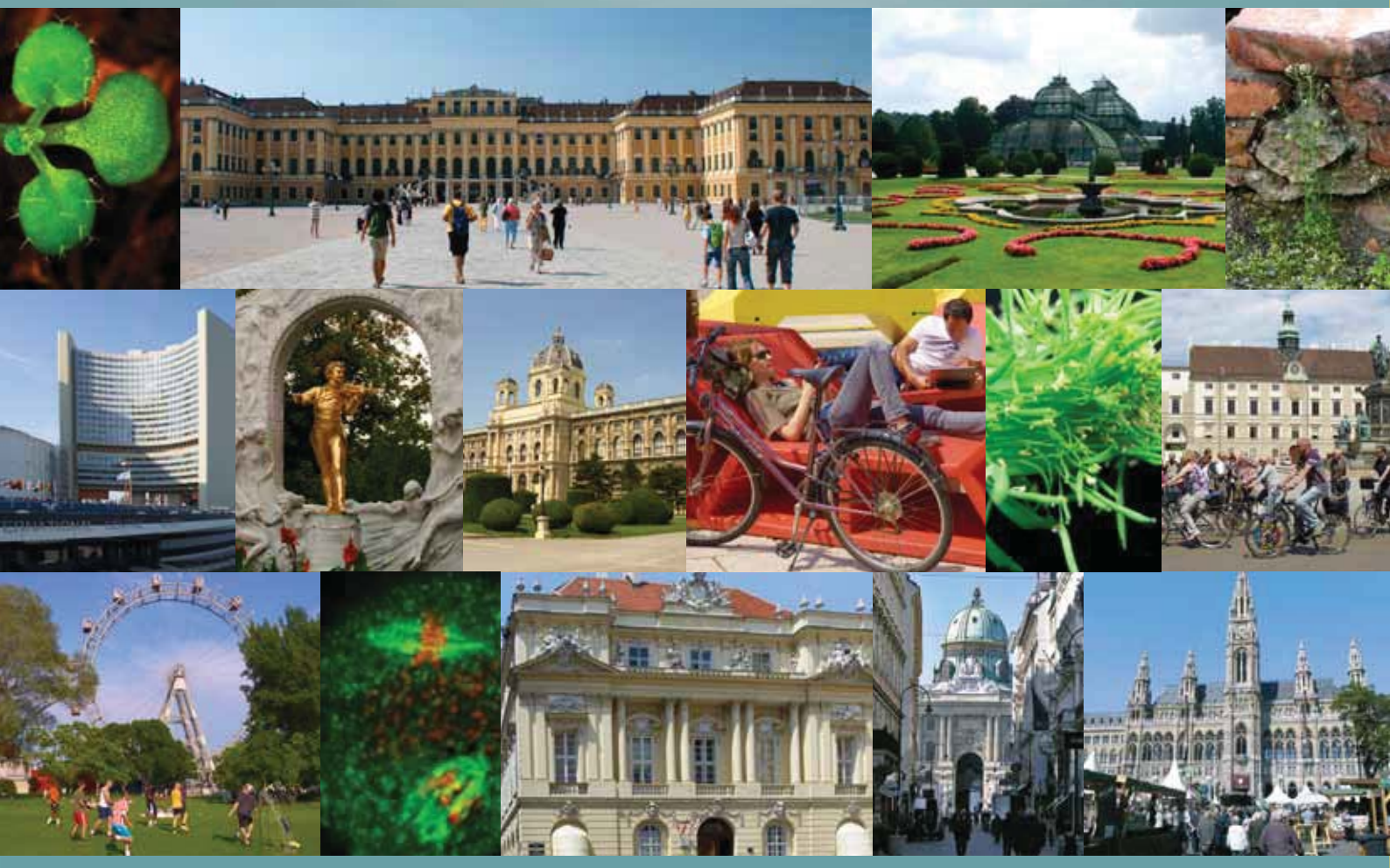
ICAR

Vienna, Austria
July 3rd-7th 2012

Hofburg Imperial Palace,
Vienna Austria



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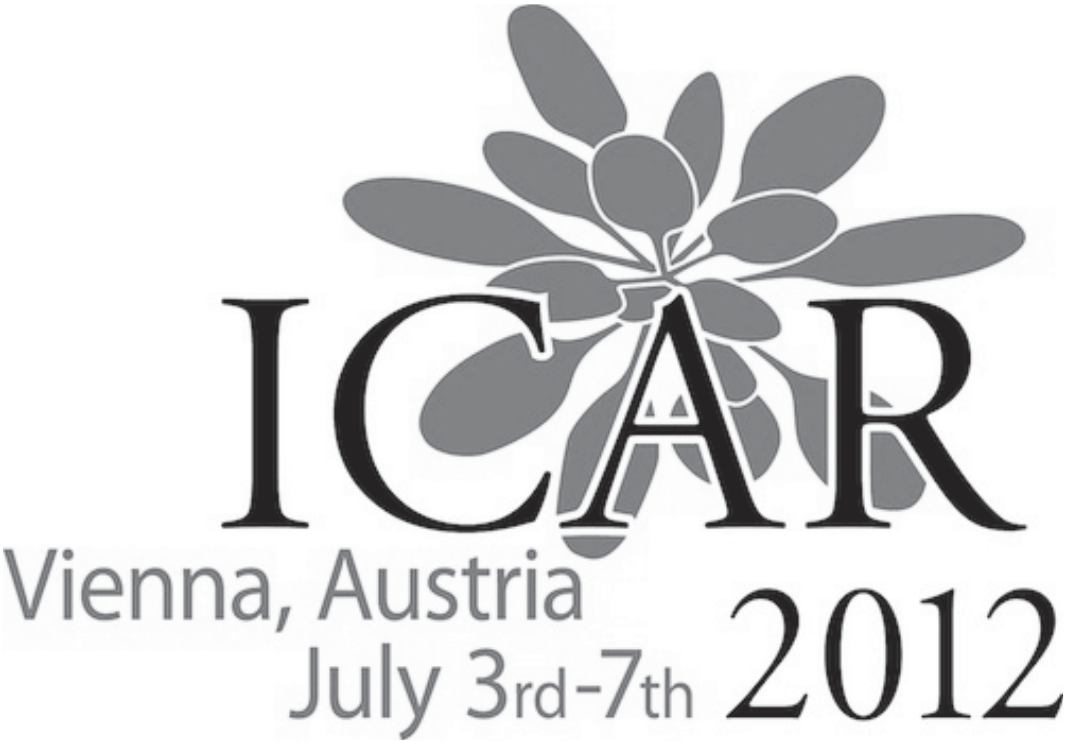
PROGRAM AND ABSTRACTS



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SESSION OVERVIEW

TUESDAY JULY 3		
14:00 – 22:00	Registration	Halle
16:00 – 17:30	Workshops 1-3	see Program
18:00 – 18:30	Welcome Addresses	Festsaal
18:30 – 19:30	Keynote Lectures	Festsaal
19:30 – 22:00	Welcome Reception	Prinz Eugensaal
WEDNESDAY JULY 4		
08:00 – 09:00	Registration	Halle
09:00 – 10:30	P1: Epigenetics	Festsaal
11:00 – 12:30	P2: Plant Defense	Festsaal
14:00 – 16:00	C1: RNA Mediated Regulation	Festsaal
14:00 – 16:00	C2: Bioenergy	Zeremoniensaal
16:30 – 18:30	C3: Interactions with Biotic Environment	Festsaal
16:30 – 18:30	C4: Novel Tools/Bioinformatics	Zeremoniensaal
18:30 – 22:00	Poster Session 1 (Odd Numbers)	Galerie/Wintergarten
19:00 – 22:00	IAIC Meeting	Radetzky Apt II
THURSDAY JULY 5		
08:30 – 09:00	Registration	Halle
09:00 – 10:30	P3: Responses to the Abiotic Environment	Festsaal
11:00 – 12:30	P4: Cell Biology	Festsaal
14:00 – 16:00	C5: Plant Hormones	Festsaal
14:00 – 16:00	C6: MASC Roadmap	Zeremoniensaal
16:00 – 19:00	ABRC Meeting	Radetzky Apt II
16:30 – 18:00	Workshops 4-6	see Program
18:00 – 22:00	Poster Session 2 (Even Numbers)	Galerie/Wintergarten
19:00 – 22:00	NAASC Meeting	Parterre office
FRIDAY JULY 6		
08:30 – 09:00	Registration	Halle
09:00 – 10:30	P5: Natural Variation	Festsaal
11:00 – 12:30	P6: Genetics and Genomics Beyond *A. thaliana*	Festsaal
14:00 – 16:00	C7: Lifting Yield Barriers in Breeding	Zeremoniensaal
14:00 – 16:00	C8: Systems Biology of Development	Festsaal
16:30 – 18:00	Workshops 7-9	see Program
19:00 – 23:00	Conference Dinner	Heuriger Alter Bach-Hengl
SATURDAY JULY 7		
09:00 – 10:30	P7: Systems Biology & Metabolism	Festsaal
11:00 – 12:30	P8: Development	Festsaal
12:30 – 12:45	Highlights – Concluding Remarks	Festsaal

225 COMPARATIVE ANALYSIS OF THE MECHANISMS UNDERPINNING SALT TOLERANCE IN PLANTS

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High salt concentrations in soil are a leading cause of salt stress restraining crop production in different parts of the globe. It is anticipated that stresses from the abiotic factors including salinity will result in over 50% decrease in average yield of major crops under current agricultural practices by 2050. Therefore, extensive work has been conducted during last 20 years to understand the basic mechanisms for salt-tolerance. The obtained knowledge has started to develop plants with higher resistance to environmental stresses including salinity. Differential expression of a set of key genes might play a crucial role in the salinity tolerance trait among few species. However, in recent research the data supporting this hypothesis lack details in terms of what is important in the observed differential response, the timing or the amplitude of the responses or both. This project aimed at exploring in details the hypothesis and to find out the main mechanisms for the observed differential gene regulation under salt-stress between *Arabidopsis thaliana* and *Thellungiella halophila*. We aimed at analyzing and comparing the kinetics of salt-stress responses as well as level (amplitude) of these salt-stress responses exhibited by these two contrasting plant systems in terms of salt-tolerance, through a time course. This analysis involved comparisons at both, very early stages of salt-stress (first 48 hours) and after prolonged salt-stress up to 10 days. The analyzed responses included the physiological responses (growth, photosynthesis), metabolic responses (production of osmo-regulators) and gene responses (P5CS1 and SOS1 genes). Our results suggest that the difference in the kinetic of the responses to salt-stress might contribute to the higher salt-tolerance exhibited by *T. halophila* by responding faster to salt-stress than *A. thaliana*.

226 IDENTIFICATION OF *VIN3* UPSTREAM COMPONENTS IN VERNALIZATION PATHWAY

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Vernalization, a long term cold inducing acceleration of flowering, is one of the important environmental factors to determine the timing of flowering in plants. In *Arabidopsis*, mitotically stable repression of floral repressor, *FLC,* is a crucial mechanism for the vernalization-dependent acceleration of flowering. Transcriptionally activated PHD finger domain protein VERNALIZATION INSENSITIVE 3 (VIN3) is known to induce the repression of *FLC* chromatin. However, the question how plants can perceive the winter signal is still elusive. One way to reveal the question is to isolate *VIN3* upstream components. For this purpose, we generated a transgenic line with the promoter of *VIN3* fused to *GUS* reporter gene and performed *Agrobacterium*-mediated activation tagging mutagenesis. Currently, we have isolated 1 vernalization insensitive mutant (*X79*) which shows decreased expression of *VIN3* in vernalization, and 2 vernalization hypersensitive mutants (*p393, p545*) which show increased expression of *VIN3* without vernalization. *p393* and *p545* show additional morphological phenotypes in SAM, leaf, silique, etc. The cloning of the corresponding genes are in progress.

227 HEAT-STRESS IN TRANSGENIC *ARABIDOPSIS THALIANA* PLANTS WITH INDUCIBLY-INCREASED LEVELS OF ENDOGENOUS CYTOKININS.

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Plants are not able to solve problems with adverse enviromental conditions by active movement. Therefore, plants have developed sophisticated system of hormonal regulations, that lead to compensation and appropriate responses. Cytokinin (CK) is one of the most important hormone. CK controls many physiological aspects and developmental processes. In this work, we studied responses of plants with elevated levels of cytokinins to aplication of heat stress to different parts of plant body. Plants were treated by heat stress for up to 3 hours: heat stress from above (leaves), heat stress from below (roots) and heat stress on the whole plant. The differences in heat-stress perception in roots and leaves between individual experiments were evident in first 30 minutes of treatment. Plants were subjected to proteomic and hormonal analysis. We found 102 differentialy regulated proteins in leaves and 36 differentialy regulated proteins in roots by 2D gel electophoresis followed by MALDI MS analysis. We measured levels of all major phytohormones and their respective derivates, and 21 transcripts of marker genes linked to hormonal signalling pathways. We observed many differences between control plants (Col) and transgenic plants according to relevant type of heat-stress, which correlated with the physiological status of the treated plants.

228 PHYTOHORMONE AND PHYTOCHELATIN METABOLISM IN *ARABIDOPSIS THALIANA* EXPOSED TO CADMIUM, COPPER AND ZINC IN DIFFERENT COMBINATIONS

Adriano Sofo* (University of Basilicata, Italy), Antonella Vitti (University of Basilicata, Italy), Antonio Scopa (University of Basilicata, Italy), Giuseppe Tataranni (University of Basilicata, Italy), Maria Nuzzaci (University of Basilicata, Italy), Jaco Vangronsveld (University of Hasselt, Belgium), Tony Remans (University of Hasselt, Belgium), Maria De Benedictis (University of Parma, Italy); Luigi Sanità di Toppi (University of Parma, Italy)

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Excess cadmium (Cd), copper (Cu) and zinc (Zn) are known to induce stress effects in plants. However, while Cu and Zn are part of many cell macromolecules, plants have no known metabolic function for Cd. *Arabidopsis thaliana* L. can be considered a model plant for -studies on metal homeostasis/detoxification, as its biochemical, physiological and morphological features are strongly affected by metal exposure. In this work, seedlings of *A. thaliana* were exposed to Cd, Cu and Zn at concentrations of 10, 5 and 150 µM, respectively. After 12 days of exposure to metals, applied separately or in combinations, plant shoots and roots were sampled and analyzed for morphological analysis (microscopy), metal content (ICP-MS), phytohormone and phytochelatin (PC) levels (LC-MS), and expression of the genes involved in phytohormone and PC metabolism (*q*-PCR). Microscopic analysis revealed that the root morphology, in terms of root apex number, branching degree and mean diameter, was strongly affected by metal exposure, both alone or in combination. The differentiated growth patterns observed in shoots and roots were accompanied by different levels and ratios of auxins and cytokinins and the main regulatory genes involved in auxin and cytokinin synthesis (*NIT1* and *IPT7*) and degradation (*AAO1* and *CKX1*) were regulated by the metal treatments. Phytochelatin synthesis was significantly induced by all metals, but the expression of the genes involved in glutathione and PC biosynthesis (*GSH1*, *GSH2*, *PCS1* and *PCS2*) was not influenced. This study could reveal cross-talks between phytohormones and PC metabolism in *A. thaliana* plants growing in a metal multi-pollution context.

229 THE ROLE OF GRO/TUP1 CO-REPRESSOR COMPLEXES IN THE PLANT CIRCADIAN CLOCK

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Circadian clocks are ubiquitous molecular time-keeping mechanisms that coordinate physiology and metabolism and provide an adaptive advantage to higher plants. The central oscillator of the plant clock is composed of multiple interlocked feedback loops. Pseudo Response Regulators (PRRs) are essential components of the central oscillator which comprise a five-member gene family. Among the multi-interlocked loops, PRR5, PRR7 and PRR9 are capable of repressing the transcription of CCA1/LHY through an unknown mechanism. Here we report that members of the plant Gro/Tup1 co-repressor family can interact with these PRR proteins, and associate with the promoters of CCA1/LHY to repress transcription only in the presence of PRR5, PRR7 and PRR9. Knock-down of this gene family significantly lengthens circadian period. Our findings show that Gro/Tup1 corepressors are novel components of the central circadian oscillator and reinforces the role of this family as a central component in multiple signaling pathways in higher plants. Since the expression of some of these components are also clock regulated, our findings further suggest a novel link between multiple signal transduction pathways and the circadian clock. Recent results in the characterization of this complex will be presented.

230 PHOSPHORYLATION - MEDIATED STRESS SIGNALING AND REDOX REGULATION

Hansjörg Stampfl* (GMI-Gregor Mendel Institute of Molecular Plant Biology, Austria), Silvia Dal Santo (GMI-Gregor Mendel Institute of Molecular Plant Biology, Austria), Julia Krasensky (GMI-Gregor Mendel Institute of Molecular Plant Biology, Austria) and Claudia Jonak (GMI-Gregor Mendel Institute of Molecular Plant Biology Vienna, Austria)

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A major consequence of various stresses is the excessive formation of Reactive Oxygen Species (ROS). Therefore, redox adjustment via the cellular antioxidant system is central to stress response. However, little is known about the signal transduction pathways that regulate the antioxidant system to counteract oxidative stress. Here we show that ASK5, a serine/threonine protein kinase from *Arabidopsis thaliana*, regulates salt stress tolerance by activating glucose-6-phosphate dehydrogenase (G6PD). G6PD is a major enzyme of the oxidative pentose phosphate pathway, essential for maintaining the cellular redox balance. Plants deficient in ASK5 show reduced G6PD activity, elevated levels of ROS and are more sensitive to high salinity conditions, whereas plants overexpressing ASK5 have an increased G6PD activity and lower levels of ROS in response to stress. Salt stress enhances ASK5 protein kinase activity which than phosphorylates and thereby stimulates the enzymatic activity of a cytosolic isoform of G6PD *in vivo*. These results reveal a novel mechanism of G6PD adaptive regulation, critical for maintaining the cellular redox state during stress response.

231 GENOME-WIDE ANALYSIS OF EGL3- AND TT8 TRANSCRIPTION FACTOR BINDING SITES USING CHIP-SEQ

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Flavonoids are a class of plant secondary metabolites playing important roles in various plant functions such as pigmentation, protection against UV light damage and phytopathogens, fertility and dormancy. The most visible function of the flavonoids is the formation of red and purple anthocyanin pigments. Anthocyanins are synthesized by the coordinated, consecutive action of