

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

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Background

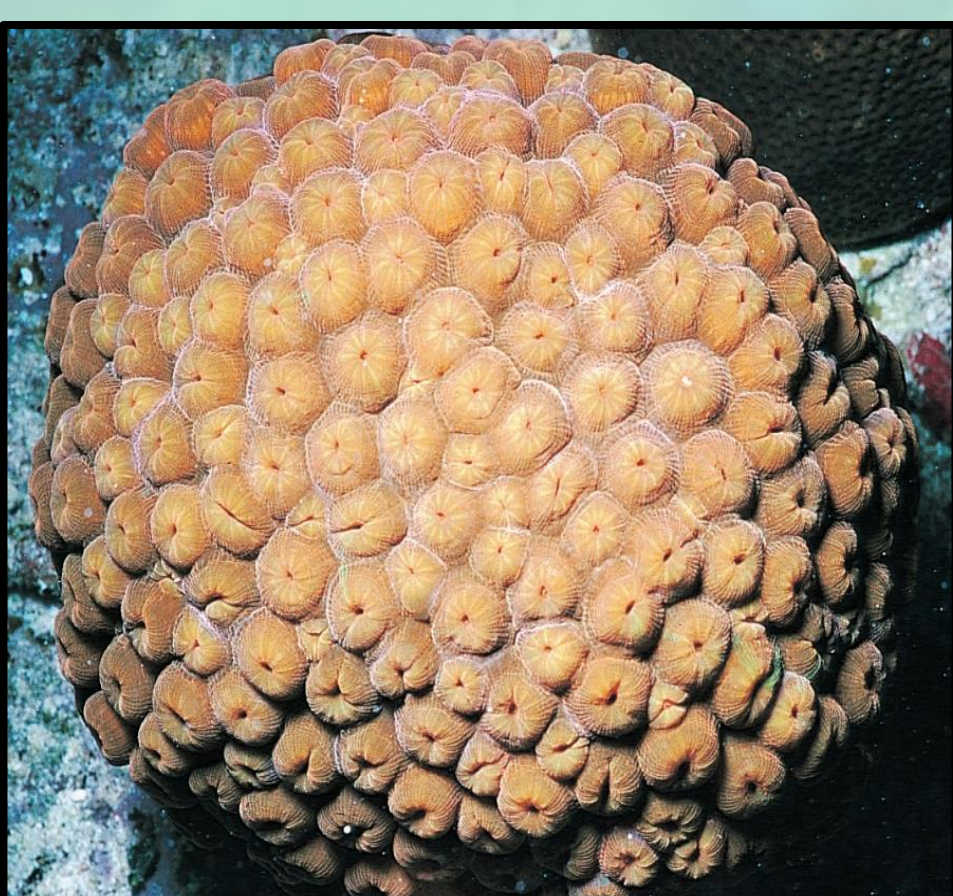
- Cuba has the largest shelf habitat in the Caribbean, supporting an estimated 3,966 km² of shallow (<30 m) and mesophotic (30–150 m) coral communities.¹
- While ongoing efforts to understand community connectivity are underway in Cuba, overall the population genetic structure of Cuba's coral communities has not been well characterized.
- Given Cuba's centrally located position and hydrodynamic regime, its hypothesized as a population source to downstream coral reefs in the U.S. A Sister Sanctuary relationship between Cuba and U.S. designed to promote effective marine resource management in both countries has been established.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

Montastraea cavernosa

- Ubiquitous coral throughout the TWA
- Extreme depth generalist³; 1–113 m
- Broadcast spawner with potential for high connectivity⁴
- Nine previously developed microsatellite loci⁵
- Available draft genome⁶
- Tissue samples collected by snorkelers (Cuba) and technical divers (BLZ, GOM) utilizing hammer and chisel and by ROV (GOM) preserved in TRIzol reagent for genetic analysis



Research Questions

- What is the population genetic structure of *M. cavernosa* among sites in Cuba?
- Is there genetic evidence of horizontal connectivity among populations across the Tropical Western Atlantic?

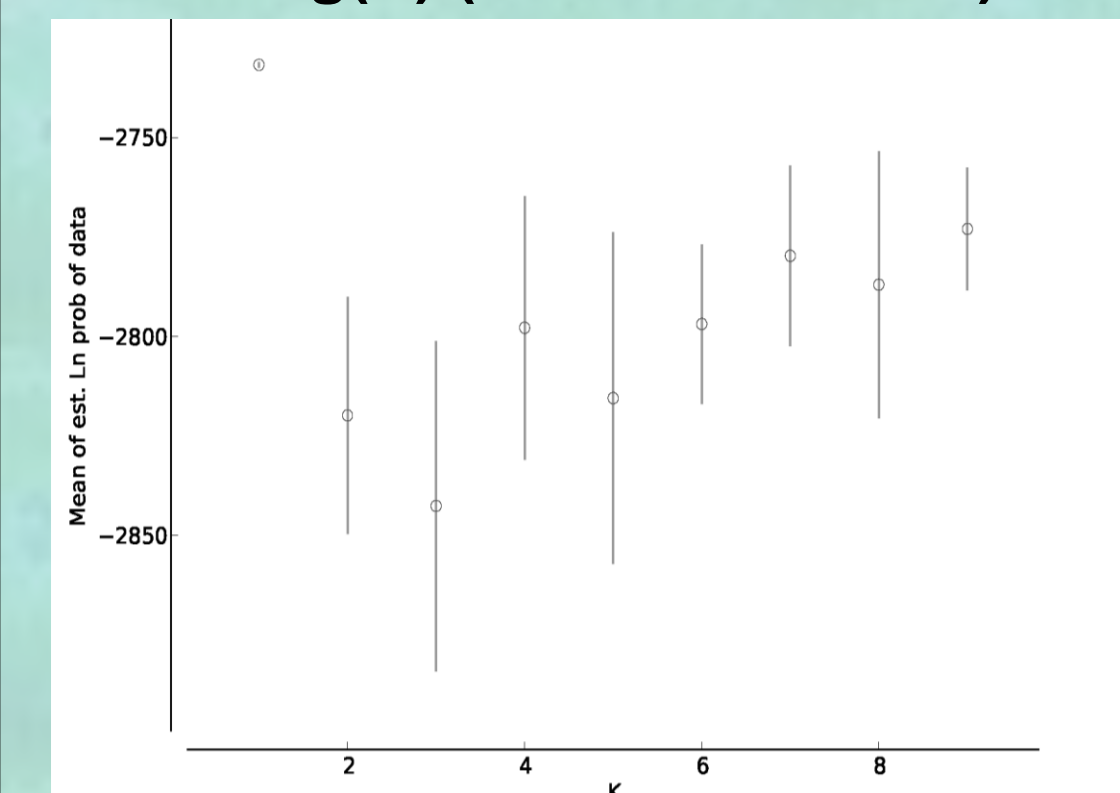
M. cavernosa Population Structure in Cuba

- 86 samples from 6 sites; 2–8 m depths
- DNA extracted via modified CTAB protocol⁷
- Amplified 9 *M. cavernosa* microsatellite loci⁵



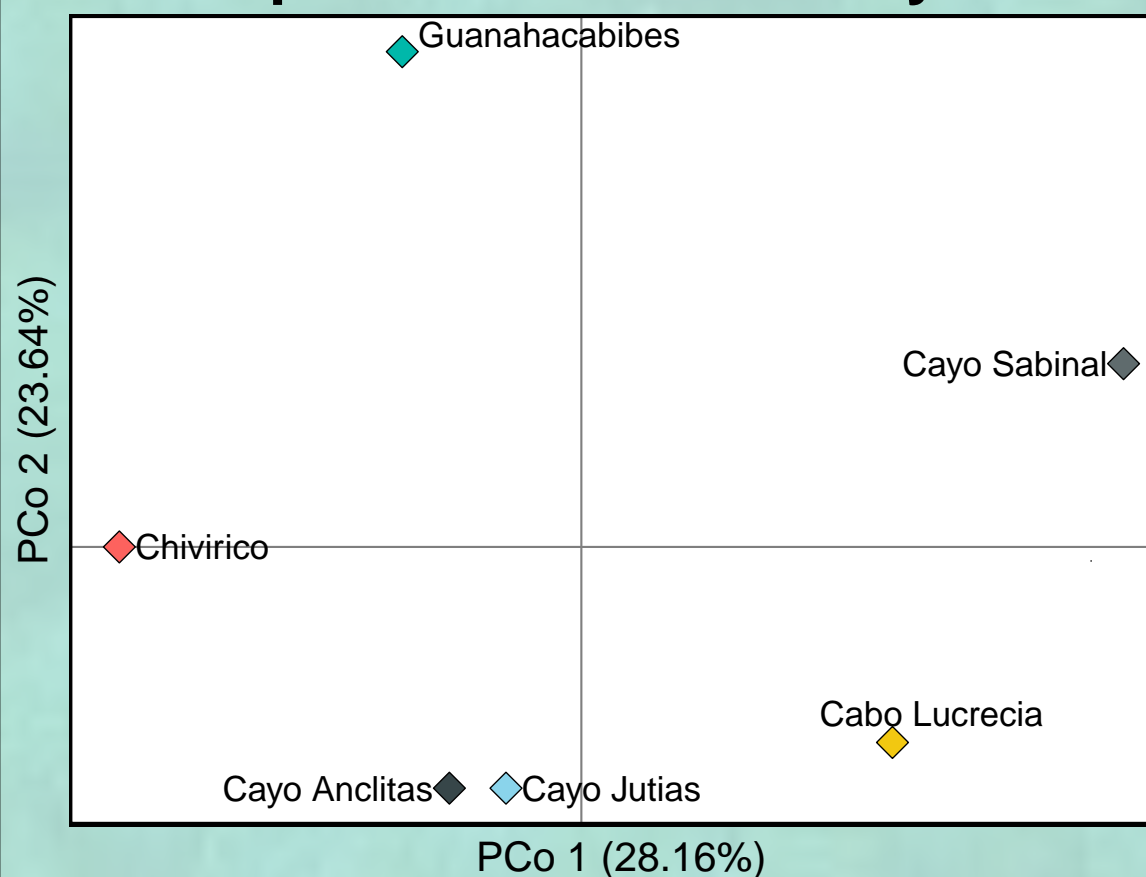
Map of the 6 Cuban populations sampled with sample size (n).
*Sites located within a Marine Protected Area

Log(K) (Mean ± Std. Dev.)



Plot of delta log likelihood values across ten replicate model simulations of historical source populations (K, ranging from 1-9) produced in the program Structure 2.3.4⁸ to estimate the most likely value of K following the Evanno method⁹.

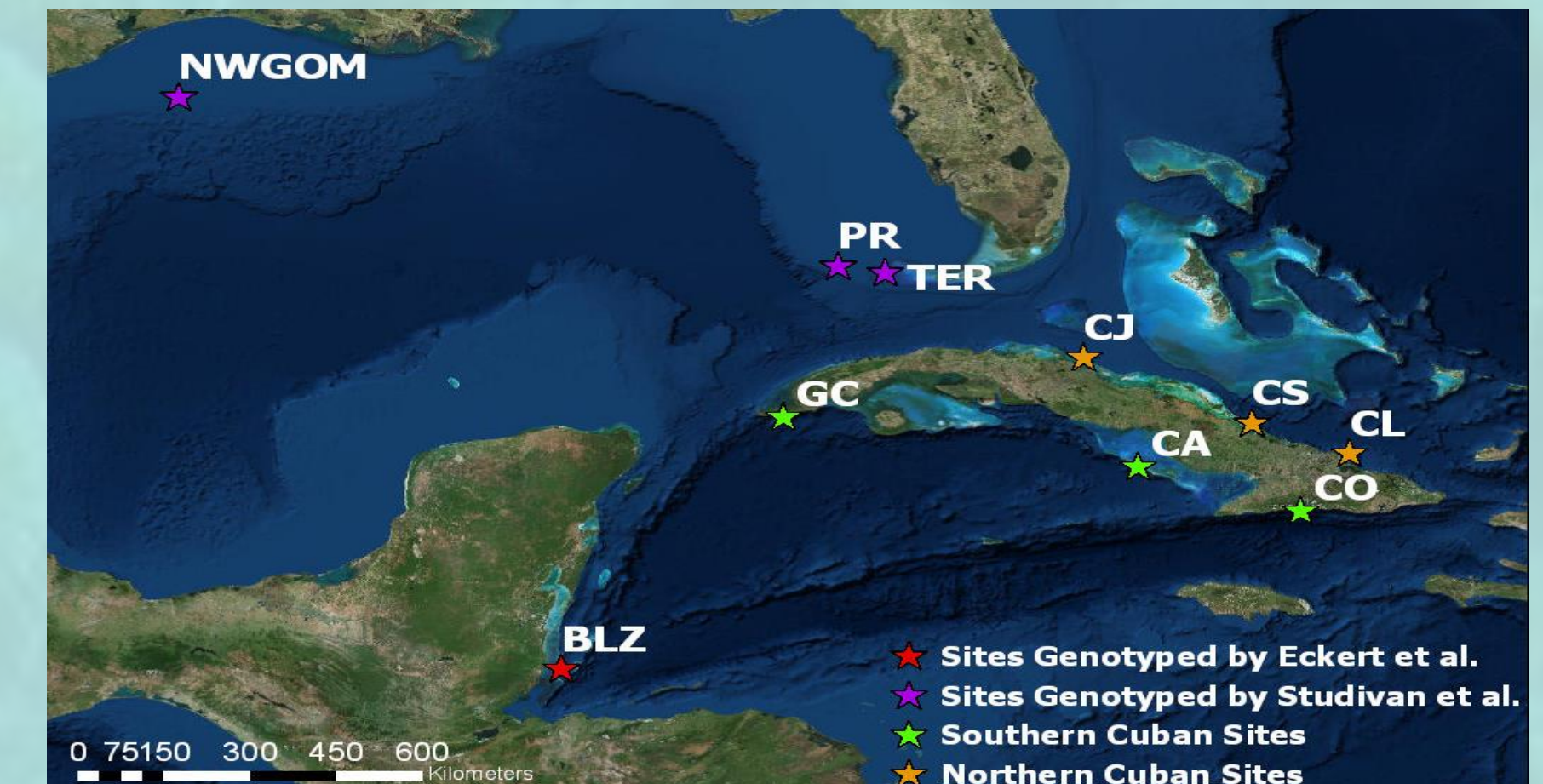
Principal Coordinates Analysis



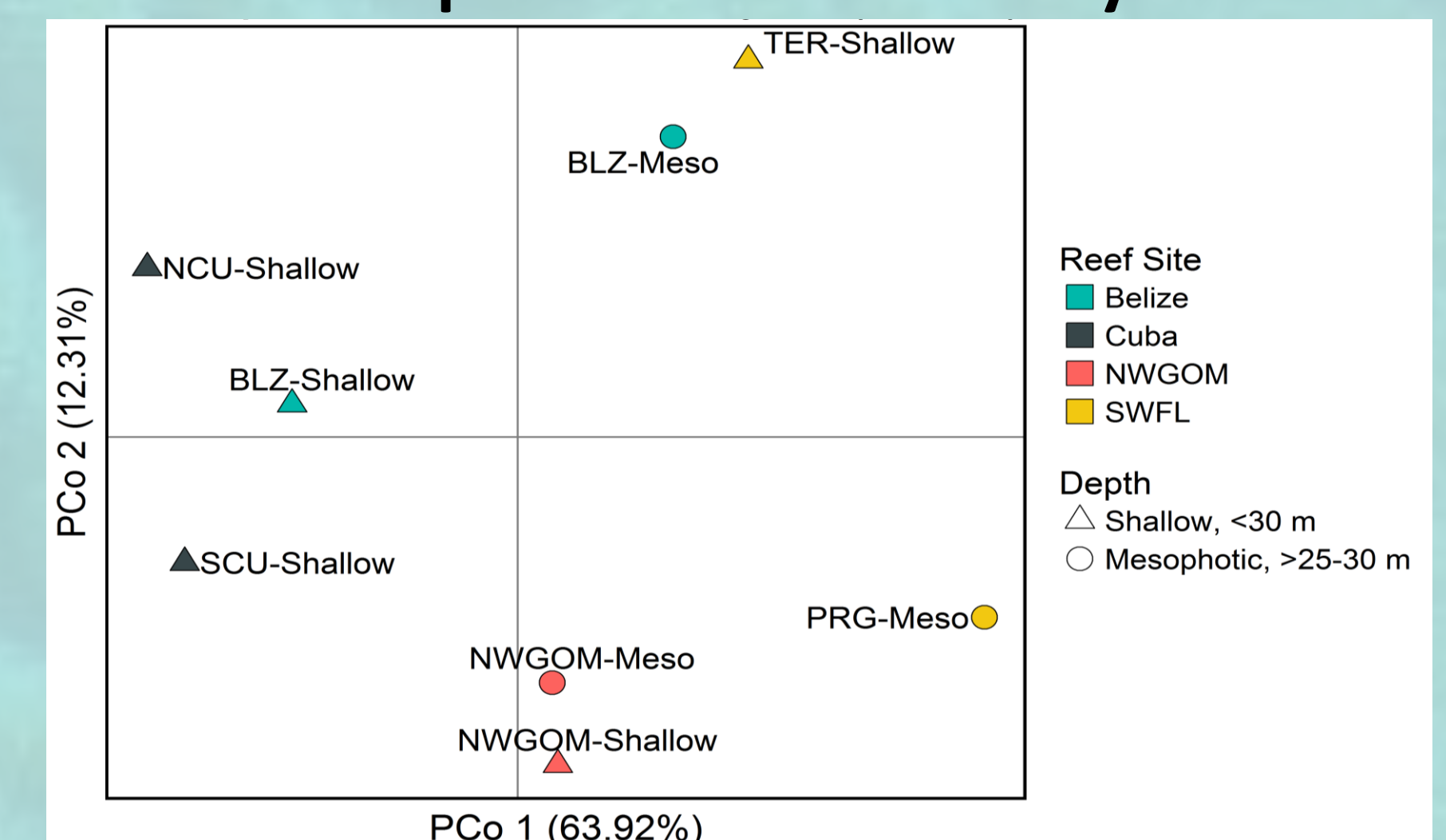
PCoA Plot based on Nei genetic distance among sites. Distance among points illustrate the degree of genetic differentiation among sites.

- An Analysis of Molecular Variance (AMOVA; 9,999 model and pairwise permutations) analysis demonstrated no significant pairwise population differentiation among the 6 sites in Cuba ($p > 0.05$)¹⁰
- Population structure analysis suggests that sites are a single panmictic population with one historical source population
- However, PCoA visualization suggests that there may be genetic differentiation among Cuban sites
- Limited samples sizes in preliminary analyses; additional samples needed to improve statistical power (i.e. $n=30$ per site)

Horizontal Connectivity Across the TWA



Principal Coordinates Analysis



	TER-Shallow	SCU-Shallow	PRG-Meso	NWGOM-Shallow	NWGOM-Meso	NCU-Shallow	BLZ-Shallow	BLZ-Meso
TER-Shallow		0.043	0.083	0.022	0.015	0.014	0.029	0.029
SCU-Shallow			0.036	0.023	0.024	0.008	0.008	0.008
PRG-Meso				0.035	0.003	0.003	0.003	0.003
NWGOM-Shallow					0.029	0.029	0.029	0.029
NWGOM-Meso						0.029	0.029	0.029
NCU-Shallow							0.029	0.029
BLZ-Shallow								0.029
BLZ-Meso								

Pairwise population differentiation heat map measured by fixation index (Fst). Differentiation level indicated by the shade of red. 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 are needed for a more robust analysis.
- M. cavernosa* populations in Cuba are most genetically similar to shallow populations in Belize and are significantly differentiated from populations at Pulley Ridge.
- Cuba may represent an important stepping stone in the dominant gene flow patterns across the TWA and among Marine Protected Areas.

Ongoing Research

- Planned Cuba technical dive mission to collect mesophotic coral samples and investigation of the vertical connectivity of *M. cavernosa* between shallow and mesophotic coral communities in Cuba
- Analysis of *M. cavernosa* algal symbionts
- SNP genotyping analysis of coral samples

Acknowledgements and Citations

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