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Genetic structure and temporal stability in the horse mackerel (*Trachurus trachurus*)

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Abstract

This study aimed at assessing the temporal and spatial genetic structure of the horse mackerel (*Trachurus trachurus*) using allozymes, within the frame of a multidisciplinary research project directed at the stock assessment of this species. To this end, 19 samples were taken from a large part of the geographical range of the species, providing more than 2200 specimens analysed. Samples from 14 localities were caught twice in different years, so that the temporal stability of their genetic structure could be investigated. The genotypes and the allele frequencies obtained at different times from the same locality were statistically consistent, suggesting that the genetic structure of horse mackerel populations is stable overtime.

Allozyme analysis showed that all the horse mackerel populations studied, although geographically separated, were genetically homogeneous and connected by high levels of gene flow. Attempts to highlight subtle genetic structure only revealed a slight differentiation between eastern Mediterranean samples (Ionian and Aegean Seas) versus the western Mediterranean and Atlantic ones, in agreement with the horse mackerel's migration routes so far identified and with the results obtained using different approaches (parasites as biological tags, otoliths).

A further objective of the research was to assess the level of genetic variability in this species. We found very high variability in all the studied samples, among the highest recorded in the literature for many pelagic and demersal fishes. Since the levels of genetic variability are increasingly used as indicators of the state of exploited and human-impacted populations, the results obtained suggested that the biomass depletion suffered by the horse mackerel has not impoverished its genetic resources yet. However, it is worth noting that the significantly lowest values were recorded for the samples from the so-called north-western stock, where the catches are rapidly decreasing since 1996.

Keywords: Horse mackerel; Allozymes; Stock structure; Genetic variability; Stock status

1. Introduction

The idea that the marine realm hosts genetically homogeneous populations of fish due to the absence of environmental barriers has been challenged by a number of studies (i.e. Hilbish (1996) with references herein). The finding of genetically structured populations even over a small geographical scale has produced many questions on the evolutionary and ecological forces generating and maintaining these differences (Nielsen et al., 2004). The same problems concerned the species found as genetically uniform, as the apparent lack of barriers was sometimes not able to explain the observed homogeneity. Other forces possibly involved could be the high dispersal ability (Waples, 1998), but also the large size frequently attained by marine fish populations, leading to low levels of genetic drift and so delaying in time the coalescence of alleles (Nesbø et al., 2000). However, it is for the same reasons that fish species having "classical" features (high fecundity, wide mobility, large populations, etc.) could show a uniform structure due to their ancient gene flow even if they are subject to recent events of subdivision (Nesbø et al., 2000). Recent splits are usually detected by fast evolving markers but, more recently, many authors evidenced the study of the temporal structure of fish populations as relevant to provide valuable information on this topic. Indeed, the assessment of both spatial and temporal genetic structure of fish populations can allow a better distinction of the roles of ancient and present events in producing the extant population patterns, with relevant implications for the management of the commercially harvested species (Tessier and Bernatchez, 1999; Garant et al., 2000).

The horse mackerel, *Trachurus trachurus* (Linnaeus, 1758), is a carangid fish having a high relevance in the fisheries of

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