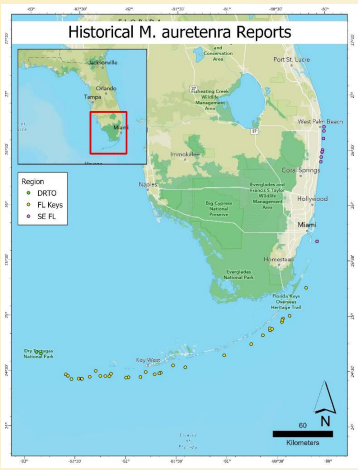
Persistence and Reproductive Potential of the Largest Known Patches of Yellow Finger Coral, *Madracis auretenra*, in an Era of Environmental Stress: Resilience or Refuge?

[1]Robert Spekis*, [1]Reagan Sharkey, [1]Hunter Noren, [2]Alicia Vollmer, [3]Sophie Cook, [4]Arthur Gleason, [1]D. Abigail Renegar, [1]Brian K Walker

[1]Nova Southeastern University [2]Florida Fish and Wildlife Conservation Commission [3]National Oceanic and Atmospheric Administration [4]University of Miami

ABSTRACT

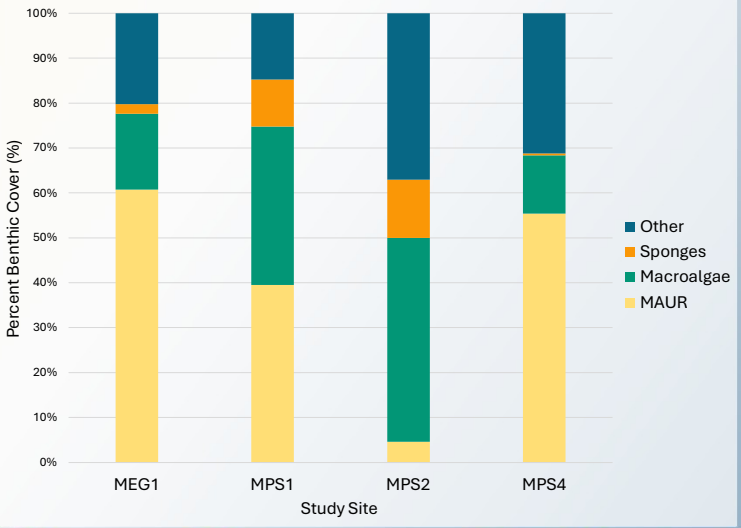
Florida's Coral Reef (FCR) has undergone extensive degradation due to warming, nutrient enrichment, and disease outbreaks. However, several large, persistent patches of Madracis auretenra in Southeast Florida have survived despite chronic stress. This project investigates whether these populations persist due to resilience (biological tolerance and reproductive potential) or refugia (protective environmental conditions). Integrating genetic (NGS) and histological analyses, this study explores connectivity, fecundity, and site conditions to understand persistence mechanisms and inform coral conservation management.



PROJECT OBJECTIVES

- **Characterize genetic diversity and connectivity** of *Madracis auretenra* across the Florida Coral Reef, identifying genotype clusters and assessing how genetic relatedness changes with geographic distance.
- **Compare fecundity among genetic clusters** to determine whether reproductive output varies between genetically distinct populations.
- **Evaluate the influence of environmental and site characteristics** on fecundity to identify potential habitat refuges or environmentally driven reproductive patterns.
- **Use structure-from-motion (SfM) 3D models** of representative patches (MPS1 and MEG1) to investigate how structural and spatial features influence coral patch health and resilience.

Benthic Composition and *M. auretenra* Cover Across Study Sites



METHODS

NEXT GENERATION SEQUENCING

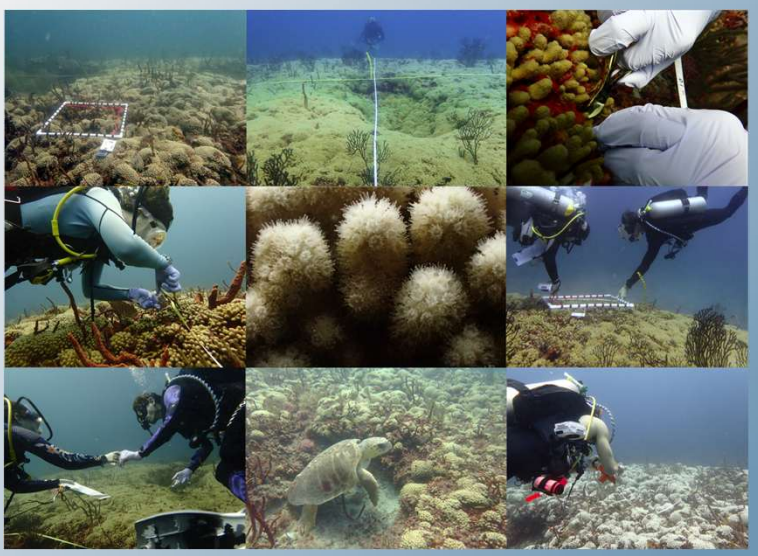
Collaboration: FWC Geneticist Alicia Vollmer (SAL-25-1702-SRP)
Sampling Sites: MPS1, MPS2, MEG1, MPS4
Collection: ~0.5 cm² branch tips clipped from M. auretenra colonies
Preservation: Stored in ethanol on ice, then at –80 °C until analysis
Dataset: 125 samples were collected combined with 62 archived samples from the Lower Keys & Dry Tortugas for full FCR coverage
Goal: Assess genetic diversity, kinship, and clone thresholds
Protocol: Genotyping-by-sequencing (GBS) following Vollmer et al., 2022

HISTOLOGY

Study Sites: MPS1, MEG1, MPS4
Design: 10 samples per site representing depth and fragmentation gradients
Timing: 120 samples were collected across 4 time points spanning the *M. auretenra* spawning season (Vermeij et al., 2004)
Collection: 3–5 cm branch tips clipped and preserved in Z-Fix buffer
Processing: Samples were trimmed to best display polyps
Staining Protocol: Heidenhain's hematoxylin (Megías et al., 2019)
Goal: Track gamete development, spawning activity, and reproductive mode

STRUCTURE-from-MOTION (SfM) 3D MODELING

Collaboration: *Dr. Arthur Gleason*, University of Miami
Sites: MPS1 & MEG1 selected as potential patches for long-term monitoring
Approach: 3D photogrammetry to reconstruct patch structure and continuity
Protocol: Methods follow Pedersen et al., 2025
Goal: Quantify structural complexity and spatial metrics linked to patch health and resilience



EXPECTED OUTCOMES

- **Quantify genetic connectivity** of *M. auretenra* along the Florida Coral Reef.
- **Identify factors linked to dense, persistent patches** to distinguish refuge vs. resilience dynamics.
- **Determine reproductive modes** (sexual vs. asexual) within dense patches through histological analysis.
- **Reveal variation in fecundity** across sites and genotypes, highlighting potential links between genetics and reproduction.
- **Inform conservation priorities** by pinpointing high-fecundity patches as potential reproductive source areas.

ACKNOWLEDGEMENTS

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