

# Genetic Population Dynamics and Management of Nassau Grouper Within the Bahamas

## Dinámica de Población Genética y Gestión de Nassau Grouper Dentro de las Bahamas

### Dynamique de la Population Génétique et Gestion du Groupe Nassau au Sein des Bahamas

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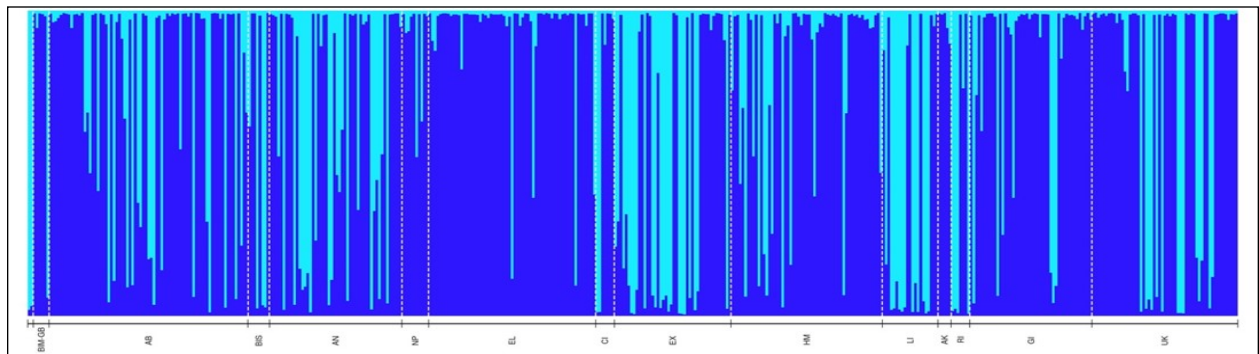
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#### EXTENDED ABSTRACT

The exploitation of fish spawning aggregations (FSAs) has contributed to substantial declines in abundance of Nassau grouper (*Epinephelus striatus*), an important marine predator, naturally distributed throughout The Bahamas and Caribbean (Sadovy de Mitcheson et al. 2013, Sherman et al. 2016). Evaluating the capacity of fish species to withstand exploitation when faced with both stochastic natural and anthropogenic stressors is of critical importance for improving fisheries management. Progress in the field of molecular biology and population genetics have proven very useful in this regard. In the present study, a panel of 15 polymorphic microsatellite loci was optimised and used to investigate genetic population structure, diversity and differentiation, provide the first estimates of effective populations size ( $N_e$ ), and determine whether bottlenecks have impacted contemporary populations of Nassau grouper sampled throughout the Bahamian archipelago. Nassau grouper fin clips were collected during August 2014 – January 2017 from 13 islands and an active FSA (sampled over three spawning seasons). Results from DNA microsatellite analysis of 454 genotyped Nassau grouper suggest weak genetic differentiation (Global  $F_{ST}$  0.00236,  $p = 0.0001$ ), no geographic structure (Figure. 1) and similar levels of diversity (Sherman et al. 2017). *VarEff* analysis of temporal changes in  $N_e$  over the last 1,000 generations show significant reductions in  $N_e$  compared to historic values that are probably due to past climatic disturbances which impacted The Bahamas (Sherman et al. 2017). Recent bottlenecks observed in three islands as well as an active Nassau grouper FSA are likely to have been caused by more recent anthropogenic impacts (e.g., FSA fishing and habitat degradation) (Sherman et al. 2017). This research has provided new information that can contribute to future monitoring assessments and advancing the management of critically endangered Nassau grouper stocks.

KEYWORDS: Bottleneck, connectivity, effective population size, endangered species, FSA, genetic diversity, microsatellites



**Figure 1.** STRUCTURE plot ( $K = 2$ ) showing 454 Nassau grouper (*Epinephelus striatus*) sampled throughout the Bahamian archipelago (Sherman et al. 2017).

#### LITERATURE CITED

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