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# PREVALENCE OF *WOLBACHIA* IN POPULATIONS OF *APHELOCHEIRUS AESTIVALIS* INHABITING RIVERS IN SOUTHERN EUROPE AND ITS POTENTIAL IMPACT ON THE HOST'S GENETIC DIVERSITY

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The bacterium *Wolbachia* infects about 52% of aquatic species. Since *Wolbachia* is co-inherited with mitochondria, natural selection acting over the bacterium will also affect mitochondria. Depending on the infection context, this hitchhiking effect may increase or decrease the host's genetic diversity at the mitochondrial level and thus cause problems in phylogeny inference. In the present study, *Aphelocheirus aestivalis* (Insecta: Heteroptera) was selected as a model species. The riverine water bug is the only reported species of the monogeneric family Aphelocheiridae occurring in most parts of Europe. Its limited dispersal abilities are predicted to limit the gene flow between populations, promoting population fragmentation, genetic divergence, local adaptation, and endemism. Here, we determined the phylogenetic relationships among six populations of *A. aestivalis* inhabiting rivers in Southern Europe (Hungary and Romania). Analyses were performed on both mitochondrial and nuclear levels (*cox1* and nine microsatellite loci, respectively). Moreover, each sample was screened for the presence of *Wolbachia*. As a result, *Wolbachia* was found in each selected sample and at least 60% of tested specimens were infected per sample. The highest percentage of specimens infected with the bacterium was observed in the sample collected from the Caraș river in Romania (93%). Analyses performed at the mitochondrial and nuclear levels revealed close relationships among selected populations. Those close relationships may be connected with various factors, e.g., common origin and belonging to a single phylogenetic lineage. Thus, the hypothesis on the *Wolbachia*-induced reduction of *A. aestivalis* genetic diversity seems less likely.

**Keywords:** *Wolbachia*, mitochondrial markers, microsatellites, phylogeny, *Aphelocheirus aestivalis*

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