AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

GENOME SEQUENCES

First Complete Genome Sequence of a Feline Alphacoronavirus 1 Strain from Brazil

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ABSTRACT We identified a strain of *Alphacoronavirus 1*, FCoV-SB22, from a pool of fecal samples from domestic cats from a rural settlement in the municipality of Santa Bárbara, Pará, Brazil. The nucleotide identity with feline coronavirus was 91.5%. The present study reports the first complete genome sequence of a feline coronavirus from Brazil.

Feline coronaviruses (FCoV) are common pathogens in domestic and wild cats in several regions of the world and may cause lethal infections, such as feline infectious peritonitis (FIP) (1). These viruses are classified in the order *Nidovirales*, family *Coronaviridae*, and genus *Alphacoronavirus* and are subdivided into two serotypes, FCoV 1 and FCoV 2. The FCoV virion is pleomorphic and enveloped and contains a single-stranded positive-sense RNA genome (27 to 32 kb). The genome of the species *Alphacoronavirus 1* has 11 open reading frames (ORFs) (2, 3). In domestic cats, FCoV 1 is predominant, leading to subclinical infections (4). In December 2016, 5 fecal samples from nondiarrheic domestic felines aged 5 months to 6 years were collected from a rural community located in the municipality of Santa Bárbara in the state of Pará, Brazil. These samples were pooled and processed for Illumina sequencing. A cDNA library was prepared using a Vilo superscript reverse transcriptase (RT) and sequenced on an Illumina MiniSeq platform using the methodology described in the Nextera XT DNA library preparation kit (5), using paired-end reads with 150 bp.

The genome was assembled using a hybrid methodology of *de novo* assembly and reference mapping with the Minia (kmer-size = 32, abundance-min = 3, abundance-max = 500, nb-cores = 8) (6) and Geneious (with default parameters) version 8.1.9 (7) programs, respectively.

Taxonomic annotation was performed using the Kraken software (with default parameters) (8). The DNA sequencing produced 8,137,466 reads. Using a *de novo* assembly methodology, 39,267 contigs were generated, 25 of which were related to the family *Coronaviridae*, 107 that were for uncultured cross-assembly phage (crAssphage), 2 that were for RD114 retrovirus, 1 that was for feline picornavirus, 4,987 that were for bacteria, and 34,140 that were undetermined by Kraken 1.0. The *Coronaviridae* contigs were characterized as *Alphacoronavirus 1* FCoV and after reference mapping generated a single unitig formed by 1,597 reads, which was related to feline coronavirus strain UG-FH8, isolated from Denmark (GenBank accession no. KX722529). The new FCoV-SB22 strain showed a genome of 29,137 bp, exhibiting 91.5% nucleotide identity with the strain used for reference mapping. The average read coverage was 8×, and the GC content was 38.7%. We report here the almost complete genome sequence of *Alphacoronavirus 1* obtained from nondiarrheic domestic felines that inhabited rural environments in Brazil. The role of this pathogen in feline infection remains poorly under-

Citation de Barros BDCV, Castro CMOD, Pereira D, Ribeiro LG, Júnior JWBD, Casseb SMM, Holanda GM, Cruz ACR, Júnior ECS, Mascarenhas JDP. 2019. First complete genome sequence of a feline Alphacoronavirus 1 strain from Brazil. Microbiol Resour Announc 8:e01535-18. https://doi.org/10.1128/MRA.01535-18.

Editor Jelle Matthijnssens, KU Leuven

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Received 12 November 2018
Accepted 5 February 2019
Published 7 March 2019

stood, and more studies are needed for a better understanding of its role. Therefore, the continuous surveillance of this agent and the improvement of diagnostic methods and their implementation are needed, in addition to strategies to prevent and control infection.

Data availability. The complete genome sequence reported here was deposited in GenBank under the accession no. MH817484 and in the SRA under accession no. SRR8352624.

ACKNOWLEDGMENTS

This research was financially supported by the Coordination for the Improvement of Higher Education Personnel (CAPES) (grant 2303800717/2013-52), the Brazilian Institutes National Council for Scientific and Technological Development (CNPq), and the Evandro Chagas Institute, Ministry of Health, Ananindeua, Brazil. B.D.C.V.D.B. and C.M.O.D.C. are recipients of CAPES fellowships, and J.D.P.M., D.P., L.G.R., and J.W.B.D.J. are recipients of a CNPq fellowship.

REFERENCES

1. Tekes G, Thiel HJ. 2016. Feline coronaviruses: pathogenesis of feline infectious peritonitis, p 193–218. *In* Ziebuhr J (ed), Advances in virus research: coronaviruses. Academic Press, Amsterdam, The Netherlands.
2. Kipar A, Meli ML. 2014. Feline infectious peritonitis: still an enigma? Vet Pathol 51:505–526. https://doi.org/10.1177/0300985814522077.
3. Le Poder S, Pham-Hung d'Alexandry d'Orangiani A-L, Duarte L, Fournier A, Horhogea C, Pinhas C, Vabret A, Eloit M. 2013. Infection of cats with atypical feline coronaviruses harbouring a truncated form of the canine type I non-structural ORF3 gene. Infect Genet Evol 20:488–494. https://doi.org/10.1016/j.meegid.2013.09.024.
4. Zhong S, Joung JG, Zheng Y, Chen YR, Liu B, Shao Y, Xiang JZ, Fei Z, Giovannoni JJ. 2011. High-throughput Illumina strand-specific RNA sequencing library preparation. Cold Spring Harb Protoc 2011:940–949. https://doi.org/10.1101/pdb.prot5652.
5. Chikhi R, Rizk G. 2013. Space-efficient and exact de Bruijn graph representation based on a Bloom filter. Algorithms Mol Biol 8:22. https://doi.org/10.1186/1748-7188-8-22.
6. Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, Thierer T, Ashton B, Meintjes P, Drummond A. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics 28:1647–1649. https://doi.org/10.1093/bioinformatics/bts199.
7. Carstens EB. 2010. Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2009). Arch Virol 155:133–146. https://doi.org/10.1007/s00705-009-0547-x.
8. Chang HW, de Groot RJ, Egberink HF, Rottier PJM. 2010. Feline infectious peritonitis: insights into feline coronavirus pathobiogenesis and epidemiology based on genetic analysis of the viral 3c gene. J Gen Virol 91:415–420. https://doi.org/10.1099/vir.0.016485-0.