

# Genetic Population Structure, Diversity, and Connectivity of Endangered Nassau Grouper (*Epinephelus striatus*) in the Bahamas

## Estructura Genética Poblacional, la Diversidad y la Conectividad del Mero Nassau (*Epinephelus striatus*) en Peligro de Extinción en las Bahamas

### Structure de la Population Génétique, la Diversité et la Conectivité des Espèces Nassau Merou (*Epinephelus striatus*) aux Bahamas

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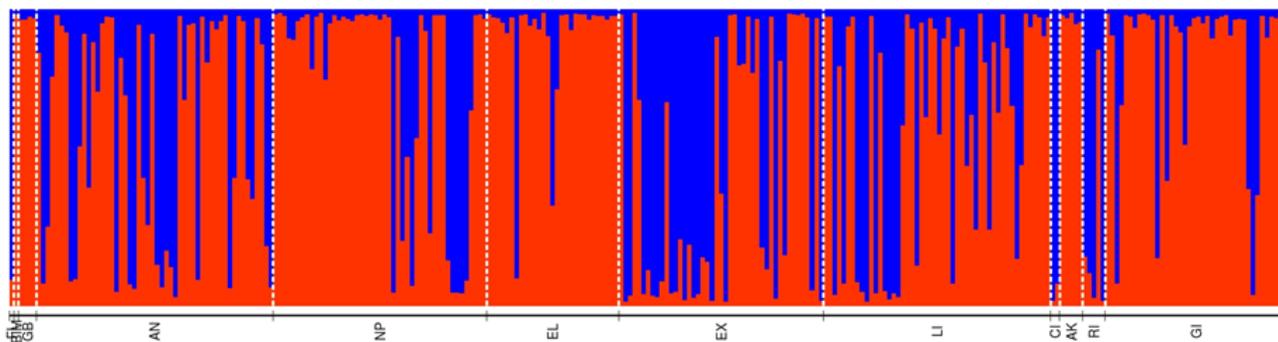
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#### EXTENDED ABSTRACT

Effective fisheries management requires a sound understanding of the reproductive biology, source-sink dynamics and genetic population structure of harvested species. The Nassau Grouper (*Epinephelus striatus*) fishery in The Bahamas has declined by up to 86% in the last two decades and has included the collapse of populations at several major spawning aggregation sites (Sherman et al. 2016). The status of Nassau Grouper spawning stocks throughout The Bahamas has not been comprehensively assessed and little is known about the genetic structure of Grouper populations in this area. Available evidence suggests Bahamian populations of Nassau Grouper may be genetically distinct from Caribbean populations (Jackson et al. 2014). We used 15 species-specific polymorphic microsatellite loci to investigate population structure, diversity and connectivity of Nassau Grouper throughout the Bahamian archipelago. A total of 365 Nassau Grouper fin clips were collected from 12 islands throughout the country between August 2014 - September 2016. Genomic DNA for microsatellite analysis was extracted from fin clip tissues using the HotSHOT method (Truett et al. 2000) and its quality assessed via spectrophotometry. PCR amplification was performed in three multiplexes and PCR products were visualized on a Beckman Coulter sequencer. Microsatellite profiles obtained for 281 fish were used to determine genetic diversity and differentiation. GenAlex (Peakall and Smouse 2012) was used to calculate expected and observed heterozygosity, AMOVA, pairwise and total  $F_{ST}$  values for populations with the largest sample sizes, corresponding to a total of 263 individuals from 6 islands. STRUCTURE (Pritchard et al. 2000) was used (10 independent runs) to test for the presence of genetically distinct populations using profiles for 281 fish from all sampled locations. Results from DNA microsatellite analysis of genotyped Nassau Grouper revealed no definitive geographical population structure (Figure 1). Genetic differentiation based on pairwise  $F_{ST}$  values ranged from 0.000 - 0.001, with total  $F_{ST}$  estimates ranging between 0.006-0.011 (Table 1). These values are consistent with panmixia, i.e. unrestricted gene flow between sampled populations. Two tests for genetic bottlenecks; M-ratio tests (Peery et al. 2012) and BOTTLENECK (Piry et al. 1990), showed the occurrence of both an historical population bottleneck and a recent bottleneck for Eleuthera fish. These data are preliminary, but provide evidence in support of a severe historic decline in Nassau Grouper populations, which may be linked to anthropogenic activities. Findings stemming from our research are beginning to generate key insights into understanding genetic population structure and connectivity, which will contribute to the development of a sustainable management plan for the Bahamian Nassau Grouper fishery.



**Figure 1.** STRUCTURE plot (K = 2) showing 281 individuals from Florida (n = 1) and The Bahamas (n = 280) for all 12 sample locations

**Table 1.** Pairwise population matrix of  $F_{ST}$  values for the total population with  $F_{ST}$  values shown below the diagonal (highlighted in grey). AN = Andros, EL = Eleuthera, GI = Great Inagua, LI = Long Island and NP = New Providence.

AN	EL	EX	GI	LI	NP	
0.000	0.068	0.005	0.077	0.068	0.010	AN
0.009	0.000	0.004	0.926	0.055	0.490	EL
0.008	0.011	0.000	0.001	0.020	0.002	EX
0.007	0.006	0.010	0.000	0.246	0.350	GI
0.006	0.009	0.007	0.007	0.000	0.037	LI
0.008	0.007	0.009	0.007	0.007	0.000	NP

**KEYWORDS:** Microsatellite analysis, fisheries management, genetic diversity

#### LITERATURE CITED

- Jackson, A.M., B.X. Semmens, Y. Sadovy de Mitcheson, R.S. Nemeth, S.A. Heppell, et al. 2014. Population Structure and Phylogeography in Nassau Grouper (*Epinephelus striatus*), a Mass-Aggregating Marine Fish. *PLoS ONE* **9**: e97508. <http://doi:10.1371/journal.pone.0097508>.
- Peakall, R. and P.E. Smouse 2012. GenALEx 6.5: Genetic analysis in Excel. Population genetic software for teaching and research—an update. *Bioinformatics* **28**:2537-2539.
- Peery, M.Z., R. Kirby, B.N. Reid, R. Stoelting, E. Doucet-B eer, S. Robinson, C. V asquez-Carrillo, et al. 2012. Reliability of genetic bottleneck tests for detecting recent population declines. *Molecular Ecology* **21**:3403-3418.
- Piry, S., G. Luikart, and J-M. Cornuet 1990. BOTTLENECK: a computer program for detecting recent reductions in effective population size using allele frequency data. *Journal of Heredity* **90**:502-503
- Pritchard, J.K., M. Stephens, and P. Donnelly 2000. Inference of population structure using multilocus genotype data. *Genetics* **155**:945-959.
- Sherman, K.D., C.P. Dahlgren, J.R. Stevens, and C.R. Tyler. 2016. Integrating population biology into conservation management for endangered Nassau Grouper *Epinephelus striatus*. *Marine Ecology Progress Series* **554**:263-280.
- Truett, G.E., P. Heeger, R.L. Mynatt, A.A. Truett, J.A. Walker, and M.L. Warman 2000. Preparation of PCR-quality mouse genomic DNA with hot sodium hydroxide and tris. (HotSHOT). *BioTechniques* **29**:52-54.