

POSTER

PRELIMINARY OXPPOS GENES ANALYSIS IN THE STRIPED RED MULLET (*MULLAS SURMULETUS LINNAEUS*, 1758)

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The striped red mullet (*Mullus surmuletus* L., 1758) is a key target species with high commercial value for small-scale fisheries in the Mediterranean Sea. The species is widely distributed along the Mediterranean coasts as well as the northeastern Atlantic Ocean, from Scandinavia to Senegal. As ectotherms, aquatic species depend on heat exchange with their surrounding environment to regulate metabolism and adaptation. Consequently, climatic variation across their range can result in differing bioenergetic requirements. Mitochondrial OXPPOS (mtOXPPOS) genes are critically involved in these processes and have been extensively studied in the last decades as a system that is subject to selection under determined environmental constraints. Based on the above, the aim of this study was to analyze the nucleotide sequence of two mitochondrial OXPPOS genes, Cy-

tochrome Oxidase I (COI) and NADH dehydrogenase subunit 1 (ND1), in five Mediterranean populations of the target species to detect the presence of positive selection based on different models of evolution. Various selection tests were conducted. In particular, the CodeML test identified the presence of one site under positive selection in the COI gene; the FUBAR test detected one site under positive selection and three under negative selection in the COI gene, as well as two sites under positive selection and twelve under negative selection in the ND1 gene. Finally, the MEME test indicated the presence of a single site under positive selection in the ND1 gene. Overall, these findings provide preliminary evidence of localized positive selection in mitochondrial OXPPOS genes of *M. surmuletus*, likely reflecting adaptive responses to spatial environmental variability across the Mediterranean Sea.