

HOW HUMAN FORCINGS AFFECT ECOLOGICAL PROPERTIES OF LARGE PELAGIC FISH IN THE MEDITERRANEAN? HISTORICAL GENETIC CHANGES IN THE OVEREXPLOITED BLUEFIN TUNA (*THUNNUS THYNNUS*)

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Abstract

Based on a comparative analysis of genetic diversity at 7 microsatellite loci in ancient (archived skeletal specimens) and modern (freshly collected individuals) samples of *Thunnus thynnus* collected in the Mediterranean Sea, we assessed temporal changes and spatial variation of genetic and demographic (genetically-related) features in the overexploited Mediterranean stock of bluefin tuna. From the analysis of more than 300 individuals, a temporal stability of genetic diversity over about 90 years but significant changes in the genetic structure of the stock were achieved. Such results argue for an evidence that, in the Mediterranean, stock overexploitation has not yet corrupted the genetic potential of such living resource and that bluefin tunas are not fully panmictic.

Keywords : *Biotechnologies, Conservation, Genetics, Fisheries, Western Mediterranean.*

The estimation of genetic variability and the identification of temporal variation in genetic structure of a population is crucial for the conservation of endangered species undergoing dramatic ecological and demographic changes linked to strong overexploitation [1], such as the Atlantic bluefin tuna *Thunnus thynnus*. Fishery is having strong impact on bluefin tuna population abundance and serious consequences on genetic potential of Mediterranean populations may occur [2].

Tab. 1. Genetic variation at the 7 microsatellite loci in ancient and modern Mediterranean samples of *Thunnus thynnus*. A_r , allelic richness; H_o , observed heterozygosity; H_e , unbiased expected heterozygosity; P , Hardy-Weinberg equilibrium test: ** $P < 0.01$, * $P < 0.05$. ^a For each genetic diversity estimator, the statistical difference between ancient and modern bluefin tunas was tested by one-way ANOVA (not significant) and pairwise χ^2 (not significant)

Locus		Ancient	Modern
Ttho-4	A_r	13.8	18.0
	H_o	0.383	0.797
	H_e	0.721	0.814
	P	**	
Tth-5	A_r	3.0	3.0
	H_o	0.769	0.400
	H_e	0.542	0.488
	P	**	*
Tth-10	A_r	8.9	6.9
	H_o	0.681	0.482
	H_e	0.523	0.486
	P	**	**
Tth-34	A_r	14.0	17.9
	H_o	0.674	0.769
	H_e	0.736	0.833
	P	**	**
Tth 1-31	A_r	15.9	19.9
	H_o	0.757	0.813
	H_e	0.861	0.897
	P	**	**
Tth 208	A_r	25.0	28.9
	H_o	0.775	0.708
	H_e	0.910	0.920
	P	**	**
Tth 112	A_r	9.9	13.0
	H_o	0.715	0.927
	H_e	0.697	0.853
	P	**	**
Mean ^a	A_r	12.9	15.4
	H_o	0.710	0.669
	H_e	0.713	0.756
	P	**	**

Owing to i) the general interest in assessing and predict historical changes in fish communities of the Southern European Seas (henceforth SES) to develop ecological and socio-economic models for an integrated management of the marine ecosystems at the regional scale [3], ii) the specific interest for the conservation, ownership and sustainable management of

bluefin tuna stocks [2], it becomes critical to resolve structure and dynamics of the SES populations of this large pelagic fish over time.

A molecular approach becomes fundamental to unlock ancient genetic features of populations and for genetic comparisons to modern populations. This can be decisive for assessing genetic and demographic changes in fishery resources overexploited since decades [4, 5]. The demonstration of loss of genetic variability in wild populations is empirically limited by lack of samples before heavy overexploitation started. Although rare, archived samples represent a unique opportunity to access ancient populations [4, 5]. In the framework of an Italian PRIN 2005-2007 research project (TUNING; <http://www.dipartimentobiologia.it/tuning/index.htm>) and of the EU-FP6 2006-2010 Integrated Project (SESAME), a comparative analyses of genetic diversity at 7 microsatellite loci in ancient (skeletal records collected from 1911 to 1926 by Massimo Sella) and modern samples (from fishing vessels) of Mediterranean bluefin tunas have been carried out to infer historical changes of genetic and demographic properties.

The analysis of about 300 bluefin tunas revealed a temporal stability of genetic diversity over about 90 years and more than 50 years of industrial exploitation of the stock (Table 1). On the other hand, significant changes in the genetic structure of Central Mediterranean bluefin tuna samples were detected. In addition, the results of such work argue for an evidence that, in the Mediterranean, stock overexploitation has not yet corrupted the genetic potential of such relevant fishery resource and that bluefin tunas are not fully panmictic [2, 6]. In general, the results did outcome from the analysis of temporal genetic variation in fishery resources that include comparisons between ancient unexploited and modern (over)exploited populations can really contribute to assess the conservation of fish stocks, based on quantitative genetic data sets that were obtained independently from fishery and tagging data.

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