

## **SUGARCANE GENOMICS: GENE DISCOVERY FOR AN ENERGY GRASS**

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Modern sugarcane cultivars are complex hybrids resulting from crosses among several species of the *Saccharum* genus. Traditional breeding methods have been extensively employed in different countries along the past decades to develop varieties with increased sucrose yield, and resistant to plagues and diseases. Conventional varietal improvement is, however, limited by the narrow pool of suitable markers. In this sense, molecular genetics is seen as a promising tool to assist in the process of molecular marker identification. The SUCEST-FUN Project (<http://sucest-fun.org>) aims to associate function to sugarcane genes using a variety of tools, in particular through the study of the sugarcane transcriptome. Expression data was obtained using cDNA microarray and quantitative PCR technologies that can be used to identify, distinguish, characterize and/or develop plants with increased sucrose content. We identified genes associated with sucrose content that are also responsive to drought indicating common pathways modulate sucrose accumulation and stress responses. Genes for hormone biosynthesis, SNF-related kinases, transcription factors, oxidative stress responses and calcium metabolism were often found to be differentially expressed when high sucrose and low sucrose plants and populations of plants were compared and/or when high and low sucrose internodes were compared which may indicate a role for them in stem development. Extensive validation in genotypes contrasting for brix revealed a possible use for the genes as molecular markers in breeding programs. Gene promoters are being cloned that may help in generating sugarcane plants with increased brix and altered drought responses.