Phylogeography of an iconic sportfish, the Giant Trevally (*Caranx ignobilis*), and implications for fisheries management

J. Glass, P. Cowley, T. Near
Yale University, United States and South African Institute for Aquatic Biodiversity, South Africa
South African Institute for Aquatic Biodiversity, South Africa
Yale University, United States
jessica.glass@yale.edu

The Giant Trevally (*Caranx ignobilis*) inhabits the Indo-West-Pacific and is a top predator associated with rocky and coral reefs. *Caranx ignobilis* is coveted by recreational fishermen and heavily targeted by small-scale and commercial fisheries throughout its range. Despite its trophic role and economic importance, only one study thus far has investigated the population genetic structure of *C. ignobilis*, and sampling was limited to the Hawaiian Islands, where overfishing has previously occurred. Consequently, we are investigating the contemporary and historical genetic structure of *C. ignobilis* across the full extent of its range. An analysis of the mitochondrial gene cytochrome-b for 123 specimens of *C. ignobilis* revealed subtle evidence of geographic structure between the western Indian and western Pacific Oceans. To tease apart finer-scale differences amongst sampling localities, we conducted analyses using double digest restriction enzyme-associated DNA sequencing (ddRADseq) for 30 individuals from Seychelles, Saudi Arabia, Australia, and South Africa. We recovered a mean of 64,908 loci for each sample after filtering, and extracted 213,900 single-nucleotide polymorphisms (SNPs). Results indicate genetic mixing in the western Indian Ocean, with a separate Australian population. Our observed homogeneity across the Western Indian Ocean is interesting in light of recent acoustic tagging studies that indicate a high level of territoriality, which would presumably result in geographic structure of genetic variation. Future research will incorporate samples from additional locations throughout the Indo-Pacific, with the objectives of identifying potential phylogeographic breaks, population bottleneck and/or expansion events, and modeling the direction and magnitude of gene flow. Understanding the population structure of *C. ignobilis* is essential for the sustainable management of this understudied species in the Indian and Pacific Oceans.