

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

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## Abstract

2019-nCoV and SARS-CoV seriously threatened human health. In order to know the genetic relations of the two dangerous clades and genetic mechanism of origin of 2019-nCoV, we compared whole genomic sequences of SARS-CoV and 2019-nCoV clades, and dissected phylogenetic histories of them. To our surprise, we found that the two clades may frequently exchange their genetic materials through homologous recombination in recent decades, resulting in 2019-nCoV and its sister branch represented by CoVZC45. Particularly the 2019-nCoV lineage might thereby acquire the receptor-binding domain from the SARS-CoV clade, enabling it to make use of angiotensin-converting enzyme 2 as well and thus spread rapidly in humans. Our findings suggest the accomplice role of a virus of SARS-CoV clade in COVID-19 and warn of the possible emergence of more mosaic CoVs capable of launching severe epidemic.

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