

Towards biofuels tolerant photosynthetic cyanobacteria using integrated OMICS approaches

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Abstract

Fermentation production of biofuels consumes agricultural crops, which will compete directly with the food supply. As an alternative, photosynthetic cyanobacteria have been proposed as microbial factories to produce various biofuel products directly from solar energy and CO₂. However, the biofuel productivity from photoautotrophic cyanobacteria is currently very low, mostly due to the low tolerance of cyanobacterial systems to the toxicity of biofuels. To build a foundation necessary to engineer robust biofuel-producing cyanobacterial hosts, we have applied an integrated approach coupling quantitative iTRAQ proteomics, RNA-seq transcriptomics and metabolomics to reveal the global metabolic responses to several major biofuel products in the model cyanobacterium *Synechocystis* sp. PCC 6803. In addition, we have applied the tolerance-related gene targets to engineer *Synechocystis* with improved biofuel tolerance.