Smithsonian Indian River Lagoon Species Inventory: Documenting and Barcoding Benthic Infauna

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Background

The Indian River Lagoon (IRL) and St. Lucie Estuary (SLE) are undergoing considerable environmental disturbance. Infaunal monitoring is a useful indicator for tracking the effects of these disruptions on biodiversity. The Smithsonian Marine Station has been monitoring infauna in the IRL and SLE since 2005. Over 900 taxa from 16 phyla have been identified across 15 sites selected for their proximity to environmental stressors. Specimens are being photographed, preserved, and sequenced for the COI gene to create a voucher collection that will help inform management practices and increase our knowledge of cryptic biodiversity in the estuaries.

Methods

Collection:
A petite ponar was used to collect sediment grabs from 5 sites in the IRL & SLE (Fig. 1 & 5).

Identification:
Organisms were isolated and identified based on morphology.

Documenting:
Specimens were filmed and photographed, preserved in 95% ethanol, and photographed again.

DNA Extraction & Amplification:
DNA was extracted from tissue, amplified and sequenced for the COI gene (Fig. 2).

DNA Analysis:
Sequenced DNA (barcodes) were aligned and compared to the public reference database GenBank to aid in-identification and expand representation of these taxa in the database. Results will be shared on the open access IRL Species Inventory (IRLspecies.org) (Fig. 3).

Figure 1: Ponar grab being preformed pre-pandemic.

Figure 2: DNA extraction of voucher tissues.

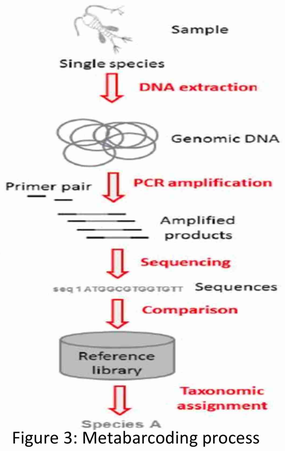

Figure 3: Metabarcoding process (Corell and Rodríguez-Ezpeleta 2014).

Figure 4: Voucher organisms top to bottom, *Prionospio* sp., *Pagurus maclaughlinae*, *Tellina* sp.

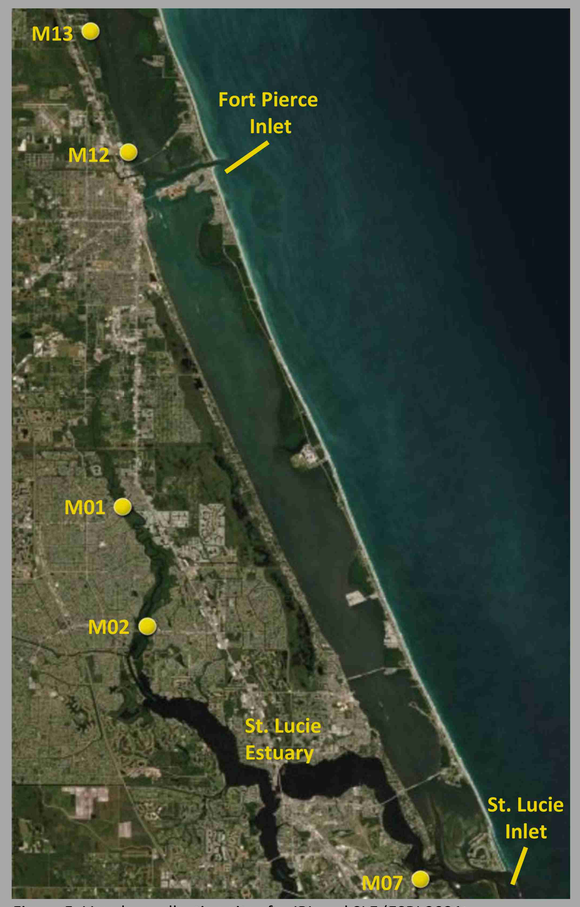

Figure 5: Voucher collection sites for IRL and SLE (ESRI 2021).

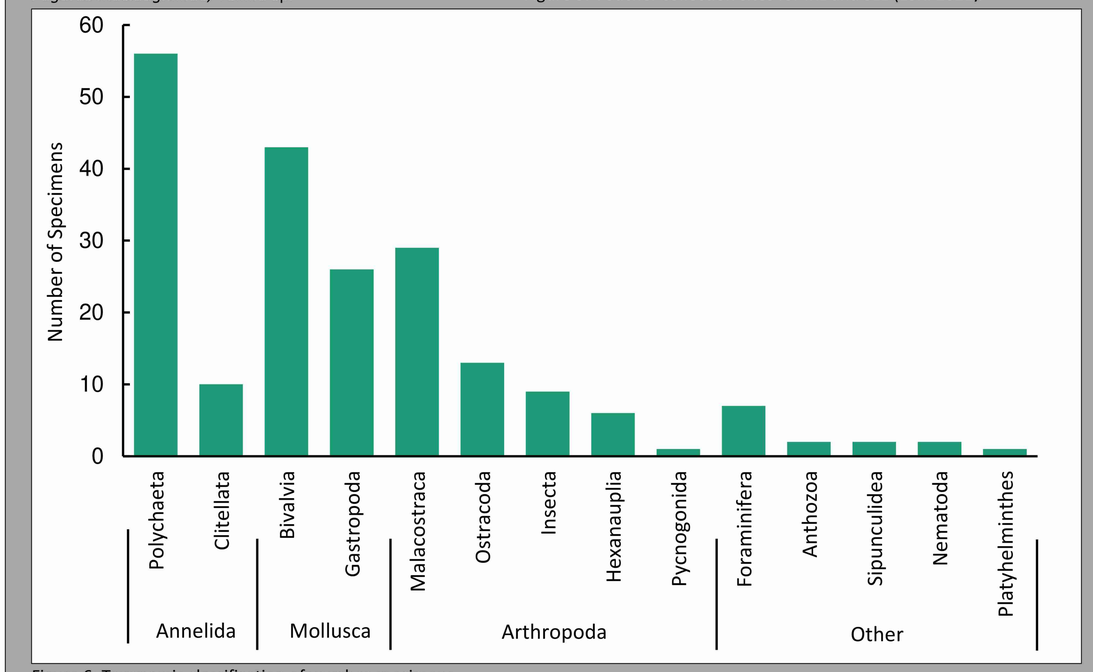

Figure 6: Taxonomic classification of voucher specimens.

Outcome & Future Expectations

Over 200 infaunal specimens were collected, containing approximately 80 taxa across 9 phyla (Fig. 6). COI sequences were compared to the GenBank; 35.6% percent were matchable to a species level (Fig. 7, dark teal) and 7.7% percent were unknown (Fig. 7, gray). This collection will strengthen the IRL Species Inventory biodiversity database and will continue to expand as more specimens are processed.

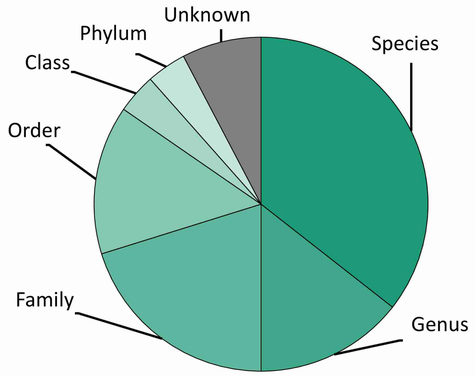

Figure 7: Percent of sequences matched to different taxonomic levels with sequences in GenBank.

Two abundant organisms, *Fabricinuda trilobata* and *Mediomastis californiensis*, have already been identified as new records for the IRLSI (Fig. 8). There will also be an initiative to sequence the genomes of key widespread and abundant species to identify genomic traits associated with tolerance to environmental stressors.

Figure 8: Voucher organisms left to right, *Fabricinuda trilobata*, *Mediomastis californiensis*.

Acknowledgements

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