How Do Specific Mutated Genes Affect Metabolic Functioning in Prochlorococcus?

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Prochlorococcus is a cyanobacterium that produces 20% of Earth's oxygen. This organism is a key organism for balancing global CO2 levels. However, anthropogenic CO2 production exceeds the absorption abilities of Prochlorococcus. The purpose of this project was to analyze and identify the mutations and functional metabolic changes in my force-evolved strain of Prochlorococcus Marinus CCMP 1375 from my previous years' experiment. This year, I performed a functional/genetic analysis of the raw mutations observed, and then compared my mutations to those identified in strains used in other research studies and sequenced wild-type strains (specifically, Prochlorococcus MIT 9211, SS51, and SS2). If identical mutations were found in highly active strains, it is probable that the forced mutations benefit the organism's carbon fixation cycle and survivability. I observed mutations in 11 genes. These genes have been linked to glycolysis, tRNA ligase, and glycine production. Three mutated genes contained mutations identified in other studies, as well as, wild-type genomes of active strains, as hypothesized. Based on these results, some genes that are likely beneficial to carbon fixation ability and metabolic rate include genes that catalyze the production of proline and alanine, produce DNA-directed RNA polymerase, and produce glutamine- fructose-6-phosphate transaminase. These mutated genes, in combination, resulted in a more active carbon-fixing strain of Prochlorococcus. Mutation analysis of Prochlorococcus in this project provides genetic targets for future CRISPR genetic engineering research in order to create a more robust Prochlorococcus that may have global environmental impacts beyond currently proposed solutions for atmospheric CO2 mitigation.

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