USING kDNA PCR FOR THE MOLECULAR DIAGNOSIS OF LEISHMANIASIS

(UTILIZAÇÃO DO kDNA PCR NO DIAGNÓSTICO MOLECULAR DE LEISHMANIOSES)

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Visceral leishmaniasis is a zoonosis of utmost importance regarding public health aspects. It is caused by trypanosoma protozoa of the genus Leishmania and has the domestic dog as the main carrier in the urban environment. Enzootic diseases often precede the occurrence in humans, which is an important parameter in predicting the occurrence of human cases (Ramos et al., 2010). Molecular techniques have acquired great prominence in the current scenario as a diagnostic tool due to increasing cases of this disease. This study aims to evaluate the occurrence of leishmaniasis in Bauru, endemic region for this disease, due to the impact that causes in public health and the importance of its diagnosis in dogs. A total of 164 samples of bone marrow of dogs were collected by the CCZ, in Bauru, regardless of gender, breed or age, prior to euthanasia. The n sampling was defined statistically with the software Epi Info (CDC, 2002), using as reference an expected prevalence of LVC (clinical and laboratory) of 70.1% (SMS-Bauru, 2011), level of significance (α) of 5%, a confidence level of 95% and a margin of error of 7%. All samples were subjected to PCR, using the primers 150(sense)5'-GGGKAGGGGCGTTCTSCGAA-3` and 152(antisense)5'- SSSWCTATWTTACACCAACCCC -3', which amplify a fragment of 120bp of a conserved region of the kDNA mini-circle of all species of Leishmania. Of the 164 dogs examined, 115 were positive for infection as indicated by the parasite DNA detected in the samples, a prevalence of 70.13%. The results reinforce the importance of the role of the dog as a carrier of this zoonosis, and main link to the maintenance of the disease in urban environments, in addition to serving as data to be used for adopting control measures.

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