

APPLICATION OF MOLECULAR BIOLOGY METHODS FOR THE DETECTION OF BABESIA CANIS

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Canine babesiosis is a widely distributed tick-borne infectious disease caused by the intraerythrocytic protozoan *Babesia canis*. During the past two decades, the number of cases of disease has increased across Europe, with a growing number also reported in Lithuania. Given the rapid spread of the disease, accurate diagnosis and effective treatment are becoming increasingly important. Conventional diagnostic approaches used in veterinary practice, including clinical examination and microscopic evaluation of blood smears, may lack sufficient sensitivity and often do not enable precise identification of the causative agent. This study aimed to assess the prevalence of *B. canis* isolated from shelter dogs in Lithuania through sequence analysis of the *B. canis Bc28.1* gene fragment. Blood samples were collected from 50 clinically symptomatic and asymptomatic shelter dogs between spring and autumn 2024. *B. canis* DNA was identified in 2 out of 50 samples (4%). Sequence analysis revealed identical *Bc28.1* gene fragments in both symptomatic and asymptomatic dogs. These findings highlight the value of molecular methods for detecting and characterizing *B. canis*, contributing to improved diagnostic accuracy and enhanced epidemiological surveillance of canine babesiosis.

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Keywords: canine babesiosis, *Babesia canis*, shelter animals, Bc28.1 gene.