

# Characterizing Nearshore Fish Assemblages at Intact and Altered Mangrove Shorelines in Southern Biscayne Bay

## Caracterización de Conjuntos de Peces en Costas de Manglares Intactas y Alteradas en el Sur de la Bahía de Biscayne

### Caractérisation des Assemblages de Poissons Côtiers sur les Rivages de Mangrove Intacts et Altérés dans le Sud de la Baie de Biscayne

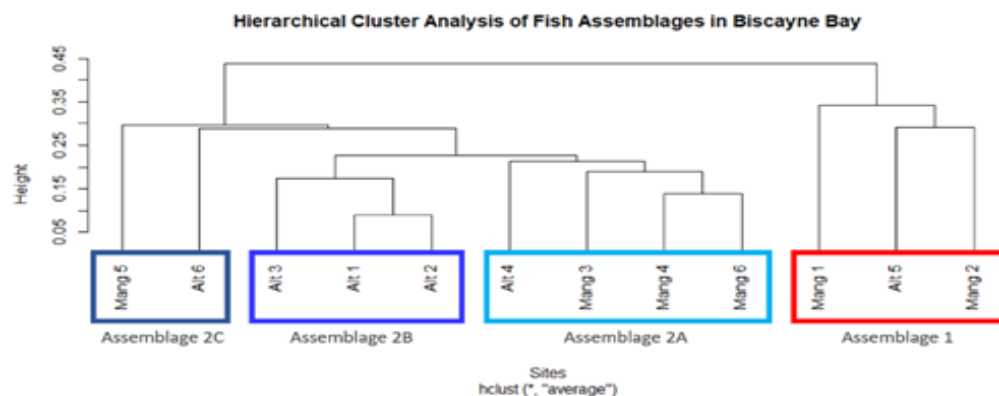
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#### EXTENDED ABSTRACT

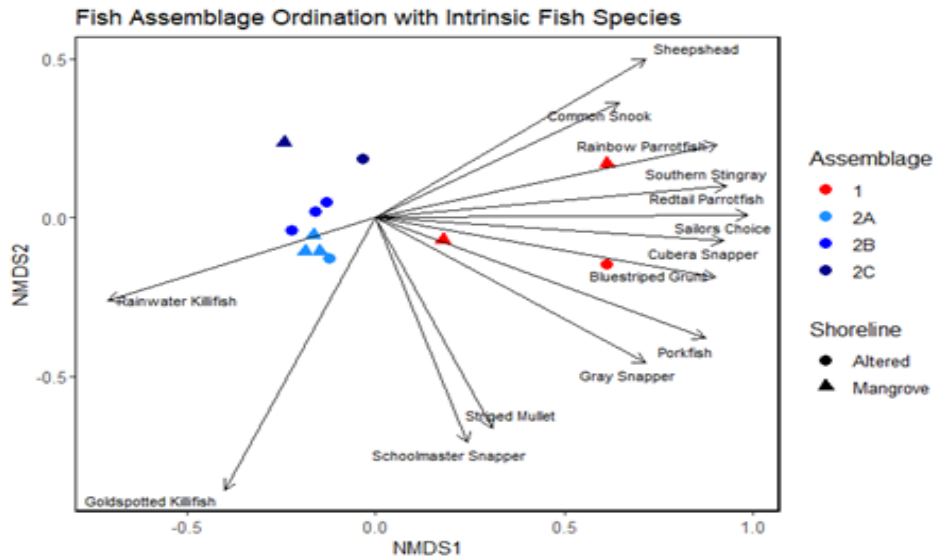
Fish do not just rely on mangroves as habitat; they are critical components of the whole coastal ecosystem. Fish form a significant component of the heterotrophic biomass in marine systems, so they can represent the scale of secondary production in ecosystems. (Day et al. 2018). Fish support many ecosystem regulating functions, linking functions, and demand-derived services (Holmlund & Hammer 1999). They regulate trophic structure, food web dynamics, ecosystem resilience, nutrient recycling, sediment processes, and maintain biodiversity (Holmlund & Hammer 1999). Fish transport nutrients, carbon, and energy, thereby facilitating connectivity between marine ecosystems, which increases system-wide biodiversity and productivity (Holmlund & Hammer 1999). Not only does fish biodiversity improve functionality, but also increases the stability of those functions (Yachi & Loreau 1999, Loreau et al. 2001, Maestre et al. 2012).

Biscayne Bay in South Florida is a heavily-altered watershed and while Southern Biscayne Bay is dominated by mangroves, it contains drainage, agricultural, and residential canals (Cantillo et al. 2000). Drainage canals were used to convert mangrove wetlands to dry land and to control flooding (Cantillo et al. 2000). These canals also serve as point-sources of pollution and cause pulses of freshwater, which harm nearby estuarine habitats (Browder et al. 2005). Reduced freshwater inflow has led to reduced mangrove functionality, while associated saltwater intrusion has facilitated scrub mangroves migrating into former freshwater wetlands (Browder et al. 2005).

All data used in this analysis was retrieved from the Integrated Biscayne Bay Ecological Assessment and Monitoring Project, a very large set of publicly available data. Visual surveys were conducted along a 30-m-long transect running parallel to the shore. To examine current fish assemblages, the five most recent years of available surveys (2015 – 2019) are considered. Six sites were in front of intact mangrove shorelines and six sites were adjacent to altered mangrove shorelines that contained a canal. Each transect is a snapshot of the fish community present for each site, so the fish abundances of all the transects at each site were added together to create the representative samples for each site. Silversides have been removed from the samples because they exist in high abundances and are not useful in discriminating species assemblages. Abundances were fourth-root transformed, then a Bray-Curtis dissimilarity matrix was created for all 12 survey sites. The matrix was used to create a cluster dendrogram and run a SIMPROF analysis to determine how many significant clusters were formed., which was confirmed with an ANOSIM. Rank-abundance plots were created to visualize differences in



**Figure 1.** Cluster analysis dendrogram showing the formation of different fish assemblages based on species composition.



**Figure 2.** NMDS plot (stress = 0.0786) showing fish assemblages overlaid with statistically significant intrinsic fish species.

species composition between assemblage clusters. SIMPER analyses were then conducted to determine which species most contributed to the dissimilarity between fish assemblages. SIMPER results and fish abundances were used to create a list of distinguishing species for each cluster. nMDS plots were created to show how sites were arranged into clusters and how both fish species and environmental factors were correlated with the distribution pattern.

Intact mangrove sites typically had higher species richness and diversity values than altered sites, but diversity does not equate to similarity in species composition. Twelve sites formed two main clusters, or fish assemblages ( $R = 0.8917$ ,  $p = 0.006$ ). Assemblage 1 contains three sites, while Assemblage 2 is made up of the nine remaining sites. Both abundant and less-abundant species are responsible for dissimilarities between the assemblages. Assemblage 1 is more diverse and is distinguished from Assemblage 2 by bluestriped grunt, schoolmaster snapper, grey snapper, sailors choice, sergeant major damselfish, rainbow parrotfish, mosquitofish, and porkfish. Assemblage 2 is distinguished by having more goldspotted killifish and rainwater killifish. The nine sites from Assemblages 2 can be further divided to form three distinct sub-clusters ( $R = 0.7$ ,  $p = 0.003$ ). Assemblage 2A is formed from four sites, Assemblage 2B consists of three altered sites, while Assemblage 2C is made up of two sites. Both abundant and less-abundant species are also responsible for dissimilarities between Assemblage 2A, 2B, and 2C. Assemblage 2A is more diverse and is distinguished from Assemblage 2B and 2C by mosquitofish, sailfin molly, yellowfin mojarra, gray snapper, pinfish, goldspotted killifish, and redfin needlefish. Assemblage 2B is distinguished by goldspotted killifish, schoolmaster snapper, yellowfin mojarra, rainwater killifish, common mojarra, and sergeant major damselfish. Assemblage 2C is distinguished by sergeant

major damselfish and redfin needlefish. Salinity and depth were correlated with the cluster distribution patterns, indicating that fish assemblages may be responding to these factors. Fish assemblages do not appear to be correlated with dissolved oxygen, temperature, visibility, latitude, or shoreline type.

Utilizing large pre-existing data sets is important as they can be used to produce statistically robust analyses and forecast ecological changes. Fish do form distinct assemblages in Biscayne Bay with different species composition. These fish assemblages appear to be responding primarily to salinity and depth, indicating that water quality plays an important role in driving fish assemblages and should be considered when planning shoreline restoration. While temperature and dissolved oxygen were not linked to different fish assemblages, this is likely because these factors were not changing between sites, not because these factors are unimportant. Notably, fish assemblages are not responding to adjacent shoreline characteristics, which may be because the alterations at canal-mangrove sites in southern Biscayne Bay were not on a scale to impact observed fish assemblages. The complexity of Biscayne Bay requires a data-intensive study of fish assemblages to understand restoration implications, because some degree of alteration does not seem to affect the surrounding fish assemblages in a largely intact mangrove landscape. Assemblage 1 has greater diversity than sites in Assemblage 2, indicating that these are higher functioning sites within southern Biscayne Bay. Sites in Assemblage 2 had lower diversity and had lower, more variable salinities at the sampling time than sites in Assemblage 1. The Comprehensive Everglades Restoration Plan aims to restore the flow of freshwater through South Florida, which would result in lower salinities. If future salinity regimes look more like the salinity of

Assemblage 2, albeit with less variability, future fish assemblages may be more similar to that of Assemblage 2 as well.

**KEYWORDS:** Assemblage characterization, Species composition, Mangroves, Canals, Cluster analysis.

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