Assessing population connectivity of the coral species, *Montastraea cavernosa*, in Cuba and the Tropical Western Atlantic

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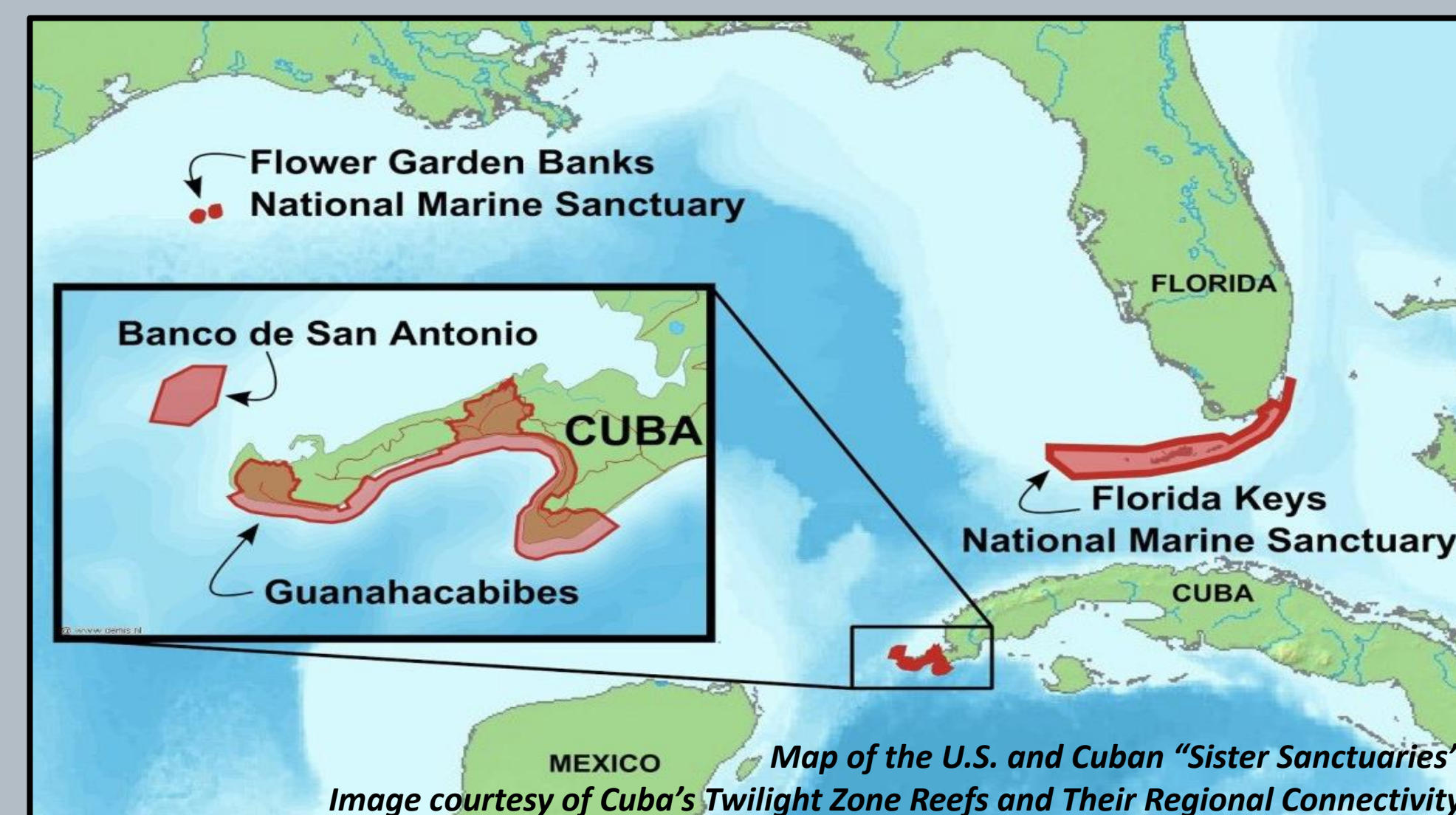
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Introduction

- Cuba has the largest shelf habitat in the Caribbean, supporting an estimated 4,000 km² of shallow (<30 m) and mesophotic (30–150 m) coral communities.[1]

- Given Cuba's centrally located position and hydrodynamic regime, it's hypothesized to be a population source to downstream coral reefs in the U.S. A Sister Sanctuary relationship was recently established between Cuba and the U.S. to promote effective marine resource management in both countries.[2]

- This study employed molecular approaches to investigate potential connectivity of the coral species *Montastraea cavernosa* among sites in Cuba and assess the potential role of these communities in the population dynamics of the Tropical Western Atlantic (TWA).

Map of the U.S. and Cuban "Sister Sanctuaries"
Image courtesy of Cuba's Twilight Zone Reefs and Their Regional Connectivity

- *M. cavernosa* is a cosmopolitan, extreme depth generalist, and a broadcast spawner with potential for high levels of connectivity throughout the TWA.[3,4]

Research Objectives

1. Assess the population genetic structure of *Montastraea cavernosa* among sites in Cuba

2. Quantify the level of horizontal connectivity among populations of *M. cavernosa* across the Tropical Western Atlantic
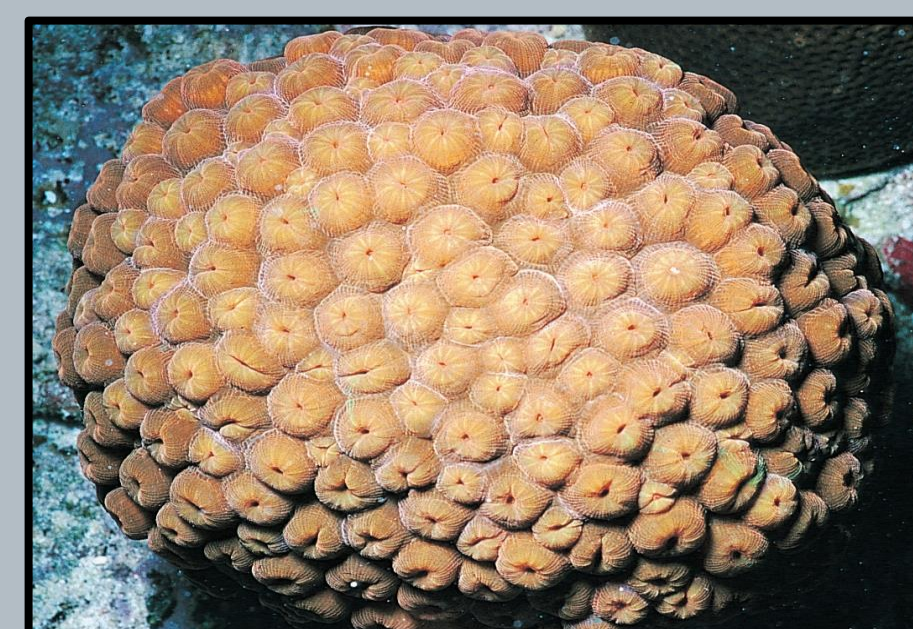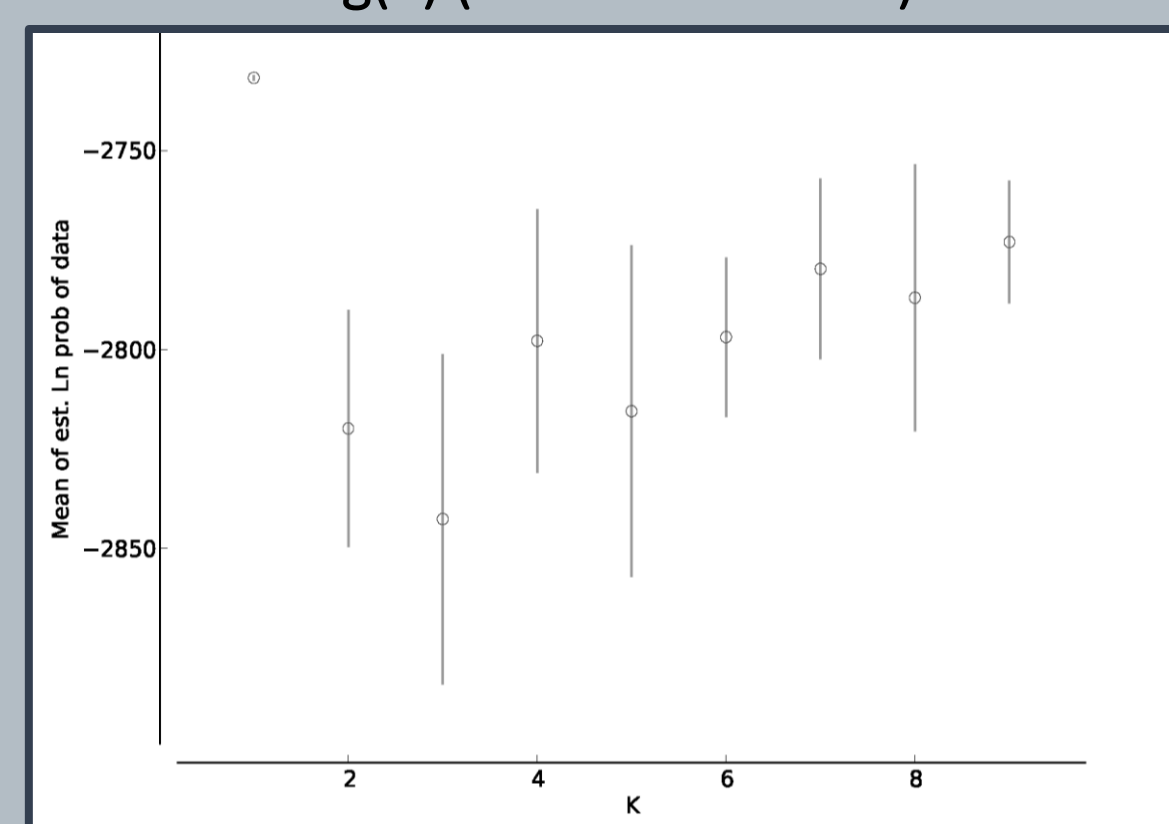

Methods

- 86 tissue samples collected by snorkelers utilizing hammer and chisel from 6 sites between 2–8 m depths

- Samples preserved in TriZol reagent for genetic analysis

- DNA extracted via modified CTAB protocol[5]

- Amplified and analyzed 9 *M. cavernosa* microsatellite loci[6]

Population Structure in Cuba

Map of the 6 Cuban sites sampled with sample size (n)
*Cayo Jutías n=13
*Cayo Sabinal n=14
*Guanahacabibes n=14
Cabo Lucrecia n=17
*Cayo Anclitas n=14
Chivirico n=14
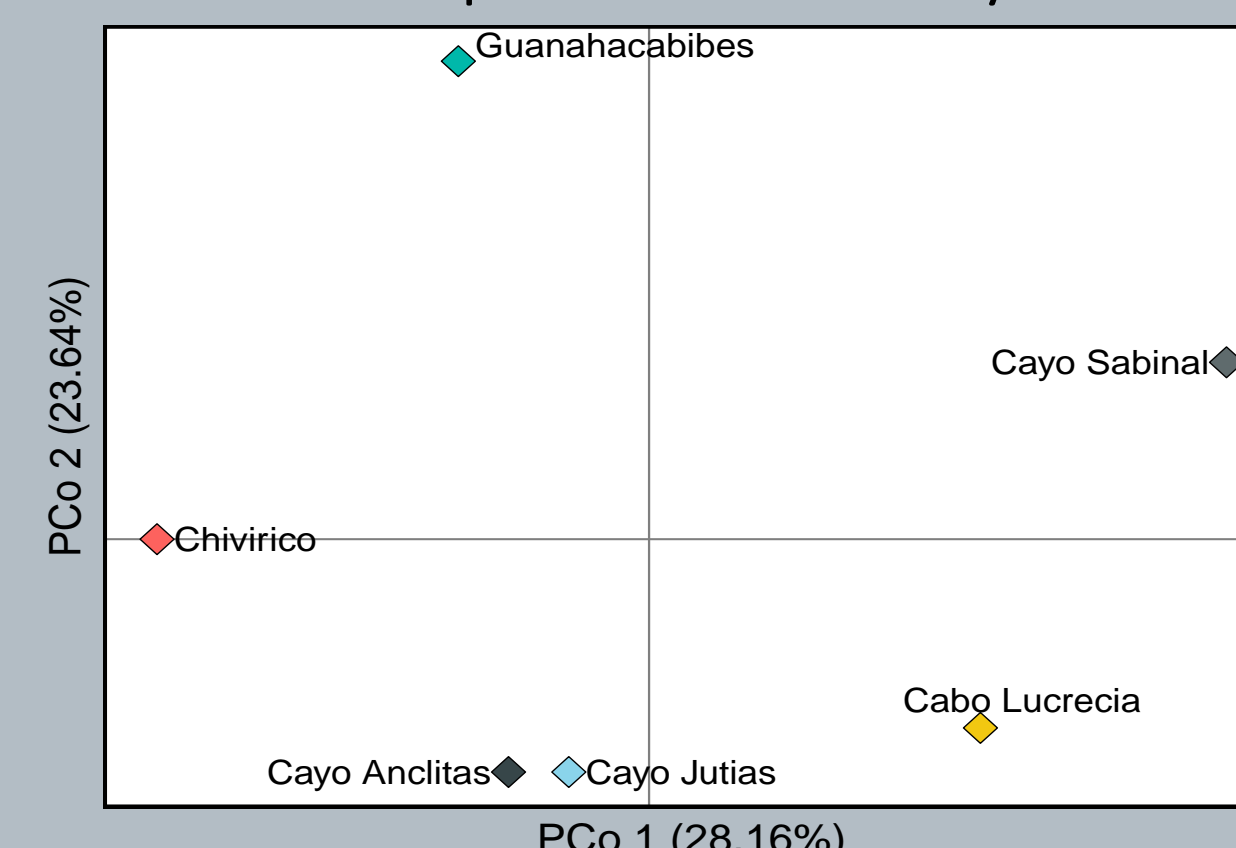*Sites located within a Marine Protected Area
★ Sampling Sites

Log(K) (Mean ± Std. Dev.)
Plot of log likelihood values across ten replicate model simulations of historical source populations (K, ranging from 1-9) produced in the program Structure 2.3.4[7] to estimate the most likely value of K.
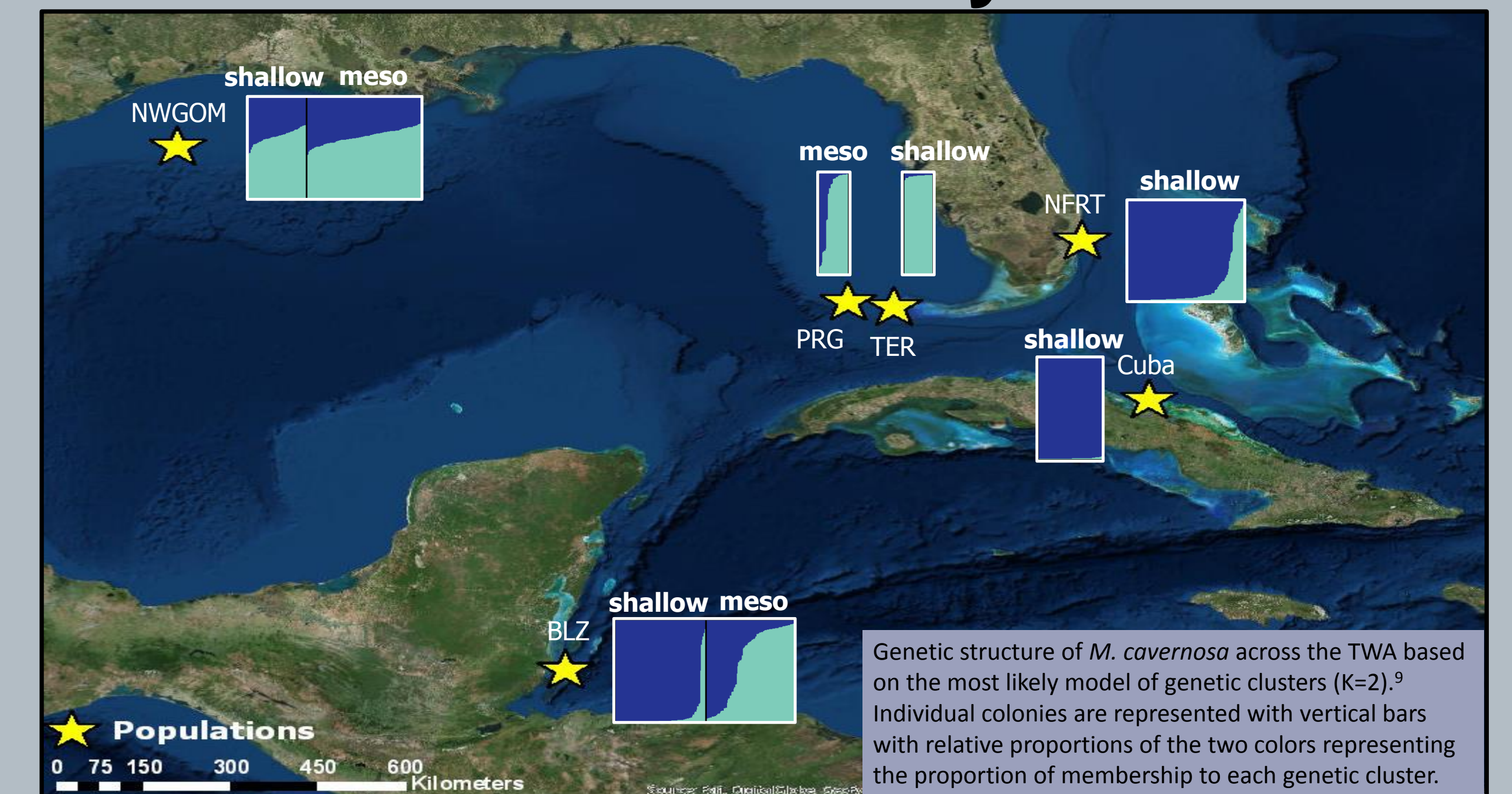

Principal Coordinates Analysis
PCoA Plot based on Nei genetic distance among sites. Distance among points illustrate the degree of genetic differentiation among sites.

Population structure analysis suggests that sites are a <u>single panmictic population</u> with one historical source population
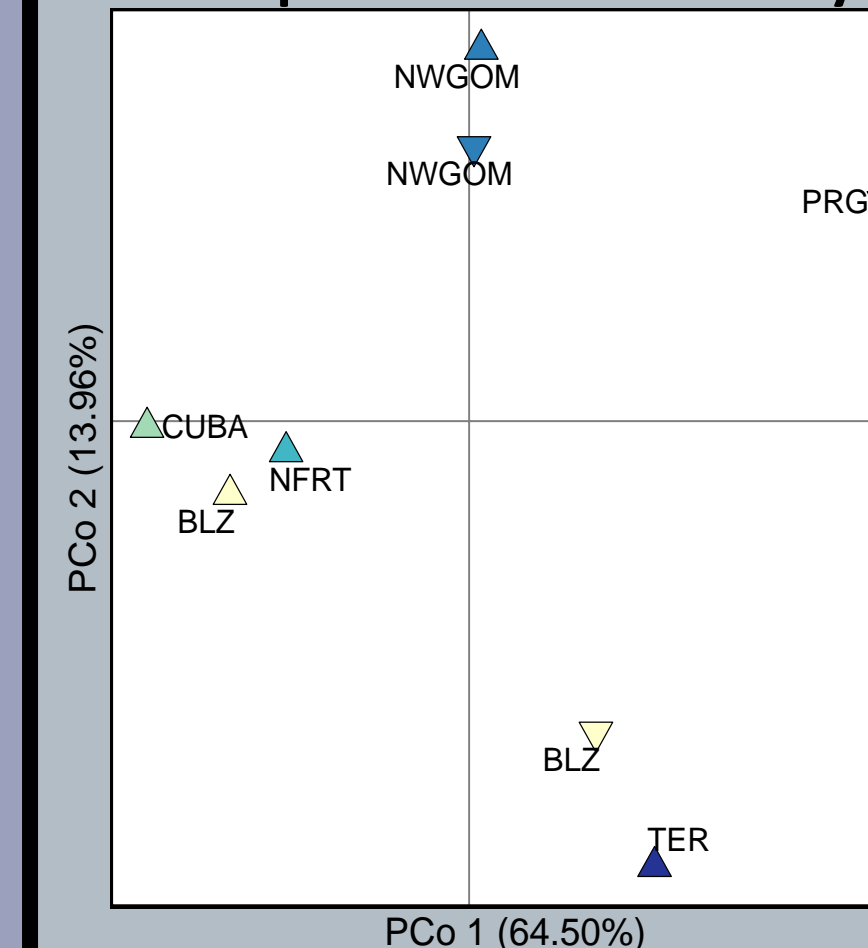
However, PCoA ordination suggests that there may be <u>genetic differentiation among Cuban sites</u>

- An Analysis of Molecular Variance (AMOVA; 9,999 model and pairwise permutations) demonstrated no significant pairwise population differentiation among the 6 sites in Cuba (p>0.05)[9]

- Limited samples sizes in preliminary analyses; additional samples (i.e. n=30 per site) or an increased number of genetic markers generated via SNP genotyping needed to improve statistical power.
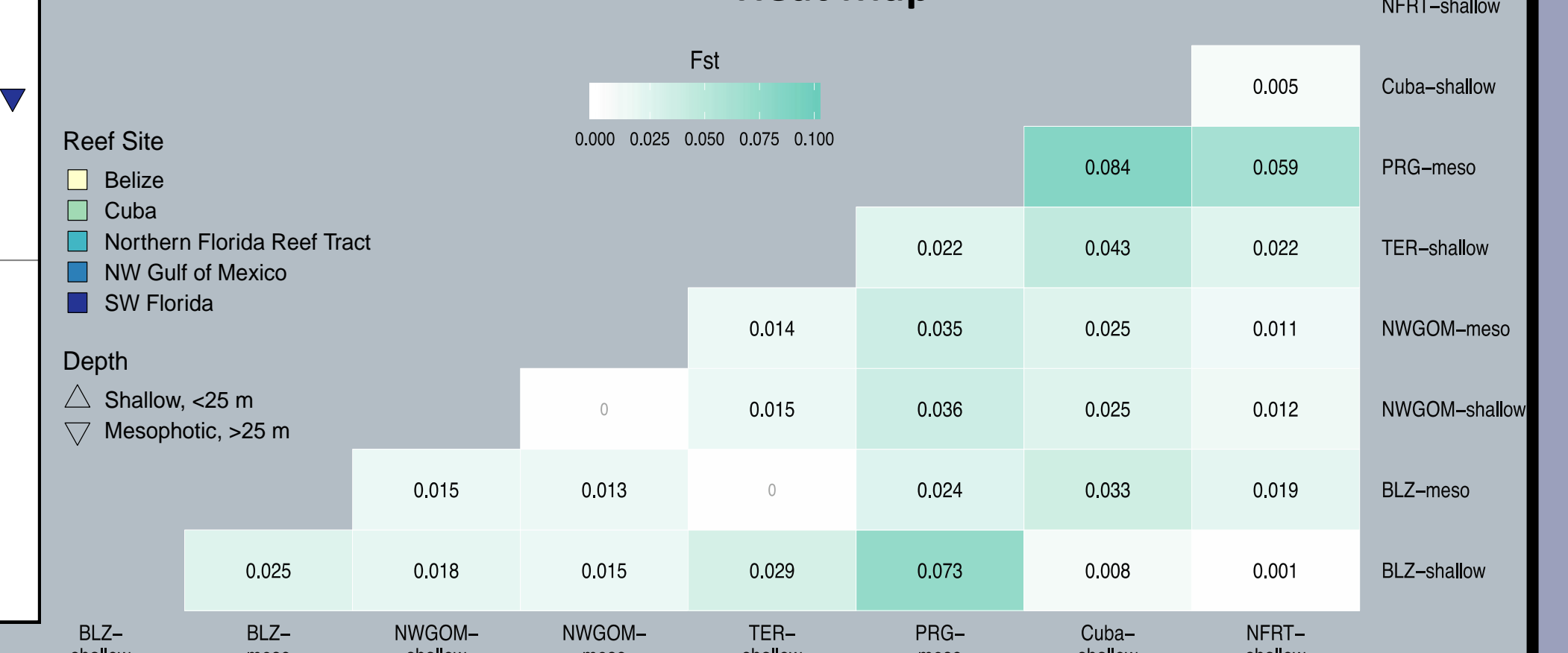
Horizontal Connectivity in the TWA

Genetic structure of *M. cavernosa* across the TWA based on the most likely model of genetic clusters (K=2).[9] Individual colonies are represented with vertical bars with relative proportions of the two colors representing the proportion of membership to each genetic cluster.

Principal Coordinates Analysis
Reef Site
Belize
Cuba
Northern Florida Reef Tract
NW Gulf of Mexico
SW Florida
Depth
△ Shallow, <25 m
▽ Mesophotic, >25 m

Pairwise Population Differentiation (Fixation Index, Fst) Heat Map

Differentiation level indicated by the shade of teal.
Black text indicates significantly differentiated Fst (p<0.05 post-FDR correction).

Conclusions

- Preliminary analyses indicate little genetic differentiation among *M. cavernosa* populations within Cuba. Additional samples or fine-scale genotyping techniques are needed for a more robust analysis.

- *M. cavernosa* populations in Cuba are most genetically similar to shallow populations in the Northern Florida Reef Tract and are significantly differentiated from populations at Pulley Ridge.

- Cuba represents an important stepping stone in the dominant gene flow patterns across the TWA and among Marine Protected Areas.

Acknowledgements and Citations

References: 1. Creary et al. (2008) ReefBase 2. NOAA (2015) Sister Sanctuary: Memorandum of Understanding 3. Lesser et al. (2009) J Exp Mar Bio Ecol 4. Brazeau et al. (2013) PLoS One 5. Mieog et al. (2009) Mol Ecol Resour 6. Serrano et al. (2014) Mol Ecol 7. Pritchard et al. (2000) Genetics 8. Peakall & Smouse (2001) GenAlEx V5 9. Evanno et al. (2005) Mol Ecol