

Fine-scale population structure and local adaptation despite high population connectivity in a marine teleost (*Chrysophrys auratus*)

Tom Oosting¹, Bastiaan Star², Maren Wellenreuther³, and Peter Ritchie¹

¹Victoria University of Wellington

²Oslo University

³New Zealand Institute for Plant and Food Research Ltd

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Abstract

Accelerated climate change is forcing species to adapt at unprecedented rates, but molecular mechanisms of how wild marine species adapt remain unclear. Here we use the marine teleost *Chrysophrys auratus* (Australasian snapper) as an exemplar high gene flow species to evaluate its ability to adapt to environmental pressures. Despite its commercial and cultural value in New Zealand, no detailed genomic analyses of its population structure have been performed. Using whole-genome sequencing of 382 individuals across 13 locations covering the New Zealand species range, we uncovered two distinct genetic clusters, a northeastern (NE-cluster) and a southwestern (SW-cluster) group, separated by distinct genetic discontinuities around Tauroa and Mahia Peninsulas. PCA, F_{ST} and admixture analyses clearly supported this split, revealing strong ancestry shifts at these geographic breaks, and areas around the genetic discontinuities where mixing of individuals from both clusters is occurring. Despite this high gene flow, we found compelling evidence of local adaptation in 38 significantly differentiated genomic regions. Two regions showed strong signs of a recent or ongoing selective sweep, each containing candidate genes linked to growth rate. For both regions, the NE-cluster exhibited directional selection, while the environmentally heterogeneous SW-cluster showed signatures of balancing selection. These patterns highlight the nuanced interplay between population connectivity, selection, and local environments and highlights the need to monitor both standing and adaptive genetic variation. As climate change accelerates, managing adaptive variation in marine teleosts like snapper will be critical to maintaining their resilience and sustainability under intensifying environmental pressures.

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