

Unveiling the Impact of Microbiomes on Host Marine Microalgae in Open Raceway Ponds using Comparative Metatranscriptomics

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Marine microalgae are increasingly studied for sustainable fuel, feed, and food production due to their rapid growth, efficient resource use, and minimal land or freshwater requirements. They also play a crucial role in oceanic oxygen production. While conventional efforts to optimize algae cultivation have focused on genetic modification and environmental adjustments, less attention has been directed towards the influence of microbial interactions in enhancing biomass production. This study aimed to assess how different inorganic carbon sources shape microbial gene expression in *Nannochloropsis oceanica* C018 ponds. Four outdoor raceway ponds (1000 L) were used, with two aerated using CO₂ and two supplemented with bicarbonate (HCO₃⁻). Over a six-day period, data on algae growth, pond conditions, and RNA samples were collected. Differential gene expression analysis revealed that CO₂ treatments significantly upregulated gene expression in microbial taxa such as *Nitrosomonadales* and *Oceanospirillales* by day 4, with pathways related to photosynthesis and carbon metabolism enhanced. In contrast, HCO₃⁻ treatments showed downregulation in these taxa and pathways, along with a decline in key groups such as *Alteromonadaceae* and *Gammaproteobacteria*. These findings underscore how different carbon sources drive distinct patterns of metabolic activity in microbial communities, influencing algal production and potentially offering new strategies for optimizing industrial algae cultivation.

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