

Lyme borreliosis (LB) is the most commonly diagnosed tick-borne disease in Europe. The estimated incidence of LB in Poland increased dramatically from 20.3 per 100,000 inhabitants in 2007 to 56.0 per 100,000 inhabitants in 2017 (an estimated average increased from 7,735 cases per year in 2007 to 21,516 cases per year in 2017). However, the reliability of LB incidence data is uncertain because of diagnostic problems and limited reporting. At least five species of *Borrelia* – *Borrelia burgdorferi* sensu stricto, *Borrelia garinii*, *Borrelia afzelii*, *Borrelia spielmani* and *Borrelia bavariensis* – are known to be pathogenic to humans and each genospecies is believed to be associated with different clinical manifestations. Recently, *Borrelia miyamotoi* has been identified as a human pathogen causing relapsing fever in Europe, and little is known about its local impact on human health.

The primary vector tick for *B. burgdorferi* throughout Europe is *Ixodes ricinus* which also serves as a vector for numerous other pathogens (*Babesia*, *Anaplasma*). Consequently, individual ticks are often infected with more than one pathogenic organism, which may have medical significance (increased severity of symptoms and ineffective treatment). Ticks have been well-studied because of their impact on human health, but new microbial associations continue to be described and newly emerging infectious diseases are being recognized. There is emerging evidence that tick microbiome – defined as a community of commensal, symbiotic and pathogenic microorganisms – diversity can affect the efficiency of pathogen transmission. We are planning, for the first time, to evaluate the impact of coinfection with other pathogens (*Anaplasma*, *Babesia*, *Rickettsia*, *Neohhrlichia*), *Borrelia* intra-species competition and tick microbiome on *Borrelia* occurrence and density inside the tick and tick-to-human transmission success under natural conditions. We are also planning to extend our knowledge of the factors like time of tick feeding, *Borrelia* species and number of spirochetes which could influence on *Borrelia* transmission success from tick to human. Our proposal in the field of parasitology, molecular biology, including NGS, bioinformatics as well as the epidemiology have an interdisciplinary dimension in line with the global 'One Health' concept.

Despite the growing number of studies, the microbiomes of most tick species remain unexplored, and further research into the functional role of these microorganisms in ticks at an individual and community level is needed. So far, most tick and tick-borne diseases control strategies focus on the use of acaricides and vaccines, however, tick populations can become resistant to chemical acaricides, and vaccine development takes an average of ten years. It is likely that obtained results would extend our knowledge on factors affecting *Borrelia* dynamics transmission. In the future, this kind of knowledge could be developed to manipulate the tick microbiome to decrease the vectorial capacity of ticks by hindering pathogen acquisition, development, and horizontal and vertical transmission, which could have a long-term impact on tick-borne pathogen transmission and could ultimately reduce morbidity and mortality caused by tick-borne diseases.