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

# MOLECULAR DETECTION OF EHRLICHIA CANIS IN DOGS IN THE MICROREGION OF UNAÍ, MINAS GERAIS: PRELIMINARY RESULTS

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Canine monocytic ehrlichiosis (CME) is an endemic disease widely distributed in Brazil, caused by Ehrlichia canis, a Gram-negative, obligate intracellular bacterium that primarily infects cells of the mononuclear phagocytic system. It is mainly transmitted by the Rhipicephalus linnaei tick, and its occurrence is favored by tropical and subtropical climates, with prevalence rates ranging from 4.8% to 65% in dogs from both urban and rural environments. Studies have identified immunoreactive proteins of E. canis, some of which are species-

specific, that are involved in parasite-host interactions and immune evasion. These proteins, in addition to contributing to the understanding of pathogenesis, highlight the genetic diversity of the agent, underscoring the need for molecular investigations to clarify regional variability and its diagnostic and epidemiological implications. The objective of this study was to detect E. canis DNA in the blood of naturally infected dogs in the microregion of Unaí, Minas Gerais. To conduct the molecular investigation, the required sample size was estimated based on an expected prevalence of 50% and a significance level of 5%. With these parameters, a minimum sample size of 384 animals was calculated, ensuring sufficient statistical power for the proposed analyses. In this study, 386 whole blood samples from dogs in the Unaí microregion (MG) were subjected to DNA extraction using the Wizard® Genomic DNA Purification Kit. To confirm the viability of the extracted DNA, all samples were initially tested using Polymerase Chain Reaction (PCR) to amplify a fragment of the endogenous gapdh gene (≈400 bp). Subsequently, an 843-bp fragment of the p28 gene, a widely used marker for E. canis, was amplified using the Ecp28F and Ecp28R primers. A 10 µL volume of the PCR products was applied to a 1.5% agarose gel, separated by electrophoresis, stained with ethidium bromide, and visualized under a UV transilluminator. All samples analyzed showed positive amplification for the endogenous gapdh gene, confirming the integrity and viability of the extracted DNA. Regarding the specific detection of E. canis via the p28 gene, 3.6% (14/386) of the blood samples were positive. Although the detection rate was relatively low, these results suggest the circulation of the pathogen within the studied population. These findings emphasize the importance of ongoing molecular monitoring to understand the dynamics of CME in different regions. Additionally, further molecular markers will be employed to identify the circulating genotypes in the Unaí microregion, contributing to a more detailed genetic characterization of E. canis in the area.

Palavras-chave: molecular biology; dogs; ehrlichiosis; p28.