

Study of Genetic structure and variation of pikeperch (*Sander lucioperca*) in Lake of Aras dame and Anzali Wetland

Farshad Mirza Ahmadi¹
Mehrnoush Norouzi^{2*}
Ameneh Amirjanati³
Mohammad Hadi Samiei⁴
Mohammad Behrouz⁵

1, 2, 3, 4, 5. Department of Marine
Biology and Fisheries Sciences,
Islamic Azad University, Tonekabon,
Iran

*Corresponding author
mnoroozi@toniau.ac.ir

Received date: 2014.05.23

Reception date: 2014.11.06

Abstract

This study aimed to determine the population genetic variation of pikeperch, *Sander lucioperca*, investigated in Anzali Wetland and Lake of Aras dame using microsatellite markers. Totally 60 samples of adult pikeperch were collected from these regions in summer 2012. Five sets of microsatellite primers tested on genomic DNA of pikeperch. All primer sets as polymorphic loci were used to analyze the genetic variation. Analyses revealed that average of alleles (N_a) per locus was 5 (range 4 to 7 alleles). All sampled regions contained private alleles. The average observed and expected heterozygosity was 0.650 and 0.731 respectively. The average estimates of inbreeding coefficient (F_{is}) values of five microsatellites were negative. Deviations from Hardy-Weinberg equilibrium were in all cases ($P < 0.01$). F-statistics (F_{st}) and gene flow (N_m) estimates in Allele frequencies were 0.092 and 2.4 respectively. Rst and Fst estimates in AMOVA indicated significant genetic differentiation among regions ($P \leq 0.01$). Genetic distance was 0.616, indicating that the genetic difference among the studied populations is pronounced. The data generated in this study provides the genetic variation and differentiation in populations of pikeperch in the Anzali Wetland and Lake of Aras dame.

Keywords: Genetic variation, Microsatellite, Pikeperch, *Sander lucioperca*.