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Transcriptomic Analyses of Kappaphycus alvarezii under Different Wavelengths of Light

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Abstract : Transcriptomes associated with the process of photosynthesis have offered insights into the mechanism of gene regulation in terrestrial plants; however, limited information is available as far as macroalgae are concerned. This investigation aims to decipher the underlying mechanisms associated with photosynthesis in the red alga, Kappaphycus alvarezii, by performing a differential expression analysis on a de novo assembled transcriptomes. Comparative analysis of gene expression was designed to examine the alteration of light qualities and its effect on physiological mechanisms in the red alga. High-throughput paired-end RNA-sequencing was applied to profile the transcriptome of K. alvarezii irradiated with different wavelengths of light (blue 492-455 nm, green 577-492 nm and red 780-622 nm) as compared to the full light spectrum, resulted in more than 60 million reads individually and assembled using Trinity and SOAPdenovo-Trans. The transcripts were annotated in the NCBI non-redundant (nr) protein, SwissProt, KEGG and COG databases with a cutoff E-value of 1e-5 and nearly 30% of transcripts were assigned to functional annotation by Blast searches. Differential expression analysis was performed using edgeR. The DEGs were designated to six categories: BL (blue light) regulated, GL (green light) regulated, RL (red light) regulated, BL or GL regulated, BL or RL regulated, GL or RL regulated, and either BL, GL or RL regulated. These DEGs were mapped to terms in KEGG database and compared with the whole transcriptome background to search for genes that regulated by light quality. The outcomes of this study will enhance our understanding of molecular mechanisms underlying light-induced responses in red algae.

Keywords : de novo transcriptome sequencing, differential gene expression, Kappaphycus alvareziired, red alga

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