

## EVA WHEAT & BARLEY NETWORK – SOUTHERN ZONE DATASET

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*Triticum aestivum, Triticum durum, Hordeum vulgare, Disease Evaluation, GWAS*

EVA is an international project aimed at increasing and improving the use of genetic diversity present in PGRFA available in European Genebanks. Through crop-specific public-private partnerships, EVA generates and links phenotypic and genotypic data to develop genetic markers and information for the enhanced use of landraces and ancient varieties in breeding and research. EVA is centrally coordinated by the European Cooperative Programme for Plant Genetic Resources (ECPGR) Secretariat.

The Wheat and Barley Network (EVA-WB) is the largest and most complex ECPGR EVA networks, bringing together 48 partners from 21 countries, and interacting also with the Horizon2020 project AGENT ([www.agent-project.eu](http://www.agent-project.eu)). EVA-WB divides its activities into 3 geographic zones across Europe (Northern, Central and Southern Europe) and evaluates spring and winter barley, spring and winter wheat, as well as durum wheat accessions, mostly for biotic stress responses in field evaluations. CREA-GB coordinates the activities in the Southern zone. Here we present initial results from 2 years of field trials on 2 sets (150 accessions each) of bread wheat (TA), durum wheat (TD), and barley (HV).

The accessions i) were provided with SMTA from seven European Genebanks/Research Institutes in '19, ii) multiplied as SSD between '20 and '21 at CREA-GB, and iii) evaluated for adult resistance to natural field infection of all occurring diseases, as well as heading date, plant height and lodging, during 2 growing season starting in '20-'21, with the '21-'22 season providing overlap for the 2 sets. In each of 13 locations across 6 countries in Southern Europe 2 replicas per acc. were evaluated in a randomized scheme.

All acc. were genotyped with Illumina Infinium iSelect arrays: Wheat 25k for *Triticum* species and Barley 15k for HV at SGS (Germany). Quality check of data, genomic diversity and population structure were computed. Physical anchoring to reference genomes was achieved by blasting SNP flanking sequences vs: i) Chinese spring genome v.2.1 ('22) for TA, ii) Svevo v.1 ('20) for TD, and iii) Morex v.3 ('21) for HV (JHI).

The phenotypic data were analysed in R for ANOVA and heritability was estimated. The averages between the 2 replicas of each acc. for each trait in each year were used as input data for genome-wide association study. The analysis were conducted for each species on Set1 ('20-'21 and '21-'22),

Set2 ('21-'22) and Sets1+2 ('21-'22) with the linear mixed models implemented in the GAPIT R package, to identify loci associated with the different traits. The most significant marker trait associations (shared between sets and/or site x year combinations) have been detected for yellow rust in TA and TD, for Septoria in TD, and for powdery mildew in HV. These results must be confirmed by the analysis of scoring data coming from the latest field trials ('22-'23).

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