

ABSTRACT

GENETIC STOCK IDENTIFICATION OF STRIPED RED MULLET (*Mullus surmuletus* L.) IN THE SEAS OF TURKEY

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Striped red mullet (*Mullus surmuletus*) is an economically important demersal species in fisheries. The present study is aimed to determine the genetic stocks and genetic variability of striped red mullet across Turkish seas using sequence data from the control region of mtDNA and genotype data of 14 microsatellite loci of nuclear genome. Striped red mullet samples has been collected from the following localities: Mersin and Antalya from the Mediterranean Sea; Marmaris, Kuşadası, Ayvalık and Saroz Bay from the Aegean Sea; Bandırma from the Marmara Sea. Higher genetic variation has been determined between populations in striped red mullet based on both the allele numbers of microsatellite loci and haplotype diversity of mtDNA. Results of mtDNA analyses have shown that populations of striped red mullet were divided into three clades. These three mtDNA lineages did not displayed a meaningful partition between the populations from the different seas studied. Each three different genetic group displays a homogenous distribution between the populations of striped red mullet. According to the results of both mtDNA and microsatellite data analyses, it has been found that striped red mullets from Saroz Bay were constituted a genetically different group which were different from the other localities in the Aegean Sea. A different genetic structuring has also found between striped red mullets from Mersin and Antalya localities in the Mediterranean. As a result, since striped red mullet from Turkish seas have displayed a different genetic differentiation in a certain degree, these information should be taken into account for a new sustainable fishery management strategies for this species.

Keywords: Red striped Mullet, *Mullus surmuletus*, Turkish Seas, microsatellites, mtDNA, Control region