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## Salt & Water Stress in Plants

June 24-29, 2012  
The Chinese University of Hong Kong  
Hong Kong, China

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### Contributors



## **Systems biology approach on the elucidation of the response of *Medicago truncatula* plants towards salinity stress**

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Salt stress is one of the most important factors limiting plant productivity, with salinity affecting plant physiology and metabolism at multiple levels. The aim of this study was to explore, elucidate and decipher the role of antioxidant and salt tolerance mechanisms in the model legume *Medicago truncatula*. For this reason, three ecotypes of *M. truncatula* showing differential response to salinity were used: Jemalong A17 (moderate response), TN6.18 (sensitive to salinity) and TN1.11 (tolerant to salinity). Cellular damage levels were monitored in roots and leaves after 48 h of salt stress application with 200 mM NaCl by measuring lipid peroxidation levels, as well as nitric oxide and hydrogen peroxide content, further supported by leaf stomatal conductance and chlorophyll fluorescence readings. The salt-tolerant genotype TN1.11 displayed the lowest cellular damage and ROS/RNS content, while the salt-sensitive TN6.18 was affected the greatest. Transcriptional profiling using microarray analysis of salt-stressed *M. truncatula* displayed differential gene expression that was both genotype and tissue-dependent. A large number of regulatory genes (associated or not previously linked with salinity stress) from a variety of biochemical pathways showed a significant induction/suppression pattern. Furthermore, metabolite profiling of *M. truncatula* plants was employed to analyse the effect of salt stress in the accumulation of key metabolites and their interrelationships, leading to exclusive insights into the plants' metabolic networks which however appear to be genotype- and not tissue-dependent. This global approach (with the addition of currently performed proteomics analysis) will hopefully contribute in gaining new insights into the cellular response to salt stress in *M. truncatula* plants.