

## **EVOLUTIONARY PATTERNS OF ADAPTIVE GENE EXPRESSION IN MARINE AND FRESHWATER DIATOMS**

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Understanding how species colonize and diversify in new environments, including whether independent environmental transitions require the same genetic changes, are central questions in evolutionary biology. Gene expression variation is one of the mechanisms utilized by organisms to cope with highly variable environmental factors, such as temperature or salinity. Diatoms are common in both marine and freshwater habitats, a pattern resulting from many independent transitions across the salinity barrier. A number of such transitions are found in the order Thalassiosirales, a diverse group of centric diatoms that occurs in the full range of naturally occurring salinities. We want to determine what role gene expression played in these transitions and which genes facilitated them. We will measure and compare variation of gene expression in taxa across the lineage to reconstruct ancestral patterns of gene expression. Analysis of these data will reveal whether variation in expression levels is the result of natural selection or neutral drift. A total of 40 species, sampled across Thalassiosirales, will be grown across a range of salinities in a laboratory common garden experiment to characterize reaction norms indicative of salinity generalists and specialists. Transcriptome sequencing will allow us to reconstruct patterns of natural selection on gene expression and identify candidate genes involved in adaptation to low salinity. Successful colonists of novel salinity environments must first mitigate the stressors imposed by the new environment, so another set of experiments will characterize patterns of short-term (10 minutes to 48 hours) gene expression in response to exposure to a new, non-native salinity.