

## Gene expression analysis and network construction using a massive microarray data set derived from drought stress treatments in rice

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To elucidate global responses to drought stress in rice, a 60 mer oligomer microarray covering 22K unique genes based on the sequence of full-length cDNA clones was used to profile gene expression changes in the rice shoot at the seedling stage and in the peduncle at heading. As reported by Ji et al. (2005) *Plant Mol Biol.* 59:945-964, peduncle elongation in rice is inhibited by drought stress. Cluster analysis of genes up- and down-regulated by drought stress in these two different growth stages revealed stage-specific gene expression profiles. Gene expression analysis using the metabolic pathway data in Rice Cyc (<http://www.gramene.org/pathway/>) showed that genes encoding many enzymes of sugar metabolism, such as degradation of sucrose, glucose and galatose, are down-regulated, along with genes encoding enzymes of cell-wall biosynthetic, while genes encoding enzymes of some amino acid biosynthetic pathways are up-regulated. Drought-induced ABA is clearly involved in antagonizing GA-dependent events underlying peduncle elongation, but the biosynthetic genes related to these hormones are not clearly affected by the drought stress treatment. Among 613 differentially expressed transcription factor-related genes, the C3H, AP2-EREBP, bHLH, NAC, MYB and WRKY types of TF-related genes showed differential expression during drought stress treatment and re-watering treatment. Finally, the promoter regions (1kb upstream sequence) of the genes clustered after microarray experiments were examined using a newly developed *cis*-element analysis tool; the results of this analysis will also be discussed. Data mining using gene annotation data (ex. GO term), pathway data, and genome mapping data suggests the existence of transcription network of drought stress-responsive genes.