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

Chan Ju Lim, Kyung Ae Yang, Joon Ki Hong, Jin Soo Choi, Dea-Jin Yun,
Jong Chan Hong, Woo Sik Chung, Sang Yeol Lee, Young Ju Choi¹, Chae Oh Lim

Division of Applied Life Science (BK21), Environmental Biotechnology National Core Research Center and
PMBBRC, Gyeongsang National University, Jinju 660-701, Korea

¹Department of Food and Nutrition, Silla University, Busan 617-736, Korea

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 cells and observed the global gene expression profiling.

Materials and Methods

Genes - 12,288 ESTs (7989 unique genes) from 6 different *Arabidopsis thaliana* cDNA libraries.

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

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

Results and Discussion

The heat acclimated *Arabidopsis thaliana* L. (Heynh.), ecotype Columbia, suspension culture cells at 37°C were 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 not positively regulate the target genes of *DREB1A* which are involved with cold, drought and salt. These results suggest that the distinct unknown pathways are existed for heat acclimation responses, and, at least, four *DREB2* subfamily genes participate in these pathways.