

## **cDNA MICROARRAY ANALYSIS OF TOMATO RESPONSE TO SALT STRESS**

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Salt stress affects plant physiology and metabolism at different levels often reducing the productive performance of the cultivated crops. The cost of salinity to irrigated horticultural crops like tomatoes is very high and is constantly increasing since irrigation is the main cause of soil salinization.

In this study, we present the physiological and molecular analysis of the dwarf-like Micro-Tom tomato variety grown in a closed hydroponic system under two NaCl concentrations (60 mM and 120 mM).

Salinity stress caused a statistically significant ( $P < 0,05$ ) decrease in plant fresh weight, leaf area development, leaf number, fresh and dry weights of leaves and roots, whereas shoot/root ratio in salinized plants increased. Total leaf water potential and osmotic potential decreased at increasing salinity of the irrigation water. No significant differences were observed for these traits, between the two NaCl treatments.

To monitor the expression profiles of tomato roots and leaves under salt stress, and to identify new salt-responsive genes we used a 13,440-clone (8700 unigenes) TOM1 microarray. Statistical analyses (t-test  $P < 0.05$ ) revealed 731 and 676 EST clones differentially expressed in response to salt stress (60 mM), respectively in leaves and roots. Many genes represented by these clones encoded proteins involved in signal transduction, protein metabolism, primary metabolism and transcriptional regulation. A total of 78 differentially regulated clones were common between leaves and roots. Microarray results have been validated by RT-PCR.

To our knowledge this is the first report of microarray analysis of tomato response to salt stress. These results may contribute to a better understanding of the physiological and molecular basis of salt stress response in tomato.