



**HAL**  
open science

## Genetic architecture of semolina yield and of its components in durum wheat (*Triticum turgidum* spp. durum)

Muriel Tavaud-Pirra, Morgane Ardisson, Frederic Compan, Jacques David, Aline Rocher, Dimitri Sanchez, Pierre Roumet

### ► To cite this version:

Muriel Tavaud-Pirra, Morgane Ardisson, Frederic Compan, Jacques David, Aline Rocher, et al.. Genetic architecture of semolina yield and of its components in durum wheat (*Triticum turgidum* spp. durum). From Seed to Pasta III: FSTP3 2018, Sep 2018, Bologne, Italy. , 1 p., 2018. hal-02786927

**HAL Id: hal-02786927**

**<https://hal.inrae.fr/hal-02786927>**

Submitted on 5 Jun 2020

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

## **Genetic architecture of semolina yield and of its components in durum wheat (*Triticum turgidum* spp. *durum*)**

M. Tavaud-Pirra, M Ardisson, F. Compan, J. David, A. Rocher, D. Sanchez, I. Vilmus, P. Roumet

During the durum wheat domestication and selection processes, some 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.

For 2 years, we measured the phenotypic variability of 181 lines for semolina yield (SY) and its most important components. We estimated the Thousand Kernel Weight (TKW), the Specific Weight SW, the Grain Protein Content GPC using near infrared spectroscopy according to our own calibrations ( $0.89 < R^2 < 0.95$ ). Phenotypic variance, heritability and correlation patterns have been carried out underlining 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 mapped on the Zavitan's genome as 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 variations. 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 complementarity between this panel and EPO to specify the highlighted locus involved in the trait variation.