

Bi-level proteome-wide analyses of *Arthrospira platensis* C1 under temperature shifts for construction of key stress-regulated protein-protein networking

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Feasibility of algae and cyanobacteria to use as a source for production of bio-product(s) has been studied due to their ability to absorb greenhouse gas (carbon-dioxide) and to be grown in large-scale outdoor cultivation. *Arthrospira (Spirulina) platensis* is the only cyanobacterium that can be mass cultivated in outdoor ponds, thus it is a candidate model-organism for bio-factory. Under temperature stress conditions that the cells encounter in outdoor mass cultivation system, proteome-wide analyses for protein expression level and post-translational modification were carried out, which led to information required for understanding of cellular response and regulation. Large-scale datasets generated were then mined, managed and in-depth analyzed by using a bioinformatics tool, SpirPro. Cellular protein-protein interaction networks under the stress conditions were constructed based on the two levels proteome-wide data. After the two-level protein networks were integrated, the proteins that were differentially expressed and also phosphorylated were classified into the group of bi-level regulated proteins. This group of proteins possibly plays key roles in cell response and survival under the stress conditions. Chaperones and proteins involved in signal transduction systems, photosynthesis, nitrogen assimilation and energy production are in the group of bi-level regulated proteins. The networking of these proteins will be elucidated further by using multi techniques e.g. flux balance analysis, binding-motif analysis and yeast two hybrid system.

Keywords: Cyanobacteria, Proteome-wide analyses, Protein-protein interaction network, Stress tolerance and Temperature stress response