

EXPLORING THE MOLECULAR BASES OF ROOT GROWTH ANGLE AND ITS REGULATION IN BARLEY AND WHEAT

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Root system architecture has a profound effect on water uptake capacity, nutrient use efficiency, and consequently crop yield. A “steep, cheap, and deep” root ideotype that facilitates water or nutrient absorption from deep soil layers was recently proposed to enhance crop stress resilience. However, root architecture has been largely neglected in crop breeding and few developmental and regulatory genes and circuits have been identified so far.

ENHANCED GRAVITROPISM 1 and 2 (*EGT1* and *EGT2*; Fusi *et al.*, PNAS *in press*; Kirschner *et al.*, 2021 PNAS 31;118(35):e2101526118) are two genes controlling root growth angle in barley and wheat and recently isolated in our group. Both *egt1* and *egt2* mutants exhibit a steeper growth of seminal and lateral roots. Molecular and transcriptomic analysis revealed that the two genes act independently on root growth angle regulation in response to gravity, roles that are evolutionary conserved between barley and wheat. Interestingly, natural variation within the *EGT1* coding sequence was found associated to steeper root angle in barley germplasm collection. We are now expanding the study of natural variation at both *EGT* genes including bread and durum wheat germplasm collections. In parallel, a genome wide association study (GWAS) analysis for seminal root growth angle was performed on the Global Durum Genomic Resource (https://wheat.pw.usda.gov/GG3/global_durum_genomic_resources). One thousand durum cultivars, landraces and domesticated emmer have been assessed for RGA at seminal stage. The results pointed to three major QTLs on chromosomes 2A, 6A and 7A, with “narrow” and “shallow” alleles at these

QTLs detectable in various combinations in the modern durum wheat cultivars. The lines combining two or three contrasting haplotypes showed opposite root angle phenotypes and were used in field trials under well-watered and drought conditions. Contrasting genotypes were furthermore instrumental 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 root angle regulation. Altogether, the obtained results will offer an exceptional starting point for breeding new varieties with root architecture traits better adapted to climate change and low input farming challenges.