

The objective of this thesis is to contribute to the general understanding and to fill some gaps in our knowledge of *Eubosminas*' biology, especially evolutionary biology, taxonomy and systematic, applying methods of molecular genetics. The main aim was to elucidate the origin of *Eubosmina* morphotypes, their taxonomic significance, and evolutionary meaning. To test possible European refugium or refugia for *Eubosmina* was the goal as well. For available paleolimnological record, occurrence in sympatry in relatively homogenous pelagial of freshwater bodies and mixed breeding system *Eubosmina* represents evolutionary system with unique and advantageous features. In spite of it, it stays in the background of modern research. It is through mainly in evolutionary, taxonomic, and systematic aspects. Although *Eubosmina* specimens are often mentioned in the paleolimnological or ecological studies their taxonomical system is based solely on morphological features that are plastic. The group itself, mainly European specimens, is known to exhibit enormous cyclomorphosis and local variance. That is why the system of *Eubosmina* differs according to the authors. Nearly each author came up with different system despite the same morphological characters have been used. Since no detail genetic study and complex morphometric comparisons were done the controversy exists over the distinctness, evolutionary significance and the taxonomical status of morphotypes and hypotheses range from one morphologically variable species to dozens of local species. The advantage of paleolimnological record (the carapace and the antennules with the main morphological features used for morphotypes distinction) brings some useful knowledge but still does not answer the question of origin of morphotypes that most likely originated after the last glaciation nor the existence and the localization of possible refugium or refugia.

The newest and the most complex taxonomical system from U. Lieder was followed in this work. The subspecies of this system were handled as distinct units called morphotypes or morphospecies that were analyzed morphologically (in four cases of morphospecies living in sympatry) and genetically. The first used genetic marker (mitochondrial gene COI) showed up unsuitable (not very informative) thus the framework of this thesis is based on faster evolving genetic marker ND2. (The detection of the pseudogene of this mitochondrial gene complicated the work and recruitment of the data itself). Besides, two nuclear genes were tested (HSP and TBP 70), but only HSP analyses was used (in four cases of morphospecies living in sympatry) to make some conclusions and answer some of the questions till now. Results obtained by this work contributed to better understanding of *Eubosmina* evolutionary biology – evolutionary meaning of the morphotypes, their taxonomic validity and proved the group to be suitable for biologically-evolutionary studies as general model.

The DNA-sequence of the complete *Eubosmina* mitochondrial genome (*Bosmina (Eubosmina) tanakai*), which was obtained as a part of this work applying a new method, facilitated comparisons with members of other close genera (*Bosmina (Eubosmina) coregoni*, *Chydorus brevilabris*, *Daphnia pulex*, and *Artemia franciscana*). This comparison suggested a different mutation-selection balance among the species.