Genomic and transcriptomic analysis of the oleaginous microalga Marinichlorella sp. NKG400014

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Abstract

Microalgae have gathered increasing attention for sustainable biofuel production. Our screening study revealed that a marine microalga strain NKG400014, which was selected from 1393 strains, exhibited excellent lipid production, indicating its potential for biofuel application. In this study, we conducted comprehensive characterization of this oleaginous microalga and multi-omics analyses, including genomics, transcriptomics studies to elucidate molecular mechanism underlying their oleaginous phenotypes.

Phylogenetic analysis revealed that strain NKG400014 was classified as *Marinichlorella* sp., which is recognized as marine species. Comparative genome analysis revealed that genes involved in protein phosphorylation and modification were identified as unique genes in *Marinichlorella* sp. NKG400014. These genes may play a crucial role in salt tolerance of *Marinichlorella* sp. in marine environments. Transcriptomic analysis in nitrogen-depletion condition demonstrated that diacylglycerol acyltransferase (DGAT), a key enzyme in triacylglycerol synthesis, was predominantly expressed at different stages of stress response. These results indicate that DGAT will be one of main targets to enhance the oil productivity by metabolic engineering. Moreover, key stress-responsive genes were identified, which may serve as crucial targets for strain improvement in the future.

Keywords: Microalgae, Lipid accumulation, Transcriptomic analysis

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