The article presents the results of examination of stray dogs from Havana, Cuba for six ixodid tick-borne diseases. Analysis was carried out using real-time PCR. Overall 107 dogs, 95 (89.09 %) were infected. 41 dogs (38.31 %), 66 (61.68 %), 28 (26.17 %) and 40 (37.38 %) were found to be infected with Anaplasma platys, Ehrlichia canis, Rickettsia spp. and Hepatozoon canis, respectively. Sequence analysis of 16S rRNA and groEL genes for Rickettsia spp. revealed 99 % identity with Rickettsia felis. There were no dogs infected with A. phagocytophilum and Borrelia spp.

Key words: tick-borne infections, dogs, Cuba


Infectious diseases caused by pathogens transmitted by ticks and other vectors are an important cause of morbidity and mortality in both humans and dogs. Tick-borne pathogens remain an important cause of disease among canine populations worldwide. In Cuba there are not many published studies on tick-borne pathogens affecting dogs, the only hemoparasite molecularly confirmed in dogs, is Anaplasma platys and in tick collected from dog’s molecular detection of Ehrlichia canis and Babesia spp. in Rhipicephalus sanguineus sensu lato was published. The aim of this research was to screen, identify and characterize selected tick-borne pathogens in stray dogs from Havana, Cuba.

MATERIALS AND METHODS

Blood samples from 107 stray dogs with and without clinical signs associated with tick-borne diseases, were analyzed by real-time PCR for E. canis, A. platys, Anaplasma phagocytophilum, Borrelia spp., Hepatozoon canis and Rickettsia spp. Real-time PCR positive samples for different pathogens were further analyzed by PCR and sequencing.

RESULTS AND DISCUSSION

Overall 107 dogs, 95 (89.09 %) were positive for one or more hemoparasite and 12 (10.91 %) were not infected. None of the dogs were detected infected...
with *A. phagocytophilum* nor *Borrelia* spp., while 41 dogs (38.31 %), 66 (61.68 %), 28 (26.17 %) and 40 (37.38 %) were found to be infected with *A. platys*, *E. canis*, *Rickettsia* spp. and *H. canis*, respectively. Sequence analysis of 16S rRNA and groEL genes for *A. platys*, 16S rRNA and gltA for *E. canis* showed high identity with known sequences available in the GenBank database. In addition, htrA gene sequence analysis for *Rickettsia* spp. revealed 99 % identity with *Rickettsia felis*. This first molecular study of different tick-borne pathogens in stray dogs points to the need of more intensive epizootic investigation, for pathogens with zoonotic potential.

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