

Population Genetics of Sponge Restoration in Florida Bay

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Sponges are crucial benthic animals and dominate the heterotrophic biomass of Florida Bay's hard bottom habitats. They serve as habitats for commercially important invertebrates like spiny lobsters and stone crabs and provide foraging grounds for juvenile fish. However, in the past century, sponges have experienced significant die-offs due to overfishing, diseases, cyanobacterial blooms, and thermal stressors. In response, the Florida Fish and Wildlife Commission (FWC) initiated a sponge propagation project targeting six key species in Florida Bay. This sponge nursery was built only from fragments of donors (clones), and the levels of clonality, inbreeding, and genetic diversity remain unclear. Our aim is to assess the genetic diversity and the effectiveness of the sponge propagation restoration efforts. Four key sponge species were targeted from both FWC sponge nursery and wild populations. Tissue samples were collected from larvae, recruits and adults to analyze genotypes, clonality, inbreeding, heterozygosity, and genetic diversity. Preliminary results suggest that *Spongia barbara* and *S. graminea* clones are fecund and therefore genetic diversity at the sponge nursery might be higher than expected, though larval settlement success is low. This study enhances FWC's restoration efforts by identifying genetic patterns and strategies for spatially distributing sponge individuals, which would increase sponges' genetic diversity and resilience to climate change.