

Abstract

Arthrospira (Spirulina) *platensis* C1 (PCC9438) is a well-known cyanobacterium used in a production of many industrial products, health supplements, animal feeds, and cosmetic products. Based on its ability to produce a large range of product, System Biology and Bioinformatics research group (SBI) at King's Mongkut University of Technology Thonburi developed a genome-scale model of *A. platensis* C1 to assist in a prediction of a gene/metabolic pathway for a high value compound. However; lack of transporter gene in the current metabolic model decreases a prediction's performance of the model substantially.

In this study, we used a comparative genomic method to predict a list of transporter gene from *A. platensis* C1 genome. First, we used BLAST to compare amino acid sequence of *A. platensis* with transporter database TCDB to filter a preliminary list of transporter gene. This list of transporter gene was refined using a define function from ortholog group of *A. platensis* with closely related species. We found 57 transporter genes with a clear defined substrate, 45 transporter genes associate with group of substrate (e.g. Amino acid), and 17 transporter genes with new substrates. We believe that these predicted transporter genes cover most of important transportation reaction in *A. Platensis* C1 and can be used to improve metabolic model. Further literature reviews are suggested before add these transporter genes into metabolic model.