Population-Level Genomics Enable Bioengineering of Biomass Cell Wall Properties and Sustainability Traits

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Undomesticated and outcrossing plant species such as *Populus trichocarpa* exhibit high levels of allelic variation across their species ranges. As such, high-resolution genome-wide association mapping (GWAS) utilizing these populations provides an unparalleled opportunity to resolve loci with large allelic effects on complex cell wall and adaptive traits that have been shaped by decades to centuries of genome evolution. Here, we summarize results of GWAS studies leveraging a panel of > 60 million single nucleotide polymorphisms (SNPs) segregating in population of 1,500+ *P. trichocarpa* genotypes established in replicated field sites in California and Oregon. We reveal allelic variants that are associated lignin and carbohydrate properties, root and shoot architecture, bud phenology, photosynthetic efficiency, disease resistance and tolerance to biotic stresses including drought. CRISPR-Cas genome editing targeting these alleles is providing systems-level understanding of the function of these variants and their specific roles in bioengineering biomass for industrial applications.