Contents lists available at ScienceDirect



Journal of Experimental Marine Biology and Ecology

journal homepage: www.elsevier.com/locate/jembe



CrossMark

Bayesian analyses of Pacific swordfish (*Xiphias gladius* L.) genetic differentiation using multilocus single nucleotide polymorphism (SNP) data

Ching-Ping Lu^{a,*}, Brad L. Smith^b, Michael G. Hinton^c, Jaime R. Alvarado Bremer^{a,d}

^a Department of Wildlife and Fisheries Science, Texas A&M University, College Station, TX, USA

^b Department of Biology, Brigham Young University Hawaii, Laie, HI, USA

^c Inter-American Tropical Tuna Commission, IATTC, La Jolla, CA, USA

^d Department of Marine Biology, Texas A&M University at Galveston, Galveston, TX, USA

ARTICLE INFO

Article history: Received 3 June 2015 Received in revised form 17 March 2016 Accepted 18 March 2016 Available online 6 May 2016

Keywords: Pacific swordfish Single nucleotide polymorphisms (SNPs) Genetic population structure High resolution melting analysis (HRMA) Early life stages (ELS)

ABSTRACT

There is no consensus on the population structure of Pacific swordfish, and current-working hypotheses based on genetic and fisheries data include variations of two, three, and four stocks. In this study the hypothesis of panmixia for Pacific swordfish was tested using multilocus analyses of single-copy nuclear DNA loci on 891 swordfish collected in 16 localities. Sampling coverage differs from all previous genetic studies by offering a more comprehensive representation of tropical areas and by including early life history stages (ELS). Accordingly, samples of larvae, juveniles, and adults were characterized at 10 loci containing 20 informative SNPs, 19 of which were genotyped using high resolution melting analysis (HRMA) and one as a restriction fragment length polymorphism (RFLP). Additionally, two short sequence repeat (SSR) loci were characterized. Exact tests of genetic differentiation, analyses of molecular variance (AMOVA), principal coordinates analysis (PCoA), Bayesian analyses using STRUCTURE and GENELAND conducted on these data all rejected the hypothesis of panmixia for Pacific swordfish, and identified Taiwan as the most highly differentiated sample. Samples from temperate areas differed from most tropical samples (SST > 24 °C), but genetic heterogeneity was also detected among several tropical samples. By contrast, no differences were detected among temperate samples despite the considerable geographic distances (up to 18,000 km) separating them. Further, Bayesian analyses using both STRUCTURE and GENELAND suggested a pattern of genetic differentiation in Pacific swordfish more complex than a simple separation of tropical and temperate regions, with no clear delineation of geographic boundaries as those displayed by Atlantic swordfish. AMOVAs conducted to test models of population structure based on fisheries data failed to yield significant proportions of among-group variance. The observed patterns of genetic differentiation of Pacific swordfish are discussed in reference to studies of reproductive biology, tagging experiments, and previous genetic studies conducted on this species.

© 2016 Elsevier B.V. All rights reserved.

1. Introduction

Swordfish (*Xiphias gladius* L.) is a highly migratory teleost of commercial and ecological importance found in all oceanic waters of the world from 45° N to 45° S (Carey and Robinson, 1981). In the Pacific Ocean swordfish is targeted primarily using longlines with an estimated capture production of 55,351 t in 2012, equivalent to roughly half the global swordfish catch (114,296 t) for that year (FAO, 2014). Currently, there is no consensus on Pacific swordfish population structure. Based upon catch statistics, several models varying in number from a single panmictic population to four subpopulations have been proposed (Fig. 1). Two-stock working hypotheses divide Pacific swordfish into North Pacific and South Pacific populations, though there is disagreement on the placement of the latitudinal boundary of these stocks (Ichinokawa and Brodziak, 2008; Nakano, 1998). Similarly, four alternative three-stock hypotheses differ in the placement of boundaries (Bartoo and Coan, 1989; Ichinokawa and Brodziak, 2008; Nakano, 1998; Bell, 1980). Finally, the two four-stock models while coinciding in a regional subdivision of this basin into western North Pacific Ocean (WNPO), western South Pacific Ocean (WSPO), eastern North Pacific Ocean (ENPO), and eastern South Pacific Ocean (ESPO) subpopulations, like both the two- and the three-stock hypotheses, fail to reach a consensus on the regional placement of boundaries (Hinton, 2003; Hinton and Deriso, 1998; Sosa-Nishizaki, 1990; Sosa-Nishizaki and Shimizu, 1991). In addition to fisheries data, studies characterizing the reproductive biology and rates of growth suggest population subdivision of

^{*} Corresponding author at: Texas A&M University at Galveston, Ocean and Coastal Studies Building 3029 Room 216A, 1001, Texas Clipper Road, Galveston, TX 77553, USA. *E-mail addresses*: michellecplu@gmail.com, chingping@tamu.edu (C.-P. Lu).

A Two stocks











Bartoo and Coan (1988).



Nakano (1998).





C Four stocks





Sosa-Nishizaki and Shimizu (1991), Hinton and Deriso (1998) and Hinton (2003).



Sosa-Nishizaki (1990) and Sosa-Nishizaki and Shimizu (1991)



Download English Version:

https://daneshyari.com/en/article/4395231

Download Persian Version:

https://daneshyari.com/article/4395231

Daneshyari.com