

Poster 39. Mapping QTL related to drought tolerance in durum wheat (*Triticum turgidum* L. subsp. *durum*).

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Durum wheat (*Triticum turgidum* L. subsp. *durum*) is largely grown in Mediterranean environments where drought stress affects grain yield and yield stability. Mapping quantitative trait loci (QTL) in segregated populations allows the detection of chromosome regions controlling traits of agronomic interest with the opportunity to dissect complex traits. To understand the genetic basis of quantitative traits involved in drought stress tolerance, 130 F₆ recombinant inbred lines (RILs), derived from a cross between the cultivar Zardak and genotype 249 (a local variety and a genotype of the Kermanshah province, Iran, respectively) were analyzed with a total of 85 microsatellite markers. Most of the markers were mapped to the 13 linkage groups (83.5%). Interval mapping was employed for QTL detection using a linkage map sequence repeat (SSR) markers. Chromosomal regions with QTL were identified for several traits related to drought tolerance. The identified genomic regions controlling wheat traits can be targeted during further studies for their genetic dissection.

Poster 40. Expression analysis of genes involved in gibberellin biosynthesis under drought stress in wild emmer wheat.

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Drought tolerance mechanisms play an important role in plant adaptation to arid environments. Aiming to identify candidate genes for drought resistance, we recently have compared the transcriptome of drought resistant (R) vs. susceptible (S) genotypes of wild emmer wheat (*Triticum turgidum* subsp. *dicoccoides*) under water stress. These studies revealed differential expression of genes involved in metabolism and signaling of abscisic acid (ABA), auxin (IAA), and gibberellin (GA) in response to drought stress. However, while ABA- and IAA-related genes had a similar pattern of expression in leaves and roots, some of the GA-related genes showed opposite expression pattern in the two tissues. GA is an essential hormone involved in many aspects of plant development, but it is not recognized as an important hormone in relation to plant stress response. In order to clarify whether modulation of specific genes in the GA metabolic pathway play a role in adaptation to drought stress, we studied the expression pattern of additional genes encoding for enzymes in the GA biosynthetic pathway. Gene expression was tested in leaves and roots of the R genotype after 3, 5, and 7 days of withholding water and in well-watered plants. The analysis showed complex pattern of gene expression, in which genes functioning at the beginning and at the end of the pathway were differentially expressed under drought in the roots, confirming the idea of different GA roles in leaves and roots. In addition, the promoter regions of the GA-related genes and GA-receptor gene (*GID1*) were scanned for abundance of transcription factors binding sites (TFBSs). The promoter regions of these genes were obtained by BLAST of the cDNA sequences against the survey sequence of wheat (IWGSC Survey Sequencing Initiative). Interestingly, promoters of the differentially expressed genes were enriched with TFBSs related to abiotic stress (e.g., DREB/CBF/ERD/COR). Our results are in agreement with recent publications showing that the cross-talk of GA with ABA and IAA contributes to developmental plasticity of root systems under water stress. These processes result in morphological changes that extend the water-absorbing surface area of the roots, including the increase in rooting depth.