



# Comparative and joint analyses of gene expression profiles under drought and rewatering in *Arabidopsis*

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**ABSTRACT.** Drought is a major limiting factor in crop production. Rewatering is a process opposite to drought, allowing plants to recover to their normal physiological state. To understand more thoroughly the set of genes involved in plant response to drought, we comparatively and jointly analyzed the microarray data of drought and rewatering experiments in *Arabidopsis*. A total of 3833 differentially expressed genes (DEGs) were identified. Among them, ~74% were proven to be co-regulated by drought and rewatering. Drought and rewatering showed contrary regulatory effects on almost all of these co-regulated genes. Only ~6% of the DEGs were significantly regulated by drought alone, and the remaining ~20% were significantly regulated by rewatering alone. However, gene ontology analysis suggested that those “rewatering-only” genes also appeared to be related, either directly or indirectly, to drought response.

**Key words:** Drought; Rewatering; Microarray; *Arabidopsis*; Differentially expressed genes