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Reconstruction and analysis of a carbon-core metabolic network for Dunaliella salina

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Dunaliella salina; Metabolic network reconstruction; Central carbon metabolism; Flux balance analysis

Abstract

Background The green microalga Dunaliella salina accumulates a high proportion of beta-carotene during abiotic stress conditions. To better understand the intracellular flux distribution leading to carotenoid accumulation, this work aimed at reconstructing a carbon core metabolic network for D. salina CCAP 19/18 based on the recently published. Results The reconstruction resulted in a network model with 221 reactions and 212 metabolites within three compartments: cytosol, chloroplast and mitochondrion. The network was implemented in the MATLAB toolbox CellNetAnalyzer and checked for feasibility. Furthermore, a flux balance analysis was carried out for different light and nutrient uptake rates. The comparison of the experimental knowledge with the model prediction revealed that the results of the stoichiometric network analysis are plausible and in good agreement with the observed behavior. Accordingly, our model provides an excellent new tool to interrogate and better understand the carbon core metabolism of D. salina. Conclusions The reconstructed metabolic network of D. salina presented in this work is able to predict the biological behavior under light and nutrient stress and will lead to an improved process understanding for the optimized production of high-value products in microalgae.

Full-text

Due to technical limitations, full-text HTML conversion of this manuscript could not be completed. However, the manuscript can be downloaded and accessed as a PDF.

Figures

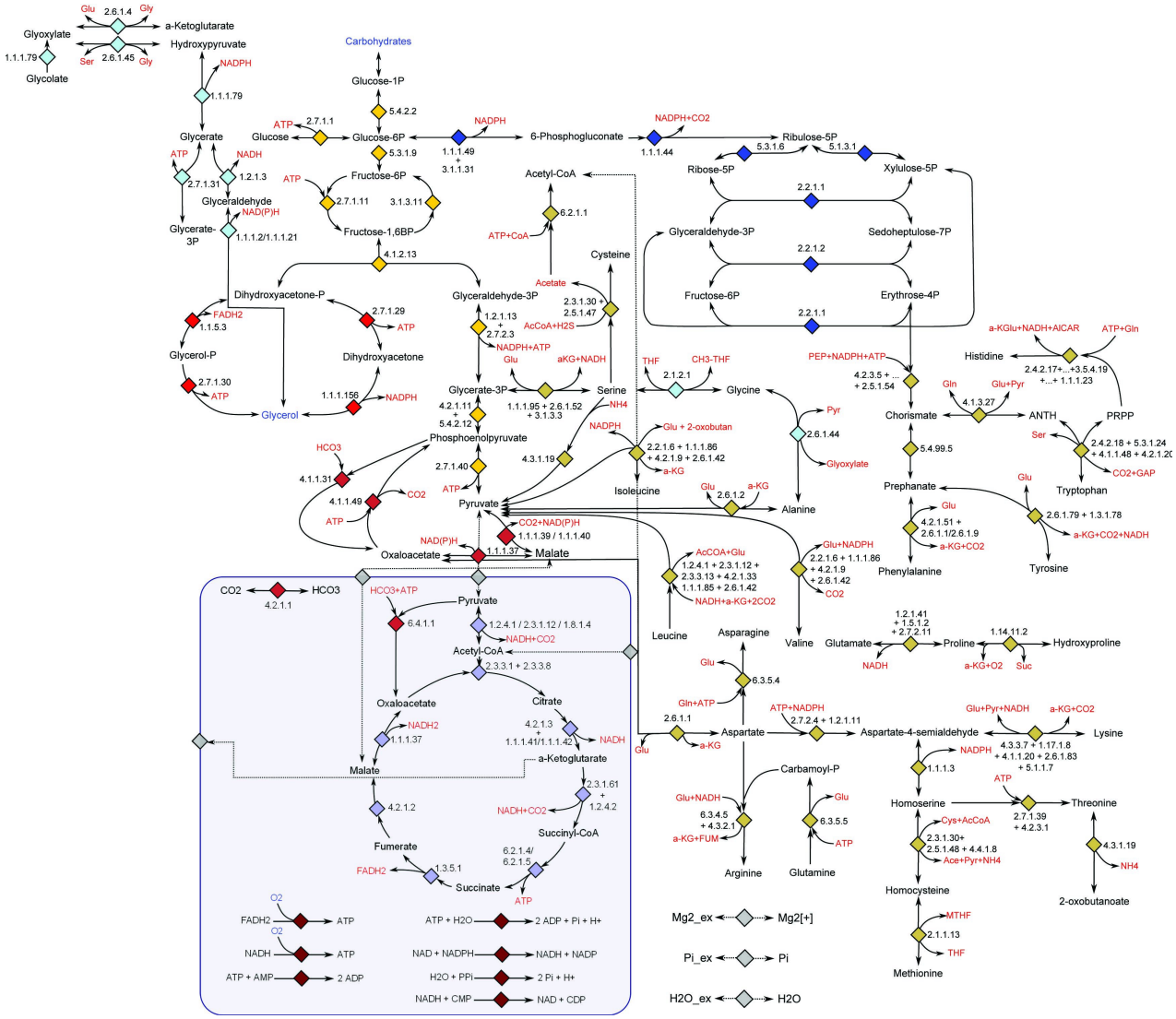


Figure 1

Network map of carbon core metabolism in the cytosol and mitochondrion. For reasons of simplicity linear reactions were merged. The arrows display the direction and reversibility of the reactions. The blue font color refers to metabolites modeled as biomass compounds and the red font color refers to key reaction components such as energy and reduction equivalents.

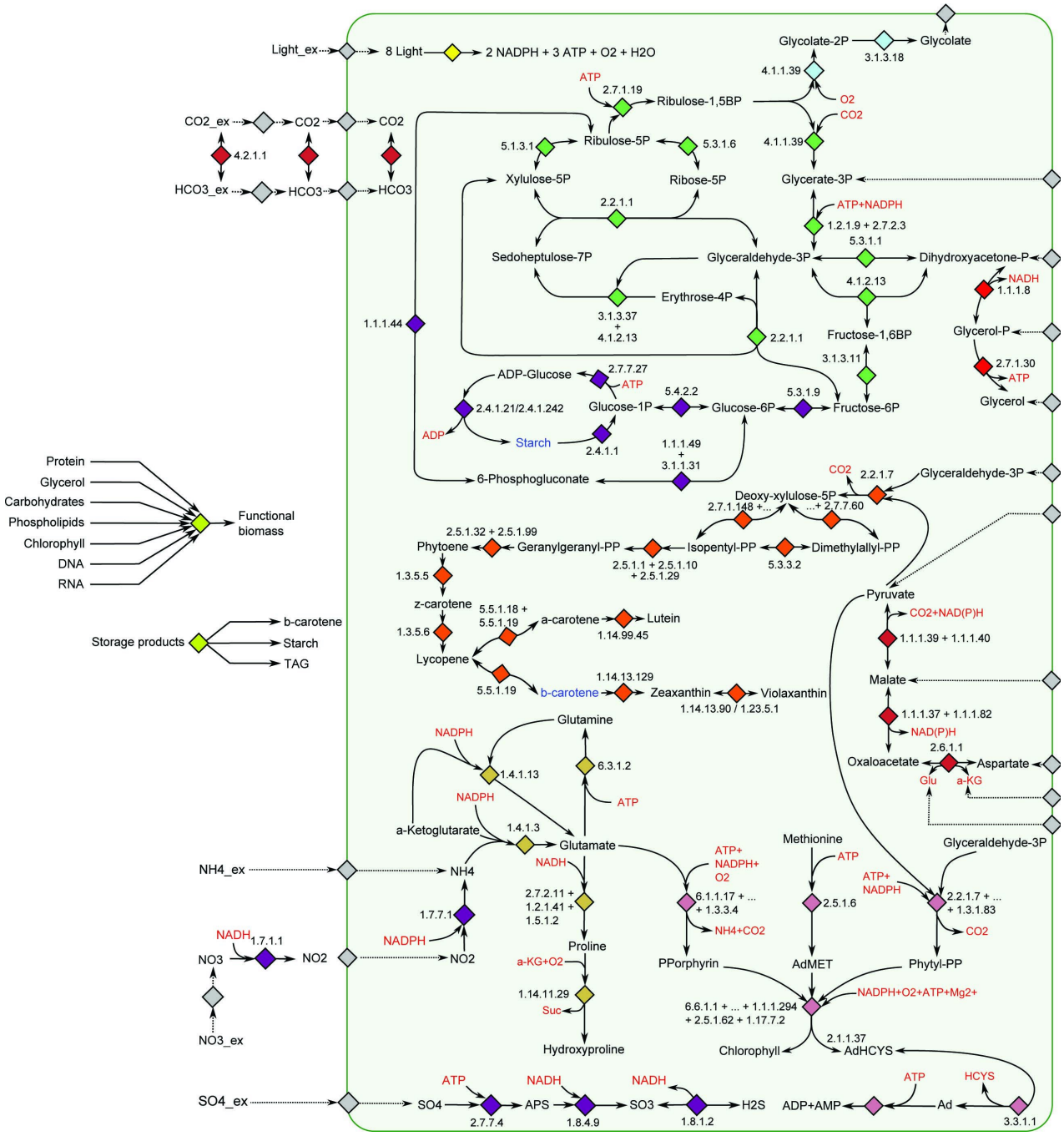


Figure 2

Network map of carbon core metabolism in the chloroplast. For reasons of simplicity linear reactions were merged. The arrows indicate the direction and reversibility of the reactions. The gray boxes indicate shuttling of metabolites between the considered compartments. The blue font color refers to metabolites modeled as biomass compounds and the red font color refers to key reaction components such as energy and reduction equivalents.

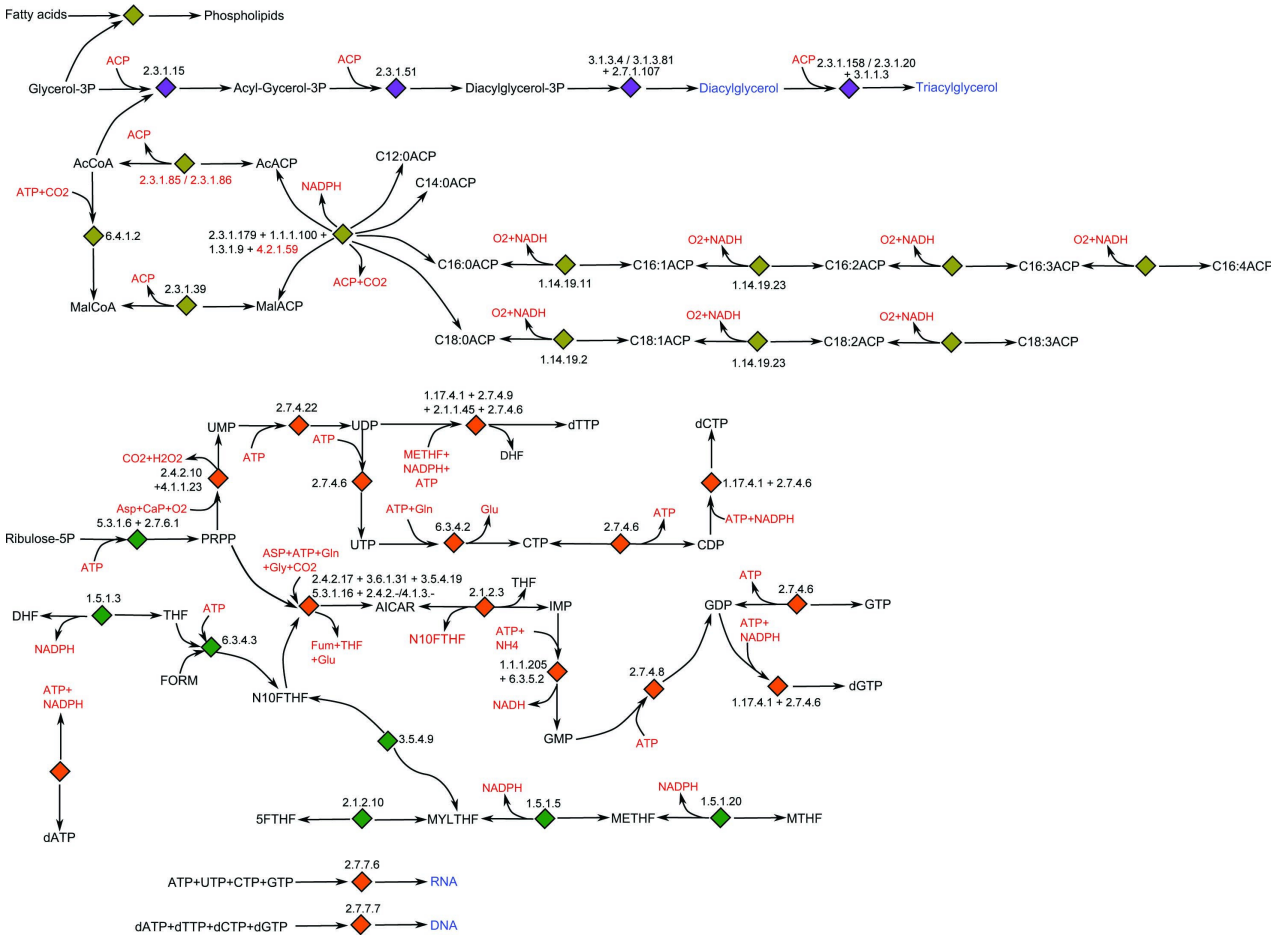


Figure 3

Network map of the fatty acid and nucleic acid metabolism. The arrows indicate the direction and reversibility of the reactions. For reasons of simplicity linear reactions were merged. The gray boxes indicate shuttling of metabolites between the considered compartments. The blue font color refers to metabolites modeled as biomass compounds and the red font color refers to key reaction components such as energy and reduction equivalents.

Supplementary Files

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Supp1_Reactions_Biomass.pdf
Dsalina_190517.xml
Flux_scenarios.zip