



The Interactions between the Long Non-coding RNA NERDL and Its Target Gene Affect Wood Formation in *Populus tomentosa*

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Long non-coding RNAs (lncRNAs) are important regulatory factors for plant growth and development, but little is known about the allelic interactions of lncRNAs with mRNA in perennial plants. Here, we analyzed the interaction of the NERD (Needed for RDR2-independent DNA methylation) *Populus tomentosa* gene *PtoNERD* with its putative regulator, the lncRNA NERDL (NERD-related lncRNA), which partially overlaps with the promoter region of this gene. Expression analysis in eight tissues showed a positive correlation between NERDL and *PtoNERD* ($r = 0.62$), suggesting that the interaction of NERDL with its putative target might be involved in wood formation. We conducted association mapping in a natural population of *P. tomentosa* (435 unrelated individuals) to evaluate genetic variation and the interaction of the lncRNA NERDL with *PtoNERD*. Using additive and dominant models, we identified 30 SNPs ($P < 0.01$) associated with five tree growth and wood property traits. Each SNP explained 3.90–8.57% of phenotypic variance, suggesting that NERDL and its putative target play a common role in wood formation. Epistasis analysis uncovered nine SNP-SNP association pairs between NERDL and *PtoNERD*, with an information gain of -7.55 to 2.16% , reflecting the strong interactions between NERDL and its putative target. This analysis provides a powerful method for deciphering the genetic interactions of lncRNAs with mRNA and dissecting the complex genetic network of quantitative traits in trees.

Keywords: association genetics, NERDL, lncRNA-mRNA interactions, epistasis, wood formation

INTRODUCTION

DNA methylation is a conserved epigenetic silencing mechanism that functions in many crucial plant growth and developmental processes, such as genomic imprinting and abiotic stress responses (Bird, 2002; Song et al., 2016). RdDM (RNA-directed DNA methylation), the most important and well-characterized DNA methylation pathway, is guided by 24-nt siRNAs, induces *de novo* cytosine methylation, and regulates gene expression (Le et al., 2014). RdDM occurs only in plants performing transcriptional gene silencing (TGS) involving the Pol IV-RDR2-DCL3