

Transcriptome Wide Computational Mining and Differential Expression Of Genes Involved in Fatty Acid and Triacylglycerol Metabolism in *Scenedesmus* sp.

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Abstract—Biodiesel production from microalgae has still not gained momentum as only few microalgal strains are available having high biomass productivity along with high lipid content. Research has been carried out to increase the oil content and growth rate of existing strains or selection of new strains with high oil content. *Scenedesmus* has been emerged as a potential oil producing microalgae having high growth rate and lipid content in comparison to other green algae. We have identified genes involved in the metabolism of fatty acids and triacylglycerol pathway in *Scenedesmus* and performed differential expression analysis of these genes in two lipid content contrasting *Scenedesmus* species viz. *Scenedesmus dimorphus* (26%) and *Scenedesmus quadricauda* (14%). Identified genes are classified into different categories i.e. fatty acid biosynthesis, fatty acid elongation, fatty acid degradation, triacylglycerol biosynthesis and catabolism. Transcript abundance of majority of genes regulating fatty acid biosynthesis, fatty acid elongation and triacylglycerol biosynthetic pathway were found to be upregulated in *Scenedesmus dimorphus* while fatty acid degradation and triacylglycerol catabolism were downregulated in *Scenedesmus dimorphus* compared to *Scenedesmus quadricauda*. The identified genes linked with high lipid content can be considered as potential targets for metabolic engineering aiming to enhance lipid content in algae. Furthermore, validation of the genes showing higher expression could provide evidence about molecular determinants for high lipid accumulation in *Scenedesmus* species.