



Genome-wide identification and phylogenetic analysis of the AP2/ERF gene superfamily in sweet orange (*Citrus sinensis*)

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ABSTRACT. Sweet orange (*Citrus sinensis*) plays an important role in the economy of more than 140 countries, but it is grown in areas with intermittent stressful soil and climatic conditions. The stress tolerance could be addressed by manipulating the ethylene response factor (ERF) transcription factors because they orchestrate plant responses to environmental stress. We performed an *in silico* study on the ERFs in the expressed sequence tag database of *C. sinensis* to identify potential genes that regulate plant responses to stress. We identified 108 putative genes encoding protein sequences of the AP2/ERF superfamily distributed within 10 groups of amino acid sequences. Ninety-one genes were assembled from the ERF family containing only one AP2/ERF domain, 13 genes were assembled from the AP2 family containing two AP2/ERF domains, and four other genes were assembled from the RAV family containing one AP2/ERF domain and a B3 domain. Some conserved domains of the ERF family genes were disrupted into a few segments by introns. This irregular distribution of genes in the AP2/ERF superfamily in different plant species could be a result of genomic losses or duplication events in a common ancestor. The *in silico*

gene expression revealed that 67% of AP2/ERF genes are expressed in tissues with usual plant development, and 14% were expressed in stressed tissues. Because the AP2/ERF superfamily is expressed in an orchestrated way, it is possible that the manipulation of only one gene may result in changes in the whole plant function, which could result in more tolerant crops.

Key words: Expressed sequence tags; *In silico* analysis; Gene expression; Amino acid sequences