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MOLECULAR DIVERSITY OF DOLPHINFISH  
(*CORYPHAENA HIPPURUS*) SHOWS THE MERGING OF ENDEMIC  
AND WIDESPREAD HAPLOTYPES IN THE MEDITERRANEAN SEA

*EVIDENZE MOLECOLARI SULLA COESISTENZA DI APLOTIPI ENDEMICI  
E AD AMPIA DISTRIBUZIONE DI LAMPUGA (CORYPHAENA HIPPURUS)  
NEL MAR MEDITERRANEO*

**Abstract** - Molecular data on *Coryphaena hippurus* (Linnaeus, 1758) from western and central Mediterranean Sea were reported and compared. The aim of the study was to study the mitochondrial molecular structuring of the species at different geographical scales: localities, sub-basins, and oceans. Results show the absence of a sharp population structure inside the Mediterranean Sea, and the isolation of the Mediterranean dolphinfishes from those inhabiting the Atlantic Ocean.

**Key-words:** population genetics, *Coryphaena hippurus*, Mediterranean Sea.

**Introduction** - The dolphinfish *Coryphaena hippurus* (Linnaeus, 1758) is a cosmopolitan migratory epipelagic fish inhabiting tropical and subtropical waters (Palko *et al.*, 1982). In the Mediterranean Sea, the dolphinfish is considered a seasonal target of artisanal and recreational fisheries. Because of its large-scale distribution, the dolphinfish represents an interesting model for phylogeographical studies and research aimed at the identification of stock units. There are few molecular data available for Mediterranean populations (Díaz-Jaimes *et al.*, 2010). This study presents mtDNA-based population genetic analyses of *C. hippurus* from western and central Mediterranean Sea and the Atlanto-Indian region with the aim of assessing genetic diversity among localities at both regional and oceanic scale.

**Materials and methods** - A total of 61 tissue samples of dolphinfish were collected at seven sites from western and central Mediterranean Sea and one location in the Indian Ocean: Majorca (Spain, n=10), Ancona (Italy, n=5), Porticello (Italy, n=8), Capo Passero (Italy, n=4), Malta (n=9), Tabulbah (Tunisia, n=10), Tripoli (Libya, n=10), and Pakistan (n=5). The mitochondrial NADH dehydrogenase subunit 1 (ND1) was amplified and sequenced according to Díaz-Jaimes *et al.* (2010). MtDNA sequences were compared to 17 sequences from Atlantic (n=15) and Indo-pacific Oceans (n=2) downloaded from public repositories. Haplotype (*h*) and nucleotide ( $\pi$ ) diversities, and Tajima's *D* neutrality test were computed to assess population diversity and recent population dynamics. Analysis of Molecular Variance (AMOVA) was conducted to test whether significant differences occurred among sampling sites, sub-basins (i.e. Tyrrhenian Sea, Sicilian channel and Ionian Sea, Adriatic Sea) and Oceans (i.e. Mediterranean sea, Atlantic and Indo-Pacific oceans). All analyses were performed using Arlequin 3.5 (Excoffier e Lischer, 2010).

**Results** - The sequencing of ND1 fragments resulted in 750-bp long sequences. A total of 14 haplotypes were recorded with 13 haplotypes exclusive to the Mediterranean Sea. The single non-exclusive haplotype described in the Mediterranean was shared with the Atlantic and Indo-pacific samples, and present in all localities investigated by our study. Two haplotypes were shared among the majority of the investigated Mediterranean samples, while the others were *private haplotypes*, exclusive to each specific site. Average haplotype and nucleotide diversities of Mediterranean populations were  $h=0.769$  and  $\pi=0.004$ . This picture, high  $h$  + low  $\pi$ , along with the support of the significant negative value of Tajima's  $D$  ( $D= -2.15387$ ,  $p<0.05$ ), suggested a recent population expansion of the species after a population bottleneck. AMOVA, performed at the geographical scale of sites and sub-basins, showed no significant differences inside the Mediterranean sea ( $\Phi_{ST}=0.021$ ,  $p=0.696$ ;  $\Phi_{CT}=0.002$ ,  $p=0.498$ ). Conversely, the comparison among the Mediterranean sea and oceans showed a sharp separation ( $\Phi_{CT}=0.115$ ,  $p=0.036$ ). The pairwise  $\Phi_{ST}$  confirmed the differences occurring among each of the sub-basins of Mediterranean Sea vs the Atlantic Ocean (Tyrrhenian Sea  $\Phi_{ST}=0.062$ ; Sicilian Channel and Ionian Sea  $\Phi_{ST}=0.117$ ; Adriatic Sea  $\Phi_{ST}=0.058$ ;  $p<0.05$ ). AMOVA revealed a significant difference between the Indo-pacific Ocean, the Mediterranean Sea and the Atlantic Ocean (respectively  $\Phi_{ST}=0.077$ ,  $0.167$ ;  $p<0.05$ ).

**Conclusions** - Though connection with the Atlantic, Mediterranean dolphinfish samples seem to maintain a degree of isolation, which preserve an endemic gene pool. Current genetic diversity of Mediterranean dolphinfishes is probably the result of a vicariance event followed by a secondary contact between Mediterranean and Atlantic populations. Our study shows the absence of a sharp molecular structuring of the species in the western and central Mediterranean basin, as commonly scored in other species (Lo Brutto *et al.*, 2004; Maggio *et al.*, 2009).

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