

Tracking viral transmissions between humans and animals could help identify successful SARS-CoV-2 mutations

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The COVID-19 pandemic was probably caused by the transmission of the SARS-CoV-2 virus from animals to humans, and it has been reported anecdotally that the virus can pass from humans to different animal species, too.

To find out how the [transmission](#) of the virus between humans and animals affects its ability to infect and cause disease in humans an international team led by McGill University researchers has begun tracking the rates of inter-species transmission. By doing so, the researchers hope to gain insight into the likely ongoing trajectory of the virus.

Their goal was to discover both the rates of transmission, and whether there were specific viral [mutations](#) that occurred frequently enough to suggest they were helping the virus adapt to a particular animal.

Transmission of the virus in different non-human animals, such as [mink](#) and deer, could put the virus on different evolutionary trajectories that could affect its ability to infect and cause disease in humans—either in a positive or negative way.

Humans transmit COVID virus to animals more frequently than vice versa

The researchers carried out statistical analyses based on all the available viral genome sequence data from four different [animal species](#).

"We found that humans transmitted the virus to cats, dogs, minks, and deer dozens of times," said Jesse Shapiro, an associate professor in McGill's Department of Microbiology and Immunology and the senior author on a paper that was recently published in *eLife*. "But transmission from these [animals](#) back to humans is rarely observed—except for minks, which transmitted the virus back to humans on dozens of separate

occasions."

Mutations of virus in mink and deer associated with COVID infections

The researchers identified just three mutations, all in the viral spike protein, which are most likely to help the virus adapt to infecting and transmitting in mink. They also found several mutations, many of which had not been previously reported, that were significantly associated with SARS-CoV-2 infections in deer.

"Other recent studies have found that SARS-CoV-2 evolves particularly rapidly in deer, consistent with our discovery of a relatively large number of deer-associated mutations," said Sana Naderi, the first author on the paper and a graduate student at McGill University. "While many of these mutations are likely to help the virus replicate in deer, it remains to be seen if they make the virus more or less likely to infect humans."

A need for further sampling and more lab work

The researchers hope that their results will spur greater sampling of SARS-CoV-2 from different animal species—including more poorly sampled species such as cats and dogs, as well as further sampling from both [deer](#) and mink which could be important reservoirs of genetic diversity for the virus.

They suggest that these mutations could also be studied in lab experiments to determine if, and under what conditions, they affect replication and transmission of the [virus](#)—and, importantly, if their adaptation to one animal [species](#) comes with a trade off in terms of reduced adaptation to humans (or not).

More information: Sana Naderi et al, Zooanthroponotic transmission of SARS-CoV-2 and host-specific viral mutations revealed by genome-wide phylogenetic analysis, *eLife* (2023). [DOI: 10.7554/eLife.83685](https://doi.org/10.7554/eLife.83685)

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