

# The genetic diversity of *Babesia canis* infecting dogs in the Mazowieckie voivodship

Wioletta Rożej-Bielicka, Aleksander Masny, Elżbieta Gołąb

Department of Parasitology, National Institute of Public Health – National Institute of Hygiene, Chocimska 24, 00-791 Warszawa, Poland

Corresponding Author: Wioletta Rożej-Bielicka; email: wrozej@pzh.gov.pl

*Babesia canis* infections are common in dogs in Poland. Babesiosis caused by *B. canis* may range from mild to severe disease in dogs. Two genotypes of *B. canis* 18S RNA-A and 18S RNA-B have been described in Poland, and those genotypes were postulated to differ in virulence (Adaszek et al. 2009). The aim of this study was to determine the genetic diversity of *B. canis* detected in dogs from the Mazowieckie voivodship.

From 61 samples of peripheral blood of dogs from Mazowieckie voivodship diagnosed with babesiosis, DNA was extracted and subjected to PCR amplification. The amplification of *B. canis* DNA was performed using the primer pair BAB GF2 and BAB GR2, which amplifies 559-bp region of the 18S rRNA gene of *B. canis*. PCR was performed as described by Bonett al. (2007), with slight modifications. The amplification products were sequenced, then DNA sequence analysis was performed using NCBI BLAST and CLC Main Workbench.

*B. canis* DNA was detected in all 61 tested samples from dogs diagnosed with babesiosis. Two genotypes of *B. canis*, 18S RNA-A (genotype A) and 18S RNA-B (genotype B), were present in the samples: four samples contained genotype A, two samples contained genotype B, and 55 tested samples contained genotypes A and B. The obtained DNA sequences were submitted to GenBank; ID numbers from KT844881.1 to KT844912.1.

In the samples from the investigated region, the majority of the *B. canis* infections were associated with the mixed genotypes 18S RNA-A and 18S RNA-B. Since the virulence of *B. canis* was postulated to depend on the 18S rRNA genotype of the parasite, the phenomenon of the domination of mixed genotype infections over single genotype infections might have clinical implications.

This is the first report to indicate that mixed genotype infections constitute the vast majority of infections with *B. canis* among dogs in Poland. Further research is required to explain why infections with mixed 18S RNA *B. canis* genotypes are more frequent.