

ABSTRACT

Phylogenetics is a field of systematic biology which aims to uncover the evolutionary relations between all species on the principle of finding their common ancestor. Phylogeny can be applied on many different markers, but among the most common are genetic and morphological ones. The results of the phylogenetic analyses can be applied in many other fields of research. We can use them e.g. in answering questions concerning geological events (when using fishes as model, most often in some river flow changes). Cobitoidea is a superfamily of fishes, which belongs to cypriniformes - the biggest group of primary freshwater fishes. Cobitoidea contain 10 families - Gyrinocheilidae, Cobitidae, Balitoridae, Botiidae, Vaillantellidae, Ellopostomatidae, Barbuccidae, Serpenticobitidae, Nemacheilidae, Gastromyzontidae, and the Catostomidae might be considered as belonging into Cobitoidea as 11th family. The distribution area of Cobitoidea covers almost whole Europe and Asia and that of Catostomidae also North America. There is no major river system in whole Eurasia that would not be inhabited by loaches. Every major river basin contains one to tens of loach species, therefore loaches can be considered one of the most characteristic element of the Eurasian freshwater fauna. In Cobitoidea, we can also find many interesting ecological adaptations. This bachelor thesis aims to summarise published hypothesis of phylogenetic and taxonomic relationships between lineages in this group of fishes.

Key words: phylogenetics, evolution, taxonomy, systematics, genetic markers, morphological markers, Cobitoidea, Cypriniformes, Eurasia