

# Chapter 6

## SARS-CoV-2 Is a Robot Bioweapon

**Li-Meng Yan**

*Rule of Law Society, USA & Rule of Law Foundation, USA*

**Adrian David Cheok**

 <https://orcid.org/0000-0001-6316-2339>

*Professional University of Information and Management for Innovation,  
iUniversity, Tokyo, Japan*

### ABSTRACT

*Two possibilities should be considered for the origin of SARS-CoV-2: natural evolution or laboratory creation. In the authors' earlier report titled "Unusual Features of the SARS-CoV-2 Genome Suggesting Sophisticated Laboratory Modification Rather Than Natural Evolution and Delineation of Its Probable Synthetic Route," they disproved the possibility of SARS-CoV-2 arising naturally through evolution and instead proved that SARS-CoV-2 must have been a product of laboratory modification. Despite this and similar efforts, the laboratory creation theory continues to be downplayed or even diminished. This is fundamentally because the natural origin theory remains supported by several novel coronaviruses published after the start of the outbreak. Here, however, the authors use in-depth analyses of the available data and literature to prove that these novel animal coronaviruses do not exist in nature.*

### INTRODUCTION

SARS-CoV-2 is a novel coronavirus and the causative agent of the COVID-19 pandemic. Despite its tremendous impact, the origin of SARS-CoV-2, however, has been a topic of great controversy. In our first report titled "*Unusual Features of the*

DOI: 10.4018/978-1-7998-4679-6.ch006

*SARS-CoV-2 Genome Suggesting Sophisticated Laboratory Modification Rather Than Natural Evolution and Delineation of Its Probable Synthetic Route*” (Yan et al., 2020), we used biological evidence and in-depth analyses to show that SARS-CoV-2 must be a laboratory product, which was created by using a template virus (ZC45/ZXC21) owned by military research laboratories under the control of the Chinese Communist Party (CCP) government. In addition, resources and expertise are all in place in the Wuhan Institute of Virology (WIV) and related, other CCP-controlled institutions allowing the creation of SARS-CoV-2 in approximately six months.

What have not been fully described in our earlier analyses are details of the novel animal coronaviruses published by the CCP-controlled laboratories after the outbreak (Yan et al., 2020). While no coronaviruses reported prior to 2020 share more than 90% sequence identity with SARS-CoV-2 (Wu et al., 2020; Hu et al., 2018), these recently published, novel animal coronaviruses (the RaTG13 bat coronavirus (Zhou et al., 2020), a series of pangolin coronaviruses (Lam et al., 2020; Liu et al., 2020; Xiao et al., 2020; Zhang et al., 2020), and the RmYN02 bat coronavirus (Zhou et al., 2020) all share over 90% sequence identities with SARS-CoV-2. As a result, these SARS-CoV-2-like viruses have filled an evolutionary gap and served as the founding evidence for the theory that SARS-CoV-2 has a natural origin (Andersen et al., 2020; Boni et al., 2020; Hu et al., 2020). In this report, we provide genetic and other analyses, which, when combined with recent findings (Chan & Zhan, 2020; Hassanin, 2020; Lin & Chen, 2020; Rahalkar & Bahulikar, 2020a; Rahalkar & Bahulikar, 2020b; Segreto & Deigin, 2020; Seyran, 2020; Zhang, 2020a; Zhang 2020b), prove that these novel animal coronaviruses do not exist in nature and their genomic sequences are results of fabrication.

## **1. EVIDENCE PROVING THAT THE RATG13 VIRUS IS FRAUDULENT AND DOES NOT EXIST IN NATURE**

On February 3<sup>rd</sup>, 2020, Dr. Zhengli Shi and colleagues published an article in *Nature* titled “*A pneumonia outbreak associated with a new coronavirus of probable bat origin*” (manuscript submitted on January 20<sup>th</sup>) (Zhou et al., 2020), which was one of the first publications to identify SARS-CoV-2 as the pathogen causing the disease now widely known as COVID-19. Also reported in this article was a novel bat coronavirus named RaTG13, the genomic sequence of which was shown to be 96.2% identical to that of SARS-CoV2. The close evolutionary relationship between RaTG13 and SARS-CoV-2 as suggested by the high sequence identity had led to a conclusion that SARS-CoV-2 has a natural origin. These striking findings have consequently made this article one of the most cited publications in the currently overwhelmed field of coronavirus research. Interestingly, an article published by

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