

Sugarcane sucrose accumulation: a transcriptomic and proteomic view.

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Sugarcane is a important crop in the Brazilian economy for both, sugar and green biofuel production, accounting for more than US\$ 20 billions/year, placing Brazil as the most important country in this trade. On the other hand sugarcane has reached a limit in sucrose production, an effect of the narrow gene pool used in current commercial breeding programs. Our objective was to assess the dynamics of sucrose accumulation in sugarcane stalks, by investigating the gene expression in the storage parenchyma of sugarcane plants during development, using transcriptomic and proteomic approaches. Sugarcane variety (SP80-3280) was cultivated under greenhouse conditions and internodes 4-to-9 were harvested at 7 and 10 months. In order to increase the sugar content, 10 month old plants were subjected to a period of water stress before sampling. All internodes were analyzed to evaluate the soluble sugars content, the internodes 5 and 9 were used in transcriptomic, and 9 was used in proteomic analyses. Expression profiles of genes involved in sucrose cycling from the 7 and 10 month old plants were studied using qRT-PCR. Proteomic approaches (2D-PAGE) were done by comparing protein expression profiles between mature internode, at both ages, and the selected spots were identified by LC-ESI-Q-TOF-MS/MS. Total soluble sugars in the storage parenchyma increased around 2,5-fold when 7 and 10 month old internodes were compared. This rise could be explained by a change in the expression of genes involved in sucrose metabolism. Endogenous and exogenous signals trigger the mechanism of sucrose synthesis which is often regulated by enzymes and signaling sugars. We identified 254 proteins from the 7 and 10 month old which included differentially expressed and exclusive spots. The data from the gene expression and proteome analyses are compared in order to understand the molecular mechanisms involved in sucrose storage.

Key word: proteome; Saccharum; sucrose content; transcriptome

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