Identifying population structure of the Gulf Pipefish, *Syngnathus scovelli*, across Florida

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The Gulf Pipefish

Syngnathus scovelli (Figure 1) is a member of the family Syngnathidae, which includes seahorses, sea dragons, and pipefish. Members of this family are characterized by a fused jaw and males that have a pouch-like structure into which females lay eggs. He then fertilizes the eggs and carries them until they hatch. As a result, *S. scovelli* juveniles lack a larval pelagic stage and dispersal in this species occurs primarily via ocean currents and rafting. *S. scovelli* inhabits shallow waters from Brazil to the Carolinas.[1] *S. scovelli* can tolerate a wide range of salinities, with one population recorded in a strictly freshwater lake.[2]

Previous studies have shown that *S. scovelli* exhibits significant population structure among coastal populations, with less structure in populations that are interconnected by streams, rivers, and bays.[3] Here we examine the population structure of *S. scovelli* across the state of Florida to determine if there are multiple subpopulations.

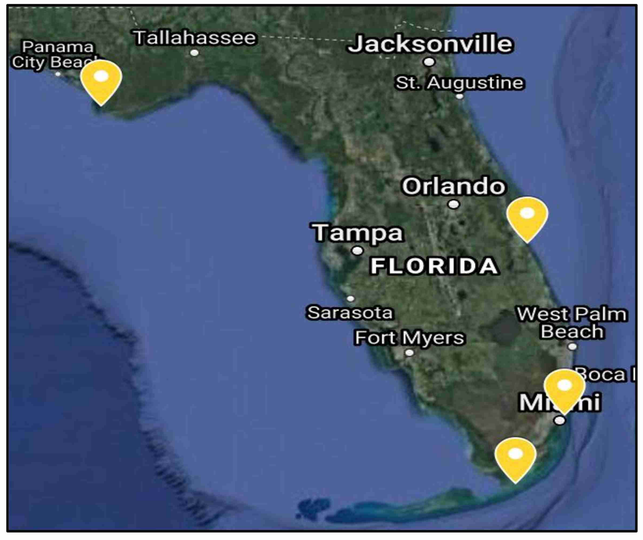

Figure 2. Map of sampling locations and number of individuals from East to West: Indian River Lagoon (22), Biscayne Bay (31), Florida Bay (23), St. Joseph Bay (24). Map generated using Google Earth (earth.google.com)

Methods

We generated DNA sequence data for the mitochondrial Cytochrome c Oxidase Subunit 1 (CO1) barcoding gene. Individuals were collected at four locations around Florida (Figure 2) by collaborators at NOAA, FWC, and Dauphin Island Sea Lab. These data were analyzed using Geneious Prime® v2021.0.3 and visualized with a median-joined haplotype network using PopART v1.7. An analysis of molecular variance (AMOVA) was conducted in Arlequin v3.5.2.2 and pairwise F_{ST} values were calculated.

Figure 1. Image of *S. scovelli* from Mississippi State University (cfr.misstate.edu), these fish inhabit shallow seagrass beds along the Gulf of Mexico and other Atlantic coastlines.

Results

A 626 bp sequence of the CO1 gene was resolved in 100 individuals. From these sequences, 33 haplotypes were identified (Figure 3).

Overall F_{ST} was high and significant (F_{ST} = 0.562) suggesting a high degree of population structure among the four sample populations. All pairwise comparisons indicated significant population structure except between Indian River Lagoon and St. Joseph Bay (Table 1).

The high levels of differentiation detected in Biscayne Bay and Florida Bay populations (Figure 3) may be caused by significant environmental differences as both populations occur in south Florida. Similarly, the estuarine populations of Indian River lagoon and St. Joseph Bay do not show significant variation. This correlation between habitat and population structure will need to be looked at more closely in future studies.

	Biscayne Bay	Florida Bay	St. Joseph Bay	Indian River
Biscayne Bay	0			
Florida Bay	**0.61683**	0		
St. Joseph Bay	**0.71454**	**0.10913**	0	
Indian River	**0.71894**	**0.1089**	0.04143	0

Table 1. F_{ST} values are blow the diagonal. *P* value < 0.005 for all populations.

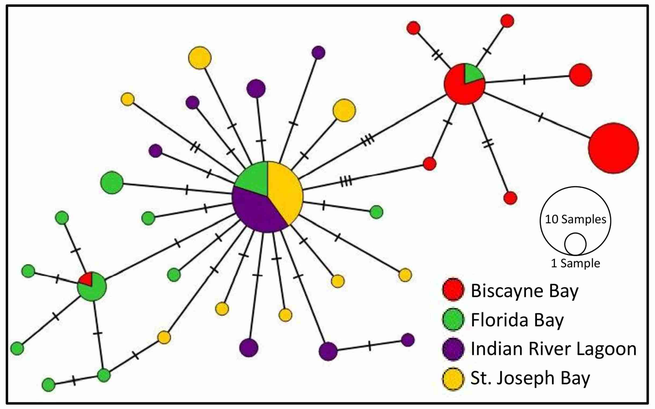

Figure 3. Median-joining Haplotype network created using PopART v1.7 for CO1 sequences. Each circle represents one haplotype where size is proportional to individuals with that haplotype; dashed lines indicate the number of base pair mutations.

Study Significance

Coastal and estuarine systems are in a constant and increasing state of change due to seasonal environmental shifts, climate change, and anthropogenic effects.

Findings from this study, and future studies like this, can be used to infer how environmental factors such as salinity and habitat fragmentation may affect habitat population connectivity and dispersal in marine and estuarine populations.

Future Studies

To determine the possible reason for the level of variation between South Florida populations of *S. scovelli* from other sample locations, future studies will have to consider collecting larger sample sizes, more sampling populations, and the use of other genomic sequencing techniques (i.e., RADSeq analysis).

As well as analysis of environmental data at the sampling locations to determine if there are any significant differences.

References

1 Bolland & Boettcher 2005 *Estuarine Research Federation*
2 Martin et al. 2013 *Southwestern Naturalist*
3 Partridge et al. 2012 *Journal of Heredity*