

United States House of Representatives
Oversight and Accountability Committee
Select Subcommittee on the Coronavirus Pandemic
“Investigating the Proximal Origin of a Cover Up.”
Tuesday, July 11, 2023
2154 Rayburn House Office Building
Washington, DC 20515

**Written Statement of Dr. Robert F. Garry
Professor & Associate Dean, Tulane University School of Medicine**

Chairman Wenstrup, Ranking Member Ruiz, distinguished members of the Subcommittee, thank you for inviting me to testify today. For the last forty years, I have worked as a professor at Tulane University School of Medicine. I’ve devoted my life’s work to understanding emerging viruses, such as HIV, Ebola virus, Lassa virus and the first SARS virus, and helping to develop diagnostics, drugs and vaccines to help stop those viruses. At the outset, it is important to note that I make these statements in my personal capacity, and I am not speaking on behalf of Tulane University.

Although we have all lived through a very challenging viral pandemic, my personal perspective has been different than most. For nearly 20 years, I’ve worked closely with scientists and clinicians at the Kenema Government Hospital (KGH) in Sierra Leone. KGH is a major site for research on the virus that causes Lassa fever. Ten years ago, Ebola virus emerged just 50 miles from KGH.¹ Ultimately, the Ebola outbreak that occurred in Sierra Leone between 2013 and 2016 claimed 12,000 lives, including the lives of dozens of healthcare workers at KGH. Having previously lost many close colleagues to an outbreak of a deadly virus, the December 2019 reports of cases of a novel pneumonia in Wuhan, China were ominous. The reports raised the specter of a

¹ Goba A *et al.* 2016. An Outbreak of Ebola Virus Disease in the Lassa Fever Zone. *J Infect Dis* 15: S110-S121; *see also*

possible impending global disaster caused by a novel airborne virus – one I worried that the world would be ill-equipped to handle.

Shortly after the first release of the SARS-CoV-2 genetic sequence,² I participated in an in-depth molecular and phylogenetic analysis of the virus with a group of three other scientists, Dr. Kristian Andersen, Dr. Eddie Holmes, and Dr. Andrew Rambaut. The four of us, as well as a fifth co-author, Dr. Ian Lipkin, wrote a peer-reviewed publication, titled “The Proximal Origin of SARS-CoV-2.” In the paper, we concluded that it was likely that SARS-CoV-2 had evolved naturally.³

Importantly, however, we specifically did not rule out a laboratory origin. Instead, in our paper, we discussed three possible origin scenarios. The first scenario was direct spillover from a bat to a human, and the second scenario was spillover from a bat to an intermediate animal and then to a human. The third scenario we discussed in the paper was a lab origin. Specifically, we discussed the possibility that some of the SARS-CoV-2 Spike protein’s features, including a receptor binding domain (RBD) that effectively binds human angiotensin-converting enzyme 2 (ACE2) and a furin cleavage site (FCS), may have arisen during passage in a laboratory.⁴ However, because we observed these notable features in related coronaviruses, which provided a straightforward evolutionary route for SARS-CoV-2 to emerge in nature, we concluded that the natural origin scenarios were most plausible and that, based on the then-available scientific evidence, we did not believe that laboratory-based scenarios, including bioengineering, were plausible.

² Holmes E. 2020. Novel 2019 coronavirus genome, available at <https://virological.org/t/novel-2019-coronavirus-genome/319>.

³ Andersen KG *et al.* 2020. The proximal origin of SARS-CoV-2. *Nat Med* 26:450-452.

⁴ Passage is the process of growing a virus in iterations in different environments (either in cultures or animals), either to observe or achieve mutations and changes.

Based on evidence that has accumulated since we wrote *Proximal Origin*, it is my opinion that SARS-CoV-2 emerged via the wildlife trade in a market in Wuhan, China.⁵ Peer-reviewed papers provide robust evidence supporting that the virus spilled over from a bat through an intermediate animal or animals to humans, one of three origin scenarios discussed in *Proximal Origin*. First, the Huanan Market in Wuhan, China was the early epicenter of the COVID-19 outbreak.⁶ Most of the earliest diagnosed human COVID-19 cases from December 2019 lived in the immediate neighborhood around this market, including those that did not work or shop there. The ascertainment of cases in late 2019 was by local health officials, not the central Chinese Centers for Disease Control, and was not biased by linkage to the Huanan Market [6].⁷ The two campuses of the Wuhan Institute of Virology (WIV) are considered the prime suspects for a lab origin of SARS-CoV-2 because they are the sites of the most advanced research programs on coronaviruses in the city.⁸ However, there was no clustering of diagnosed cases of COVID-19 in December 2019 around either the Wuchang or Jiangxi campuses of the WIV, which are 7 and 15 miles respectively, from the Huanan Market, as would be expected if entry of SARS-CoV-2 into humans involved a laboratory accident.

Second, despite official denials from China, it was determined that Huanan Market vendors sold illegal SARS-CoV-2 susceptible wildlife in November 2019, the most likely timeframe in

⁵ Garry RF. 2022. The evidence remains clear: SARS-CoV-2 emerged via the wildlife trade. *Proc Natl Acad Sci USA*. 119:e2214427119.

⁶ Holmes EC *et al.* 2021. The origins of SARS-CoV-2: A critical review. *Cell* 184:4848-4856; Worobey M. 2021. Dissecting the early COVID-19 cases in Wuhan. *Science* 374:1202-1204; Worobey M *et al.* 2022. The Huanan Seafood Wholesale Market in Wuhan was the early epicenter of the COVID-19 pandemic. *Science* 377:951-959.

⁷ Worobey M. 2021. Dissecting the early COVID-19 cases in Wuhan. *Science* 374:1202-1204.

⁸ Chan A and Ridley M. *Viral: The Search for the Origin of COVID-19* (News Corp: Harper-Collins, New York, 2021); Harrison NL and Sachs JD (2022), A call for an independent inquiry into the origin of the SARS-CoV-2 virus. *Proc Natl Acad Sci USA* 119(21):e2202769119.

which SARS-CoV-2 emerged.⁹ Environmental sampling was performed at the Huanan Market after it was shut down on January 1, 2020 and after illegal wildlife had been removed.¹⁰ SARS-CoV-2 positive samples clustered in the southwest corner of the Huanan Market, where live SARS-CoV-2 susceptible mammals were sold. Specifically, an iron cage, carts used to move cages and animals, and drainage from this area were positive for SARS-CoV-2.¹¹ It is difficult to reconcile this striking distribution of the SARS-CoV-2 positive environmental samples in the Huanan Market with the theory that SARS-CoV-2 originated at the WIV or another Wuhan laboratory.

Third, analyses of the environmental samples also indicated that at least two separate spillovers of SARS-CoV-2 from animals to humans occurred at the Huanan Market.¹² In this regard, the emergence of SARS-CoV-2 resembles the first outbreaks of a SARS coronavirus in China that happened between 2002 and 2004 in which there were multiple spillovers from live animals sold in the wildlife trade. There are no plausible lab origin scenarios that are compatible with two independent spillovers of SARS-CoV-2 at the same market location.

Finally, in November 2022, my co-authors and I obtained access to large files containing the DNA and RNA sequences from the environmental samples taken at the Huanan Market in early 2020. This long-suppressed data not only showed that live raccoon dogs, civet cats, and other mammals susceptible to SARS-CoV-2 infection were present, but also pin-pointed their precise

⁹ Xiao X *et al.* 2021. Animal sales from Wuhan wet markets immediately prior to the COVID-19 pandemic. *Sci. Rep.* 11:11898 (2021); Huang C *et al.* 2020. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. *Lancet* 395: 497–506.

¹⁰ Liu WJ *et al.* 2023. Surveillance of SARS-CoV-2 at the Huanan Seafood Market. *Nature*. 2023 Apr 5. doi: 10.1038/s41586-023-06043-2.

¹¹ Liu WJ *et al.* 2023. Surveillance of SARS-CoV-2 at the Huanan Seafood Market. *Nature*. 2023 Apr 5. doi: 10.1038/s41586-023-06043-2; Crits-Christoph *et al.* 2023. Genetic evidence of susceptible wildlife in SARS-CoV-2 positive samples at the Huanan Wholesale Seafood Market, Wuhan: Analysis and interpretation of data released by the Chinese Center for Disease Control <https://doi.org/10.5281/zenodo.7754299>.

¹² Pekar JE *et al.* 2022. The molecular epidemiology of multiple zoonotic origins of SARS-CoV-2. *Science*. 377:960-966.

locations within the market. Raccoon dog and civet cat DNA and RNA were present in the wildlife stall that contained the highest numbers of SARS-CoV-2 positive samples in the market.¹³ This is equivalent to finding a smoking gun carrying the main suspect's DNA at the exact scene of the crime. All of this evidence demonstrates that the simplest explanation is that live animals were shedding SARS-CoV-2 at the Huanan Market in late 2019.

Theories of COVID-19 origin must be investigated in a transparent manner. In prior testimony, this Subcommittee has heard scientific testimony regarding SARS-CoV-2 that is not fully accurately. For example, the Subcommittee has been told that there is no FCS in any other SARS-like virus.¹⁴ However, an FCS exists in the first SARS-CoV near putative fusion peptides.¹⁵ Moreover, other SARS-like viruses are but a single mutation from having an FCS, which could evolve in a single step.¹⁶ The Subcommittee was also told that cleavage at the FCS reorients the RBD so it can specifically bind to human ACE2.¹⁷ This is inaccurate. The same witness described “human” arginines, which do not exist.

Three and a half years into the COVID-19 pandemic, it is still my opinion that there is no credible scientific evidence to support a lab-based origin for SARS-CoV-2. I support the efforts of the Subcommittee to better understand the origins of coronavirus pandemics, as understanding viral origin plays an important role in developing strong policies to help prevent the next potential

¹³ Crits-Christoph *et al.* 2023. Genetic evidence of susceptible wildlife in SARS-CoV-2 positive samples at the Huanan Wholesale Seafood Market, Wuhan: Analysis and interpretation of data released by the Chinese Center for Disease Control <https://doi.org/10.5281/zenodo.7754299>.

¹⁴ Testimony of Nicholas Wade on 8 March 2023 to the House Select Subcommittee on Coronavirus Pandemic; Testimony of Jamie Metzl, PhD on 8 March 2023 to the House Select Subcommittee on Coronavirus Pandemic.

¹⁵ Sainz B Jr *et al.* 2005. Identification and characterization of the putative fusion peptide of the severe acute respiratory syndrome-associated coronavirus spike protein. *J Virol* 79: 7195-206.

¹⁶ Sander, AL., Moreira-Soto, A., Yordanov, S. *et al.* 2022. Genomic determinants of furin cleavage in diverse European SARS-related bat coronaviruses. *Commun Biol* 5: 491.

¹⁷ Testimony of Robert Redfield, MD on 8 March 2023 to the House Select Subcommittee on Coronavirus Pandemic.

pandemic. The global community remains ill-equipped to prevent or manage the emergence of novel viruses.¹⁸ Prevention efforts for the next coronavirus emergence should focus on obtaining a greater understanding of the diversity of the *Coronaviridae* family in wild animals, increased surveillance at the animal-human interface, and stringent oversight of the wildlife and fur trade. As mentioned earlier, I've spent much of my career developing countermeasures for emerging viruses. Diagnostics, vaccines and therapeutics for potentially pandemic coronaviruses and other high-risk viruses, can and must be developed and prepositioned.¹⁹

¹⁸ Goodrum F, et al. 2023. Virology under the microscope—a call for rational discourse. *J Virol* 97:e00089-23.

¹⁹ Graham B and Corbett KS. 2020. Prototype pathogen approach for pandemic preparedness: world on fire. *J Clin Invest* 130: 3348-3349.