Thursday, September 27, 2018
2:00-2:30 p.m.

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Compartmentalized metabolic networks in a model photosynthetic eukaryotic microbe

Diatoms are unicellular photosynthetic protists in the Stramenopile lineage. Evolutionarily derived from serial endosymbiotic events between Eukaryotes, diatom genomes and metabolism are a mosaic unique relative to other model systems. Diatoms possess certain metabolic pathways that are anomalous for phototrophs, such as a urea cycle, mitochondrially-targeted glycolysis pathway, and a chloroplast ornithine biosynthetic pathway, but their biological roles are largely unknown. Using phylogenetic, functional genomics, and systems biology approaches, we have investigated the origin and significance of these pathways in diatoms. Additionally, we have generated key new insights into long standing enigmas in diatom biology related to iron acquisition and biosynthesis of the potent neurotoxin domoic acid (DA). New data suggest that diatoms utilize distinct pathways for assimilation of different forms of dissolved iron including uncomplexed inorganic ferric iron, organically complexed iron and highly transient ferrous iron. These data also suggest that carbonate ions are required for activity of the ferric iron assimilation system, suggesting that ocean acidification might affect iron uptake and the relative contribution of distinct iron acquisition pathways. We have also recently identified the DA biosynthesis (*dab*) genes in the harmful algal bloom (HAB) diatom *Pseudo-nitzschia multiseries*. We have successfully characterized the encoded enzyme activities using heterologous expression in *Escherichia coli* and *Saccharomyces cerevisiae*. The biosynthetic pathway for DA is predicted to involve several subcellular compartments, including the diatom chloroplast. Using molecular genetics, we have initiated efforts to reprogram the model diatom *Phaeodactylum tricornutum* to produce DA biosynthetic intermediates and further investigate subcellular localization of Dab enzymes. Strategies and progress to date related to this synthetic biology-driven approach to fully reconstitute DA biosynthesis in a heterologous host will be discussed.