

## TRITICUM AESTIVUM SUBSPECIES: EXPLORING ANCIENT DIVERSITY

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Bread wheat (*Triticum aestivum* L.) is among the first domesticated crop species and the most widely cultivated crop on Earth; moreover, it contributes about a fifth of the total calories consumed by humans. Crop breeding is a continuous effort to ensure sustainable food production despite the challenges posed by growing global population, changing climate, and emerging virulent strains of pathogens and pests.

Selection has dramatically shaped genetic and phenotypic variation in bread wheat. Wheat ancient subspecies may represent a reservoir of untapped and potentially important genes for crop improvement that have been left behind during the processes of range extension and breeding for high yields under intensive agricultural systems.

A collection of 184 wheat accessions coming from all over the world was created. This panel, beside some reference cultivars of *Triticum aestivum* ssp. *aestivum*, includes a significant representation of 4 *T. aestivum* subspecies: ssp. *compactum*, ssp. *sphaerococcum*, spp. *macha*, and ssp. *spelta*. The selected accessions represent cultivars, most of them marginally cultivated nowadays, landraces and wild materials.

The accessions have been phenotyped for three years in North Italy for several phenological, morphological, physiological, and yield-related traits.

A single plant from each accession has been genotyped with the Illumina Infinium 20K SNP and 25K SNP assays, giving information on the allelic state at >20K genome-wide markers. For more than 10K SNPs, a unique

physical position has been determined using the IWGSC RefSeq v2.0.

Molecular data have been used to study the genetic structure of the collection and to investigate the diversity between and within the subspecies; together with the phenotypic data, they will be used to identify genomic regions involved in recorded traits. A detailed genetic and phenotypic characterization of this unique germplasm will allow leveraging of the full potential of this collection through association genetics and will pave the way to explore the untapped variation for pre-breeding. Furthermore, with aim to assess the genomic basis of historical phenotypic changes, and the potential for future improvement, a crossing program has been undertaken to produce experimental populations that attempt to undo selection through the randomizing effects of recombination.

In details, two Nested Association Mapping populations, using alternatively 'Chinese spring' (for spring type) or 'Arina' (for winter type) as common parents, and different subspecies as donor parents are under development.

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