

## Abstract

In this study comparative phylogenetic analyses of huchonid fishes (*Brachymystax* and *Hucho* genera) were carried out by application of various computational methods based on the supermatrix data retrieved from NCBI Gene Bank. For this purpose, the available mitochondrial (3575 bp) and nuclear (2037 bp) DNA data originated from all extant huchonid species were used. Additionally, molecular dating was carried out to estimate time background of huchonids divergence. Phylogenetic analyses were conducted using the Neighbor-joining (NJ), Maximum likelihood (ML), Maximum parsimony (MP) and Bayesian approach (BA) methods. The ancestral position of *Brachymystax/Hucho* cluster within Salmoninae subfamily was resolved and dated to emerge c.a. 24.7–25.6 million years ago (Mya). The evolutionary age of the most recent ancestor of contemporary huchonids was estimated to 10.6–13.6 Mya, while the oldest lineage within huchonid fishes was the genus *Brachymystax* (5.5–6.1 Mya). All three extant *Hucho* species were dated to split about 2.5 Mya, suggesting their disjunctive distribution during speciation. The highest heterogeneity was observed within *Hucho taimen* and *Hucho bleekeri* species, which clustered into two distinct phylogeographic groups, implying their vicariant origin from different glaciation refuges. The lowest level of genetic differentiation was recorded in *Hucho hucho* species, which may reflect past low population size, bottlenecks, founder effect and/or low rate of molecular clock. The carried out comparative analyses evidenced the discordance between nuclear and mitochondrial DNA data, indicating probable introgression between *H. bleekeri* and *Brachymystax lenok* that was estimated to take place around 5.5 Mya. The monotypic *Parahucho* genus was resolved as evolutionary younger and separate from huchonid lineage, that emerged around 15.8–13.2 Mya.