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## Microarray analysis during heat acclimation in *Arabidopsis* suspension culture cells

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### Objectives

Thermotolerance by mild heat acclimation is a genetically controlled manner in plants to overcome transiently temporal heat shock. Recently, this thermotolerance phenomenon have been extensively studied and focused on HSPs production. Despite these efforts and ubiquitous nature of the heat shock response, little is known how the plant senses an increase in temperature or signaling pathways resulting in HSPs. To expand this limited knowledge, we adopted microarray technology to the heat acclimated *Arabidopsis* suspension culture cells and observed the global gene expression profiling.

### Materials and Methods

#### 1. Material

Genes - 12,288 ESTs from 6 different *Arabidopsis thaliana* cDNA libraries

Plants - Heat acclimated *Arabidopsis thaliana* (L.) Heynh., ecotype Columbia suspension cultures

#### 2. Methods

DNA amplification and purification, Printing, Hybridization, Data analysis, Expression profiling. FDA staining, Chlorophyll assay.

### Results and Discussion

The heat acclimated *Arabidopsis thaliana* L. (Heynh.), ecotype Columbia, suspension culture cells at 37°C were also shown thermotolerance against lethal heat shock (9 min, 50°C) by tests of chlorophyll assay and fluorescein diacetate (FDA) staining. To monitor the genome-wide transcriptome change by heat acclimation at 37°C, we fabricated a *Arabidopsis thaliana* cDNA microarray containing 7989 unique genes and used it to heat acclimated *Arabidopsis* suspension culture cells at various times (0.5, 1, 2.5, 6, and 16 h). From the data analysis, differentially expressed 192 genes were identified, grouped into 10 clusters, and found several known or unknown regulatory common motifs in promoters. The heat shock proteins (HSPs) showed strong expression as previously reported, and several up-regulatory genes encoding detoxification and regulatory proteins were also detected. Among them, strong induction of four *DREB2* (dehydration responsive element-binding factor 2) subfamily genes could positively regulate the target genes of *DREB1A* which are involved with cold, drought and salt. These results suggest the cross-talk occur between heat and other abiotic stress pathways. In addition, at least, four *DREB2* subfamily genes participate in these pathways.