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Regulation of NAGK activity in photosynthetic organisms: the role of the PII nitrogen regulator

Asunción Contreras

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In the paradigmatic Ntr (Nitrogen Regulation) system of enteric bacteria PII proteins (encoded by paralogous genes glnB and glnK) regulate their targets by protein-protein interactions in response to nitrogen signals. PII proteins are believed to be also key players in the coordination of nitrogen assimilation and carbon metabolism in other bacteria, archaea and plants. However, the identity of PII receptors remains elusive in most organisms, and in particular in those that perform oxygenic photosynthesis.

We are using yeast two-hybrid approaches to identify new PII receptors and to explore functional links between nitrogen regulators in cyanobacteria. In this context, the screening of a Synechococcus sp. PCC 7942 yeast two-hybrid library with PII as bait resulted in the identification of N-acetyl glutamate kinase (NAGK), a key enzyme in arginine biosynthesis, and PipX (Protein Interacting with PII), a protein of unknown function.

In Synechococcus, PII stimulates NAGK activity, a function dependent on the presence of Ser49, a residue conserved in the T-loops of all organisms performing oxygenic photosynthesis. Phylogenetic and yeast two-hybrid analysis suggests conservation of the NAGK-PII regulatory interaction in the evolution of cyanobacteria and chloroplasts, thus providing the first clue to the function of eukaryotic PII proteins. It appears that in these systems, the driving force for the strong conservation of Serine in the T-loops of PII proteins has been interaction with NAGK, instead of the so far presumed phosphorylation-dependent regulation of PII targets.