

PHYSIOLOGICAL AND MOLECULAR ANALYSIS OF SALT STRESS IN SUGARCANE PLANTS

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Salinity afflicts plant agriculture in many regions of the world. Increase of salt levels in the soil results in the disturbance of the ionic and hydric steady state of cells. The plant adaptation to saline conditions involves a complex molecular response by alterations in the levels of numerous mRNAs, proteins, and metabolites. The identification and analysis of these genes allows understanding the mechanisms associated to plant tolerance. The present work focused on the physiological and molecular effects of salt stress in sugarcane. Thus, sugarcane cultivars (RB72454 and CB4789) were treated with 1,0% of NaCl. Analysis of the photosynthetic quantum yield (Fv/Fm) and lipid peroxidation showed that salinity provoked moderate reduction of the Fv/Fm, and inductions of the lipid peroxidation levels. The effect of salt stress on gene expression was analyzed by macroarray. In this way, 360 cDNA clones related with ion transport, osmoprotectant metabolism, antioxidant system, photosynthesis, aquaporins were analyzed in leaves and root of the cultivar CB4789. The analyses revealed the differential transcription of several genes after 48 hours of stress, revealing the activation of specific response pathways