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## A Genome-wide transcriptional analysis in NaCl-treated barley seedlings

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### Objectives

Salinity is a major problem in crop production in large areas worldwide. The objective of this study was to examine the genetic mechanisms of the response in barley to high salinity.

### Materials and Methods

#### 1. Material

Plant: Three-week-old barley seedlings

#### 2. Methods

Salt treatment: 200 mM NaCl treatment for 1 and 5 days.

Genome-wide transcript analysis: Affymetrix barley GeneChip probe array system

### Results and Discussion

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

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