

Differentially Expressed Genes in Drought Stressed Sugarcane

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Drought is one of the most challenging agricultural issues limiting sustainable sugarcane production. In some cases, yield losses due to drought are estimated up to 50%. This stress induces series of biochemical, physiological and developmental responses in plants, which can reduce the corresponding damage. In this study, we aimed to identify a set of transcript fragments that are differentially expressed in response to sub-optimal soil water supply in sugarcane plants. Key candidate genes were selected for this study using the *GeneSnare*TM technique, which allowed fast and accurate identification of differentially expressed sequences in sugarcane. The validation of candidate genes was conducted by submitting sugarcane plants under different levels of drought stress: ($\psi_t = 1$ MPa, without stress; $\psi_t = 1.5$ MPa, moderate stress and $\psi_t = 3$ MPa, severe stress). Analysis of *Northern blot* and RT-qPCR demonstrated that six tested genes showed the expression pattern in accordance to typical drought stress. Our results suggest that these genes are potentially involved in drought stress tolerance in sugarcane. Based on this information, expression cassettes containing these coding sequences were constructed and will be utilized to evaluate its efficiency to prevent and/or minimize the drought effect in the model plant *Brachypodium distachyon*. Data obtained from this experiment will provide a suite of genes involved in the plant's response to drought in sugarcane.