

ESTABLISHMENT OF A GLOBAL TETRAPLOID WHEAT COLLECTION TO FACILITATE THE DISSECTION OF THE NATIVE VARIATION PRESENT IN THE A AND B WHEAT GENOMES

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Current cereal crop improvement must cope with a climate change scenario leading to increased temperatures and altered precipitation regimes, which will affect (i) phenology, (ii) resilience to abiotic stresses (drought and heat), and (iii) susceptibility to diseases (rusts, septoria/stagonospora, fusarium head blight, other *Fusaria* complexes and soil-borne mosaic virus). Durum wheat (AABB) is a major cereal and staple in the Mediterranean basin and belong to the diverse tetraploid wheat gene pool, including up to 11 *T. turgidum* subspecies, all interfertile with common wheat (AABBDD).

Common hexaploid wheat originated from two domestication bottlenecks of wild emmer and tetraploid hybridization with *Aegilops tauschii* (DD). The tetraploid germplasm has spread from the Fertile Crescent across Europe,

North Africa, Asia, India and Ethiopia. This evolution has produced a huge diversity valuable for the identification of beneficial alleles for enhancing both durum and bread wheat resilience to abiotic stresses and disease resistance.

Based on an international effort, we have assembled a comprehensive global durum wheat resource comprising (i) the Tetraploid wheat Global Collection (TGC, 1,856 accessions), including wild and domesticated emmer and landraces of durum wheat and related subspecies, (ii) the Global Durum Panel (GDP, 1,033 accessions) including cultivated and locally grown durum wheat varieties supplied by breeders from various nations, and (iii) the Tetraploid wheat Core Collection (TCC, 300 accessions). The iSelect 90K SNP array anchored to the Svevo genome sequence allowed us to study population structure and perform association mapping studies. The TCC captures 95% of molecular variation of tetraploids and is thus particularly suited for allele mining.

The TGC and GDP have been characterized to dissect the QTLome for resistance to yellow rust, leaf rust, soil-borne cereal mosaic virus (SBCMV), root growth angle (RGA) and ear fertility traits. Examples of genome wide association study (GWAS) will be presented for key traits. The combined analysis of the GDP and TGC allowed to identify novel QTL and/or cross-validate major common QTLs. The combined resources allowed us to trace the origin, spread and physical extent of conserved haplotypes (haplo-blocks) at the target loci, an information essential to better define the SNP-tags relevant for KASP® design and marker assisted selection (MAS).

Passport and genotypic data of the collection are available in GrainGenes (https://wheat.pw.usda.gov/GG3/global_durum_genomic_resources). The three combined collections provide unprecedented opportunities to exploit at best the native diversity of the A and B genomes for the identification and deployment of novel beneficial haplotypes in both durum and common wheat