Journal of Medical Virology / Accepted Articles

RESEARCH ARTICLE | Free Access

Homologous recombination within the spike glycoprotein of the newly identified coronavirus may boost cross-species transmission from snake to human

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First published: 22 January 2020
https://doi.org/10.1002/jmv.25682
Citations: 2

This article has been accepted for publication and undergone full peer review but has not been through the copyediting, typesetting, pagination and proofreading process, which may lead to differences between this version and the Version of Record. Please cite this article as doi: 10.1002/jmv.25682

Abstract

The current outbreak of viral pneumonia in the city of Wuhan, China, was caused by a novel coronavirus designated 2019-nCoV by the World Health Organization, as determined by sequencing the viral RNA genome. Many patients were potentially exposed to wildlife animals at the Huanan seafood wholesale market, where poultry, snake, bats, and other farm animals were also sold. To determine the possible virus reservoir, we have carried out comprehensive sequence analysis and comparison in conjunction with relative synonymous codon usage (RSCU) bias among different animal species based on existing sequences of the newly identified coronavirus 2019-nCoV. Results obtained from our analyses suggest that the 2019-nCoV appears to be a recombinant virus between the bat coronavirus and an origin-unknown coronavirus. The recombination occurred within the viral spike glycoprotein, which recognizes cell surface receptor. Additionally, our findings suggest that snake is the most probable wildlife animal reservoir for the 2019-nCoV based on its RSCU bias resembling snake compared to other animals. Taken together, our results suggest that homologous recombination within the spike glycoprotein may contribute to cross-species transmission from snake to humans.

Citing Literature

Supporting Information

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