Prof. Wolfgang R. Hess
Genetics & Experimental Bioinformatics (www.cyanolab.de)
University of Freiburg
Institute of Biology III
Schänzlestrasse 1
D-79104 Freiburg, Germany

Master thesis in Genetics (AG HESS)

Topic: A LysR-type regulator that might be involved in transcriptional control of RubisCO in cyanobacteria

Plants and other photoautotrophs including cyanobacteria perform oxygenic photosynthesis using solar energy to convert atmospheric CO_2 into organic compounds in the Calvin-Benson-Bassam (CBB) cycle. Inorganic carbon (Ci) assimilation into living cells needs to be tightly controlled to allow acclimation to fluctuations in external Ci availabilities. In the model cyanobacterium *Synechocystis* sp. PCC 6803 the mechanisms of adaptation to changes in Ci supply have been extensively studied (see **Figure 1**).

The cyanobacterial acclimation to varying amounts of Ci mainly involves fine tuning of the carbon concentrating mechanism (CCM), which comprises active Ci uptake systems and the enrichment of CO_2 in close proximity to RubisCO within proteinaceous structures, the carboxysomes. Expression of genes encoding uptake systems is strongly up-regulated under Ci-limiting conditions and controlled by the major LysR-type transcriptional regulators (LTTRs) CmpR and NdhR (also known as CcmR). However, our understanding of expression regulation of genes encoding enzymes involved in the CBB cycle and associated pathways in cyanobacteria is still fragmentary.

In addition to the well-characterized LTTRs CmpR and NdhR, *Synechocystis* also harbours a so far uncharacterized LTTR which appears to perform important regulatory function since a knockout mutant could not be obtained. Thus, its presence is crucial for cell viability and it could be speculated that this LTTR activates expression of essential genes. In agreement with the described observations in *Synechocystis*, a closely related protein was shown to activate transcription of the Rubisco operon *rbcLS-cbbX* in the chloroplast of red algae. Thus it is tempting to speculate that this LTTR is responsible for active transcription of the RubisCO-encoding genes also in *Synechocystis* as well as many other cyanobacteria.

The potential Master candidate will be involved in generating inducible knock-down mutants for the respective regulator gene. Once a stable mutant is available, transcript profiling will be performed to identify its target genes. Afterwards, the promoters of the identified target genes will be analyzed for similarities, i.e. putative LTTR binding motifs. Finally, promoter binding of the purified LTTR will be analyzed *in vitro*.

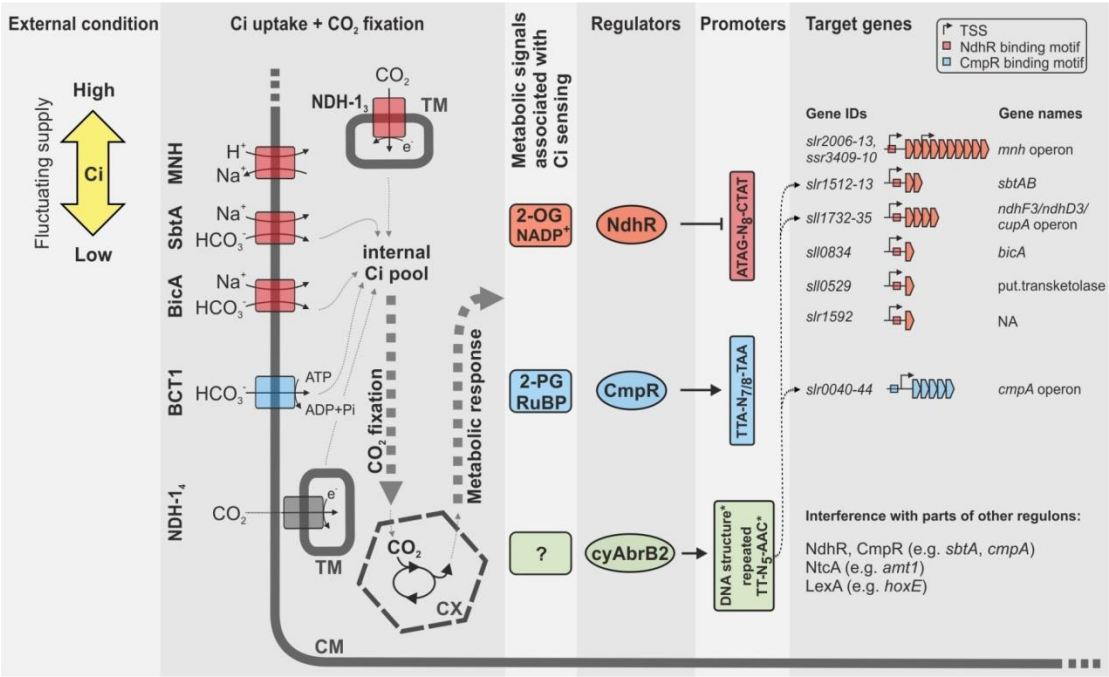

Figure 1: Overview of the inorganic carbon acquisition and its regulation on the transcriptional level in *Synechocystis* sp. PCC 6803. CCM - carbon concentrating mechanism, Ci - inorganic carbon, CM - cytoplasmic membrane, TM - thylakoid membrane, CX - carboxysomes, 2-OG - 2-oxoglutarate, 2-PG - 2-phosphoglycolate, RuBP - ribulose-1,5-bisphosphate, TSS - transcriptional start site.

Related references:

Orf I, Schwarz D, Kaplan A, Kopka J, Hess WR, Hagemann M, Klähn S. CyAbrB2 Contributes To The Transcriptional Regulation Of Low CO_2 Acclimation In *Synechocystis* sp. PCC 6803. (2016) *Plant and Cell Physiology*, in press.

Orf I, Klähn S, Schwarz D, Frank M, Hess WR, Hagemann M, Kopka J. (2015) Integrated analysis of engineered carbon limitation in a quadruple CO_2/HCO_3^--uptake mutant of *Synechocystis* sp. PCC 6803. *Plant Physiology* 169: 1787-1806.

Klähn S, Orf I, Schwarz D, Matthiessen JKF, Kopka J, Hess WR, Hagemann M. (2015) Integrated transcriptomic and metabolomic characterization of the low-carbon response using an *ndhR* mutant of *Synechocystis* sp. PCC 6803. *Plant Physiology* 169: 1540-1556.

If you are interested please contact us via Email: (wolfgang.hess@biologie.uni-freiburg.de, stephan.klaehn@biologie.uni-freiburg.de)