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SHORT COMMUNICATION

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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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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.

KEYWORDS

cat, COVID-19, dog, one health, SARS-CoV-2, spillback, variant of concern

1 | INTRODUCTION

The evolution and emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants have caused concern for increased transmissibility (Davies, et al., 2021), pathogenicity (Davies et al., 2021), and altered effectiveness of diagnostics (Ascoli, 2021), therapeutics and vaccines (Altmann et al., 2021). Human-to-animal transmission of SARS-CoV-2 is well-documented

TABLE 1 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[a]				Viral neutralization endpoint titre	Viral isolation	Genome sequence GISAID accession[b]
	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: N1/N2, virus nucleocapsid gene target region 1 and 2; na, not attempted; nd, not detected.

[a]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.

[b]Texas dog and cat viral genome sequences available at GISAD 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).

in pets (Hosie et al., 2021), which typically become infected after exposure to owners with COVID-19 (OIE 2021). 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-19 (Hamer et al., 2020) 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 12 February 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 methods (Hamer et al., 2020), 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 using a 96-well virus neutralization test as previously described (Table 1; McAloose et al., 2020). 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 1).

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 myocarditis (Ferasin et al., 2021). These results support public health guidance that recommends people with COVID-19 isolate from animals (CDC, 2021) and the continued application of a One Health approach to SARS-CoV-2 investigations. Given the continued emergence (Galloway et al., 2021) and enhanced transmissibility and pathogenicity of B.1.1.7 in humans (Davies, Abbott, et al., 2021), onward transmission of this and other variants of concern from animals should remain the subject of ongoing research.

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[Correction added on 27 May 2021, after first online publication: The funding statement has been added before the last sentence of the Acknowledgments in this current version.]

CONFLICTS OF INTEREST

The authors declare no conflict of interest.

AUTHOR CONTRIBUTIONS

S.A.H, R. R. G, C.B.B. and G.L.H.: involved in conceptualization. S.A.H., I.B.Z., L.D.A., C.M.R., E.D., R.E.B., W.T., A.P.-C., M.L.K., M.J.-M., M.K.T., S.R.A., A.L. and G.L.H.: involved in methodology. M.L.K., M.J.-M. and M.K.T.: involved in validation. S.A.H., R.R.G., M.J.-M., M.K.T., S.R.A. and G.L.H.: involved in formal analysis. S.A.H., I.B.Z., L.D.A., C.M.R., E.D., R.E.B., W.T., M.J.-M., M.K.T., S.R.A. and A.L.: involved in investigation. S.A.H, R.R.G., Y.A., R.S.B.F., C.B.B. and G.L.H.: involved in resources. S.A.H., L.D.A. and C.M.R.: involved in data curation. S.A.H. and G.L.H: involved in writing—original draft preparation. all authors: involved in writing—review and editing. S.A.H, R. R. G, C.B.B. and G.L.H.: involved in supervision. S.A.H, L.D.A., Y.A., R.S.B.F. and G.L.H.: involved in project administration. S.A.H., R.R.G.,C.B.B., G.L.H.: involved in funding acquisition. All authors have read and agreed to the published version of the manuscript.

ETHICAL APPROVAL

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). Research was exempt from Institutional Review Board oversight.

DATA AVAILABILITY STATEMENT

The whole-genome sequences from this study are available at GISAID accession numbers hCoV-19/dog/USA/TX-TAMU-21–005988–002-466/2020 and hCoV-19/cat/USA/TX-TAMU-21–005988–005-467/2020.

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