

# Cryptic genetic adaptation despite high gene flow in a range-expanding population

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March 12, 2024

## Abstract

Signals of natural selection can be quickly eroded in high gene-flow systems, severely challenging efforts to understand how and when genetic adaptation occurs in the ocean. This long-standing, unresolved topic in ecology has renewed importance because rapidly changing environmental conditions are driving range expansions that, in many cases, necessitate rapid evolutionary responses. To test for genetic adaptation in a coastal marine species with high dispersal potential, we performed a series of crosses on Kellet's whelk (*Kelletia kelletii*) collected from its historical and recently colonized range, and conducted RNA-Seq on offspring that we reared in a common garden environment. We identified 2,770 differentially expressed genes between 54 samples with historical-range and expanded-range ancestry. Using SNPs called directly from the differentially expressed genes, we revealed parental population structure that enabled us to assign "unknown" samples back to their range of origin with unprecedented accuracy for a marine species (92.6 to 94.5%). The SNP with the highest predictive importance occurred on triosephosphate isomerase (TPI), an essential enzyme for glycolysis and glucogenesis, which also plays a role in cold stress response. TPI is both highly upregulated and contains a non-synonymous mutation in the expanded range, where ocean temperatures are colder than in the historical range. Our findings pave the way for accurately identifying patterns of dispersal, gene flow, and population connectivity in the ocean by demonstrating that rapid genetic adaptation can occur even in high gene flow species and that experimental transcriptomics can reveal mechanisms for how marine organisms respond to changing environmental conditions.

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