

## **Expression profiling of sugarcane varieties differing in their tolerance to drought stress**

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Sugarcane is a highly productive C4 grass used for centuries as the main source of sugar and recently to produce ethanol. Sugarcane originated from crosses of *Saccharum* species and is noted for its unique capacity to accumulate high amounts of sucrose in its stems. Environmental stresses limit enormously sugarcane productivity and are the main cause of losses in agriculture worldwide. Little is known about the molecular and physiological basis of drought tolerance in sugarcane and some evidences indicate that this variability has a genetic component. Our goals are to unravel the physiological changes resulting from drought in contrasting sugarcane varieties and identify the molecular basis of tolerance through a focus on transcriptomics. For this study, we selected six genotypes for an evaluation of drought responses. The experiment was conducted using four biological replicates in 2 experimental fields under irrigation and drought conditions in Campo Alegre-AL. Samples were collected after 7 months of planting. Physiological studies in these six genotypes were conducted to define the most tolerant and sensitive varieties which were further profiled for transcriptome alterations through microarray experiments using a Custom 44K oligo array (*Agilent*). The most sensitive variety was RB855536, but there was no difference that distinguished what was the best tolerant variety. RB857515 and RB92579 were profiled based on its high yield under drought conditions and for its commercial importance. A total of 1040 SAS (Sugarcane Assembled Sequences) were found to have differential expression. We found several genes involved in general drought responses as seen in other studies, but this was the first time that physiological data was correlated with molecular data to describe varieties with different tolerance levels. Collectively these results are valuable information that can guide further studies for the development of improved sugarcane varieties and can be used as molecular markers in breeding programs.

Funding by FINEP, CNPq and FAPESP.

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