

Determination of Genetic Structure of Trout Populations Using mtDNA-RFLP Analysis Method in Turkey

Project Leader: Dr. Yılmaz ÇİFTÇİ– CFRI

In this study, genetic and morphometric structures of anadromus and non-anadromus brown trout (*Salmo trutta*) and flathead trout (*Salmo platycephalus*) populations from different part of Turkey were studied by means of mtDNA-RFLP analysis and Truss network system. After amplifying three segments of mtDNA by PCR, ND1 amplified product was digested with 5 restriction enzymes, Cyt. b/D-loop product with 5 and ND5/6 product with 7. Thirty one composite haplotypes were identified. The nucleotide divergence between composite haplotypes was ranged from 0.0004 to 0.0289 and phylogenetic tree of the haplotypes constructed by using the UPGMA method showed that brown trout populations clustered into two different groups namely Danubian (DA) and Adriatic (AD), which includes *S. platycephalus* as well. The haplotype and nucleotide diversity within populations were 0.270 and 0.001 respectively, and pairwise nucleotide divergence and diversity between populations were 0.009 and 0.010 in that order. Genetic heterogeneity between populations was tested by using Monte-carlo simulation and distribution of

haplotype frequencies was significant ($\chi^2=8647.20$, $P<0.001$). But no heterogeneity was found between anadromus and resident ecotypes ($\chi^2=15.28$, $P<0.1350$). Significant genetic differentiation ($\Phi_{ST}=0.92$) and small number of effective gene flow ($N_e m$) = 0.045 among the populations were observed. On the contrary, genetic differences seem to be less ($\Phi_{ST}=0.084$) and gene flow very high ($N_e m$)=5.5 among anadromus and resident groups. No significant correlation was observed between geographical and genetic distance including Black Sea and Mediterranean Sea drainage populations when geographical distance smaller than 2000 km ($R^2 = 0.0136$, $P=0.176$). However, good correspondence was found when geographical distance larger than 2000 km ($R^2=0.4893$, $P<0.001$). According to assignment test for morphological differences %84.36 of individuals from the all taxa were classified correctly. According to UPGMA phenogram resulting from squared Mahalanobis distance for all taxa *S. t. abanticus* and *S. platycephalus* separated from other subspecies grouped together.

