Metagenomics, Metabolic Reconstruction, and High-Resolution Proteomics of Biomass Degradation in a Thermophilic Bacterial Community

Patrik D'haeseleer[1]*(PDHaeseleer@lbl.gov), John Gladden[1], Joshua Park[1], Alyssa Redding[1], Chris Petzold[1], Martin Allgaier[1], Dylan Chivian[1], Steve Singer[1], Terry Hazen[1], Blake Simmons[1]

[1]Joint BioEnergy Institute, Lawrence Berkeley National Laboratory, Emeryville, CA

www.jbei.org

Project Goals:

The Microbial Communities group at JBEI aims to develop a fundamental understanding of how microbial communities degrade targeted biomass feedstocks, and to utilize a targeted, function-based screening approach to genomics and proteomics to identify, isolate, and characterize new enzymes that are capable of efficiently degrading lignocellulosic feedstocks. Focusing on a thermophilic switchgrass-adapted enrichment community yields an order of magnitude more useful enzyme sequences compared to our previous work on a more complex community, and the resulting enzymes are more likely to be well suited to our targeted feedstock, pretreatment, and processing conditions. Combining enzymatic assays, metagenomics, zymography, MS proteomics, and metabolic modeling provides a multidimensional view of the internal functioning of this highly active biomass degrading bacterial community.

A microbial enrichment culture with high biomass degrading activity was selected for metagenomic sequencing, annotated using JGI's IMG/M system, and binned into phylogenetic groups. Metabolic reconstructions were generated using Pathway Tools, allowing us to assign metabolic roles to the different members of the bacterial community. High resolution MS metaproteomics by EMSL was mapped to the community members to analyze differential expression of their metabolic pathways and identify highly expressed biomass degrading enzymes.

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