Combined GWAS And eQTL Analysis Uncovers Novel Genetic Regulatory Networks for Lignin and Carbohydrate Biosynthesis in *Populus trichocarpa*

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Lignocellulose, primarily composed of cellulose, hemicellulose, and lignin, constitutes the main components of plant cell walls. Poplars (*Populus* spp.), due to their rapid growth and broad geographic distribution, have become an economically important tree species, providing lumber, paper, and bioenergy feedstocks. Despite the economic and ecological significance of poplar, the genetic regulation of lignocellulose biosynthesis remains poorly understood. In this study, we utilized an integrative approach, combining 1) robust genome-wide association study (GWAS) using multiple traits measured in three distinct techniques, 2) expression quantitative trait loci (eQTL) analysis, and 3) co-expression analysis, to investigate the genetic regulation of lignocellulose biosynthesis in the model species *Populus trichocarpa*. Our study identified four key genes significantly involved in lignocellulose formation, with one known gene and three novel genes discovered. Among these genes, Potri.005G116800 has been previously established as a critical regulator of secondary cell wall formation. Genes Potri.012G130000, Potri.004G202900, and Potri.002G216300 exhibit both upstream and downstream networks involved in cell wall biosynthesis and defense responses. Furthermore, we uncovered the importance of candidate genes in lignocellulose formation and present a gene network based on information in the eQTL analysis. The integration of these methodologies enabled the discovery of new putative regulators of lignocellulose development. Our findings provide valuable insights into the genetic regulation of lignocellulose development in *P. trichocarpa* and lay the foundation for future genetic engineering of cell wall properties to optimize biomass traits.