

The Adaptation Mechanism of *Synechocystis* sp. PCC6803 in Organic-rich Water Environment: Metabolism and Transcriptome

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Abstract

In the long-term eutrophic environment, many inorganic nutrients are supplied to algae, and their residues are enriched in the water as organic nutrients. In order to explore the metabolic reaction of photoautotroph Cyanobacteria in the organic-rich environment, Culturing *Synechocystis* sp. PCC6803 in BG11-glucose solution with different glucose concentrations (0 g/L, 0.7 g/L, 1.4 g/L, 2.1 g/L, 2.8 g/L, 3.5 g/L) at the temperature of (30 ± 1) °C and the light intensity of 2000 Lux. Cell density, chlorophyll-a, and other indicators were measured every 2 days. The results showed that, contrary to the control, under the glucose treatment, the cell density of algae decreased sharply on 2th day and then fluctuated up and down. Observing the microstructure of cell by scanning electron microscopy, the surface of cells appeared wrinkle cracks with increasing glucose concentration, cell's shape became irregular, and the intercellular adhesion gradually increased. Chlorophyll-a of glucose solution decreased gradually. The chlorophyll-a of T1 (0.7 g/L) decreased from 0.28 mg/L at 0th to 0.06 mg/L at 6th, which was reduced by 70% significantly; T5 (3.5 g/L) was reduced by 97% during the same period, and the algae solution lost green. Inversely, alkaline phosphatase activity of treatment was 4.7 times, 2.5 times, 9.2 times, 8.3 times, and 7.4 times of the control on 8th, respectively. According to the transcriptome, among the differential gene expression (DEGs) screened from the blank, 187 genes of 0.7g/L were up-regulated and 91 genes were down-regulated significantly. Under 2.1g/L treatment, 393 genes were up-regulated and 466 genes were down-regulated significantly. Only 1.4 g/L concentration difference can increase the number of up-regulated and down-regulated genes by 1.1 times and 4.1 times, respectively. Through KEGG enrichment analysis, 6 DEGs in the Photosynthesis pathway were all up-regulated at 0.7 g/L, and 2 DEGs in the Carbon fixation pathways of prokaryotes were all up-regulated; at 2.1 g/L group, 18 DEGs in the Photosynthesis pathway of algae, of which only 3 were up-regulated, and among the three DEGs concerning Carbon fixation pathways of prokaryotes, only one was up-regulated. It showed that in the water environment with abundant organic matter, the photosynthesis, carbon fixation metabolism and biomass of Cyanobacteria decreased, weakening Cyanobacteria's competitiveness, so they will be replaced by other mixed-nutrient algae.

Keywords

Cyanobacteria, Organic Nutrients, Eutrophication, Transcriptome