ABSTRACT

MOLECULAR PHYLOGENY OF BROWN TROUTS (Salmo trutta L.) IN TURKEY

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Ph. D. Thesis, Department of Biology Supervisor: Prof. Dr. Fevzi BARDAKCI 2013, 72 pages

Salmo trutta L. is a native salmonid species with a range from Eurasia and North Africa. Its natural range extends from northern Norway to the Atlas Mountains of North Africa. In this study, mitochondrial displacement loop (D-loop) and nuclear DNA ITS1 were used for determining the phylogenetic relationships of *Salmo trutta* L. in Turkey. Mitochondrial DNA data was analysed by combining the sequences of the same mitochondrial DNA region deposited in GenBank belonging to brown trout lineages from other geographic regions. As a result, six main evolutionary lineages were defined, and it was determined that four of them (Adriatic, *marmoratus*, Tigris, Danubian) are existed in Turkey. The existence of *marmoratus* lineage was reported in this study for the first time. Phylogenetic inferences has been made by evaluating both mitochondrial and nuclear DNA sequence data. The results of this study indicated the secondary contacts, especially among Danubian, Adriatic and Tigris lineages. In addition, the lineages of Turkish brown trout populations are highly divergent and mainly have a unique genetic structure.

Key words: Salmo trutta L., mitochondrial DNA, nuclear DNA, phylogeny, Turkey