

Identification and analysis of microRNAs in *Chlorella sorokiniana* using high-throughput sequencing

ABSTRACT

Chlorella is a popular microalga with robust physiological and biochemical characteristics, which can be cultured under various conditions. The exploration of the small RNA content of *Chlorella* could improve strategies for the enhancement of metabolite production from this microalga. In this study, stress was introduced to the *Chlorella sorokiniana* culture to produce high-value metabolites such as carotenoids and phenolic content. The small RNA transcriptome of *C. sorokiniana* was sequenced, focusing on microRNA (miRNA) content. From the analysis, 98 miRNAs were identified in cultures subjected to normal and stress conditions. The functional analysis result showed that the miRNA targets found were most often involved in the biosynthesis of secondary metabolites, followed by protein metabolism, cell cycle, and porphyrin and chlorophyll metabolism. Furthermore, the biosynthesis of secondary metabolites such as carotenoids, terpenoids, and lipids was found mostly in stress conditions. These results may help to improve our understanding of regulatory mechanisms of miRNA in the biological and metabolic process of *Chlorella* species. It is important and timely to determine the true potential of this microalga species and to support the potential for genetic engineering of microalgae as they receive increasing focus for their development as an alternative source of biofuel, food, and health supplements.

Keyword: *Chlorella sorokiniana*; MiRNA; Metabolites; Transcription regulation