4th International Symposium on
Energy Challenges & Mechanics
- working on small scales

11-13 August 2015
Aberdeen, Scotland, UK

Computational approaches and metabolic network reconstructions of *Chlamydomans Reinhardtii* in the quest for biofuel optimization.

Joseph Koussa[1*], Amphun Chaiboonchoe[1], Bushra Dohai[1], Ashish Jaiswal[1] and Kourosh Salehi-Ashtiani[1#]

[1] *Division of Science and Math, New York University Abu Dhabi and Center for Genomics and Systems Biology (CGSB), New York University Abu Dhabi Institute, Abu Dhabi, UAE*

Accepted for publication on 16th April 2015

The increased demand and consumption of fossil fuels have raised interest in finding renewable energy resources throughout the globe. Much focus has been placed on optimizing microorganisms, and primarily microalgae, to efficiently produce compounds that can substitute for fossil fuels. However, the path to achieving economical feasibility is likely to require strain optimization through using available tools and technologies in the fields of systems and synthetic biology. Such approaches invoke a deep understanding of the metabolic networks of the organisms and their genomic and proteomic profiles. Metabolic network reconstructions represent one major milestone in such a quest for biofuel production optimization. Several tools are available and allow such reconstructions most importantly the COBRA toolbox and Pathway-tools. A comprehensive metabolic network, reconstructed and curated, sets forth a major resource allowing for a targeted investigation of the metabolism in the organism of interest. Flux Balance Analysis (FBA) builds on the reconstructed network offering a model with predictive power and subsequently, high accuracy simulations of targeted gene knockouts and pathway optimization endeavors. Herein, we describe our latest effort in the reconstruction of a genome-scale metabolic model for the alga *Chlamydomonas reinhardtii*, a choice stemming from a worldwide interest in the development of algal-based biofuels, using diverse experimental and computational platforms to obtain functional FBA models for this species. Using this model, we define condition-specific sets of genetic synthetic interactions. Even further, we detail topological and functional network analyses to investigate the interplay between gene function and phylogenetic affinities. The results suggest that the metabolic network of *C. reinhardtii* is assembled with an architecture to minimize phylogenetic profile distances topologically, while it includes an expansion of such distances for functionally interacting genes. Such findings give more insight into the specific metabolic network arrangement providing guidance to downstream applications and gene targeting approaches. All of these datasets, together with advances in molecular biology tools and procedures, represent a promising leap forward in the quest for algal biofuel optimization and the establishment of a sustainable renewable source of clean energy.

Keywords: Biofuels, *Chlamydomonas reinhardtii*, metabolic network reconstruction, FBA.