M9 NEW SNP MARKERS IN EUROPEAN ANCHOVY AND ALBA-CORE: USEFUL GENETIC TOOLS FOR STOCK DELIMITATION

Urtzi Laconcha[178], Iratxe Montes[179], Haritz Arrizabalaga[180], Andone Estonba[181]

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 CONCLUSSIONS

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 and 57 (49.1%) for albacore as being potentially useful in population genetic structure analyses, as they were neutral, independent and meet Hardy-Weinberg equilibrium.

In the case of European anchovy, the genetic structure of populations was analyzed using Structure v2.3.3 [8], pairwise FST [9], and a hierarchical analysis of molecular variance (AMOVA; [10]). These tests revealed that studied samples for European anchovy are separated into 5 main populations (Figure 1): North Sea, Atlantic (including samples from Cadiz and Canary Islands), Mediterranean, and two anchovy populations in the Bay of Biscay (the main one related to offshore environments and the other one to inshore habitats).

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
[1] Arrizabalaga H., Costas E., Juste J., González-Garcés A., Nieto B. & López- Rodas V. "Population structure of albacore Thunnus alalunga inferred from blood groups and tag-recapture analyses". Mar. Ecol. Prog. Ser. 282, 245-52. 2004.
[2] Helyar SJ, Hemmer-Hansen J, Bekkevold D, Taylor MI, Ogden R, Limborg MT, Cariani A, Maes GE, Diopere E, Carvalho GR, Nielsen EE. "Application of SNPs for population genetics of non-model organisms: new opportunities and challenges". Mol Ecol Resour 11: 123-136.2011.
[3] Kumar S, Banks TW, Cloutier S "SNP discovery through Next-Generation Sequencing and its applications". Int J Plant Genomics 2012:831460. 2012.
[4] Zarraonaindia I, Iriondo M, Albaina A, Pardo MA, Manzano C, Irigoien X. and Estonba A. "Multiple SNP markers reveal fine-scale population and deep phylogeographic structure in European anchovy (Engraulis encrasicolus L.)". PLoS One 7: e42201. 2012.
[5] Albaina A, M. Iriondo, I. Velado, U. Laconcha, I. Zarraonaindia, H. Arrizabalaga, N. Goñi, M. Lutcavage, W. S. Grant and A. Estonba "Single nucleotide polymorphism discovery in albacore and Atlantic bluefin tuna provides insights into worldwide population structure". Anim. Genet. In press. 2013.
[7] ICCAT "Atlantic wide research programme for Bluefin Tuna" (GBYP). 2009-2013.
[6] Montes I, Conklin D, Albaina A, Creer S, Carvalho GR, Santos M, Estonba A . "SNP discovery in European anchovy (Engraulis encrasicolus, L) by high-throughput transcriptome and genome sequencing". PLoS ONE (submitted). 2013.
[8] Pritchard JK, Stephens M, Donnelly P "Inference of population structure using multilocus genotype data". Genetics 155: 945-959. 2000.
[9] Weir BS, Cockerham CC "Estimating F statistics for the analysis of population structure". Evolution 38: 1358-1370. 1984.
[10] Excoffier L, Smouse PE, Quattro JM "Analysis of molecular variance inferred from metric distances among DNA haplotypes: application to human mitochondrial DNA restriction data." Genetics 131: 479.491. 1992
[11] Guillot G, Mortier F, Estoup A. "GENELAND: a computer package for landscape genetics." Mol Ecol Notes, 5:712-715. 2005.