

Opinion

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The Covid-19 Lab Origin Theory Has No Case



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Abstract

To explain how COVID-19 originated, a lab theory has been put forward that researcher in Wuhan, China engineered SARS-CoV-2, the virus that causes COVID-19, and/or leaked the virus. Despite intense interest, the theory has no evidential support and can be dismissed based on scientific knowledge and judgment.

Keywords: COVID-19; SARS-CoV-2; origin

Abbreviations: WIV: Wuhan Institute of Virology; CoV: Coronavirus; GOF: gain-of-function

Introduction

The origin of COVID-19 has been a highly charged issue since late December 2019, when the first cases were reported in Wuhan, China. There are two theories: the natural origin or zoonotic spillover theory, which proposes that SARS-CoV-2 arose naturally in animals, likely involving bats, and then infected humans, and the lab origin theory, which implicates research facilities in Wuhan, in particular the Wuhan Institute of Virology (WIV). Of the two, the natural origin theory is supported by the long history of human experiences with infectious diseases and results of SARS-CoV-2 sequence analyses and other studies. For example, Anderson et al found no sign of human engineering in the virus genome [1]. Features of SARS-CoV-2 are present in other coronaviruses (CoVs), and the repertoire of CoVs in nature vastly exceeds what humans have examined. For these reasons, most biologists favor the natural origin theory: SARS-CoV-2 evolved by mutations, recombination, or both, in animals and spread to humans.

A small minority of scientists, however, advocate the lab made/leak theory. No evidence exists other than certain researchers in Wuhan studying bat CoVs. There is also the reality that the immediate precursor of SARS-CoV-2, e.g., a CoV more than 99% identical, and animal hosts have yet to be identified, but such, tentative discoveries in other diseases have taken many years, and for some such as Ebola, those questions have remained unanswered for decades. Lab leak is a thinly disguised

version of the lab made theory, because for lab leak to occur, WIV must first have the virus. Then how did WIV get it? One is WIV invented it, i.e., lab made. The other is WIV collected it during field survey before it escaped. To which Dr Anthony Fauci has a response : "But that means it was in the wild to begin with. That's why I don't get what they're talking about [and] why I don't spend a lot of time going in on this circular argument." [2]. Anyway, there is no indication WIV possessed SARS-CoV-2 prior to December 2019. During numerous domestic and international visits and interviews since January 2020, WIV researchers have consistently and unequivocally rejected the lab theory (e.g., [3]). WIV is a public research institution not unlike others around the globe. It publishes its findings in scientific journals, and records show that the closest WIV (or China) had worked on prior to 2020 were SARS-like CoVs, distantly related to SARS-CoV-2.

Much focus has been on Gain-Of-Function (GOF) studies. GOF is an idea or strategy widely applied in biological research, but for the lab theorists it means that WIV engineered a CoV to produce SARS-CoV-2. A 2015 paper has been cited to implicate Dr Shi Zhengli at WIV, yet the experiments were conducted at the University of North Carolina, with Dr Shi merely providing materials in collaboration [4]. The paper was on SARS-like CoVs; importantly, because the work involved splicing known CoVs, genesis of the resulting CoV is apparent by bioinformatics. On the contrary, sequence analyses have discounted human manipulation in the 30-kilobase-long genome of SARS-CoV-2. How can GOF foil

bioinformatics detection, in theory? The only credible method is to propagate a precursor CoV or recombine CoVs in Vero cells or human ACE2 transgenic mice, and then select for a certain phenotype. But what is the research aim? What phenotype to select for and how? What is the end point? Most critically, can the CoV coming out of the screen, if ever, in cells or mice, overcome the immune system and other barriers in humans? There is no precedent of success with large viruses such as CoVs in the literature, and just considering those practically insurmountable difficulties would dissuade most attempts.

Moreover, what might the starting CoV be? Frequently invoked is RaTG13, the closest known relative of SARS-CoV-2 [5]. But with 96.2% identity and the scattered 1.2-kilobase differences, it would take decades of evolution for RaTG13 to yield SARS-CoV-2 in nature [3]. RaTG13 probably doesn't bind the human ACE2 receptor well [6] and is only weakly infectious in human cells, so it would be difficult to establish infection to begin with. And WIV did not even have the live RaTG13 virus, records showing sequencing its RNA only [3,5].

Lastly, a GOF experiment would consume a great deal of resources for a long period of time, and a lot of people must know about it. WIV has collaboration inside and outside China, with constant mobility for its students and researchers. But nobody ever associated with WIV has alleged WIV working on COVID-19 prior to 2020, whereas whoever had spoken all denied any knowledge or anything unusual at WIV [7]. A combination of facts and biology-based knowledge, therefore, are sufficient to dismiss the lab made theory. How about the lab leak angle [8]? Even in its most benign form, in which a WIV worker was infected while collecting samples in the wild or working with collected samples at WIV, neither of which had any evidence, isn't the virus still of natural origin [2]? Even then one cannot conclude COVID-19 started as a result. No matter how much fieldwork WIV has performed, it is dwarfed by orders of magnitude by natural human interactions with CoVs around the world [9]. For example, WIV collected samples only in places where the locals had found bats. Then if a WIV worker with protective equipment were infected,

the locals who have lived around the bats and other animals for years would already be infected. Wuhan being a major city and transportation hub, with an alert medical system, perhaps also by chance, first reported COVID-19, but it does not mean COVID-19 originated there.

Conclusion

The lab origin theory has no evidence and faces the technical impossibility of WIV engineering SARS-CoV-2. Some proponents have claimed agnostic or simply wanting more research. More research is indeed needed to study how SARS-CoV-2 evolved and spilled over to humans. And if the goal of asking questions is to improve lab safety in general, then sure. But questions and further investigation must be based on existing knowledge, solid evidence, and sound judgment.

References

1. Andersen KG, Rambaut A, Lipkin WI, Holmes EC, Garry RF (2020) The proximal origin of SARS-CoV-2. *Nat Med* 26(4): 450-452.
2. <https://www.nationalgeographic.com/science/article/anthony-fauci-no-scientific-evidence-the-coronavirus-was-made-in-a-chinese-lab-cvd>
3. scim.ag/ShiZhengli.
4. Menachery VD, Yount BL Jr, Debbink K, Agnihothram S, Gralinski LE, et al. (2016) A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence. *Nat Med* 22(4): 446.
5. Zhou P, Yang XL, Wang XG, Hu B, Zhang L, et al. (2020) A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature* 579(7798): 270-273.
6. Guo H, Hu B, Si HR, Zhu Y, Zhang W, et al. (2021) Identification of a novel lineage bat SARS-related coronaviruses that use bat ACE2 receptor. *Emerg Microbes Infect* 10(1): 1507-1514.
7. <https://www.bloomberg.com/news/features/2021-06-27/did-covid-come-from-a-lab-scientist-at-wuhan-institute-speaks-out>.
8. Bloom JD, Chan YA, Baric RS, Bjorkman PJ, Cobey S, et al. (2021) Investigate the origins of COVID-19. *Science* 372(6543): 694.
9. Cecilia A Sánchez, Hongying Li, Kendra L Phelps, Carlos Zambrana-Torrel, Lin-Fa Wang, et al. (2021) A strategy to assess spillover risk of bat SARS-related coronaviruses in Southeast Asia. *medRxiv*.



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