

Detection and identification of *Borrelia spirochaetes* in hard ticks removed from deer in the Warmia-Mazury Voivodeship – preliminary studies

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Ticks are second to mosquitoes as vectors of human arthropod-borne diseases and play a role primary for animals in the process of diseases transmission. *Ixodes ricinus* is a main vector of Lyme borreliosis, a multisystematic zoonosis caused by pathogenic spirochaetes of the *Borrelia burgdorferi* complex. In this group comprising 20 species, five (*B. burgdorferi* s. s., *B. afzelii*, *B. garinii*, *B. bavariensis* and *B. spielmanii*) are pathogenic to humans. The pathogenicity of *B. valaisana*, *B. bissetti* and *B. lusitaniae* is also not excluded. In recent years, disease symptoms caused by *B. myamotoi* have been observed, including in Russia, the USA, Europe and Japan. The transmission of *Borrelia spirochaetes* from *Dermacentor reticulatus* to humans has not yet been confirmed but these ticks plays an important role in the maintenance of pathogens of medical and veterinary importance in the environment. In the spreading of spirochaetes, not only ticks, but also reservoir animals play an important role. Reservoir animals have different functions depending on the respective species. Small rodents and some birds are responsible for retaining pathogens, while the large domestic and wild animals contribute to the increase the tick population in the area and to the transmission of *Borrelia* spirochaetes among themselves through the co-feeding phenomenon.

Therefore, the aim of the present study was to identify *Borrelia* genomic species in hard ticks *I. ricinus* and *D. reticulatus* isolated from deer. 91 females of *I. ricinus* and 39 males of *D. reticulatus* isolated from deer, shot during hunting in the choosing districts of Warmia-Masury Voivodeship (north-eastern Poland) in the autumn of 2018, were analysed. In order to identify the *Borrelia* DNA, nested PCR was applied according to the method of Wodecka *et al.* (2010) using two primer pairs 132f / 905r, and 220f / 823r complementary to the fla gene. The genomic species of spirochaetes were determined using PCR-RFLP.

Detection of the fla gene was observed in 10/130 ticks (9 – *I. ricinus* and 1 – *D. reticulatus*), which constituted 7.69% of all analysed ticks (Table 1). Out of the examined DNA lysates, we identified two enzyme digestion patterns specific for the *B. afzelii* (8) and *B. miyamotoi* (1). In one case, *B. afzelii* was co-infected with another genomic species (X), whose full identification will be possible after sequence analysis in the next step of research (Table 1).

Table 1. Identification of *Borrelia* spirochaetes in hard ticks removed from deer in the choosing districts of Warmia-Mazury Voivodeship

Tick species	District	N infected ticks/N collected ticks	Genomic species
I. ricinus	Bartoszyce	2/5	1. Coinfection *B. afzelii*/X *2. B. miyamoto*i
	Gietrzwałd	2/18	*B. afzelii*
	Giżycko	0/9	–
	Kowale Oleckie	1/23	*B. afzelii*
	Olsztynek	0/24	–
	Reszel	4/12	*B.afzelii*
D. reticulatus	Giżycko	1/39	*B. afzelii*

REFERENCE. Wodecka B., Leońska A., Skotarczak B. 2010. A comparative analysis of molecular markers for the detection and identification of *Borrelia spirochaetes* in *Ixodes ricinus*. J. Med. Microbiol. 59:309-314

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