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Possible Human-to-Dog Transmission of SARS-CoV-2, Italy, 2020

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We detected severe acute respiratory syndrome coronavirus 2 in an otherwise healthy poodle living with 4 family members who had coronavirus disease. We observed antibodies in serum samples taken from the dog, indicating seroconversion. Full-length genome sequencing showed that the canine and human viruses were identical, suggesting human-to-animal transmission.

Coronavirus disease (COVID-19), caused by infection with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), emerged in humans in Wuhan, China, in late December 2019, probably because of spillover from an unidentified animal host (1). Dogs and cats, to which some coronaviruses are endemic (2), are also susceptible to SARS-CoV-2 infection (3,4). Although the spread of SARS-CoV-2 is maintained mainly by human-to-human transmission, the epidemiologic implications of animal susceptibility remain uncertain (4). We characterized the full genome of a SARS-CoV-2 isolate detected in a dog.

A female poodle, who was 1.5 years of age, lived with 4 family members in Bitonto, Italy. All family members had signs and symptoms of COVID-19, the illness caused by SARS-CoV-2 infection. High temperature (37.5°C–38.5°C), coughing, anosmia, and ageusia developed in the mother, who was 54 years of age, on October 31, 2020. The woman tested positive for SARS-CoV-2 by a rapid antigen test conducted on November 3, 2020. The local health authority

collected nasopharyngeal swab samples and used molecular testing to confirm SARS-CoV-2 infection in the woman's husband and 2 daughters. Clinical signs in the other family members ranged from mild fatigue and high temperatures (37.5°C–37.8°C) in the daughters to moderate respiratory signs and persistent high temperature (37.8°C–38.6°C) in the husband. This study was approved by the Ethics Committee of the Department of Veterinary Medicine at the University of Bari (approval no. 15/2020).

On November 4, 2020, the owners collected oral and nasal swab samples from the family's poodle according to our instructions. The pooled samples tested positive for SARS-CoV-2 by real-time reverse transcription PCR selective for the N gene (5). During the next 11 days, the owners collected nasal, oral, and rectal swab samples from the dog. Of 20 samples collected during November 6–15, a total of 4 samples (all of which were collected during November 6–9) tested positive for SARS-CoV-2 (Table). Viral shedding occurred at low titers. We did not isolate the virus. The dog did not show any clinical signs, and no other pets lived in the household.

We tested a serum sample collected by the dog's veterinarian on November 27 with 2 commercial multispecies ELISA tests: ID Screen SARS-CoV-2 Double Antigen Multi-species ELISA (ID.vet, <https://www.id-vet.com>) and Eradikit COVID19-Multispecies (In3Diagnostic, <http://www.in3diagnostic.com>). We also conducted a plaque reduction neutralization test (PRNT) (4) and a virus neutralization test (VNT) (6). We detected antibodies with the Eradikit (23%), PRNT (1:80), and VNT (1:10). We used serologic as-

says to confirm the presence of antibodies against SARS-CoV-2 in an additional serum sample collected on December 12, 2020; the antibody titers were 1:80 for PRNT and 1:20 for VNT (Table).

We submitted the positive pooled oral and nasal swab samples from the dog and the oropharyngeal swab sample from the index patient, all of which were collected on November 4, for next-generation sequencing (7). Next-generation sequencing obtained total reads of 929,736 with a mean coverage of 4,300× for the index patient and 969,837 with a mean coverage of 1,800× for the dog. Complete genomes were obtained using the pipeline SARS-CoV-2 RECOVERY in the Galaxy public server ARIES (Istituto Superiore di Sanità, <https://w3.iss.it/site/aries>). The 2 SARS-CoV-2 genomes shared 100% nucleotide identity. The Pangolin COVID-19 Lineage Assigner (<https://pangolin.cog-uk.io>) and Nextclade (<https://clades.nextstrain.org>) assigned the sequences to the lineage B.1.177 (denoted by Nextclade as 20A.EU1) in Europe. Phylogenetic analysis confirmed the clustering of the 2 strains within the GV clade and the B.1.177 lineage already detected in Italy (Figure).

Despite the massive number of persons with SARS-CoV-2, only a few cases of active infection in pets have been reported (3). SARS-CoV-2-specific antibodies in pets have been reported on a few occasions, and higher seroprevalence rates have been found in animals from households in which family members have COVID-19 (4,6,8). The scarce reports of natural infection in dogs reflect their low susceptibility to SARS-CoV-2; for this infection, dogs are asymptomatic, produce limited titers, and have a reduced

Table. Molecular and serologic testing of dog with severe acute respiratory syndrome coronavirus 2 infection, Italy, 2020*

Date of sample collection	Real-time reverse transcription PCR C _t values			Serologic assay results			
	Oral	Nasal	Rectal	ELISA ID.vet†	ELISA In3Diagnostic‡	PRNT ₈₀ §	VNT¶
2020 Nov 4	35.7**	35.7**	ND	ND	ND	ND	ND
2020 Nov 6	ND	37.64	ND	ND	ND	ND	ND
2020 Nov 7	35.61	–	ND	ND	ND	ND	ND
2020 Nov 8	ND	–	40.71	ND	ND	ND	ND
2020 Nov 9	ND	–	36.04	ND	ND	ND	ND
2020 Nov 10	–	–	–	ND	ND	ND	ND
2020 Nov 11	–	–	ND	ND	ND	ND	ND
2020 Nov 12	–	–	ND	ND	ND	ND	ND
2020 Nov 13	–	–	ND	ND	ND	ND	ND
2020 Nov 14	–	–	ND	ND	ND	ND	ND
2020 Nov 15	–	–	ND	ND	ND	ND	ND
2020 Nov 27	ND	ND	ND	–	+ (23%)††	1:80	1:10
2020 Dec 12	ND	ND	ND	–	–	1:80	1:20

*C_t, cycle threshold; ND, not done; PRNT₈₀, 80% plaque reduction neutralization test; VNT, virus neutralization test; –, negative; +, positive.

†ID Screen SARS-CoV-2 Double Antigen Multi-species ELISA (ID.vet, <https://www.id-vet.com>).

‡Eradikit COVID19-Multispecies (In3Diagnostic, <http://www.in3diagnostic.com>).

§Antibody titer expressed as the highest serum dilution with 80% reduction in plaques in inoculated VERO-E6 cells compared with the control. 1:20 was the lowest serum dilution tested.

¶Antibody titer expressed as the highest serum dilution preventing the appearance of cytopathic effect in inoculated VERO-E6 cells. 1:10 was the lowest serum dilution tested.

**Pooled oral and nasal swab specimens.

††Ratio between the optical densities of the tested serum and the positive control (cutoff value = 20%).

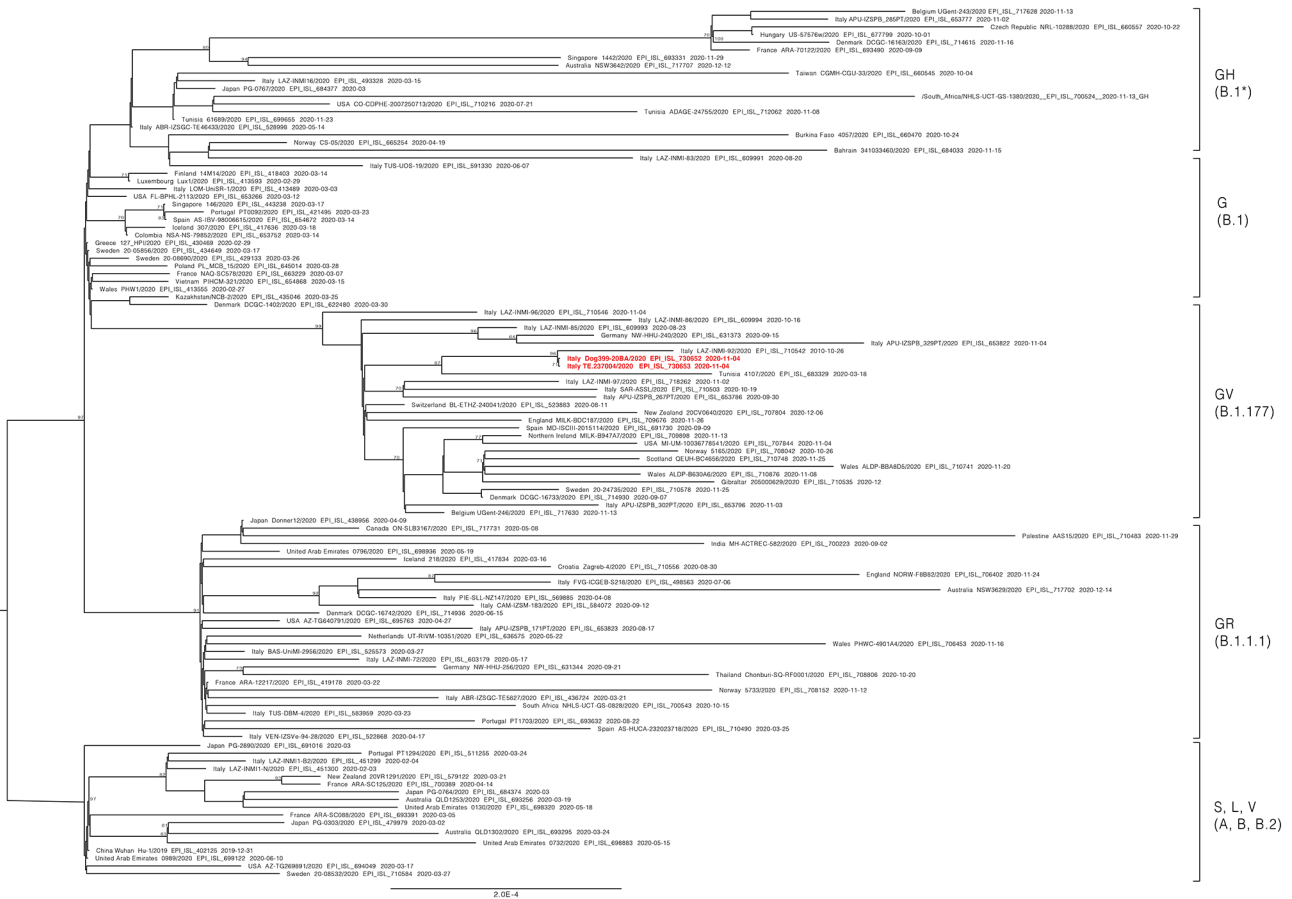


Figure. Maximum-likelihood tree comparing 108 strains of severe acute respiratory syndrome coronavirus 2 circulating among humans and canines. Tree shows 107 complete genomes downloaded from the GISAID database (<https://www.gisaid.org>) and the strains sequenced from an infected dog and family member in Italy (bold red text). The tree was built with IQ-TREE version 1.6.10 (<http://www.iqtree.org>) using the best fit model indicated by the Model Finder with 1,000 bootstrap replicates. Text at nodes indicates bootstrap values >70. Brackets to the right indicate clades. Scale bar indicates number of nucleotide substitutions per site.

duration of viral shedding (9). Upon experimental infection, dogs shed SARS-CoV-2 at lower titers and for a shorter period than cats (10). Patterson et al. (4) found no actively infected dog or cat in a sampled population of 494 pets, including 67 dogs from households in which family members had COVID-19; however, SARS-CoV-2-specific antibodies were detected in a small proportion of pets (4). Delayed sampling of animals, caused by restrictions on human and animal movement during the pandemic, probably contributed to the negative results of molecular testing in that study. The infected poodle we report was monitored after the identification of the index case in the family, enabling the detection of SARS-CoV-2 RNA in swab samples collected during the observational follow-up. Because the canine virus shared 100% nucleotide identity with the virus detected in the index case, we believe human-to-dog transmission of the virus probably occurred in the household.

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Dr. Decaro is professor in the Department of Veterinary Medicine at the University of Bari in Valenzano, Italy. His research interests include the study of viral pathogens of dogs and cats, especially coronaviruses and parvoviruses.

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Postoperative *Paenibacillus thiaminolyticus* Wound Infection, Switzerland

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Paenibacillus thiaminolyticus is a nonvirulent organism found in human and ruminant microbiota. However, *P. thiaminolyticus* can act as an opportunistic pathogen in humans. We describe a case of abdominal wall hematoma secondarily infected by *P. thiaminolyticus*. Our findings emphasize the risk for unusual *Paenibacillus* infections in otherwise healthy persons.

The genus *Paenibacillus* comprises a growing number of species of rod-shaped, motile bacteria with peritrichous flagella (1). *Paenibacillus* species share 89.6% similarity of 16S rDNA gene sequences and grow as nonpigmented colonies on tryptic soy agar (1). Best known as a nearly ubiquitous environmental bacteria, many *Paenibacillus* species are potential opportunistic pathogens in humans (2). We report a case of isolated surgical site infection caused by *P. thiaminolyticus* in an otherwise healthy patient.

A 33-year-old woman came to the emergency department with a fever and reported having a painful and fluctuating abdominal wall mass for 3 days. She had undergone lipoabdominoplasty in a different hospital 7 days earlier. Laboratory tests showed anemia (hemoglobin 88 g/L, hematocrit 0.24 L/L) and isolated C-reactive protein elevation (117 mg/L). Computed tomography of the abdomen demonstrated a fluid collection in the abdominal wall measuring 22 × 9.5 × 5 cm. The patient was admitted for observation. Blood cultures performed at 38.5°C showed no bacterial growth.

Empirical intravenous antimicrobial drug therapy for suspected infected hematoma was initiated with amoxicillin/clavulanate (2.2 g 3×/d), according to local hospital guidelines. Under antimicrobial drug treatment, the patient's fever resolved, but her abdominal pain persisted.

On day 3, we aspirated a sample of the fluid collection in the abdominal wall for microbiological examination. The aspirate was cultured on blood agar incubated at 35°C with 5% CO₂ for 48 h; on MacConkey