

EXPLORING TRAIT VARIATION IN A SEQUENCED AEGILOPS TAUSCHIIDIVERSITY PANEL FOR FAST TRACKING WHEAT BREEDING

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Abstract

Aegilops tauschii is the diploid progenitor of the D 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, *T. aestivum* has been strongly depleted in polymorphisms particularly in the D subgenome. Crop wild relatives offer a wide range of novel alleles due to the broad genetic variability still present in natural populations. Our objective was to assess the phenotypic diversity of 242 accessions from the Open Wild Wheat Consortium (OWWC; <http://www.openwildwheat.org/>), all provided with whole-genome resequencing. Traits of agronomic interest were considered, including phenology, growth habit, tillering, spike traits, anthocyanin accumulation, shoot and root biomass as well as root system architecture (RSA). The collection includes Lineage 1 from Turkey through Afghanistan to Central Asia and Lineage 2, primarily from the southwestern coastal area of the Caspian Sea, with the latter being involved in wheat domestication. Agronomic data were gathered from two field experiments conducted in

Cadriano, Italy, in 2019/2020 and 2020/2021. RSA data were obtained from growing the accessions in a growth chamber on filter paper sheets on polycarbonate plates soaked in a modified Hoagland solution. Root growth angle, root length, root diameter, root network area, lateral root density and length were assessed on ten-day-old roots. Field data were analyzed and corrected for outliers and spatial effects while RSA growth chamber data were analyzed including replicates and blocks. High heritability (0.70 - 0.94) was observed for days to heading, flag leaf length, peduncle length, plant height and anthocyanin presence and for root growth angle among the root traits. Lowest values (< 0.50) were observed for root dry weight and tiller score. The relationship between phenotypic traits was significant. A high value ($p < 0.01$) was observed between culm dry weight, number of culms and root dry weight ($r > 0.60$). A positive correlation was also observed between senescence and elevation angle ($r = 0.37$), plant height and internode length ($r = 0.59$). Overall, the preliminary findings suggest that an important genetic variability exists in the OWWC collection.

A *k-mer* based GWAS is underway with the aim of identifying novel QTLs governing the examined traits (Gaurav et al. 2021, bioRxiv 2021.01.31.428788). Eventually, novel beneficial RSA alleles could be introgressed into bread and durum wheat through direct crossing and synthetic hybridization.

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