Identifying the most efficient algal degrading communities: diversity, composition and mechanisms

Xiaoqian Yu[1][*](xy43@mit.edu), Christopher H. Corzett,[1] **Martin F. Polz[1] and Eric J. Alm**[1]

[1]Massachusetts Institute of Technology, Cambridge, MA, USA

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 fast growing primary producers representing half of the carbon production and three-quarters of the biomass in coastal oceans. They are thus a rapidly replenishing resource for bioenergy applications. We are currently studying the degradation of macroalgae by natural microbial communities addressing three principal questions: (i) How does the diversity of a microbial community affect its productivity? (ii) Are there specific microbial communities that are especially productive when growing on algal material? (iii) What are the community compositions of these microbial communities and what are the relevant mechanisms?

We performed a microcosm experiment where marine microbial communities with different diversity and composition were generated from a natural seawater community using a removal-of-species-by-dilution method. All communities were supplemented with one of the three following substrates: macroalgal (*Fucus*) extract, alginate (major structural polysaccharide of *Fucus*), or mannose (monosaccharide precursor for many sugars in *Fucus*). For all substrates, we found that the most productive communities were not those with the highest diversity, but those that were dominated by 3-4 species of bacteria after a period of growth during which the more productive species have been selected for. Specifically, for communities supplemented with alginate, we were able to identify a few genera of bacteria that were important predictors of community productivity using a random forest model. The most important predictor genera in the model was *Shewanella*, known for having versatile electron-accepting capacities that allow them to couple organic matter decomposition to various terminal electron receptors in different environments. All other top predictors belonged to the order *Alteromonadales* or *Oceanospirillales*, both known for their abilities to degrade dissolved organic material. We are currently in the process of scaling up the microcosm experiment so we can apply ecological models to identify the relative roles of selection, resource partitioning, and interactions in the most productive communities. We will also perform comparative transcriptomics across communities with high, medium and low productivity to reveal how different organisms could cooperate to degrade algae and form a highly productive community. This will allow us to no longer be restricted to one single organism when packaging metabolic genes into useful genetic modules for algae degradation and biofuel production; the suite of genes can now be picked from and optimized across multiple organisms.