medium; upon reaching the equilibrium, carbon was then used for cell division. The initial investment of carbon for osmoregulation processes can explain the differences in the lag phase duration in response to the decrease of medium sucrose concentration. However, calli cultured on medium added with 30 g L^{-1} of sucrose used carbon both to adjust their osmotic potential and to restore the growth whilst the calli on sucrose free medium entered in a quiescent state. The growth rates compared to the transcript accumulation trends suggested that a threshold effect, rather than a quantitative regulation model, governed the relation between *CycB* gene transcription and cell division. The findings showed that poplar calli used the carbon following a "hierarchical" model based on their physiological state and the sugar concentration available in the medium.

Key words: poplar callus, sucrose, osmotic potential, callus proliferation, B-type cyclins.

Survive or die? A molecular insight into salt-dependant signaling network

Alice Trivellini^{1*}, Mariella Lucchesini², Antonio Ferrante³, Giulia Carmassi², Guido Scatena¹, Paolo Vernieri², Anna Mensuali-Sodi¹

¹ Istituto di Scienza della Vita, Scuola Superiore Sant'Anna, Pisa

² Dipartimento di Scienze Agrarie, Alimentari e Agro-ambientali, Università di Pisa

³ Dipartimento di Scienze Agrarie e Ambienali, Università di Milano

The response of plants to salt stress involves dynamic changes in growth and signaling leading to successful adaptation or death. To elucidate how these opposed events are coordinated we identified a salt-tolerant (obesifruticosa) and a salt-sensitive (aestiva) Antirrhinum majus mutants using shoots as sensitive indicator of stress magnitude. A series of physiological tests were performed that compared the response after 6 h and 3 days of these contrasting mutants grown in agar under a single (200 mM) NaCl concentration, including shoot area, root length, relative water content, plant height, and overall biomass accumulation. Additional measurements of ABA content, chlorophyll degradation, ethylene production, net photosynthesis rates and Na⁺, K⁺, Ca²⁺, and Mg²⁺ content were also reported. RNA-seq analysis was performed on the two mutants after 6 h and 3 days under 200 mM NaCl. A total of 9199 transcripts were found to be differentially expressed in response to NaCl treatment in the two mutants. A large collection of known genes, including MAPKs, CDKs, CDPKs, CIPKs, various transcription factors, various ion transport proteins, and various genes involved in ABA and ethylene signaling pathways were described in detail that displayed differential expression profiles. Overall these data provided evidences of a putative osmotic tolerance sensing and signaling mechanism through a better integration and transduction of environmental cues into growth programs. The reprogramming of calcium-signaling components, generates specific stress signatures affecting differentially the salinity tolerance traits, such as tissue tolerance and anion exclusion. Interestingly, the hormones ABA and ethylene may action as a positive regulators of salt acclimation by the modulation of their signal transduction pathway.

Key words: *Antirrhinum majus* L., NaCl stress, RNAseq, transcriptome, ABA, ethylene, snapdragon, Ca²⁺, signaling, cell cycle progression.

^{*} alice.trivellini@gmail.com