

IDENTIFICATION AND *IN SILICO* ANALYSIS OF THE *CITRUS* HSP70 MOLECULAR CHAPERONE GENE FAMILY

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The completion of the genome sequencing of the *Arabidopsis thaliana* model system provided a powerful molecular tool for comparative analysis of gene families present in the genome of economically relevant plant species. In this investigation, we used the sequences of the *Arabidopsis* Hsp70 gene family to identify and annotate the citrus Hsp70 genes represented in the CitEST data base. Based on sequence comparison analysis, we identified 18 clusters that were further divided into five sub groups encoding four mitochondrial mtHsp70s, three plastid csHsp70s, one ER luminal Hsp70 BiP, two HSP110/SSE-related proteins and eight cytosolic Hsp/Hsc70s. We also analyzed the expression profile by digital Northern of each Hsp70 transcript in different organs and in response to stress conditions. The EST database revealed a distinct population distribution of Hsp70 ESTs among isoforms and across the organs surveyed. The Hsp70-5 isoform was highly expressed in seeds, whereas BiP, mitochondrial and plastid HSp70 mRNAs displayed a similar expression profile in the organs analyzed, and were predominantly represented in flowers. Distinct Hsp70 mRNAs were also differentially expressed during *Xylella* infection and *Citrus tristeza* viral infection as well as during water deficit. This *in silico* study represents the groundwork for future investigations to fully characterize functionally the citrus Hsp70 family and underscores the relevance of Hsp70s in response to abiotic and biotic stresses in *citrus*.