

Corona B.G.<sup>1</sup>, Díaz-Sánchez A.A.<sup>1</sup>, Meli M.L.<sup>2,3</sup>, Cañizares E.V.<sup>1</sup>, Arias L.R.<sup>1</sup>, Dorta Y.L.<sup>1</sup>,  
Rivero E.L.<sup>1</sup>, Hofmann-Lehmann R.<sup>2,3</sup>

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

<sup>1</sup> National Center for Animal and Plant Health (CENSA), Carretera de Tapaste y Autopista Nacional  
(P.O.B. 10, CP 32700, San José de las Lajas, Mayabeque, Cuba)

<sup>2</sup> Center for Clinical Studies, Vetsuisse Faculty, University of Zurich  
(Rämistrasse 71, Zürich CH-8006, Switzerland)

<sup>3</sup> Clinical Laboratory, Vetsuisse Faculty, University of Zurich  
(Rämistrasse 71, Zürich CH-8006, Switzerland)

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)

Корона Б.Г.<sup>1</sup>, Диас-Санчес А.А.<sup>1</sup>, Мели М.Л.<sup>2,3</sup>, Канисарес Э.В.<sup>1</sup>, Ариас Л.Р.<sup>1</sup>,  
Дорта Й.Л.<sup>1</sup>, Риверо Э.Л.<sup>1</sup>, Хофманн-Леманн Р.<sup>2,3</sup>

<sup>1</sup> National Center for Animal and Plant Health (CENSA), Carretera de Tapaste y Autopista Nacional  
(P.O.B. 10, CP 32700, San José de las Lajas, Mayabeque, Cuba)

<sup>2</sup> Center for Clinical Studies, Vetsuisse Faculty, University of Zurich  
(Rämistrasse 71, Zürich CH-8006, Switzerland)

<sup>3</sup> Clinical Laboratory, Vetsuisse Faculty, University of Zurich  
(Rämistrasse 71, Zürich CH-8006, Switzerland)

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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#### Information about the authors

**Corona Belkis González** – PhD, Senior Research Officer, National Center for Animal and PlantHealth (CENSA), Carretera de Tapaste y Autopista Nacional (Cuba, CP 32700, Mayabeque, San José de las Lajas, P.O.B. 10; e-mail: bcorona@censa.edu.cu)

**Díaz Sánchez Adrian Alberto** – MSc, Junior Research Officer, National Center for Animal and PlantHealth (CENSA), Carretera de Tapaste y Autopista Nacional (Cuba, CP 32700, Mayabeque, San José de las Lajas, P.O.B. 10; e-mail: adiaz@censa.edu.cu)

**Meli Marina L.** – PhD, Senior Research Officer at Clinical Laboratory, Vetsuisse Faculty, Center for Clinical Studies, Vetsuisse Faculty, University of Zurich (Switzerland, CH-8006, Zürich, Rämistrasse, 71, e-mail: mmeli@vetclinics.uzh.ch)

**Cañizares Ernesto Vega** – PhD, Senior Research Officer, National Center for Animal and PlantHealth (CENSA), Carretera de Tapaste y Autopista Nacional (Cuba, CP 32700, Mayabeque, San José de las Lajas, P.O.B. 10; e-mail: evega@censa.edu.cu)

**Arias Lisset Roblejo** – Junior Research Officer, National Center for Animal and PlantHealth (CENSA), Carretera de Tapaste y Autopista Nacional (Cuba, CP 32700, Mayabeque, San José de las Lajas, P.O.B. 10; e-mail: lroblejo@censa.edu.cu)

**Dorta Yanet López** – MSc, Junior Research Officer, National Center for Animal and PlantHealth (CENSA), Carretera de Tapaste y Autopista Nacional (Cuba, CP 32700, Mayabeque, San José de las Lajas, P.O.B. 10; e-mail: ylopez@censa.edu.cu)

**Rivero Evelin Lobo** – PhD, Senior Research Officer, National Center for Animal and PlantHealth (CENSA), Carretera de Tapaste y Autopista Nacional (Cuba, CP 32700, Mayabeque, San José de las Lajas, P.O.B. 10; e-mail: elobo@censa.edu.cu)

**Hofmann-Lehmann Regina** – Professor, PhD, Senior Research Officer at Clinical Laboratory, Vetsuisse Faculty, Center for Clinical Studies, Vetsuisse Faculty, University of Zurich (Switzerland, CH-8006, Zürich, Rämistrasse, 71, e-mail: rhofmann@vetclinics.uzh.ch)