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OCCURRENCE OF TICK-BORNE PATHOGENS IN STRAY DOGS FROM HAVANA, CUBA

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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

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ВСТРЕЧАЕМОСТЬ ВОЗБУДИТЕЛЕЙ КЛЕЩЕВОГО ЭНЦЕФАЛИТА У БРОДЯЧИХ СОБАК Г. ГАВАНА (КУБА)

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В работе приведены результаты обследования популяции бродячих собак г. Гавана на заражённость шестью инфекциями, передаваемыми при укусах иксодовых клещей. Исследование проводили с помощью ПЦР с учётом результатов в режиме реального времени. Из 107 обследованных животных было заражено 95 (89,09 %). Среди них 41 (38,31 %), 66 (61,68 %), 28 (26,17 %) и 40 (37,38 %) были заражены, соответственно, *Anaplasma platys*, *Ehrlichia canis*, *Rickettsia* spp. и *Hepatozoon canis*. Нуклеотидные последовательности генов 16S rRNA, *gltA* и *htrA* *Rickettsia* spp. были на 99 % идентичны последовательностям соответствующих генов *Rickettsia felis*, опубликованных в базе данных GenBank. Не было обнаружено случаев заражения собак *A. phagocytophilum* и *Borrelia* spp.

Ключевые слова: клещевые инфекции, собака, Куба

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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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