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Manuscript Title:

The gibberellin oxidase gene family in *Liriodendron chinense*: genome-wide identification and expression in response to abiotic stress and phytohormones

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Abstract:

Studying the gibberellin (GA) synthesis pathway can provide a basis for the directional breeding of *Liriodendron chinense* to meet market demand. However, a systematic analysis of GAox in the angiosperm *L. chinense* has not yet been reported. Here, we identified all LcGAox gene family members in *L. chinense*, which were classified into the three subgroups of GA20ox, C19GA2ox, and C20GA2ox. Comparison of the gene structure, conserve motifs, phylogenetic relationships, and syntenic relationships of gibberellin oxidase gene families in different species indicated that the gene functional differences may be due to the partial deletion of their domains during evolution. Furthermore, evidence for purifying selection was detected between orthologous GAox genes in rice, grape, *Arabidopsis*, and *L. chinense*. Analysis of the codon usage patterns showed that mutation pressure and natural selection might have induced codon usage bias in angiosperms; however, the LcGAox genes in mosses, lycophytes, and ambarella plants exhibited no obvious codon usage preference. These results suggested that the gibberellin oxidase genes were more primitive. The gene expression pattern was analyzed in different tissues subjected to multiple abiotic stresses, including GA, abscisic acid (ABA), and chlormequat (CCC) treatment, by RNA-seq and qRT-PCR, ...

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