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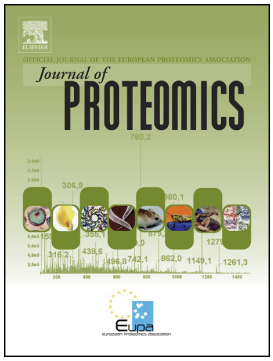

Putative model based on iTRAQ proteomics for Spirulina morphogenesis mechanisms

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Putative model based on iTRAQ proteomics for *Spirulina* morphogenesis mechanisms

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Abstract: The morphology of *Spirulina* during cultivation is susceptible to external interferences, but the morphogenesis mechanism is still unclear. Here the proteomic changes of linear *Spirulina* and spiral *Spirulina* were comparatively investigated via isobaric tag for relative and absolute quantitation (iTRAQ). Totally 165 and 167 differences in proteins expression were screened out from the TJSD2/TJSD3 and TJBC4-1/ TJBC4-2 groups, respectively. Gene ontology and metabolic pathway analysis of differences in proteins expression uncovered the metabolic pathways (photosynthesis, carbon fixation, sugar metabolism) that were significantly enriched with the proteins correlated with *Spirulina* morphogenesis. The results of differences in proteins expression in metebolic pathway were verified by quantitative real-time PCR. We also built a putative model of *Spirulina* morphogenesis mechanism and thought multiple metabolic pathways interact and take part in *Spirulina* morphogenesis.

Keywords: *Spirulina*; Morphogenesis; Putative model; Proteomics

1. Introduction

Spirulina is a multicellular and unbranched photoautotrophic prokaryote [1]. Due to adverse environmental conditions, the blue-green spiral or wavy filaments of *Spirulina* are susceptible to morphologic changes as well as physiologic, nutritional, genetic and proteomic variations [2,3,4,5,6]. As reported, high-temperature induction would structurally alter the *Spirulina*-synthesized peptidoglycan and thereby induce morphological changes [7]. *Spirulina* may also be subjected to morphologic change by laser irradiation, probably because laser would change the activity and expression of intracellular photosynthetic chromoprotein [8,9,10,11]. Two-dimensional electrophoresis reveals that many proteins are differentially expressed among different forms of *Spirulina* filaments, and these differential proteins are involved in diverse life activities, such as cell wall synthesis, nucleotide metabolism, energy metabolism, sugar metabolism, transcription, translation and photosynthesis [12,13,14].

The studies above suggest that morphogenesis of *Spirulina* is a complex process, but research on the underlying mechanism is still at the exploratory stage. Due to the limitation of genomic resources, there is insufficient data for the analysis, identification and functional annotation of proteins that are associated with *Spirulina* morphogenesis. Also research on the newly-found protein functions

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