**Abstract**

The Dinaric karst region in the Balkans is one of the hot spots of biodiversity with a high number of endemic freshwater fish. The major cause of the high degree of endemism are numerous paleoclimatic and geological events that have affected the formation of the entire area. Flows of karst poljes represent a specific ecosystem to which some fishes have adapted. The poljes have been periodically flooded and these floods may activate different underground channels, which lead to interconnection of poljes. These fish species spend a part of the year in surface water and a part in groundwater and they may use the underground flows between poljes for migration.

The aim of this thesis is to evaluate the genetic variability of two endemic fish species of the genus *Telestes* living in karst poljes in the region of eastern Herzegovina, and to detect a possible current gene flow between populations of these species due to the connection of underground flows. For this purpose, the DNA from 102 individuals from five different localities was isolated. The mitochondrial marker cytochrom *b* and 16 microsatellite loci were used for the analyses.

The results point to very low variability between species and populations. Based on mitochondrial marker analysis, no link between populations of the species was detected, with the exception of a possible connection to the *Telestes metohiensis* populations from the rivers Zalomka and Mušnica, which shared one haplotype. The populations are likely to be very small, therefore the observed heterozygosity was lower then expected and the $F_{IS}$ coefficient revealed the presence of inbreeding in the populations. Estimated effective population size was low and populations are prone to demographic changes. Species are particularly threatened by building dams and canals, which prevent periodical flooding of poljes, but also by pollution and the introduction of non-native species.

Key words: *Dinaric karst, karst polje, freshwater fishes, Telestes, cytochrome b, microsatellites, genetic diversity*