

DEER MAY SERVE AS A RESERVOIR FOR OLD SARS-COV-2 VARIANTS

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Viral sequences recovered from white-tailed deer were “highly divergent from SARS-CoV-2 sequences recovered from humans”. File | Photo Credit: AFP

A study has found widespread infection of white-tailed deer with SARS-CoV-2 virus across the U.S. State of New York. The RNA of the virus was detected in 17 of the 2,700 samples (0.6%) collected during September to December 2020, and in 583 of the 2,762 samples (21.1%) collected during September to December 2021. The researchers found cocirculation of the Alpha, Delta, and Gamma variants in the white-tailed deer, months after they were last detected in humans. Of particular concern is the fact that the viral sequences recovered from white-tailed deer were “highly divergent from SARS-CoV-2 sequences recovered from humans”. This implies rapid adaptation of the virus in white-tailed deer.

The study found multiple spillover events from humans to deer of the Alpha and Delta lineages, and subsequent transmission among white-tailed deer and adaptation of the viruses in the deer.

While the precise implication of these mutations in enabling the virus to quickly and easily spread between white-tailed deer and from the animals to humans is yet to be determined, the very presence of SARS-CoV-2 variants that is no longer in circulation among humans arises the real possibility of the white-tailed deer serving as reservoir for variant SARS-CoV-2 strains that no longer circulate in the human population. The virus is likely to have jumped from humans to white-tailed deer during feeding or targeted baiting of hunting prey. The results of the study were published in the journal Proceedings of the National Academy of Sciences.

It was already known that the ACE2 of white-tailed deer (WTD) share a high similarity to the human ACE2 receptors and this similarity, it was predicted, will allow the virus to bind and enter the cells of deer. If silico predictions too showed the animals to be highly susceptible to infection by SARS-CoV-2 virus, intranasal inoculation of the virus in white-tailed deer led to infection, replication and shedding of the virus, and eventual transmission from one deer to another. That white-tailed deer is broadly distributed in North America with an estimated 30 million population is a concern if the animal turns out to be a reservoir for the virus.

The researchers confirmed that the virus collected from the deer during 2021 was infectious and active virus replication was proven in laboratory studies. While the Delta variant was found in human samples and coincided with the detection in deer, the Alpha and Gamma variants were

rarely in circulation among humans between September and December 2021.

The Alpha and Gamma variants in the deer had numerous mutations (about 50-80) in comparison to the ancestral Wuhan strain. The Delta variant in the animals revealed similar genetic divergence from the human Delta sequences but the number of mutations accumulated in deer sequences was lower (40-65).

“These observations highlight the need to establish continuous surveillance programs to monitor the circulation, distribution, and evolution of SARS-CoV-2 in White-tailed deer populations and to establish measures to minimise additional virus introductions in animals that may lead to spillback of deer-adapted SARS-CoV-2 variants to humans,” they write.

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