



Differential gene expression in drought-tolerant sugarcane roots

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ABSTRACT. Drought is one of the most frequent abiotic stresses limiting the productivity and geographical distribution of sugarcane culture. The use of drought-tolerant genotypes is one approach for overcoming the effects of water stress. We conducted a comparative study to identify gene expression profiles under water stress in tolerant sugarcane roots. Two different cultivars, 1 drought tolerant (RB867515) and 1 drought susceptible (SP86-155), were evaluated at 4 sampling time points (1, 3, 5, and 10 days) using the cDNA-amplified fragment length polymorphism technique. A total of 173 fragments were found to be differentially expressed in response to water stress in the tolerant cultivar. Seventy of these were cloned, sequenced, and categorized. Similarity analysis using

BLAST revealed that 64% of the fragments differentially expressed code proteins classified as no hits (23%), hypothetical (21%), or involved in stress response (20%), with others were involved in communication pathways and signal transduction, bioenergetics, secondary metabolism, and growth and development. Four genes were analyzed and validated using real-time quantitative polymerase chain reaction to determine their expression and showed consistency with the cDNA-amplified fragment length polymorphism analyses. Our results contribute insight into the molecular responses to water stress in sugarcane and possibility to the development of cultivars with improved tolerance to drought.

Key words: Abiotic stress tolerance; *Saccharum* spp; Chaperones; cDNA-amplified fragment length polymorphism; Quantitative reverse transcription-polymerase chain reaction