CHRACTERIZATION OF *Synechocystis* sp. PCC 6803 GENE CLUSTERS INVOLVED IN GLIDING MOVEMENT: SEQUENCE SIMILIRITY TO THE CHEMOTAXIS PROTEINS OF ENTERIC BACTERIA AND THE TWITCHING BACTERIUM *Pseudomonas aeruginosa*

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Using transposon mutagenesis, we isolated 12 nongliding mutants of the unicellular cyanobacterium *Synechocystis* sp. PCC 6803 (Syn6803) on the surface of agar plate. Protein responsible for gliding motility was identified as a methyl-accepting chemotaxis protein (MCP) homolog encoded by slr1044. Disruption of MCP gene such as slr1044 and sll1294 also resulted in a loss of gliding motility. Surrounding gene clusters including MCP were found to be high similarity to *che* genes of enteric bacteria and *Pseudomonas*. One gene cluster, named R1, included slr1041, slr1042, slr1043 and slr1044, which are sequence homology to *che* genes. The slr1042 gene product exhibits significant amino acid identity (47%) with the enteric reponse regulator, *che*Y. The putative proteins of slr1041, slr1043 and slr1044 are homo;ogous to the PilG (32%, CheY homolog in enterics), CheW (27%) and PilJ (35%, MCP homolog in enterics) genes in a twitching bacterium *Pseudomonas aeruginosa*, respectively. The other gene cluster, named L1, is organized in the same gene arrangement of R1 cluster. Inactivation of slr1044 or sll1294 impaired gliding ability severely on the surface of agar or glass. It was previouly reported that *che* gene homlogs were involved in pilus biosynthesis and twitching motility of *Pseudomonas* (Darzins *et al.*, 1994, *Mol. Microbiol.* 1, 137-153). These results suggest that R1 and L1 *che* gene clusters in Syn6803 control pili formation and gliding motility.