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Saito Lab Marine Bioinorganic Chemistry: Proteomics of Colimitation in Diatoms

Collaborators

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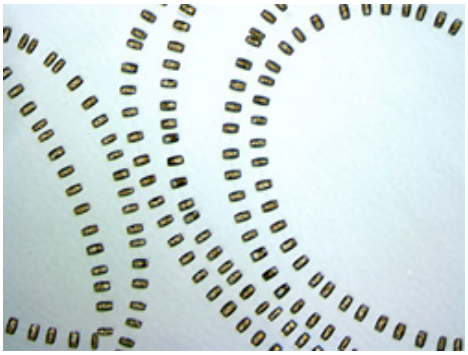

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The marine diatom Thalassiosira rotula. (Tatiana Rynearson)

PROJECT SUMMARY

Diatoms are an abundant and widespread functional group of phytoplankton, responsible for significant amounts of primary production in the ocean. As such, they exert a profound influence on the global cycling of carbon. In recognition of this significance, the diatom *Thalassiosira pseudonana* was the first eukaryotic marine phytoplankton model selected for whole genome sequencing by the DOE JGI. The annotated genome of this model diatom highlighted unexpected aspects of *T. pseudonana* metabolism (e.g. a mosaic of pathways derived from plant and animal ancestors), and emphasized that despite their importance, there are fundamental gaps in our understanding of diatom physiology and how these organisms function in the sea.

The supply of micronutrients (e.g. Fe) and macronutrients (e.g. P) are considered to be primary drivers of diatom biomass in many marine systems. In fact, models predict there are large regions of both the Atlantic and the Pacific where diatoms are limited by Fe or P. The proposed research will use transcriptional and proteomic profiling to examine the underlying molecular mechanisms involved in the response of marine diatoms to Fe and P limitation. Since multiple factors can be limiting for growth in the environment, we are also proposing experiments to dissect the impact of nutrient co-limitation on marine diatoms with a molecular test of Liebig's Law. This genome-enabled work will first be pursued with *T. pseudonana* using long-serial analysis of gene expression (Long-SAGE) for the transcriptome profiling and advanced mass spectrometry for the proteome profiling, with the closed *T. pseudonana* genome as a frame-work for gene discovery and annotation. We will then apply these methods to understand how nutrient limitation impacts another ecologically important, unsequenced diatom species, *T. rotula*. This will work will result in the following benefits and outcomes; 1) Characterize P and Fe metabolism and stress responses in two species, 2) Determine if gene expression patterns are consistent with the proteome observations, 3) Examine heterogeneity in the P-limitation response between *T. pseudonana* and *T. rotula*, 4) Test Type I – Minimum form versus the Type I – Multiplicative form co-limitation, and 5) Address the utility of the *T. pseudonana* genome for genome-enabled work in other diatom species. In summary, this approach will address key gaps in our understanding of diatom physiological ecology.

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