



# American Resistance Party

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**FOR IMMEDIATE RELEASE  
ACTION ALERT**

## **HOW CHINA COULD HAVE MADE COVID-19 While Hiding Its Origin**

**04/23/2020 – FROM THE DESK OF:**

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### **How China could have made COVID-19 while hiding its origin**

Apr 23, 2020 Written By: [Lawrence Sellin](#)

<https://www.wionews.com/opinions-blogs/how-china-could-have-made-covid-19-while-hiding-its-origin-294223>

The coronavirus, COVID-19, which originated in China and is responsible for the global pandemic, has a unique structural feature that none of its closest viral relatives yet identified have, a furin polypeptide cleavage site.

Cleavage sites similar to that found in COVID-19 are present in some naturally-occurring coronaviruses, but in completely separate evolutionary pathways from COVID-19.

It has also been demonstrated that such coronavirus cleavage sites can be modified by genetic engineering to alter viral pathogenicity, sometimes increasing it.

For example, in a 2011 study, using site-directed mutagenesis, a non-infective influenza virus was transformed into a pathogenic one by the replacement of two native amino acids in its cleavage site with two new basic amino acids.

Scientists in China [have used site-directed mutagenesis](#) to alter the cleavage site of an infectious bronchitis virus by introducing basic amino acids, thereby increasing its pathogenicity and resulting in a “gain of function” such that the new virus was capable of infecting the brain producing “severe encephalitis.”

An alternative method for introducing a polybasic cleavage site and producing a pathogenic virus from a naturally-occurring non-pathogenic one is by a technique called [“reassortment”](#) or mixing two or more viruses in a host animal or cell culture system from which a new virus emerges through a natural recombination process.

The scientific “conventional wisdom” claims that COVID-19 is a naturally-occurring bat beta-coronavirus that “jumped” from animals to humans presumably in the Wuhan Seafood Market, an assertion with which the Chinese Communist Party and the World Health Organisation wholeheartedly agree.

There is also general, if unproven, agreement within the scientific community that [the closest relative](#) to COVID-19, and perhaps the strain from which it evolved, is another bat beta-coronavirus named RaTG13.

But RaTG13 does not have COVID-19’s furin polybasic cleavage site nor do any of the other close relatives that have been so far identified.

One of the main reasons we do not yet know the origin of COVID-19 is because China has not opened its research files and databases for inspection, sources containing information about the vast number of coronaviruses they have isolated and the experiments conducted on them.

One example is RaBtCoV/4991 (GenBank KP876546), which is one of the many bat coronaviruses isolated from an [abandoned mineshaft](#) in Yunnan Province, often mentioned as a potential starting point for a human disease outbreak.

Although isolated in 2013, RaBtCoV/4991 has never been fully sequenced or practically studied at all, even though, [according to one source](#), the RaBtCoV/4991 short sequence is a 100 per cent match for RaTG13 and SNU01, the viral isolate from the first COVID-19 patient in South Korea.

Applying the bioengineering techniques of recombination, site-directed mutagenesis and reassortment, CoVid-19 could have been created through the introduction of a furin polybasic cleavage site onto an appropriate coronavirus “backbone” from the catalogue of isolated strains in Chinese laboratories.

China also has [animal models](#) to test the ability of such new viruses to infect humans.

It is only the lack of candour by the Chinese government that prevents the world from knowing the true origin of COVID-19.

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