The Ecology of Algal Polysaccharide Utilization: Novel *Verrucomicrobia* Isolates Efficiently Degrade Fucoidan

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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.

Marine macroalgae are vital players in the global carbon cycle, and polysaccharides represent a significant output of their primary production. Identifying the microbes and metabolic pathways responsible for degrading these sugars is not only crucial to understanding marine carbon flow, but also offers potential for biofuel production using 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. Enrichment cultures from coastal samples yielded numerous isolates from diverse genera (*Vibrio, Stappia, Neptunomonas, Alteromonas, Tenacibaculum*) implicated in the breakdown of fucoidan polysaccharides, and novel *Verrucomicrobia* isolates performing an especially critical role in facilitating this process were sequenced. Draft genomes reveal Polysaccharide Utilization Loci (PULs) enriched with numerous and diverse Carbohydrate-Active Enzymes (CAZymes), with some isolates encoding as many as 60 genes with homology to established fucosidases. Differences in the dynamics and extent of fucoidan utilization among closely related isolates suggest variation in enzymatic capabilities and may reflect resource partitioning. Specific combinations of natural isolates appear to complement one another and yield greater overall biomass accumulation, suggesting engineered organisms or communities with a full repertoire of enzymatic machinery may facilitate the efficient conversion of algal biomass.