

First look into the evolutionary history, phylogeographic and population genetic structure of the Danube barbel in Croatia



The Danube barbel, *Barbus balcanicus* is small rheophilic freshwater fish, belonging to the genus *Barbus* which includes 23 species native to Europe. In Croatian watercourses, three members of the genus *Barbus* are found, *B. balcanicus*, *B. barbus* and *B. plebejus*, each occupying a specific ecological niche. This study examined cytochrome b (cyt b), a common genetic marker used to describe the structure and origin of fish populations to perform a phylogenetic reconstruction of the Danube barbel. Two methods of phylogenetic inference were used: maximum parsimony (MP) and maximum likelihood (ML), which yielded well supported trees of similar topology. The Median joining network (MJ) was generated and corroborated to show the divergence of three lineages of *Barbus balcanicus* on the Balkan Peninsula: Croatian, Serbian and Macedonian lineages that separated at the beginning of the Pleistocene. Croatian lineage of *B. balcanicus* shows a uniform structure with many recently diverged haplotypes, which was further supported by the star-like shape of the MJ network. Effective size estimates were obtained for

populations inhabiting separate river catchments and the results imply the good reproductive potential of *Barbus balcanicus* in Croatia, which is in positive correlation with the overall high genetic diversity calculated for its populations. Nevertheless, population sizes of several population seem to be reduced as a consequence of habitat degradation and fragmentation.

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