

Infections of *Ixodes ricinus* ticks with bacteria of *Rickettsia* and *Borrelia* genus in selected Forest Inspectorates (Lower Silesia, SW Poland)

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In Poland, *Ixodes ricinus* is the most abundant tick species which play an important role in transmitting tick-borne diseases, including borreliosis being the most often reported. Among other tick-borne diseases recognized as an emerging disease are rickettsioses, caused by bacteria from the spotted fever group of the genus *Rickettsia*.

The aim of the study was to estimate the prevalence of infection rate of *Borrelia* spp. and *Rickettsia* spp. in *I. ricinus* ticks collected in chosen Forest Inspectorates, Lower Silesia (SW Poland).

The study was conducted in three Forest Inspectorates (Milicz, Henryków, Miękinia) in Lower Silesia (SW Poland). Ticks were collected by flagging method during the spring peak of activity in April/May 2018. A nested PCR targeting the *fla* gene and the nested PCR targeting the *gltA* were used to detect *Borrelia* spp. and *Rickettsia* spp, respectively. Additionally, PCR-RFLP method was used to determine the *Borrelia* genospecies. Randomly selected positive samples of *Rickettsia* spp. were sequenced.

A total of 514 *I. ricinus* ticks, including 226 nymphs, 136 females and 152 males, were individually tested. *Borrelia* spp. was detected in 121 (23,5%) samples, whereas *Rickettsia* spp. in 131 (25,4%). *Borrelia* spp. and *Rickettsia* spp. co-infections were found in 5% of ticks. The analysis of randomly selected 45 *Borrelia* positive samples revealed the presence of 5 species from the *B. burgdorferi* s.l. complex: *B. afzelii*, *B. garinii*, *B. lusitaniae*, *B. burgdorferi* s.s., *B. valaisiana* and additionally *B. miyamotoi*. Sequencing confirmed the presence of *R. helvetica*.

Our results show the potential risk of *Borrelia* spp. and *Rickettsia* spp. infection in tested Forest Inspectorates in Lower Silesia (SW Poland) as well as the possibility of co-infection.