



Population Genetic Analysis of Grouper Species (*Epinephelus* spp.) in Turkish Seas

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Abstract

In this project, it is aimed to determine population genetic structure of grouper species belonging to *Ephinephelus*, *Hyporthodus* and *Mycteroperca* genera distributed in the Aegean and Mediterranean Seas with sequence analysis of mitochondrial DNA (mtDNA) gene. With the population genetic analysis of grouper species we elucidate whether there are enough migration or gen flow among populations which lead to one panmictic populations, or there are partial genetic isolation among populations which lead to genetically different local populations. It is also aimed to reveal results of the negative effect of overfishing and other environmental factors on genetic structure of the species, and determine preferential populations and species for conservation. Grouper species distributed in the Mediterranean and Aegean Seas are represented with 6 species (*Epinephelus aeneus*, *E. caninus*, *E. costae*, *E. marginatus*, *Hyporthodus haifensis*, *Mycteroperca rubra*) in Turkish marine waters. Fishing tonnage of grouper species are extremely decreased within the last decade according to Fishery statistics. According to IUCN criteria, dusky grouper *E. marginatus* is indicated as critically endangered and white grouper *E. aeneus* is indicated as nearly endangered species, and they are faced to be extinct in the nature. The other grouper species cannot be evaluated due to deficient data on them in Turkey. As is known in our country and around world, these species and their populations have high economic value and shown to be under threat of extinction. In this context, analysis of the genetic structure of the grouper species, belonging to *Ephinephelus* genera distributed in Turkish Marine waters with a very high economic value, is very important in terms of sustainability. This project was supported by TUBITAK (214O575).

Keywords:

Turkish seas, grouper species, *Ephinephelus* spp., population genetics, mtDNA sequencing
