

Chapter 5

Unusual Features of the SARS-CoV-2 Genome Suggesting Sophisticated Laboratory Modification as a Biological Robot

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ABSTRACT

The COVID-19 pandemic caused by the novel coronavirus SARS-CoV-2 has led to deaths worldwide and decimation of the global economy. Despite its tremendous impact, the origin of SARS-CoV-2 has remained mysterious and controversial. The natural origin theory, although widely accepted, lacks substantial support. The alternative theory that the virus may have come from a research laboratory is, however, censored on peer-reviewed scientific journals. Nonetheless, SARS-CoV-2 shows biological characteristics that are inconsistent with a naturally occurring, zoonotic virus. In this report, the authors describe the genomic, structural, medical, and literature evidence, which, when considered together, strongly contradicts the natural origin theory. The evidence shows that SARS-CoV2 should be a laboratory product created by using bat coronaviruses ZC45 and/or ZXC21 as a template and/or backbone. Building upon the evidence, the authors further postulate a synthetic

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route for SARS-CoV-2, demonstrating that the lab-creation of this coronavirus is convenient and can be accomplished in approximately six months.

INTRODUCTION

COVID-19 has caused a world-wide pandemic, the scale and severity of which are unprecedented. Despite the tremendous efforts taken by the global community, management and control of this pandemic remains difficult and challenging.

As a coronavirus, SARS-CoV-2 differs significantly from other respiratory and/or zoonotic viruses: it attacks multiple organs; it is capable of undergoing a long period of asymptomatic infection; it is highly transmissible and significantly lethal in high-risk populations; it is well-adapted to humans since the very start of its emergence (Zhan et al., 2020); it is highly efficient in binding the human ACE2 receptor (hACE2), the affinity of which is greater than that associated with the ACE2 of any other potential host (Mou et al., 2020; Piplani et al., 2020).

The origin of SARS-CoV-2 is still the subject of much debate. A widely cited *Nature Medicine* publication has claimed that SARS-CoV-2 most likely came from nature (Andersen et al., 2020). However, the article and its central conclusion are now being challenged by scientists from all over the world (Maiti, 2020; Lin & Chen, 2020; Bengston, 2020; Segreto & Deigin, 2020; Rahalkar & Bahulikar, 2020b; Robinson, 2020a; Robinson, 2020c; Sørensen et al., 2020; B. Zhang, 2020a; Sirotkin & Sirotkin, 2020; Seyran et al., 2020). In addition, authors of this *Nature Medicine* article show signs of conflict of interests (Columbia Mailman School of Public Health, 2020; Holmes, 2020), raising further concerns on the credibility of this publication.

The existing scientific publications supporting a natural origin theory rely heavily on a single piece of evidence – a previously discovered bat coronavirus named RaTG13, which shares a 96% nucleotide sequence identity with SARS-CoV-2 (P. Zhou, 2020). However, the existence of RaTG13 in nature and the truthfulness of its reported sequence are being widely questioned (Lin & Chen, 2020; Bengston, 2020; Segreto & Deigin, 2020; Rahalkar & Bahulikar, 2020a; Rahalkar & Bahulikar, 2020b; Singla et al., 2020; D. Zhang, 2020a). It is noteworthy that scientific journals have clearly censored any dissenting opinions that suggest a non-natural origin of SARS-CoV-2 (Segreto & Deigin, 2020; Robinson, 2020b). Because of this censorship, articles questioning either the natural origin of SARS-CoV-2 or the actual existence of RaTG13, although of high quality scientifically, can only exist as preprints (Maiti, 2020; Lin & Chen, 2020; Bengston, 2020; Segreto & Deigin, 2020; Rahalkar & Bahulikar, 2020a; Rahalkar & Bahulikar, 2020b; Singla et al., 2020; D. Zhang, 2020a) or other non-peer-reviewed articles published on various online platforms (Robinson, 2020a; Robinson, 2020c; Sørensen et al., 2020; B. Zhang,

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