



# Association Studies in *Populus tomentosa* Reveal the Genetic Interactions of *Pto-MIR156c* and Its Targets in Wood Formation

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MicroRNAs (miRNAs) regulate gene expression in many biological processes, but the significance of the interaction between a miRNA and its targets in perennial trees remains largely unknown. Here, we employed transcript profiling and association studies in *Populus tomentosa* (*Pto*) to decipher the effect of genetic variation and interactions between *Pto-miR156c* and its potential targets (*Pto-SPL15*, *Pto-SPL20*, and *Pto-SPL25*) in 435 unrelated individuals from a natural population of *P. tomentosa*. Single-SNP (single-nucleotide polymorphism) based association studies with analysis of the underlying additive and dominant effects identified 69 significant associations ( $P < 0.01$ ), representing 51 common SNPs (minor allele frequency  $> 0.05$ ) from *Pto-MIR156c* and its three potential targets, with six wood and growth traits, revealing their common roles in wood formation. Epistasis analysis uncovered 129 significant SNP-SNP associations with ten traits, indicating the potential genetic interactions of *Pto-MIR156c* and its three putative targets. Interestingly, expression analysis in stem (phloem, cambium, and xylem) revealed that *Pto-miR156c* expression showed strong negative correlations with *Pto-SPL20* ( $r = -0.90$ ,  $P < 0.01$ ) and *Pto-SPL25* ( $r = -0.65$ ,  $P < 0.01$ ), and a positive correlation with *Pto-SPL15* ( $r = 0.40$ ,  $P < 0.01$ ), which also indicated the putative interactions of *Pto-miR156c* and its potential targets and their common roles in wood formation. Thus, our study provided an alternative approach to decipher the interaction between miRNAs and their targets and to dissect the genetic architecture of complex traits in trees.

**Keywords:** association genetics, *Pto-miR156c*, miRNA-mRNA, interaction, epistasis, wood formation

## INTRODUCTION

MicroRNAs (miRNAs) are small non-coding RNAs (20–24 nt) that function in gene regulation as sequence-specific regulators, via post-transcriptional mRNA cleavage or inhibition of gene expression in eukaryotes (Voinnet, 2009). In plants, miRNAs have influential roles in development (Rubio-Somoza and Weigel, 2011) and resistance to stresses such as drought and salinity (Frazier et al., 2011; Kruszka et al., 2012). Thus, studying miRNAs can provide important information