

GWAS-eQTL Integration – Uncovering Regulators of Lignocellulose Biosynthesis in *Populus*

Background

- Genome-Wide Association Studies (GWAS) in *Populus* often face challenges in providing biological context for trait-associated loci, making it challenging to identify the underlying genes and regulatory networks. This limitation constrains the potential to solely leverage GWAS results for improving lignocellulose traits critical for bioenergy production.

Approach

- We integrated GWAS, expression quantitative trait loci (eQTL) analysis, and co-expression networks to link nucleotide variants to measured lignocellulose traits in *Populus trichocarpa*. This multiple lines of evidence approach enabled the identification of candidate genes involved in lignocellulose formation by providing a comprehensive biological context around the associated loci.

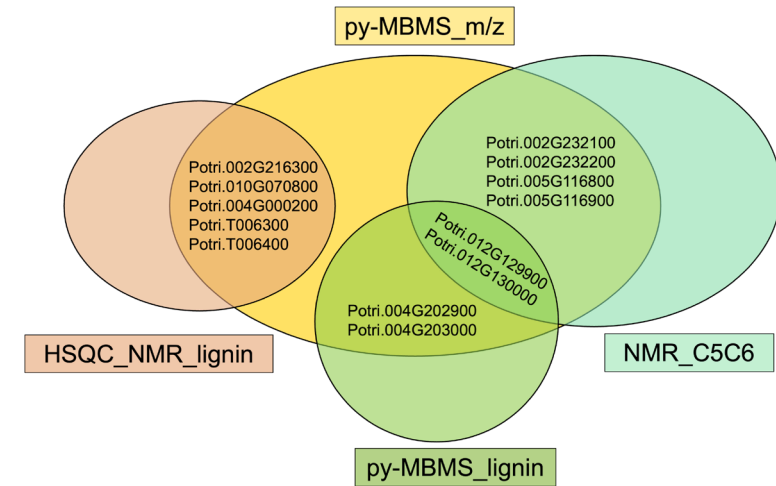
Results

- We identified candidate genes linked to lignocellulose biosynthesis including:
 - Potri.005G116800/VND1: A critical regulator of secondary cell wall formation.
 - Potri.012G130000/AtSAP9: Newly associated with lignin biosynthesis and stress responses.
 - Potri.004G202900/BIC1: Newly linked to lignin biosynthesis and defense mechanisms.
- Our integrative framework demonstrated that combining GWAS with eQTL and co-expression network analysis enhances the biological interpretation of GWAS results, providing deeper insights into the genetic regulation of lignocellulose traits.

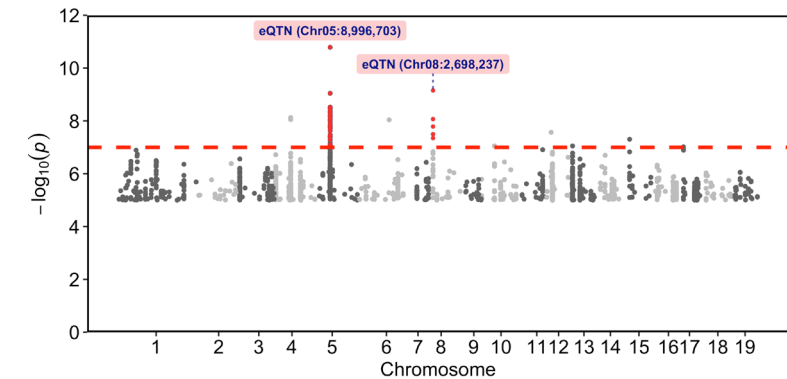
Significance

- This study demonstrates the power of integrating genomic and transcriptomic data to uncover key regulators of lignocellulose biosynthesis. By providing a deeper understanding of the genetic networks controlling biomass traits, the findings offer valuable targets for genetic manipulation to improve both biomass yield and quality, crucial for advancing bioenergy production.

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Overlapping genes identified via GWAS analyses on four sets of lignocellulose traits in *Populus trichocarpa*. Traits include: 28 py-MBMS_m/z, 2 py-MBMS_lignin, 6 NMR_C5C6, and 11 HSQC_NMR_lignin).



Manhattan plot of eQTL analysis for the annotated gene Potri.005G116800 for SNP Chr05:9012 325 in xylem tissue.