

Phylogenetic Analysis of the *WRKY* Transcription Factors Gene Superfamily in Coffee Plants

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SUMMARY

WRKY family proteins are transcription factors involved in the regulation of development and plant defense response pathways. The *Arabidopsis thaliana* WRKY superfamily is made of 75 members. Common to these proteins is a DNA-binding region of approximately 60 amino acids in length which comprises the absolutely conserved sequence motif WRKY adjacent to a novel zinc-finger motif. A comparative phylogenetic analysis of the *WRKY* gene family in coffee and *A. thaliana* was conducted to assess the diversity of this family in coffee and to identify homologous coffee genes with putative function in defense responses to pathogens. Bioinformatic analysis of around 200 000 coffee Expressed Sequence Tags (ESTs) identified 313 ESTs with BLAST homologies to WRKY proteins. Almost 30 different putative WRKY genes were obtained, but only 25 unigenes encoding a protein with a WRKY domain were identified. Alignment of the WRKY domain sequences of the 25 coffee unigenes together with those of 72 *A. thaliana* WRKY genes showed a high conservation of the WRKY motif and the zinc-finger motif in the coffee WRKY domain. The 25 coffee WRKY members were distributed among the 3 main *A. thaliana* WRKY subgroups, with group I members displaying two WRKY domains, as expected. Conservation of the intron position within the WRKY domain sequence was evidenced when cloning the genomic sequence of one *WRKY* coffee gene (*CaWRKYI*). Clustering of the coffee *WRKY* genes based on the EST distribution in cDNA libraries made from tissues under several physiological conditions allowed to identify genes associated with development or with plant defense responses. To assess the involvement of *WRKY* genes in the coffee defense response pathways, gene expression patterns are being tested in coffee plants under several defense-related conditions.