

## GENOME WIDE ASSOCIATION STUDY UNCOVERS THE QTLOME FOR OSMOTIC ADJUSTMENT AND RELATED DROUGHT ADAPTIVE TRAITS IN DURUM WHEAT

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Osmotic adjustment (OA) is a major component of drought resistance in crops. The genetic basis of OA in wheat and other crops remains largely unknown. In this study (Concorelli *et al.* 2022), a panel of 248 field-grown durum wheat elite accessions grown under well-watered conditions until flowering, underwent a progressively severe drought treatment started at heading. Leaf samples were collected at heading and 17 days later. The following traits were considered: flowering time (FT), leaf relative water content (RWC), osmotic potential ( $\psi_s$ ), osmotic adjustment (OA), chlorophyll content (SPAD) and leaf rolling (LR). The high variability (3.89-fold) in OA among drought-stressed accessions resulted in high heritability (72.3%) of the trait. Notably, a high positive correlation ( $r = 0.78$ ) between OA and RWC was found under severe drought conditions. GWA analysis revealed 15 significant QTLs for OA ( $R^2 = 63.6\%$ ) as well as 8 major QTL hotspots/clusters on chromosome arms 1BL, 2BL, 4AL, 5AL, 6AL, 6BL and 7BS where a higher OA capacity was positively associated with RWC and/or SPAD, and negatively with LR, indicating a beneficial effect of OA on the water status of the plant. The comparative analysis with the results of 15

previous field trials conducted under varying water regimes showed concurrent effects of five OA QTL cluster hotspots on normalized difference vegetation index (NDVI), thousand-kernel weight (TKW) and/or grain yield (GY). Gene content analysis of the cluster regions revealed the presence of several candidate genes, including bidirectional sugar transporter SWEET, rhomboid-like protein and S-adenosyl-L-methionine-dependent methyltransferases family protein and DREB1. Our results support OA as a valuable proxy for marker-assisted selection (MAS) aimed at enhancing drought resistance in wheat.