

Recombination may frequently occur between 2019-nCoV and SARS-CoV clades

Cheng-Qiang He¹, Chun-Xue Qin¹, Mei He¹, Sheng-Wen Li¹, Wei Wang¹, Hongbin He¹, and Nai-Zheng Ding¹

¹Affiliation not available

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Abstract

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV) and 2019 novel coronavirus (2019-nCoV) pose a serious threat to human health. To determine the genetic relationships between the two clades and the genetic mechanism of origin of 2019-nCoV, we compared the whole genomic sequences of SARS-CoV and 2019-nCoV and dissected their phylogenetic histories. Surprisingly, we found that the two clades have frequently exchanged genetic material through homologous recombination in recent decades. Nearly 2/3 of the genetic material of CoVZC45 comes from 2019-nCoV lineage, while the other 1/3 descends from SARS-CoV clade. In particular, the 2019-nCoV lineage might have acquired its receptor-binding domain from the SARS-CoV clade, enabling 2019-nCoV to bind to human angiotensin-converting enzyme 2 receptor and helping it to spread rapidly in humans. Our findings suggest the role of a virus of the SARS-CoV clade in causing COVID-19 and warn of the possible emergence of more mosaic CoVs capable of causing severe epidemics.

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