

se interazioni tra piante e comunità microbiche della rizosfera. Il ruolo delle micorrize nel fitorimedio è incentrato soprattutto sull'incremento della tolleranza delle piante agli inquinanti; esiste infatti un'ampia letteratura sugli effetti delle micorrize nelle piante sottoposte a stress da metalli, ma anche su numerose applicazioni nella degradazione di inquinanti organici (Göhre e Paszkowski, 2006).

Le tecniche di coltura *in vitro* sono poi direttamente coinvolte nella realizzazione della trasformazione genetica. L'introduzione di geni estranei nel genoma della piante è una pratica che si sta sempre più diffondendo e che offre interessanti prospettive anche nel campo del fitorimedio, grazie alla sovraespressione, negli organismi modificati, di geni coinvolti nell'assorbimento, nel trasporto e nel metabolismo di specifici inquinanti. Sono ormai innumerevoli i lavori che documentano la trasformazione di piante per l'aumento della tolleranza e della capacità di estrazione, accumulo e traslocazione. In particolare, tra le specie arboree grande attenzione si è concentrata sui pioppi: *Populus alba* (Balestrazzi *et al.*, 2009), *P. nigra* (Bittsanszki *et al.*, 2005), *P. deltoides* (Che *et al.*, 2003), *P. tremula* x *P. alba* (Samuilov *et al.*, 2016). In questo settore, a parte gli aspetti legali coinvolti, è comunque necessaria un'attenta considerazione dei rischi correlati; ne consegue l'opportunità di testare in campo gli organismi transgenici per una loro approfondita valutazione, tenendo anche in dovuto conto la problematica dell'accettazione sociale degli OGM.

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B-Type cyclin modulation in response to carbon balance in callus of *Populus alba*

Giovanni Emiliani^{1*}, Silvia Traversari^{2*}, Anna De Carlo¹, Maria Laura Traversi¹, Claudio Cantini¹, Alessio Giovannelli^{1,2}

¹ Istituito per la Valorizzazione del Legno e delle Specie Arboree (IVALSA-CNR), Sesto Fiorentino (Fi)

² BioLabs, Istituto di Scienze della Vita, Scuola Superiore Sant'Anna, Pisa

In plants, sucrose is the principal transported carbon compound. Sucrose and/or glucose and fructose are relevant in the regulation of meristematic cell proliferation. The aim was to define the sugar balance and the relationship between the osmoregulation processes and the cell division patterns in callus of *Populus alba* in response to different sucrose medium concentra-

tions. Callus proliferation and metabolism were assessed through biometric measures, non-structural soluble carbohydrates quantification, osmotic potential determination, as well as by quantification of mRNA accumulation of B-type cyclin genes. Calli were cultured on proliferation medium without sucrose or supplemented with 10, 20 or 30 g L⁻¹ of sucrose. A large amount of non-structural soluble carbohydrates was used to restore the osmotic balance between callus and

* s.traversari@santannapisa.it

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 Ambientali, 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