New SNP Markers in European Anchovy and Albacore: Useful Genetic Tools for Stock Delimitation

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Abstract
Albacore and European anchovy fisheries require a management regime based on integral information. Genetic markers like SNPs are elementary for this purpose. In this paper, newly discovered SNPs in both species and their utility for stock delimitation is described.

Keywords - Fisheries management, population structure, SNP discovery, Thunnus alalunga, Engraulis encrasicolus

INTRODUCTION
The high commercial value of the albacore tuna (Thunnus alalunga, Bonn.) and the European anchovy (Engraulis encrasicolus L.) makes them highly vulnerable to fishing impacts. Preventing overfishing and therefore the risk of collapse requires a sustainable management regime based on solid knowledge about population structure [1]. In this respect, genetic markers such as single nucleotide polymorphisms (SNPs) have proven to be useful in describing the genetic variation within and between populations in high gene flow marine taxa. For non-model species such as European anchovy and albacore, the lack of genomic data is a limiting factor for SNP discovery and it has been a challenge until the development of next generation sequencing (NGS) technologies [3]. In fact, to date, no more than 62 SNPs have been described on European anchovy [4] and 128 on albacore [5].

MATERIAL AND METHODS
In this study European anchovy SNPs were discovered by transcriptome and genome sequencing through NGS technologies [6] and a subset of 530 SNPs was genotyped in 990 samples. Whereas, the 116 SNPs genotyped on 1,330 albacore individuals were discovered by cross-species amplification using arrays designed for a closely related species, the Atlantic bluefin tuna (BFT, Thunnus thynnus), kindly provided by the BFT project [7].

RESULTS AND CONCLUSIONS
In all, 441 (83.2%) SNPs were validated in European anchovy and 82 (70.7%) in albacore. From them, a subset of 424 (80.0%) markers were selected for European anchovy [4] and 128 on albacore [5].

Regarding the genetic structure of albacore populations, same tests were applied in addition to Geneland software [11]. Results depict three main populations worldwide: Mediterranean Sea, Atlantic and Pacific-Indian Oceans (Figure 2).

In conclusion, and with the long term objective of providing valuable information to stock managers, in this study a new set of SNP markers has been developed and the delimitation of several populations for both species has been proposed.

REFERENCES