

Bacterial Succession Patterns in Algal Degradation: Identifying the Most Efficient Algal Degrading Communities

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Project Goals: Marine algae hold great promise for biofuel production and have advantages over terrestrial biomass and freshwater algae. Despite this potential, little effort has been made to date to harness the enzymatic machinery that bacteria use to convert marine algal carbohydrates into bioenergy substrates. Our project capitalizes on this unexplored opportunity via three distinct activities: bioprospecting for novel algal polysaccharide-degrading genes, functional screening for enzymes with desired biochemical properties, and repackaging pathways in reusable genetic modules.

In the marine ecosystem, macroalgae are both fast growing carbon producers and major carbon sinks; they represent half of the carbon production and three-quarters of the biomass in coastal oceans. Studying the organisms and metabolic pathways that are involved in natural degradation of macroalgae could help improve our understanding of marine energy flow. This research also has potential to provide guidelines for synthetic community design in using macroalgae as a feedstock for biofuel production. In a microcosm experiment with *Fucus* extract as the sole carbon source provided, we found that different natural marine communities (surface seawater/sediment) followed similar community succession patterns. Only five bacterial families (*Halomonadaceae*, *Oceanospirillaceae*, *Pseudoalteromonadaceae*, *Rhodobacteraceae*, *Vibrionaceae*) increased to a relative abundance of 10% or more in the microcosm communities. The expansion of these families followed a strict sequential order. In another microcosm experiment performed, random subsets of a natural seawater community were generated by a removal-of-species-by-dilution method. Some of these subset communities were found to be 2-4 fold more productive than the original natural seawater community in terms of degrading *Fucus* extract. These two microcosm experiments suggest that specific combinations of bacteria from certain families may be optimal at degrading a complex carbon source such as *Fucus* material. These specific combinations will be further identified and characterized using a combination of culture-free and culture-based methods.

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