Modeling carbon metabolism of the diatom *Phaeodactylum tricornutum* during nitrogen starvation and during high light and low light conditions

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Pt has the ability to store up to 45% of dry cell weight as triacylglycerol (TAG), a neutral lipid and precursor to biodiesel[1]. To take advantage of this innate ability, we need to understand how metabolic pathways adjust to changing environmental conditions. The goal of the project is to promote efficient production of high-value and fuel-related compounds through optimization of metabolic fluxes in the diatom *Phaeodactylum tricornutum* (Pt), a model photosynthetic eukaryotic microbe. Our lab focuses on using ^{13}C metabolic flux analysis (MFA) to understand changes in metabolism by generating a quantitative flux map of the metabolic reaction network.[2,3] To create the flux map, we use experimental measurements of growth, product formation, and stable isotope labeling to constrain a model of central carbon metabolism. We developed a model of Pt based on genomic annotations and incorporated subcellular compartments to reflect the organization of central carbon metabolism within the cell. We combined our model with experimental isotope labeling studies to elucidate the metabolism of Pt under conditions relevant for biomanufacturing.

Our current focus is to investigate metabolic adjustments to variations in light and nitrogen availability, two variables which strongly impact Pt growth and lipid accumulation. Under low light growth conditions (60μE), we observed significantly higher chlorophyll content compared to the chlorophyll content at high light growth conditions (250μE). We also unearthed dramatic shifts in metabolic fluxes and pool sizes in Pt under nitrogen-limiting conditions. Particularly, most of the TCA cycle metabolite pool sizes were elevated while pool sizes of most nitrogen-containing metabolites, except urea, decreased significantly. Our near-term goal is to use ^{13}C MFA to understand how Pt metabolism adapts to various environmental conditions that are essential for maximizing TAG biosynthesis.

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2 Jazmin, L.J. et al. Isotopically nonstationary ^{13}C flux analysis of cyanobacterial isoburyaldehyde production. *Metabolic Engineering* **42**, 9-18, https://doi.org/10.1016/j.ymben.2017.05.001 (2017)

3 Ma, F. et al. Isotopically nonstationary ^{13}C flux analysis of changes in Arabidopsis thaliana leaf metabolism due to high light acclimation. *Proc Natl Acad Sci U S A.* **111**(47), 16967-16972, doi: 10.1073/pnas.131948511 (2014)