Salt & Water Stress In Plants
From Molecules To Crops

June 13-18, 2010
Les Diablerets Conference Center
Les Diablerets, Switzerland

Chairs:
Anna Amtmann & **Jian-Kang Zhu**

Vice Chairs:
Julian I. Schroeder & **Teun Munnik**

Contributors

BASF The Chemical Company

Bayer CropScience

King Abdullah University of Science and Technology KAUST

MONSANTO imagine

Characterization of carbonylated and nitrated proteins in response to hydrogen peroxide and nitric oxide in salt-stressed citrus plants

Georgia Tanou*, Athanassios Molassiotis*, Vasileios Fotopoulos¶, Maya Belghazi [1], Dominique Job[2], Grigorios Diamantidis*

* Faculty of Agriculture, Aristotle University of Thessaloniki, 54 124, Thessaloniki, Greece

¶ Department of Agricultural Sciences, Biotechnology and Food Science, Cyprus University of Technology, PC 3036, Limassol, Cyprus

[1]Centre d'Analyse Protéomique de Marseille, Institut Fédératif de Recherche Jean Roche, Marseille, France

[2]Centre National de la Recherche Scientifique-Université Claude Bernard Lyon-Institut National des Sciences Appliquées-Bayer CropScience Joint Laboratory (UMR 5240), Bayer CropScience, Lyon, France

Hydrogen peroxide (H_2O_2) and nitric oxide ($^{\bullet}NO$) have a fundamental role in plant resistance and signalling responses, and protein carbonylation and nitration are emerging as an important mechanism for the transduction of H_2O_2 and $^{\bullet}NO$ bioactivity. A key step towards elucidating the mechanisms by which these molecules function during abiotic stress responses is the identification of the proteins that are subjected to these modifications. The present study aimed to identify proteins that are targets of these molecules in citrus leaves upon root treatment with H_2O_2 or the $^{\bullet}NO$ donor sodium nitroprusside (SNP) in the absence or presence of salt stress. Data indicated that pre-treatment with H_2O_2 or SNP prior to salinity reduces the damaging phenotypical and physiological effect of direct NaCl stress. Gene transcript levels of components of the antioxidant system were tightly regulated by both molecules. Expression patterns of citrus proteins were undertaken by IEF/SDS-PAGE and tandem mass spectrometry. This proteomic approach revealed an array of proteins that are either carbonylated or tyrosine-nitrated in citrus leaves. Proteins with a function in photosynthesis, protein stability and stress response were over-represented among the identified carbonylated or nitrated citrus proteins. Identification of proteins modified by H_2O_2 or the $^{\bullet}NO$ allows for a deeper understanding of the oxidative and nitrosative signaling networks in citrus plants.