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A CANDIDATE GENE ANALYSIS OF QTLS FOR ROOT GROWTH ANGLE IN DURUM WHEAT

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Optimization of root system architecture (RSA) traits is an important objective for modern wheat breeding. Durum wheat *Triticum turgidum* L. var. *durum* Desf.), germplasm, including two recombinant inbred line populations and one association mapping panel of 183 elite cultivars was searched for RSA QTLs. Seven QTLs were selected for investigation of gene content in the QTL confidence interval based on the Chinese Spring *T. aestivum* IWGSC1.0+POPSEQ (Mayer et al, 2014, Chapman et al. 2015) as well as based on the golden standard wheat genome assemblies of *T. dicoccoides* accession Zavitan (Avni et al, 2017), *T. durum* cultivar Svevo (Maccaferri et al, unpublished) and *T. aestivum* IWGSC RefSeq v1.0 (IWGSC, 2018). The TriAnnot v4.3 pipeline was used for gene prediction and annotation. Candidate genes were prioritized based on annotation, expression analysis, evidence mining for association to auxin response/signaling, root hair formation/elongation, gravitropism and root meristem (KnetMiner). Candidate genes were functionally validated in orthologs. The QTL confidence intervals ranged from 1.8 to 14.0 Mb and contained 4 from to 37 candidate genes. Candidate genes were involved in MYB transcription factor, auxin response factors (ARF) family, PIN-formed (PIN) protein family of auxin transporters, zink finger protein family and other candidates. All these gene families have been shown to be involved in controlling RGA in both rice and *Arabidopsis*. The tissue expression of candidate genes was investigated in 13 varieties of durum wheat and in wheat expression databases expVIP (Borrill et al, 2016), WheatExp (Pearce et al, 2015). The most promising candidate genes will be validated by re-sequencing the alleles from the relevant parents/representative cultivars, investigating of their transcriptome profiles and identification of TILLING mutants in Kronos collection.

ABSTRACT