

International Conference

Plant Gene Discovery Technologies

Programme and Abstracts

Vienna, Austria

23-26 February 2011

Organising Committee

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N15. Expression Profiles of Barley (*Hordeum vulgare* L) Reveal Differences Between Responses under Boron Toxicity and Deficiency

Oz, M.T., Eyidogan, F., Yucel, M., Oktem, H.A.

Boron (B), one of the essential micronutrients for plants, causes toxicity at high or deficiency at low soil concentrations. Moreover, our understanding of molecular responses of plants to B-toxic or B-deficient conditions is incomplete. In this study, transcriptome changes associated with B toxicity or deficiency were investigated in barley (*Hordeum vulgare* L. cv. Tarm-92) using DNA microarrays. Eight day old aseptically grown seedlings were subjected to 0.02 μM H_3BO_3 (B-deficient) or 5000 μM H_3BO_3 (B-toxic) treatments for 5 days. Expression profiles were determined with Barley1 GeneChip using total RNA from leaf or root tissues. Among 22,840 transcripts - each represented with a probe set on the GeneChip - significantly ($P < 0.05$) altered genes were determined. Compared to control (10 μM H_3BO_3) conditions, toxicity and deficiency resulted in significant changes in gene expressions in leaf and root tissues, respectively. Deficiency resulted in up-regulation of B transporter orthologs in root tissues. Furthermore, a noticeable feature was the crosstalk between responses to high B and various environmental stresses. Determination of responsive genes will shed light on successive studies aiming to elucidate molecular mechanism of B toxicity, deficiency or tolerance to these stresses.

N16. Molecular Cloning and Characterization of Ribosomal Protein L24 (RpL24) from Melon (Cucumis melo L.)

Baloglu, M.C., Negre Zakharov, F., Oktem, H.A., Yucel, M.

One of the ribosomal protein L24 (CmRpL24) gene was firstly isolated from a melon (Cucumis melo L.) using the RACE (Rapid amplification of cDNA ends) method. The complete sequence of the CmRpL24 gene (GenBank accesion no: EU853460) with a size of 848 bp was obtained. The cloned cDNA had an ORF extending from position 220 in frame to position 699, coding for a mature 159 amino acid protein with a predicted molecular mass of 17.6 kDa. There was a conserved domain for ribosomal protein L24 at positions 13^107, but no mitochondrial type RpL24 signature sequences was found. KOW motif generally found in ribosomal proteins was also identified at positions 17-48. The predicted polypeptide sequence of CmRpL24 shows the highest similarity (above 90%) with RpL24s from soybean, castorbean, poplar, grape and Arabidopsis. Neighbor-joining trees were constructed from homologies of RpL24 sequences. The tree architecture reflected the divergence between both gymnosperm-angiosperm and monocot-dicot plant species. We showed here for the first time that CmRpL24 gene was cloned and characterized by amino acid sequences. It is known that some ribosomal proteins have functions outside the ribosome. So, RNAi constructs for CmRpL24 gene was prepared to determine function of CmRpL24 gene in melon.