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Abstract

Plant anion channels belonging to the SLAC/SLAH family have been characterized in great detail. While SLAC1 expression is restricted to guard cells, its homolog SLAH3 is expressed in various tissues including guard and mesophyll cells or roots. Moreover, SLAH3 activity is modulated in different ways. SLAH3 anion channels are not active per se but require extracellular nitrate as well as phosphorylation by calcium-dependent kinases from the CPK or CIPK family. In the root xylem-pole pericycle adjacent to the xylem vessels AtSLAH3 co-localizes with AtSLAH1 and direct interaction between both channels was demonstrated via FRET/FLIM measurements. Interestingly, when co-expressed in *Xenopus* oocytes, the electrically silent SLAH1 subunit interacts with and gates SLAH3 open independent of the presence of nitrate and kinases, thereby increasing its chloride conductance. Under high soil salinity, AtSLAH1 expression markedly declined and the chloride content of the xylem sap in AtSLAH1 loss-of-function mutants was half of the wild-type level only. Apparently, SLAH1/SLAH3 heteromerization facilitates SLAH3-mediated chloride efflux from pericycle cells into the root xylem vessels. Our results indicate that under salt stress, plants control the shoot NO₃ - /Cl⁻ ratio via differential expression and assembly of SLAH1/SLAH3 anion channel subunits.

Functional Interactomics

Akyla Maria Martins Alves - Poster-B187

Abstract Title: DIFFERENT ADAPTATION STRATEGIES OF TWO CITRUS SCION/ROOTSTOCK COMBINATIONS IN RESPONSE TO DROUGHT STRESS

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Abstract

Scion/rootstock interaction is important for plant development and for breeding programs. In this context, polyploid rootstocks presented several advantages, mainly in relation abiotic stresses. Here we analyzed the response to drought of two different scion/rootstock combinations presenting different ploidy: the diploid (2x) and autotetraploid (4x) Rangpur lime rootstocks grafted with 2x Valencia Delta sweet orange scions (V/2xRL and V/4xRL). We developed an interactomic approach to identify proteins involved in V/2xRL and V/4xRL response to drought. A main interactomic network was built from V/2xRL and V/4xRL data. Exclusive proteins of the V/2xRL and V/4xRL networks, as well as common to both networks were identified. Functional clusters were obtained and two models of drought stress response were designed. Even if the V/2xRL plant implement some tolerance mechanisms, the global plant response to drought was rapid and quickly exhaustive resulting in a general tendency to dehydration avoidance, which presented some advantage in short and strong drought stress conditions. At the contrary, the V/4xRL plants presented a response which strong impacts on development but that present some advantages in case of prolonged drought. Finally, some specific central proteins were

identified as good candidates for subsequent functional analysis of citrus genes related to drought response.

Gene and Metabolic Regulatory Network

Ashish Srivastava - Poster-S224

Abstract Title: Molecular basis of thiourea mediated enhanced plant growth and reduced arsenic accumulation in rice

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Abstract

Arsenic (As) is a ubiquitously present environmental carcinogen that enters into human food chain mainly through rice grains. In present study, we have evaluated the potential of thiourea (TU; a non-physiological ROS scavenger) for ameliorating the negative impacts of arsenite (As III) stress in rice. At both seedling and mature plant stage, TU supplementation along with As III significantly improved the plant growth as compared to that under As III alone. Besides, 30% reduction in arsenic accumulation was observed in grains and LC-MS data showed no residual TU accumulation. Microarray analysis in seedlings subjected to As III stress with/without TU treatment for 24 h identified a set of TAR (T U dependent A rsenic R esponsive) genes which were specifically regulated under As III +TU treatment. TAR genes were mainly associated with multiple processes including carbon metabolism, redox balancing and hormone signalling. Top-ranked differential genes including arsenic transporters and hormones like abscisic acid, salicylic acid, gibberellic acid, jasmonic acid were quantified to validate their association with TU mediated response. Thus, the study not only demonstrates TU potential for reducing arsenic load from rice grains but also, highlight the key genes and metabolic pathways that can be targeted to minimize arsenic stress induced damages in rice.

Gene and Metabolic Regulatory Network

Marie Pireyre - Poster-S221

Abstract Title: TRANSCRIPTIONAL NETWORKS GOVERNING UV-B PHOTORECEPTOR RESPONSES IN ARABIDOPSIS

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Abstract

Perception of light signals is important to optimize plant growth and development. Exposure to low doses of UV-B is sufficient to induce specific transcriptional changes and inhibit cell elongation. UV-B is perceived by homodimeric UV RESISTANCE LOCUS 8 (UVR8) photoreceptors, triggering their monomerization. UVR8 monomers interact with the E3 ubiquitin ligase CONSTITUTIVELY