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**FOR IMMEDIATE RELEASE
ACTION ALERT**

**U.S. Expertise
Contributed to COVID-19?**

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How U.S. Expertise May Have Inadvertently Contributed to COVID-19

by [Col. Lawrence Sellin \(Ret.\)](#) May 4, 2020

<https://ccnationalsecurity.org/how-u-s-expertise-may-have-inadvertently-contributed-to-covid-19/>

While the media eagerly picked up on a quote this past week from the Office of the Director of National Intelligence (ODNI) that while the virus did in fact originate in China, “The Intelligence Community also concurs with the wide scientific consensus that the COVID-19 virus was not man-made or genetically modified,” that is by no means the final word on the matter.

There are only three possible origins for the COVID-19 pandemic:

- (1) It is a naturally-occurring disease, where coronaviruses circulating in a bat population mutated and acquired the ability to infect humans, which was then transmitted to people either visiting or working in the Wuhan Seafood Market;
- (2) A yet unknown and undescribed coronavirus of natural origin, now named COVID-19, was one of the many bat coronaviruses isolated from bat populations by Chinese scientists and leaked from a Wuhan laboratory;
- (3) COVID-19 was man-made and leaked from a Wuhan laboratory.

The Chinese government, the media and some scientists are desperately trying to convince the public that COVID-19 is a naturally-occurring disease because certain vested interests may be affected, including the potentially devastating political and economic consequences for China, global corporate and private investment in China and an effect on ongoing scientific collaboration and research funding.

Viruses, which can undergo frequent mutation, do “jump” from animals to humans after acquiring an ability to infect humans. That may prove to be the case for COVID-19.

Arguing against that conclusion are the facts that the initial patients hospitalized between December 1st and 10th, 2019 had [not visited](#) the Wuhan Seafood Market, there were [no bats](#) in that market and there is no clear evolutionary pathway yet identified that explains the unique features of COVID-19.

The claim that COVID-19 is naturally-occurring is based nearly entirely on a single, but widely-cited Nature Medicine article entitled “The Proximal Origin of SAR-CoV-2,” which compares the structure of COVID-19 to what the authors consider its closest relatives found in animal populations, specifically, the bat coronavirus RaTG13 and a coronavirus from the scaly anteater, called pangolins.

There are, however, inconsistencies that do not fully support that claim.

Although COVID-19 bears a striking structural similarity to the bat coronavirus RaTG13, the critical receptor binding domain, which initiates attachment to human cells, is [closer](#) to that of pangolins.

In addition, there is no explanation for the origin of the furin polybasic cleavage site as represented by the proline-arginine-arginine-alanine (PRRA) amino acid insertion, which does not exist in any of the bat or pangolin close relatives yet identified, a structure that is known to enhance [pathogenicity](#) and [transmissibility](#) in coronaviruses.

Alternatively, the inconsistencies of the naturally-occurring argument could be resolved if one assumes that COVID-19 was bioengineered.

There are two U.S. patents related to that type of bioengineering, “Methods and Compositions for Chimeric Coronavirus Spike Proteins” and “Insertion of Furin Protease Cleavage Sites in Membrane Proteins and Uses Thereof,” patent numbers US9884895B2 and US7223390, respectively.

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 binding and membrane-fusing capability of COVID-19 resides in a structure called the spike protein, specifically sections of the “S” protein, which contain the receptor binding domain and the furin polybasic cleavage site.

The bioengineering capabilities to “splice” the receptor binding domain from one virus to another and to insert a furin polybasic cleavage site are both well-established laboratory techniques for which I provide the following specific examples.

In 2015, Ralph Baric from the University of North Carolina, co-patent holder of US9884895B2, and Zheng-Li Shi, the “[bat woman](#)” from the Wuhan Institute of Virology, jointly published a [scientific article](#) describing the combination of the receptor-binding spike protein from a newly isolated coronavirus (SHC014) and the “backbone” from SARS-CoV, the coronavirus responsible for the 2002-2003 pandemic.

The above experiment produced a novel virus, chimera SHC014-MA15, which showed “robust viral replication both in vitro [cell cultures] and in vivo [animals],” using models adapted to test human infectivity.

In 2013, Chinese scientists [demonstrated](#) the capability to insert a furin polybasic cleavage site, similar to that of COVID-19, into a protein, an article which cited U.S. patent “Insertion of Furin Protease Cleavage Sites in Membrane Proteins and Uses Thereof.”

One of the authors of that 2013 article, Chinese scientist Shibo Jiang, has a joint appointment at the Lindsley F. Kimball Research Institute in New York and Fudan University in Shanghai and is a long-time collaborator of Zheng-Li Shi and Ralph Baric in coronavirus research.

All of the above is not meant to assign complicity or culpability in any way, but to demonstrate that the bioengineering capability to manufacture COVID-19 clearly exists and should be investigated as its possible origin.

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