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ANALYSIS OF NUCLEOTIDE SEQUENCE OF THE MITOCHONDRIAL CYTOCHROME B GENE IN THREE *SARDA SARDA* (BLOCH 1793) STOCKS FROM MEDITERRANEAN SEA

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The characterization of fish stocks was usually carried out from phenotypic data sets which now are known to be accompanied by a considerable uncertainty with regard to the accuracy of the results. Here we used as genetic marker the mtDNA because of its characteristics of simple gene organization, maternal inheritance, absence of recombination and rapid rate of sequence divergence (Ferris *et al.*, 1987). We analyzed three samples of *S. sarda* of 37, 26 and 31 individuals respectively, coming from Gulf of Taranto, Gulf of Evvoia and Marmara Sea.

By using the Polymerase Chain Reaction we amplified, with universal primers (Kocher *et al.*, 1989, Meyer *et al.*, 1990), a fragment of about 400 nucleotides of the cytochrome b gene and sequenced about 300 nucleotides of all 94 available fishes.

We found thirteen variable nucleotide positions (twelve mutations are transitions and only two of them produce aminoacidic substitutions) that define seven genotypes named from A through G, as shown in Table 1.

TABLE I
The seven genotypes and their thirteen mutation sites.

	Mutation sites												
	1	2	3	4	5	6	7	8	9	10	11	12	13
Genotype A	C	C	T	G	G	G	C	T	C	C	C	G	T
Genotype B	T	—	C	—	A	C	T	C	T	T	—	—	C
Genotype C	—	—	—	—	—	—	—	—	—	—	T	—	—
Genotype D	—	—	—	A	—	—	—	—	—	—	—	—	—
Genotype E	—	—	—	—	A	—	—	—	—	—	—	—	—
Genotype F	T	—	C	—	A	C	T	C	T	T	—	A	C
Genotype G	—	T	—	—	—	—	—	—	—	—	T	—	—

Keeping the A sequence as standard, the other six genotypes differ for 1 to 10 base pairs from it.

In first approximation it is possible to note two philetic lines, each one characterized by concurrent mutation sites: line 1 comprises A, B, D and G genotypes and line 2 E, B and F genotypes.

Frequency analysis indicates that there is not a single characteristic genotypes for each group of fishes, but it is possible to find different genotypes proportions inside the three stocks. A and B are the main genotypes in Turkish and Italian stocks, respectively; these stocks show the highest degree of differentiation.

The Greek stock presents a frequency distribution more uniform showing a lower genetic differentiation if compared with the Italian and the Turkish stocks.

These data show only a different proportion of the genotypes frequencies in the three stocks indicating that they do not come from one undifferentiated panictic population.

In conclusion, although it is not possible to identify the origin of a single fish, it is possible to assign a group of individuals to a determinate stock.

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