

Phylogeography of *daphnia magna straus* (Crustacea: Cladocera) in Northern Eurasia: Evidence for a deep longitudinal split between mitochondrial lineages

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Abstract

© 2018 Bekker et al. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited. Species with a large geographic distributions present a challenge for phylogeographic studies due to logistic difficulties of obtaining adequate sampling. For instance, in most species with a Holarctic distribution, the majority of studies has concentrated on the European or North American part of the distribution, with the Eastern Palearctic region being notably understudied. Here, we study the phylogeography of the freshwater cladoceran *Daphnia magna* Straus, 1820 (Crustacea: Cladocera), based on partial mitochondrial COI sequences and using specimens from populations spread longitudinally from westernmost Europe to easternmost Asia, with many samples from previously strongly understudied regions in Siberia and Eastern Asia. The results confirm the previously suspected deep split between Eastern and Western mitochondrial haplotype super-clades. We find a narrow contact zone between these two super-clades in the eastern part of Western Siberia, with proven co-occurrence in a single lake in the Novosibirsk region. However, at present there is no evidence suggesting that the two mitochondrial super-clades represent cryptic species. Rather, they may be explained by secondary contact after expansion from different refugia. Interestingly, Central Siberia has previously been found to be an important contact zone also in other cladoceran species, and may thus be a crucial area for understanding the Eurasian phylogeography of freshwater invertebrates. Together, our study provides an unprecedented complete, while still not global, picture of the phylogeography of this important model species.

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