

Natural Variation of Lignin Metabolism in Poplar

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Lignin is a major biopolymer found in nature, especially in woody plant cell walls, with important economic implications for papermaking and biorefining industries. Natural genetic diversity within plant species can be used as a valuable resource in genome-wide association studies (GWAS) for identifying genes that contribute to phenotypic variation in physiological traits. In this study, we measured lignin amount and composition by thioacidolysis GC-MS in developing xylem samples from 433 individuals of a *Populus trichocarpa* population distributed along the Northwest coast of North America. Whole-genome resequencing data of these trees, coupled with multitrait association analyses, were used to detect genes underlying the variation in lignin amount and monomer composition. A subgroup of individuals with phenotypically extreme lignin composition was selected for further gene expression analyses and saccharification assays. Our results show a wide variation in the two major monolignols (G and S) among natural poplar variants. In addition to association with the biosynthetic gene Ferulate-5-Hydroxylase (F5H), we found that the polymerization of lignin by laccases (Lac) has a major role driving the lignin composition changes observed, with PtLac4 and PtLac17 displaying higher affinity for sinapyl alcohol as substrate. Furthermore, trees with extreme S/G ratios displayed different gene expression patterns and cell wall saccharification efficiency for biofuel production. Our work expands our knowledge on the regulation of lignin composition in trees and paves the way to generate natural biopolymers and high value chemicals from poplar.