Omics Research at the Joint BioEnergy Institute (JBEI)

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Omics research at JBEI is part of the Technologies division and provides enabling tools for a variety of cell wide and analytical measurements required for a Biofuels research program. For the conversion of sugars derived from deconstructed lingo-cellulosic biomass to fuel compounds, an important area of research is on engineered organisms that contain combinations of native and non-native biochemical pathways for the production of a target metabolite and also efforts to understand the causes of toxicity/ stress during such applications. For example, the incorporation of exogenous biochemical pathways into a host organism places unregulated strain on the cell by consuming metabolites, energy and critical cofactors creating an imbalance that will trigger a variety of stress response systems. While these stress responses may be useful to the cell in such an environment, they are unfavorable in an engineering context and reduce product yield or viability during production culturing. Systems biology, built on the foundations of omics studies (genomics, proteomics, metabolomics and fluxomics), enables a comprehensive view of the impact of an exogenous pathway on the host within the context of its full metabolism. To match the requirement of such high-throughput profiling of particular classes of cellular components, genes, proteins and metabolites, our capabilities now include microarray analysis and high resolution mass spectrometry (combined with LC, GC, and CE for shotgun proteomics, targeted protein studies, primary and secondary metabolite analysis and glycomics). In collaboration with the computational core we also have powerful data analysis and integration tools. These functional genomics workflows are now being applied to gather data for the effect of (1) exposure of deconstruction conditions (Ionic liquids, post saccharification mix from simple and complex cellulose sources), (2) accumulation of endogenous and exogenous target metabolites and (3) impact of different growth condition and expression of the biosynthetic pathway proteins in our model host microbes (E. coli, S. cerevisiae). Specifically the use of targeted proteomics using the MRM workflow has proved valuable in gauging the presence of a complete engineered pathway. Finally, the functional genomics and analytical tools described above are also being extensively used by the Feedstock division for a molecular characterization of cell wall and by the Deconstruction division in meta-genomic studies.