Quaderni del Centro Studi Alpino – IV

*Unione Zoologica Italiana*
*76th National Conference*

# Proceedings

Viterbo, 15-18 September 2015

a cura di Marzio Zapparoli, Maria Cristina Belardinelli

Università degli Studi della Tuscia
2015

FRANCESCO SACCO[1], EUGENIA SCHIMMENTI[1], FEDERICO MARRONE[1], SABRINA LO BRUTTO[1], AMINA BESBES[2], AHMED NFATI[3], MARK GATT[4], SAMAR SABER[5], FABIO FIORENTINO[6], MARCO ARCULEO[1]

[1] Dipartimento STEBICEF, Università di Palermo, Via Archirafi 18, 90123 Palermo, Italia
[2] INSTM, Centre de Monastir, Tunisie
[3] Marine Biology ResearchCenter, Tajura, Lybia
[4] Ministry for Sustainable Development, the Environment and Climate Change, Malta
[5] Instituto Espanol de Oceanografia, Malaga, Spain
[6] IAMC- CNR Mazara del Vallo (TP), Italia

# GENETIC VARIATION OF THE DOLPHINFISH *CORYPHAENA HIPPURUS* (PISCES, CORYPHAENIDAE) IN THE MEDITERRANEAN SEA

*Coryphaena hippurus* is a cosmopolitan migratory epipelagic species and represents a target species for artisanal fisheries and recreational fishing. Moreover, in some parts of the Mediterranean Sea, it constitutes one of the most important species for commercial fishery. In the present study we analysed the mtDNA genetic diversity of dolphinfish throughout the Mediterranean Sea with the aim to support future management plans aimed at ensuring the sustainability of this important marine resource. Genetic variation was investigated by the sequencing of two mtDNA markers, i.e. the cytochrome c oxidase subunit 1 (COI) and the NADH dehydrogenase subunit 1 (ND1). Tissue samples were obtained from 10 different landing localities of the Mediterranean Sea: Palma de Majorca (Balearic islands, Spain), Ancona (Adriatic coast of peninsular Italy), Ischia (Naples, Tyrrhenian coast of peninsular Italy), Porticello (Palermo, Sicily), Capo Passero (Syracuse, Sicily), La Valletta (Malta), Teboulba (Monastir, Tunisia), Tripoli (Libya), Larnaca (Cyprus) and Izmir (Aegean coast of Turkey). A fragment of the mitochondrial ND1 was amplified using the primer described by DIAZ-JAIMES *et al.*, (2010), whereas a fragment of mitochondrial COI was amplified using the primer described by FOLMER *et al.*, (1994). Haplotype ($h$) and nucleotide ($\pi$) diversity, AMOVA, Mismatch analyses, and the neutrality tests were performed with ARLEQUIN 3.5 (EXCOFFIER *et al.*, 2010). Fragments of 751bp and 551 bp of the mitochondrial ND1 and COI were amplified and sequenced from 88 *C. hippurus* individuals. 26 polymorphic sites and 23 different haplotypes were scored for ND1, whereas for COI 6 polymorphic site sand 8 different haplotypes were identified. Populations structure and genetic differentiation was investigated using F-statistics with AMOVA. Comparison among the Mediterranean samples did not show any significant difference for both markers highlighting a general genetic homogeneity within the basin ($\Phi CT = 0.043$, $P = 0.179$ for ND1 and $\Phi CT = 0.072$, $P = 0,083$ for COI). In conclusion, based on our results, the Mediterranean dolphinfishes could be considered as a single-stock management unit, which needs a large regional scales management plan involving all countries interested in the exploitation of this important marine resource. Research realised with the financial support of RITMARE. We are grateful to CONISMA and FAO-MEDSUDMED project.