

50003

Engineering enzyme networks for biomass deconstruction in synthetic microbial communities

Steven J. Hallam

University of British Columbia

Abstract: Lignocellulose, the main component of plant cell walls, is arguably the most abundant biopolymer on the planet. Through biorefining, it is also a renewable input for energy and materials production. Valorization of the three major components of lignocellulose biomass “cellulose, hemicellulose and lignin” is critical for the sustainability of next generation biorefineries. Production of energy and materials from plant biomass will lower our dependence on fossil fuels and reduce greenhouse gas emissions ushering in a more sustainable bioeconomy. Particular types of woody biomass (e.g., poplar, pine), agriculture residues (e.g., corn stover) and perennial grasses (e.g., miscanthus, switchgrass) have emerged as preferred feedstocks, in part because they do not compete with food crops. To harvest fermentable sugars and aromatics provided in plant biomass, mechanical, chemical and biological processes have been developed. However, efficient deconstruction of biomass remains a significant barrier to its utilization. This recalcitrance is due principally to heterogeneity of lignin and its complex association with polysaccharides. The discovery and design of cost effective and efficient biocatalysts enabling generation of a “funneling platform” for biomass deconstruction is integral to scalable production in modern biorefining ecosystems. While rot-fungi are traditionally associated with the process of lignin transformation in a free radical process compared to combustion, recent studies indicate a role for bacteria in converting lignin into a range of potentially useful monoaromatic product profiles. Given the increased tractability of bacterial expression systems and the wide range of product profiles offered by bacterial lignin transforming enzymes there is increasing interest in determining the functional capacities bacterial networks driving lignin transformation in the environment and harnessing this information in the design of whole cell biocatalysts that improve biorefining process streams. Here, we will use ‘omic studies spanning multiple levels of biological information (DNA, RNA and metabolites) to monitor and reconstruct bacterial biomass deconstruction processes in synthetic microbial communities constructed from environmental genomic (fosmid) libraries. These libraries are sourced from soil ecosystems through a long-term soil productivity (LTSP) study of soil organic matter relating to tree harvesting practices at over 110 sampling sites throughout North America. The construction of synthetic bacterial communities from LTSP sites through pooling and selective enrichment will provide a platform for examining catabolism of lignocellulose substrates and resolve novel genes and gene cassettes mediating this process in soil microbiomes. Resulting genomic resources and sequence information will guide assembly of more efficient biological platforms (i.e. synthetic consortia, novel enzymatic cocktails, etc.) for energy and materials production in modern biorefining ecosystems.