

Diversity and Distribution of Barnacles on Natural and Artificial Substrates in a Mangrove-Dominated Tidal Creek

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BACKGROUND

This study was conducted in the Biscayne Bay Coastal Wetlands, where red mangrove (*Rhizophora mangle*) roots attract larvae from multiple epibiont species. This research, which focused on one of the experimental block's tidal creeks, aimed to (1) **assess variations in the distribution of root epibionts** with distance from the tidal creek mouth, and (2) use a molecular systematic approach to **identify species of juvenile and adult barnacles** on *R. mangle* roots and artificial substrate colonization samplers (ASCs)

SUBSTRATE TYPES

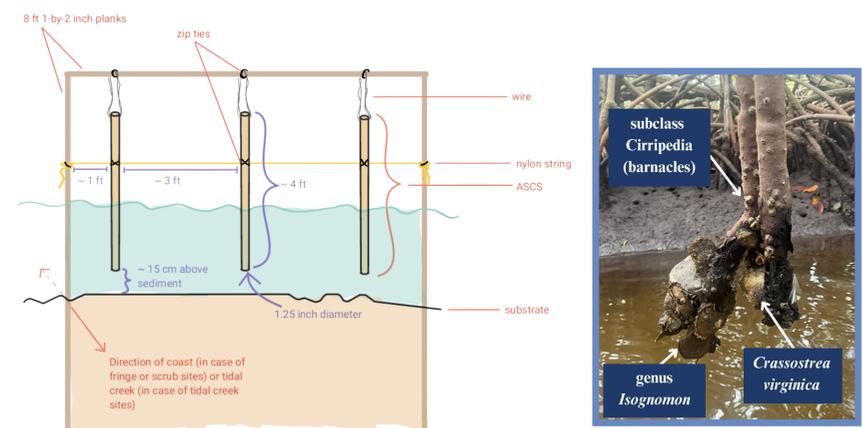


Figure 1. Artificial Substrate Colonization Sampler (ASCs) Design & Mangrove Roots. ASCs includes 3 pine dowels suspended from a frame to simulate suspended mangrove roots. Colonized mangrove roots served as natural substrate.

GENETIC METHODS

• DNA Extractions:

- Extractions performed on individual barnacles collected in the tidal creek



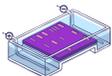
• Polymerase Chain Reaction (PCR):

- Using Folmer (1994) primers to amplify the cytochrome c oxidase I (COI) gene fragment



• Gel Electrophoresis:

- To visualize successful amplification



• Sanger Sequencing:

- Sequences produced were blasted via NCBI GenBank Database using the Blastn function



• Phylogenetic analysis:

- Matches determined with reciprocal monophyly between our sequence fragments and top GenBank matches



GENETIC RESULTS

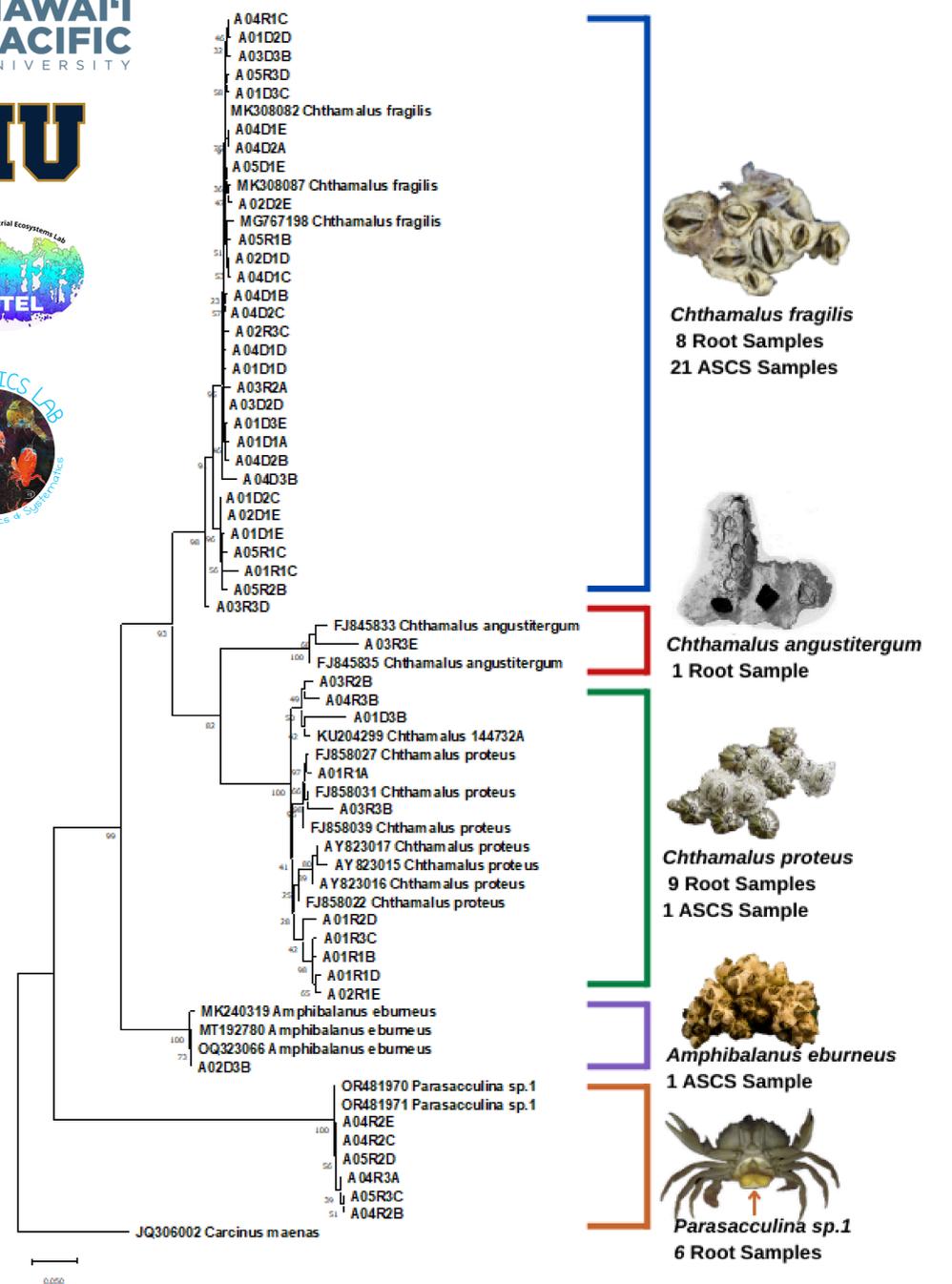


Figure 3. Phylogenetic Analysis. Tree was generated using Maximin-Likelihood and Hasegawa-Kishino-Yano model with 1000 bootstrap replicates. Sequences with species names were downloaded from GenBank. Tidal creek barnacles begin with a site number A01-A05, an indication of substrate type (R indicating root samples and D indicating ASCs samples), the replicate within the site (1-3), and the position the barnacle was collected at (A-E).

- **Roots were colonized by 4 species:** *Chthamalus fragilis*, *Chthamalus angustitergum*, *Chthamalus proteus*, and *Parasacculina sp.1*
- **ASCs were colonized by 3 species:** *Chthamalus fragilis*, *Chthamalus proteus*, and *Amphibalanus eburneus*

POPULATION METHODS & RESULTS

Presence-absence data on the tidal creek's *R. mangle* roots was recorded every 10 meters for *Crassostrea virginica* oysters, *Isognomon* oysters, Mytilidae mussels, and barnacles. After 11 weeks, ASCs were collected and **barnacle settlement was quantified.**

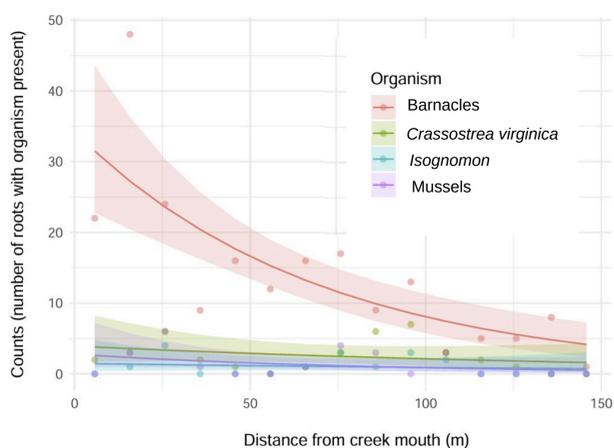


Figure 4. Site map showing approximate sampling locations. Each labeled blue diamond represents one set of three ASCs (s). Each unlabelled red circle represents one 3-meter strip where existing roots were surveyed.

Figure 5. Negative binomial GLMMs for barnacle, Mytilidae, *C. virginica* and *Isognomon* root counts. Graphed with data points, trend lines and 95% confidence intervals.

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ANALYSIS

- The presence of **4 native species** was confirmed to reside in the tidal creek: *Chthamalus fragilis*, *C. proteus*, *C. angustitergum*, and *Amphibalanus eburneus*.
- **1 invasive species**, *Parasacculina sp.1*, was also identified.
 - This species belonging to a genus of **barnacles that parasitize green crabs**, resulting in sterilization
- ASCs exhibited lower species evenness with 90% of samples identified as *Chthamalus fragilis* (20 of 22)
- Root survey results indicated that:
 - The presence of mussels from the Mytilidae family, *Crassostrea virginica* oysters, and oysters from the *Isognomon* genus did not change significantly with distance from the tidal creek mouth.
 - **Barnacle abundance decreased significantly** with distance from the tidal creek mouth: According to the above GLMM, $p = 0.001$.
- ASCs barnacle counts generally corroborated the root survey results.
- Literature indicates that barnacle settlement patterns may be a combined result of **differential mortality and settlement preferences influenced by tidal flow, current direction, and interactions with other epibionts.** (critical citations)