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High resolution SNPs selection in *Engraulis encrasicolus* through Taqman OpenArray

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ABSTRACT

The European anchovy (*Engraulis encrasicolus*) is one of the most important species in fisheries, representing the majority of landings worldwide. Identification of genetic stocks and assessment of divergence among them, is critical in order to implement management strategies. Population genetic structure in the Mediterranean basin is not clear and has not been extensively investigated with highly informative markers for population analyses. In this work, we aimed to identify a small SNP panel to be utilized for fine scale population genetic analysis within the Mediterranean basin. In order to do that, we used a set of 424 species-specific SNPs for assessing differentiation among *E. encrasicolus* populations within the Mediterranean and between Atlantic and Mediterranean Sea. Hence, we applied a Fst ranking method, for selecting a SNP sub-set from the large 424 SNPs panel and we compared the results obtained with the two sets of markers. Population assignment power and patterns of population differentiation were comparable. Analyses revealed a clear distinction between anchovies in the Atlantic and Mediterranean areas, and lower differentiation among Mediterranean populations. Our approach was successful in selecting a 96 SNP subset with high resolution and cost effectiveness to genotyping that can represent a useful tool for population genetic studies and stock management in this economically important species.

1. Introduction

The European anchovy (*Engraulis encrasicolus*; Family: Engraulidae), one of the most important species in fisheries worldwide, is distributed in the whole Mediterranean Sea, including the Black and the Azov Seas, and also along the eastern Atlantic coast, from Norway to South Africa (Whitehead et al., 1988).

Together with sardines, anchovies represent the majority of landings in the world and in particular in the Mediterranean Countries (Whitehead et al., 1988). Mediterranean and Black Sea give 5% of the world's anchovy catch, which is equivalent to 563,000 t. The largest supplying countries of this area are Turkey, Italy, Georgia and Greece. In recent years, the high commercial demand has caused an excessive exploitation of the resource, forcing authorities to adopt measures for the development of management plans and for monitoring the stock status (UE Council Regulation No 1967/2006).

In order to implement management strategies, it is critical to identify spawning areas, to unravel population genetic structure and to assess genetic divergence among stocks. The distribution of spawning habitats along the coasts of the Mediterranean is only known for areas where detailed acoustic surveys have been conducted (Giannoulaki et al., 2013). Adults seem to have a limited dispersal from restricted areas of high productivity allowing that particular regions could harbor distinct populations or stocks. Previous studies using molecular markers, showed a complex population structure for European anchovies in the Atlantic Ocean, and in distinct areas of the Mediterranean Sea (Spanakis et al., 1989; Keskin and Atar, 2012; Bembo et al., 1996a,b; Kristoffersen and Magoulas, 2008; Grant, 2005; Borsa, 2002; Borsa et al., 2004). Mitochondrial DNA markers identified two major mitochondrial lineages within the Mediterranean and Black Seas: one was predominant in the Black Sea and the Aegean Sea, and the other much more frequent in the western basin (Magoulas and Zouros 1993; Magoulas et al., 1996). A recent secondary contact between previously isolated Atlantic and Mediterranean populations has been suggested (Magoulas et al., 2006). Nuclear markers such as allozyme loci (Borsa et al., 2002; Erdogan et al., 2009), introns

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