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Introduction

- The Dwarf Seahorse is one of four seahorse species in N. America
- Smallest seahorse in the U.S., max size 2.5 to 3 cm (Fig. 1)
- Disperse by rafting on free floating seagrass or algae (Fig. 2)
- Florida
 - Relatively well studied
 - Classified as Least Concern by the IUCN
 - Gene flow documented among bays (Fedrizzi et al. 2015)
- Texas
 - Understudied
 - Only 8 individuals in previous genetics study (Rose et al. 2014)
- Objective:** This study investigates the relationships between Dwarf Seahorse populations among bay systems in Texas and Florida to aid in the management and conservation of the species

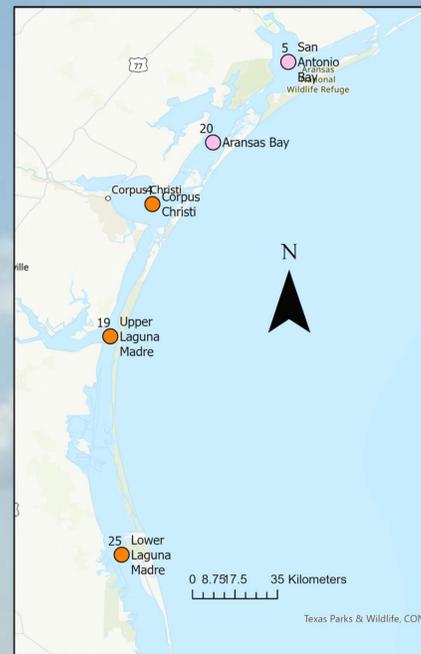


Figure 3. Bay systems sampled in Texas. Color corresponds to Fig. 5.

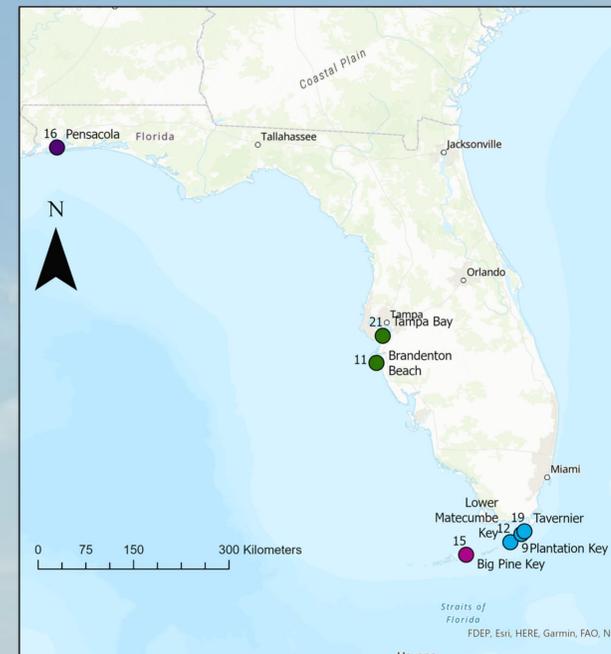


Figure 4. Bay systems sampled in Florida. Color corresponds to Fig. 5.

Conclusions

- Genetic lineages in Texas are distinct from Florida
- Pensacola population represents a genetic lineage distinct from the other Florida lineages with minimal gene flow
- Tampa Bay and Bradenton Beach likely represent a distinct lineage
 - More gene flow from this lineage to southern populations is observed
- Evidence of southern migration direction in Florida
 - Southern populations appear to have influence from more lineages
- Evidence of migration among the bays of Texas
 - Northern and southern lineage with a gradient between
- Trends may indicate likely migration paths through rafting

Methods

- 72 Dwarf Seahorses were collected from 5 bay systems in Texas (Fig. 3)
- 121 Dwarf Seahorses were provided from 7 bay systems in Florida (Fig. 4) (Fedrizzi et al. 2015)
- Double digest restriction-site associated DNA sequencing (ddRADseq) was used to sequence the DNA
- Sequenced DNA was put through ADMIXTURE to determine the most likely population structure (Alexander et al.)
 - Population structure was visualized using CLUMPAK (Kopelman et al.)

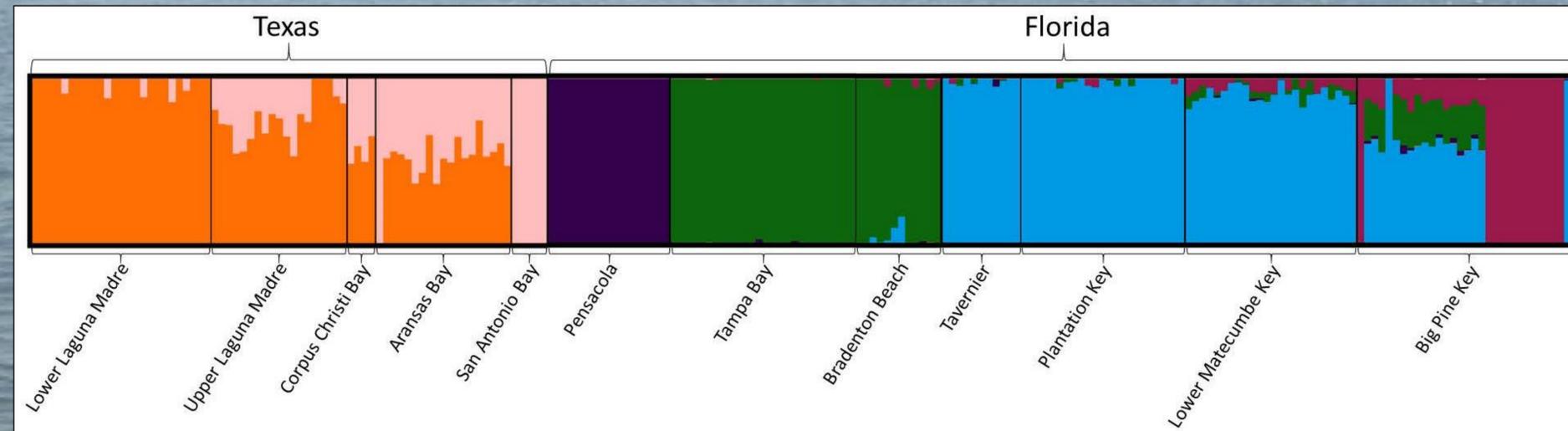


Figure 5. A visualization of the population structure of the Dwarf Seahorses in Texas and Florida. Each color represents a distinct genetic cluster, and each bar represents an individual. Created using CLUMPAK (Kopelman et al.)

Future Directions:

- Data analysis is on-going
 - Investigate migration rates using *BayesAss*
 - Determine loci under selection using *BAYESCAN*
 - Estimate effective population size using *NeEstimator*
- This work will allow for a better understanding of the genetic ecology of Dwarf Seahorses and inform conservation efforts for the species

Literature Cited:

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Figure 1. Juvenile Dwarf Seahorse on an index finger to demonstrate scale.



Figure 2. Dwarf Seahorse captured from Aransas Bay, TX in mixed Algae.

Results

- Based on the Best K value from ADMIXTURE, the most likely explanation for the population structure is 6 genetic lineages (Fig. 5).