

ROOT GROWTH ANGLE IN DURUM WHEAT AS A PROXY FOR DROUGHT TOLERANCE: A HIGHLY HERITABLE AND VARIABLE TRAIT IN DURUM WHEAT GERMPLASM

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Root system architecture has a profound effect on water and nutrient uptake capacity, and consequently on crop yield, especially under drought- and nutrient-limited conditions. However, root architecture has been largely neglected in crop breeding and few developmental and regulatory genes and circuits have been identified so far.

This study presents the results of the characterization of both natural and induced variation in the Triticeae for root growth angle (RGA), a trait relevant for water and nitrogen uptake efficiency. Importantly, no major QTL has been reported for RGA in bread wheat. RGA have been assessed on a wide panel of tetraploid wheat, including two bi-parental populations (Colosseo x Lloyd and Meridiano x Claudio), a Global Durum Panel collection including 1,000 accessions (Mazzucotelli et al. 2020), mainly cultivars from world-wide and landraces, a set of additional 250 *T. turgidum*

landraces and a T.dicoccum panel from the Tetraploid Global Collection (TGC, Maccaferri et al. 2019). (https://wheat.pw.usda.gov/GG3/global_durum_genomic_resources). The results of the GWAS unveiled three major QTLs on chromosomes 2A, 6A and 7A, with narrow and shallow alleles detectable in various combinations in modern durum wheat cultivars. The 6A was the QTL with the highest PVE and the highest effects. KASP® markers tagging the narrow and shallow haplotypes have been obtained for each QTL, thus allowing for efficient marker-assisted selection and germplasm screening in breeding materials. SNP haplotype analysis in the three QTL confidence interval was carried out and haplotypes associated to narrow and shallow RGA to various extent were identified. The three-QTL haplotypes were recombined to various extent in varieties of the GDP, leading to varieties with combined narrow haplotypes and very narrow RGA phenotype (ICARDA genotypes) and very shallow RGA on the opposite (CIMMYT genotypes). Finally, the lines combining two or three contrasting haplotypes showed markedly different RGA phenotypes and were evaluated in field trials under well-watered and drought conditions. Contrasting genotypes for RGA were used for root transcriptome analyses aimed at the identification of allelic variation and haplotype-specific expression at the candidate genes, together with regulatory networks associated to RGA regulation. Altogether, these materials will provide a unique opportunity for field evaluation of contrasting RGA and its effects on grain yield and its stability according to the availability of water and nutrients.

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