Genomic and Transcriptomic Analysis of a Nannochloropsis oceanica Strain Displaying a Greater Thermal Tolerance Towards the Engineering of a Heat Tolerant Marine Microalgal Strain

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Global warming has led to a significant escalation of the rate of coral bleaching, with 90% of reefs projected to experience bleaching annually by 2050. Coral bleaching often occurs when marine microalgae within corals die or get expelled due to their surrounding temperatures surpassing their thermal threshold. As symbiotic microalgae provide ~90% of the corals' energy, the absence of such algae causes the reefs to bleach. Hence, past studies have aimed to investigate genes associated with the thermal tolerance of marine microalgae species. The following study aimed to first analyze the DNA sequencing data of a mutant strain of a model marine microalgal species Nannochloropsis oceanica that displayed a greater thermal tolerance compared to the wild-type strain; 48 mutated genes were identified. Transcriptomic analysis included culturing the two strains under control and elevated temperatures to conduct RNA sequencing. However, the differentially expressed genes unique to the mutant strain under elevated temperatures did not correspond to any of the 48 candidate genes identified. A limitation accounting for such discrepancy is the inadequate read counts that presumably arose from low sequencing yield rate, challenges enriching for mRNAs, and the lacking reference genome annotation. Steps being taken to improve RNA sequencing quality include reannotating the reference genome and re-conducting RNA sequencing. Future steps involve reanalyzing the DNA and RNA sequencing data to identify overlapping candidate genes between the sequencing results. Plasmids including the candidate genes will be designed and inserted into wild-type N.oceanica cells (utilizing electroporation), which will undergo heat-screening trials to validate the function of the unregulated candidate genes.

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