



The Role of DNA Methylation in Xylogenesis in Different Tissues of Poplar

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In trees, xylem tissues play a key role in the formation of woody tissues, which have important uses for pulp and timber production; also DNA methylation plays an important part in gene regulation during xylogenesis in trees. In our study, methylation-sensitive amplified polymorphism (MSAP) analysis was used to analyze the role cytosine methylation plays in wood formation in the commercially important tree species *Populus tomentosa*. This analysis compared the methylation patterns between xylem tissues (developing xylem and mature xylem) and non-xylem tissues (cambium, shoot apex, young leaf, mature leaf, phloem, root, male catkin, and female catkin) and found 10,316 polymorphic methylation sites. MSAP identified 132 candidate genes with the same methylation patterns in xylem tissues, including seven wood-related genes. The expression of these genes differed significantly between xylem and non-xylem tissue types ($P < 0.01$). This indicated that the difference of expression of specific genes with unique methylation patterns, rather than relative methylation levels between the two tissue types plays a critical role in wood biosynthesis. However, 46.2% of candidate genes with the same methylation pattern in vascular tissues (cambium, phloem, and developing xylem) did not have distinct expression patterns in xylem and non-xylem tissue. Also, bisulfite sequencing and transcriptome sequencing of *MYB*, *NAC* and *FASCICLIN-LIKE AGP 13* revealed that the location of cytosine methylation in the gene might affect the expression of different transcripts from the corresponding gene. The expression of different transcripts that produce distinct proteins from a single gene might play an important role in the regulation of xylogenesis.

Keywords: DNA cytosine methylation, different transcripts, methylation-sensitive amplified polymorphism (MSAP), tissue-specific DNA methylation, gene expression, poplar

INTRODUCTION

Trees constitute major parts of the biosphere and provide renewable resources for energy, pulp, paper products, and building materials (Plomion et al., 2001). *Populus tomentosa*, an important commercial tree species in northern China has been used as a model tree for biochemical analysis of lignin synthesis and for identification of candidate genes that function in lignocellulosic biosynthesis and growth, using association analysis (Du et al., 2013). However, the epigenetic