

Transcriptome Analysis in NaCl-Treated Barley (*Hordeum vulgare* L) Seedlings

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Objective

Salinity is a major problem in crop production in large areas worldwide. To understand the genetic mechanisms of the response in barley to high salinity we examined genome-wide changes in transcript accumulation in barley (*Hordeum vulgare* L.) seedlings following exposure to high salinity.

Materials and Methods

The Affymetrix barley GeneChip probe array, containing 22K probe sets was used to examine gene expression in roots at 1 and 5 days after salinity treatment (200 mM NaCl).

Results and Discussion

Transcript accumulation from over 5,000 genes was altered by high salinity, and more than 900 transcripts differentially accumulated 5-fold or more. Genes that exhibited 5-fold or more differential transcript accumulation included novel genes as well as genes involved in osmotic adjustment, transport across membranes, stress signal transduction, oxidative stress amelioration, and general plant defense mechanisms. Complex and overlapping expression profiles of the genes indicated distinct responses of barley to high salinity. This work was supported by a grant from the BioGreen 21 program, Rural Development Administration, Republic of Korea.

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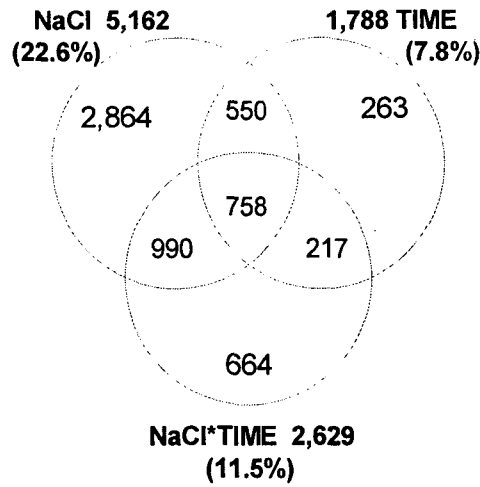


Fig. 1. Numbers of probe sets showing significant difference in transcript levels by salinity, time and interaction effects in barley roots.

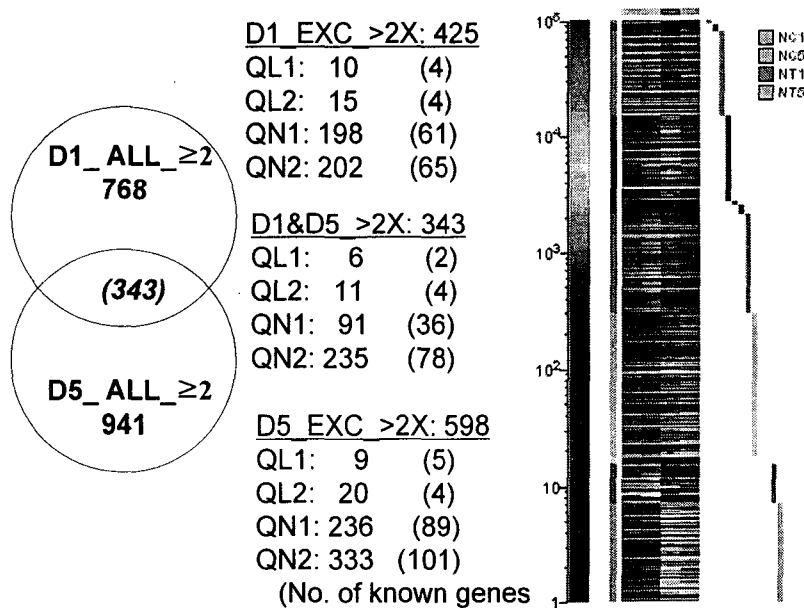


Fig. 2. Numbers of probe sets showing over two-fold difference in transcript levels by salinity effect in barley roots. Changes in the transcript profiles were grouped as qualitative (QL) and quantitative (QN) by the presence and absence test and clustering analysis of the expression levels. 1 indicates changes from absence to presence in QL and from low to high in QN. 2 indicates changes from presence to absence in QL and from high to low in QN.