Modeling carbon metabolism of the diatom *Phaeodactylum tricornutum*

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Phaeodactylum tricornutum (Pt), a unicellular diatom species, has the ability to store up to 45% of dry cell weight as triacylglycerol (TAG), a precursor to biodiesel [1]. To take advantage of this innate ability, we need to understand the metabolic pathways that supply the substrates needed to synthesize TAG.

Our lab focuses on using ^{13}C metabolic flux analysis (MFA) to map the central metabolism of numerous autotrophic systems, such as plants and cyanobacteria, using $^{13}CO_2$ labeling experiments [2,3]. In this project, we are developing a detailed metabolic model that describes the primary metabolism of Pt and encompasses precursors necessary for TAG biosynthesis. In addition, we are adapting our analytical methods (GC-MS and LC-MS/MS) to obtain the measurements needed to perform MFA in Pt under photoautotrophic conditions.

This presentation will discuss the construction, testing, and validation of an initial network model as well as optimal experiment design to maximize pathway resolution and flux precision. Our long term goal is to develop a ^{13}C MFA pipeline that would be integral for guiding rational metabolic engineering to optimize TAG production in Pt.

(Supported by grant *DE-SC0018344: Design, Synthesis, and Validation: Genome Scale Optimization of Energy Flux through Compartmentalized Metabolic Networks in a Model Photosynthetic Eukaryotic Microbe* from the Department of Energy.)

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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)