

IDENTIFICATION OF COMMON KEY GENES AND REGULATORY PATHWAYS INVOLVED IN DROUGHT TOLERANCE IN FOUR GRAMINEAE SPECIES THROUGH A COMPARATIVE TRANSCRIPTOMIC META-ANALYSIS

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Drought negatively affects plant growth and development. The ability to tolerate abiotic stresses varies among species, and among genotypes within species. Unravelling the molecular mechanisms behind drought response is essential to identify the genes involved in tolerance. Comparative transcriptomic studies, analysing different genotypes with contrasting drought responses (tolerance *vs* sensitiveness), allow the exploitation of the natural genetic variation of plant species for discovering genes involved in drought tolerance. Here, a meta-analysis on RNA-Seq data related to comparative transcriptomic studies of different Gramineae species was performed to identify the genes representing common key players in response to drought, as well as the regulatory pathways in which these genes are involved. In particular, four published studies, investigating the transcriptomic response to drought in the leaf of two contrasting genotypes (tolerant and sensitive) in *Brachypodium*, barley, maize and rice, were selected for the transcriptomic meta-analysis. We re-analysed the RNA-Seq data with a unique pipeline and detected the differentially expressed genes (DEGs) in both genotypes of the four experiments. The drought-induced variation in DEG expression was compared between tolerant and susceptible genotypes of each species. We assumed that the genes whose expression regulation differs between the two contrasting genotypes represent key players in the differentiation between the tolerant and the sensitive response to drought. The rice orthologues of the selected genes were identified to obtain comparable datasets. We found 69 common genes that are putatively involved in drought tolerance in the four species. Clustering analysis and protein-protein interaction underlined a prominent role of genes involved in photosynthesis and chlorophyll degradation (*i.e.*, the *Stay-Green* gene, *SGR*) for all the considered species. Moreover, genes of unknown function that may be crucial in plant tolerance were identified. Finally, gene co-expression networks of the 69 genes and the DEGs encoding transcription factors were developed to reveal regulatory pathways that putatively differentiate the response of tolerant and susceptible genotypes in the four Gramineae species. Specific transcription factors for each species were identified as putative major players in the regulation of drought tolerance.