Species or Populations? Investigation of Genetic Divergence in western Atlantic Bathygobius fishes

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Introduction
- Bathygobius is a genus of gobies found in the Atlantic and Pacific Oceans.
- The genus was previously thought to comprise three western Atlantic species, but based on molecular analyses using the mitochondrial marker cytochrome c oxidase-I (CO1) and morphology, Tornabene et al. (in press) recognize six species (Fig. 1).
- CO1 also reveals two sublineages within two species, B. soporator and B. geminatus.
- The genetic divergence is intermediate between that observed as inter- and intra-specific variation in other Bathygobius species.
- Previous morphological analyses could not distinguish between sublineages.
- In both species, one sublineage is more broadly distributed (Fig. 2), but all four lineages occur sympatrically in the western Atlantic and have been collected from the same site in southeast Florida.

Methods
Labwork
- Sequenced five independent nuclear loci (four coding genes and one intron)
- Nuclear genes used in this analysis: S7, Rag1, plagl2, ptr, and SH3PX3

Data Analyses
- Used Akaike information criterion (AIC) to determine the optimal evolutionary model for each gene
- Generated five nuclear gene trees and a concatenated tree with all genes combining all genes using Paup* version 4.0

Morphology & Habitat
- Compared meristic, morphometric and pigment characters between sublineages in attempts to identify diagnostic features.
- Visited existing and explored new collecting sites in Florida to collect and photograph new specimens and to quantify small-scale differences in habitat.

Results
- The 49 new gobies collected in Florida include specimens from all four sublineages, in one case all from the same site - around two rocks 200 cm apart, 300 cm from shore and 25 cm deep (Figs. 3, 4).
- One morphological character - shape of posterior margin of genital papilla of females - distinguishes sublineages A & B of B. geminatus (Fig. 5).
- A consensus gene tree derived from parsimony analysis using all CO1 and nuclear data supports the monophyly of B. geminatus and B. soporator (Fig. 6).
- This analysis suggests two subclades within B. soporator and one within B. geminatus, results not supported by nuclear data alone.
- Nuclear data increase support for B. soporator A and B. geminatus B.

Objectives of Study
- Further investigate genetic divergence in B. soporator and B. geminatus by adding nuclear markers
- Travel to Florida to collect specimens and observe micro-habitat preferences between species and sublineages
- Seek morphological characters that distinguish the sublineages within each species

Implications and Future Research
Implications
- Molecular data suggest the possibility of recent divergence, shown by stronger resolution from mtDNA vs. slower-evolving nDNA.
- With no morphological characters separating all four sublineages, we do not formally recognize the sublineages as separate species.
- The phylogenetic breaks between B. geminatus sublineages A&B and B. soporator A&B correspond to an ecological break between tropical (Caribbean) and subtropical (Florida/Gulf of Mexico) waters, suggesting that ecology could be driving speciation.

Ideas for Future Research
- Sequence more nuclear markers, AFLPs, microsatellites
- Continue seeking morphological differences between sublineages
- Observe courtship and spawning behavior of B. geminatus and B. soporator in captivity to study interactions among sublineages
- Investigate distributions of other shorefishes in search of similar patterns of phylogenetic and ecological breaks
- Increase collecting efforts worldwide to better understand the distributions of B. geminatus and B. soporator sublineages

Acknowledgements and Literature Cited
- Thomas Heier & Lab at Yale University
- Amy Dinsel, Maggie Ragan and the Smithsonian Lab