

A selective breeding program to improve aquaculture performance of eastern oyster *Crassostrea virginica* in different salinity environments

Un programa de selección genética para mejorar el rendimiento acuícola de la ostra oriental *Crassostrea virginica* en diferentes ambientes de salinidad

Un programme de sélection génétique pour améliorer les performances de l'huitre américaine *Crassostrea virginica* cultivée a différentes salinités

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EXTENDED ABSTRACT

The greater amberjack (GAJ), *Seriola dumerili*, is a popular gamefish found circumglobally in tropical and subtropical waters. GAJ are also commercially exploited in the US Gulf (Gulf) and South Atlantic. In US waters, a two-stock model for management that distinguishes a Gulf and an Atlantic stock has been implemented, but this division has yet to be supported with genetic data. Incorrect management of a subdivided stock, ignoring sub-units for example, can lead to local overexploitation and extirpation as well as the loss of unique genetic characteristics of local stocks (Carvalho & Hauser 1994). Accordingly, the definition of management units and their geographic boundaries requires understanding of the structure of populations and their connectivity patterns.

Unfortunately, the available information regarding GAJ life history and population structure is fairly limited. Through tagging data around Florida, Murie et al. (2011) suggested GAJ exhibit regional fidelity with a mean of 69km and median of 8km travel distance for an adult. The species' has also been reported to move off reef structures to areas along the outer continental shelf and the upper slope for spawning which occurs from February to April in the Gulf of Mexico (Harris et al. 2007). Post-spawning, GAJ young of the year have been found associating with, but not dependent on, sargassum and other fish aggregating devices (FADs; (Wells & Rooker 2004; Sinopoli et al. 2007). Evidence of regional site fidelity coupled with off-shore spawning and association with FADs may promote connectivity and lend GAJ to a pattern of isolation by distance whereby genetic distance increases with physical distance.

Currently, information on population genetic structure is limited to two studies based on mitochondrial DNA variation and microsatellite markers, respectively, which indicated weak support for divergence between Atlantic and Gulf of Mexico stocks (Gold & Richardson 1998; Hargrove et al. 2018). However, the delineation of these two stocks, patterns of mixing between them, and the possible of occurrence of additional distinct stocks within US waters within the Gulf of Mexico. remain unknown. This study will apply genome scans generated by the double digest Restriction-site Associated DNA (dd-RAD) sequencing protocol and a comprehensive sampling from the Carolinas to the Western Gulf of Mexico to describe stock structure of the species in the region. Analysis is in progress for samples collected between 2021 and 2024 during tagging and fishery-dependent and independent sampling surveys along the US East coast (North Carolina, South Carolina and Southeast Florida), from the eastern, central and western Gulf of Mexico. Each US region was sampled over two years to assess temporal stability of inferred patterns. Genomic resources needed to interpret genome scans were developed in a first project component by sequencing the genome of one GAJ specimen using the PACBIO Sequel HiFi and the Illumina Novaseq platforms.

Assembly efforts yielded a 625Mb reference in 223 contigs with an N50 over 18 Mb. The reference genome will be applied to analyze and interpret sequencing results of all population samples. A first group of 384 samples from all regions surveyed during sampling have been sequenced so far and initial data analysis indicates overall very weak divergence between regional populations within the Gulf and weak but more pronounced divergence between Gulf and US East Coast populations. Additional sampling in other Atlantic populations potentially connected to US ones is in progress and will be sequenced analyzed alongside additional samples from US regions.

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