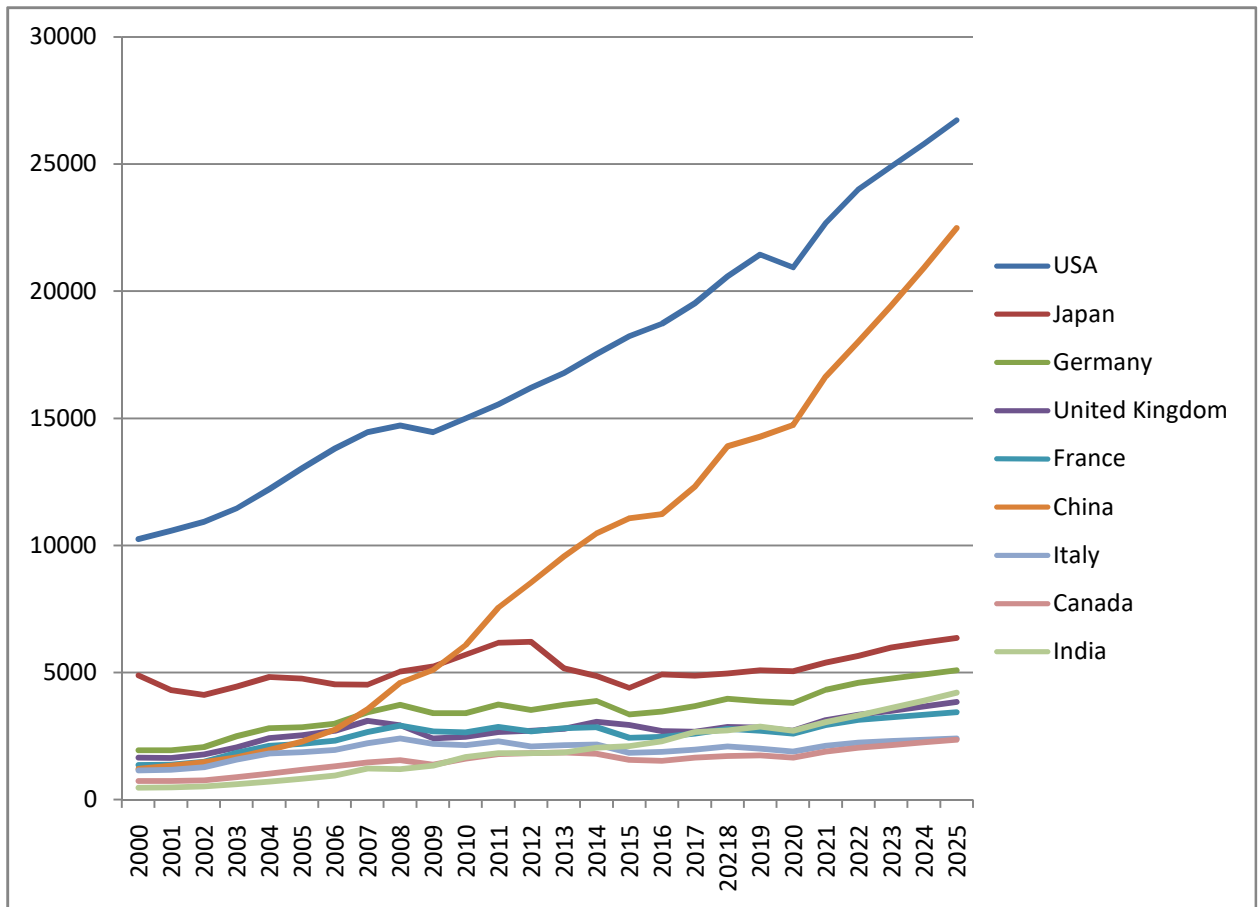
What is a Strategic Biological Warfare?

A very instructive program was telecast on June 10, 2009 on *Biological Warfare and Terrorism – The Military and Public Health Response*.¹. It had resulted from a joint collaboration between United States Army Medical Research and Materials Command and the Center for Disease Control of the Human and Health Services of the US Government. In a prophetic warning the then Secretary of Health and Human Services Dianna F Shalala started off the program by saying that “*make no mistake, these threats (of biological warfare) could become a reality and potentially overwhelm this country’s medical and public health infrastructure.*”

Thereafter Lt.Col. Ted Cieslak, MD of the Operational Medicine Division, US Army Medical Research Institute of Infectious Diseases explained strategic biological warfare. It is one in which a biological agent is used to alter course of global power.. He went to state that there are ‘*very very few biological agents*’ which can launch a pandemic and alter the course of global politics. He named Small pox, plague and anthrax as such biological agents.

From January 2020, we know Covid 19 or SARS 2 is one more such biological agent. **Without any fear of exaggeration or contradiction it , can be legitimately said that Covid 19 has altered the course of global economic power.**

**India and China Compared to G-7
2000 -2025**



As of 2019, China was already well ahead of all nations bar USA. The three economies following China by 2025 are set to be Japan, Germany and India.

Japan

China has a very bitter historical memory of Japanese occupation. During the World War II, China (as also much of South East Asia) was subjected to brutal biological warfare by Japan. Unit 731 of the Imperial Army of Japan is infamous for conducting horrifying experiments on live human beings². Some of them were cut open while still alive without being anesthetized. Furthermore the researchers involved were never prosecuted as War criminals. They were given immunity by the United states in exchange for their data, which was used in the US Offensive Biological Warfare unit that is known to have existed until 1969. So have the Chinese forgiven Japan?.

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They overtook Japan around 2008 and in next ten years, grew their economy three times as big as that of China. Whatever they may have done in World War II, Japan today is forced to treat China with utmost respect.

Germany

China has no serious historical baggage with Germany. In any case, Germany is well entrenched within the larger entity of European Union. Covid 19 did cause the German economy to contract in 2020 while China grew, increasing the gap between the two nations.

India

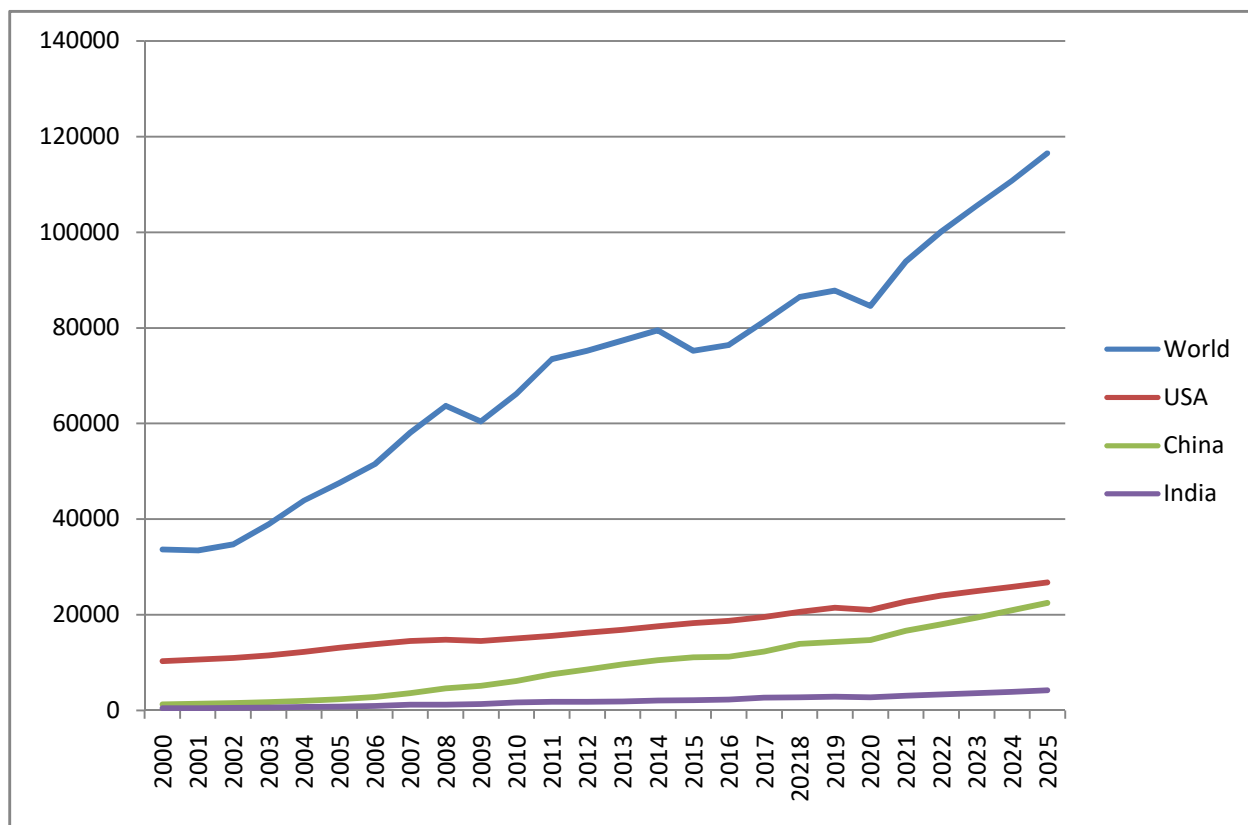
India has a complex relation with China. In 1980, when my generation started its professional life, Indian GDP was \$ 186 billion while China was \$ 191 billion .Forty years later, Indian GDP is \$ 2,860 billion while China is five times higher at \$ 14,280 billion.

Yet China knows well that with a population of 1.3 billion, India is a potentially more serious long term rival than Germany. **Besides economic rivalry and the growing tensions on the border, China and India have many unresolved structural problems between them**

- a) India has given shelter to Dalai Lama since he fled from Chinese occupation of Tibet in late 1950s
- b) Both countries are vying for emerging as a dominant power in Asia and Africa.
- c) The fact that China has a seat in the Security Council with a Veto power while India does not – rankles Indians. On the other hand, China has not forgotten the role of Indian traders profiteering from 19th century opium wars foisted on China by colonial powers.

It is also the nation devastated by the Delta variant on an unimaginable scale just when India's leaders started boasting about having conquered the pandemic and declared themselves as saviours of the world for exporting vaccine to nations who had paid for the same on a commercial basis.

**The State of Global Economy
The Big Picture
2000-2025**



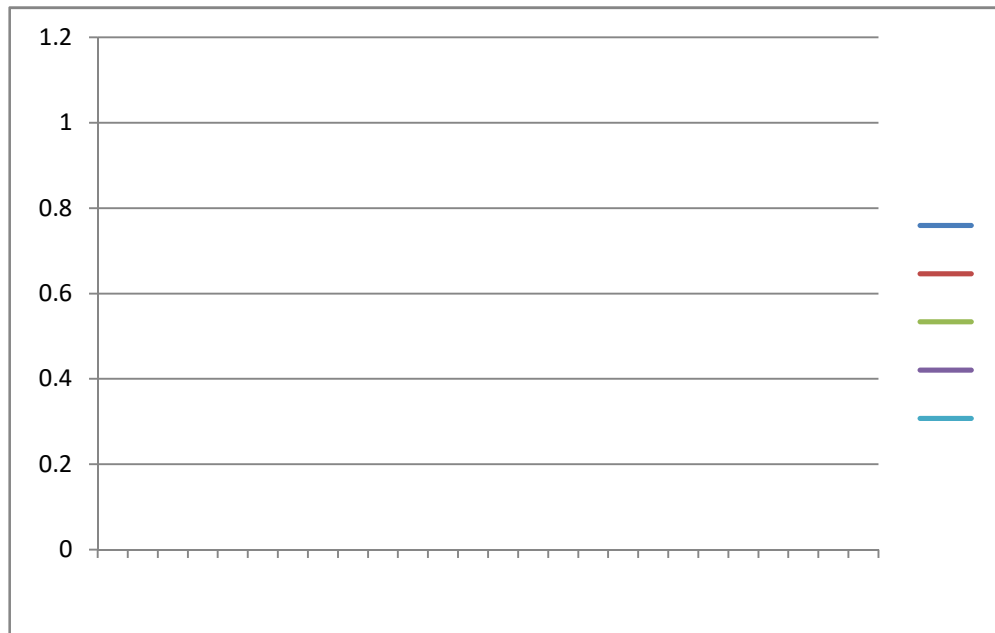
The Gap between USA and China has narrowed considerably and India comes into the picture, though far behind but all projections in respect of Indian economic growth are pre Second wave. The full extent of the economic impact of the second wave is not yet know. In all probability, the Covid 19 and its Delta variant has cost India, two years of economic decline and stagnation even while China continues to gallop ahead increasing the already big gap between them.

Source: <https://statisticstimes.com/economy/countries-by-projected-gdp-growth.php>

BRICS

At one time, Brazil, Russia, India, China and South Africa were considered the BRICS nations, capable of being the locomotive of global economic growth. Here too, China is well ahead but India being in the distant second place but far ahead of Russia which is in the third place..

**BRICS NATIONS
2000 – 2025**



India, which till very recently, was an aspiring super power; has been reduced by the Delta variant to an object of worldwide pity and derision – a failed state or a flailing state, which cannot even provide oxygen to patients in its hospitals.

South Africa and Brazil have not fared much better. Russia has withstood the Covid test but just about and certainly not as well as China.

QUAD

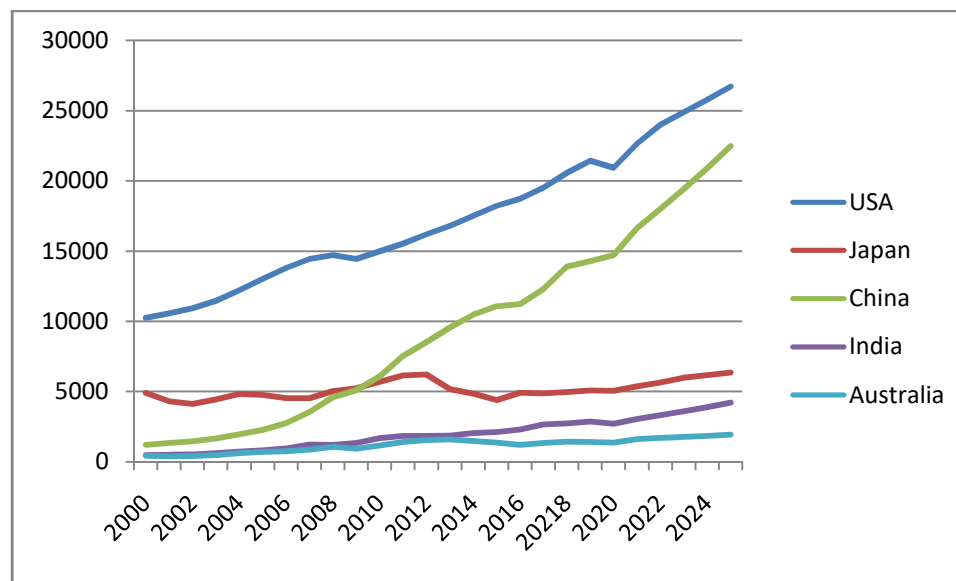
Worried by ascendancy of China, a Quadrilateral Security Dialogue (QUAD) was initiated between United States, Australia, Japan and India between 2006 -2008. Then after a brief hibernation, it was revived in 2017

Due to the Pandemic - Japan was forced to postpone showcase Olympics. Australia has saved itself by shuttering down, not allowing its own citizens to return. The United States – the reigning superpower, was laid low until it bounced back with the help of its technological prowess in the area of vaccine development

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An India devastated by the Delta Variant of Covid 19 is on economically on its own, as can be seen from the tight embrace of Chinese Dragon on QUAD members.

China and QUAD 2000-2025



China is the biggest customer of Japan buying \$ 142 billion.³, i.e. 22% of its total exports while India accounts for only \$ 13 billion⁴ or 1.8% of Japanese exports. Australia is far more dependent on China for its exports (34%) and imports (25%) Total financial transaction of Australia with China is about \$ 144 billion, 10 times that with India⁵

The US has, with China, an annual financial transaction of \$ 788 billion⁶ against \$ 197 billion with India⁷. US has another big financial dependence on China. The dollar COFER⁸ for individual countries is not known. Globally \$ holding accounts for 60% of foreign exchange reserves⁹. On this basis China holds US \$ assets worth about \$ 1.9 Trillion. A big strategic lever over US.

IMPACT OF CONTAGION AND MORTALITY OF COVID - 19

It will not be out of place to quote Dr David Asher, Senior Fellow of the Hudson Institute from a Virtual Discussion The Origins of COVID-19: Policy Implications and Lessons for the Future | March 12, 2021¹⁰

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“The world of biology that Andy and Jamie have been writing about and warning about for years, where you could use even the common flu and other viruses as exceptionally good weapons.

If you believe, as I do, that this might have been a weapons vector gone awry, not deliberately released but in development and then somehow leaked, this has turned out to be the greatest weapon in history. You've taken out 15% to 20% of global GDP. You've killed millions of people. The Chinese population has been barely affected. Their economy has roared back to be number one in the entire G20.

It doesn't mean that they did this, but when you look as I do having run criminal investigations as well, you've got to say, "Motive, cover up, conspiracy." All the hallmarks of guilt are associated with this thing.

The fact that the initial cluster of victims surrounded the very institute that was doing the highly dangerous if not dubious research is significant. And the fact that they massively covered it up, destroyed evidence, and denied access in a way that they didn't do in SARS-COVID-1 back in 2002, 2003. I was the Senior State Department Official involved in discussing that issue with the Chinese government and they had more than enough to tell us about that. They kept it pretty secret from our own people, but they did warn us that they had a big problem on their hands. In this case, they told us nothing”

One need not necessarily agree with Dr Asher but that a **biological agent Covid, 19 has altered the course of global power is a Fact and that is a key hall mark of Strategic Biological Warfare .**

THEREFORE this one factor alone ought to significantly enhance the probability of Covid 19 being a Bio Weapon and NOT reduce it as Rootclaim has done.

References

- 1 <https://www.youtube.com/watch?v=fowreAPpQeE>
- 2 https://en.wikipedia.org/wiki/Unit_731
- 3 <https://tradingeconomics.com/japan/exports/china>
- 4 https://www.mea.gov.in/Portal/ForeignRelation/India-Japan_Bilateral_Brief_feb_2020.pdf
- 5 <https://wits.worldbank.org/countrysnapshot/en/AUS>
- 6 <https://ustr.gov/countries-regions/china-mongolia-taiwan/peoples-republic-china>
- 7 <https://ustr.gov/countries-regions/south-central-asia/india>
- 8 Currency Composition of Official Foreign Exchange Reserves
- 9 <https://data.imf.org/regular.aspx?key=41175>

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- 10 Virtual Event | The Origins of COVID-19: Policy Implications and Lessons for the Future
<https://www.hudson.org/events/1934-virtual-event-the-origins-of-covid-19-policy-implications-and-lessons-for-the-future-32021>

9.2 Location – Wuhan

View

- A bio weapon would be more likely to be released in an urban area, especially if the point was to attack the economy (as reasoned before, due to the highly contagious nature of COVID-19)
 - Wuhan isn't a particularly desirable target for a bio weapon to be released. It is not a capital city so it doesn't have a large psychological effect. Although China is the second largest economy in the world, there are much better targets in China and around the world. It is the 9th largest economy in China, but it doesn't make the top 100 economies in the world.
- Since there are rumors that Wuhan contained a Chinese bio weapon lab, this could be a potential location to release a bio weapon to make it look like a lab escape, so that the actual source of the virus would not be suspected. However
 - Rumors of a bio weapon facility were circulated mostly after the outbreak of COVID-19 (a Google search for key terms before December 2019 revealed almost nothing relevant).
 - Since a pandemic could naturally break out in many cities, the first priority would probably be having the biggest effect and not releasing it somewhere near a bio weapon lab.

Because Wuhan is not a particularly attractive target in terms of economy or psychology, its initial likelihood as a target is estimated in proportion to its portion of the global urban population: 0.2%. One particular reason to target Wuhan is the presence of the Wuhan Institute of Virology - since the release of a virus could be blamed on a lab leak.

Therefore, this likelihood is increased 5x, bringing the effective likelihood to 1%.

Supporting View

Wuhan could not have been the intended target release for a bio-weapon. It could be a case of accidental release of the Bio weapon while transporting it FROM Wuhan to the intended target outside China. Is it not curious that Wuhan Metro Line 2 is blamed for spreading of the virus world wide with its connection to the Wuhan International Airport but not a whimer is raised as to how the virus – whether of natural origin or lab leak simply resulted in its export outside China without spreading to other provinces of China itself?

The effective likelihood therefore has to be significantly enhanced.

9.3 Virus Sources Near Wuhan

View

There are no obvious natural sources for COVID-19 in the Wuhan area (Hubei province). The most similar coronavirus is found among bats that don't live nearby, and scientists have not been able to pinpoint the exact point where SARS-CoV-2 transferred to humans. On the other hand, the initial cluster of cases in the Wuhan wet market is significantly more likely if the virus originated Zoonotically.

Wet market: If the source was either a lab escape or a bio weapon, then the wet market is no more likely than the many other possible breakout locations in Wuhan. If it was certain that the wet market was the breakout location this would have a very large effect based on the large number of such locations, perhaps by 50x. But since it is not certain, this potential breakout location reduces the likelihood of a lab escape, Zoonotic collection, or bio weapon by 20x.

Not finding the origin is more likely if the virus was developed in a lab (either as a bio weapon or during gain of function research), since it would not exist in nature. However, the overall impact is conservatively assumed to be negligible, as it often takes a while to find animals with viruses that originated Zoonotically.

Counter View

The View is dated. Further more – as noted earlier, Wuhan Wet market is no longer considered as the source of the pandemic. The blog of Jamie Metzler – Origins of SARS-Cov-2 / <https://jamiemetzler.com/origins-of-sars-cov-2/>, notes –

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“A Broad Institute study asserts that genetic examination of four samples containing the virus from the seafood market to those taken from the Wuhan patient are ‘99.9 per cent’ identical. This suggests it came from infected visitors or vendors, indicating ‘Sars-CoV-2 had been imported into the market by humans’. The authors found no evidence ‘of cross-species transmission’ at the market”.. It also states - “After months of speculation and with the market origin story indefensible, the Chinese Centers for Disease Control and Prevention finally admitted only in late May 2020 that it has ruled the site out as the origin point of the outbreak. According to Gao Fu, the director of the Chinese CDC, “It now turns out that the market is one of the victims.”

As such, now this factor should contribute to increasing the probability of the Bio weapon and not reducing it.

9.4 Chimera

SARS-CoV-2 has parts in common with two different viruses, but those individual viruses do not share these similarities with each other, indicating it is a chimera. Such chimeras are found both in nature and in labs that conduct gain-of-function research. However, this specific chimera seems less likely to combine in nature, while the WIV is known to have access to both viruses

Chimeras are often created in labs, and the WIV could have produced this particular chimera. WIV knows of both CoV RaTG13 and pangolin CoV, and could have accessed both virus strains.

For such a combination to happen naturally, an animal needs to be infected with both viruses simultaneously in order for them to exchange genetic material, and there needs to be enough time for the other mutations to arise naturally

- Chimeras happen occasionally, when an animal is simultaneously infected with both a virus typical to its species and a virus that had crossed over from another species
- Chinese pangolins and bats don't usually cohabit, making this somewhat unlikely in nature
- Bats have been found cohabitating with the giant pangolin in Africa, but their burrows are much larger than those of Chinese pangolins.

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- Giant pangolin burrows are 30-60 cm wide and up to 100 feet (30m) long
- Chinese pangolin burrows are 5-41 in (13-104 cm) wide and 1.5-11 feet (0.5-3.3m) in length.
- Coronaviruses from both bats and pangolins were studied in Chinese labs, where they could have mixed naturally, without human intervention on the genetic level. It is also possible for the two to come in contact if smugglers were storing or transporting many different types of animals.
- The dwindling pangolin population makes this less likely to have occurred naturally. Additionally, there could be an intermediate host that wasn't yet identified.
- The pangolin strain with a matching RBD may not exist in nature
- **All the matching samples are from one batch of smuggled pangolins, so they may have all caught the virus from the same host.**
- In this case, WIV research may have been the only place for such a recombination event involving these known viruses (although there could be another virus with a similar RBD that has not yet been identified)
- **If SARS-CoV-2 developed naturally, its ancestors have not yet been identified.**
- Receptor binding studies of reconstituted RaTG13 showed that it does not bind to pangolin ACE2, so if there was a pangolin recombination event, it probably involved a virus other than RaTG13.
- The 96% similarity between SARS-CoV-2 and RaTG13 (found in 2012) suggests many decades of mutations, meaning that a Zoonotic ancestor has not yet been identified.
- The WHO mission failed to find any conclusive Zoonotic source

Probabilistic Estimates:

Chimeras are created on a regular basis in labs, and the WIV could have created this chimera via a process they have employed before using two viruses that they had access to. At the same time, this chimera is less likely to occur in nature, and it is unlikely that mutations in the known potential Zoonotic ancestors would have resulted in SARS-CoV-2.

Therefore, the likelihood that COVID-19 emerged Zoonotically is decreased by 10x.

Additional View

The Author offers no Counter view except to point out that For about six months, the pangolin, a scaly anteater, was suspected to be the intermediate host but finally Dr. Daszak reported that CoV-2 was not found in pangolins in the wild or from the (illegal) market trade.

<https://link.springer.com/article/10.1007/s10393-020-01503-x>

9.5 Furin Cleavage

View

SARS-CoV-2 has a furin cleavage site - an amino acid sequence that causes the protease furin to cut the virus in a way that facilitates its entry into cells. This feature is missing in related coronaviruses, and its placement in the genetic code looks like an insertion rather than a mutation, making it less likely to develop in nature.

Confidence: 90% (probability of 1/10 the effect analysis is wrong)

Relevant Factors:

The furin cleavage site is part of what makes SARS-CoV-2 especially contagious

- Furin cleavage sites are not common in other related coronaviruses, and did not appear in other coronaviruses related to SARS-CoV-2
- SARS and many SARS-related coronaviruses found in bats (including RaTG13) do not utilize furin and do not have cleavage sites

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- MERS, a different type of coronavirus, seemed to have a furin cleavage site, although it probably didn't contribute to infection. One study questioned whether furin contributes to MERS-CoV infectivity in cell culture. Another study concluded that furin does not play a role in the entry of MERS-CoV into cells

The code for the furin cleavage site in SARS-CoV-2 is notable because it is present where there wasn't one in other related viruses like RaTG13 and Pangolin M789 (see Royal Genealogy), and it looks like it was inserted into the existing sequence rather than being generated by nucleotide mutations.

At least one other coronavirus, RmYN02, has a furin cleavage site in a similar location. Some posit that the fusion cleavage site in RmYN02 evolved by insertion. An examination of the nucleotides makes this look like a nucleotide mutation and not an insertion.

Although the cleavage sites can increase human infections, there may be evolutionary disadvantages to such recombinations in the wild, explaining why it is not prevalent.

In contrast, various gain-of-function experiments have researched the effect of adding furin sites to coronaviruses. US researchers created a SARS mutation with a furin cleavage site in 2006. Additional Japanese, Dutch and other scientists have conducted similar research. Chinese scientists did this as well with a live chicken coronavirus in 2019.

The furin cleavage site in SARS-CoV-2 includes two subsequent appearances of the amino-acid Arginine, both encoded with the nucleotide codons CGG. The CGG codon is not common, found in only 5% of SARS-CoV-2 or RaTG13 arginines, and this is the only case where two successive CGG codes are found. Using this unique code may have advantages in a lab setting, for example for easier identification of the modified virus.

Probabilistic Estimates:

Adding a furin cleavage site is a known procedure in gain-of-function research involving coronaviruses, while almost no other SARS-related coronaviruses contain furin cleavage sites (out of hundreds of related viruses). Since this virus resulted in a pandemic, it is much more likely to have such a feature, and we thus conservatively estimate it is equally likely for a zoonotic virus and a gain-of-function virus.

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However, the placement in the genetic code looks like it was the result of an insertion and not a mutation, which is estimated to be at least 5x less likely to occur Zoonotically. Additionally, it is estimated that the appearance of two successive CGG codons are at least 3x less likely if SARS-CoV-2 developed Zoonotically.

Therefore, the likelihood that COVID-19 developed Zoonotically is reduced by 15x, conservatively adjusted to 10x.

Evidence

The furin cleavage site is part of what makes SARS-CoV-2 especially contagious.

Sources: Markus Hoffman, et. al.

Dr. Robert Garry, virologist at Tulane University in New Orleans, Louisiana

A newly isolated bat SARS-like coronaviruses, RmYN02, contains a multibasic furin cleavage site.

Source: Cold Spring Harbor Laboratory

Counter View – None

9.6 Already Well Developed

It appears that there was one index case of COVID-19, rather than multiple jumps from nature to humans, as was the case in many other pandemics. Additionally, SARS-CoV-2 was already well adapted for human infection from the first known cases.

Confidence: 80% (probability of 1/5 the effect analysis is wrong)

Relevant Factors:

Viruses often mutate after a Zoonotic jump, but SARS-CoV-2 seemed to be well adapted for human infection from the first known cases

A successful virus will often develop mutations and generate new strains as it adapts to the host-specific immunological defenses of a new host species.

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- Avian flu (H5N1) caused a number of human deaths, but did not rise to epidemic proportions because it was still suited to birds, and did not develop mutations that would allow for easier human-to-human transmission.
- SARS-CoV-2 showed high affinity with human ACE2 and mice hACE2 receptors. Transgenic mice with human hACE2 are used for Sars-CoV research. SARS-CoV-2 showed very weak binding to bat ACE2. This is less likely if bats were the zoonotic source.
- **The furin cleavage site in SARS-CoV-2 is very well suited for human airway cells. The furin cleavage site quickly mutated away in non-human cells. The furin cleavage site was extremely stable in human airway cells.**
- There was one index case of COVID-19, as opposed to many other pandemics that started with multiple Zoonotic jumps, which matches well with a lab leak.
- Other pandemics are characterized by genome base diversity even in early stages, indicating multiple Zoonotic jumps.
- One analysis suggests that MERS has jumped from camels to humans hundreds of times. An astounding 137 out of 255 of the earliest human infections of MERS and CoV-1 studies are attributed to independent zoonotic infections and not human-to-human infections. It seems that HIV jumped from chimpanzees to humans at least four separate times.
- Early cases of SARS-CoV-2 showed limited genetic diversity, indicating that it started with a single index case. A single source is expected from a lab escape (one infected lab worker, one animal escaping), but is not so likely if there was a Zoonotic origin.
- Alternatively, it's possible that multiple mutations could have developed from a single person in order to adapt to human hosts, even if there was a Zoonotic origin.
- There is a known case of COVID-19 in which a virus mutated over the course of a few months inside one immune compromised individual receiving various treatments, resulting in viruses with multiple new mutations.
- However, it seems that would require a very unique individual contracting the disease at the very beginning of the pandemic, so it is less likely.

Probabilistic Estimates:

The single infection point and capacity for human infection from the beginning increases the likelihood of a lab leak or bio weapon by an estimated 2x.

Counter View **None**

9.7 WIV Lab Procedures

There is some weak evidence regarding lax security and procedures at the Wuhan Institute of Virology.

Confidence: 90% (probability of 1/10 the effect analysis is wrong)

Relevant Factors:

The majority of lab infections and undetected leaks are due to human error. Indicators of lax security and procedures at the Wuhan Institute of Virology, which would increase the likelihood that it escaped from the local lab:

There were bio containment security failures in Wuhan laboratories, including at least one WIV project from 2017 Coronaviruses and other pathogens were found in a sequencing laboratory in Wuhan outside of the biocontainment labs. One of the coronaviruses was found in a dataset of mice (*Mus musculus*) from WIV in 2017. In 2018 there were allegations that WIV's procedures were subpar. A 2019 Chinese review team confirmed that there were five non-conformities at WIV

Mitigating Factors

- The 2019 Chinese review also offered constructive criticism and outlined the changes that needed to be enacted.
- A document on the lab's official website (which has been removed) said that the review team gave a high evaluation of the lab's overall safety management
- Any high level lab would face at least some criticism and any audit would make suggestions on how they could improve. Some non-Chinese scientists who have visited the lab have praised its standards and safety conditions and said they were on par with labs in the US and Europe.

Probabilistic Estimates:

Labs with lax security and procedures are conservatively estimated as 2x more likely to produce a lab escape (either from the lab directly or during the collection process). However, since the reports are not very reliable, and safety procedures may have been updated, this is reduced to 1.5x.

Counter View

It is difficult to understand the impact of lack of procedures or otherwise on the prospect of development of a Bio weapon in the lab. At best, it can be said that a Bio weapon should not be developed in a lab where safety standards are lower. This is far cry from stating that in such a lab Bio weapons could not have been developed.

The Author therefore strongly disagrees with reduction of probability of Covid 19 being a Bio weapon from 9% to 6% on this account.

9.8 WIV Disassociation

The WIV explicitly stated that they were not working on SARS-CoV-2 prior to the outbreak.

However, on December 30, when Dr. Shi Zheng-Li was informed of the COVID-19 outbreak, changes were made to her bat virus database, making it look like she was trying to dissociate her lab's research from the COVID-19 outbreak.

Then, in January 2020, WIV researchers published a paper claiming to have found a previously unknown coronavirus named RaTG13 that was a 96% match with SARS-CoV-2. But RaTG13 is a new name given to BtCoV/4991, a coronavirus that the WIV discovered (along with many other viruses) when they examined a bat cave after six miners contracted a pneumonia-like disease and three died.

This, and other anomalies surrounding WIV's handling of RaTG13, are indicative of attempts to minimize WIV involvement.

Confidence: 60% (probability of 1/2.5 the effect analysis is wrong)

Relevant Factors:

The WIV said they were not working on SARS-CoV-2 prior to the outbreak.

- If the lab didn't actually have any similar samples that would be very meaningful, but there is no independent verification that this is true, especially since they didn't release a full list of everything being studied at the lab.
- **The WIV has no incentive to say that the virus came from the lab.**

Dr. Shi Zheng-Li's reaction

On December 30, when Dr. Shi Zheng-Li was informed of the COVID-19 outbreak, changes were made to her bat virus database. She had previously said that it included data on virus variants in other wild animals, but certain terms such as “bat,” “rodent,” and “virus” were replaced with “wild animal samples,” “viral pathogen data,” “emerging infectious diseases,” and “cross-species infection.”

The database was later deleted.

This kind of behavior makes it look like Dr. Zheng-Li was trying to dissociate her lab from the COVID-19 outbreak. Dr. Zheng-Li has been associated with coronavirus research and bats for years, and had already warned of an outbreak like this occurring, so an attempt to disassociate herself or her lab from zoonotic coronaviruses seems futile.

The speed with which Dr. Zheng-Li reacted is somewhat suspicious, since in December 2019, at the beginning of the outbreak, it was not immediately obvious that COVID-19 had bat origins.

It seems strange that Dr. Zheng-Li immediately started to dissociate her lab from the COVID-19 outbreak unless she already knew that it had bat origins. However, it doesn't require a large logical leap to link COVID-19 with bats. Many other coronaviruses have bat origins. Dr. Zheng-Li and other scientists had been warning about bats as coronavirus reservoirs for years. SARS was believed to have originated in a bat population.

Overall, Dr. Zheng-Li's reaction is more likely if she knew that COVID-19 could have escaped from her lab.

Anomalies surrounding RaTG13, the closest known relative of SARS-CoV-2 (96% similar)

- There were some irregularities regarding the sequencing of RaTG13. It G13 was fully sequenced in 2018. A paper published by WIV researchers in February 2020 implied that RaTG13 had been sequenced only after the COVID-19 outbreak (“We carried out full-length sequencing on this RNA sample”). The WIV paper referenced RaTG13 without mentioning that it was previously known and sequenced as BtCoV/4991.
- Long after the relationship was pointed out, an addendum published in November 2020 by Shi and her co-authors confirmed that BtCoV/4991 is indeed identical to RaTG13
- Why was BtCoV/4991 renamed as RaTG13?
 - According to Dr. Zheng-Li, the virus had only been partially sequenced when it was first published as BtCoV/4991 in 2016, and when technological developments enabled the full sequencing, it was eventually renamed RaTG13 to reflect the bat species, location, and the year the samples were obtained..
 - However, this explanation does not address why the authors themselves didn't initially mention that they had previously published this virus, and why they only acknowledged the connection months after being asked if this was a new name for the same virus.
 - If RaTG13 was actually the basis for SARS-CoV-2, it may not have been published in full because they were still working on it (the 2016 paper may have been part of that research). In that case, after COVID-19 broke out, they could have released the information about RaTG13 in 2020 in order to misdirect attention to a possible natural origin.
 - Renaming the virus without connecting it to BtCoV/4991 would further support the claim that RaTG13 wasn't being used in active research and had just been found in the search for a virus that was similar to SARS-CoV-2.
 - Claiming that BtCoV/4991 had been only partially sequenced and that they didn't keep any copies of the original BtCoV/4991 would mean that it could not be compared to RaTG13 or SARS-CoV-2 so it could not be definitively proved that RaTG13 is actually BtCoV/4991

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- A paper co-authored by Dr. Shi Zheng-Li that analysed novel features of RaTG13 and similarities to SARS-CoV-2 did not note the furin cleavage site. Since she had previously researched furin cleavage sites in coronaviruses, and should have identified it, this may have been an attempt to divert attention.
- The director of the WIV biosafety lab, Yuan Zhiming, initially denied that RaTG13 came from the Mojiang mineshaft.

Probabilistic Estimates:

The actions of the WIV conservatively increase the likelihood of a lab escape by 2x and a Zoonotic collection by 1.5x.

If the virus came from a deliberately released bio weapon, the WIV is not a likely source, making this evidence irrelevant.

Counter View

The view *“If the virus came from a deliberately released bio weapon, the WIV is not a likely source, making this evidence irrelevant”* and consequently reducing the probability of a Bio weapon from 6% to 3.2% defies logic.

We need to take into account the possibility that Covid 19 is a Bio weapon and simply got wrongly released in wuhan instead of its intended target elsewhere in the world. Such a possibility explains why WIV/Dr Shi chose to disassociate themselves from Covid 19 leaking from their lab.

Thus on this account, the probability of Covid 19 being a Bio weapon needs to be increased – not reduced.

9.9 Chinese Response

The official Chinese response was not transparent, though not particularly surprising even if the virus developed zoonotically. They restricted WHO access, destroyed samples, and withheld information, which might be construed as an attempt to hide evidence that could be used to blame China for COVID-19.

Additionally, they sent Major General Chen Wei from the Academy of Military Medical Sciences to oversee COVID-19 efforts at the WIV, which could potentially indicate the involvement of a bio weapon, but it is probably immaterial.

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The Chinese government was not transparent at first: they did not share information and silenced Chinese doctors who were talking about COVID-19, didn't release the sequenced genome (until after it was already leaked by an individual researcher), and destroyed some samples of SARS-CoV-2.

Indicators that China was responsible for the COVID-19 pandemic:

- If there was concern about China being held responsible then the government would be more careful about controlling information
- **This could indicate that there was a lab mistake that led to a pandemic, or that they were developing bio weapon.**

Alternative explanations

:

- Many governments withhold some information even when they're not at fault
- There may have been concerns China could be blamed simply for conducting risky research, even if COVID-19 was zoonotic in origin. China explained that they destroyed some samples due to safety concerns, when those samples were not contained in secure facilities. The Chinese position is that they were forthright and shared information as it was confirmed to be reliable.

China's interactions with the WHO investigative team lacked transparency:

- China initially refused to allow an international investigation led by the WHO.
- Strong limitations were imposed on the WHO team that was eventually allowed in, a year after the initial outbreak. China secured veto rights over participants and insisted its scope encompass other countries as well. The team didn't receive raw data regarding the earliest infections. WHO team members said they didn't have the mandate, expertise, or access to investigate a potential lab leak
- Peter Daszak says the WHO team had full access to everything they asked for. However, he is motivated to focus on a zoonotic source, as he himself supported gain –of-function research, including coronavirus research and partnered with the WIV.

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- These interactions with the WHO investigators seem to imply guilt. Alternatively, China may have just been protecting unrelated proprietary material in their labs. Additionally, China could be concerned about other negative findings unrelated to a lab leak

Journalists were barred access to the mine where RaTG13 was found.

- The journalists claimed that they were stopped by plainclothes policemen. There were some concerns when Major General Chen Wei went to oversee COVID-19 efforts at the WIV, but the arguments are probably immaterial.
- **There is some evidence that she has connections to a bio weapon program: Wei is China's top bio warfare expert.** There is a much stronger explanation for why Wei would be involved, as she is recognized as a top expert in her field, with ideal qualifications to head a pandemic response. Wei is a leading epidemiologist and virologist, the doctoral supervisor of the Academy of Military Medical Sciences (AMMS), and an academic at the Chinese Academy of Engineering. She also has key experience combating epidemics as a leading figure in a team of experts at China's Biological Hazards Prevention and Control Program. She made great contributions in fighting SARS, and treated many other viruses including Ebola and anthrax. The WIV is probably the best suited lab in China to work on a vaccine for COVID-19.
- It has been claimed that Huang Yan Ling, who worked at the WIV, could not be located after rumors that she was the first to contract COVID-19. Ling disappeared, and her biography and image were deleted from the WIV website. Chinese officials censored online reports about Ling. An impersonal message was posted from Ling's WeChat account asking people to ignore rumors about her. A Chinese news agency claimed that it had spoken with her new employer but provided no other details.

Probabilistic Estimates:

Many aspects of this response are likely under all scenarios, but overall this increases the likelihood that COVID-19 escaped from either a lab or a research team after collection by 1.5x.

Counter View

Given the range of evidence presented, it is surprising that probability of Covid 19 being a Bio weapon is reduced instead of being increased.

9.10 Missing Information

No one from the Wuhan Institute of Virology was reported as being infected with, or dying from, COVID-19, and no one has come forward to give first hand testimony or evidence of any link between COVID-19 and a lab, even though some doctors and researchers have spoken out about other incidents where they believed that China mishandled information regarding COVID-19. There were also no published records of SARS-CoV-2 in virus databases or research grants.

Confidence: 80% (probability of 1/5 the effect analysis is wrong)

Relevant Factors:

Likely methods by which a virus could escape from a lab to cause a pandemic include Researchers getting infected while collecting samples. A lab worker getting infected. Since many COVID-19 cases are asymptomatic or very mild, it is very possible that the lab worker would not be aware of the infection, and they may have spread it only to strangers (e.g. in public transportation). Improper disposal of waste materials containing the virus, which then infects someone not associated with the lab. Some WIV researchers were sick before the breakout, and the US suspects that there were early COVID-19 infections at the WIV. There were confirmed sicknesses at the WIV. They may have been routine flu-like infections. The WIV claimed that staff tested negative for SARS-CoV-2

The US may have additional reliable information. There are reasons to doubt the reliability of this statement. No details or concrete evidence was released. This statement could have been a parting shot at China before President Trump left office.

Reasons to believe there were no infections:

The staff health monitoring program did not report COVID-19 or other respiratory illnesses during the weeks or months prior to December 2019. There was no serological evidence of SARS-CoV-2 infection in lab workers.

Would there be a Whistleblower?

In case of a lab escape, there is a good chance people in the lab would know or suspect it. There is some chance one of them would choose to go forward, either publicly or anonymously, despite the personal cost. For example, doctors like Li Wenliang and Yan Li-Meng have come forward to share their experiences because they felt the Chinese government mishandled the situation.

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If the virus was a bio weapon, the details would be kept confidential to trusted military or government figures with an interest in keeping the information secret. A terrorist organization may choose to publicize the attack, but that is less likely for an economic weapon, as indicated by the previous evidence. There were no published records of SARS-CoV-2 in virus databases or research grants. If SARS-CoV-2 was developed in a lab, it could have been listed in a grant or could have appeared in a published paper prior to the pandemic. On the other hand, many unpublished novel viruses including coronaviruses were found in Wuhan.

Probabilistic Estimates:

If the pandemic was a result of an incident at the WIV, we would expect there to be incidents within the WIV. However, WIV personnel might not be aware of the initial leak or they might choose to hide it. The lack of such reports lowers the likelihood of a lab escape by 2x and a zoonotic collection by 1.5x. If the virus came from a deliberately released bio weapon, it could have been produced in many locations throughout the world, and the WIV is not a likely source of infections, so the lack of infections at the WIV does not affect that hypothesis. However, there were no reported whistleblowers from other sources where the bio weapon would have been produced, reducing the likelihood by 1.2x.

Counter View

Missing Information is missing information that calls for investigation rather than being used to change probability one way or the other

10 Author's Conclusions on Probability of Covid 19 Being a Bio Weapon

That Covid 19 is a lab leak and a direct result of a Gain of Function research appears to be a probability that can no longer be dismissed. What remains to be seen is whether the Gain of Function research was being done in China with – as in many laboratories across the World, to find a Vaccine in the event of a pandemic breaking out or with more sinister motives remains to be seen.

Rootclaim remains the only source which did analysis with respect to the probability of Covid 19 being a bio weapon and reduced it to 3.5% from Initial State of 16%. Even 3.5% probability is high when more than 4 million deaths have occurred.

The Author's view based on arguments detailed above is that the probability is significantly higher than 3.5% and is estimated below

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% Probability of Covid 19 being a Bio Weapon

		Rootclaim view	Author's View	
	Initial State	16		
1	Contagion and Mortality	1.5	Strongly Disagree retain at Initial State	16
2	Outbreak Location: Wuhan	0.5	Strongly Disagree no case for reduction	16
3	Virus Sources near Wuhan	0.3	Strongly Disagree no case for reduction	16
4	Chimera	2.4	Agree but to be safe increase only by 1.1 and not the RC factor	17.6
5	Furin Cleavage	8	Agree but to be safe increase only by 1.1 and not the RC factor	19.36
6	Well Adopted to Humans	9	Agree but to be safe increase only by 1.05 and not the RC factor	20.32
7	WIV Lab Procedures	6	Disagree - No case for reduction	20.32
8	WIV Disassociation	3.2	Disagree - No case for reduction	20.32
9	Chinese Response	2.2	Disagree - No case for reduction	20.32
10	Missing Evidence	3.5	Disagree - No case for increase	20.32
	Final Conservative View			20

20% probability is without doubt something that warrants a serious investigation into whether or not Covid 19 is indeed a Bio Weapon

11 The Key to the Mystery – Origin of Delta Variant

Any investigation into whether or not Covid, originated naturally or in a lab is necessarily contingent upon cooperation of China. There are no signs of any such cooperation emerging.

With a 15 trillion dollar economy that is second only to the United States in the World, having a Veto power in the Security Council, a nuclear power state like China simply cannot be coerced into cooperation.

Inflammatory calls for Reparations from China when even Lab Leak, let alone Covid 19 being a bio weapon, is proven, is hardly helping matters

The Communist Party of China does not allow an investigation because it fears that were Covid 19 be proved to have originated in a lab resulting from a Gain of Function research for whatever motives, the resulting outrage **within** Chinese Society will force it out of power. Such an outrage can hardly be expected to result from any assessment of the Intelligence Community of the United States

But where is scientific proof going to come from if no access to data or records within China – where the Virus originated from, is allowed. And without convincing scientific proof, people of China cannot be expected to side with Outsiders against their own Government which has powered their nation to the very top of the World.

So this is a Catch 22 situation.

The Author submits that the answer lies in investigating the Origin of the Delta variant for the following reasons..

11.1 The Delta variant emerged from India. Repeated mutations have had to occurred within India before it emerged in its highly infectious form. The trail of mutations of Covid 19 into Delta variant has to lie within India. Whatever data that is required to prove whether or not the Delta variant is a natural mutation or a synthetic pathogen lies within India.

11.2 India is not an Outlier State with respect to following or not following Covid 19 protocol. It did some terribly wrong things such as holding massive religious festivals, holding mask less election rallies, goof ups in vaccine procurement but so did many many other countries.

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- 11.3 The carnage that India witnessed between April – June 2021, was not entirely attributable to these events but for the Delta variant, India could possibly have got away.
- 11.4 After all India did hold similar elections in the State of Bihar in November 2020 without there being witnessing anything remotely similar to the horrible scenes for relatives of hospitalized patients begging for oxygen.
- 11.5 India was also extremely careless in guarding itself There was no Genome sequencing worth the name, being carried out. It simply had no knowledge that the ravages of the second wave were fuelled by Delta variant of Covid 19.**

Finally India has no reason whatsoever to block any serious credible scientific investigation to uncover the trail of mutation. Well known Chinese scientists can be invited to participate in the investigation. If they refuse, that is their prerogative. However, in that case, the results of the investigation cannot become tainted

The Author will therefore like to conclude on the note that there is an urgent need to investigate the origins of the Delta variant and establish whether it resulted from natural mutation or is a synthetic pathogen.

This seems to be the only way of coming to some definitive conclusion on the issue of the Origins of Covid 19 in the short term.