

Genetic and Biophysical Modeling Assessment of Red Grouper (*Epinephelus morio*) Connectivity in the Gulf of Mexico and Southeastern USA

Evaluación Genética y Biofísica Modelado de Red Mero (*Epinephelus morio*) Conectividad en el Golfo de México y el sureste de USA

Évaluation Génétique et Biophysique Modélisation de Red Grouper (*Epinephelus morio*) Connectivité dans le Golfe du Mexique et du sud-USA

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EXTENDED ABSTRACT

Introduction

Conserving biological diversity and sustainably managing coral reef organisms is contingent upon understanding connectivity linkages between distant populations that form meta-populations. Genetics, biophysical modeling, and animal tagging are often utilized to measure connectivity - and individually, each technique can provide insight into population structure. Employing a singular approach, however, has limitations as each are prone to inherent errors. Thus, adopting multiple methodologies, may better resolve reef connectivity dynamics and also lend insight into the factors driving it.

The Red Grouper (*Epinephelus morio*) is found throughout the Gulf of Mexico (GOM) and Southeast USA (SE-USA) and is of high commercial value, as it is heavily targeted by Cuban, Mexican, and United States (US) fishers within these waters. A prior genetic study suggests that Red Grouper populations in the Atlantic form one large meta-population (Zatcoff et al. 2004); however, only four microsatellite markers were employed – providing only limited spatial resolution of genetic population structure. The extent of connectivity between geographically-separated populations of the fish in the GOM and SE-USA, however, is largely undocumented. This broad-basin connectivity is important as Red Grouper fisheries in the region are managed as two separate units within the US and are relatively unregulated outside US waters. The purpose of this study, therefore, was to first analyze the population structure of the Red Grouper throughout the SE-USA and GOM using high-resolution genetic microsatellite markers obtained from sampled grouper populations in the region. And, secondly, we used a biophysical model that incorporated life history traits of the grouper and ocean conditions in the SE-USA and GOM to forecast connectivity between the same sampled sub-populations over multiple generations of the fish. This twofold approach is better able to resolve connectivity and population dynamics of the Red Grouper and can be used to provide management advice for this economically important, international reef fishery.

Methods

Red Grouper tissue samples were collected from 304 individuals from six geographic locations spanning US and Mexican waters (Figure 1 - Southeastern US Atlantic, n = 49; Florida Keys, n = 35; Dry Tortugas, n = 48; Pulley Ridge, n = 44, West Florida Shelf of the Gulf of Mexico, n = 51; Campeche Bank, Gulf of Mexico, n = 78) and were cross-amplified and genotyped at 13 non-species specific microsatellite markers (Chapman et al. 1999, Zatcoff et al. 2012, Bernard et al. 2012). Population genetic structure was assessed by estimating pairwise values of differentiation between locations, and by performing Bayesian and multivariate individual-based clustering analyses (STRUCTURE and Discriminant Analysis of Principle Coordinates, respectively).

The biophysical connectivity model we employed was previously used to study the diffusion and recruitment of reef fishes in the GOM and SE-USA (Johnston and Purkis 2015, Johnston and Akins 2016) and snappers and groupers in the Hawaiian Islands (Johnston and Purkis 2016). The model implements a three-dimensional Lagrangian diffusion algorithm that coupled GOM and SE-USA ocean conditions, as simulated by the HYbrid Coordinate Ocean Model, with Red Grouper life strategies to forecast the dispersal, recruitment, and resultant connectivity between sub-populations in the study area. Simulations using the model were run for ten years, a length of time that spanned five generations of Red Grouper - important to compare model connectivity with genetic connectivity, the latter which reflects population structure on decadal scales. To match the spatial scope of the model runs with the genetics, geographic founder locations of simulated breeding groupers were the same locations where samples were obtained for the genetic analysis. As sampled locations on the Campeche Bank, Mexico, were unknown, ten random locations were used instead to seed the model. The model outputs are diffusion and recruitment maps of Red Grouper larvae over generations and a connectivity matrix that plots larval founder locations with recruitment positions to illustrate population connectivity within the study region.

Results and Discussion

The population genetic survey of Red Grouper in the GOM and SE-USA suggested a single genetic population and high connectivity between sampled locations. Population-level values of divergence among collection sites showed no indication

of genetic heterogeneity ($F_{ST} < 0.004$, $p < 0.05$) – nor was any significant genetic population structure found among fishery management units (SE-USA, GOM, and Mexico) when samples within units were pooled ($F_{ST} < 0.0008$, $p < 0.05$). Both individual-based clustering analyses also suggested that Red Grouper throughout the sampled area comprise a single homogenous genetic population.

Modeling generational connectivity of GOM and SE-USA Red Grouper indicated similar panmixia as the genetic population structure in the same region (Figure 1). Larval flow was generally from west-to-east and south-to-north, following prevailing ocean current in the study region over the grouper's long pelagic larval duration of 50 days. Populations from locations upstream in the study area, such as on the Campeche Bank, showed high connectivity to populations downstream, such as on the east coast of Florida. Interestingly, upstream recruitment was seen in the simulation from the region of Pulley Ridge (offshore of the southwestern Florida coast) to the Campeche Bank as a result of anti-cyclonic eddy shedding from the Loop Current. This finding suggests that bi-directional exchange of Red Grouper larvae occurs between US and international fishery units and, therefore, all three managed units are reliant upon dispersal from one another.

The concordant outcomes from our dual theoretical and empirical approaches enhance confidence in the results of high connectivity in this region. The study results also

suggest that the GOM and SE-USA Red Grouper populations, now managed separately, should be considered one unit given the population mixing demonstrated by these combined analyses.

KEYWORDS: Red Grouper, *Epinephelus morio*, connectivity, biophysical modeling

LITERATURE CITED

- Bernard, A.M., Richard, V.P., Nemeth, R.S., Shivji, M.S. (2012) Development and characterization of fifteen novel microsatellite loci for the Nassau grouper (*Epinephelus striatus*) and their utility for cross-amplification on a suite of closely related species. *Conservation Genetics Resources* 4:983-986.
- Chapman, R.W., Sedberry, G.R., Koenig, C.C., Eleby, B.M. (1999) Stock identification of Gag, *Mycteroperca micropilis*, along the southeast coast of the United States. *Marine Biotechnology* 1:137-146.
- Johnston, M.W., Purkis, S.J. (2015) A coordinated and sustained international strategy is required to turn the tide on the Atlantic lionfish invasion. *Marine Ecology Progress Series* 533:219-235.
- Johnston, M.W., Akins, J.L. (2016) The Non-native royal damselfish (*Neopomacentrus cyanomos*) in the southern Gulf of Mexico; an invasion risk? *Marine Biology* 163(1):1-14.
- Johnston, M.W., Purkis, S.J. (2016) Forecasting the success of invasive marine species; lessons learned from purposeful reef fish releases in the Hawaiian Islands. *Fisheries Research* 174:190-200.
- Zatcoff, M.S., Ball, A.O., Chapman, R.W. (2002) Characterization of polymorphic microsatellite loci from the black grouper, *Mycteroperca bonaci* (Teleostei: Serranidae). *Molecular Ecology Notes* 2:217-219.
- Zatcoff, M.S., Ball, A.O., Sedberry, G.R. (2004) Population genetic analysis of Red Grouper, *Epinephelus morio*, and scamp, *Mycteroperca phenax*, from the southeastern U.S. Atlantic and Gulf of Mexico. *Marine Biology* 144:769-777.

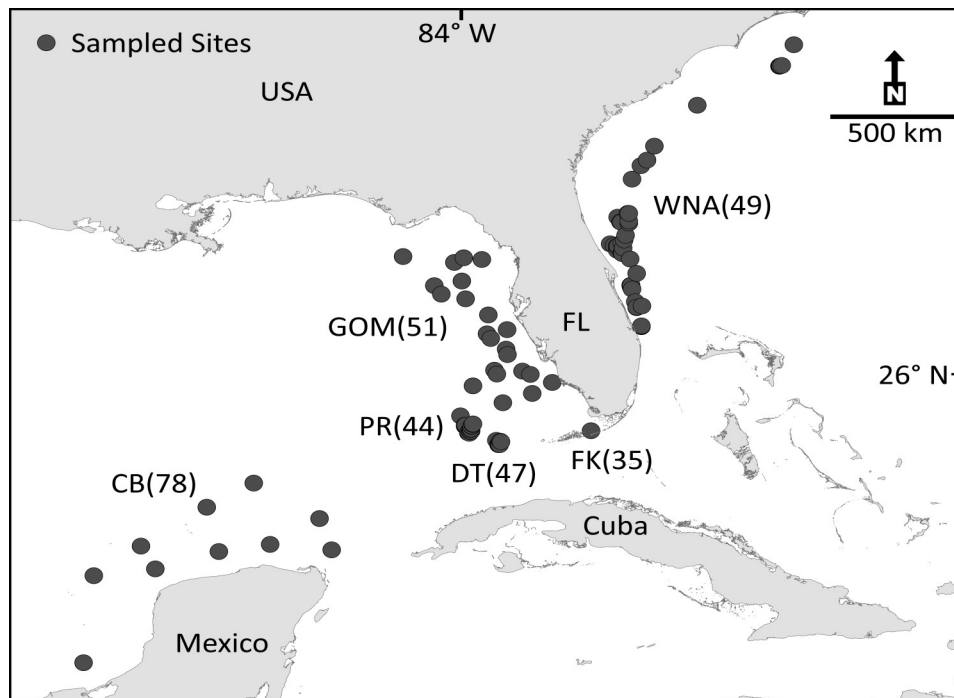


Figure 1. Map of sampling distribution of Red Grouper (*Epinephelus morio*) with sample sizes in brackets; dots indicate exact Red Grouper collection location and modeling larval source location (WNA, FLK, DT, PR, GOM). Sampled sites were unknown on the CB and so ten random locations were used for modelling.

Abbreviations: WNA, Western North Atlantic; FLK, Florida Keys; DT, Dry Tortugas; PR, Pulley Ridge; GOM, Gulf of Mexico; CB, Campeche Bank.