

# A genetic multi marker approach to estimate spatial and temporal structuring and $N_e$ of albacore (*Thunnus alalunga*)

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## Introduction

Albacore (*Thunnus alalunga*) is a mostly over-exploited commercially important pelagic species [1]. Population genetic structure definition, along with effective population size ( $N_e$ ) estimation, are essential for the sustainable management and conservation of exploited species [2]. While defining population genetic structure is essential in order to define stocks or fisheries management units,  $N_e$  determines how vulnerable populations are to losing genetic diversity due to genetic drift and, consequently, assesses their responsiveness [3]. However, despite the great importance of this parameter for species' conservation, nowadays there is no a published work with a  $N_e$  estimation for the albacore.

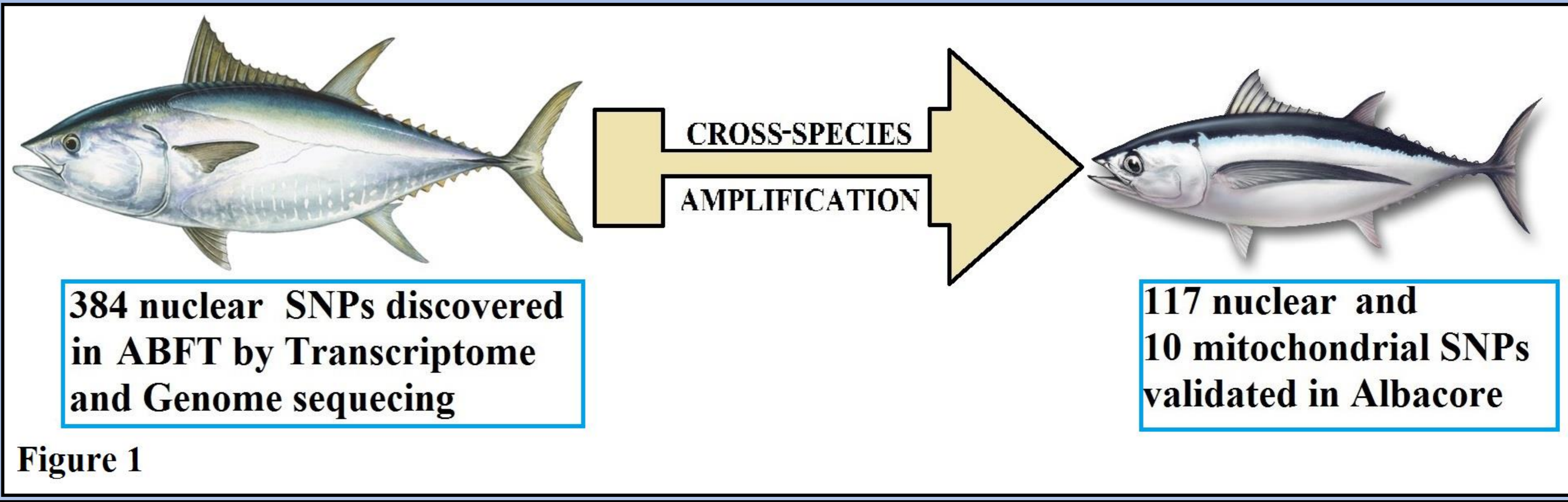


Figure 1

## Material and methods

The nuclear SNP markers used in this study were previously discovered in the Atlantic Bluefin tuna (*Thunnus thynnus*) through transcriptome and genome sequencing (Fig.1) while mitochondrial SNPs were discovered directly in the Albacore.

Multiple softwares (Populations v1.2.32; IBDWS; Structure v2.3.4; Geneland v3.2.2; Fstat v2.9.3; DNAsp 5) were used in order to define the number and limits of Albacore Populations.

Long- and short-term  $N_e$  estimations for the North Atlantic were calculated with Migrate v3.2.1 software and Waples (1989) [4] method respectively.

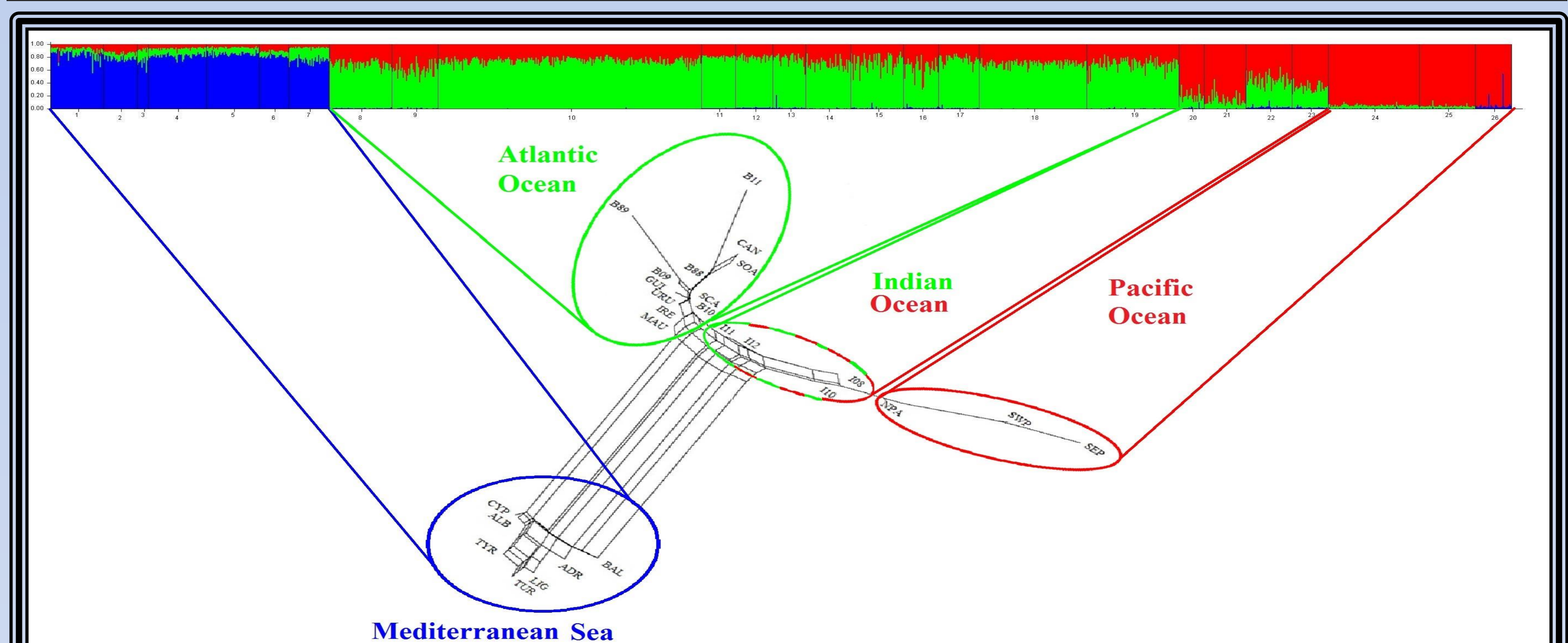


Figure 2. Results of Structure (above) and Populations (below) softwares together indicating four albacore populations.

## Results and conclusions

Four Albacore populations were detected, one in each Ocean and another one in the Mediterranean Sea (Fig.2), which actually are managed as 6 independent stocks, results indicate that no one stock includes more than one population. Mediterranean population is the most differentiated based on both nuclear and mitochondrial SNPs.

Both *long-term*  $N_e$  estimation (median= 16,729 individuals) and *short-term*  $N_e$  estimations and also  $N_e/N_c$  ratios for the North Atlantic Ocean (Table 1) indicate that the genetic diversity and the response capacity of the stock have not been significantly affected by the overexploitation.

## References

1. Majkowski J. (2007) Global fishery resources of tuna and tuna-like species. Food and Agriculture Organization of the United Nations. 483.
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3. O'Leary S.J., Hice L.A., Feldheim K.A., Frisk M.G., McElroy A.E., Fast M.D. and Chapman D.D. (2013) Severe Inbreeding and Small Effective Number of Breeders in a Formerly Abundant Marine Fish. *PLOS One* 8: e66126.
4. Waples R.S. (1989) A generalized approach for estimating effective population size from temporal changes in allele frequency. *Genetics* 121: 379-391.

	Short term $N_e$	$N_c$	$N_e/N_c$
North Atl <sub>1986</sub>	14,040	3,200,270	0.004
North Atl <sub>1987</sub>	8,388	2,397,944	0.003
North Atl <sub>2005</sub>	18,147	2,796,804	0.006
North Atl <sub>2006</sub>	10,232	2,238,867	0.005
North Atl <sub>2007</sub>	5,466	2,090,050	0.003
North Atl <sub>2008</sub>	23,330	2,373,467	0.010

Table 1. Short-term  $N_e$  and  $N_e/N_c$  ratios for North Atlantic albacore calculated for six cohorts