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## Letter to the Editor

# Molecular detection of *Bartonella clarridgeiae* in domestic cats from Midwest Brazil



Dear Editor,

Cat scratch disease (CSD) is caused by *Bartonella henselae* a hemotropic bacterium that infects human, domestic and wild mammals. Closely related to *B. henselae*, the *B. clarridgeiae* comprises approximately 10–30% of *Bartonella* isolates from clinically healthy cats and was found in cardiac and hepatic lesions in dogs.<sup>1</sup> Moreover, *B. clarridgeiae* has been serologically associated with CSD-like illness in humans.<sup>2</sup>

Cats are considered the major reservoir and carriers of *B. henselae*, *B. clarridgeiae* and *B. koehlerae*. *Bartonella* spp. can be a vector transmitted by flea to susceptible cats. Few cats naturally infected have clinical signs. Medical problems of cats associated with *Bartonella* infections are variable, ranging from transient fever and lymphadenopathy to abscesses or microabscesses in different organs, endocarditis, and central nervous signs.<sup>1</sup> Transmission from cats to humans and dogs mainly occurs through cat scratches or bites. In humans, this infection may be asymptomatic and can disappear spontaneously without any treatment; however, in some cases the disease may be fatal if left untreated.<sup>3</sup>

In order to identify arthropod-borne pathogens in domestic feline, 182 cats from different places of Cuiabá and Varzea Grande cities, both located in Mato Grosso State, Midwest Brazil, have been analyzed. Cats were seen at the Veterinary Hospital of the Federal University of Mato Grosso (HOVET-UFMT), Veterinary Hospital of the University of Cuiabá (UNIC-HV), and animal shelters and Zoonosis Control Centers (ZCC) of Cuiabá and Várzea Grande cities. Sample collection was conducted in agreement with the Ethical Principles for Animal Research under the institutional watch of the UFMT Committee for Ethics in Animal Research.

Collected blood samples were subjected to a DNA extraction using the Axyprep Blood Genomic DNA Miniprep Kit (Axygen Biosciences, Hangzhou, China). Extracted DNA was then used as a template for *Bartonella* spp. PCR assay using the primer BARTON-1 (5'-TAACCGATATTGGTTGTGTGAAG-3') and BARTON-2 (5'-TAAAGCTAGAAAGTCTGGCAACATAACG-3'), which amplifies a segment of 585–588 bp of *Riboflavin synthase C (ribC)* gene of *Bartonella* genus.<sup>4</sup>

Three (1.6%) cats were positive to the presence of *Bartonella* DNA according to PCR targeting portions of the *ribC* gene. Partial DNA sequences of all PCR-positive samples were generated yielding a sequence (GenBank accession: KR092386) that was identical to KC331014 and HM588660 and 99% similarity to HQ12585, KC331017, KC331014, which corresponds to *B. clarridgeiae* sequences available in GenBank.

The positive cats were found in the ZCC of Várzea Grande city. Usually, these animals are taken off the streets and kept until adoption. Boulouis et al. observed that stray cats present higher prevalence of *Bartonella* spp. infection than pet cats, mainly due to close contact between infected animals in large groups of cats, demonstrating that differences in the occurrence of the infection are associated with the type of feline population studied.<sup>5</sup> Due to vigorous flea control among cat populations, the prevalence of *Bartonella* infection in cats have reduced and the risk of *Bartonella*-associated disease in pet owners decreased. However, cat owners and animal health professionals should be cautioned to avoid behaviors that increase the risk of animal bites or scratches, since the feline population acts as a source of zoonotic agents and represents a potential risk of infection.<sup>1</sup>

In Brazil, the occurrence of *Bartonella* infection in human was previously described. In the State of Rio de Janeiro, 41.6% of clinically asymptomatic HIV-positive patients were found seropositive for *Bartonella* species.<sup>3</sup> In fact, veterinarians and medical doctors should consider the presence of these zoonotic pathogens in their diagnostic routine.

## Conflicts of interest

The authors declare no conflicts of interest.

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