

A TETRAPLOID CORE COLLECTION (TCC) FROM THE GLOBAL DURUM GENOMIC RESOURCE ASSESSED FOR RESILIENCE TRAITS INCLUDING ROOT SYSTEM ARCHITECTURE, STEM ANATOMY AND DEVELOPMENTAL TRAITS

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Durum wheat (*Triticum turgidum* L. ssp. *durum*) is a major cereal for the semi-arid regions of the Mediterranean Basin, including Southern Europe, North Africa, and West Asia. It originates from a wild tetraploid wheat domesticated in the Neolithic era and then evolved to domesticated emmer and then to primitive tetraploid wheat, durum wheat landraces and finally durum wheat cultivars. After the transitions from wild emmer to domesticated emmer and from emmer to primitive durum, tetraploids underwent two similar star-like radial expansions from the Fertile Crescent to Western (North Africa, Balkans, Southern Europe) and Eastern (India and Ethiopia, Iran and Transcaucasia, Russian Federation/Central Asia). This happened under two overlapping though independent events, for both domesticated emmer populations and, subsequently, for primitive *T. ssp. turgidum*, *turanicum*, *polonicum*, *durum* and *carthlicum* populations.

With the support of the International Durum Sequencing Consortium, the Wheat Initiative, CIMMYT and ICARDA we have assembled the Global Durum Genomic Resource (https://wheat.pw.usda.gov/GG3/global_durum_genomic_resources), composed by the Tetraploid Germplasm Collection (TGC, Maccaferri et al. Nature Genetics 2019) and by the Global Durum Panel (GDP, Mazzucotelli et al. Frontiers in Plant Science, 2020).

The Tetraploid Global Collection (TGC) consists of 1856 genotypes, comprehensively sampling wild emmer wheat, domesticated emmer wheat, durum landraces, and other durum subspecies. The Global Durum Panel (GDP) is a wheat collection including 800 durum modern cultivars and durum landraces from worldwide. The population structure and expansion dynamics have been assessed by means of the Illumina iSelect 90K wheat SNP array.

Based on haplotype analysis and stratified sampling, a highly representative Tetraploid Core Collection (TCC) of 432 accessions sampling all main populations and subpopulations of tetraploids from wild emmer to modern durums have been assembled. TCC is organized as a pyramid with top, intermediate and basal level. Ideally, the TCC is relevant for pangenome analysis and allele mining. Currently, the collection is provided with the 90K wheat SNP genotypes and, limited to 250 accessions, with the whole exome capture

We characterized the TCC with traits relevant for adaptation to the diverse Mediterranean and Eurasian environments, as heading date, peduncle length, flag leaf size and area, anatomical root and nodal traits, root growth angle, spike fertility traits and kernel weight and shape traits in two nurseries grown in Cadriano at the University of Bologna experimental farm.

We therefore performed trait analysis distribution within and among populations and subpopulations based on population structure analysis and run preliminary GWAS based on 90K and exome capture data.

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