New Report Claims to Shed Light on SARS-CoV-2 Origin

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STORY AT-A-GLANCE

- A paper by Dr. Li-Meng Yan — a former researcher at the University of Hong Kong School of Public Health, a top coronavirus research lab — claims to present evidence showing SARS-CoV-2 likely underwent genetic manipulation
- Yan previously accused the Chinese government and World Health Organization representatives in Hong Kong of covering up the Wuhan outbreak
- On the morning of September 14, 2020, Yan posted a link to her paper on Twitter. Shortly thereafter, she posted another tweet saying Zenodo was "immediately hacked" and taken down once the report was posted
- Yan and colleagues propose SARS-CoV-2 was made using the ZC45/ZXC21 bat coronavirus as the backbone. The receptor-binding motif in the spike protein was then manipulated to give the virus the ability to strongly bind to the human ACE2 receptor
- Alina Chan, a molecular biologist at the Broad Institute of Harvard and MIT, is yet another scientist who questions the zoonotic nature of SARS-CoV-2. Since it sprang into action fully evolved for human transmission, Chan believes the missing intermediate phase of evolution took place in a lab

July 31, 2020, I wrote about a Hong Kong whistleblower scientist who claims[1] the Chinese government and World Health Organization representatives in Hong Kong covered up the Wuhan outbreak, allowing it to spread unchecked around the world.

In a Fox News interview in July 2020, the whistleblower, Dr. Li-Meng Yan — who worked at the University of Hong Kong School of Public Health, a top coronavirus research lab — said her investigation into the SARS-like outbreak in Wuhan could have helped prevent a global pandemic from developing, had her supervisors shared her findings.

Yan was interviewed by Fox News again September 15, 2020 (above), this time about the report she just published, and Twitter promptly began censoring the interview from its platform.[2]

Yan claims her supervisor, WHO consultant Leo Poon, asked her to, secretly, investigate reports of a SARS-like illness spreading in Wuhan, China, in late December 2019. The Chinese government had refused overseas experts from getting involved, and Poon wanted her to figure out what was really going on.

Yan turned to a professional colleague who works in the Chinese Center for Disease Control and Prevention and had first-hand information about the outbreak. Yan was told there was likely human-to-human transmission occurring, as they had found family clusters of cases.

The WHO, however, did not confirm the human-to-human spread potential for several weeks. On the contrary, an official WHO statement said the virus "does not transmit readily between people."

January 16, 2020, Yan was again asked to reach out to her contacts in China to see if she could learn more. Her CDC contacts were fearful, but it became clear that patients and front-line doctors were not being properly protected, and that Chinese authorities were trying to keep a lid on the flow of information.

When she updated Poon, he told her to stay silent and not cross the Chinese government, or else they'd both be "disappeared." The co-director of the University of Hong Kong School of Public Health laboratory, professor Malik Peiris, also stayed quiet. Yan told Fox News she believes WHO colluded with the China Communist Party (CCP) government to prevent information about the virus from coming out.

The Yan Report Is Instantly Censored

Back in July 2020, Yan claimed she had proof that SARS-CoV-2 was manmade, and that once she released it, she would make it accessible to all. September 11, 2020, The Sun quoted statements made by Yan during a British TV interview that same morning, in which she said:[3]

> *"The genome sequence is like a human fingerprint. Based on this you can identify these things. I will [use this] evidence to tell people why this has come from the lab in China, why they are the ones who made it. Anyone, even if you have no biology knowledge, will be able to read it, and check and identify and verify it yourself."*

Three days later, September 14, 2020, Yan and her Ph.D. colleagues, Shu Kang, Jie Guan and Shanchang Hu, published the report,[4] "Unusual Features of the SARS-CoV-2 Genome Suggesting Sophisticated Laboratory Modification Rather Than Natural Evolution and Delineation of Its Probable Synthetic Route" on the preprint server Zenodo.

On the morning of September 14, Yan posted a link to the paper on her Twitter account.[5] Shortly thereafter, she posted another tweet saying Zenodo was "immediately hacked" once the report was posted. The following day, September 15, Twitter suspended her account.[6] According to Yan's report:[7]

> *"The evidence shows that SARS-CoV-2 should be a laboratory product created by using bat coronaviruses ZC45 and/or ZXC21 as a template and/or backbone.*
>
> *Building upon the evidence, we further postulate a synthetic route for SARS-CoV-2, demonstrating that the laboratory-creation of this coronavirus is convenient and can be accomplished in approximately six months."*

Before I get into the content of Yan's report, it's worth noting that questions have arisen as to whether she might be "controlled opposition." Her report also appears very similar to the work[8] of Yuri Deigin. In a September 16 Twitter post, Deigin says:[9]

> *"While it is flattering to see the Yan report citing our preprint with @Rossana38510044, I have to admit, I expected a whistleblower to present much more convincing (and new) evidence than just a rehash of what was already known months ago. Also, why no mention of the 2012 outbreak?"*

Interestingly, a formerly anonymous scientist has now stepped forward as one of the three co-authors of Yan's paper. The anonymous scientist has detailed scientific evidence showing SARS-CoV-2 is a manmade virus, and that there appears to be a

concerted effort to promote the idea that SARS-CoV-2 is a natural occurrence, in a blog called Nerd Has Power.[10]

I reviewed some of the key take-home points of this work in "**Why Was Wuhan Lab Locked Down When Outbreak Began**" and "**Undetectable Engineering Methods Used to Create SARS-CoV-2**."

Steven Mosher, president of the Population Research Institute (a nonprofit research group that exposes human rights abuses and the myth of overpopulation[11]) has previously noted that because Nerd Has Power "published his raw data, I and others have been able to check and verify his work."[12]

In a September 14, 2020, Twitter post,[13] Nerd Has Power identifies himself as Shu Kang, one of the four authors of the Yan report. "Like my co-authors, I stand by this report 100%," Kang says.

Yan Report Claims SARS-CoV-2 Was Genetically Engineered

As of this writing, the Zenodo website is back up and Yan's paper is again available for viewing. Below are a few chosen excerpts.[14] (If you like, you can compare it to Yurin's Medium article.[15])

> *"The receptor-binding motif of SARS-CoV-2 Spike cannot be born from nature and should have been created through genetic engineering.*
>
> *The Spike proteins decorate the exterior of the coronavirus particles. They play an important role in infection as they mediate the interaction with host cell receptors and thereby help determine the host range and tissue tropism of the virus.*
>
> *The Spike protein is split into two halves (Figure 3). The front or N-terminal half is named S1, which is fully responsible for binding the host receptor.*
>
> *In both SARS-CoV and SARS-CoV-2 infections, the host cell receptor is hACE2. Within S1, a segment of around 70 amino acids makes direct contacts with hACE2 and is correspondingly named the receptor-binding motif (RBM) (Figure 3C).*

In SARS-CoV and SARS-CoV-2, the RBM fully determines the interaction with hACE2. The C-terminal half of the Spike protein is named S2. The main function of S2 includes maintaining trimer formation and, upon successive protease cleavages at the S1/S2 junction and a downstream S2' position, mediating membrane fusion to enable cellular entry of the virus.

Similar to what is observed for other viral proteins, S2 of SARS-CoV-2 shares a high sequence identity (95%) with S2 of ZC45/ZXC21. In stark contrast, between SARS-CoV-2 and ZC45/ZXC21, the S1 protein, which dictates which host (human or bat) the virus can infect, is much less conserved with the amino acid sequence identity being only 69%.

Figure 4 shows the sequence alignment of the Spike proteins from six β coronaviruses. Two are viruses isolated from the current pandemic (Wuhan-Hu-1, 2019-nCoV_USA-AZ1); two are the suspected template viruses (Bat_CoV_ZC45, Bat_CoV_ZXC21); two are SARS coronaviruses (SARS_GZ02, SARS).

The RBM is highlighted in between two orange lines. Clearly, despite the high sequence identity for the overall genomes, the RBM of SARS-CoV-2 differs significantly from those of ZC45 and ZXC21.

Intriguingly, the RBM of SARS-CoV-2 resembles, on a great deal, the RBM of SARS Spike. Although this is not an exact 'copy and paste,' careful examination of the Spike-hACE2 structures reveals that all residues essential for either hACE2 binding or protein folding (orange sticks in Figure 3C and what is highlighted by red short lines in Figure 4) are 'kept.'

Most of these essential residues are precisely preserved, including those involved in disulfide bond formation (C467, C474) and electrostatic interactions (R444, E452, R453, D454), which are pivotal for the structural integrity of the RBM (Figure 3C and 4).

The few changes within the group of essential residues are almost exclusively hydrophobic 'substitutions' … which should not affect either protein folding or the hACE2-interaction. At the same time, majority of the

amino acid residues that are non-essential have 'mutated' (Figure 4, RBM residues not labeled with short red lines).

Judging from this sequence analysis alone, we were convinced early on that not only would the SARS-CoV-2 Spike protein bind hACE2 but also the binding would resemble, precisely, that between the original SARS Spike protein and hACE223. Recent structural work has confirmed our prediction ...

The way that SARS-CoV-2 RBM resembles SARS-CoV RBM and the overall sequence conservation pattern between SARS-CoV-2 and ZC45/ZXC21 are highly unusual. Collectively, this suggests that portions of the SARS-CoV-2 genome have not been derived from natural quasi-species viral particle evolution."

Why Natural Origin Theory Fails

Yan's paper goes on to explain why the natural evolution origin theory fails to hold water. She points out that were it the result of wholly natural evolution, its RBM would have to have been acquired either through a) an ancient recombination event followed by convergent evolution, or b) a natural and fairly recent recombination event. Yan dismisses the ancient recombination/convergent evolution option, stating, in part:[16]

" … the virus would have to adapt extensively in its new host, where the ACE2 protein is highly homologous to hACE2 [human ACE2]. Random mutations across the genome would have to have occurred to eventually shape the RBM to its current form — resembling SARS-CoV RBM in a highly intelligent manner.

However, this convergent evolution process would also result in the accumulation of a large amount of mutations in other parts of the genome, rendering the overall sequence identity relatively low.

The high sequence identity between SARS-CoV-2 and ZC45/ZXC21 on various proteins (94-100% identity) do not support this scenario and, therefore, clearly indicates that SARS-CoV- 2 carrying such an RBM cannot

come from a ZC45/ZXC21-like bat coronavirus through this convergent evolutionary route."

She also dismisses the second, recent recombination event, option stating:[17]

"In the second scenario, the ZC45/ZXC21-like coronavirus would have to have recently recombined and swapped its RBM with another coronavirus that had successfully adapted to bind an animal ACE2 highly homologous to hACE2. The likelihood of such an event depends, in part, on the general requirements of natural recombination:

1. *that the two different viruses share significant sequence similarity;*
2. *that they must co-infect and be present in the same cell of the same animal;*
3. *that the recombinant virus would not be cleared by the host or make the host extinct;*
4. *that the recombinant virus eventually would have to become stable and transmissible within the host species.*

In regard to this recent recombination scenario, the animal reservoir could not be bats because the ACE2 proteins in bats are not homologous enough to hACE2 and therefore the adaption would not be able to yield an RBM sequence as seen in SARS-CoV-2. This animal reservoir also could not be humans as the ZC45/ZXC21-like coronavirus would not be able to infect humans.

In addition, there has been no evidence of any SARS-CoV-2 or SARS-CoV-2-like virus circulating in the human population prior to late 2019. Intriguingly, according to a recent bioinformatics study, SARS-CoV-2 was well-adapted for humans since the start of the outbreak."

Pangolin and Other Animals Are Unlikely Intermediary Hosts

There is a third possibility for natural evolution, Yan notes, that of an intermediary host, but this theory also has a significant flaw. "The ZC45/ZXC21-like virus and a

coronavirus containing a SARS-like RBM could have recombined in an intermediate host where the ACE2 protein is homologous to hACE2," the paper states.

It also added that several laboratories have reported that Sunda pangolins carrying coronaviruses with a near-identical receptor-binding domain to that of SARS-CoV-2 have been smuggled into China from Malaysia. Some have argued that these pangolins were likely intermediary hosts. There are several problems with this theory, however, including the following:

- Even though Sunda pangolins have been sampled between 2009 and 2019, no coronaviruses have ever been found in those samples
- Recent research shows the receptor-binding domain shared by SARS-CoV-2 and the reported pangolin coronaviruses binds 10 times stronger to the human ACE2 receptor than it does to the pangolin ACE2 receptor
- Other research has demonstrated that none of the animal ACE2 proteins examined have more favorable binding potential to the SARS-CoV-2 spike protein than the human ACE2 receptor. According to Yan:[18]

> *"This study virtually exempted all animals from their suspected roles as an intermediate host, which is consistent with the observation that SARS-CoV-2 was well-adapted for humans from the start of the outbreak.*
>
> *This is significant because these findings collectively suggest that no intermediate host seems to exist for SARS-CoV-2, which at the very least diminishes the possibility of a recombinant event occurring in an intermediate host"*

Restriction Enzyme Digestion — The Smoking Gun?

Yan goes on to review what she believes is the smoking gun proving SARS-CoV-2 is a laboratory creation. In a nutshell, she and her colleagues believe SARS-CoV-2 was created by swapping out the receptor-binding motif or RBM, not the entire spike protein.

The feasibility of such a swap has already been proven by none other than Dr. Zhengli Shi, one of the researchers arguing for a natural origin of SARS-CoV-2 (as reviewed in this September 10, 2020, article[19] on Minerva). According to Yan:

> *"In 2008, Dr. Zhengli Shi's group swapped a SARS RBM into the Spike proteins of several SARS-like bat coronaviruses after introducing a restriction site into a codon-optimized spike gene ... They then validated the binding of the resulted chimeric Spike proteins with hACE2.*
>
> *Furthermore, in a recent publication, the RBM of SARS-CoV-2 was swapped into the receptor-binding domain (RBD) of SARSCoV, resulting in a chimeric RBD fully functional in binding hACE2 … It is noteworthy that the corresponding author of this recent publication, Dr. Fang Li, has been an active collaborator of Dr. Zhengli Shi since 2010 ...*
>
> *The striking finding of EcoRI and BstEII restriction sites at either end of the SARS-CoV-2 RBM, respectively, and the fact that the same RBM region has been swapped both by Dr. Shi and by her long-term collaborator, respectively, using restriction enzyme digestion methods are unlikely a coincidence. Rather, it is the smoking gun proving that the RBM/Spike of SARS-CoV-2 is a product of genetic manipulation."*

Yan's paper also details evidence suggesting the Chinese scientists tried to cover their tracks to hide the genetic manipulation, and reviews how the furin-cleavage site in SARS-CoV-2 is further indication that genetic engineering was used.

Summary

In summary, Yan and colleagues propose SARS-CoV-2 was made using the ZC45/ZXC21 bat coronavirus as the backbone. The RBM in the spike protein was then manipulated to give the virus the ability to strongly bind to the human ACE2 receptor.

> *"This is supported by the finding of a unique restriction enzyme digestion site at either end of the RBM. An unusual furin-cleavage site may have been introduced and inserted at the S1/S2 junction of the Spike protein, which*

contributes to the increased virulence and pathogenicity of the virus," Yan writes.

The diagram below illustrates the steps required to create SARS-CoV-2:

Why the Cover-Up?

As reported by Aksel Fridstrom in a September 10, 2020, article[20] posted on Minerva, as well as a September 9, 2020, article[21] written by Rowan Jacobsen in Boston Magazine, Alina Chan, a molecular biologist at the Broad Institute of Harvard and MIT, is yet another scientist who questions the zoonotic nature of SARS-CoV-2.

> **"If the public and politicians really knew about the dangerous pathogen research being conducted in many laboratories, they'd be outraged. Denying the possibility of a catastrophic incident like this then could be seen as a form of career preservation. ~ Rowan Jacobsen, Boston Magazine"**

Importantly, Chan discovered that SARS-CoV-2 has not evolved in the manner you'd expect had it jumped from an animal to a human. It sprang into action fully evolved for human transmission. Like Yan and several other scientists, Chan has come to the conclusion that the missing intermediate phase of evolution from animal to human transmissibility must have taken place in a lab.

Chan published her paper,[22] "SARS-CoV-2 Is Well Adapted for Humans. What Does This Mean for Re-Emergence?" on the preprint server bioRxiv May 2, 2020. As in most cases, the pushback she and her co-authors received was enormous.

In his article,[23] Jacobsen points out that one of the obvious reasons for this response is that "if the public and politicians really knew about the dangerous pathogen research being conducted in many laboratories, they'd be outraged." Hence, "Denying the possibility of a catastrophic incident like this … could be seen as a form of career preservation."

Interestingly, The Lancet COVID-19 Commission, which has vowed to "leave no stone unturned" in its investigation into the origins of SARS-CoV-2 and the possibility of a lab escape, is being led by none other than Dr. Peter Daszak,[24] a scientist who has already concluded the virus is natural.

As the president of the EcoHealth Alliance, Daszak is also steeped in conflicts of interest, seeing how EcoHealth Alliance received grants from the NIH for coronavirus research that was then subcontracted to the Wuhan Institute of Virology.

What's more, the NIH is demanding EcoHealth Alliance produce records detailing its work with the Wuhan lab before further funding will be released.[25] It seems the purpose for this "fix" is best summarized by a quote from Boston Magazine:[26]

> *"Antonio Regalado, biomedicine editor of MIT Technology Review, put it more bluntly. If it turned out COVID-19 came from a lab, he tweeted, 'it would shatter the scientific edifice top to bottom.'"*

Indeed, safeguarding the continuation of dangerous gain-of-function research would be a powerful motivator to preserve the zoonotic origin narrative.

According to Chan, there are solutions, however. One would be to conduct this kind of research using "neutered viruses that have had their replicating machinery removed in advance, so that even if they escaped confinement, they would be incapable of making copies of themselves," Jacobsen writes.[27] Another would be to locate high biosafety level laboratories in sparsely populated areas rather than right smack in the middle of large cities.

New Engineered Coronaviruses Are Under Development

Getting to the bottom of where SARS-CoV-2 actually came from is important, because if it came from a high-security bioweapons lab, then it's proof positive that something must be done to prevent a repeat. This is even more important now that biosafety labs around the world are looking at modifying live SARS-CoV-2 even further.[28]

As just one example, researchers at the University of Pittsburgh are looking to insert the SARS-CoV-2 spike protein, which is what allows the virus to gain entry into human

cells, into Bacillus anthracis, the causative agent of anthrax,[29] an already devastatingly dangerous pathogen.

Researchers are also arguing for infectious SARS-CoV-2 research to be permitted in biosafety level 2 laboratories, which have nowhere near the same level of biosafety procedures in place as BSL 3 and BSL 4 labs do.

If the SARS-CoV-2 pandemic is in fact the result of a lab escape, then the responsible way forward is to halt all gain-of-function research until safety protocols are massively upgraded. If we really want to avert another catastrophe, this kind of research should probably be abolished altogether.

Be Prepared

As it stands right now, the weaponization of pathogens continues unabated, and is likely to continue unless or until the public becomes sufficiently aroused to demand real change.

In the meantime, it is important to make sure you're prepared at home. I strongly recommend reviewing **my interview with Dr. David Brownstein**, in which he explains the benefits of nebulized hydrogen peroxide. It's important to have something in your own arsenal to protect yourself against whatever they come up with next. I also added a new video to the page that describes how to do the nebulization therapy.

This needs to be a central player in your emergency medical kit as I fully believe it could be the difference for many, especially the elderly, those who are vitamin D deficient and/or metabolically unfit and insulin resistant. I believe nebulized peroxide is one of the best options available for any respiratory virus, including even more dangerous ones than SARS-CoV-2 that are likely to be introduced in the future.