

## A TRANSCRIPTOMIC APPROACH TO IDENTIFY CANDIDATE GENES AT QTLS FOR ROOT GROWTH ANGLE IN DURUM WHEAT

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Root systems architecture (RSA) affects water and nutrients uptake and is crucially important for crop performance, particularly under non-optimal water and nutrients supply conditions. RSA variation for root growth angle, root length, density or architecture of lateral roots, can potentially affect root distribution in soil profile and belowground competitive interactions between neighbouring plants. For instance, narrow root growth angle (RGA) generally results in deeper rooting systems that could better capture soluble nitrogen and/or water in the deep soil layers. On the contrary, a shallow root system with a wider RGA and a greater distribution in the upper soil layers, enable crop plants to better capture phosphorous in the topsoil.

Previous analysis in durum wheat (*Triticum turgidum* L. var. *durum* Desf.) using two recombinant inbred line populations and an association mapping panel of 183 accessions allowed the identification of seven main QTLs controlling root growth angle (RGA; Maccaferri et al., 2016).

In this study we present new results on the molecular genetic control of RGA based on a wider genome wide association study and integrated with RNA-Seq analysis. An improved GWAS pipeline applied to the Global Durum Panel (GDP), a world-wide tetraploid collection composed of 755 accessions, confirmed the previously identified major RGA-QTLs on chromosomes 2A, 6A and 7A and also allowed the identification of two additional RGA-QTLs on chromosomes 5B and 7A, that are under further investigation.

RNA-Seq analysis was performed on root samples collected from cultivars

with contrasting RGA and different haplotypes at the identified QTLs. Samples from root tips (including root cap and meristematic region), elongation and transition/maturation zones were collected from 'Altar-84' (shallow RGA), 'Svevo' (intermediate RGA) and 'Geromtel' (narrow RGA) cultivars, representative of contrasting haplotypes. Differentially expressed genes (DEGs) showing RGA-dependent expression levels mapped in the RGA-QTL intervals were therefore investigated at functional level. Interesting candidate genes involved in auxin signalling, melatonin biosynthesis, hormone signalling and cross-talk and cell wall biosynthesis were identified. Analysis of co-expressed genes and regulatory networks associated to wide or narrow RGA in durum wheat are underway, with preliminary results pointing to a main role for abscisic acid signalling.

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