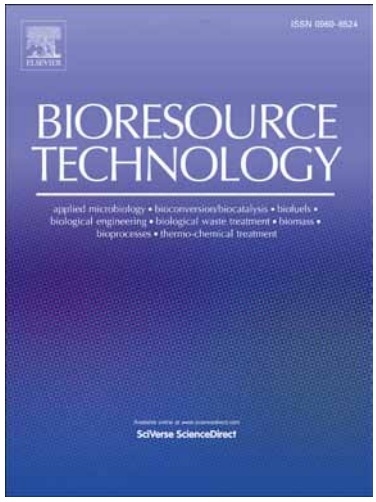

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Metabolic model of *Synechococcus* sp. PCC 7002: prediction of flux distribution and network modification for enhanced biofuel production

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Abstract

Flux Balance Analysis was performed with the Genome Scale Metabolic Model of a fast growing cyanobacterium *Synechococcus* sp. PCC 7002 to gain insights that would help in engineering the organism as a production host. Gene essentiality and synthetic lethality analysis revealed a reduced metabolic robustness under genetic perturbation compared to the heterotrophic bacteria *E.coli*. Under glycerol heterotrophy the reducing equivalents were generated from tricarboxylic acid cycle rather than the oxidative pentose phosphate pathway. During mixotrophic growth in glycerol the photosynthetic electron transport chain was predominantly used for ATP synthesis with a photosystem I/photosystem II flux ratio higher than that observed under autotrophy. An exhaustive analysis of all possible double reaction knock outs was performed to reroute fixed carbon towards ethanol and butanol production. It was predicted that only ∼10% of fixed carbon could be diverted for ethanol and butanol production.

Keywords: Cyanobacteria, *Synechococcus* sp. PCC 7002, Genome scale metabolic network reconstruction, Flux balance analysis, Gene essentiality analysis, Synthetic lethality analysis, Minimization of Metabolic Adjustments (MOMA)

1. Introduction

Cyanobacteria are a group of gram negative bacteria capable of fixing CO_2 and performing oxygenic photosynthesis. Concerns over depletion of fossil fuel reserves and rising levels of atmospheric CO_2 levels have drawn attention towards cyanobacteria, a potential source of renewable energy (Parmar et al., 2011). Cyanobacteria grow significantly faster compared to other oxygenic