

Twitter Suspends Account Of Chinese Scientist Who Published Paper Alleging Covid Was Created In Wuhan Lab

By Jim Hayek September 15, 2020

On Sunday afternoon we asked how long before the twitter account of the “rogue” Chinese virologist, Dr. Li-Meng Yan, who yesterday “shocked” the world of establishment scientists and other China sycophants, by publishing a “smoking gun” scientific paper demonstrating that the Covid-19 virus was manmade, is “silenced.”



zerohedge

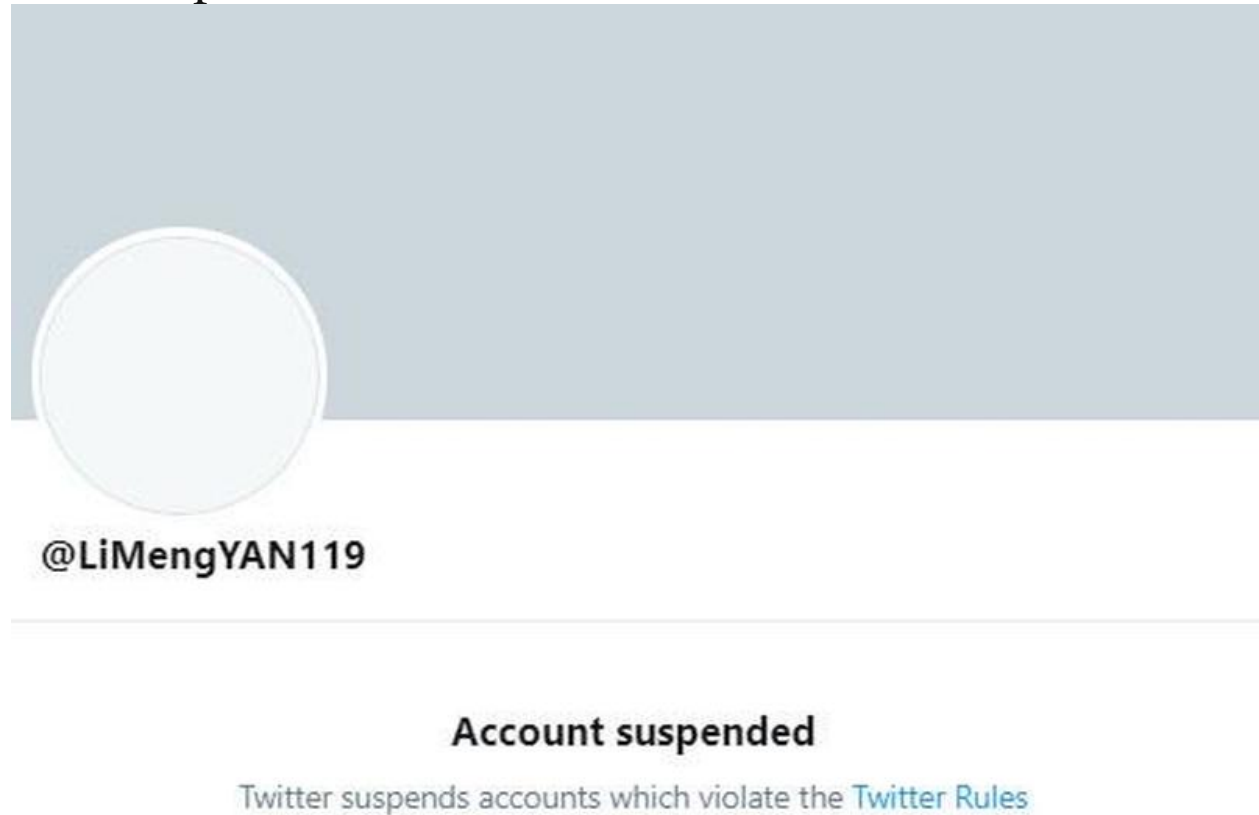
@zerohedge

How long before the [@LiMengYAN119](#) account is silenced

2:21 PM · Sep 13, 2020

437 people are Tweeting about this

We now have the answer: less than two days. A cursory check of Dr Yan's twitter page reveals that the account has been suspended as of this moment.



The suspension took place shortly after Dr Yan had accumulated roughly 60,000 followers in less than 48 hours. The snapshot below was taken earlier in the day precisely in anticipation of this suspension.



It was not immediately clear what justification Twitter had to suspend the scientist who, to the best of our knowledge, had just 4 tweets as of Tuesday morning none of which violated any stated Twitter policies, with the only relevant tweet being a link to her scientific paper co-written with three other Chinese scientists titled “Unusual Features of the SARS-CoV-2 Genome Suggesting Sophisticated Laboratory Modification Rather Than Natural Evolution and Delineation of Its Probable Synthetic Route” which laid out why the Wuhan Institute of Virology had created the covid-19 virus.

While we appreciate that Twitter may have experienced pressure from either China, or the established scientist community, to silence Dr Yan for proposing a theory that flies in the face of everything that has been accepted as undisputed gospel - after all Twitter did just that to us - we are confident that by suspending her account, Jack Dorsey has only added more fuel to the fire of speculations that the covid virus was indeed manmade (not to mention countless other tangential conspiracy theories).

If Yan was wrong, why not just let other scientists respond in the open to the all too valid arguments presented in Dr. Yan's paper? Isn't that what "science" is all about? Why just shut her up?

Because if we have already crossed the tipping point when anyone who proposes an "inconvenient" explanation for an established "truth" has to be immediately censored, then there is little that can be done to salvage the disintegration of a society that once held freedom of speech as paramount.

For those who missed it, here is our post breaking down Dr. Yan's various allegations which twitter saw fit to immediately censor instead of allowing a healthy debate to emerge.

We hope Twitter will provide a very reasonable and sensible explanation for this unprecedented censorship. For those who missed it, her paper is below:

Laboratory Modification Rather Than Natural Evolution and Delineation of Its Probable Synthetic Route

Li-Meng Yan (MD, PhD)¹, Shu Kang (PhD)¹, Jie Guan (PhD)¹, Shanchang Hu (PhD)¹

¹Rule of Law Society & Rule of Law Foundation, New York, NY, USA.

Correspondence: team.lmyan@gmail.com

Abstract

The COVID-19 pandemic caused by the novel coronavirus SARS-CoV-2 has led to over 910,000 deaths worldwide and unprecedented decimation of the global economy. Despite its tremendous impact, the origin of SARS-CoV-2 has remained mysterious and controversial. The natural origin theory, although widely accepted, lacks substantial support. The alternative theory that the virus may have come from a research laboratory is, however, strictly censored on peer-reviewed scientific journals. Nonetheless, SARS-CoV-2 shows biological characteristics that are inconsistent with a naturally occurring, zoonotic virus. In this report, we describe the genomic, structural, medical, and literature evidence, which, when considered together, strongly contradicts the natural origin theory. The evidence shows that SARS-CoV-2 should be a laboratory product created by using bat coronaviruses ZC45 and/or ZXC21 as a template and/or backbone. Building upon the evidence, we further postulate a synthetic route for SARS-CoV-2, demonstrating that the laboratory-creation of this coronavirus is convenient and can be accomplished in approximately six months. Our work emphasizes the need for an independent investigation into the relevant research laboratories. It also argues for a critical look into certain recently published data, which, albeit problematic, was used to support and claim a natural origin of SARS-CoV-2. From a public health perspective, these actions are necessary as knowledge of the origin of SARS-CoV-2 and of how the virus entered the human population are of pivotal importance in the fundamental control of the COVID-19 pandemic as well as in preventing similar, future pandemics.

1.4 Summary

Evidence presented in this part reveals that certain aspects of the SARS-CoV-2 genome are extremely difficult to reconcile to being a result of natural evolution. The alternative theory we suggest is that the virus may have been created by using ZC45/ZXC21 bat coronavirus(es) as the backbone and/or template. The Spike protein, especially the RBM within it, should have been artificially manipulated, upon which the virus has acquired the ability to bind hACE2 and infect humans. 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. These transformations have then staged the SARS-CoV-2 virus to eventually become a highly-transmissible, onset-hidden, lethal, sequelae-unclear, and massively disruptive pathogen.

Evidently, the possibility that SARS-CoV-2 could have been created through gain-of-function manipulations at the WIV is significant and should be investigated thoroughly and independently.

2. Delineation of a synthetic route of SARS-CoV-2

In the second part of this report, we describe a synthetic route of creating SARS-CoV-2 in a laboratory setting. It is postulated based on substantial literature support as well as genetic evidence present in the SARS-CoV-2 genome. Although steps presented herein should not be viewed as exactly those taken, we believe that key processes should not be much different. Importantly, our work here should serve as a demonstration of how SARS-CoV-2 can be designed and created conveniently in research laboratories by following proven concepts and using well-established techniques.

Importantly, research labs, both in Hong Kong and in mainland China, are leading the world in coronavirus research, both in terms of resources and on the research outputs. The latter is evidenced not only by the large number of publications that they have produced over the past two decades but also by their milestone achievements in the field: they were the first to identify civets as the intermediate host for SARS-CoV and isolated the first strain of the virus⁷¹; they were the first to uncover that SARS-CoV originated from bats^{72,73}; they revealed for the first time the antibody-dependent enhancement (ADE) of SARS-CoV infections⁷⁴; they have contributed significantly in understanding MERS in all domains (zoonosis, virology, and clinical studies)⁷⁵⁻⁷⁹; they made several breakthroughs in SARS-CoV-2 research^{18,35,80}. Last but not least, they have the world's largest collection of coronaviruses (genomic sequences and live viruses). The knowledge, expertise, and resources are all readily available within the Hong Kong and mainland research laboratories (they collaborate extensively) to carry out and accomplish

Motives aside, the following facts about SARS-CoV-2 are well-supported:

1. If it was a laboratory product, the most critical element in its creation, the backbone/template virus (ZC45/ZXC21), is owned by military research laboratories.
2. The genome sequence of SARS-CoV-2 has likely undergone genetic engineering, through which the virus has gained the ability to target humans with enhanced virulence and infectivity.
3. The characteristics and pathogenic effects of SARS-CoV-2 are unprecedented. The virus is highly transmissible, onset-hidden, multi-organ targeting, sequelae-unclear, lethal, and associated with various symptoms and complications.
4. SARS-CoV-2 caused a world-wide pandemic, taking hundreds of thousands of lives and shutting down the global economy. It has a destructive power like no other.

Judging from the evidence that we and others have gathered, we believe that finding the origin of SARS-CoV-2 should involve an independent audit of the WIV P4 laboratories and the laboratories of their close collaborators. Such an investigation should have taken place long ago and should not be delayed any further.

We also note that in the publication of the chimeric virus SHC015-MA15 in 2015, the attribution of funding of Zhengli Shi by the NIAID was initially left out. It was reinstated in the publication in 2016 in a corrigendum, perhaps after the meeting in January 2016 to reinstate NIH funding for gain-of-function research on viruses. This is an unusual scientific behavior, which needs an explanation for.

What is not thoroughly described in this report is the various evidence indicating that several coronaviruses recently published (RaTG13¹⁸, RmYN02³⁰, and several pangolin coronaviruses^{27-29,31}) are highly suspicious and likely fraudulent. These fabrications would serve no purpose other than to deceive the scientific community and the general public so that the true identity of SARS-CoV-2 is hidden. Although exclusion of details of such evidence does not alter the conclusion of the current report, we do believe that these details would provide additional support for our contention that SARS-CoV-2 is a laboratory-enhanced virus and a product of gain-of-function research. A follow-up report focusing on such additional evidence is now being prepared and will be submitted shortly.