

The Summer Undergraduate Research Fellowship (SURF) Symposium
6 August 2015
Purdue University, West Lafayette, Indiana, USA

The identification of optimal pathways in *Synechocystis sp.* PCC 6803 by flux balance analysis

Ning Xuan Yip, John A. Morgan
School of Chemical Engineering, Purdue University
Longyun Guo
Department of Biochemistry, Purdue University

ABSTRACT

Cyanobacteria are microorganisms considered advantageous for producing valuable compounds because of their high growth rates compared to plants. They also can be grown at large scale in photobioreactors. This research aims to use metabolic engineering strategies to maximize the phenylalanine yield in *Synechocystis sp.* PCC 6803. Our hypothesis is flux balance analysis will give different flux distributions with different objective functions. The scope of the project is modeling photoautotrophic metabolism of cyanobacteria with a genome scale stoichiometric model, testing several alternative objective functions. We also examined the tradeoff between growth and L-phenylalanine production with flux balance analysis. A linear programming problem is constructed to solve for the fluxes. Using an available genome-scale model and the COntstraint Based Reconstruction and Analysis (COBRA) toolbox available in MATLAB, we solved for the flux value for each reaction in the wild type strain with different objective functions such as maximizing biomass, maximizing carbon dioxide uptake and minimizing total flux. Of particular interest to metabolic engineers is the production of L-phenylalanine, an essential amino acid. In plants, Phe is the precursor to phenylpropanoids, a family of thousands of compounds with wide ranging applications from pharmaceuticals to cosmetics. Using FBA, we quantitatively defined the tradeoff between directing the carbon flux towards phenylalanine instead of biomass. Future work will involve validating the model's predictions and making improvements to it, as well as exploring the tradeoff in the production of other molecules in cyanobacteria.

KEYWORDS

Keywords – cyanobacteria, phenylalanine, flux balance analysis, genome scale model

Key concepts – flux balance analysis, linear programming, genetic engineering, metabolic engineering