

MITOCHONDRIAL DNA SEQUENCE VARIATION IN TUNISIA SARDINE (*SARDINA PILCHARDUS*) STOCKS

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Abstract

The genetic diversity and population genetic structure of the Tunisian sardines *Sardina pilchardus* were investigated. A total 92 individuals were sampled from 3 localities of the coastal zones of Tunisia. Genetic variation in DNA sequences were examined from the cytochrome b (cytb) gene of the mitochondrial DNA. High levels of haplotype diversity were detected, indicating a high level of genetic diversity. Phylogenetic trees demonstrated a divergence between the populations examined in the present study. The knowledge on genetic diversity and genetic structure will be crucial to establish appropriate fishery management stocks for the species.

Keywords: *Genetics, Fishes*

Introduction

The sardine, *Sardina pilchardus* (Walbaum, 1792), is an important fish species of great economic importance to Tunisia, as well as to many other countries [1] [2]. For the management and sustainability of fish populations, studying genetic diversity is critical. Nevertheless, studies on the geographic distribution and genetic population structure of many commercial fish species stocks have not been completed [3]. Data concerning sardine populations inhabiting Tunisia coastal waters are currently very limited [4]. To the best of our knowledge the genetic diversity of Tunisia's sardine populations has yet to be investigated using modern DNA technology which provides suitable markers to examine genetic structure such as mitochondrial DNA.

Mitochondrial (mt) DNA has many attributes that make it particularly suitable for population genetic studies, including its rapid rate of evolution, lack of recombination, and maternal inheritance.

The aim of the present study was to determine whether there is genetic diversity among the sardine populations inhabiting the coastal zones surrounding Tunisia.

Materials and methods

A total of 3 samples of *Sardina pilchardus* were collected from representative regions along the coastal zones of Tunisia (Gulf of Tunis, Sahel and Gulf of Gabes). For each sample, a fragment of cytochrome b (cytb) gene was amplified by PCR analysis and subsequently sequenced. Sequences of the 307-bp cytb region were aligned using the BioEdit v.7.0.7 program. Haplotype frequencies, gene diversity (h) and pairwise genetic distances (Fst) were calculated with ARLEQUIN vers. 3.01 [5].

Pairwise FSTs genetic distance was used to construct the population phenogram using the neighbor-joining algorithm [6] implemented in Phylip v3.6.1 [7].

Results and discussion

This work provides the first molecular data for the species *Sardina pilchardus* along the coast of Tunisia.

Among the 92 specimens studied, 24 different haplotypes were defined by 45 polymorphic sites. Significant heterogeneity in the distribution of haplotypes was revealed between the three populations analysed.

Of the 24 haplotypes, 5 were singletons and of the remaining 19 haplotypes, one was shared among populations.

Haplotype diversity (h) within populations ranged from 0.827 at Gulf of Tunis to 0.910 at Gulf of Gabes. This result demonstrates that Gulf of Gabes is the most diversified.

FST values calculated between populations indicated significant difference ($p < 0.05$) in each pairwise combination of these 3 sampled areas.

The phylogenetic tree constructed using neighborjoining and maximum likelihood methods indicated that population from Gulf of Tunis was closely related to the Adriatic and Ionian sardine samples [8], whereas the two other populations were most divergent. The result suggested that the sardine stocks investigated in the present study were from different populations.

Besides the possible contribution of the history and hydrographic barriers, evolutionary processes such as genetic drift and founder effect, and or selection, may have produced the observed genetic differentiation between the populations analysed.

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