Characterizing Bermuda's baitfish populations to improve management and fishery sustainability

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Introduction

- In Bermuda, small bony fishes provide food for larger fishes and water birds, but are also exploited by recreational and commercial fishers for bait. The reef silverside, dwarf herring and endemic Bermuda anchovy are presumed to be annual species, but information on their life history characteristics are poor.
- Populations of Baitfish around Bermuda have been drastically declining, but it is unclear whether that is due to changes in fishing practices or a decline population.
- This project aims to assess several aspects of an eco-system based approach, that includes **life history, genetics, abundance, and distribution**, to improve management plans and promote sustainable fishery practices.

Objectives

- To genetic barcode samples to confirm taxonomic identity down to the species level a universal fish gene, cytochrome c oxidase (COI).
- To compare differences between populations and locations across the island using population genetics analysis including genetic diversity and connectivity indices.
- To create maximum likelihood phylogenetic trees that include all focal species and species of similar genotypes.

Methods

- **Qiagen DNA Extraction Protocols** were performed on 100+ samples of 5 species from 10 locations across the island of Bermuda.
- Focal species included: *Anchoa choerostoma*, *Hypoatherina harringtonensis*, *Harengula humeralis*, *Jenkinsia lamprotaenia*, and *Sardinella spp.*
- 10 locations included: East Bay, West Bay, Bermuda Aquarium, Museum and Zoo Dock, Whalebone Bay, Bailey's Bay, Frank's Bay, Deep Bay, Coney Island, South Bay, and Turtle Bay.

Figure 1: Bermuda Aquarium, Museum and Zoo provides BIOS will samples from across the island.

Methods (Continued)

- **Standard PCR** protocols were performed to isolate and multiply a universal fish gene that is commonly used in genetic barcoding, cytochrome c oxidase (COI).
- **Gel Electrophoresis** and **Spectrophotometer** were used to visualize the final PCR product.
- Samples were sent to Genewiz for sequencing. Once returned, sequences were run in **Blast** for identification and **Sequencher** was used to align and edit each forward and reverse DNA sequence.
- **Mega** Software was used to determine genetic diversity, connectivity, and create phylogenetic trees based on 96 sample sequences.

Initial Results

- 94.79% (91/96) samples were barcoded successfully and cleaned for further analysis.
- 11% (10/91) of samples were incorrectly morphologically identified. *Jenkinsia lamprotaenia* was misidentified as *Hypoatherina harringtonensis,* and a non-target species *Opisthonema oglinum* was commonly mistaken for *Sardinella spp.* and *Harengula humeralis.*

Figure 4, 5, 6: Three morphologically similar species that were incorrectly identified before genetic barcoding. Samples labeled *H. humeralis* and *Sardinella spp.* were genetically identified as *O. oglinum*.

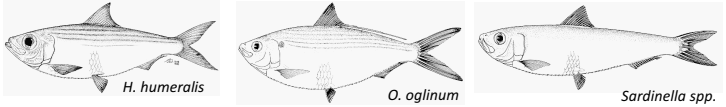


Figure 6,7: Two morphologically similar species that were incorrectly identified before genetic barcoding. Samples labeled *H. harringtonensis* were genetically identified as *J. lamprotaenia*.

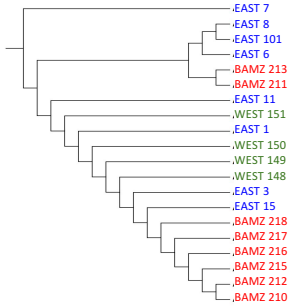
Table 1: Mean Genetic Diversity Indices

	Within Subpopulations	Entire Population
A. choerostoma	0.004	0.004
H. humeralis	n/c	n/c
J. lamprotaenia	0.002	0.002
O. oglinum	0.003	0.003
H. harringtonensis	0.001	0.001
S. longiceps	n/c	n/c

- The Mean Genetic Diversity Indices were very similarly low across all species. This could be because of the stable nature of the selected gene, cytochrome c oxidase (COI). A wider focus, specifically genes that code for characteristics or responses that are likely to be different between species, is necessary to fully assess the diversity levels between groups.

Conclusions/Future Work

Figure 8: Phylogenetic Tree of *Anchoa choerostoma* (Bermuda Anchovy; Hogmouth Fry) throughout all three locations: East Bay, West Bay, and BAMZ dock. This distributions of locations in this tree suggests there is mixing between populations, either as adults or after birth as juveniles. This pattern was seen in all six species' phylogenetic trees.



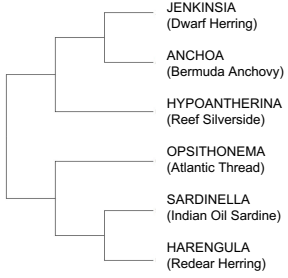


Figure 9: Phylogenetic Tree of all six focus genuses. The closer one species is to another represents how closely related the two are. The top three species are morphologically similar to each other with wider, shorter bodies. The bottom three species are morphologically similar to each other with elongated, slimmer bodies.

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