Rapid gene discovery and validation using the BESC *Populus* association population

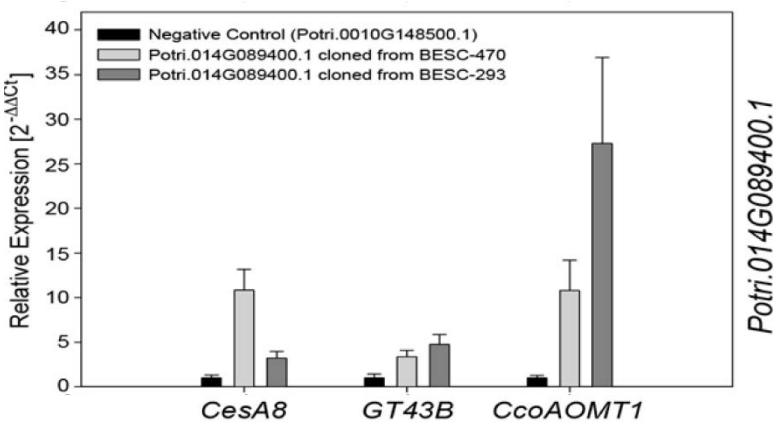
U.S. DEPARTMENT OF ENERGY | Office of Science

Background

- The process for Identifying genes mediating cell wall recalcitrance in long-lived perennial trees has largely been restricted to inferring candidate genes from model plant systems.

Approach

- Common gardens with a thousand *Populus* individuals were established.
- Whole-genome resequencing (with JGI) and SNP genotyping were used to saturate candidate intervals and identify causal mutations with single-gene resolution.
- Multi-year and multi-environment cell wall phenotypes were measured in this interspecific mapping pedigree and two partially overlapping populations of unrelated *P. trichocarpa* genotypes using biomass composition and saccharification.
- QTL mapping was conducted using a high-density genetic map with 3,568 SNP markers distributed across 19 chromosomes.



One example of gene discovery: Differences in activation of reporter genes CesA8 (cellulose), GT43B (hemicellulose) and CCoAOMT1 (lignin) by allelic variants of Angustifolia CtBP transcription factor in a protoplast assay.

Outcome

- 37 significant SNPs were mapped within or adjacent to the 6 candidate genes on chromosome XIV which exhibited reproducible significant association with cell wall chemistry phenotypes in drastically different environments.
- Transient protoplast assays were used to validate predicted functions of 3 transcription factors identified in this study.

Significance

- Complementary QTL and association mapping are powerful tools for rapid gene discovery with no *a priori* candidate gene selection. This proof of concept in a perennial organism opens up opportunities for discovery of novel genetic determinants of economically important but complex traits in plants.

A four-year-old *P. trichocarpa* in a common garden

BESC BioEnergy Science Center

Muchero, *et al*., "High-resolution genetic mapping of allelic variants associated with cell wall chemistry in *Populus*," *BMC Genomics,* 16:24 2014. doi: 10.1186/s12864-015-01215-z