

Pleiotropic and Epistatic Network-Based Discovery: Integrated SNP Correlation, Co-Expression and Genome-Wide Association Networks for *Populus trichocarpa*

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Project Goals: The BioEnergy Science Center (BESC) is focused on the fundamental understanding and elimination of biomass recalcitrance. BESC's approach to improve accessibility to the sugars within biomass involves (1) designing plant cell walls for rapid deconstruction and (2) developing multi-talented microbes or converting plant biomass into biofuels in a single step (consolidated bioprocessing). BESC researchers provide enabling technologies in biomass characterization, 'omics, modeling and data management in order to (1) understand chemical and structural changes within biomass and (2) to provide insights into biomass formation and conversion mechanisms.

Biological organisms are complex systems that are composed of pleiotropic functional networks of interacting molecules and macro-molecules. Complex phenotypes are the result of orchestrated, hierarchal, heterogeneous collections of expressed genomic variants. However, the effects of these variants are the result of historic selective pressure and current environmental and epigenetic signals, and, as such, their co-occurrence can be seen as genome-wide correlations in a number of different manners. Biomass recalcitrance (i.e., the resistance of plants to degradation or deconstruction, which ultimately enables access to a plant's sugars) is a complex polygenic phenotype of high importance to the U.S. Department of Energy's biofuels programs. We are using data derived from the re-sequenced genomes from over 1000 alternate *Populus trichocarpa* genotypes in combination with transcriptomics, metabolomics and phenomics data across this population in order to better understand the molecular interactions involved in recalcitrance. The resulting Genome Wide Association Study networks, integrated with SNP (single nucleotide polymorphism) correlation and co-expression networks, are proving to be a powerful approach to determine the pleiotropic and epistatic relationships underlying cellular functions and, as such, the molecular basis for complex phenotypes, such as recalcitrance.

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