

## GENOME WIDE ASSOCIATION STUDY REVEALS NOVEL QUANTITATIVE LOCI FOR OSMOTIC ADJUSTMENT UNDER DROUGHT STRESS IN DURUM WHEAT

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Drought stress is one of the most devastating stressors limiting crop survival and adaptability, thereby affecting yield loss. Osmotic adjustment (OA) is one of the major components of drought resistance in crops (Blum 2017) thanks to an active accumulation of solutes in response to a water potential reduction, thereby maintaining turgor (Turner 2018). Although yield differences in wheat yield have been correlated to OA capacity, the genetic basis of this trait is basically unknown due to the difficulty to measure OA in an adequately large number of accessions, an essential prerequisite to detect reproducible and reliable Quantitative Trait Loci (QTLs). This work reports the first Genome Wide Association Study (GWAS) in durum wheat for OA as well as for relative water content (RWC), osmotic potential ( $\psi_s$ ) and dry biomass (DB) under full and deficit irrigation conditions.

In the field trial conducted in 2018 at the Maricopa Agricultural Center (AZ), 248 durum wheat elite lines and cultivars from worldwide (Durum Panel) were evaluated according to a randomized block design with two replicates. Leaf samples were first collected at flowering under well-irrigated conditions and 14 days later under both well-irrigated and water-stressed conditions. To analyze OA, eight fully expanded flag leaves were sampled from each plot before dawn, re-hydrated to full turgor for 8 hours and stored in freezer. The extracted leaf sap was collected for measuring  $\psi_s$  using a vapor pressure osmometer. The resulting osmolality ( $\text{mosmol kg}^{-1}$ ) was converted to osmolarity (MPa) to evaluate OA as  $\psi_s$  (control) -  $\psi_s$  (water-stressed).

The genetic characterization of the Durum Panel was carried out with the Illumina iSelect wheat 90K SNP assay. GWAS analysis was performed using a Mixed Linear Model (MLM) including both a fixed effect as the population structure matrix (Q) and a random effect as the kinship matrix (K) in Tassel 5.2.7 in order to identify the genetic intervals harboring loci controlling OA, RWC,  $\psi_s$  and DB. A total of four, six, four and nine significant QTLs were detected for OA, RWC,  $\psi_s$  and DB, respectively. In particular, two major QTL hotspots on chromosomes 6AS and 6AL were found to concurrently affect OA, RWC and DB with a positive effect of OA on both RWC and DB. These results support OA as a prime drought-stress adaptive trait in support of plant production under water-stressed conditions in durum wheat.