

A Key Regulator is Confirmed for Adventitious Root Formation in Populus

Background

- Clonal propagation and plant establishment is utilized to conserve elite plant genotypes. The formation and growth of adventitious roots (AR) are essential for success of clonal propagation for perennial tree species and for rapid deployment of the best poplar genotypes.

Approach

- Taking advantage of natural variation within our GWAS *Populus trichocarpa* common gardens and transcriptomics data, we identified genetic determinants of plant growth and development and elucidated the underlying transcriptional regulatory networks using eQTL (expression quantitative trait loci) methods.
- After identifying potential master regulators of transcriptional regulation, we validated their function by molecular and genetic studies. We further used Omics analyses and biochemical assays to determine the molecular signatures and the underlying molecular mechanism in *P. trichocarpa*.

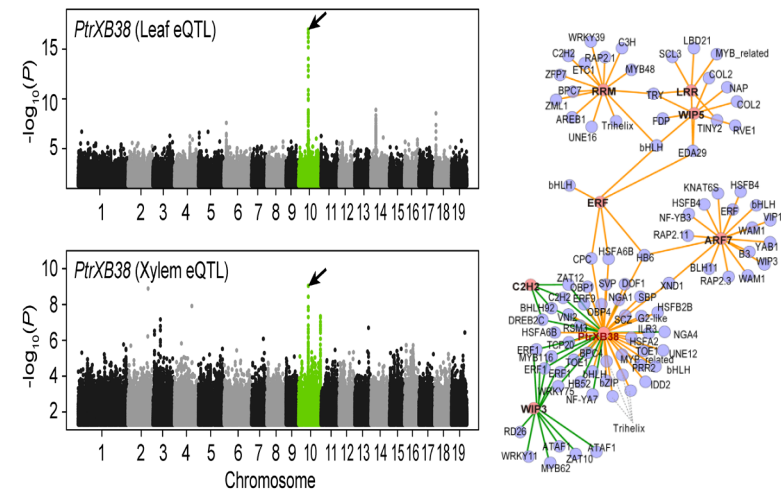
Results

- We identified a member of C3HC4-type E3 ligase family, designated as PtrXB38, as a hub regulatory gene that is associated with expression of over 500 genes in *Populus*.
- Overexpression of PtrXB38 resulted in drastic increase in callusing and formation of both stem-born roots and base-born adventitious roots in *Populus*.
- Omics studies revealed that genes and proteins controlling auxin transport and signaling were involved in PtrXB38-mediated adventitious root formation. Protein-protein interaction assays indicated that PtrXB38 interacts with components of endosomal sorting complexes required for transport machinery, revealing a possible underlying mechanism of action of PtrXB38 in the regulation of endocytosis pathway.

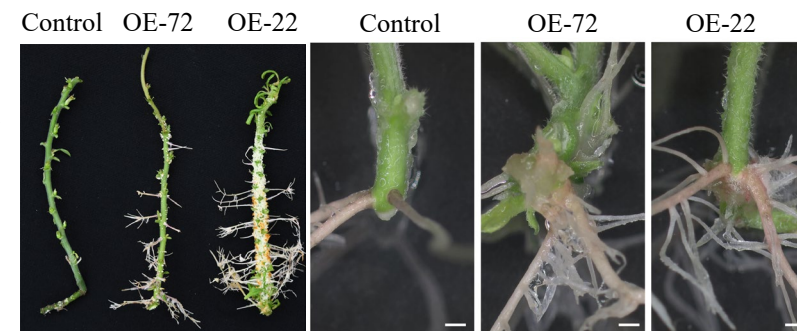
Significance

- This work identified a crucial root development regulator involved in hormone signaling, nitrate uptake and hypoxia tolerance -- making it a target for engineering elite plant feedstocks in marginal environments.
- These results show the power of association genetics, followed by reverse genetics validation and omics analyses, for discovering novel plant development regulators in woody plants.

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eQTL mapping of *P. trichocarpa* population identified PtrXB38 as a developmental regulator via a cis-eQTL hotspot in leaf and xylem. Associated single nucleotide polymorphisms in the *PtrXB38* locus on chromosome 10 (green) is marked with arrow. TF-based PtrXB38 regulatory network from eQTL network and expression profiles represent first layer (brown nodes) and second layer (blue nodes).



Validation of AR formation from stem (left) and stem base (right) of *Populus PtrXB38* overexpression transgenic lines (OE-72 and OE-22) in comparison with wild type control.