

Genetic Population Structure of Caribbean Spiny Lobster

Estructura Genética de la Población de la Langosta Espinosa del Caribe

Structure Génétique des Populations de Langouste Blanche des Caraïbes

NATHAN TRUELOVE^{1,2*}, STEVE BOX², DON BEHRINGER, JR³, MARK BUTLER IV⁴, and RICHARD PREZIOSI¹

¹University of Manchester, Faculty of Life Sciences, Manchester, M13 9PT United Kingdom.

*nathan.truelove@manchester.ac.uk.

²Smithsonian National Museum of Natural History, Smithsonian Marine Station, Fort Pierce, Florida 34949 USA.

³University of Florida, School of Forest Resources and Conservation, Gainesville, Florida 32653 USA.

⁴Old Dominion University, Department of Biological Sciences, Norfolk, Virginia 23529 USA.

EXTENDED ABSTRACT

Our research combined population genetics data from microsatellite markers with data from biophysical modeling to explore associations among levels of connectivity, genetic population structure, and potential barriers to larval dispersal throughout the range of spiny lobster, *Panulirus argus*. The results from our large-scale population genetics study of the spiny lobster among several advective and retentive oceanographic environments throughout the Caribbean suggest that the long-lived larvae of *P. argus* disperse among sites throughout their range frequently enough to homogenize the genetic population structure of this species, except for a few sites where self-recruitment is enhanced by persistent offshore gyres.

Despite the high levels of connectivity among distant spiny lobster populations there was substantial variation in geneflow among populations. Striking examples of this variation were observed in the Mesoamerican barrier reef (MBRS). Pairwise levels of genetic differentiation (F_{ST}) were low yet significantly different between the Sapodilla Cayes and Caye Caulker in Belize, which are separated by < 200 km. Since the levels of connectivity were high among the majority of spiny lobster populations that we surveyed, it's unlikely that genetic isolation due to a lack of connectivity explains the higher levels of genetic differentiation over small spatial scales (Christie et al. 2010, Hogan et al. 2011). These results, though perhaps counterintuitive, indicating that some adjacent sites exhibit higher levels of genetic differentiation than more distant sites, is in agreement with a growing body of population genetics research on species with extensive dispersal potential. Johnson and Black (1982) originally identified this phenomenon as "chaotic genetic patchiness". The consensus among several studies of 'chaotic genetic patchiness' in marine species suggests these types of spatial patterns are surprisingly common in species with widespread dispersal and most likely the result of temporal variation in the genetic composition of new recruits (Johnson and Black 1982, Planes and Lenfant 2002, Selkoe et al. 2006, Iacchei et al. 2013).

Recent population genetics studies that have combined analyses of kinship and F_{ST} have uncovered potential drivers of chaotic genetic patchiness among populations of marine species that exhibit high levels of connectivity (Iacchei et al. 2013). A similar methodology was used in to help explain chaotic patterns of genetic differentiation among spiny lobster populations in the MBRS. Kinship analysis of spiny lobster populations residing in marine protected areas (MPAs) in the MBRS found significantly more genetically determined migrants in northern MPAs compared to southern MPAs. Our findings of increased levels of migrants within local populations in the northern MBRS are supported by biophysical modeling studies suggesting that northern regions of the MBRS are more dependent on larval recruitment from distant source populations located upstream of the Caribbean current than southern regions of the MBRS (Butler et al. 2011).

Kinship analyses also found significantly more siblings than expected by chance in the majority of spiny lobster populations than were examined. Higher than expected numbers of siblings have also been reported in populations of other species of spiny lobster and reef fish (Selkoe et al. 2006, Christie et al. 2013, Iacchei et al. 2013). These results may be explained by self-recruitment, a sweepstakes recruitment event, or an unknown mechanism that prevents larvae from mixing throughout their pelagic larval phase (Selkoe et al. 2006). Biophysical modeling studies of spiny lobster larval and coral reef fish connectivity suggests self-recruitment may be common due to larval behavior coupled with local oceanographic characteristics (Cowen et al. 2006, Butler et al. 2011). Several population genetics studies of coral reef fish species in the MBRS, which have much shorter PLDs than spiny lobsters, have provided evidence of both self-recruitment and limited connectivity in the MBRS (Hogan et al. 2011, Puebla et al. 2012, Chittaro and Hogan 2012). Sweepstakes recruitment events may also explain higher than expected levels of siblings that were found in this thesis (Christie et al. 2010). There is growing evidence to suggest that self-recruitment and sweepstakes recruitment may be predominant ecologically processes that shape patterns of larval dispersal in many marine species (Cowen 2000, Christie et al. 2010, Hogan et al. 2011).

The findings of this research highlight the importance of international cooperation for the sustainable management of Caribbean spiny lobster. Genetic connectivity analyses suggest that populations of spiny lobster are highly interconnected throughout its range. However, our findings only present a single snapshot in time. Temporal replication and comparisons

of larvae to adults will clearly be required to understand if the patterns we observed are stable or simply a shifting mosaic over time (Hellberg 2009). Long-term genetic studies will be required to resolve this uncertainty. However, until the uncertainties regarding the ecological and physical drivers of genetic differentiation among Caribbean spiny lobster populations can be resolved, the findings of our research suggest that MPA managers should plan for uncertainty, whilst providing the flexibility for refinement as research provides additional clarity.

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