

# Transcriptional regulation and coordination of photosynthetic genes in *Synechocystis*: a comprehensive study based on CyanoExpress

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We know in great detail structures and functions of the main components of photosynthesis, from the absorption of light particles by pigment-binding protein-complexes to the assimilation of inorganic carbon into carbohydrates by the Calvin-Benson cycle. However, our knowledge of the regulation of photosynthesis and its coordination with other cellular processes is still limited hindering an optimal usage in green biotechnology. Therefore, the substantial amount of expression data that has been accumulated for cyanobacterium *Synechocystis* sp. PCC6803 - an important photosynthetic model organism - provides a unique opportunity to clarify how its photosynthetic apparatus adapts to environmental changes, and how photosynthesis is co-regulated with other processes on a systems level.

For this purpose, we utilized **CyanoExpress** (<http://cyanoexpress.sysbiolab.eu>), a database for *Synechocystis* transcriptome data, to examine the regulation of photosynthetic genes across a large variety of environmental conditions. Global clustering of expression data revealed strong co-regulation of genes encoding subunits of the two photosystems, the cytochrome  $b_6f$  complex, the phycobilisome, respiratory terminal oxidases, and enzymes involved in the synthesis of tetrapyrrole compounds that are prosthetic groups in these complexes. The observed co-expression of functionally related genes allowed the prediction of novel genes involved in the photosynthetic capacity of *Synechocystis* through application of a “guilt by association” principle. Notably, this approach predicted 19 genes to be newly linked to photosystem I (8 genes), photosystem II (2 genes), and phycobilisomes (9 genes) functional categories. Finally, network-based analysis of co-expression indicated a tight coordination of photosynthesis with various processes such ATP synthesis and translation.