## P001 Towards Cyanobacterial Systems Biology: Transcriptome and Proteome 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 transcriptomic 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 transcriptomic 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 subjected to a 12-hour light-dark cycle. To assess the physiology of this cyanobacterium, mRNA and protein samples were obtained throughout each cycle. Transcriptome profiling was performed with cDNA microarrays and key genes were verified using RT-PCR. Differences in protein expression were assessed using both 2-D gel electrophoresis and gel-free "shotgun") proteomics. In the latter method, proteins were first fractionated either using iso-electric focusing or LC-strong cation exchange (SCX) columns, and then fractions were digested with trypsin. The peptides from these digested fractions were further fractionated on SCX and C18 reverse-phase columns before analysis in an electrospray ionization quadrupole time-of-flight tandem mass spectrometer. Spectra from MS and MS-MS studies were analysed using Mascot and Pro ID software. Over 400 proteins were identified 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 transcriptome and proteome.