Virologists Say Genetic “Fingerprints” Prove COVID-19 Man-Made, ‘No Credible Natural Ancestor’

Description

via ZeroHedge

Two notable virologists **claim to have found “unique fingerprints” on COVID-19 samples that only could have arisen from laboratory manipulation**, according to an explosive 22-page paper obtained by the *Daily Mail*.

The paper’s authors, Norwegian scientist Dr. Birger Sørensen (left) and British Professor Angus Dalgleish (right) via the Daily Mail

British professor Angus Dalgleish – **best known for creating the world’s first ‘HIV vaccine’**, and Norwegian virologist Dr. Birger Sørensen – chair of pharmaceutical company, Immunor, who has published 31 peer-reviewed papers and holds several patents, wrote that while analyzing virus samples last year, the pair discovered “unique fingerprints” in the form of “six inserts” created through **gain-of-function** research at the Wuhan Institute of Virology in China.

They also conclude that “SARS-Coronavirus-2 **has “no credible natural ancestor**” and that **it is “beyond reasonable doubt” that the virus was created via “laboratory manipulation.”**

Birger Sørensen, Andres Susrud & Angus Dalgleish

Immunor & St Georges University of London

May 26 2021

ABSTRACT (299 words)

We published the mode of action of our first-in-class third generation vaccine in QRB-D on 2 June 2020, making clear that we built outwards from analysis of the mode of action of SARS-Coronavirus-2. By 17 March 2020 we had discovered that the spike has six inserts which are unique fingerprints with five salient features indicative of purposive manipulation and we circulated an interim account in July 2020. In this paper we publish an updated and more complete account of the underlying virus aetiology and posit that the likelihood of it being the result of natural processes is very small. Since all relevant biological, computer-record and direct testimony from Wuhan has been destroyed or is unavailable, absolute proof cannot be provided. There is therefore a choice to be made between an agnostic and passive or an active methodological response which can more efficiently form and assess hypotheses. We employ an active scientific logic. First we describe here principles of engineering a virus for Gain of Function experiments. Then we update our bio-chemical analysis of the SARS-Coronavirus-2 virus's Mode of Action. We then set out the logic of our methodological choices. Fourthly, we add a diachronic dimension by analysing a sequence of five linked projects which, we suggest, shows by reasonable deduction how, where, when and by whom the SARS-Coronavirus-2 Spike acquired its special characteristics. We posit that this reconstructed historical aetiology meets the criteria of means, timing, agent and place to reverse the burden of proof. Henceforth, those who would maintain the zoonotic transfer hypothesis need to explain precisely why our simpler account of laboratory manipulation is wrong, before asserting that their evidence is persuasive. This is more especially when, as we also show here, the evidence used to support some of their arguments is actually in contradiction of them.

DailyMail.com exclusively obtained the 22-page paper which is set to be published in the scientific journal Quarterly Review of Biophysics Discovery. In it, researchers describe their months-long 'forensic analysis' into experiments done at the Wuhan lab between 2002 and 2019 (Daily Mail)

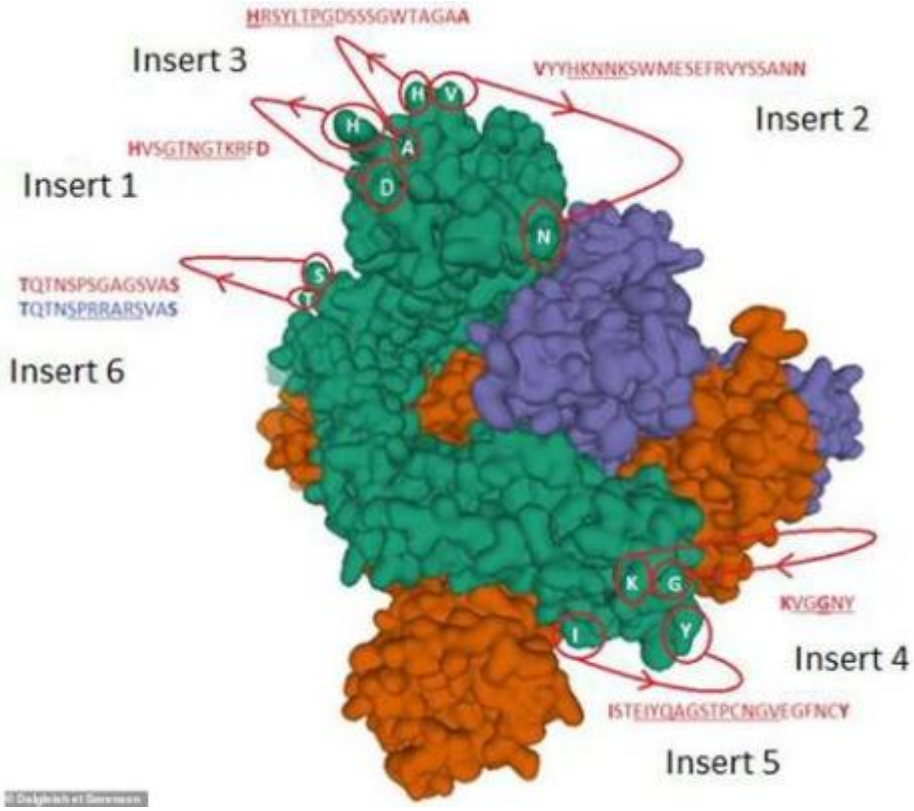
Table 2: GenBank details for the named strains aligned in table 1.

Sequence #	Origin of sequence	Comments	Collection date	Submitted date

1	Human – SARS-Coronavirus-2(Covid-19)	GenBank: MN908947.3	05-Dec-2019	05-Jan-2020
2	Pangolin	GenBank: MT084071.1 A complete virus has still not been verified	29-Mar-2019	23-APR-2020
3	Bat – SARS like Coronavirus SZ45	GenBank: AVP78031.1	Feb-2017	05-Jan-2018
4	Bat SARS like Coronavirus ZXC21	GenBank: AVP78042.1	Jul-2015	05-Jan-2018
5	Bat – RaTG13	GenBank: MN996532.1 [WARNING] On Oct 13, 2020 this sequence was replaced by MN996532.2.	24-Jul-2013	27-Jan-2020 24-MAR-2020
6	RmYN02	GenBank: MW201982.1	25-Jun-2019	22-NOV-2020
7	WIV16	GenBank: KT444582.1	21-Jul-2013	13-JAN-2016
8	Bat – SARS like Coronavirus LYRa11	GenBank: AHX37558.1	2011	22-Aug-2013
9	Human – SARS-Coronavirus	GenBank: AY278741.1 – Urbani	NA (2002-2003)	17-APR-2003

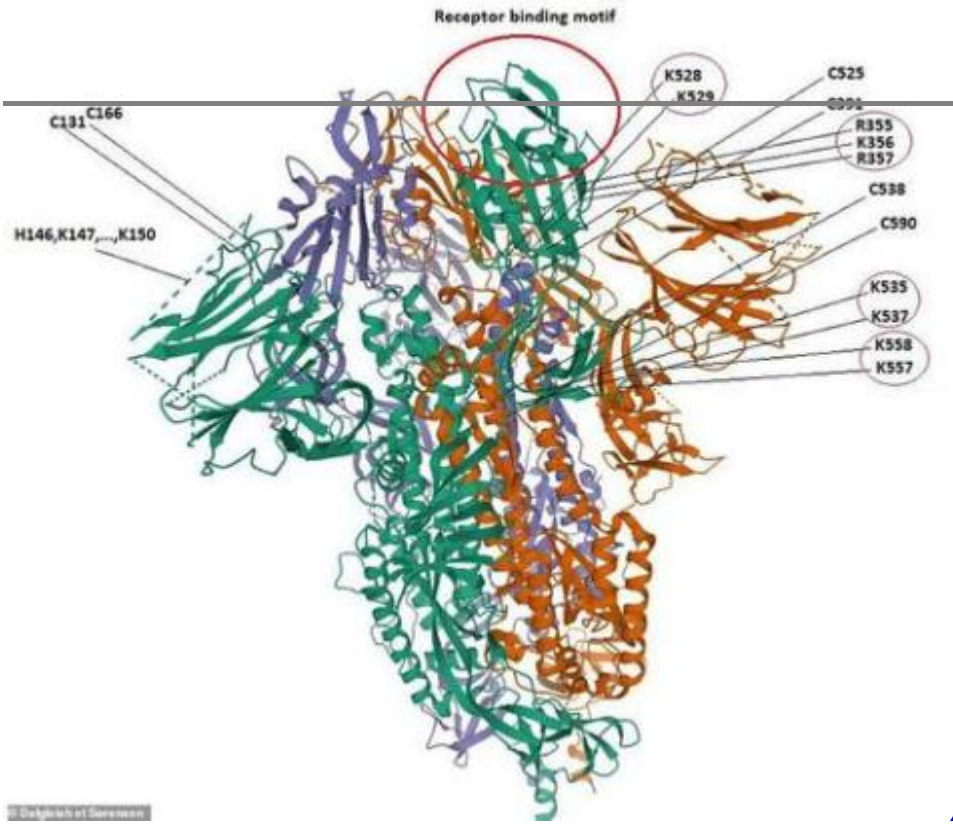
Table 2 shows that isolates 7,8 and 9 were collected between 2003 and 2013 and submitted to GenBank between 2003 and 2016. The other isolates 1-6 were isolated from 2013 onwards and submitted to GenBank between 2018 and 2020. The collection dates stated must be considered as indicative only. There is also lack of clarity about exactly what was collected and when by Dr Shi Zheng-li and her colleagues including Dr Peter Daszak, and when and what was submitted to GenBank. This is the subject of continuing research.

A 'GenBank' table included in the paper lists various coronavirus strains, with the dates they were collected and then when they were submitted to the gene bank, showing a delay of several years for some (Daily Mail)



19 has properties which have
ollaborated for many years on
China.

One diagram of the coronavirus



A second diagram showed how a row of four amino acids found on the SARS-Cov-2 spike have a positive charge that clings to human cells like a magnet, making the virus extremely infectious (Daily Mail)

The paper detailing their months-long "forensic analysis," which looked back at experiments done at the Wuhan Institute of Virology between 2002 and 2019, is set to be published in the scientific journal Quarterly Review of Biophysics Discovery.

More via the *Mail*:

> *Digging through archives of journals and databases,* ***Dalgleish and Sørensen pieced together how Chinese scientists, some working in concert with American universities, allegedly built the tools to create the coronavirus.***
>
> *Much of the work was centered around controversial '****Gain of Function****' research – temporarily outlawed in the US under the Obama administration.*
>
> *Gain of Function involves tweaking naturally occurring viruses to make them more infectious, so that they can replicate in human cells in a lab, allowing the virus's potential effect on humans to be studied and better understood.*
>
> *Dalgleish and Sørensen claim that* ***scientists working on Gain of Function projects took a natural coronavirus 'backbone' found in Chinese cave bats and spliced onto it a new 'spike', turning it into the deadly and highly transmissible SARS-Cov-2.***

One tell-tale sign of alleged manipulation the two men highlighted was a row of four amino acids they found on the SARS-Cov-2 spike.

In an exclusive interview with DailyMail.com, ***Sørensen said the amino acids all have a positive charge, which cause the virus to tightly cling to the negatively charged parts of human cells like a magnet, and so become more infectious****.*

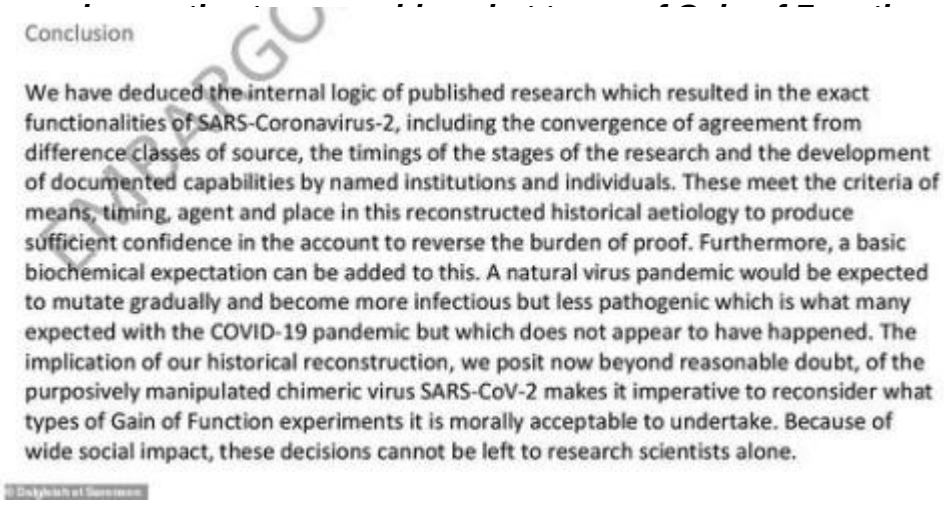
But because, like magnets, the positively charged amino acids repel each other, ***it is rare to find even three in a row in naturally occurring organisms, while four in a row is 'extremely unlikely,'*** *the scientist said.*

'The laws of physics mean that you cannot have four positively charged amino acids in a row. ***The only way you can get this is if you artificially manufacture it,'*** *Dalgleish told DailyMail.com.*

Their new paper says these features of SARS-Cov-2 are 'unique fingerprints' which are 'i ***ndicative of purposive manipulation****', and that* ***'the likelihood of it being the result of natural processes is very small.'***

*'****A natural virus pandemic would be expected to mutate gradually*** *and become more infectious but less pathogenic which is what many expected with the COVID-19 pandemic but which does not appear to have happened,' the scientists wrote.*

*'****The implication of our historical reconstruction, we posit now beyond reasonable doubt, of the purposively manipulated chimeric virus SARS-CoV-2 makes it*** ***experiments it is morally***

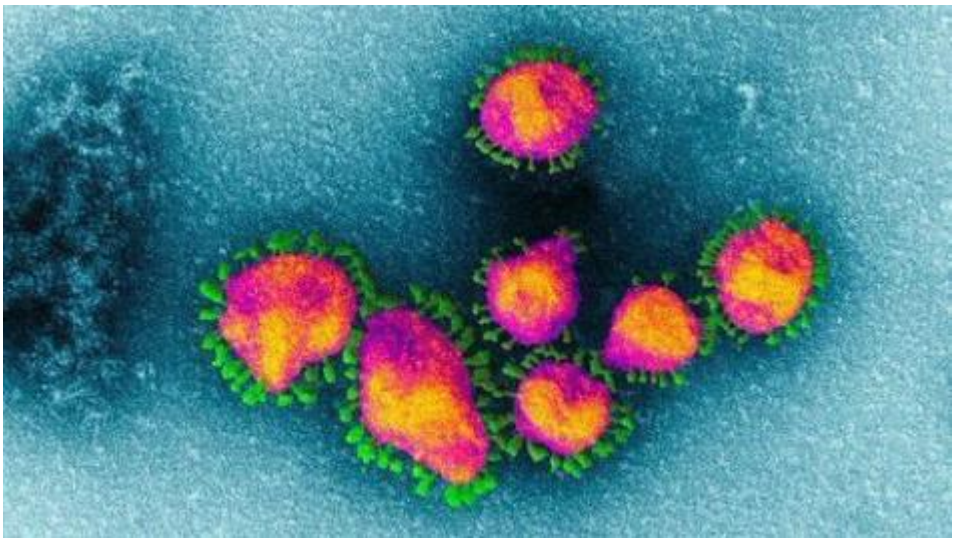


Conclusion

We have deduced the internal logic of published research which resulted in the exact functionalities of SARS-Coronavirus-2, including the convergence of agreement from difference classes of source, the timings of the stages of the research and the development of documented capabilities by named institutions and individuals. These meet the criteria of means, timing, agent and place in this reconstructed historical aetiology to produce sufficient confidence in the account to reverse the burden of proof. Furthermore, a basic biochemical expectation can be added to this. A natural virus pandemic would be expected to mutate gradually and become more infectious but less pathogenic which is what many expected with the COVID-19 pandemic but which does not appear to have happened. The implication of our historical reconstruction, we posit now beyond reasonable doubt, of the purposively manipulated chimeric virus SARS-CoV-2 makes it imperative to reconsider what types of Gain of Function experiments it is morally acceptable to undertake. Because of wide social impact, these decisions cannot be left to research scientists alone.

The study concluded 'SARS-Coronavirus-2 has no credible natural ancestor' and that it is 'beyond reasonable doubt' that the virus was created through 'laboratory manipulation' (Daily Mail)

When Sørensen and Dalgleish floated their findings last year, **it was 'debunked' with the thinnest of logic** – however **former MI6 chief Sir Richard Dearlove pointed to the pair's findings as an "important" developmentwhich could prove that the pandemic may have originated at the WIV.**



Sørensen and Dalgleish aren't the first scientists to find **unusual features** within COVID-19. Last June, the *Daily Telegraph* reported that there are ***two*** unique features to COVID-19:

First, the virus binds more strongly to *human* ACE2 enzymes than any other species, including bats.

Second, SARS-CoV-2 has a "furin cleavage site" missing in its closes bat-coronavirus relative, RaTG-13, which makes it significantly more infectious – a finding we reported in late February.

According to Israeli geneticist, Dr. Ronen Shemesh, **the Furin site is the most unusual finding**.

"I believe that the most important issue about the differences between ALL coronavirus types is the insertion of a Furin protease cleavage site at the Spike protein of SARS-CoV-2," he said. "**Such an insertion is very rare in evolution, the addition of such 4 Amino acids alone in the course of only 20 years is very unlikely**."

"There are many reasons to believe that the COVID-19 generating SARS-CoV-2 was generated in a lab. Most probably by methods of genetic engineering," he said, adding "**I believe that this is the only way an insertion like the FURIN protease cleavage site could have been introduced directly at the right place and become effective.**"

> Dr Shemesh, who has a PhD in Genetics and Molecular Biology from the Hebrew University in Jerusalem, and over 21 years of experience in the field of drug discovery and development, said **it is even "more unlikely" that this insertion happened in exactly the right place of the cleavage site of the spike protein – which is where it would need to occur to make the virus more infectious**. –*Daily Telegraph*

"What makes it even more suspicious is that fact that this insertion not only occurred on the right place and in the right time, but also turned the cleavage site from an Serine protease cleavage site to a

FURIN cleavage site," he added.

In January 2020, a team of Indian scientists wrote in a now-retracted paper that the coronavirus may have been genetically engineered to incorporate parts of the HIV genome, writing "This uncanny similarity of novel inserts in the 2019- nCoV spike protein to HIV-1 gp120 and Gag is **unlikely to be fortuitous in nature**," meaning – it was unlikely to have occurred naturally.

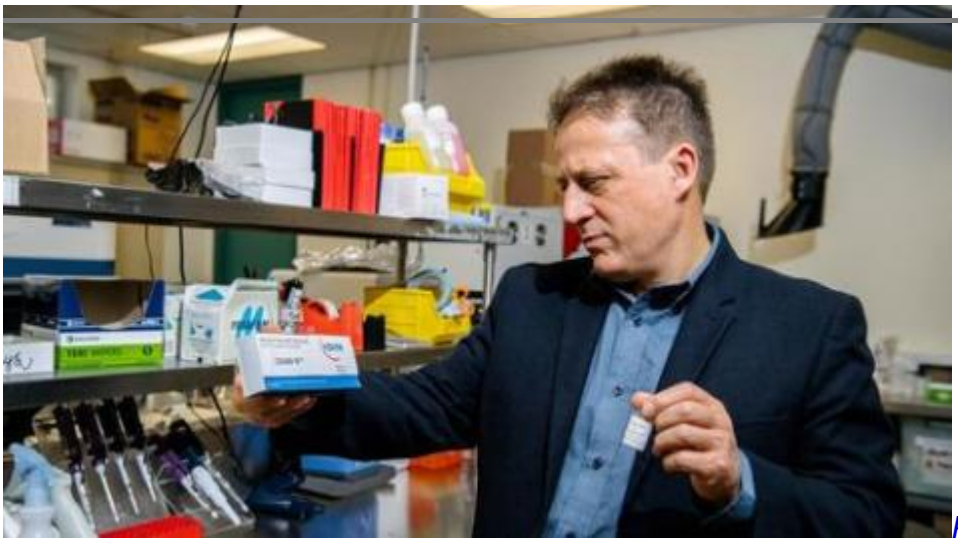
The next month, a team of researchers in Nankai University noted that COVID-19 **has an 'HIV-like mutation' that allows it to quickly enter the human body by binding with a receptor called ACE2 on a cell membrane.**

> **Other highly contagious viruses, including HIV and Ebola, target an enzyme called furin**, which works as a protein activator in the human body. Many proteins are inactive or dormant when they are produced and have to be "cut" at specific points to activate their various functions.
>
> When looking at the genome sequence of the new coronavirus, Professor Ruan Jishou and his team at Nankai University in Tianjin **found a section of mutated genes that did not exist in Sars, but were similar to those found in HIV and Ebola**. –*SCMP*

According to the Nankai University study, **the furin binding method is "100 to 1,000 times as efficient' as SARS at entering cells.**

"**This protein cleaving protein is highly promiscuous**, it's found in many human tissues and cell types and is involved in many OTHER virus types activation and infection mechanisms (it is involved in HIV, Herpes, Ebola and Dengue virus mechanisms)," said Dr. Shemesh. "**If I was trying to engineer a virus strain with a higher affinity and infective potential to humans, I would do exactly that**: I would add a Furin Cleavage site directly at the original less effective and more cell specific cleavage site."

Meanwhile, Flinders University Professor Nikolai Petrovsky found last year either "a remarkable coincidence or a sign of human intervention" within COVID-19 telling the *Telegraph* that COVID-19 is **"exquisitely adapted to humans."**



Professor Nikolai Petrovsky

“We really don’t know where this virus came from – that’s the truth. The two possibilities is that it was a chance transmission of a virus…the other possibility is that it was an accidental release of the virus from a laboratory,” he said, adding “One of the possibilities is that an animal host was infected by two coronaviruses at the same time and COVID-19. **The same process can happen in a petri-dish.”**

“In other words COVID-19 could have been created from that recombination event in an animal host or it could have occurred in a cell-culture experiment. I’m certainly very much in favour of a scientific investigation. Its only objective should be to get to the bottom of how did this pandemic happen and how do we prevent a future pandemic.”

Keep in mind – reporting any of this last year was punishable by social media banishment, demonetiziation, and hit-piece articles from propagandists peddling CCP talking points.