Poster Communication Abstract – 1.40

UNRAVELING SEED MORPHOLOGY IN WHEAT FOR FUTURE BREEDING

SANSONI F.*, VOLANTE A.**, POZZI V.*, BIANCHI E.*, PECCHIONI N.*,
VACCINO P.*

*) CREA, Centro di Ricerca Cerealicoltura e Colture Industriali, Vercelli
**) CREA, Centro di Ricerca Orticoltura e Florovivaismo, Sanremo

Triticum aestivum, plant genetic resources, GWAS, heritability, QTL

In the perspective of ensuring food security for the next generations, grain yield is one of the main focuses. Among grain yield traits, thousand kernel weight (TKW) has been described to have the highest heritability, and to be highly correlated and influenced by many seed morphological traits. The AGENT (Activated Genebank NeTwork, H2020, Grant Agreement No. 862613; www.agent-project.eu) project aims to unlock the potential contained in the genebanks by using FAIR standards and an open digital infrastructure for the management of plant genetic resources. The research program is focused on a panel of 6,700 wheat and 5,200 barley accessions, created by sharing part of the collections of the project partners, genotyped by high throughput technologies and phenotyped for agronomic and physiological characters, in order to identify important loci through Genome Wide Association Studies (GWAS) and to develop models for the prediction of the breeding value through Genomic Selection (GS). In the frame of the project, CREA-CI is studying a set of 1,000 common wheat (*Triticum aestivum*) cultivars, made by two thirds of Italian genotypes, from landraces to old cultivars to modern ones, released until the 90'.

The other accessions have been selected, according to the project's decisions, to maximize global diversity. The genotypes were grown for two consecutive years in open field at Cigliano (VC, Italy); agronomic traits (plant height, flowering time, heading date) and climatic data were collected. After harvest, thousand kernels weight was measured and seed morphology (seed length, width, area, perimeter, curvature and roundness) was recorded using a scanner (Epson, Perfection V850) and the software WinSEEDLE (Reagents Instruments Inc.). Descriptive statistics, normality, correlations and Principal Component Analysis (PCA) on the overall data

were performed using R-Studio (packages FactoMineR, factoextra, corr, nlme, multtest). The heritability (h^2) of the measured traits was assessed by META-R. GWAS (R-Studio, GAPIT3 package) was performed on a subset of accessions for which SNP markers were already available. Genotypic data were filtered with PLINK 1.07 with thresholds of 10% missing data and 5% MAF (Minor Allele Frequency); imputation of the missing data was carried out with Beagle 5.4.

Significant associations were identified for seed length, width, area, and perimeter, confirming previous results reported in literature, but also suggesting new possible QTLs (Quantitative Trait Loci).

These results can be valuable for researchers and breeders, for a more focused and precise improvement of wheat varieties.