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***Borrelia burgdorferi* s.l. genospecies and genotypes in *Ixodes ricinus* ticks from different neuroborreliosis-risk areas in Denmark**

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Neuroborreliosis (NB), the most severe Lyme borreliosis form, is linked to *Borrelia garinii* and *B. bavariensis*. However, it is unclear if all genotypes cause disease. The database for *Borrelia* multilocus sequence typing (MLST) shows a higher diversity of sequence types (STs) in ticks than in humans, suggesting that not all STs cause symptoms. Our study explores *Borrelia* prevalence, genospecies, and ST diversity in three NB risk area types: significantly high, non-significant (medium risk), and significantly low.

In 2023, ticks were collected from the vegetation on Funen, Denmark, in high, medium, and low NB risk areas, based on reported incidence data from Odense University Hospital. Tick DNA was tested for *Borrelia* via qPCR and further analyzed using MLST. After sequencing, the results were compared to the MLST database. A total of 2007 *I. ricinus* ticks were collected. Nymphs (87.3%) were the dominant life stage. *Borrelia* DNA was found in 11.7% of ticks (n=234), with a slightly higher prevalence in medium risk areas (13.9%) than in high and low risk areas (10.4% each). So far, 46 samples out of 85 with Ct $\leq$ 37.5 have been sequenced, revealing 6 genospecies, *B. afzelii*, *B. bavariensis*, *B. burgdorferi* s.s., *B. garinii*, *B. spielmanii*, and *B. valaisiana*, belonging to 41 different STs (26 pre-existing and 20 with novel allele combinations). 11 STs found in our study showed known pathogenic profiles. They were found in all three NB risk area types. Three of them were detected for the first time in ticks.

Further analysis of this ongoing study will be presented at the conference. This work has been supported by the German Academic Exchange Service (DAAD).

Keywords

Borrelia, genospecies, ticks, *Ixodes ricinus*, MLST, genotypes, sequence type, neuroborreliosis

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Junior Scientist Status

No, I am not a Junior Scientist.

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