

Genetic connectivity among populations of Bandedtail Goatfish (*Upeneus vittatus*) in Fiji

Elora H. López¹, Joshua A. Drew^{1,2}

¹Department of Ecology, Evolution and Environmental Biology, Columbia University, New York, NY, USA ²Department of Ichthyology, American Museum of Natural History, New York, NY, USA

Abstract

Genetic connectivity across populations is crucial in maintaining genetic diversity and is therefore a priority for effective conservation management. Marine reserves designed to protect and link genetically connected populations improve species resilience and can benefit local fisheries. Species' life histories, habitat fragmentation, and manmade and natural physical barriers to dispersal affect the extent of genetic connectivity or isolation across geographically distinct populations. We will assess the degree of genetic connectivity among populations of *Upeneus vittatus* (Forsk., 1775) by comparing two mitochondrial DNA (mtDNA) genes, cytochrome b (cyt-b) and mitochondrial control region (d-loop), of specimens from the reefs of five Fijian islands. The islands are separated by up to 370 km and lie in different orientations relative to the Bligh Waters, a major oceanic current of the Fijian archipelago. Here we discuss the patterns of genetic connectivity of *U. vittatus* in relation to major oceanographic features and spatial distance throughout the Fijian archipelago. These results are then placed in a conservation context. Conservation of *U. vittatus* will be critical in conserving coral reef ecosystems in Fiji, as this species is an ecosystem engineer whose food-foraging actions in benthic substrate create bioturbation and benefit the reef system's functioning as a whole. The species is also a target of commercial and subsistence fisheries in Fiji, so its conservation is economically and nutritionally important.



Figure 2. Two adult *Upeneus vittatus*. Photo by H. Scales.

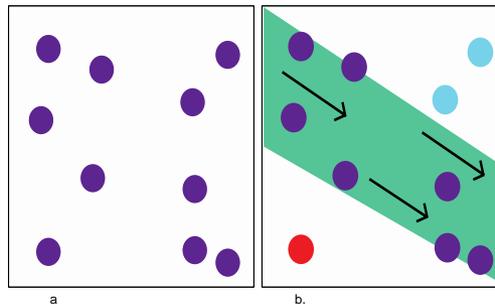


Figure 3. A comparison of genetic connectivity among a.) populations not separated by physical barriers to dispersal and b.) populations affected by a strong oceanic current, leading to differentiation between populations separated by the current (indicated in red and blue).

Thesis Statement and Hypotheses

I will study the genetic connectivity of five *Upeneus vittatus* populations in Fiji to investigate how spatial distance and the Bligh Waters relate to *U. vittatus* dispersal, and thereby inform conservation management strategies for this species. I will test the following hypotheses:

- H1a. There is no difference in genetic connectivity between populations that live on opposite sides of the Bligh Waters.
- H1b. There is less genetic connectivity between populations that lie on opposite sides of the Bligh Waters.
- H2a. There is no difference in genetic connectivity between spatially distant and close populations.
- H2b. There is less genetic connectivity between spatially distant than close populations.



Figure 1. *U. vittatus* at a Fijian fish market. Photo by E. Eastwood.

Materials and methods

We will collect *Upeneus vittatus* samples by purchase from local fish markets and by the researchers' own SCUBA spearfishing efforts. To be consistent with recommendations made by Keyse *et al.*'s (2014) meta-analysis of marine phylogeographic studies, we will collect at least 15 individuals per population. We will extract DNA and sequence two mtDNA genes, cyt-b and the d-loop. Both of these genes have demonstrated enough variability to show differences between divergent populations of the same species (Keyse *et al.*, 2014). We will calculate haplotype diversity (h); average pairwise differences (π); and the population fixation index (Φ_{st}) to determine diversity within and among the five sampled populations. Migration estimation and the relationship between spatial scale and genetic connectivity will also be calculated by using MIGRATE and an analysis of molecular variation (AMOVA) in Arlequin. We will calculate isolation by distance using IBDWS Version 3.23.



Figure 4. A map of the main islands of the Fijian archipelago, with the five sampling sites as well as the location and direction of the Bligh Waters indicated. Map data ©2014, Google.

Predictions

The fieldwork will be conducted from late June to early August of 2014. We predict that populations on the reefs of Nagigi and Taveuni will be highly connected to each other due to their geographic proximity. We expect there to be some divergence between populations in Nagigi and Taveuni and the one in Suva because it may be difficult for larvae to move perpendicular to the direction of the Bligh Waters, though Drew & Barber (2012) did not find that current to be a barrier to dispersal for other fishes. The Yasawa population may be divergent because of its spatial distance from the other sites, but it is also downstream from Taveuni, so it is possible that larvae spawned in Taveuni could end up on reefs in Yasawa as adolescents. The Lau population may be the most isolated due to its distance from the other reefs.

Implications

The results of this study will be presented to the Fiji Locally Managed Marine Area (FLMMA) network, a group of marine conservation practitioners that works to preserve biodiversity and improve fishery resources on Fiji's reefs. Management suggestions will be made based on the patterns of connectivity or divergence found through this study. This study will also fit into the broader framework of increasing the base of phylogeographic research done on marine taxa in the Pacific Ocean. Currently there is a lack of consistency of connectivity patterns among closely related taxa, even when measured across similar seascape barriers. By increasing the number of taxa and geographic regions represented in the phylogeographic literature, we can help to resolve, elucidate, or explain some of the idiosyncrasies present in the current literature. In doing so, we can better understand the biological and physical causes of specific genetic connectivity patterns.

Literature Cited

- Drew, J.A., and Barber, P.H. (2012). Comparative phylogeography in Fijian coral reef fishes: a multi-taxa approach towards marine reserve design. *PLoS ONE* 7(10):e47710.doi:10.1371/journal.pone.0047710
- Keyse, J., Crandall, E.D., Toonen, R.J., Meyer, C.P., Trembl, E.A., Riginos, C. (2014). The scope of published population genetic data for Indo-Pacific marine fauna and future research opportunities in the region. *Bulletin of Marine Science* 90(1):47-78.

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For further information

Please contact ehl2130@columbia.edu. More information on this and related projects can be obtained at www.labroides.org. The authors can be found on Twitter via @EloraHL and @Drew_Lab