

Genomics reveals fine-scale Patterns of Dispersal for a Reef Fish along the ecologically significant Coast of Northwestern Australia

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An important ecological driver underpinning coastal marine management is dispersal, but it has proven difficult to directly measure in this setting. The coast of Northwestern Australia provides an emerging frontier for implementing new genomic tools, which allows testing of dispersal under a management framework given its diverse and extreme environmental conditions. This study focuses on the Stripey Snapper (*Lutjanus carponotatus*), which is important to recreational, charter-based, and customary fishers in coastal waters throughout the Indo-West Pacific. We collected 1016 *L. carponotatus* samples at 51 locations in coastal Australia ranging from the Northern Territory in the northeast to Shark Bay in the southwest and adopted a genotype-by-sequencing approach to test the influences of extreme gradients in coastal hydrodynamics on realized connectivity via larval dispersal. Hydrodynamic simulations using Connie provided a null model for comparison. Based on 4,402 polymorphic Single Nucleotide Polymorphism (SNP) loci shared across all individuals we demonstrated significant genetic sub-division illustrated in pairwise F_{st} and STRUCTURE plots between the Shark Bay Bioregion in the south and all locations within the five more northern bioregions. More importantly, we identified a genetic 'transition zone' of retention less than 80 km across the tip of the Dampier Peninsula in the south of the Kimberley Bioregion, which experiences the largest tropical tidal range and some of the fastest tidal currents in the world. These results will be discussed in the context of long term conservation management initiatives of the unique marine environment in Northwestern Australia.



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