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CANINE BABESIOSIS: PREVALENCE, INTENSITY AND MOLECULAR IDENTIFICATION OF *Babesia* SPECIES IN DOGS BROUGHT TO VETERINARY TEACHING HOSPITAL, PERADENIYA

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Canine babesiosis is a globally distributed and clinically significant tick-borne disease caused by an intra-erythrocytic haemoprotozoan parasite belonging to the genus *Babesia*. Two species of *Babesia* infect dogs: *B. canis* and *B. gibsoni*. The present study determined the prevalence, intensity and phylogeny of *Babesia* species in dogs brought to the Veterinary Teaching Hospital (VTH) at the University of Peradeniya. The study compared the morphological and molecular methods of diagnosis and investigated the potential tick vectors of babesiosis. Blood samples from dogs brought to the VTH were collected from January to June 2019. Giemsa stained blood smears were examined under light microscopy. Blood samples from 42 dogs were collected and were subjected to PCR using genus-specific primers to amplify a 411-450 bp region in the *18S rRNA* gene. The DNA from 20 positive blood samples was sequenced and phylogenetic analysis was conducted using MEGA7 software. Results show that 19 (45.2%) and 33 (78.6%) dogs were positive for babesiosis from microscopic and molecular methods, respectively. This highlights a significant difference in the two methods of diagnosis (χ^2 = 9.462, p = 0.002) with 33.3% infected dogs diagnosed microscopically negative. All the parasites identified either through microscopy or genetically were confirmed as *B. gibsoni*. Nine dogs were infested with ticks (21.4%) and 17 ticks were collected from them. The tick species were identified as: *Rhipicephalus haemophysaloides, Haemophysalis bispinosa,* and *Rhipicephalus sanguineus*. Further studies are needed to confirm the vector capacity of these tick species and the presence of *Babesia* in ticks. The results of the study show a high prevalence of canine babesiosis among the dogs brought to the VTH and most of these infections may go undetected if only the microscopic method is used in the diagnosis. Moreover, since the infection is mostly asymptomatic, improved diagnostic method is needed to control and prevent the disease distribution, effectively.

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