Abstract

Arthrospira platensis (*A. platensis*) C1 are kind of cyanobacteria that contain high protein content and high valuable substances. Many industries are interested in using *A. platensis* C1 as a cell factory to produce desired substances. The aim is to increase their biomass that is usually grown in outdoor cultivation. *A. platensis* C1 have to face several stresses including high temperature, nutrient sufficiency, and etc. In this study, we focused on *A. platensis* C1 in response to high temperature stress. We first analyzed microarray data of *A. platensis* C1 under high temperature and 250 responsive genes were obtained. Genes were clustered into 5 groups on the basis of similar gene expression profiles. We searched for common motifs of genes expressing similarly and then compared predicted motifs with known motifs of prokaryotic organisms. We have inferred the regulatory relationship from the information whether genes that express similarly and share a common motif would be connected with a predicted regulator. Finally, we constructed a regulatory network of responsive mechanism under high temperature stress of *A. platensis* C1.