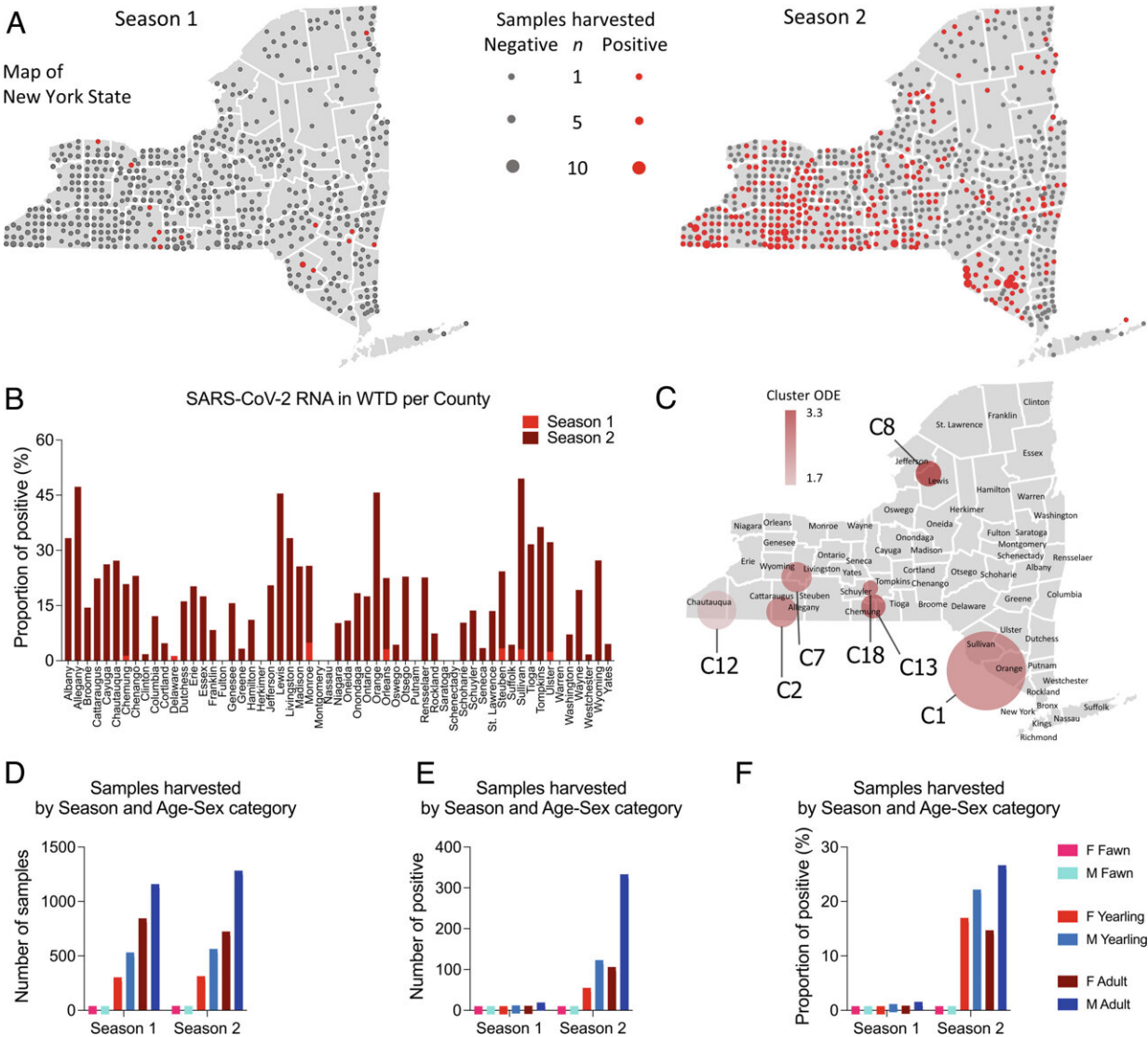


Researchers find deer carry SARS-CoV-2 variants that are extinct in humans

January 31 2023



Demographics of WTD population sampled and tested for SARS-CoV-2. Retropharyngeal lymph node (RPLN) samples were collected from free-ranging

hunter-harvested WTD during the hunting Season 1 (September to December 2020, $n = 2,700$) and Season 2 (September to December 2021, $n = 2,762$) in the State of New York (NY). (A) Sampling distribution and positivity across NY. SARS-CoV-2 RNA was detected in 17 samples (0.6%) from Season 1 and 583 samples (21.1%) from Season 2. (B) Proportion of SARS-CoV-2–positive samples in Season 1 and Season 2 per county of NY. (C) High-risk areas or hotspots of SARS-CoV-2 infection in WTD in NY. Spatial cluster analysis performed with the samples from Season 2 ($n = 2,762$). Nineteen spatial clusters (C1 to C19) containing from 3 to 57 positive samples collected within a radius of 10.6 to 55 km from each other were identified. Seven hotspots with high-risk for SARS-CoV-2 infection in WTD (relative risk [RR] > 1.76) are highlighted in the map. (D) Total number of collected samples based on sex and age of WTD during Season 1 and Season 2. Animals were distributed in three age groups as follows: younger than 1.5 y old (fawns), ≥ 1.5 and younger than 2.5 y old (yearlings), and ≥ 2.5 y old (adults). (E) Number of SARS-CoV-2–positive samples based on sex and age of WTD during Season 1 and Season 2. (F) Proportion of positive samples based on sex and age of WTD during Season 1 and Season 2. Credit: *Proceedings of the National Academy of Sciences* (2023). DOI: 10.1073/pnas.2215067120

Cornell University researchers have found that white-tailed deer—the most abundant large mammal in North America—are harboring SARS-CoV-2 variants that were once widely circulated, but no longer found in humans.

Whether or not deer could act as long-term reservoirs for these obsolete variants is still unknown, as scientists continue to collect and analyze new data.

The study, published January 31 in the journal *Proceedings of the National Academy of Sciences*, represents one of the most comprehensive studies to date to assess the prevalence, [genetic diversity](#) and evolution of SARS-CoV-2 in [white-tailed deer](#).

"One of the most striking findings of this study was the detection of co-circulation of three variants of concern—alpha, gamma and delta—in this wild animal population," said Diego Diel, associate professor of population medicine and diagnostic sciences at Cornell.

Over the course of the pandemic, deer have become infected with SARS-CoV-2 through ongoing contact with humans, possibly from hunting, wildlife rehabilitations, feeding of wild animals or through wastewater or water sources.

"A virus that emerged in humans in Asia, most likely after a spillover event from an animal reservoir into humans, apparently, or potentially, has now found a new wildlife reservoir in North America," Diel said.

The 5,700 samples used in the study were collected over two years in New York from 2020-22.

When the researchers compared the genomic sequences of the variants found in deer with sequences of the same variants taken from humans across New York, they found the viruses had mutated in the deer, suggesting the variants had likely been circulating in deer for many months. By the time alpha and gamma variants were detected in deer, for example, there was no evidence of these viral strains still circulating in humans. In fact, when they were found in deer, neither [variant](#) had been detected in humans in New York for four to six months.

"When we did sequence comparisons between those viruses recovered from white-tailed deer with the human sequences, we observed a significant number of mutations across the virus genome," Diel said, adding that some of the viruses had up to 80 mutations compared with the [human](#) sequences, providing further evidence that the viruses had likely been circulating in the deer for some time. The mutations suggest the virus has adapted to deer, possibly making it more transmissible

between them.

More study is needed to confirm whether these variants will disappear in deer over time or whether there is risk of SARS-CoV-2 spreading to other wildlife, including predators.

"Because of the evidence obtained in our study, it is very important to continue to monitor the [virus](#) in these [animal populations](#) to really understand and track changes that could lead or favor spill back into humans and other wildlife," Diel said.

There are an estimated 30 million white-tailed deer in the United States. A 2022 study by Diel and others found that across five states surveyed in 2021, SARS-CoV-2 was found in up to 40% of white-tailed deer.

More information: Leonardo C. Caserta et al, White-tailed deer (*Odocoileus virginianus*) may serve as a wildlife reservoir for nearly extinct SARS-CoV-2 variants of concern, *Proceedings of the National Academy of Sciences* (2023). [DOI: 10.1073/pnas.2215067120](https://doi.org/10.1073/pnas.2215067120)

Provided by Cornell University

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