

PHYSIOLOGICAL AND TRANSCRIPTOMIC CHARACTERIZATION OF DROUGHT STRESS IN THREE DIFFERENT DURUM WHEAT GENOTYPES

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Crop productivity is threatened by climate change, which has led to increasing water scarcity in various regions of the world, including Europe, and in particular the Mediterranean area. Drought is one of the most common environmental stresses, and it negatively impacts on the normal plant physiology and growth in many ways. Although durum wheat is adapted to semi-arid climates, extreme weather conditions and prolonged drought have a negative effect on yield potential and survival. Accordingly, the identification of more resilient genotypes able to cope with suboptimal water could allow to counteract yield losses. This study describes the physiological and transcriptomic characterization of drought stress in three *Triticum turgidum* genotypes, Svevo, Svems16 and LCYE*. Plants were grown hydroponically and exposed to drought for six days through the application of 10% (w/v) polyethylene glycol (PEG) 6000 to the nutrient solution. The plant response to drought was investigated through the evaluation of shoot and root fresh weight, chlorophyll levels, proline and malondialdehyde (MDA) concentration. The observed physiological changes were then related to the morphological traits of root system. The results revealed that Svems16 and LCYE* genotypes were more tolerant to drought than Svevo, as indicated by their lower MDA content, higher root proline concentration and medium-depth rooting system. RNA-seq analysis identified a total of 3150 differentially expressed genes (DEGs) related to the stress response of which 122 and 14 shared among all three genotypes respectively in root and shoot tissues. The transcriptome reprogramming induced by PEG treatment was more intense in the sensitive genotype compared to the tolerant ones and in root than in shoot tissue. The root specific-response included genes involved in nicotianamine biosynthesis, membrane

modification, and glycosylation whereas the leaf specific-response was mainly associated to the metabolic processes related to carbohydrates and amino acids. Interestingly, a positive modulation by drought was observed in all genotypes for genes involved in glutathione and sulfur compound metabolic processes, confirming the functional role of sulfur in plant response to oxidative stress. In conclusion, the data presented here provide broad information about genes and physiological changes involved in drought tolerance occurring in wheat roots and shoots, that can be used to improve grain yield and quality under unfavorable conditions.

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