

Abstract

I studied the genetic structure of cladocerans from the *Daphnia longispina* complex in several European mountain ranges. The population genetic structure of the *D. longispina* complex was studied using mitochondrial (mtDNA; partial sequencing of the 12S rRNA gene) and nuclear markers (nine microsatellite loci).

Major part of the work was done in the Tatra Mountains; the genetic structure of populations of the *Daphnia longispina* complex from two parts of this range (the West and the High Tatras) was compared. The pattern of mtDNA confirmed multiple colonization of lakes from different source populations, detected haplotype diversity was high and haplotype sharing only within the West or the High Tatras was observed. The observed genetic differentiation indicates low level of gene flow and persistent founder effect, consistent with the monopolization hypothesis. The alternation of asexual and sexual reproduction in the life cycle of *Daphnia*, cyclical parthenogenesis, may affect genetic structure of their populations. This was the topic of a study described in the first chapter. A detailed analysis of population structure of two closely related *Daphnia* species (*D. galeata* and *D. longispina*) living in similar habitats (permanent dimictic mountain lakes) in the Tatra Mountains revealed that populations show strikingly different genetic composition depending on their reproductive strategy during unfavourable periods (overwintering as parthenogenetic females vs. ephippial dormant eggs). The next chapter focused on the past changes of taxonomic composition of a *Daphnia* population in a single Tatra Mountain lake, and shows the usefulness of paleogenetic methods for such a purpose. The use of internal primers amplifying only short fragments of the target mitochondrial gene overcame the problem of degraded DNA in the old ephippial eggs, and enabled the correct species determination from 80-years old sediments.

Daphnia populations from other European mountainous regions extended the scope of my studies. In the third chapter, populations of *Daphnia longispina* and *Eucyclops serrulatus* complexes from the Tatra Mountains were compared with populations from other mountain ranges in South-Eastern Europe. All studied lakes were inhabited by single lineages of the respective species complexes (one of the *Eucyclops* clades, and *Daphnia longispina* sensu stricto) and their sequence variation suggests that many of the studied regions were colonised multiple times by both species. *D. longispina* haplotypes were highly variable, representing a substantial proportion of the known haplotype diversity of the species. We detected six divergent lineages of *Eucyclops* cf. *serrulatus*, confirming that this taxon represents a diverse species complex. The last chapter deals with the population genetic and phylogeographic structure of *D. longispina* in Pyrenean lakes. The diversity in the sampled region is mostly the result of a single colonization event. The post-colonization gene flow has been very rare indicating that priority effects are major drivers of genetic structure at various spatial scales. Although the presence of cryptic lineages in the mountain lakes does not seem to be a general pattern, studies of the mountain populations of zooplankton may advance the knowledge on processes shaping the within- and among-population diversity in this group of organisms.