

SARS-CoV-2 B.1.1.7 variant of concern detected in a pet dog and cat after exposure to a person with COVID-19, USA

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Case Report

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Abstract

As part of a longitudinal household transmission study of pets living with persons with COVID-19 in Texas, two pets were confirmed to be infected with the SARS-CoV-2 B.1.1.7 variant of concern (VOC). The pets were a dog and a cat from the same household, sampled two days after their owner tested positive for COVID-19. The oral, nasal, and fur swabs for both pets tested positive for SARS-CoV-2 by qRT-PCR and consensus whole genome sequences from the dog and cat were 100 % identical and matched the B.1.1.7 VOC. Virus was isolated from the cat's nasal swab. One month after initial detection of infection, the pets were re-tested twice at which time only the fur swabs (both pets) and oral swab (dog only) remained positive, and neutralizing antibodies for SARS-CoV-2 were present in both animals. Sneezing by both pets was noted by the owner in the weeks between initial and follow-up testing. This study documents the first detection of B.1.1.7. in companion animals in the United States, and the first genome recovery and isolation of B.1.1.7 variant of concern globally in any animal.

Main Text

The evolution and emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants have caused concern for increased transmissibility¹, pathogenicity², and altered effectiveness of diagnostics³, therapeutics, and vaccines⁴. Human-to-animal transmission of SARS-CoV-2 is well-documented in pets⁵, which typically become infected after exposure to owners with COVID-19⁶. However, the impact of infections with SARS-CoV-2 variants of concern on the clinical presentation and duration of infection in pets and the transmissibility between people and pets remains unknown. Since June 2020, we have conducted a longitudinal household transmission study of pets living with one or more persons with COVID-19⁷ to better understand the role of virus transmission between humans and pets.

As part of this ongoing study, two pets from the same household were sampled for SARS-CoV-2 on February 12, 2021, two days after their owner—one of two residents in a home in Brazos County, Texas—received a positive test result for COVID-19 through a commercial laboratory; no viral sequence was generated from the owner. The pets—the only animals in the home—were a 15-year-old Labrador retriever mix dog and a 12-year-old domestic shorthair cat. On initial visit, the animals were asymptomatic. The owner described a high degree of contact with both pets, including sleeping in the same room (dog) and bed (cat). Following previously described methods⁷, oral, nasal, and fur swabs from both pets were found to be positive for SARS-CoV-2 by real-time (RT) PCR. Rectal swabs tested negative. Sera tested negative for SARS-CoV-2 neutralizing antibodies (Table). Live virus isolation was attempted from all positive samples and was successful from the cat's nasal swab. SARS-CoV-2 whole genome sequencing was attempted and successful from the cat's nasal swab and the dog's oral swab. Consensus sequences from both animals were 100% identical to each other and were identified as the B.1.1.7 variant of concern by single-nucleotide polymorphism (SNP) analysis and alignment. In addition to characteristic B.1.1.7 mutations, sequences from both animals also showed 8 SNPs in ORF1ab and ORF8.

These pets were resampled on March 11, at which time the owner disclosed both had been sneezing over the past weeks. Pets were resampled again on March 15, and clinical signs had resolved. Nasal and rectal swabs from both resample time points tested negative, while fur swabs (both animals) and the oral swab (dog) remained positive with high Ct. Neutralizing antibodies were detected in both animals (Table).

This study documents the first detection of B.1.1.7. in companion animals in the United States, and the first genome recovery and isolation of B.1.1.7 variant of concern globally in any animal. These findings are coincident

with detection of B.1.1.7 infection in rectal swabs of three U.K. pets with myocarditis⁸. These results support public health guidance that recommends people with COVID-19 isolate from animals⁹ and the continued application of a One Health approach to SARS-CoV-2 investigations. Given the continued emergence¹⁰ and enhanced transmissibility and pathogenicity of B.1.1.7 in humans¹, onward transmission of this and other variants of concern from animals should remain the subject of ongoing research.

Declarations

Acknowledgments

We appreciate the participation of the owner and their pets in this study. All samples were obtained from privately-owned animals in accordance with guidelines approved by the Texas A&M University's Institutional Animal Care and Use Committee and Clinical Research Review Committee on May 14, 2020 (2018 – 0460 CA). We thank Dr. Susan Rollo of Texas Animal Health Commission and Drs. Laura Robinson, Paul Gruenwald, and David Smonko of Texas Department of State Health Services for assistance in the case investigation. The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention or the USDA. Project funds provided in part by Texas A&M AgriLife Research and the Centers for Disease Control and Prevention RFP 75D 301-20-R-68167. The authors declare no conflicts of interest.

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Table

Table. Longitudinal SARS-CoV-2 test results for a pet dog and cat from the same household in Texas that were confirmed for infection with the B.1.1.7. variant of concern.

| Animal ID number, date of sample collection | N1/N2 real-time (RT) PCR Ct values for swab testing* | | | | Viral neutralization endpoint titer | Viral isolation | Genome sequence GISAID accession† |
|---|--|-----------|---------|-----------|-------------------------------------|------------------------------------|--|
| | oral | nasal | rectal | fur | | | |
| Dog TAMU-466) | | | | | | | |
| Feb 12 2021 | 28.8/28.7 | 28.5/28.8 | nd/nd | nd/37.9 | nd | Oral, nasal, fur negative | hCoV-19/dog/USA/TX-TAMU-21-005988-002-466/2020 |
| Mar 11 2021 | nd/nd | nd/nd | nd/nd | 35.9/38.4 | 1:16 | na | na |
| Mar 15 2021 | 36.9/39.4 | nd/nd | nd/nd | nd/nd | 1:8 | na | na |
| Cat TAMU-467 | | | | | | | |
| Feb 12 2021 | 31.4/31.7 | 24.8/24.3 | nd/39.2 | 35.2/34.9 | nd | Oral, fur negative; nasal positive | hCoV-19/cat/USA/TX-TAMU-21-005988-005-467/2020 |
| Mar 11 2021 | nd/nd | nd/nd | nd/nd | 34.6/37.4 | 1:64 | na | na |
| Mar 15 2021 | nd/nd | nd/nd | nd/nd | 36.7/38.1 | 1:64 | na | na |

Abbreviations: nd (not detected); na (not attempted); N1/N2 (virus nucleocapsid gene target region 1 and 2)

*Testing was conducted at both the Wisconsin Veterinary Diagnostic Laboratory and National Veterinary Services Laboratory (NVSL). When detected in both laboratories, the Ct values were averaged by target.

†Texas dog and cat viral genome sequences available at GISAID under these accession numbers, which include state of origin (TX); submitting laboratory (TAMU/Texas A&M University); NVSL accession (21-00598): and animal ID (dog, 466; cat, 467).