

Population genetic structure of common Kilka (*Clupeonella cultriventris*) in the South Caspian Sea costline (Mazandaran province) using microsatellite markers

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Abstract

Common kilka, *Clupeonella cultriventris* is an economic fish in Caspian sea and we investigate population genetic structure of common kilka in the South Caspian Sea costline (Mazandaran province) using microsatellite markers. Totally, 60 individuals of adult common kilka from two seasons were sampled. Eight sets of microsatellite primers were developed from American shad and Pacific herring tested on genomic DNA of common kilka. At this point only the five successfully used primer sets and were used to analyze the genetic variation in adultsof the common kilka population. Analyses revealed that average of alleles per locus was 11.7 (Na range 6 to 17 alleles per locus). Both of sampled seasons contained private alleles. Average observed and expected heterozygosity were 0.543 and 0.866 respectively. Deviations from Hardy-Weinberg equilibrium were in most cases ($P < 0.01$). Basis on AMOVA for both F_{ST} values among pairs them indicated a significant difference between the two seasons ($P \leq 0.01$). These results support the existence of different genetic populations along the South Caspian Sea costline (Mazandaran province) in different seasons.

Keywords: Population genetic, South Caspian Sea, Microsatellite, *Clupeonella cultriventris*