INTRODUCTION

Coronaviruses belong to the Coronaviridae family, which comprises a group of enveloped single-stranded RNA viruses. The SARS-CoV-2, which is the causal agent of the new coronavirus disease of 2019 (COVID-19), is closely related to bats and pangolin coronaviruses (Zhang et al., 2020; Zhou et al., 2020).

Since the World Health Organization declared the pandemic situation related to COVID-19 (WHO, 2020), different animals, including dogs, minks and felines, were reported to test positive for the SARS-CoV-2. In general, the infected animal can become ill, but the clinical manifestation seems to be mild and self-limited (Belgium OIE, 2020; Davidson, 2020a, 2020b; Rijksoverheid, 2020; Sit, 2020a, 2020b).

Cats, due to close contact with humans, have received great attention of studies aimed at detecting the SARS-CoV-2 virus in animals, since the first report in Belgium in March 2020 (Belgium OIE, 2020). In addition, their angiotensin-converting enzyme 2 (ACE2), used by the virus as receptor and entry route, shares high amino acid sequence identity with human ACE2 (Wan et al., 2020). Noteworthy, to date, there are no reports of SARS-CoV-2 transmission from cats or dogs to humans.

In fact, since the first report in Belgium, some natural infection cases in cats were reported in Hong Kong (Sit, 2020a), United States of America (Davidson, 2020b) and France (Sailleau et al., 2020). In this study, we report the first case of SARS-CoV-2 infection in a cat in Latin America, and describe genomic sequences obtained from the viruses detected in the cat and its owner.

RAPID COMMUNICATION

First genome sequencing of SARS-CoV-2 recovered from an infected cat and its owner in Latin America

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Abstract
An 11-year-old male mixed-breed cat, with exclusively indoor life, presented 3 cough episodes after the owners tested positive by RT-PCR for SARS-CoV-2. The house is inhabited by 5 people (3 adults and 2 children), and 2 of the adults have shown mild symptoms associated with throat discomfort. The cat was vaccinated, had no history of any previous disease, and tested negative for feline coronavirus (FCoV), feline immunodeficiency virus (FIV) and feline leukaemia virus (FeLV). Rectal sample collected from the cat was positive for SARS-CoV-2 by RT-PCR. Viral genome sequences recovered from human and cat samples showed an average 99.4% sequence identity. This is the first report of genome sequences of SARS-CoV-2 recovered from a cat and its owner in Latin America.

KEYWORDS
Brazil, cat, next-generation sequencing, SARS-CoV-2
An 11-year-old male mixed-breed cat, with exclusively indoor life, presented 3 cough episodes 2 days after the owners tested positive by RT-PCR for SARS-CoV-2. The house is inhabited by 5 people (3 adults and 2 children), and 2 of the adults have shown mild symptoms associated with throat discomfort, started one week earlier from RT-PCR test. The second cat that inhabited the house was a 9-year-old female cat that is also kept exclusively indoor and did not present any clinical signs.

The cat was vaccinated, had no history of any previous disease and tested negative for feline coronavirus (FCoV), feline immunodeficiency virus (FIV) and feline leukaemia virus (FeLV). Anti-coronavirus antibodies, anti-FIV antibodies and FeLV antigens were searched using commercially available kits (Feline Infectious Peritonitis Virus IFA Antibody Kit, Fuller Laboratories, Fullerton, CA, USA, and FIV Ac/FeLV Ag Test Kit, Alere, Abbott Laboratories, Abbott Park, IL, USA, respectively) according to the manufacturer’s instructions.

Nasopharyngeal and rectal samples were collected from the cat to SARS-CoV-2 detection. Laboratory confirmation was performed by RT-PCR through the protocol developed by Charité Hospital, Universitätsmedizin Berlin, Germany (Corman et al., 2020), using GoTaq® Probe 1-Step RT-qPCR System (Promega). This protocol is based on the detection of the SARS-CoV-2 E gene using a pair of primers (F: 5’-3’ ACACGTCATGAATTTAGTTAAGGCT; R: 5’-3’ ATATGGCAGCAGTGACCGACA) and a TaqMan probe (MGB FAM-ACTGACCATCATCTTCGCCCTCC); and sequencing was performed with the Ion AmpliSeq™ SARS-CoV-2 Research Panel (Thermo Fisher Scientific, CA, USA), using an Ion 540 chip in the Ion S5 instrument (Thermo Fisher Scientific). Raw sequencing data are available at NCBI SRA database under accession numbers SRR12980649 and SRR12980650.

Further studies also using serological assays could add new evidence about the SARS-CoV-2 infections between felids and humans.
its owners in domestic environments. However, in this study, unfortunately, we do not have appropriate equipment and reagents to run serology assay. In addition, there are no data in the literature showing how long specific antibodies last in felids. Therefore, obtaining cat blood at another time to test for the presence of specific antibodies against SARS-CoV-2 could not
reflect the animal’s infection status at the time when RT-PCR test was performed.

Regarding clinical presentation, the cat showed mild self-limiting clinical signs, as seen in other reports (Belgium OIE, 2020; Davidson, 2020b; Sailleau et al., 2020). In addition, the cat was positive only in the rectal swab, similar to what occurred in the case reported in France (Sailleau et al., 2020), suggesting that this sampling site is important for animals, in addition to being easily accessible for the species in question.

Finally, it is important to notice that there is no proof currently that dogs and cats can transmit COVID-19 to humans, and probably, they have no important epidemiological roles on transmission. In a research conducted in New York City, during the pandemic peak in the city, only 3 cats were positive, in a city full of cats (Davidson, 2000a). In Wuhan, about 11% of 102 cats were positive in ELISA after the outbreak (Zhang, Zhang, et al., 2020). Also, there are a low number of diagnosed animals compared with the numbers of cases in humans, showing that the transmission between humans and cats is not common. Considering our report and previous studies, the authors of the present report do not recommend any kind of abandonment of cats or dogs because of SARS-CoV-2, once these animals do not seem to have any role in transmission or infection in humans.

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CONFLICT OF INTEREST
There was no conflict of interest with others.

ETHICAL APPROVAL
We declare that ethical statement is not applicable.

DATA AVAILABILITY STATEMENT
The data that support the findings of this study are openly available in NCBI SRA database at [https://www.ncbi.nlm.nih.gov/sra], reference number SRR12980649 and SRR12980650.

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