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Natural variation in *Arabidopsis thaliana*: Molecular genetic architecture of stress tolerance under water deficit

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The functional genomics tools available for studying *Arabidopsis thaliana* are a great resource for researchers trying to characterize and understand the genetic basis of natural variation. Genome wide transcript profiling can simultaneously monitor the gene expression programs regulated by growth and development and signal transduction pathways in response to environmental stress conditions. The responses of plants to water deficit depend on the extent and rate of water loss and its timing and duration. As a physical stress, water deficit triggers biochemical responses through a cascade that includes stress perception, signal transduction and regulation of gene expression. *Arabidopsis* accessions differ largely in their adaptation to stress tolerance. To understand the genetic basis of this intra-specific variation we analyzed five accessions under gradual water deficit leading to severe stress conditions. The changes in the gene expression profiles under water deficit conditions were studied using functional genomics tools, microarray and quantitative real time PCR and the regulatory roles of stress induced and developmental related transcripts will be discussed.