

92. The Ecology of Algal Polysaccharide Degradation: Characterizing Novel Fucoidan-Degrading Bacteria

Christopher Corzett^{1*} (corzett@mit.edu), Jan-Hendrik Hehemann,¹ **Martin Polz,¹** and **Eric Alm¹**

¹Massachusetts Institute of Technology, Cambridge, MA

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.

Marine macroalgae are vital players in the global carbon cycle, and polysaccharides represent a significant output of their primary production (~90% dry mass). Identifying the microbes and metabolic pathways responsible for degrading these sugars is not only crucial to understanding marine carbon flow, but also offers vast potential for biofuel production utilizing seaweed feedstocks. Fucoidans are an important class of structurally heterogeneous sulfated polysaccharides found in brown seaweeds, yet few organisms have been shown to metabolize this abundant carbohydrate. Using environmental samples from coastal waters we have isolated and characterized numerous representatives from diverse genera (*Vibrio*, *Lentimonas*, *Stappia*, *Neptunomonas*, *Alteromonas*, *Tenacibaculum*) capable of using fucoidan as a sole carbon source, and demonstrated enzymatic degradation of fucoidan polysaccharides using cellular extracts.

Preliminary findings also reveal differences in the dynamics and extent of fucoidan degradation among closely related isolates. These differences in enzymatic capabilities could reflect metabolic specialization and indicate resource partitioning occurs during the degradation of specific algal polysaccharides. Ongoing comparative genomic and transcriptional analyses aim to identify and characterize the enzymatic machinery and metabolic modules required for the efficient conversion of algal biomass.

This work is supported by the Office of Biological and Environmental Research in the Department of Energy Office of Science (DE-SC0008743).