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ACTION ALERT**

**Col. Lawrence Sellin (Ret.)
Evidence Suggesting CoVid-19 is Man-Made**

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Evidence Suggesting CoVid-19 is Man-Made

by [Col. Lawrence Sellin \(Ret.\)](#) April 16, 2020

Identifying the unique characteristics of CoVid-19, understanding the techniques that have been used to study coronaviruses and analyzing the scientific publications going back two decades or more will all be key in determining the origin of the Wuhan pandemic.

Since the 2002-2003 SARS coronavirus pandemic (SARS-CoV), which also originated in China, it has been known that human infectivity depends on the coronavirus' capability to bind to a human lung cell receptor, in this case, angiotensin converting enzyme-2 (ACE2), a property that CoVid-19 also possesses.

In 2008, scientists at the Wuhan Institute of Virology, led by Zhengli Shi, [demonstrated](#) the importance of the human ACE2 binding capability by using bioengineering techniques to “splice” the receptor binding domain of SARS-CoV onto a non-human-infecting bat coronavirus, thereby creating the capability for the “new” virus to infect humans.

By 2013, a growing number of horseshoe bat coronaviruses, capable of binding to the human ACE2 receptor, were [isolated](#) by the Wuhan Institute of Virology under the direction of Zhengli Shi.

Given the possibility that CoVid-19 could be a naturally-occurring mutation within the bat population that “jumped” to humans, scientists world-wide have attempted to match CoVid-19’s genetic and amino acid sequence with coronaviruses found in nature.

Up until now, they have been unable to do so, but the nearest naturally-occurring relatives or “progenitors” of CoVid-19 have been suggested.

In the March 2020 scientific [article](#) “The proximal origin of SARS-CoV-2,” which has been widely cited both in the scientific literature and the mainstream media as evidence for CoVid-19 being a naturally-occurring coronavirus, the authors identified a number of close relatives to CoVid-19 and, from that, quickly concluded that CoVid-19 must occur in nature.

Yet, the authors cannot explain the presence of a unique amino acid sequence composed of Arginine-Arginine-Alanine-Arginine (RRAR), called a furin (polybasic) cleavage site that does not exist in any of the identified close relatives.

The [minimum sequence](#) for a furin cleavage site is R-X-X-R, where Arginine (R) occurs in the first and last positions and the middle two positions 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 second position, as occurs in CoVid-19.

Furin cleavage sites have been found to be important factors contributing to the pathogenicity in human ([MERS](#)) coronavirus infections and in [animals](#), like the bird infectious bronchitis Beaudette coronavirus strain, which has a furin cleavage site sequence of Arginine-Arginine-Lysine-Arginine, closely matching that of CoVid-19.

It is important to note that furin cleavage sites have been “[introduced](#)” into coronaviruses using widely-known genetic engineering techniques since, at least, 2006 in order to study the effect of cleavage to mediate cell-to-cell fusion and affect viral infectivity.

In the absence of conclusive evidence that CoVid-19 is naturally-occurring either within the bat population or as a Chinese laboratory isolate, it is postulated that CoVid-19 may have been manufactured as part of a research program and accidentally leaked from a high containment facility.

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