



American Resistance Party

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**FOR IMMEDIATE RELEASE
ACTION ALERT**

IS BAT CORONAVIRUS 4991 A Smoking Gun

04/25/2020 – FROM THE DESK OF:

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Is Bat coronavirus 4991 a smoking gun in China's COVID-19 cover-up?

Apr 25, 2020 - Written By: [Lawrence Sellin](#)

<https://www.wionews.com/opinions-blogs/is-bat-coronavirus-4991-a-smoking-gun-in-chinas-covid-19-cover-up-294760>

There is no doubt that COVID-19 is a novel coronavirus, but from where did it originate?

No one knows. There have been hints. Yet, now, for some reason, some of those hints have disappeared from the debate.

In the February 3, 2020 article in the prestigious journal Nature, scientists at the Wuhan Institute of Virology, led by Zheng-Li Shi, [claimed](#) that the coronavirus RaTG13, isolated from bats in Yunnan Province, China, showed a 96.2% sequence identity with COVID-19 and, therefore, “RaTG13 is the closest relative” of COVID-19 and forms a distinct lineage from other coronaviruses.

A month later on March 17, 2020, in now the most widely-cited article both by scientists and the media, “The proximal origin of SARS-CoV-2,” published by Nature Medicine, the authors supported the conclusion that RaTG13 is CoVid-19’s closest relative, which “jumped” from animals to humans in the Wuhan Seafood Market.

But is that conclusion warranted?

In an article that appeared on February 6, 2020, scientists at the State Key Laboratory of Virology, Modern Virology Research Center, College of Life Sciences, Wuhan University [wrote](#) that the partial RdRp gene sequence of bat coronavirus strain BtCoV/4991 (GenBank KP876546) had a 98.7% nucleotide identity with COVID-19.

On March 16, 2020 and maybe earlier, it was [noted](#) that BtCoV/4991's short sequence was a 100% match for the same short sequence in RaTG13 and was also a 100% match for [SNU01](#), the viral isolate from the first COVID-19 patient in South Korea.

The obvious question [then](#) as [now](#) remains, are RaTG13 and BtCoV/4991 the same coronavirus? If true, it could reveal a cover-up by China as to the true origin of COVID-19.

Both bat coronaviruses [RaTG13](#) and [BtCoV/4991](#) were isolated from bats in Yunnan Province, China in July 2013. Their GenBank accession designations are [MN996532](#) and [KP876546](#), respectively.

BtCoV/4991 was partially sequenced in 2016, but its full sequence has never been published. Oddly, although isolated in 2013, the sequence of RaTG13 was not submitted until January 27, 2020.

It is also strange that with all the information publicly available, the most widely cited article by many scientists and media, "The proximal origin of SARS-CoV-2," never mentions BtCoV/4991.

And how did a coronavirus, whether it be RaTG13 or BtCoV/4991, isolated from bats in Yunnan Province, nearly 1,000 miles away, end up in the Wuhan Seafood Market, if that was indeed the source of the outbreak?

Or, more likely, was it the result of a leak from a Wuhan laboratory, where experiments were being conducted on a variety of bat coronaviruses?

In addition, no one has explained the origin of COVID-19's furin polybasic cleavage site, which exists in none of the yet identified close coronavirus relatives and may be partially responsible for its [enhanced transmissibility](#) in humans.

Furthermore, as an April 22, 2020 comment [states](#):

“If they [the Chinese] obfuscated the origin of this virus, how can we be sure the RaTG13 genome is accurate and not manipulated? In this context, we would need independent third-party access to the original specimen to extract the genetics.”

Indeed. The science coming out of China seems to raise more questions than it answers.

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