

Transcription Profiling of Signal Transduction-Related Genes in Sugarcane

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Over 3,500 components involved in several aspects of signal transduction, transcription, development, cell cycle, stress responses and pathogen interaction are being studied using cDNA microarrays. Sugarcane signal transduction components were compiled into the Sugarcane Signal Transduction (SUCAST) Catalogue. Microarrays were used to profile individual variation of plants cultivated in the field and transcript abundance in six plant organs (flowers, roots, leaves, lateral buds, 1st and 4th internodes). From 1280 distinct elements analyzed, 217 (17%) presented differential expression in two biological samples of at least one of the tissues tested. A total of 153 genes (12%) presented highly similar expression levels in all tissues. A virtual profile matrix was constructed and the expression profiles were validated by real-time PCR. Expression data was also obtained for sugarcane varieties contrasting for biotic and abiotic stresses as well as sucrose accumulation. Over 400 genes have been shown to be differentially expressed in at least one of the 10 conditions analyzed. A gene expression database was constructed to host and allow efficient analysis of the data obtained. The data can aid in assigning function for the sugarcane genes and be useful for promoter characterization of this and other economically important grasses (Supported by FAPESP, Centralcool and Cane Technology Center).