



CHARACTERIZATION OF *EUCALYPTUS GRANDIS*' DOF GENE FAMILY OF TRANSCRIPTION FACTORS

Gabriel Silveira d'Almeida¹; Michèle Claire Breton¹; Patrícia Dalcin Martins¹; Vítor da Silveira Falavigna¹; Andréia Carina Turchetto-Zolet¹; Luís Fernando Revers²; Giancarlo Pasquali^{1*}

¹PPG Biologia Celular e Molecular, Centro de Biotecnologia, Univ. Fed. Rio Grande do Sul, Porto Alegre, RS, 91.501-970. ²Lab. Genética Molecular de Plantas, EMBRAPA Uva e Vinho, Bento Gonçalves, RS, 95700-000.

*E-mail: pasquali@cbiot.ufrgs.br

Palavras-chave: Dof, *Eucalyptus*, gene expression, RT-qPCR, transcription factor

The Dof protein family comprehends plant exclusive transcription factors characterized by the presence of the DNA binding Dof domain whose structure is similar to the zinc finger domain. Dof proteins are engaged in both activation and inhibition of promoters of genes involved in different plant metabolisms such as endosperm development, light response, flowering, germination and many others. The Dof domain consists of a conserved region of 52 amino acids with a unique structure containing four cysteine residues bound to a zinc atom. This domain is also capable of protein-protein interaction, therefore being considered a bifunctional domain. The region outside the Dof domain does not appear to be capable of DNA binding, featuring high structural variability. This region is most probably related to the different functions exerted by these proteins. Each gene codes for only one Dof structure and, consequently, each protein has only one DNA binding domain. The objective of the present work is to characterize genes encoding Dof proteins of *Eucalyptus grandis* by comparing them phylogenetically to related genes from *Arabidopsis thaliana* and *Populus trichocarpa*. We also intend to analyze the expression patterns of these genes in different tissues (leaf, stalk and root) and in seedlings of *E. grandis* under different hormonal (naphthaleneacetic acid and abscisic acid) and abiotic treatments (high salinity and low temperatures). Nucleic and amino acid sequences corresponding to Dof genes and proteins of *E. grandis* (27 sequences), *P. trichocarpa* (41) and *A. thaliana* (36) were obtained from the online databases Phytozome, Plant Transcription Database and The Arabidopsis Information Resource, respectively, and aligned with software MEGA (Clustal W algorithm). The alignments were then used to generate a phylogenetic tree with Mr. Bayes software, which revealed clusters of paralogous and orthologous sequences. Afterwards, 27 primer pairs were designed based on the complete encoding sequences of *E. grandis* Dof genes for RT-qPCR assays. *E. grandis* seeds were germinated in culture flasks and plastic cups containing an equivalent mix of soil and vermiculite in controlled chambers under 16 hours-light. Total RNA was extracted from leaf, stalk and root and treated with DNase. Corresponding cDNAs were subsequently synthesized by reverse transcription. Resulting cDNA samples are currently being analyzed by RT-qPCR in order to better characterize the pattern of expression of the *E. grandis* Dof genes.

Financial support: CNPq