Systems Genetics in Poplar: Identification of Candidate Genes for the Transport and Deposition of Cell Wall Precursors During Wood Formation

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Lignin is a phenolic polymer that plays critical roles, stiffening secondary cell walls for structural support to aerial organs while also protecting polysaccharides from microbial degradation, which reduces amenability of biomass for certain bio-energy applications like biofuels. The initial steps required for monolignols monomers production through the phenylpropanoid biosynthetic pathway have been extensively studied in different plants including some woody species. The subsequent steps required for monolignol export to the apoplast and polymerization into the cell wall however remain poorly characterized in a biomass crop like poplar. In model plants, members of multiple protein families were shown to contribute to lignification. This includes large families of transporters, oxidases such as laccases and peroxidases that mediate radical coupling of the monolignols to the lignin polymer, and non-catalytic dirigent proteins that are thought to guide stereoselective coupling of monolignols at the initiation sites of lignification in the cell wall. In poplar, genome-wide association studies pointed to multiple transporters, proteins involved in vesicle trafficking, and dirigent proteins as potential key determinants of biomass traits such as lignin composition and structure. By integrating population-wide genetic and transcriptomic information into systems genetics approaches, we identified a subunit of the Exocyst complex, a synaptobrevin, and several members of the dirigent protein family that could be directly involved in the transport and biosynthesis of cell wall polymers and their precursors during wood formation in poplar. We further investigate the function of these genes using reverse genetics approaches to explore the potential of these candidate genes for biomass engineering in poplar.