DISSECTION OF THE SIGNAL TRANSDUCTION PATHWAYS INVOLVED IN PHOTOTACTIC GLIDING MOTILITY IN THE CYANOBACTERIUM *Synechocystis* sp. PCC 6803 - FUNCTIONAL GENOMIC APPROACHES

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In order to search for the genes involved in the light signal transduction pathways in the cyanobacterium *Synechocystis* sp. PCC 6803 (Syn6803), we constructed a Tn*5* mutant library. Among the pool of 2,000 mutants of Syn6803, we isolated ca. 50 nongliding mutants on the surface of agar plates. The genes responsible for the mutations in 35 phototatic movement mutants were identified by DNA sequence determination after amplifying the flanking DNA sequences of the transposon by an inverse PCR method. 20 different genes were responsible for the mutations in phototatic gliding motility; a putative ABC transpoter, a MCP-like protein, aa-binding/transporter, UDP-NAG-pyrophosphorylase, transcriptional regulator, gln-binding/transporter, protein kinase(Ser/Thr), glycogen synthase, RNA polymerase sigma factor, phosphate starvation-inducible protein, catabolite gene activator protein, WD repeat, and seven hypothetical proteins.

We also recently showed that a putative methyl accepting chemotaxis protein (MCP), was involved in a signal transduction pathway of the gliding motility in Syn6803 (Chung *et al.*, 2001, *FEBS Lett.* **492**, 33-38). The Cyanobase shows that Syn6803 have 3 additional MCPs, each of which belongs to a part of a gene cluster, high similarity to the *che* gene cluster of enteric bacteria and *Pseudomonas*. Interposon mutagenesis of each gene in the gene clusters displayed altered phototaxis in the bacteria. The possible mechanism of genes involved in phototactic movement of Syn6803 by identified in this study will be discussed.