Temporal profiles unravel resource allocation mechanisms under nitrogen starvation in the diatom *Phaeodactylum tricornutum*

Juan D. Tibocha-Bonilla[1], Cristal Zuniga[1*] (crzuniga@eng.ucsd.edu), **Andrew E. Allen[2]**, and **Karsten Zengler[1]**

[1]University of California, San Diego; [2]J. Craig Venter Institute, San Diego

The goal of this project is to gain new insights into the photosynthetic eukaryote *Phaeodactylum tricornutum* for bioenergy production using a systems biology approach. We integrated time-course target metabolomics data into a metabolic modeling framework to systematically identify and quantify the partitioning of carbon and nitrogen between cellular metabolism, cross-talk between organelles, and channeling of photosynthetic electron flows.

Diverse conditions, i.e. growth during day and night, and compartmental cellular organization require phototrophs to shift their proteome demands and therefore adjust their metabolism and biomass composition during the course of growth. This complex interplay between energy and carbon metabolism and its dynamics in phototrophs is still not fully understood. Constraint-based modeling is a systems biology tool that contextualizes experimental data, such as uptake rates and biomass composition, for successful prediction of growth phenotypes. Currently, the lack of time-course biomass composition data has restricted prediction accuracy. Instead of recapitulating dynamic changes in cell composition, current models are forced to assume that the biomass remains constant. Here, we used experimentally determined metabolomics data to determine biomass composition constrains. Dynamic constraints were applied to our previously published genome-scale metabolic model of the diatom *P. tricornutum*[1]. We identified temporal profiles of metabolic fluxes that indicate long-term trends in pathways and organelle-specific activities in response to nitrogen depletion. Additionally, a growth rate sensitivity analysis of time-course flux distributions enabled identifying the main metabolite affecting growth (e.g. amino acids and lipids). Surprisingly, our dynamic simulations hinted at free energy instead of the molecular weight as the main drivers of biosynthetic cost. Our *P. tricornutum* temporal-flux-profiles will be used to enlarge the number of gene associations in the model by scanning dynamic transcriptomics data sets and by evaluating hidden metabolic and transport activities using our in-house developed tools[2].

References

1. Levering, J. *et al.* Genome-scale model reveals metabolic basis of biomass partitioning in a model diatom. *PLoS One* **11,** 1–22 (2016).

2. Zuñiga, C. *et al.* Predicting dynamic metabolic demands in the photosynthetic eukaryote *Chlorella vulgaris*. *Plant Physiol.* **176,** 450–462 (2018).