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## Abstract

Water fleas of the *Daphnia pulex* species complex inhabit diverse environments throughout the northern hemisphere, they have enormous dispersal capacity and show striking patterns of phenotypic diversity, which makes them interesting study subjects. My main intention was to better understand diversity in the water flea *D. pulicaria* Forbes. Therefore I used molecular markers. *D. pulicaria* is widely distributed across the temperate and arctic regions of North America and Eurasia, and it shows a remarkable phenotypic polymorphism in Europe. An unpigmented morphotype inhabits lowland regions throughout Europe and mountain lakes in the High Tatra, a carotenoid pigmented morphotype coexists with the unpigmented one in the High Tatra, and a melanic morphotype occurs in the Pyrenees. As yet no study assessed genetic differentiation between the morphotypes. My study therefore had three primary objectives. I first used DNA sequence variation at the mitochondrial DNA (mtDNA) ND5 gene to reconstruct phylogenetic relationships among *D. pulicaria* from different parts of its distribution and to investigate their relationships to other members in the *D. pulex* complex. The main finding was that the carotenoid and melanin pigmented populations from the European mountain lakes were not related to the unpigmented populations inhabiting the same lakes and the lowland regions throughout Europe, but were more closely related to *D. pulicaria* sampled from Canada and Greenland. This Eastern Nearctic lineage was not found in Europe before. My second objective was to test for a concordance of the morphotype divergence across different genetic markers. I quantified variation at eight microsatellite loci and found that each population was fixed for a single multilocus genotype and that genotypes were not shared among the morphotypes despite the coexistence in the High Tatra, confirming that their genetic divergence is not restricted to mtDNA. I concluded that at least two divergent species are confused under the name *D. pulicaria* in Europe, which differ in pigmentation and life history, and coexist in the same lakes without loss of the genetic integrity. My final research objective was to assess the utility of diapausing egg banks of *D. pulicaria* in the High Tatra lakes as repositories of genetic information. Very low numbers of resting eggs and their poor physical condition yielded no amplifiable DNA, making tracking long-term genetic shift in these ultra-oligotrophic lakes unfeasible. Autochthonous recovery of extinct genotypes is therefore unlikely, which underscores the importance of immigration and local selection in the spatial patterning of genotypes. In general, my study shows that a considerable part of *Daphnia* diversity, previously attributed to ecophenotypy by morphological taxonomy, has been missed.