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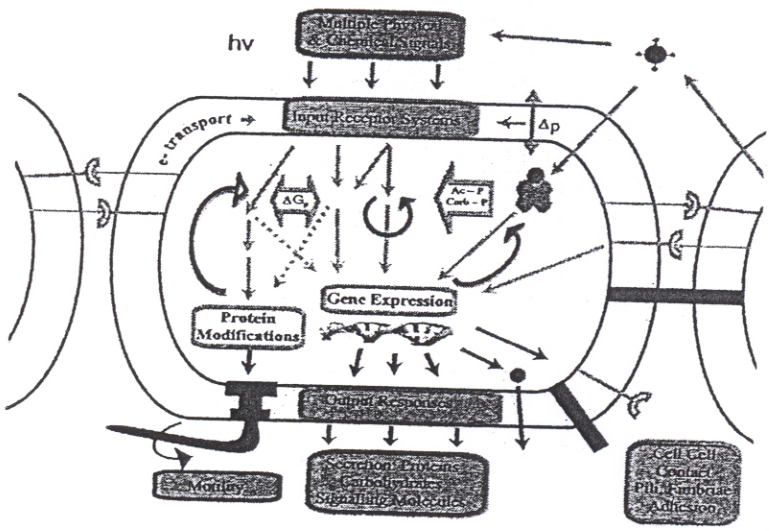
BACTERIAL NEURAL NETWORKS



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ABSTRACTS

Nitrogen regulation and interaction networks in enterobacteria

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In enterobacteria, PII proteins play a key role on both transcriptional and metabolic regulation, interacting with three different bifunctional signal transducing enzymes (UTase/UR, ATase, and NtrB) and an ammonium transporter (AmtB). Two paralogous genes, *glnB* and *glnK*, encode PII proteins in enterobacteria. The physical properties of the *E. coli* GlnB and GlnK proteins are very similar, and, under some circumstances, GlnK can substitute for GlnB. Signals that indicate carbon and nitrogen status determine the ability of PII proteins to regulate the kinase and phosphatase activities of NtrB and, as a result, the activity of the response regulator NtrC. The nitrogen status of the cell is sensed by UTase/UR enzyme, encoded by *glnD*, which uridylylates/de-uridylylates PII proteins according to the glutamine levels. In addition to transcriptional regulation, UTase/UR and PII proteins also play a role on metabolic regulation (by affecting glutamine synthetase activity) and ammonium transport (by interaction with AmtB).

With the aim to construct a nitrogen "interactome" or interaction network, we are using the known nitrogen regulators as baits in yeast two-hybrid screenings. Identification and preliminary characterisation of a number of "interactants" suggests that the paradigmatic Ntr system is part of a wider regulatory network. In addition, the finding of additional interaction partners for the UTase/UR and phenotypic analysis of *E. coli* GlnD mutants indicates that PII proteins are not the only proteins uridylylated according to the glutamine levels.

Proteins interacting with PII from *Synechococcus*: regulatory mechanisms unique to cyanobacteria and conservation of interologous partners across domains of life.

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PII proteins play a key role on both transcriptional and metabolic regulation in enterobacteria, where two paralogous genes, *glnB* and *glnK*, encoding PII proteins, have received much attention. PII proteins, encoded by orthologous *glnB* genes, are also believed to be 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, particularly in photosynthetic organisms. In this work, we have exploited yeast two-hybrid approaches to identify new PII receptors and to explore functional links between PII and NtcA, the cianobacterial global nitrogen regulator. The screening of *Synechococcus* sp. PCC 7942 libraries with PII as bait resulted in the identification of two very different receptors: N-acetyl glutamate kinase (NAGK), a key enzyme in the biosynthesis of arginine and PipX (PII-Interacting Protein), whose phylogenetic distribution is limited to cyanobacteria. We present evidences concerning a) conservation of the NAGK-PII interaction in the cyanobacteria-chloroplast lineage and b) a role of PipX in connecting the two key nitrogen regulators of cyanobacteria: NtcA and PII.