

Genomic signatures of hybridization between *Ixodes ricinus* and *Ixodes persulcatus*

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Abstract

Identifying hybridization between common pathogen vectors is essential due to the major public health implications through risks associated with hybrid's enhanced pathogen transmission potential. These hard-ticks *Ixodes ricinus* and *Ixodes persulcatus* are the two most common vectors of tick-borne pathogens that affect human and animal health in Europe. *I. ricinus* is a known native species in Finland with a well-known distribution. Over the past 60 years, *I. persulcatus* has expanded in range making the species appear in areas previously not found in Finland. Here we used double-digest restriction site-associated DNA (ddRAD) sequencing on 92 ticks (morphologically identified as 46 *I. ricinus*, and 46 *I. persulcatus*) collected across Finland to investigate whether RAD generated single nucleotide polymorphisms (SNPs) discriminate tick species and identify hybridization events. Two different clustering methods were used to infer the specific species based on how they clustered and identified hybrids among them. We were able to discriminate between the two tick species and identified five putative hybrids with admixed genomic proportions ranging from approximately 25 to 75 percent. Four of these hybrids were morphologically identified as *I. ricinus* and the other as *I. persulcatus*. Our results suggest that RAD SNPs are robust for identifying both species of the ticks as well as their hybrid individuals. These results suggest ongoing hybridization between *I. ricinus* and *I. persulcatus* in their natural populations in Finland. This study is a significant step in understanding the formation of hybridization zones due to range expansion potentially associated with climate change. Despite our findings, our data are insufficient for resolving the factors that affect population genetic structure within species.

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