

## **244a Towards a Systems Biology Understanding of the Dynamics of *Synechocystis* Sp. Pcc 6803 during Light-Dark Cycling**

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Experimental systems biology tools provide extensive information about an organism's physiology, yet the picture they provide is incomplete because only one aspect (e.g., mRNA, protein, or metabolites) is described. A more substantial understanding can be gained by integrating data from multiple methods with macroscopic physiological measurements. In addition, the dynamics of a system have rarely been considered. In this study, we sought to analyse the transient responses of *Synechocystis* sp PCC 6803 to alterations in light level using both transcript and proteomic analyses. *Synechocystis* sp PCC 6803 is a useful model cyanobacterium for future metabolic engineering exploitation to improve its production of hydrogen and other secondary metabolites. Previous research has provided information on metabolic pathways and products, and transcriptional and proteomic investigations have been facilitated by the recent sequencing of this organism's genome. *Synechocystis* sp PCC 6803 was grown in a photobioreactor at 26 C, and subjected to a 12-hour light-dark cycle. To assess the physiology of this cyanobacterium, mRNA and protein samples were obtained throughout each cycle. The transcriptional levels of key genes over the cycle were monitored using quantitative real time PCR. Differences in protein expression were assessed using isobaric mass tagging technology (iTRAQ), with key phenotypic relationships verified by 2-D gel electrophoresis. Typically 300 proteins were quantified per phenotype. Particular attention was paid to the response time scales for the induced oscillatory metabolic networks, and significant differences were noted between the dynamics of the transcript and proteome.