



Category: Functional Genomics

How cyanobacterial signalling system behaves in different media component with time? – a Genomics and Transcriptomics approach

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Abstract

In this study, we are aiming at deciphering the physiological and molecular mechanisms behind cyanobacterial IQ system i.e. the putative signalling component proteins [1] in *Mastigocladus laminosus* using a reverse genetics approach. Polymorphic *Mastigocladus laminosus* belongs to one of the least studied but most evolved family of cyanobacteria, the Stigonemataceae. Its unique properties to withstand extreme environmental conditions and economic value make it a suitable candidate for genomics and transcriptomics studies. Whole genome sequencing of *M. laminosus* was carried out using Illumina Miseq. Good quality paired end and mate pair library data were assembled into a draft genome. Annotation showed that a major portion of genes are part of several critical pathways such as two component regulatory system, ABC transporters, etc. We set up pilot experiments for finding suitable time points for checking the fatty acid production differential in strains growing in nitrogen supplemented and nitrogen depleted media. In both the conditions, between 0th day and 12th day the fatty acid production difference was the maximum. Taking the cue from this, we performed the transcriptome experiment. Results show that among the differentially expressed genes, the signalling genes of two-component systems are the predominant class. Chemotaxis family two component hybrid kinases are found in a cluster within the genome. Also several other non-ribosomal peptide synthetases /polyketide synthetases classes were the second most predominant class showing a promise of becoming a source of novel secondary metabolite production. Several heat shock protein coding genes have been identified. Phosphate and molybdate ABC transporter expression were upregulated with respect to time but not affected from the presence or absence of nitrogen in media. Our future work will include characterizing the finer details of the significant genes through pathway analysis and exploring the metabolome. From preliminary analysis of the genome and transcriptome of *M. laminosus*, it is evident that cyanobacteria have evolved to sense unfavourable condition by their huge interactive network of regulatory components and survived by producing compounds that are mostly unexplored yet from the earliest period of this planet.

References

[1] Galperin, M.Y. (2005) A census of membrane-bound and intracellular signal transduction proteins in bacteria: bacterial IQ, extroverts and introverts. *BMC Microbiol* 5: 35. <https://doi.org/10.1186/1471-2180-5-35>

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