

ARRAY ANALYSIS OF DROUGHT RESPONSE IN BREAD AND DURUM WHEAT AT GRAIN FILLING STAGE

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Drought tolerance is a complex trait where many morpho-physiological mechanisms are involved in the response/adaptation processes are supported by a complete reorganization of the cell transcriptome. To provide a global study of the changes in gene expression we have investigated the transcriptome of bread (*T. aestivum* cv Chinese Spring and its deletion line CS-5AL) and durum wheat (*T. turgidum*, cvs. Creso and Trinakria) subjected to two different levels of water stress (mild and severe stress) at the grain filling stage. Expression study was conducted with the Affymetrix 61K wheat chip on three biological replicates of mRNA extracted from flag leaves and glumes. The t-test comparing analysis between control and stressed samples have shown more than 1,000 genes up or down-regulated in each genotype. When the stress responses of tetraploid and hexaploid wheat were compared we have found that under mild stress conditions the molecular response involved much more genes in the hexaploid than in the tetraploid wheat. Data-mining on the expression data have identified some known drought response pathways (i.e. biosynthesis pathway of ABA, proline, sorbitol, glycine betaine) as well as a number of transcription factors whose expression can be associated to stress resistance. The higher number of expressed genes detected in the hexaploid bread wheat compared to the tetraploid durum wheat allowed the identification of sequences putatively located on the D genome. In the same way the comparison between Chinese Spring and CS-5AL allowed the finding of putative sequences belong to long arm of 5A chromosome. The poster will present data on genes and pathways up- or down-regulated in the different specie and cultivars and clustering organization of the genes depending on the intensity of the water stress applied.