Breaking down biomass with thermophilic bacteria

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Thermophilic bacteria, like the bacteria above that decorate the hot pools in Yellowstone National Park, hold key roles in the deconstruction of biomass. Credit: Bill Gracey

The deconstruction of biomass is a pivotal process in the biofuel industry, but the enzymes that possess a significant role in the breakdown of biomass remain relatively unexplored. To this end, DOE researchers at several national labs and user facilities are studying thermophilic bacteria, organisms that survive and thrive in high-

temperature environments, that contain these enzymes.

In a study published July 19, 2013 in *PLoS One*, a team of scientists including groups from DOE Joint Genome Institute, the Joint BioEnergy Institute, and the Environmental Molecular Sciences Laboratory researchers set out to further understand the specific proteins involved in biomass deconstruction in a thermophilic microbial community adapted to break down switchgrass, a candidate biofuel feedstock. The DOE JGI team sequenced and assembled metagenomic sequences while the EMSL team identified which proteins predicted by the metagenomics are produced by the microbial community.

The group was successful in reconstructing genomes for Thermus thermophilus and Rhodothermus marinus, two strains that made up a majority of the population samples. In addition, they were able to identify the phyla Paenibacillus and Gemmatimonadetes as important groups involved in biomass deconstruction. The results marked the first time that the functional roles of individual microbial populations within a consortium have been linked with specific enzyme activities. The team was able to identify more than 3,000 separate proteins associated with the breakdown of biomass, but the study indicates that there are even more unexplored proteins that could serve a purpose in this process.

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