

## **The Cellulose Synthase and Cellulose Synthase-Like Gene Superfamily in the *Populus* genome**

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One of the main objectives of growing forest plantation is to provide raw materials for cellulose fiber production. However, it is still unclear how cellulose biosynthesis is genetically controlled during wood formation. In this study we identified all of the possible cellulose synthase (*CesA*) and cellulose synthase-like (*CSL*) genes in the *Populus* genome. There exist multiple *CesA* and *CSL* genes represented by 18 and 26 genomic loci, respectively, in the tree species. The expression of these genes in various tissues was profiled by real-time PCR; and the wood formation-related *CesA* and *CSL* genes were identified. The analysis of the secondary structure of the gene products suggested that *CesA* and *CSL* might function in a variety of means to control cellulose properties in wood formation. The application of the genomic information to tree improvement will be discussed.

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