

ABSTRACTS

Part 1

Canyon-shaped reservoirs, characteristic by elongated morphology and by ecologically diverse conditions along both horizontal and vertical reservoir axes, are good model systems for ecological studies of zooplankton communities. Presence of ecological gradients improves habitat differentiation and may facilitate coexistence of related species. Here we provide detailed study of genetic structure of the *Daphnia longispina* complex inhabiting three canyon-shaped reservoirs. Using 12 microsatellite loci, we assessed taxonomic and genetic structure of assemblages composed by populations of *D. galeata*, *D. cucullata*, *D. longispina* and their interspecific hybrids. We focused on detailed taxon determination and on patterns of hybridization and introgression. High number of distinct hybrid genotypes in the samples suggested high frequency of hybridization; despite this, later generation hybrids were rare.

In one reservoir inhabited by a single species, *D. galeata*, we also tested if environmental gradients may cause intra-population genetic diversification similar to spatial differentiation in species composition. Subpopulations along horizontal gradient in the reservoir, as well as those in different layers of the stratified water column, were significantly genetically differentiated. We propose that this structuring of *D. galeata* population is caused by local adaptation and clonal selection facilitated by presence of ecological gradients. On the other hand, we did not observe such intraspecific differentiation in a reservoir inhabited by several taxa of the complex, although *D. galeata* was present along the whole reservoir.

Part 2

Daphnia galeata, *D. longispina* and *D. cucullata* (Crustacea: Cladocera) are closely related species often producing interspecific hybrids in natural populations. Common inconsistencies among species-specific markers using for their determination were traditionally attributed to the complexity of their relationships and to the occasional introgression. In order to test this hypothesis, we used several different approaches for the taxon identification. Using allozyme electrophoresis and ITS-RFLP, we identified more than 1200 individuals from ten localities situated in the Czech Republic as parental species or hybrids. 444 animals were additionally analyzed and identified by analysis of 12 microsatellite loci. The data set was further extended by samples from 19 sites across the whole Europe, in which the taxon was estimated using microsatellites and ITS-RFLP. Results of microsatellite analysis corresponded well with allozymes. However, two sites from the

Czechia and three sites from other European countries exhibited consistent discrepancies between ITS-RFLP and other markers. Although some marker disagreement could have been caused by occasional introgression, more serious deviations observed in ITS-RFLP more likely suggest a long-term maintenance of introgressed alleles in genomes of parental species, in which evolutionary mechanisms such as gene conversion and meiotic drive could support the maintenance of “alien” alleles.

Finally, we compared data from molecular markers with identification based on phenotypic characteristics of photographed animals for a randomly selected set of 240 *Daphnia* individuals, and quantitatively evaluated the body shape variation by geometric morphometrics. Morphological identification, at least when based on photographs, gave substantially worse results than any molecular method. The least successful was differentiation between *D. galeata*, pelagic *D. longispina*, and their hybrids; these taxa showed particularly high degree of overlap of their body shape.