

IDENTITY OF SARDA SARDA (BLOCH) STOCKS FROM
MEDITERRANEAN SEA THROUGH MITOCHONDRIAL
DNA ANALYSIS

M. ROBERTI * - G. DE METRIO ** - A. LUDOVICO *** - F. MILELLA *
- P. MEGALOFONOU ** - P. CANTATORE * - M.N. GADALETA *

* *Dipartimento di Biochimica e Biologia Molecolare, Università di Bari;*

** *Dipartimento di Produzione Animale, Università di Bari, and*

*** *Istituto Sperimentale Talassografico «A. Cerruti», Taranto.*

Reprints from:

The Italian Journal of Biochemistry, Vol. 41 - No. 4 - July-August 1992
Il Pensiero Scientifico Publishers, via Bradano 3/c, 00199 Rome

IDENTITY OF *SARDA SARDA* (BLOCH) STOCKS FROM
MEDITERRANEAN SEA THROUGH MITOCHONDRIAL
DNA ANALYSIS

M. ROBERTI * - G. DE METRO ** - A. LUDOVICO *** - F. MILELLA *
P. MEGALOFONOU ** - P. CANTATORE * - M.N. GADALETA *

* *Dipartimento di Biochimica e Biologia Molecolare, Università di Bari;*

** *Dipartimento di Produzione Animale, Università di Bari, and*

*** *Istituto Sperimentale Talassografico «A. Cerruti», Taranto.*

Sarda sarda (Bloch) 1793 is an epipelagic fish belonging to the family of Scombridae widely distributed in the Mediterranean Sea. It is one of the economically most important fish species and is mainly caught off the Turkish Black Sea coast. However, also Italy and Greece are among the greatest producers of *S. sarda*.

To obtain a genetic description of the fish stocks exploited by the commercial fleets, as well as information about migrations events and the possibility of the existence of different populations in the considered areas, we are studying the mitochondrial DNA (mt DNA). This molecule in the last 10 years has been widely used in the study of local populations for many animal species including the definition of stocks of other fish species. In our ongoing study of *S. sarda* we are analyzing individuals coming from the Ionian Sea, the Aegean Sea and the Black Sea.

The first experimental approach is the analysis of RFLPs. The digestion of *S. sarda* mt DNA with Pst I gives four fragments of about 8000, 4500, 1800, 1700 bp respectively. This has allowed us to suggest 16000 bp for the size of the mt DNA genome of *S. sarda*. This value is similar to those of the vertebrates mt DNAs studied so far. A preliminary comparison between the mt DNA of one individual from the Aegean Sea

and one from the Ionian Sea tested with ten restriction enzymes does not show any difference. An alternative and more convenient approach consists in the direct sequencing of a segment of the mt DNA, amplified by means of the polymerase chain reaction. By using a pair of primers corresponding to highly conserved regions of the mt genome we have amplified a 423 bp segment of DNA corresponding to the 5' region of the *cyt b* gene.

The comparison of 120 nucleotides-long sequences shows a single nucleotide substitution between two individuals coming from Greece. These two individual sequences when compared with that of an Italian *S. sarda* present five or six nucleotide substitutions, respectively. Further experiments are needed in order to clarify if genetic differences characterize *S. sarda* individuals coming from various geographical areas.

ACKNOWLEDGMENTS

This work has been supported financially by MURST (60%), Ministero Marina Mercantile, Comunità delle Università del Mediterraneo and by CT06.92.01202 of CNR.