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DECODING LIGNIN IN SWEDISH ASPEN

Paths to Better Feedstocks and Resilient Trees

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Abstract

Trees are vital to our environment because they support biodiversity, carbon sequestration, oxygen production, and many other environmental functions. The lignocellulosic biomass produced by trees is also a renewable source of green products that can replace fossil fuel-derived products. More recently, their importance has been recognized as carbon sinks that assimilate atmospheric carbon dioxide into organic biomass. Climate change will expose trees to various environmental stresses and pathogens, and due to their sessile nature, trees rely on genetic diversity to survive and adapt. For instance, natural variation in resistance to pathogens allows trees to pass important resistance factors to their progeny and facilitate adaptation. Genome-wide methods have been developed to elucidate the molecular mechanisms underlying natural variation in important tree traits, which could be used in breeding for improved forest feedstocks.

In this thesis, the Swedish Aspen collection of *Populus tremula* trees (the SwAsp collection) was used as a resource to study natural variation in traits influencing tree biomass accumulation, pathogen resistance, and biomass processability. In addition, a systems genetic approach, including genome-wide analysis of expression quantitative trait loci (eQTL) and genome-wide association studies (GWAS), was taken to elucidate factors influencing variation in lignin biosynthesis in the SwAsp population. We identified biomass traits, in particular stem diameter and height, as the most critical factors influencing overall saccharification yield in this population based on multivariate analyses. We uncovered new regulatory aspects of lignin biosynthesis. Through GWAS, we detected genetic associations for saccharification, guaiacyl (G)- and syringyl (S)-type lignin subunits in young ramets and fungal resistance, providing potential molecular markers for these traits. We also validated parts of our results using reverse genetics and an independent aspen collection. Finally, two soft rot fungal genera, *Ascocoryne* and *Cadophora*, were identified as highly abundant fungal pathogens in the ramets of the SwAsp trees. The symptoms of the fungal infections varied within the SwAsp population, and their extent correlated positively with the abundance of the p-hydroxyphenyl (H)-type lignin.

This thesis highlights natural variation in traits significant for forest tree improvement, such as biomass accumulation, wood traits, and pathogen resistance, within the Swedish aspen population. It also provides details that help to understand lignin biosynthesis and fungal resistance in deciduous trees cultivated in short-rotation plantations. The identification of genetic and molecular markers for many of these traits contributes to efforts in tree breeding to enhance the resilience and utility of forest trees in the face of climate change.

Keywords

Lignin, aspen, natural variation, systems genetics, cell wall, genome-wide association, fungi, saccharification, lignocellulosic biomass, transcription factor, population, single nucleotide polymorphism

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