

CyanoEXpress: An enhanced tool for on-line analysis and visualization of gene expression data from cyanobacteria

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Synechocystis sp. PCC 6803 is one of the best-studied cyanobacteria and an important model organism for our understanding of photosynthesis. The early availability of its complete genome sequence initiated numerous transcriptome studies, which have generated a wealth of expression data. To facilitate the study of the accumulated *Synechocystis* expression data, we developed CyanoEXpress (<http://cyanoexpress.sysbiolab.eu>), a web database for interactive analysis and visualization of transcriptomics data from cyanobacteria (1). As basis, we collected publicly available microarray measurements and analysed them in a standardised manner. To this date, 718 *Synechocystis* microarray measurements carried out in 33 independent studies were evaluated and included in CyanoEXpress making it the most comprehensive catalogue of *Synechocystis* gene expression data. It enables its users to explore and visualise the transcriptional response of *Synechocystis* to 177 distinct environmental conditions or genetic perturbations for 3073 chromosomal genes. CyanoEXpress can also assist researchers in the characterization and functional annotation of genes using the guilty-by-association principle. This presentation will provide an overview of CyanoEXpress and its functionality, and will highlight its recent extensions and enhancements. We will also present our newest developmental version, which includes expression data from other cyanobacterial species – a feature that will make CyanoEXpress useful to a wide community of researchers in the field of phototrophic prokaryotes.

References

1. Miguel A. Hernandez-Prieto and Matthias E. Futschik. (2012). CyanoEXpress: A web database for exploration and visualisation of the integrated transcriptome of cyanobacterium *Synechocystis* sp. PCC 6803. *Bioinformatics*. 8(13): 634–638