

ABSTRACT

I studied the genetic diversity of central European *Cyclops* (Crustacea, Copepoda) species. The present thesis deals with all species of the genus *Cyclops* known from the Czech Republic (*C. strenuus*, *C. vicinus*, *C. abyssorum*, *C. insignis*, *C. singularis* and *C. furcifer*); the occurrence of *C. singularis* and *C. heberti* there is recorded herein for the first time. Other two species under study are *C. ochridanus*, an endemic species from the Ohrid lake, and an apparently new species of the genus *Cyclops* from the Retezat Mts. in Romania. Populations of *Cyclops abyssorum* from Romania, Slovakia and Switzerland were studied as well.

The amplification of a part of the COI mitochondrial gene, using the universal arthropod primer (Folmer et al. 1994) or primers derived from it, was successful only in less than half of the populations under study. In contrast, amplification of a part of the 12S srRNA gene, using the primer of Machida et al. (2002), worked very well in all the populations.

Cyclops abyssorum, a morphologically and ecologically variable species, showed very low between-population sequence polymorphism. The ecotypes “praealpinus“, “divulsus“ and “tatricus“ seem to lack a species or subspecies status. They are likely to be, as Einsle (1980) supposed, morphological variations only. Populations of *C. strenuus*, another widespread species, were also genetically uniform.

The ecological valence of *C. singularis*, described from temporary ponds in southern Germany, is broader than expected; the species may occur in permanent water bodies (e.g., the hypolimnion of the deep Slapy reservoir and shallow permanent ponds).

Due to its low evolutionary rate, the 12S srRNA gene seems to be unsuitable for phylogeographic studies.