218. Pan-omics Biological Applications in the Genome Sciences Program

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Project Goal: The Pan-omics Program includes efforts that involve a broad spectrum of analytical measurements acquired using advanced mass spectrometry-based measurement pipelines. The Biological Applications portion of the Pan-omics Program works in collaboration with GSP scientists, and utilizes these measurements to advance the fundamental understanding of biological systems important to DOE missions. These pan- omics measurements, integrated with genomic and transcriptomics data, will increasingly enable predictive models, as well as the monitoring, manipulation or control of complex biological systems. Currently, collaborative projects range from studies involving novel microbial species to highly diverse ecosystems including interactions between bacteria, fungi, plants, and insects. The understanding of the complex regulatory and functional interactions necessary to provide predictions for optimal production for reengineered organisms or the elucidation of emergent properties in climate and carbon-cycling process will benefit from a range of pan-omics measurement capabilities.

We present below several examples from present collaborations efforts conducted under the Biological Applications portion of the Pan-omics Program. These examples illustrate misson specific areas of interest to the DOE, including terrestrial carbon cycling, ligno-cellulose deconstruction, and the impacts of climate change on ecosystems.

Leaf-cutter ants are dominant herbivores in ecosystems throughout the Neotropics that feed on fungal gardens cultivated on fresh foliar biomass. While the cycling of nutrients that takes place in these specialized microbial ecosystems is still not well understood, pan-omic investigations in collaboration with Dr. Cameron Currie (University of Wisconsin; Madison) have revealed that: the fungus, Leucoagaricus gongylophorus, plays a dominant role in breaking down cellulose, lignin, and pectin, while the bacterial community and the fungus break down simple oligosaccharides and hemicelluloses

Relative abundances of L. gongylophorus Carbohydrate-Active Enzymes (CAZyme) (blue), Lignin-degrading FOLyme (magenta), and Proteases (brown) protein families in the top (T), middle (M), and bottom (B) strata of Ac. echinatior and At. cephalotes gardens. regrading organisms ever cultured from the cow rumen, but the mechanism of cellulose degradation involving the direct attachment of the organism to the plant material has never been elucidated. Working with Dr. Garrett Suen (University of Wisconsin; Madison), pan-omics measurements have identified a novel mechanism for cellulose deconstruction that falls between cellulosome associated and fully secreted mechanisms.

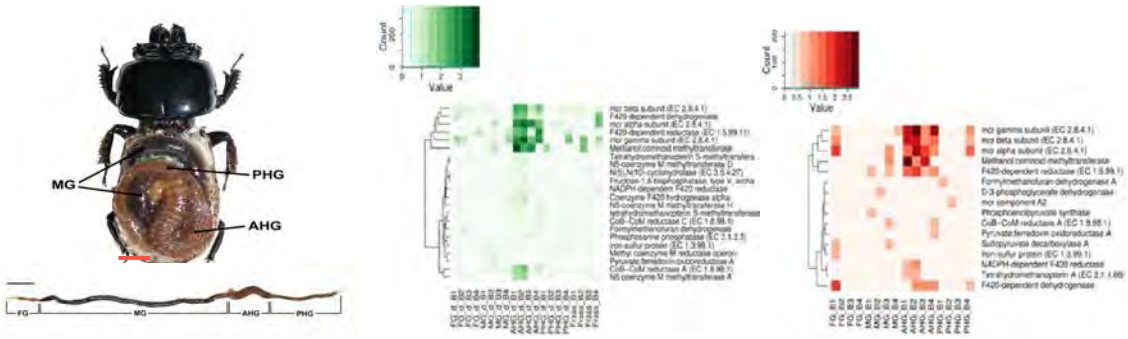
Cytoplasmic membrane Periplasmic space Outer membrane

Cellulose Fibers

Fibroslime protein
= CAZy protein
= Pilin structure= Cellulase

A proposed mechanism for cellulose deconstruction is being evaluated using pan-omics measurements, where plant fiber is mediated by fibroslime proteins, pilin like structures, and CAZy by way of ABC transporters into periplasmic space where cellulose is deconstructed through interaction with cellulases.

In phototrophic dominated microbial communities, carbon excretion by microbial mat primary producers, Cyanobacteria, is key to our understanding of carbon cycling but carbon excretion for extracellular matrix production is not well understood. In collaboration with Drs. Jennifer Pett- Ridge and Rhona Stuart (LLNL), pan-omic investigation of microbial mat extracellular matrix basic composition revealed a reservoir of starch-like (α-linked) oligosaccharides, cyanobacterial exoproteins and extracellular enzyme activity that are involved in breakdown of carbohydrates, Changes in extracellular protein abundance and enzyme activity of the Cyanobacteria in culture are diel and light dependent, and seem to be most active during the day.



Proteomics measurments determine that methanogenesis activity is localized in the anterior hind gut of the Passalid beetles.

Passalid beetles colonize decaying hardwoods, posses a high potential for lignocellulose degradation, and are a potential source of efficient xylose fermenting yeasts used for cellulosic ethanol production. Recent meta proteomic investigations into the microbial communities resident in the gut of the beetle, in collaboration with Dr. Eoin Brodie (LBNL) and Dr. Jennifer Pett-Ridge (LLNL) reveal nitrogenase and CAZY activities distributed through out the 4 regions of the gut, but methanogenesis activities localized to the anterior hind gut.