

Proteomic Analysis of *Saccharum* spp. Cultivars with Contrasting Drought Tolerance Phenotypes Under Salt Stress Conditions

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Sugarcane is one of the most important crops in Brazil used for both sugar and ethanol production. Salt is a common abiotic stress that tends to increase due to accumulation in irrigated fields and can cause losses in production. Enzymes and a number of other proteins have been related to plant tolerance to salt stress and could possibly confer a salt tolerance phenotype when introduced into non tolerant varieties of sugarcane. In terms of plant physiology and gene expression plant salt stress responses overlap with drought responses. Sugarcane has a large genome and hitherto there are no reports of how protein expression changes in response to salt stress. Therefore, salt stress tolerant proteins could be used for biomarkers production or genetic transformation of sugarcane. This project aims a proteomic analysis of sugarcane cultivars with contrasting response to drought stress under a salt stress of 100 mM NaCl. The comparative analysis was performed between six sugarcane plants irrigated with dH₂O and six other plants irrigated with 100 mM NaCl for 48 days. Leaves were ground in N₂ and submitted to protein extraction using a phenol/SDS protocol. Seven hundred micrograms of protein were applied to rehydrated 13 cm *strips* (pH 3-11) and protein separation was obtained by IEF followed by SDS-PAGE 12%. Proteins were visualized by Coomassie Blue G-250 staining and gels images were analyzed with *Bionumerics software*. *Spots* were selected by and an increase of, at least, twice and differential *spots* between treatments. Selected *spots* were digested and de-salted. MALDI-MS/MS was used to acquire MS/MS spectra and MASCOT *software* or *de novo* sequencing was carried out to identify the proteins.

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