

A phylogenetic comparison between mitochondrial DNA and nuclear DNA of *Babesia canis* in blood collected from dogs from Warsaw and its suburbs

Mohammed Alsarraf, Ewa J. Mierzejewska, Anna Bajer

Department of Parasitology, Institute of Zoology, Faculty of Biology, University of Warsaw

Canine babesiosis, is a common tick-borne protozoan disease with a wide distribution in Asia, Africa, Australia, Europe, and North America, its symptoms include fever, anemia, hemoglobinuria, pallor, anorexia, jaundice, splenomegaly, and even death in serious cases. The 18S rRNA gene is widely used in establishing phylogenetic relationships as well as to differentiate the genotypes or subspecies of canine *Babesia*. Genetic characterization and phylogenetic analysis of the 18S rRNA gene of canine piroplasms from Asia, the Midwestern United States, California, Africa and Spain conclusively proved that there are three genotypically distinct *Babesia* of canines. Mitochondrial (mt) genomes from diverse phylogenetic groups vary considerably in size, structure, and organization. Apicomplexa have the smallest (mt) genome in the form of a circular and/or tandemly repeated linear element of 6 kb, encoding only three protein genes (cox1, cox3, and cob).

The aim of this study is to compare and determine the diversity in mitochondrial and/or nuclear DNA of *Babesia canis* depending on the dogs and their origin, mainly Warsaw and its suburbs.

Blood samples were collected from 60 dogs in 2014-2015 and all were positive with *Babesia* sp. For the molecular and phylogenetic analysis of the nuclear DNA we used amplification and sequencing of the 18S rDNA (24 samples), the regions ITS1 (N=22) and ITS2 (N=23). 30 samples were obtained with complete mitochondrial genome of about 6kb. The sequences were aligned and the phylogenetic analysis was conducted using the MEGA7 tool. The results of the mentioned phylogenetic analysis of the nuclear DNA didn't show clear diversity regarding *Babesia canis*, but the phylogenetic analysis of the mitochondrial DNA of *Babesia canis* expressed better and more distinct diversity.

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