

# Harvard to the Big House

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China owns Nature magazine's ass – Debunking “The proximal origin of SARS-CoV-2” claiming COVID-19 definitely wasn't from a lab

Posted on March 19, 2020March 21, 2020 by [harvard2thebighouse](#)

Maybe you shouldn't blindly believe everything you read? Even if the source has a pretty solid reputation?

*Nature* magazine has censored over 1,000 articles (<https://www.insidehighered.com/news/2018/10/03/book-publishers-part-ways-springer-nature-over-concerns-about-censorship-china>) at the request of the Chinese government over the past several years. And it seems pretty clear that their recent article, “The proximal origin of SARS-CoV-2” (<https://www.nature.com/articles/s41591-020-0820-9>) is just one more example of their influence. China bought off the head of Harvard's chemistry department, you don't think they could buy off run-of-the-mill research scientists scrambling for tenure and funding and publication? It's absolutely horrific that so many scientists and researchers are taking part in what's really clearly a disinformation campaign orchestrated by the Chinese Communist Party, and willfully spreading a smokescreen about something that's already killed thousands and is projected to kill millions more across the planet.

And while the mainstream corporate media mindless regurgitates claims from the Chinese government that are falsifiable with the simplest of google searches, allowing the public to be lulled into a false sense of security and complacency, and Reddit rapidly censors and moderates anything that might indicate that this virus leaked from a Chinese lab and so the Chinese government is to blame for this pandemic – sites like ZeroHedge (<https://www.zerohedge.com/>), that have been at the forefront of keeping the lines of investigation open, have been banished from Twitter and marginalized.

Below is a takedown of that article, and the good news is a much more nuanced and honest look at the origins of COVID-19, the Wuhan Strain of coronavirus is just a click away (<https://harvardtothebighouse.com/2020/01/31/logistical-and-technical-analysis-of-the-origins-of-the-wuhan-coronavirus-2019-ncov/>).

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Thus, the high-affinity binding of the SARS-CoV-2 spike protein to human ACE2 is most likely the result of natural selection on a human or human-like ACE2 that permits another optimal binding solution to arise. This is strong evidence that SARS-CoV-2 is not the product of purposeful manipulation.

- As our report mentions right at the start (<https://harvardtothebighouse.com/2020/01/31/logistical-and-technical-analysis-of-the-origins-of-the-wuhan-coronavirus-2019-ncov/>), scientists passed the H5N1 Bird Flu through a series of ferret hosts until it gained ACE2 affinity and then became incredibly virulent, which is what's seen with COVID-19 since its affinity to ACE2 is orders of magnitude higher than SARS. That process would leave a genome that appears “natural” and not purposeful as well since it wouldn't leave a genomic smoking gun and would simply appear to be the result of “natural” selection. However the addition of artificial generations produced by this process of passing through ferrets in the lab would create a lot of genetic distance from any possible relatives – precisely what is seen in COVID-19: it forms its own clade and appears very distant from all other bat coronaviruses. So this is lazy research, they're either unaware of the Bird Flu study or are willfully ignoring it.

Given the level of genetic variation in the spike, it is likely that SARS-CoV-2-like viruses with partial or full polybasic cleavage sites will be discovered in other species.

- This seems like pretty intentional dissimulation. It's “likely” that other viruses with this cleavage site will be found? What? How likely? 1 in 10? 1 in 10 million? Is it likely that if my aunt grew balls she'd become my uncle? Is it “likely” that a natural intermediate animal vector will be found? Well... likely or not, until it happens it seems incredibly disingenuous to state that “likely” means a damn thing here.

The functional consequence of the polybasic cleavage site in SARS-CoV-2 is unknown, and it will be important to determine its impact on transmissibility and pathogenesis in animal models. Experiments with SARS-CoV have shown that insertion of a furin cleavage site at the S1–S2 junction enhances cell–cell fusion without affecting viral entry<sup>14</sup> (<https://www.nature.com/articles/s41591-020-0820-9#ref-CR14>).

- This doesn't seem to address the virus's provenance at all, but just as an aside it seems like a lot of the viruses with furin cleavage sites engage in ADE, which COVID-19 appears to be doing from a clinical perspective: neurological damage, the second infection is worse, and areas like Wuhan with extended infections have much higher CFRs as infections overlap.

The acquisition of polybasic cleavage sites by HA has also been observed after repeated passage in cell culture or through animals<sup>17</sup> (<https://www.nature.com/articles/s41591-020-0820-9#ref-CR17>).

- Exactly. Passage through a series of ferret hosts in a lab would have given COVID-19 this distinct cleavage site.

It is improbable that SARS-CoV-2 emerged through laboratory manipulation of a related SARS-CoV-like coronavirus. As noted above, the RBD of SARS-CoV-2 is optimized for binding to human ACE2 with an efficient solution different from those previously predicted<sup>7</sup> (<https://www.nature.com/articles/s41591-020-0820-9#ref-CR7>),<sup>11</sup> (<https://www.nature.com/articles/s41591-020-0820-9#ref-CR11>).

- Yes, again we aren't arguing that this thing was built nucleotide-by-nucleotide as the perfect

bespoke bio-weapon. This efficient solution is exactly the kind of thing that would be selected for after passage through ferrets in lab, which was already done to the Bird Flu that created a horrifically virulent strain. Isn't it funny that no one's mentioning that experiment? Or Baric's work at UNC? How come every single public-facing virologist seems to be leaving these studies out? Are they really unaware of them? That seems exceedingly hard to believe when I was able to find them on the front page of a single google search. Seems a lot more likely everyone's just covering each other's asses since they realize the magnitude of what's happening and how deep into the cover-up they already are.

Furthermore, if genetic manipulation had been performed, one of the several reverse-genetic systems available for betacoronaviruses would probably have been used<sup>19</sup> (<https://www.nature.com/articles/s41591-020-0820-9#ref-CR19>).

- This is an utterly vacuous statement. Probably doesn't mean a damn thing in science. “Okay folks, we probably won't get an earthquake anytime soon, so no reason to prepare for one or try and detect one coming!” Seriously?

Instead, we propose two scenarios that can plausibly explain the origin of SARS-CoV-2: (i) natural selection in an animal host before zoonotic transfer; and (ii) natural selection in humans following zoonotic transfer.

- As we've explained before, there was no trace of this virus before November 2019, and full zoonotic jumps don't just magically happen, especially not of a virus that's so incredibly adapted to humans and able to infect us undetected and spread undetected, and then kill us after more than enough time has passed to find multiple new hosts. It's funny so many virologists are throwing out the book of how zoonotic jumps happen... all that money in gain-of-function research must be quite blinding. Kind of amazing they don't matter how many thousands of people are dying. As far as the intermediate animal host goes: It might as well be a unicorn at this point. Until someone finds it, it's just conjecture.

Malayan pangolins (*Manis javanica*) illegally imported into Guangdong province contain coronaviruses similar to SARS-CoV-2<sup>21</sup> (<https://www.nature.com/articles/s41591-020-0820-9#ref-CR21>). Although the RaTG13 bat virus remains the closest to SARS-CoV-2 across the genome<sup>1</sup> (<https://www.nature.com/articles/s41591-020-0820-9#ref-CR1>), some pangolin coronaviruses exhibit strong similarity to SARS-CoV-2 in the RBD, including all six key RBD residues<sup>21</sup> (<https://www.nature.com/articles/s41591-020-0820-9#ref-CR21>) (Fig. 1 (<https://www.nature.com/articles/s41591-020-0820-9#Fig1>)). This clearly shows that the SARS-CoV-2 spike protein optimized for binding to human-like ACE2 is the result of natural selection.

- The most recent study, covered in our article, that examines the neutral sites that are assumed to best show heritage found that pangolins are “very unlikely” to have served as a host at all. Their assertion that *natural* natural selection is clearly shown is raw steamy bullshit. Serial passage through ferrets fits the overall big picture far better than this pangolin crap.

For a precursor virus to acquire both the polybasic cleavage site and mutations in the spike protein suitable for binding to human ACE2, an animal host would probably have to have a high population density (to allow natural selection to proceed efficiently) and an ACE2-encoding gene that is similar to the human ortholog.

- WAIT WAIT WAIT!! You mean exactly like a bunch of ferrets, which have the same ACE2 receptor as humans, all jammed into a bunch of cages together and then infected over and over again in a lab?! That's crazy talk!! Other than the fact it was exactly the process used to make the Bird Flu into something that “could make the 1918 pandemic look like a pesky cold.” (<https://www.dallasnews.com/opinion/commentary/2011/12/31/carl-zimmer-should-scientists-self-censor-their-h5n1-research/>).

It is possible that a progenitor of SARS-CoV-2 jumped into humans, acquiring the genomic features described above through adaptation during undetected human-to-human transmission. Once acquired, these adaptations would enable the pandemic to take off and produce a sufficiently large cluster of cases to trigger the surveillance system that detected it<sup>1</sup> (<https://www.nature.com/articles/s41591-020-0820-9#ref-CR1>),<sup>2</sup> (<https://www.nature.com/articles/s41591-020-0820-9#ref-CR2>).

Hence, this scenario presumes a period of unrecognized transmission in humans between the initial zoonotic event and the acquisition of the polybasic cleavage site. Sufficient opportunity could have arisen if there had been many prior zoonotic events that produced short chains of human-to-human transmission over an extended period.

- Sure this would be plausible... other than the fact that, as we cover in our report (<https://harvardtothebighouse.com/2020/01/31/logistical-and-technical-analysis-of-the-origins-of-the-wuhan-coronavirus-2019-ncov/>), that statistical analysis shows that this thing didn't hit humans until November of 2019, which this article agrees with. But zoonotic jumps only occur after a genomic trial-and-error process where the virus jumps to one host, spreads to a few new hosts, and then fizzles out. There is absolutely no evidence anywhere of this occurring. Every single data points to this thing hitting humans in November and being immediately adapted and dangerous. There is no trace whatsoever of it creating small clusters of infections and dying out – stating there could have been doesn't mean it's been seen. It hasn't. And as our report covers, this would require sustained interaction with the intermediate host – how does that happen in the middle of a massive modern urban metropolis the size of NYC? And where is this intermediate host anyways? If an intermediate host isn't needed, is it some magical sleep-flying bat that decided not to hibernate and fight crime in Wuhan when it's buddies were all hibernating, creating the sustained interactions with humans as it fought for Justice? Because that's about as plausible as what's being proposed here.

The presence in pangolins of an RBD very similar to that of SARS-CoV-2 means that we can infer this was also probably in the virus that jumped to humans.

- Again, analysis of the neutral sites shows that pangolins were almost certainly not in play.

Furthermore, a hypothetical generation of SARS-CoV-2 by cell culture or animal passage would have required prior isolation of a progenitor virus with very high genetic similarity, which has not been described

- This means nothing. There is no open-source shared database of viruses. No one has any idea what viruses are in China's BSL-4 lab, where they've been collecting these viruses for years. As mentioned, one of our persons-of-interest was the very first person to isolate a coronavirus from a bat that uses the ACE2 receptor. He also worked at UNC in Baric's lab making the hyper-virulent bat coronavirus in 2015.

Subsequent generation of a polybasic cleavage site would have then required repeated passage in cell culture or animals with ACE2 receptors similar to those of humans, but such work has also not previously been described.

- The fuck it hasn't.

Retrospective serological studies could also be informative, and a few such studies have been conducted showing low-level exposures to SARS-CoV-like coronaviruses in certain areas of China<sup>26</sup> (<https://www.nature.com/articles/s41591-020-0820-9#ref-CR26>). Further serological studies should be conducted to determine the extent of prior human exposure to SARS-CoV-2.

- Beyond the statistical analysis that indicates it only hit humans in November in 2019, is the fact that the version of COVID-19 found in the first few dozen hosts was exactly the same – there aren't any variants whatsoever, just one version. This is not what would be found with the genomic trial-and-error of a full zoonotic jump, which requires sustained human-to-human transmission as different variants of the virus try and fail to adapt to human biology. Here, only one variant was found in all the initial infected humans, instead of the multiple variants that would be expected. But does fit what would happen if a virus that already had high affinity to the ACE2 receptor, which is the same in human and ferrets, leaked out of a lab. But addressing this point in particular, oh weird, the study they cite from March of 2018 (<https://link.springer.com/article/10.1007%2Fs12250-018-0012-7>) was done mostly on people who live in villages barely a kilometer away from bat caves. A far cry from a massive urban city bout the size of NYC. Oh, and how many of these villagers, who live about a kilometer or less from bat caves, had antibodies indicating exposure to bat coronaviruses? Two-point-seven percent. (There is hand-waving about how long antibodies persist in humans, but I'm pretty sure it's more than long enough.) That study actually sampled people living in Wuhan too and found... no evidence whatsoever of exposure to “SARS-CoV-like coronaviruses.” So are these peer-reviewers just straight chugging lead paint, or are they on the take too?

The finding of SARS-CoV-like coronaviruses from pangolins with nearly identical RBDs, however, provides a much stronger and more parsimonious explanation of how SARS-CoV-2 acquired these via recombination or mutation<sup>1</sup> (<https://www.nature.com/articles/s41591-020-0820-9#ref-CR19>).

- Again, just demonstrably false.

**Get the real story here. (<https://harvardtothebighouse.com/2020/01>)**

## **/31/logistical-and-technical-analysis-of-the-origins-of-the-wuhan-coronavirus-2019-ncov/)**

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# 31 thoughts on “China owns Nature magazine’s ass – Debunking “The proximal origin of SARS-CoV-2” claiming COVID-19 definitely wasn’t from a lab”

1. Pingback: [Logistical and Technical Exploration into the Origins of the Wuhan Strain of Coronavirus \(COVID-19\) – Harvard to the Big House](#)
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3. Pingback: [Debunking Nature Magazine's "COVID-19 Definitely Didn't Come From A Lab" China Propaganda | ValuBit](#)
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17. Pingback: [Debunking Nature Magazine’s “COVID-19 Definitely Didn’t Come From A Lab” China Propaganda – Finanz.dk](#)

18. Pingback: [Debunking Nature Magazine's "COVID-19 Definitely Didn't Come From A Lab" China Propaganda | Zero Hedge](#)
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23. Pingback: [Beim wem wir uns vermutlich für Covid-19 bedanken dürfen. | How blue](#)
24. **Stanley Smith** says: [March 21, 2020 at 8:22 am](#)  
– Absolutely excellent stuff, thanks so much for reading and passing that along!!

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About Scripps Research Institute, who published the paper, here are some links to their press releases of multi-million dollars deals with chinese labs:

<https://www.scripps.edu/news-and-events/press-room/2017/20170608chempharma.html>

<https://www.scripps.edu/news-and-events/press-room/2019/20191127-szbl-collaboration.html>

<https://www.biospace.com/article/releases/yisheng-biopharma-announces-research-collaboration-with-the-scripps-research-institute-in-developing-new-aids-vaccine-/>

I invite you all to check the main researcher twitter account, there are quite a lot of china-praising statements and political stances as well. He has already started deleting some of his tweets (I have a full backup if needed).

Quick note on the wording in the paper:

“Our analyses clearly show that SARS-CoV-2 is not a laboratory construct or a purposefully manipulated virus”

“This is strong evidence that SARS-CoV-2 is not the product of purposeful manipulation”

“It is improbable that SARS-CoV-2 emerged through laboratory manipulation of a related SARS-CoV-like coronavirus”

“[...] we do not believe that any type of laboratory-based scenario is plausible”

Very assertive claims at the beginning, then going diminuendo, finally ending with “we do not believe”.

Now here is the title from Scripps Research Institute press release about the publication:

“The COVID-19 coronavirus epidemic has a natural origin, scientists say”.

Every media outlets and china internet water army agents are now using this paper to claim final victory over “debunked lab made virus conspiracy theory”. This paper is also used by moderators on social networks to delete any possible discussion on the topic.

Reply

25. Pingback: [Debunking Nature Magazine's "COVID-19 Definitely Didn't Come From A Lab" China Propaganda | Real Patriot News](#)
26. Pingback: [Desacreditando la propaganda de China "COVID-19 definitivamente no vino de un laboratorio" de China | Heaven32](#)
27. Pingback: [Debunking Nature Magazine's "COVID-19 Definitely Didn't Come From A Lab" China Propaganda | Newzsentinel](#)
28. Pingback: [coronavirus reading list #5 | gringos estupidos](#)

29. **D.P. Miller** says: March 22, 2020 at 3:34 pm

Anyone with common sense would understand immediately that China's response to this bug was not a normal reaction....People in the dark , facing the new unknown , would not go off the edge immediately...that response was what one does when one understands the nature , the real consequences , of such as the release of (this) new virus.

...it was not new to them.... Ergo , it was being studied , cultured , altered within a controlling environment...and what better place than proximate to its discovery next to a bioweapon research lab ? Not made ? Now really.....!! I read a research print within a week of the news here... it was terrifying...self destruct ?? No wonder the efforts we now must put forth....what a sad mess...

Question is , while engaging in the ID of bug's destructive nature , was there a concurrent study to get the antidote , the counter immune mechanism identified and the ways and means to augment it?

...because if so they will be way ahead of the game....and we will be hurting... AND it would be poorly planned Science if there was NOT a counter measure being sought !

..

Reply

30. Pingback: Never Yet Melted » “The COVID-19 Virus Definitely Wasn't From a Lab”

31. Pingback: “No monkey ever reheated a frozen burrito” – What “The Expanse” tells us about the COVID-19 pandemic – Harvard to the Big House

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