

## 91. Adaptive Radiation after Gene Transfer Leads to Population Specialization and Enhanced Glycan Cycling

Jan-Hendrik Hehemann<sup>1\*</sup> (hehemann@mit.edu), Manoshi Sen Datta<sup>1</sup>, Nathan Cermak<sup>1</sup>, Andreas Hentschel, Christopher Corzett<sup>1</sup>, Xiaoqian Yu<sup>1</sup>, **Martin Polz<sup>1</sup>**, and **Eric Alm<sup>1</sup>**

<sup>1</sup> Massachusetts 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.**

Polysaccharides produced by plants and algae represent the major source of food for life on Earth. The rate-limiting factor for their turnover is the activity of microbial carbohydrate active enzymes, or CAZymes, which split polysaccharides into smaller, consumable sugars. How microbes interact to drive glycan cycling in systems such as the human gut or the ocean is poorly understood. Genomic comparisons of 76 *Vibrio* genomes revealed a common degradation pathway for alginate, an important structural polysaccharide in brown algae. This pathway was acquired once via horizontal gene transfer and subsequently modified by gene loss and duplication in different lineages, leading to a cascade of interacting populations in the degradation of alginate. Some populations specialize in the breakdown of the polymer, while others have lost the dedicated enzymes for polysaccharide degradation (alginate lyases), but have retained the import proteins and enzymes (oligo-alginate lyases) for oligosaccharide degradation. Hence, some populations pioneer polymer breakdown, while others harvest the alginate oligosaccharides that diffuse away from the primary degraders, revealing an efficient mechanism of resource exploitation at the community level. Overall, this work illustrates that molecular understanding of CAZymes can be used to reconcile microbial food webs, thereby advancing our knowledge of how polysaccharides are so rapidly metabolized by natural microbial communities.

*This work is supported by the Office of Biological and Environmental Research in the Department of Energy Office of Science (DE-SC0008743). Jan-Hendrik Hehemann is supported by Human Frontiers Fellowship.*