

Molecular characterization of sugarcane genotypes contrasting for drought stress tolerance

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Key words: Drought-prone; microarray; methyl-viologen; *Saccharum*; water deficit.

The increasing demand for ethanol imposes the Brazilian sugarcane industry to expand to drought-prone regions of the 'Cerrado', requiring cultivars with yield potential adapted to marginal conditions. To investigate physiological mechanisms involved in field tolerance to water deficit, we evaluated approaches to characterize tolerance by focusing on phenotyping and gene expression profiling. We also evaluated the addition of polyethylene glycol (PEG) as a stress inducer in nutrient solution to simulate drought-response, or by evaluating electrolyte leakage after exposure of leaf segments to methyl-viologen. Ten genotypes were evaluated for drought tolerance in a field trial in Goianésia (GO), a drought-prone location. Based on physiological evaluations, we identified two contrasting genotypes for response to drought stress: 'IACSP94-2094' showed enhanced features of drought tolerance (early stomatal closure; maintenance of leaf water potential; and superior photochemical activity), absent in 'IACSP97-7065'. When plants were grown on nutrient solution containing 15% PEG, differences between genotypes for leaf water potential and gas exchange traits were apparent after 72 h, whereas differences in electrolyte leakage between genotypes after leaf-disk treatment with methyl-viologen suggested the potential application of both approaches for early selection for water deficit tolerance. To identify genes involved in drought tolerance, field trial leaf samples collected from the contrasting genotypes were analyzed for global expression by microarray. From a set of 14,522 genes, 91 (~0.63%) were differentially expressed between irrigated and non-irrigated treatment during early drought, whereas 576 (~4%) were differentially expressed during severe drought between water treatments, from which 438 were differentially expressed between genotypes, including many genes traditionally associated with drought response, together with novel ones that might play a role in drought tolerance. Some genes are being validated through qPCR for comparison of the methods and gene responses, and to be used on functional genomics studies.

Support by CAPES, CNPq, FAPESP, FUNDAG, Usina Jalles Machado.

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