## **Poster Communication Abstract – 6.51**

## A WIDE COLLECTION OF WILD EMMER ACCESSIONS TO RECOVER DIVERSITY FOR CULTIVATED WHEATS

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The wild emmer wheat, *Triticum dicoccoides* (AABB), is the progenitor of the domesticated durum wheat (AABB). It harbors a wide spectrum of alleles that were lost during domestication and breeding processes, some features being deleterious, but many others possibly useful for genetic improvement of cultivated wheat. Indeed, a number of genes and alleles positively contributing to biotic and abiotic stress tolerance, yield components, and quality, have been found in wild emmer and introgressed in cultivated wheats.

A collection of wild emmer accessions has been established c/o CREA-Research Centre for Genomics and Bioinformatics. The accessions originated from all Fertile Crescent countries and thus represent all environments where wild emmer naturally occurs. After one cycle of single seed descent, 285 lines were genotyped with the Axiom 35k Breeders' Array, yielding about 12,000 informative SNPs, with 7574 having a unique physical position on the wild emmer reference genome sequence (Zavitan accession).

Based on genotyping data, genetic diversity and population structure within the collection were assessed. Two groups, mostly corresponding to the known wild emmer races, and subgroups, corresponding to the originating countries, were identified. The LD decay (R2) as a function of physical distance was evaluated, and a genome-wide critical distance of 436 kbp was found (R2 decay threshold <0.2).

The collection is being exploited for genome wide association studies (GWAS) for a number of traits including resistance to rusts and spike fertility.

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