

TRANSCRIPTOMIC ANALYSIS OF DROUGHT AND HEAT RESPONSES IN DURUM WHEAT AND eQTLs MAPPING TO IDENTIFY THE LOCI CONTROLLING THE MOLECULAR RESPONSE TO DROUGHT

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The durum wheat cultivars “Cappelli” and “Ofanto” are characterized by contrasting behavior in response to high temperature and drought stress.

The transcriptome profiles of the two cultivars flag leaves subjected to water stress, heat stress and a combined stress at booting stage were compared based on Affymetrix microarray analysis. The analysis has identified 1850 stress responsive probe sets characterized by a significantly different stress expression profiles in Cappelli vs Ofanto. These genes are almost not differentially expressed in response to drought both in Cappelli and Ofanto. On the contrary, Cappelli showed a more pronounced molecular response to heat stress. Finally these genes showed similar expression levels in response to the combined stress.

Briefly these genes describe a complex response: perception and signal transduction were characterized by the activation of HSP, transcription factors and RNA binding protein suggesting both transcriptional and post-transcriptional regulation. Moreover expression values have indicated a regulation of stomata closure as well as the activation of fatty acid degradation pathway.

Among these genes some drought and heat response gene markers have been identified and use to test the heat and drought response of the two cultivars at young developmental stages by qRT-PCR. The gene markers were selected according to the fold change threshold of the Affymetrix dataset. These sequences were considered ideal candidates for an eQTL mapping experiment aiming to identify the key loci controlling the molecular response to drought. The mapping experiment was based on the availability of a genetic map developed on the Ofanto x Cappelli Recombinant Inbred Line (RIL) population, composed by 161 lines. Based on their expression profile, two genes were chosen to be tested on 80 RILs grown in water stress conditions by qRT-PCR. A highly significant (LOD=7) eQTL was identified on chromosome 6B which explained about 36% of observed variability for the expression of High Expression Level gene (HEL), one out of the two tested genes. HEL is a transcript, unknown annotated, shows a strong drought induction in Ofanto. The corresponding probe set matches with the contig444272 of Chinese spring draft genome assembly. The gene mapping is in progress in order to distinguish between a *cis*- or *trans*-action of the eQTL identified on the gene expression. Then, since this gene

is differentially regulated between the two cultivars contrasting for stress tolerance, additional experiments will be planned to map drought tolerance QTLs.