

Genetic diversity of a tick, *Dermacentor reticulatus*, in an expansion zone in central Europe

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A rapid expansion of the tick *Dermacentor reticulatus* has been reported recently in central European countries. In Poland, *D. reticulatus* has become common in the eastern part of the country, but another population has been newly established in the western part, near Zielona Góra and Wrocław. These two populations remained geographically separated.

The aims of our study were: (1) to determine the genetic diversity of ticks within and between the populations; (2) to compare this diversity with putative ‘source’ populations from Germany and Ukraine. Questing adult *D. reticulatus* ticks were collected by dragging in fallow lands in 2012–2014. The present study examined the genotype of ticks from three western and three eastern sites, along with samples from Potsdam area, Germany and Ukraine. Ticks were genotyped by the PCR amplification and sequencing of mitochondrial 16S rDNA (440 bp) and ITS2 region (1000 bp) (Kulakova et al. 2014). Altogether, about 100 sequences of each marker site were obtained for comparisons. The genetic variation within and between Polish populations was low, and the number of identified haplotypes was lower than in other studies in the genus *Dermacentor* sp. Similarly, almost no variance was observed in samples from Potsdam. In contrast, samples from Ukraine were found to have the highest number of unique haplotypes. We hypothesize that the low heterogeneity of ticks in the expansion zone in Poland and Germany may be the result of the ‘founder effect’ or reflect the “stepping-stone” model of expansion. Both models are associated with a loss of genetic variation. However, the lack of genetic difference between eastern and western populations, and between Polish and German populations, does not allow any conclusions to be made about the possible origin of the western population.

The study was supported by the National Science Center (NCN) grants: OPUS 2011/03/B/NZ8/02212 and Sonata Bis 2014/14/E/NZ7/00153.