COVID lab leak ‘science’ refuted

Alongside the absurd mainstream media reports that in recent weeks have sought to revive the “Wuhan lab leak” theory on the genesis of COVID-19 in sync with the geopolitical drumbeat against China, a few articles have appeared in more reputable publications which raise what seem to be legitimate scientific objections to the alternative theory that the virus responsible evolved naturally. The most influential to date is an essay titled “Origin of COVID—Following the clues: Did nature open Pandora’s box at Wuhan?”, by US-based British journalist and former *New York Times* science editor Nicholas Wade. Self-published 3 May on Wade’s Medium.com page, the essay was picked up two days later by the esteemed *Bulletin of the Atomic Scientists*, and has since been widely cited by both mainstream and “alternative” media as an impartial and authoritative analysis of each theory’s relative merits. It turns out, however, Wade is just a more sophisticated propagandist. Several highly qualified scientists, including top US virologists who were not involved with the Wuhan Institute of Virology (WIV), have pointed out that all of what Wade presents as “scientific facts” indicating that the Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2) was made in a lab is at best misrepresented and often demonstrably false. Given Wade’s own scientific training (he holds a bachelor’s degree in biology) and decades of subject-specific journalistic experience, it may be assumed that this is deliberate.


Shi Zhengli, a.k.a. Bat-Woman. Pic: Screenshot

The prevailing theory of SARS-CoV-2’s origin is that like many viruses before it, it mutated sufficiently in its host, or “reservoir”, animal— most likely a species of horseshoe bat— and that it was able to jump the “species barrier” to humans (possibly via an intermediary animal) in a process called zoonosis. This theory includes the possibility that zoonosis may have occurred months, years or even decades before the virus was first identified in Wuhan, China, in December 2019, but only recently developed the ability to sicken large numbers of people. Alternatively, it remains theoretically possible that it was created in and escaped from a laboratory. Wade does acknowledge that “so far there is *no direct evidence* for either theory. … So I have only clues, not conclusions, to offer.” (Emphasis in original.) A few legalistic equivocations notwithstanding, however, conclusions are exactly what he draws. Having stated in his opening paragraphs that blame for the pandemic “starts with … the government of China”, he closes with a call for a “reckoning” with same, along with the “international community of virologists” he paints as its accomplices.

‘Conflict of interests’, or fruitful collaboration?

Wade’s first target is New York-based British zoologist Dr Peter Daszak. An expert in disease ecology with a focus on emerging zoonotic pathogens, Daszak is the founder and president of the EcoHealth Alliance, a non-governmental organisation affiliated to the intergovernmental World Health Organisation (WHO) and the UN Food and Agriculture Organisation (FAO) which, as stated on its website, “conducts research and outreach programs on global health, conservation and international development” in collaboration with governments and NGOs around the world. “Dr Daszak’s research has been instrumental in identifying and predicting the origins and impact of emerging diseases across the globe”, the site states. “This includes identifying the bat origin of SARS”, the original Severe Acute Respiratory Syndrome coronavirus (similar in symptoms but not genetically related to SARS-CoV-2), which broke out in southern China in 2002. It was in this capacity that Daszak and EcoHealth began their collaboration with the WIV, whose lead virologist Dr Shi Zhengli (a.k.a. “Bat-Woman”) is the world’s leading authority on bat coronaviruses.

In February 2020 Daszak organised a statement[1] cosigned by dozens of scientists from around the world, lamenting that “The rapid, open, and transparent sharing of data on this outbreak [by Chinese public health professionals] is now being threatened by rumours and misinformation”, and condemning “conspiracy theories suggesting that COVID-19 does not have a natural origin … [which] do nothing but create fear, rumours, and prejudice that jeopardise our global collaboration in the fight against this virus.” Wade accuses Daszak of having done so to perpetrate a cover-up, because EcoHealth “funded coronavirus research at the Wuhan Institute of Virology. If the SARS2 [sic] virus had indeed escaped from research he funded, Daszak would be potentially culpable.” Later Wade adds US National Institute of Allergy and Infectious Disease (NIAID) director and chief presidential medical advisor Dr Anthony Fauci to the list, on the basis that “From June 2014 to May 2019, Daszak’s EcoHealth Alliance had a grant from the … NIAID, part of the National Institutes of Health [NIH], to do gain-of-function research with coronaviruses [i.e. artificially increasing infectivity to predict the effects of natural mutations]” at the WIV.

Whatever Daszak or Fauci’s real or perceived conflict of interests, however, all this actually makes the lab leak theory less likely. As the *Australian Alert Service* has previously reported,[2] due to its

participation in the WIV's research, the NIH—an agency of the United States government—had full and prompt access to all data produced in its experiments, which scientists from EcoHealth and the US Centres for Disease Control and Prevention (CDC) helped design and often participated in, as did colleagues from other countries, including Australia. Had the WIV engineered SARS-CoV-2, the US government would almost certainly already know it, since in the circumstances it is hardly conceivable such work could have been done in secret.

Science vs opinion

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Wade's second target is Dr Kristian G. Andersen, a professor of microbiology and immunology at Scripps University in California, where he is director of infectious disease genomics. On 17 March 2020 Andersen and four co-authors published a paper titled "The proximal origin of SARS-CoV-2" in the international biomedical journal *Nature Medicine*. Based on a "review of what can be deduced about the origin of SARS-CoV-2 from comparative analysis of genomic data", they wrote, "We offer a perspective on the notable features of the SARS-CoV-2 genome and discuss scenarios by which they could have arisen. Our analyses clearly show that SARS-CoV-2 is not a laboratory construct or a purposefully manipulated virus."

Andersen et al.'s paper was published as a "Letter" rather than an "Article", which Wade asserts means that it is "an opinion piece, not a scientific article". This is a lie. As *Nature* explains on its website, an Article is "a substantial novel research study that often involves several techniques or approaches", and typically runs to 3,500 words and five printed pages, whereas a Letter is a shorter report of at most 2,000 words which focuses on a single outstanding original finding. (For example, geneticists James Watson and Francis Crick published their discovery of the structure of DNA in a *Nature* Letter on 25 April 1953.) Both are subject to the same editorial and peer review processes. Wade must know this, given he was a staff writer and science editor for Nature in 1967-71.

Wade summarises Andersen et al.'s arguments against artificial origins of the virus thus: "First, they say that the spike protein of SARS2 binds very well to its target, the human ACE2 receptor, but does so in a different way from that which physical calculations suggest would be the best fit. … The authors' basic assumption, not spelt out, is that anyone trying to make a bat virus bind to human cells could do so in only one way. First they would calculate the strongest possible fit between the human ACE2 receptor and the spike protein with which the virus latches onto it. They would then design the spike protein accordingly." ACE2 stands for angiotensin-converting enzyme-2, a protein found on the surface of many cell types including the lining of the nose, mouth and lungs. Its normal function is to snip the large protein angiotensin into pieces which can enter the cell, a pathway the virus exploits to gain entry and take over.

Secondly, Wade says, due to the difficulty of manipulating RNA, the genetic molecule on which coronaviruses are based, researchers "will first convert the RNA genome to DNA … then arrange for the manipulated DNA genome to be converted back into infectious RNA. *Only a certain number of these DNA backbones have been described in the scientific literature* … and since SARS2 is not derived from any of them, therefore it was not manipulated. But … *DNA backbones are quite easy to make*, so it's obviously possible that SARS2 was manipulated using an unpublished DNA backbone. And that's it. These are the two arguments … [that] convinced the world's press that SARS2 could not have escaped from a lab." (Emphasis added.) According to actual scientists, however, Wade is wrong on both points, which are immaterial in any case since these are not Andersen et al.'s arguments anyway.

What they actually argue is that "On the basis of structural studies and biochemical experiments, CoV-2 seems to have an RBD [the receptor-binding domain of the spike protein] that binds with high affinity to ACE2 from humans", but also that from "ferrets, cats and other species". As co-author Prof. Robert Garry of Tulane University in New Orleans, a microbiologist who ranks among the USA's pre-eminent experts on emergent diseases, explained in a 29 May 2021 interview for the "This Week in Virology" podcast, "This is a pan-tropic virus; it's a generalist virus. It can infect a lot of different species, very easily. It has no trouble jumping from a human to a dog, to a cat, to a tiger, to a gorilla … the number of species can go on and on. This is a characteristic of naturally emerging viruses." SARS-CoV-2's RBD appears to have come from a virus found in Malayan pangolins (scaly anteaters)—but one which was only discovered afterwards.

Wade also makes much of the virus's "furin cleavage site", which "ensures the spike protein will be

cleaved in exactly the right place" to facilitate its entry into the cell. "Human cells have a protein cutting tool on their surface known as furin … [which] will cut any protein chain that carries its signature target cutting site", he says. "[Of] all known SARS-related beta-coronaviruses, only SARS2 possesses a furin cleavage site. All the other viruses have their S2 unit cleaved at a different site and by a different mechanism." Nonsense, says Garry. "There are five sub-genuses of beta-coronaviruses. We know that four out of the five have viruses with furin cleavage sites", several of which— including the deadly Middle East Respiratory Syndrome (MERS) virus—are known to infect humans. But according to all the computational models, he explained, SARSCoV-2's particular furin site is a "minimal" furin site that should not be anything like as infectious as it is, and as such no experienced virologist would have thought to insert it.

As for DNA backbones, the reason only a few have been described is because making them is actually extraordinarily hard. As Christian Stevens MD, a virologist at the Mount Sinai School of Medicine in New York, noted in an April 2020 blog post, most of SARS-CoV-2's genome (about 96 per cent) is identical to that of a bat coronavirus closely related to RaTG13, samples of which were kept at the WIV. To create the former from the latter, he wrote, "virus engineers (and this actually happens to be my job…)" would need to "1. Make a virus backbone from a never-before-seen virus that looks like, but isn't, RaTG13 without having any reason to believe it would be a better starting place than a previously characterised virus (like the original SARS-CoV); 2. Spend months to years building a system that is easy to engineer … when there are other virus backbones readily available; [and] 3. Choose the RBD [receptor-binding domain] region from an unknown pangolin coronavirus even though all computer models show it should be suboptimal at binding ACE2, and show that it binds well *in spite* of the models… All of these steps sound like bad ideas from a scientist's perspective: there were easier ways to engineer a coronavirus, and no one would have rationally chosen either the bat virus backbone *or* the pangolin portion of the spike protein. … [We] have zero evidence that any person or lab has attempted even one part of this process." And the final nail in the coffin of Wade's theory is that the Andersen group also identified a type of molecule called "olinked glycans" in the virus, an adaptive defence mechanism by which a virus avoids detection by the host's immune system. "This type of selection cannot occur using cell culture", wrote Stevens, "and there is no known animal model that would allow for selection of human-like ACE2 binding and avoidance of immune recognition. *This strongly implies SARS-CoV-2 could not have been developed in a lab, even by a system of simulated natural selection.*" (Emphasis in original.)

Given this thorough debunking, the lab leak hypothesis looks less likely than ever.

By Richard Bardon, Australian Alert Service, 9 June 2021

Footnotes

1. "Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19", The Lancet, 19 Feb. 2020.
2. "Still no evidence for COVID 'lab leak' theory ", *AAS*, 2 June 2021.