

EXPLOITING THE FULL POTENTIAL OF A LOW-LINKAGE DISEQUILIBRIUM, FULLY RE-SEQUENCED AGILOPS TAUSCHII COLLECTION FOR GWAS TARGETING ROOT SYSTEM ARCHITECTURE

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Aegilops tauschii is the diploid progenitor of the DD subgenome of hexaploid wheat (*Triticum aestivum* L.) and is an important source of genetic variation for wheat breeding. As a consequence of a strong domestication bottleneck, it is known that the DD genome of *T. aestivum* is strongly depleted in polymorphisms. Our objective was to assess the phenotypic diversity for root traits in the 242 accessions of the Open Wild Wheat Consortium (OWWC <http://www.openwildwheat.org/>), all provided with whole-genome resequencing and suitable to highly precise GWAS, aiming at identifying novel QTLs governing root traits.

The collection includes Turkey-to-Afghanistan-Central Asian lines (L1 lineage) and southwestern coastal Caspian Sea (L2), with the latter being involved in wheat domestication. The two lineages are strongly differentiated (Gaurav et al., 2021), representing wide genetic variability.

As for roots system architecture traits, pre-germinated seedlings were

grown on filter paper sheets placed on black polycarbonate screening plates soaked in a modified Hoagland nutrient solution. After ten days in growth chamber, images of seminal roots were collected for measuring the following traits: root growth angle, primary root and total root length, root diameter, root network area, lateral root density and length.

All phenotypic data were analyzed with linear mixed model. A k-mer based GWAS was performed in collaboration with John Innes Center (Dr. Brande Wulff lab) using the pipeline published in Gaurav et al., Nat Biotechnol 40, 422–431 (2022).

Interesting QTL peaks were detected for different traits: network area, primary root length, root length, lateral root density score, lateral root length score, root growth angle. K-mer based GWAS proved to have high resolution on peaks, ranging from 50kb to 2Mbp for different traits. Information on protein function and conserved domains were extracted for each gene included in intervals. In addition, orthologues in different species have been detected (including *Arabidopsis thaliana*, rice and wheat) to analyze molecular functions, tissue and level of gene expression. GWAS analysis identified interesting QTLs corresponding to very few candidate genes for all traits. The analysis of candidate gene sequences in L1 and L2 accessions could reveal different allelic variants specific for the phenotypic variability and for genetic distance that characterized the two *Aegilops* lineages. Most probably the *Aegilops* functional variants (alleles) will not be represented in modern wheat. Hence, this provide a fast and effective way to dissect the genetic control of a valuable trait and to provide new valuable variants for downstream pre-breeding activities at the same time.

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