

Gene Expression Associated to Sucrose Metabolism in Sugarcane

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Sucrose is the major product of photosynthesis in many higher plants. It is transported from the source tissue (mature leaves) through the phloem to various sink tissues (internodes) to support plant growth, development and reproduction. The knowledge about the signal transduction pathway involved in stem maturation is limited. The SUCEST (Sugarcane EST Project) database provides a great opportunity to understand sucrose accumulation in sugarcane at the transcriptional level, and finding the genes coding for proteins involved in signal transduction processes is an important step towards this goal. These genes are potential targets to be used as molecular markers and to develop genetically manipulated plants. Our objective was to analyze the expression profile of ~1200 sugarcane (*Saccharum* sp.) genes involved in signal transduction, as well as transcription factors and stress-related elements. To this end we used cDNA microarrays from the Sugarcane Signal Transduction (SUCAST) catalogue (<http://ipe.cbmeg.unicamp.br/sucestfun/sucast/>). We have compared the expression profile from immature and mature internodes (1, 5 and 9) from a sugarcane population segregating for sucrose content. We found 158 genes that were differentially expressed, 116 were expressed only in internodes with high sugar content and 42 in internodes with low sugar content. The insights on how signal transduction can regulate sucrose accumulation in sugarcane plants will be discussed. Supported by FAPESP.