

ELUCIDATING GENE SIGNATURES THAT CONTROL THE CIRCADIAN RHYTHM IN CYANOBACTERIA USING BIOINFORMATICS METHODS

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Background: The daily light-dark cycle governs rhythmic changes in the behavior and physiology of most species. This circadian rhythm, or biological “clock,” allows the organism to anticipate and prepare for the changes in the physical environment that are associated with day and night, thereby ensuring that the organism carries out specific processes at the right time of the day. Studies have found that the internal clock consists of an array of genes and the protein products they encode, which regulate various physiological processes throughout the body. *Cyanothece* sp. ATCC 51142 is an organism that has both photosynthetic (producing oxygen) and nitrogen fixing ability. The N₂-fixing enzyme, nitrogenase, is highly sensitive to oxygen for which it has developed a temporal regulation in which N₂ fixation and photosynthesis occur at different times throughout a diurnal cycle with very high levels of CO₂ fixation during the light and high levels of N₂ fixation in the dark. The mechanisms underlying the circadian rhythm and the signature genes elucidating this mechanism are addressed in this research.

Objective: The objective is to integrate gene expression data with data and knowledge from prior studies using bibliomics techniques, in the *de novo* construction of quasi-complete transcriptional regulatory networks to identify gene signatures in functional motifs and elucidate their role in circadian rhythms in *Cyanothece* sp. ATCC 51142.

Methodology: The sequence data of Transcription profiling time series of *Cyanothece* sp. ATCC 51142 grown in 12-hour light/12 hour dark then 24 h light from Array Express was used to construct the initial global regulatory network. Different network topological features (degree, betweenness and eccentricity) are used to identify the signature pathways during the day and night. The genes of the global regulatory network were used to construct networks of homologous species. The functions of the already known genes in well-studied homologous species were mapped to the function of the unannotated genes of *Cyanothece* sp. ATCC 51142.

Results: We have identified significant ($p < 0.05$) signature pathways like photosynthesis, pantothenate and CoA biosynthesis and Glyoxylate and dicarboxylate metabolism that operate during the day. And during the night, pathways such as ribosome, riboflavin metabolism, and fatty acid biosynthesis sulfur metabolism were found to be significant ($p < 0.05$). We will further investigate the genes that were already known to be significant using cyanobase database in a particular biological pathway and the novel genes that are identified by bibliomics approach.

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