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Expression profiling using Affymetrix GeneChip Microarrays in sugarcane during leaf senescence

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Leaf senescence was investigated in *Saccharum* spp., as a developmentally programmed degeneration process that constitutes the final step of leaf development. Leaf senescence is an active process controlled by multiple factors and therefore several genes are expressed during this process. In sugarcane, the leaf senescence was characterized by the remobilization of nutrients and by the reduction in chlorophyll content. To identify differentially expressed genes in different stages of leaf senescence, sugarcane plants were selected for three stages (T1, T2 and T3, no, intermediate and advanced leaf senescence, respectively) and RNA from each stage were extracted and used for further analyses. Subsequently targets RNA were labeled and hybridized to the ATH1-121501 GeneChipR array and scanned on a G2500A GeneArray scanner. From these results a gDNA cell intensity file (.cel file) was generated using the Microarray Analysis Suite software (MAS, v5.0, Affymetrix). This cell file were then processed by AffylmGUI library in R environment using Bioconductor. *Arabidopsis thaliana* probe-air that hybridized to the sugarcane transcript DNA on the basis of the perfect-match (PM) probe signal were then selected or the subsequent analysis using .cel file parser script to generate probe mask files. Several genes were identified as up-regulated, including genes involved in cell wall modification (e.g., pectinsterase, 6 phosphogluconate dehydrogenase), signaling proteins, transporters and proteins involved in oxyreductase activity (e.g. GA30X2 - Gibberelin 3-beta-hydrolase) among others. Genes involved in protein folding and signaling were found as down-regulated. To your knowledge, this study revealed for the first time new genes that might be involved in the leaf senescence in sugarcane at the transcriptomic level.

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