RESUMO SIMPLES - PROTOZOÁRIOS E AGENTES TRANSMITIDOS POR VETORES DE IMPORTÂNCIA EM SAÚDE

COMPARISON OF DIAGNOSTIC TECHNIQUES FOR THE DETECTION OF BABESIA VOGELI IN DOMESTIC DOGS AND CATS ATTENDING A VETERINARY HOSPITAL

Laís Da Silva De Oliveira (sialais98@gmail.com)

Larissa Costa Dos Santos (lara_acacias@hotmail.com)

Victor Silva De Souza (vicctorsilva21@gmail.com)

Thiago Dutra Dias (thiagodd15@gmail.com)

Nelson Meireles Da Silva (meirelesvet3@gmail.com)

Laís Feliciano De Souza (laisfelicici@gmail.com)

Mayara Viera Duarte Da Paz (vet.mayarapaz@gmail.com)

Cristiane Divan Baldani (crisbaldani@ufrrj.br)

Huarrisson Azevedo Santos (huarrisson@yahoo.com.br)

Maristela Peckle Peixoto (maristelapeckle@ufrrj.br)

The protozoan Babesia vogeli belongs to the phylum Apicomplexa and the family Babesiidae. This species is frequently detected in domestic dogs in Brazil and has occasionally been reported in cats, although such occurrences are rare. Transmission primarily occurs during the blood meal of the tick Rhipicephalus sanguineus sensu lato. The aim of this study was to compare the diagnostic performance of nested PCR (nPCR), quantitative real-time PCR

(qPCR), and cytology for the detection of B. vogeli in dogs and cats treated at the Small Animal Veterinary Hospital of UFRRJ (HVPA). A total of 338 blood samples were collected and sent to the Hemoparasites and Vectors Laboratory (LHV/UFRRJ) for storage and processing. Genomic DNA was extracted using the Extracta Kit MGBD-P096 (Loccus, Brazil) following the manufacturer's instructions, and DNA quality and concentration were assessed by spectrophotometry (NanoDrop®). Molecular detection was performed using qPCR targeting the hsp70 gene and nested PCR targeting a fragment of the 18S rDNA. Direct diagnosis was carried out using blood smears stained with Giemsa (1:10) and examined by optical microscopy under an oil immersion objective (1000x). Statistical analyses comparing the diagnostic techniques were conducted using IBM SPSS Statistics software (version 30). Of the 338 samples analyzed, 1.8% (6/338) were positive for B. vogeli by qPCR and 0.6% (2/338) by nPCR. All nPCR-positive samples were also positive by qPCR. Among the qPCR-positive samples, five were dogs and one was a cat, whereas all nPCR-positive samples were dogs. No intraerythrocytic merozoites were observed in the cytological examination. Statistical analysis indicated moderate agreement between nPCR and qPCR (Kappa = 0.496; $p < 0.001$), reflecting the higher sensitivity of qPCR, which detected four additional cases. Although qPCR identified four more positives, the number of discrepancies was insufficient to reach statistical significance in the McNemar test ($p = 0.125$), indicating that the superior sensitivity of qPCR did not translate into a statistically significant difference in the proportion of positive samples in this dataset. Among the qPCR-positive animals, all were older than six months. A higher number of females (n = 4) were observed among the positive dogs, while the only positive cat was male. Regarding breed, only one dog was a Dachshund, and the remaining dogs were mixed breed. Overall, qPCR demonstrated greater sensitivity for detecting B. vogeli, outperforming nPCR and cytology, although the difference between the molecular techniques was not statistically significant. The occurrence of B. vogeli was low and limited to animals over six months of age, with higher detection in mixed-breed dogs, suggesting potential host-related differences in susceptibility or exposure.

Palavras-chave: keywords: ticks; babesiosis; babesiidae.