**From:** Morens, David (NIH/NIAID) [E]
**Sent:** Wed, 4 Mar 2020 14:51:07 +0000
**To:** Folkers, Greg (NIH/NIAID) [E]
**Cc:** NIAID OD AM;NIAID OCGR Leg;NIAID COGCORE
**Subject:** Re: DAVID --- National Science Review: On the origin and continuing evolution of SARS-CoV-2 http://bit.ly/2uW6rxG
**Attachments:** image001.png, ATT00001.htm, image001.png, ATT00002.htm, Daily Mail TWO strains of the killer coronavirus are spreading around the world – and 70% of infected patients have caught the more aggressive and contagious type, study claims.eml, ATT00003.htm

[redacted] (b) (5)

Sent from my iPhone
David M Morens
OD, NIAID, NIH

On Mar 4, 2020, at 09:48, Morens, David (NIH/NIAID) [E] [redacted] (b) (6) wrote:

Greg, i just saw this and haven't had a chance to read carefully so here is a quick impression.

[redacted] (b) (5)

Sent from my iPhone
David M Morens
OD, NIAID, NIH

On Mar 4, 2020, at 08:42, Folkers, Greg (NIH/NIAID) [E] [redacted] (b) (6) wrote:

David, this may come up in ASF's 10:00 hearing. What do you make of this paper and the attendant press coverage?

# On the origin and continuing evolution of SARS-CoV-2

Xiaolu Tang, Changcheng Wu, Xiang Li, Yuhe Song, Xinmin Yao, Xinkai Wu, Yuange Duan, Hong Zhang, Yirong Wang, Zhaohui Qian ... Show more

Author Notes

*National Science Review*, nwaa036, https://doi.org/10.1093/nsr/nwaa036
Published:
03 March 2020

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## ABSTRACT

The SARS-CoV-2 epidemic started in late December 2019 in Wuhan, China, and has since impacted a large portion of China and raised major global concern. Herein, we investigated the extent of molecular divergence between SARS-CoV-2 and other related coronaviruses. Although we found only 4% variability in genomic nucleotides between SARS-CoV-2 and a bat SARS-related coronavirus (SARSr-CoV; RaTG13), the difference at neutral sites was 17%, suggesting the divergence between the two viruses is much larger than previously estimated. Our results suggest that the development of new variations in functional sites in the receptor-binding domain (RBD) of the spike seen in SARS-CoV-2 and viruses from pangolin SARSr-CoVs are likely caused by mutations and natural selection besides recombination. Population genetic analyses of 103 SARS-CoV-2 genomes indicated that these viruses evolved into two major types (designated L and S), that are well defined by two different SNPs that show nearly complete linkage across the viral strains sequenced to date. Although the L type (~70%) is more prevalent than the S type (~30%), the S type was found to be the ancestral version. Whereas the L type was more prevalent in the early stages of the outbreak in Wuhan, the frequency of the L type decreased after early January 2020. Human intervention may have placed more severe selective pressure on the L type, which might be more aggressive and spread more quickly. On the other hand, the S type, which is evolutionarily older and less aggressive, might have increased in relative frequency due to relatively weaker selective pressure. These findings strongly support an urgent need for further immediate, comprehensive studies that combine genomic data, epidemiological data, and chart records of the clinical symptoms of patients with coronavirus disease 2019 (COVID-19).

SARS-CoV-2, virus, molecular evolution, population genetics

Issue Section:

Research article

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