

## Highly Resolved Genome-Wide Association Mapping (GWAS) Reveals Novel Variants for Engineering Increased Biomass Yield in *Populus trichocarpa*

Wellington Muchero,<sup>1\*</sup> ([mucherow@ornl.gov](mailto:mucherow@ornl.gov)), Jin-Gui Chen,<sup>1</sup> Stephen P. DiFazio,<sup>2</sup> Luke Evans,<sup>2</sup> Gancho Slavov,<sup>2</sup> Eli Rodgers-Melnick,<sup>2</sup> Priya Ranjan,<sup>1</sup> Joel Martin,<sup>3</sup> Wendy Schackwitz,<sup>3</sup> Jeremy Schmutz<sup>3</sup>, Kathy Haiby,<sup>4</sup> Richard Shuren,<sup>4</sup> Brian Stanton,<sup>4</sup> and **Gerald A. Tuskan**<sup>1</sup>

<sup>1</sup> The Center for Bioenergy Innovation and BioEnergy Science Center, Oak Ridge National Laboratory, Oak Ridge, Tennessee, <sup>2</sup>Department of Biology, West Virginia University, Morgantown, West Virginia, <sup>3</sup>DOE Joint Genome Institute, Walnut Creek, California, <sup>4</sup>GreenWood Resource Inc., Portland, Oregon

<https://cbi.ornl.gov>

**Project Goals:** The Center for Bioenergy Innovation (CBI) vision is to *accelerate domestication of bioenergy-relevant, non-model plants and microbes to enable high-impact innovations at multiple points in the bioenergy supply chain*. CBI will address strategic barriers to the current bioeconomy in the areas of: 1) high-yielding, robust feedstocks, 2) lower capital and processing costs via consolidated bioprocessing (CBP) to specialty biofuels, and 3) methods to create valuable byproducts from the lignin. CBI will identify and utilize key plant genes for growth, composition and sustainability phenotypes as a means of achieving lower feedstock costs, focusing on poplar and switchgrass. We will convert these feedstocks to specialty biofuels (C4 alcohols and C6 esters) using CBP at high rates, titers and yield in combination with cotreatment or pretreatment. And CBI will maximize product value by *in planta* modifications and biological funneling of lignin to value-added chemicals.

Undomesticated and outcrossing plant species such as *Populus trichocarpa* have a surprising ability to maintain high-levels of defective alleles among genotypes across their species ranges. As such, high-resolution genome-wide association mapping (GWAS) provides an unparalleled opportunity to resolve loci with large allelic effects on complex traits like biomass yield. Here, we summarize results of a GWAS study leveraging a panel of >8.2 million single nucleotide polymorphisms (SNPs) segregating in population of 1,084 *P. trichocarpa* genotypes established in replicated field sites in California and Oregon. Multi-year measurements of biomass indicators -- height, diameter and sylleptic branching, were collected between 2009 and 2017. Genotype-to-phenotype correlations were performed using mixed liner models with kinship as a covariate. This analysis revealed twelve reproducible associations that were statistically significant after correcting for multiple testing using the Bonferroni approach. Notably, these loci harbored genes including a DELLA family transcription factor previously implicated in gibberellic acid signaling, cell proliferation and internode elongation and expansion, a Cell Division Control protein 48-homolog with established roles in cell cycle regulation, and an XBAT35, a gene with known roles in lateral root production via ethylene biosynthesis. Allelic variants of these genes conferring increased biomass yield are being incorporated in genomic selection algorithms to expedite domestication of high yielding *Populus* genotypes and cis-genic validation of the molecular basis of their function is also underway.

*The Center for Bioenergy Innovation is a U.S. Department of Energy Bioenergy Research Center supported by the Office of Biological and Environmental Research in the DOE Office of Science.*