



***In silico* characterization of putative members of the coffee (*Coffea arabica*) ethylene signaling pathway**

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ABSTRACT. The plant hormone ethylene is involved in several developmental and physiological processes in plants, including senescence, fruit ripening and organ abscission, as well as in biotic and abiotic stress responses. Initiation of these processes involves complex regulation of both ethylene biosynthesis and the ability of cells to perceive the hormone and respond in an appropriate manner, a process which is regulated both spatially and temporally. Ethylene is a gaseous hormone whose sensitivity is a key factor to limiting its response in target cells. We made a search of the Coffee Expressed Sequence Tag (CAFEST) database for expressed sequence tags related to known elements of the ethylene signaling pathway. Sequences showing a reliable similarity were clusterized, annotated and analyzed for conserved domains. Multiple alignments comprising the sequences that we found and sequences of ethylene signaling elements from other species were made, and their phylogeny was assessed by phylogenetic trees constructed with the MEGA4 software. The expression profile was assessed by *in silico* Northern blot analysis performed using the Cluster and TreeView programs. The CAFEST database was found to have a

large number of sequences related to previously described ethylene signaling pathway elements, allowing identification of putative members from almost every step of this pathway. The phylogenetic trees demonstrated high similarity between the sequences found in the CAFEST and those from other species, and the electronic Northern blot analysis detected their expression in various tissues, development stages and stress conditions.

Key words: Sensitivity; Ethylene receptors; *CTR1*; *EIN2*; *EIN3*; *ERF*