## Emergence of canine blood parasite *Babesia gibsoni* in Slovakia, clinical and molecular genetic study

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Canine vector-borne diseases have grown to represent a significant problem in veterinary medicine and present a mounting challenge in differential diagnosis and therapy for veterinary practitioners. In Europe, *Babesia canis* is considered to be the most common species responsible for canine babesiosis, a severe and potentially life-threatening infection.

The present study is the first molecular detection of *Babesia gibsoni* in two mixed pit bull terriers with clinical and hematological signs of babesiosis. Polymerase chain reaction (PCR), Restriction Fragment Length Polymorphism (RFLP) analysis and further sequencing of the 18S rRNA gene fragments isolated from blood samples of both dogs confirmed 100% similarity to each other, and 100% identity with *B. gibsoni* isolates that infect dogs worldwide.

Consequently, this study confirms that *B. canis* is not the only species responsible for canine babesiosis in Slovakia. Although infections reported in western Slovakia cannot be clearly considered as autochthonous, the study presents the first molecular characterization of clinical infections caused by small babesia, suggesting that *B. gibsoni* may be underdiagnosed here.

The results of the study alert veterinarians to a new infection that previously did not occur in Slovakia. As this infection requires different treatment than the one caused by *B. canis*, differential diagnosis and accurate identification of causative agents is crucial for the selection of appropriate therapy and successful treatment, especially in dogs with hemolytic anemia and febrile conditions.

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