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GENETIC ARCHITECTURE OF SEMOLINA YIELD AND OF ITS COMPONENTS IN DURUM WHEAT (*TRITICUM TURGIDUM* SPP. *DURUM*)

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During durum wheat domestication and selection process, successive genetic bottlenecks occurred and induced a strong reduction of genetic diversity in *Triticum turgidum ssp durum* compared to its progenitors. To enlarge genetic diversity available for breeding, we founded in 1997, the Evolutionary Prebreeding pOpulation (EPO) including a great diversity of wild, primitive and modern forms of *T. turgidum*. We maintained an allogamous rate of about 20 % in this population thanks to the presence of male sterile plants. After 17 generations of intermating coupled with a mild selection for architectural trait values, we derived an inbred line panel to study relationships between genotypes and phenotypes.

During 2 years, we measured phenotypic variability of 181 lines for semolina yield (SY), which quantify the performance of the genotype at the first step of industrial process, and its most important components. Thousand Kernel Weight TKW, Specific Weight SW, Grain Protein Content GPC, were estimated by near infrared spectroscopy according our own calibrations ($0.89 < R^2 < 0.95$). Phenotypic variance, heritability and correlation patterns have been carried out underlying the importance of the annual effect; inter annual broad sense heritability varied from 0.3 (GPC) to 0.45 (TKW). EPO lines were genotyped for 420 k array developed for the BreedWheat project and we used about 168 000 SNPs with high quality resolution and physically mapped on Zavitan reference. After correction of the phenotypic data for the spatial variation, GWAS analysis was performed, allowing us to identify genomic regions explaining from 8 to 18 % of SY, TKW, GPC and SW variation. The major TKW QTL mapped on the 2AS co-localized with the SY QTL. We discuss the potential of this panel to decipher genetic architecture of traits and the complementary between this panel and EPO to precise the highlighted locus.

ABSTRACT