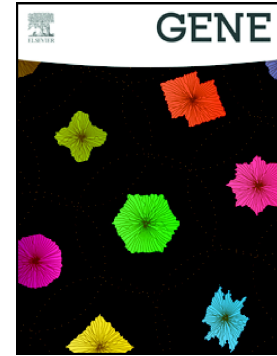


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Genome-wide analysis of *Eucalyptus grandis* WRKY genes family and their expression profiling in response to hormone and abiotic stress treatment

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Abstract: The WRKY transcription factors, a large family of proteins in plants, are involved in multiple developmental and biological processes including response to phytohormones and abiotic stress. However, little information is available regarding the WRKY family in *Eucalyptus*, which has been the most widely planted hardwood trees in tropical and subtropical areas. In this study, a total of 79 WRKY genes (named as *EgrWRKY1-79*) were identified from the *Eucalyptus grandis* genome and classified into three main groups according to the phylogenetic analysis, which was further supported by their gene structure and conserved motifs. Of which, 28 *EgrWRKYs* were involved in tandem duplication but none for segmental duplication, indicating that tandem duplication was the main cause for the expansion of WRKY gene family in *E. grandis*. Subsequently, expression profiles of *EgrWRKY* genes in eight different tissues and in response to treatments of three hormones (SA, JA, and BR) and two abiotic stresses (salt and cold) were analyzed. The results revealed that the *EgrWRKY* genes had differential expression in their transcript abundance and they were differentially expressed in response to plant hormones and salt and cold stresses, suggesting their contributions to plant developmental processes as well as abiotic stresses

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