

Global Warming Induced Salinity Shifts: Metabolic Responses by Algal-Bacterial Consortia

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Abstract: The reality of global warming predicts that the survival of many organisms will be compromised due to rapid environmental changes of the ecosystems in which they live. Aquatic ecosystems are particularly vulnerable to shifts in climate. Large incursions of fresh water or water loss from lack of rainfall will cause modification in water chemistry. As a result, aquatic organisms dwelling in marine or fresh water regions will either adjust to these changes or die. In terms of maintaining aquatic ecosystem function, algae play a keystone role. As primary producers they fix CO₂ and often, because of their high fat content, serve as a highly nutritious food source for other eco-chorts. Algae live in a complex environment where they form tight associations with bacteria that act as their metabolic partners. The alga and bacterial complex are sometime so interdependent that the partners cannot survive alone. This study will analyze the impact of changing salinity on the metabolic interplay between the alga *Chrysochromulina tobin* (Haptophyceae) and its 10-membered bacterial biome. Using a systems biology approach, we will apply a genomic, transcriptomic, HPLC/MS and flow cytometric toolbox to better understand nitrogen processing, CO₂ fixation and fatty acid production by this alga-bacterial consortium. The *Chrysochromulina* bacterial team is an excellent choice for proposed research. The 59Mb genome sequence of *Chrysochromulina* has recently been published, 8 of the 10 bacterial genomes (and their plasmids) associated with this alga are also sequenced, preliminary transcriptome analysis is accomplished, and the salinity tolerance of the organism is well studied. Understanding how algal-bacterial co-partners survive physiological stress will also provide important insight to the maintenance of commercially valuable up-scaled algal production programs that target alternative energy and food security endeavors.