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Genetic diversity and population structure of the yellowfin tuna (*Thunnus albacares*) comparing samples collected in artisanal fisheries of Ecuador and Mexico using microsatélite loci

Terán-Velástegui M. [a], Torres, ML. [a], Galván Magaña, F. [b], Canty S. [c], Muñoz Abril L. [a]

[a] Universidad San Francisco de Quito (USFQ), Colegio de Ciencias Biológicas y Ambientales, Laboratorio de Biotecnología Vegetal, Campus Cumbayá, Quito, Ecuador.
[b] Centro Interdisciplinario de Ciencias Marinas (CICIMAR), La Paz, México.
[c] Smithsonian Institute, Washington D.C., United States.

Graphical Abstract

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Abstract.

The yellowfin tuna (*Thunnus albacares*) is a bony fish belonging to the Scombridae family. It is found on tropical and subtropical pelagic waters around the world. *Thunnus albacares*, particularly, is a species of high economic, ecologic and social value as it supports a relevant sector of the fishery industry [1]. Therefore, ensure an adequate management of this resource is necessary to maintain both sustainability and commercial trade [2][3]. Moreover, as an apex predator, the conservation of the yellowfin tuna is relevant for the preservation of healthy marine ecosystems and prevent the loss of this species [4]. However, to date multiple mismatches between management units and biological populations have been reported in the case of the yellowfin tuna in different regions of the world. These mismatches put in danger the correct management of the marine resource [5][6]. Specifically in the Eastern Pacific Ocean, previous studies have suggested genetic differences between northern and equatorial samples [7][8]. Thus, the objective established in the present study was to characterize the genetic diversity and population structure of *Thunnus albacares* in a section of the Eastern Pacific. We collected 630 samples from artisanal fisheries of Ecuador and Mexico in three distinct years (2015-2017). The samples were molecularly characterized using 18 microsatellite loci. The expected heterozygosity index (HE = 0.85) together with an allelic richness per locus of 18.40 showed a high genetic diversity in the sample analyzed. No population structure was found, although low genetic differences were found between samples from Mexico and Ecuador (FST < 0.02). The low genetic differentiation found was statistically significant ($P < 0.05$). Low levels of relatedness as well as the detection of first generation migrants suggest continuous gene flow in the section of the Eastern Pacific Ocean analyzed. The results support the concordance between one biological population and the actual management unit administrated by the Inter-American-Tropical-Tuna-Commission (IATTC). However, model-based clustering STRUCTURE results also show a slight difference in the genetic pools composition of northern and equatorial samples. Additionally, differences between the genetic pool of samples collected in the same region in different years suggest temporal changes in allelic frequencies or the dependence of the collection on fishery effort. It is recommended to continue the monitoring of *T. albacares* in the Eastern Pacific Ocean, specially taking into account the actual diminish of tuna populations worldwide [9]. Future studies should consider the inclusion of samples from higher latitudes where geographical barriers like the California and Humboldt [10] cold currents occur. In addition, new approaches such as second generation sequencing analyze a greater proportion of the genome and they can provide new information that contribute to the development of better management plants for *T. albacares* in the fishery industry [11].

Key words: Genetic diversity, stock, microsatellite markers, fisheries management, yellowfin tuna.

Introduction *(optional)*

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Materials and Methods *(optional)*

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Results and Discussion *(optional)*

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Conclusions *(optional)*

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References *(mandatory)*

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