RNA-Seq Investigation of Transgenerational Acclimation to Thermal Stress in Coral Reef Fish

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If climate change persists, ocean warming and acidification will have catastrophic effects on coral reefs and marine biodiversity in the next 100 years. However, marine and coral biodiversity may be conserved through evolution or transgenerational acclimation. This project uses RNA sequencing (RNA-Seq) in a multi-generation two-population experiment for the first time to study acclimation genotypes and phenotypes. It was hypothesized that various genes would be differentially-expressed at various experimental variables, and that expression matrices would cluster by population. RNA reads were analyzed using an RNA-Seq pipeline. The sequencing data was obtained from two Acanthochromis polyacanthus populations originating in The Great Barrier Reef, Australia. Samples were treated with +1.5°C at the (F1,2) generations, with liver RNA extraction (13 samples w/replicates). The pipeline mainly comprised of short-read trimming, TopHat2 reference alignment, and DESeq2 differential-expression analysis. Differential-expression was observed in (F1P1) with cytoskeleton growth genes, and in (F2P2) with rRNA genes and genes of unknown function (10 total genes). All differential-expressions exhibited q-values<0.05. Additionally, distance matrices assembled by population, with principal component analyses (PCAs) showing no sub-population clusters (34% variance). It was concluded that differential-expression in (F1P1) was to optimize oxygen-delivery systems as a response to thermal stress, a trait that is passed to offspring. Distance matrices and PCAs suggest that acclimation catalyzes long-term effects. Characterizing acclimation pathways will help in understanding how certain organisms retain habitual biological functionality and reproduction in intolerable environments.

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