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FOR IMMEDIATE RELEASE
ACTION ALERT

THE CONCEPTUAL BASIS
For A Bioengineered COVID-19

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The Conceptual Basis for a Bioengineered COVID-19

by Col. Lawrence Sellin (Ret.) April 27, 2020

https://ccnationalsecurity.org/the-conceptual-basis-for-a-bioengineered-covid-19/

Questions remain as to whether this COVID-19 pandemic that we are living through is the result of malevolent actions by the Chinese government, i.e., some form of biological warfare. Or is it just the result of careless behavior in the Wuhan Institute of Virology or another nearby lab that accidentally resulted in the virus leaking out and spreading across the globe? Or could it be, as the World Health Organization and much of the media want us to believe, something that came from bats or other animals sold in the wet markets of China?

As I have been documenting in a series of recent articles, with very technical but vital information, the evidence is building that this was the result of genetic manipulation. If true, it could suggest that this line of research might lead in the direction that some might define as part of a biological warfare program. To explain how I've reached this conclusion, at this point, it requires a rather technical explanation. So please bear with me.

Viruses rely on the biochemical mechanisms of the host cell they invade to bind and fuse with the host cell membrane and replicate inside the cell.

The fusion part of that cascade of events can involve the virus using host cell enzymes to cleave one or more of the virus' proteins at specific sites to facilitate entry into the host cell.

Those sites are often composed of relatively short sequences of chemically basic amino acids called poly-basic cleavage sites.

At the junction of the S1 and S2 protein subunits, COVID-19 has just such a polybasic cleavage site that uses the host cell enzyme furin, which is found in many human organ systems and known to be involved in the pathogenic processes of viruses, for example, HIV, Ebola and various strains of coronavirus.

The presence of the furin polybasic cleavage site may explain clinical reports of COVID-19's ability to infect a variety of organ systems.

The furin polybasic cleavage site in COVID-19 can be roughly defined by the amino acid sequence SPRRARS, which is Serine-Proline-Arginine-Arginine-Alanine-Arginine-Serine, where the cleavage takes place at the R-S junction.

Within that broader sequence, the minimum sequence for a furin cleavage site is R-X-X-R, where Arginine (R) occurs in the 3rd and 6th positions and positions 4 and 5 can be any amino acid, but activity of the furin cleavage site can be significantly enhanced with a basic amino acid like Arginine in the 4th position, as occurs in COVID-19.

It is very important to note that the furin polybasic cleavage site in COVID-19 is unique and has not been found in any of the coronaviruses yet identified as close relatives.

Remarkably, however, such sequences do exist in other viruses, including coronaviruses not directly related to COVID-19.

For example, the feline (cat) enteric coronavirus (FECV) causes a mild, but highly-transmissible infection, in which chronically infected cats can shed infectious virus for a year or longer.

FECV isolates have an amino acid sequence at the S1/S2 junction of SRRARRS.

The alpha-coronavirus HKU1, which can infect the human respiratory system and has done so as recently as 2016, has a SRRKRRS sequence at the S1/S2 junction.

The Beaudette gamma-coronavirus strain has an amino acid sequence at the S2-prime (S2′) cleavage site of SSRRKRS, very similar to the sequence seen at COVID-19's S1 site.

It is also interesting to note that the S2′ sequence of bat coronavirus CoVZX21, often cited as a close relative of CoVid-19, has an identical amino acid sequence of SKPSKRS at that position, but is demonstrably different at the critical S1 cleavage site.

The bioengineering capability to insert polybasic cleavage sites into the coronavirus S1 protein is well-established, already from 2006.

All of the above could be considered coincidental except for the fact that no clear evolutionary pathway has been identified that would explain the presence of COVID-19's furin polybasic cleavage site, especially given its enhanced pathogenic significance.

It is, therefore, not an unreasonable alternative to assume that the unique furin polybasic cleavage site found in COVID-19 and in no other close relatives may be the result of genetic manipulation.

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