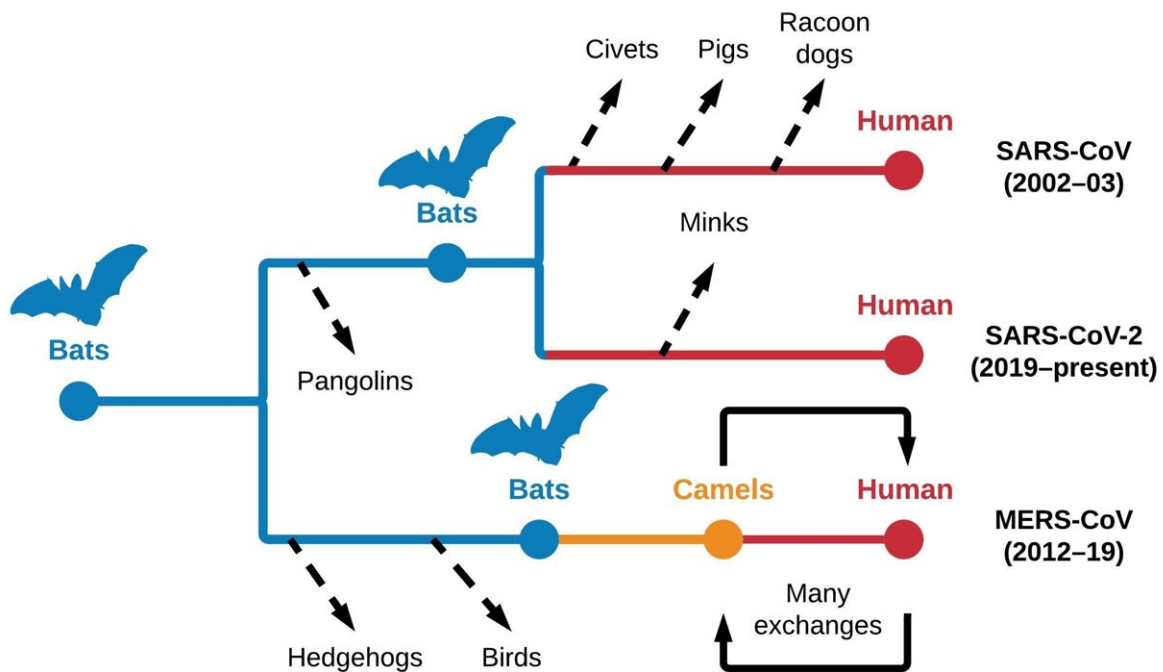


# Researchers analyze the host origins of SARS-CoV-2 and other coronaviruses

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This tree is a summary of the selected host transformations in the clade of Betacoronavirus associated with SARS-CoV, MERS-CoV, and SARS-CoV-2. Bats have been fundamental hosts of these human coronaviruses. The host transformations indicated by dotted lines are independent events that are not important to the origins of these human coronaviruses. Credit: Denis Jacob Machado

Coronavirus (CoVs) infection in animals and humans is not new. The earliest papers in the scientific literature of coronavirus infection date to 1966. However, prior to SARS-CoV, MERS-CoV, and SARS-CoV-2, very little attention had been paid to coronaviruses.

Suddenly, coronaviruses changed everything we know about personal and public health, and societal and economic well-being. The change led to rushed analyses to understand the origins of coronaviruses in humans. This rush has led to a thus far fruitless search for intermediate hosts (e.g., civet in SARS-CoV and pangolin in SARS-CoV-2) rather than focusing on the important work, which has always been surveillance of SARS-like viruses in bats.

To clarify the origins of coronavirus' infections in humans, researchers from the Bioinformatics Research Center (BRC) at the University of North Carolina at Charlotte (UNC Charlotte) performed the largest and most comprehensive evolutionary analyses to date. The UNC Charlotte team analyzed over 2,000 genomes of diverse coronaviruses that infect humans or other animals.

"We wanted to conduct evolutionary analyses based on the most rigorous standards of the field," said Denis Jacob Machado, the first author of the paper. "We've seen rushed analyses that had different problems. For example, many analyses had poor sampling of viral diversity or placed excessive emphasis on overall similarity rather than on the characteristics shared due to common evolutionary history. It was very important to us to avoid those mistakes to produce a sound evolutionary hypothesis that could offer reliable information for future research."

The study's major conclusions are:

- 1) Bats have been ancestral hosts of human coronaviruses in the case of SARS-CoV and SARS-CoV-2. Bats also were the ancestral hosts of

MERS-CoV infections in dromedary camels that spread rapidly to humans.

2) Transmission of MERS-CoV among camels and their herders evolved after the transmission from bats to these hosts. Similarly, there was transmission of SARS-CoV after the bat to human transmission among human vendors and their civets. These events are similar to the transmission of SARS-CoV-2 by fur farmers to their minks. The evolutionary analysis in this study helps to elucidate that these events occurred after the original human infection from lineages of coronaviruses hosted in bats. Therefore, these secondary transmissions to civet or mink did not play a role in the fundamental emergence of human coronaviruses.

3) The study corroborates the animal host origins of other human coronaviruses, such as HCoV-NL63 (from bat hosts), HCoV-229E (from camel hosts), HCoV-HKU1 (from rodent hosts) and HCoV-OC43 and HECV-4408 (from cow hosts).

4) Transmission of coronaviruses from animals to humans occurs episodically. From 1966 to 2020, the scientific community has described eight human-hosted lineages of coronaviruses. Although it is difficult to predict when a new human hosted coronavirus could emerge, the data indicate that we should prepare for that possibility.

"As coronavirus transmission from animal to human [host](#) occurs episodically at unpredictable intervals, it is not wise to attempt to time when we will experience the next [human](#) coronavirus," noted professor Daniel A. Janies, Carol Grotnes Belk Distinguished Professor of Bioinformatics and Genomics and team leader for the study. "We must conduct research on viruses that can be transferred from [animals](#) to humans on a continuous rather than reactionary basis."

**More information:** Denis Jacob Machado et al, Fundamental evolution of all Orthocoronavirinae including three deadly lineages descendent from Chiroptera-hosted coronaviruses: SARS-CoV, MERS-CoV and SARS-CoV-2, *Cladistics* (2021). [DOI: 10.1111/cla.12454](#)

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