
THE GENETIC STRUCTURE OF THE POPULATION OF *APHELOCHEIRUS AESTIVALIS* INHABITING RIVERS IN NORTHERN EUROPE

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The genetic structure of a population determines the amount and distribution of genetic variation within and among populations of selected species. Analyses of that structure contribute to understanding population dynamics, occurrence trends, and genetic relationships among populations. In the present study, we determined the genetic structure of five populations of selected model species, the riverine water bug *Aphelocheirus aestivalis* (Insecta: Heteroptera). Samples were collected from populations inhabiting rivers in northern Poland, Lithuania, Estonia and Finland, respectively. The preliminary insight into the genetic structure of selected populations was based on the analyses of eight polymorphic microsatellite loci. As a result, we found that all selected microsatellite loci were highly polymorphic in the tested samples. The number of alleles per locus per sample varied between 4 and 20. Moreover, private alleles were observed in each sample tested. Further analyses of F_{ST} values revealed, in general, a low level of genetic differentiation among samples. Only the sample collected from the Porvoonjoki River (Finland) was identified as genetically differentiated from other samples at a moderate level (values of F_{ST} in the range of 0.051–0.070). Principal Coordinates Analysis (PCoA) revealed that samples collected from the Šventoji (Lithuania) and the Łyna (Poland) rivers were more similar to each other than to the other analysed samples. The presented study is part of a research grant. Analyses will be continued on a wider spatial scale using mitochondrial and nuclear markers. Results will be also analysed in the context of the prevalence of known endosymbiotic bacteria infecting populations of *A. aestivalis*.

Keywords: microsatellites, genetic structure, *Aphelocheirus aestivalis*, phylogenetic relationships

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