



Allelic Interactions among *Pto-MIR475b* and Its Four Target Genes Potentially Affect Growth and Wood Properties in *Populus*

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OPEN ACCESS

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Specialty section:

This article was submitted to
Plant Genetics and Genomics,
a section of the journal
Frontiers in Plant Science

Received: 18 April 2017

Accepted: 31 May 2017

Published: 21 June 2017

Citation:

Xiao L, Quan M, Du Q, Chen J,
Xie J and Zhang D (2017) Allelic
Interactions among *Pto-MIR475b*
and Its Four Target Genes Potentially
Affect Growth and Wood Properties
in *Populus*. *Front. Plant Sci.* 8:1055.
doi: 10.3389/fpls.2017.01055

MicroRNAs (miRNAs) play crucial roles in plant growth and development, but few studies have illuminated the allelic interactions among miRNAs and their targets in perennial plants. Here, we combined analysis of expression patterns and single-nucleotide polymorphism (SNP)-based association studies to explore the interactions between *Pto-MIR475b* and its four target genes (*Pto-PPR1*, *Pto-PPR2*, *Pto-PPR3*, and *Pto-PPR4*) in 435 unrelated individuals of *Populus tomentosa*. Expression patterns showed a significant negative correlation ($r = -0.447$ to -0.411 , $P < 0.01$) between *Pto-MIR475b* and its four targets in eight tissues of *P. tomentosa*, suggesting that *Pto-miR475b* may negatively regulate the four targets. Single SNP-based association studies identified 93 significant associations ($P < 0.01$, $Q < 0.1$) representing associations of 80 unique SNPs in *Pto-MIR475b* and its four targets with nine traits, revealing their potential roles in tree growth and wood formation. Moreover, one common SNP in the precursor region significantly altered the secondary structure of the pre-*Pto-miR475b* and changed the expression level of *Pto-MIR475b*. Analysis of epistatic interactions identified 115 significant SNP-SNP associations ($P < 0.01$) representing 45 unique SNPs from *Pto-MIR475b* and its four targets for 10 traits, revealing that genetic interactions between *Pto-MIR475b* and its targets influence quantitative traits of perennial plants. Our study provided a feasible strategy to study population genetics in forest trees and enhanced our understanding of miRNAs by dissecting the allelic interactions between this miRNA and its targets in *P. tomentosa*.

Keywords: MiRNA, *Pto-MiR475b*, association study, allelic interaction, tree growth and wood formation

INTRODUCTION

MicroRNAs (miRNAs) are small, non-coding RNAs of 20 to 24 nucleotides and play key roles in post-transcriptional regulation of gene expression in eukaryotes (He and Hannon, 2004; Rogers and Chen, 2013). MiRNAs function by cleaving the transcripts or suppressing the translation of their target genes through near-perfect sequence complementation (Chen, 2005). Plant miRNAs