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Genetic analysis reveals temporal population structure in Caribbean spiny lobster (*Panulirus argus*) within marine protected areas in Mexico

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ABSTRACT

Management efforts for improving the sustainability of the Caribbean spiny lobster (*Panulirus argus*) fishery require knowledge of population connectivity. The aim of this study is to investigate population connectivity of *P. argus* at two levels: (1) spatially between two marine protected areas (MPAs) in the Caribbean coast of Mexico, and (2) temporally within MPAs; by genotyping discrete size classes lobsters using microsatellite markers. No evidence of population differentiation between lobster populations from Banco Chinchorro and Sian Ka'an MPAs was found ($P = 0.139$). In contrast significant levels of population differentiation among discrete size classes of lobsters was found ($F_{ST} = 0.0054$; $P = 0.0052$). Temporal variation among the genotypes of new larval recruits may explain these results. Future research will be required to directly test the genotypes of new larval recruits in Banco Chinchorro and Sian Ka'an MPAs to confirm this hypothesis.

1. Introduction

The Caribbean spiny lobster, *Panulirus argus* is widely distributed in the Caribbean and Western Atlantic from North Carolina to Rio de Janeiro Brazil (Diniz et al., 2005). This species of spiny lobster is one of the most economically valuable fished single species in the Caribbean (Butler et al., 2011; Ley-Cooper et al., 2013). Despite management and conservation efforts to sustain the *P. argus* fisheries, commercial landings have been in decline since the 1990s (Ehrhardt et al., 2010). Management efforts for improving the sustainability of the *P. argus* fishery requires knowledge of population connectivity among Caribbean nations (Kough et al., 2013). Several studies have used a variety of genetic methods to assess population connectivity in *P. argus* (Sarver et al., 1998; Silberman et al., 1994; Naro-Maciel et al., 2011; Tourinho et al., 2012). Phylogenetic analyses based on mitochondrial (mtDNA) and nuclear sequence markers suggest that Caribbean and Brazilian spiny lobster populations originally attributed to *P. argus* belong to different species (Tourinho et al., 2012). There have been no reports of structuring among subpopulation in the Brazilian subspecies. However, recent studies of population structuring among Caribbean subpopulations using mtDNA markers have provided conflicting results. Diniz et al. (2005) suggested that northern Caribbean subpopulations might be distinct from southern populations, yet Naro-Maciel et al. (2011) found no evidence of genetic differentiation among subpopulations in Puerto Rico, Bahamas, and Florida. Polymorphic microsatellite markers (msatDNA) are widely considered more powerful for resolving population structure than mtDNA markers, particularly at small spatial scales (Hellberg, 2009; Lukoschek et al., 2008). For example, preliminary results of spiny lobster genetic differentiation in Belize based on msatDNA suggested that subregional population structure may exist among marine protected areas (MPAs) in the Mesoamerican region (Truelove et al., 2012).

MPAs in the Mesoamerican Barrier Reef System (MBRS) often focus on locally based management such as preserving important

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habitats that serve as shelter, foraging grounds or adult movement corridors, as well as protecting local breeding stocks (Bezaury-Creel, 2005). The implementation of these regulations for the *P. argus* fishery in the Sian Ka'an and Banco Chinchorro Biosphere Reserves were an important criterion for their recent certification by the Marine Stewardship Council. Locally based MPA management of the spiny lobster fishery in Mexico could also benefit from knowledge of spatiotemporal patterns of population differentiation within and between the Sian Ka'an and Banco Chinchorro Biosphere Reserves. Spatial patterns of population differentiation are critical parameters in connectivity models for optimizing the size and spacing of MPAs (Palumbi, 2003) as well as identifying the appropriate scale for fisheries management (Kough et al., 2013; Truelove et al., 2014). Temporal genetic analyses provide insight into how stable larval recruitment patterns are over time and have helped to identify how dispersal, geneflow, and variable reproductive success interact to shape long-term patterns of population connectivity in marine ecosystems (Pusack et al., 2014; St-Onge et al., 2015).

Biophysical modelling studies of spiny lobster larval connectivity patterns over multiple years suggest lobster populations within Sian Ka'an and Banco Chinchorro MPAs are highly dependent on larval recruitment from distant source populations throughout and outside the Caribbean (Briones-Fourzán et al., 2008; Kough et al., 2013). These findings were corroborated by research that identified genetically determined outliers or migrants within Sian Ka'an and Banco Chinchorro reserves (Truelove et al., 2014). Whilst there is mounting evidence to suggest that spatial management of the *P. argus* fishery in Mexico should extend beyond MPA and geopolitical boundaries, little is known about how temporal recruitment patterns shape levels of genetic differentiation among cohorts within and among MPAs in this region.

The aim of this study was to investigate population genetic structure of *P. argus* at two levels: (1) spatially between MPAs in the Caribbean coast of Mexico, and (2) temporally within MPAs; by genotyping individual lobsters using microsatellite loci. To explore temporal changes in the levels of population differentiation cohorts were identified by estimating the age of individuals based on previous research of spiny lobster growth rates in the Sian Ka'an MPA (Lozano-Álvarez et al., 1991). The analysis of population structure among cohorts may provide an additional level of resolution that can be used to improve the understanding of the complex spatiotemporal population dynamics of the Caribbean spiny lobster.

2. Methods

2.1. Study sites and sample collection

Samples were collected in Mexico from adult lobsters captured by fishermen in general use zones of the Sian Ka'an Biosphere Reserve and Banco Chinchorro Biosphere Reserve between August 23–26, 2011 (Fig. 1A and B). The Sian Ka'an Biosphere Reserve and Banco Chinchorro Biosphere Reserve are MPAs where the lobster fishery is co-managed by the National Commission for Protected Areas (CONANP) and the National Commission for Fisheries and Aquaculture (CONAPESCA). It should be noted that no samples were collected from the no-take zones of either MPA. The lobster fisheries of Banco Chinchorro and Sian Ka'an MPAs have been reviewed previously by Ley-Cooper et al. (2011, 2013, 2014). Briefly, the spiny lobster fisheries at the Sian Ka'an use casitas, which are large artificial shelters that provide habitat for a broad size range of spiny lobsters. In Banco Chinchorro, the fishers use skin diving to search for spiny lobsters in reef habitats and extract them by hand, but there are plans to substitute this method for casitas. Casitas are confined to shallow areas (15–20 m) allotted to individual fishers that are associated with a cooperative. The cooperatives comply with internal and federal fishing regulations that include a four month

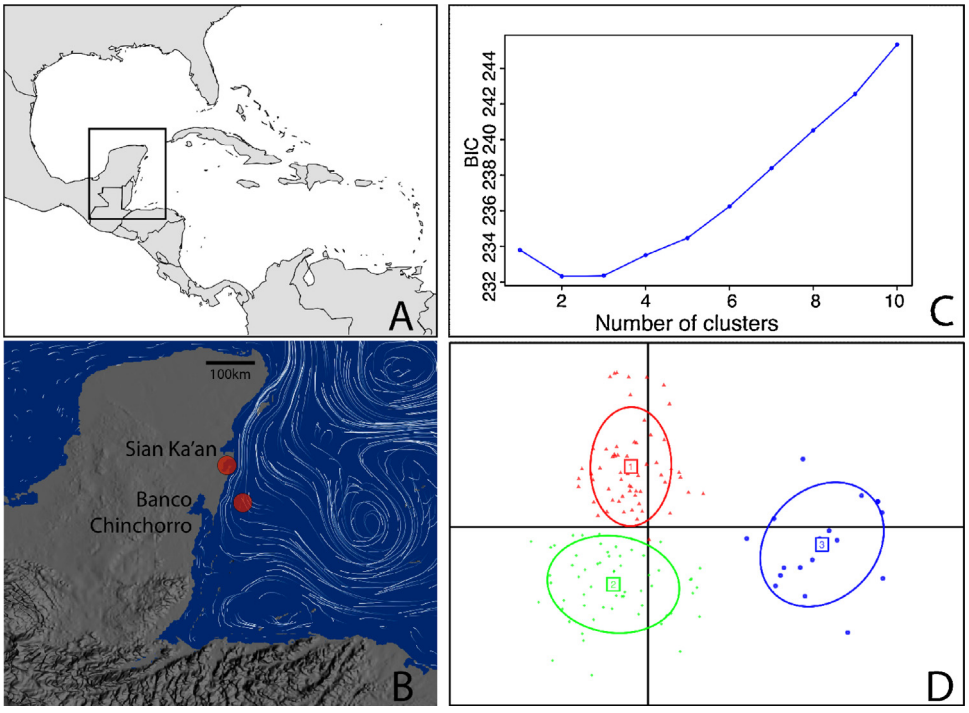

Fig. 1. *Map of study Sites and K-means clustering analysis.* (A) Regional map of the study area with the sampling sites located within the inset in panel (B). (B) Approximate locations of sampling sites in Sian Ka'an and Banco Chinchorro marine reserves in Mexico. The NASA/GSFC Scientific Visualization Studio provided flow data from the ECCO2 model for the visualization Caribbean ocean currents. (C) Plot of Bayesian Information Criterion (BIC) values used for selecting the number of clusters for the discriminant analysis of principle components (DAPC) method. The lowest BIC values indicate the optimal numbers of clusters. (D) Subdivision of clusters according to the DAPC method. Unique genetic clusters are indicated with different colours (red = cluster 1, green = cluster 2, and blue = cluster 3). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)