



当前位置: 网站首页 >> 成果一览 >> 重要论文 >> 正文

Transcriptome sequencing of active buds from *Populus deltoides* CL. and *Populus×zhaiguanheibaiyang* reveals phytohormones involved in branching

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论文题目: Transcriptome sequencing of active buds from *Populus deltoides* CL. and *Populus×zhaiguanheibaiyang* reveals phytohormones involved in branching

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论文摘要:

Branching in woody plants affects their ecological benefits and impacts wood formation. To obtain genome-wide insights into the transcriptome changes and regulatory mechanisms associated with branching, we used high-throughput RNA sequencing to characterize cDNA libraries generated from active buds of *Populus deltoides* CL. 'zhonglin2025' (BC) and *Populus×zhaiguanheibaiyang* (NC). '*Populus×zhaiguanheibaiyang*' has more branches and rapid growth, while *P. deltoides* CL. 'zhonglin2025' has fewer branches than NC. In this study, a total of 198.2 million high-quality clean reads were obtained from the NC and BC libraries. We detected 3543 differentially expressed genes (DEGs) between the NC and BC libraries; among them, there were 1418 down-regulated and 2125 up-regulated genes in the NC/BC comparisons. Gene Ontology functional classification of the differentially expressed genes indicated that they included 89 genes encoding proteins related to hormones biosynthesis, 364 related to hormone signaling transduction, and 104 related to the auxin efflux transmembrane transporter. In addition, we validated the expression profiles of the 16 DEGs by real-time quantitative PCR, and the results displayed similar expression patterns to those generated from high-throughput sequencing. Here, we identified global hormone regulatory patterns and differences in gene expression between NC and BC, and constructed a hormone regulatory network to explain branching in *Populus* buds. Moreover, candidate genes were also excavated for molecular breeding of particular plant types, and provides a starting point that will help in future investigations into the molecular mechanisms of branching in *Populus*.

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