

Prevalence and phylogeny of *Borrelia burgdorferi* s.l.- infected ticks in central and southern Sweden

Popular summary

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The tick, *Ixodes ricinus*, is a well-known vector of the bacteria, *Borrelia burgdorferi*. When ticks bite and attach to humans, they can transfer the bacteria and thus infect their host. Up to ten thousand cases of *Borrelia* infection (also called Lyme Borreliosis, LB) are reported in Sweden every year. Symptoms vary but include a ring-shaped rash surrounding the tick bite, achiness or fatigue, fever, and other flu-like symptoms. Studies in the past fifteen years have shown that the prevalence of *Borrelia* species is approximately 15-20% in adult ticks in Sweden and may be increasing. Climate change, increased time spent in tick-dense environments, and increased public and clinical awareness of the disease are some of the factors that seem to play a role in the rise of reported LB cases in Sweden. Little information exists about the current prevalence of *Borrelia* in Sweden or about how prevalence may vary depending on specific location within the country. Therefore, the aims of this project work were to determine the current prevalence of *B. burgdorferi* s.l. in specific locations in central and southern Sweden and to determine the phylogenetic relationships among the bacteria in these same areas. Polymerase chain reaction and analysis of DNA sequences were used during this study in an attempt to accomplish these goals.

Neither aim was completed in full. Difficulties with the PCR analysis presented a challenge and work to pinpoint the problem is continuing. Standard PCR troubleshooting such as using new materials, changing PCR machines, and optimizing protocol has been performed. To date, only 21 ticks from the 879 total sample collection (about 2.8%, much lower than expected) were found to be positive for *Borrelia* using nested PCR with IGS primers. All positive samples were purified and sent to an outside company for DNA sequencing; only 7 of the 21 samples provided enough *Borrelia* DNA for analysis. This was not enough information to study the phylogenetic relationships in Sweden but it was possible to assign species to each specimen. Two of the specimens most closely matched *B. miyamotoi*, a species entering Sweden with unknown dominance from the east.

More work continues in order to positively classify the remaining samples as either positive or negative for *Borrelia* species. Since the completion of the project report, a trip to Umeå University for help from Sven Bergström's group was made. Nothing new was elucidated from that trip and the samples which had been found positive in Uppsala (and subsequently sequenced) were not shown to be positive by PCR in Umeå despite the use of different machines and all materials. However, repetition of the experiment using different primers (as originally recommended by the author) will be completed by the group in Umeå. Reverse transcriptase PCR, which would identify positive samples but provide no information that may be used for sequence analysis, will likely be done at the university in August. The samples identified would then be the focus of further PCR amplification, with the hope that sequence analysis could be performed later.