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

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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 (π) diversities, and Tajima’s D neutrality test were computed to assess population diversity and recent population dynamics. Analisys of Molecular Variance (AMOVA) was conducted to test whether significant differences occurred among sampling sites, sub-basins (i.e. Tyrrenhian 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 (Tyrrenhenian 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 basin, as commonly scored in other species (Lo Brutto et al., 2004; Maggio et al., 2009).

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References

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