

100 - Exploiting the potential of Global Durum Panel for plant and human health

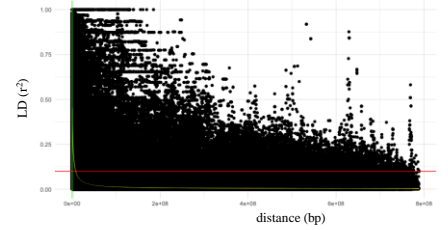
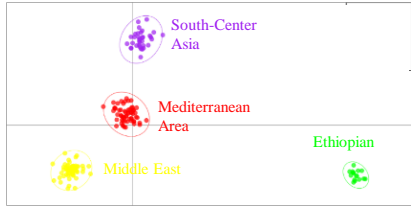
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Background

Durum wheat (*Triticum turgidum* L. ssp. *durum* (Desf.) Husn.) is the 10th most important cultivated cereal worldwide with a yearly production average of 40 million tons. Empirical and modern breeding has created new high-yielding varieties increasing production in the last century. A side effect of the breeding activities is the genetic erosion of the cultivated durum wheat germplasm compared to their wild relatives, which might hamper the long-term improvement of this crop. To overcome this genetic erosion and sustain breeding, **Global Durum Panel (GDP)** has been recently established. GDP is a genetic collection developed and genotyped by the international durum wheat research community to collect, share and exploit available genetic diversity. GDP is a freely shared wide collection composed by modern germplasm and landraces, with a selection of emmer and primitive tetraploid wheats [doi: 10.3389/fpls.2020.569905].

For our purposes, we selected a subset of the collection of **215 genotypes, including 193 landraces**, to address **two important topics in durum wheat farming and seed processing through genome wide association studies (GWAS)**.



Structure population analysis confirmed about 95 % of the original genetic variability in our sub-population and identified four groups, matching the geographic origin of the genotypes.

Pairwise marker correlations (r^2 values) were calculated on the SNP dataset using TASSEL5. Linkage Disequilibrium was calculated with a distance of 4.4 Mbp.

The first topic concerns the wheat disease caused by the **soil-borne cereal mosaic virus (SBCMV)**. The virus transmission occurs via roots by *Polymyxa graminis* Led, a plasmodiophorid protist that persists in soil up to 20 years. Both new SBCMV variants and climate change are contributing to a significant impact of virus infection.

The second topic is related to human health. **Acrylamide** has been detected in many foods after high temperature processing. In wheat derivatives, the quantity of free asparagine (**fAsn**) is the key factor in acrylamide formation. Exploring natural variation for fAsn content in wheat seeds allows to identify candidate genes controlling this trait.

The level of resistance to SBCMV in the durum wheat genotypes of the GDP subset was evaluated at CNR-IPSP (Torino, Italy) using two different approaches. The data related to symptoms evaluation will be used for **GWAS** to identify genomic regions of durum wheat associated to SBCMV response.

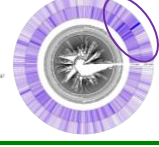
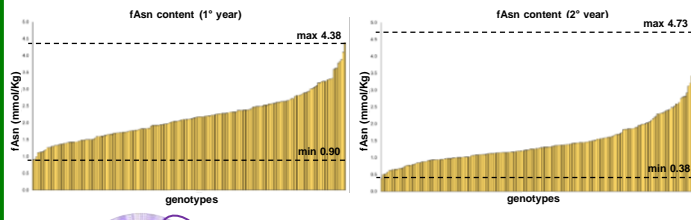
The 215 durum wheat genotypes were grown in Fiorenzuola d'Arda (PC, Italy) for three years.



Vector-mediated transmission - This approach mimics natural conditions. The durum wheat genotypes were sown and grown outdoor during the winter-spring period in pots containing soil collected in infested fields. The resulting durum wheat phenotype (susceptibility/resistance) depends on the reaction of the roots to both SBCMV and the attack of *Polymyxa*. Infection was evaluated by visual evaluation of symptoms. Quantification of viral RNA by qRT-PCR is in progress.



The fAsn quantification in the whole-grain samples was performed using K-ASNAM enzymatic assay (Megazyme) for the first two years of field trials. The analysis indicated the presence of a good variability for fAsn content in the population. The analysis of the third year is still in progress.

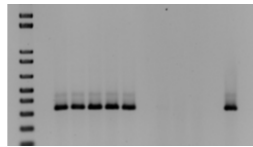


A neighbour joining phylogenetic tree was constructed based on SNPs data with 1000 bootstrap replications, using poppr (R package). The associated heatmap shows the two years fAsn values. A high fAsn content clade was found (the purple ellipse).

Artificial transmission - The susceptibility of seedlings to mechanical inoculation was measured in growth chamber conditions. This artificial transmission is not the way SBCMV infects plants in field, but produces data on the direct interaction between the host plant and the virus.



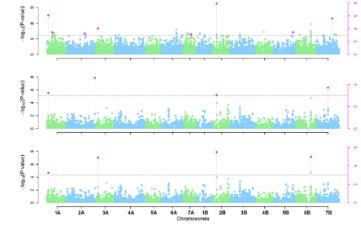
Comparison between SBCMV mechanically inoculated (I+) and non-inoculated (I-) plants in cv. Meridiano.



Virus detection by end-point RT-PCR in mechanically inoculated plants.

A first group of 70 genotypes has been artificially inoculated. The genotypes showed variable levels of symptoms on leaves and reduction of growth, but all tested positive in RT-PCR. Analyses on the remaining genotypes are in progress.

A multi locus GWAS was performed using mrMLM (R package) using the phenotypic data generated in the first two years. The Manhattan plots show an example of our results. These analyses identified 6 QTNs (Quantitative Trait Nucleotides) associated to 144 genes for a total of 398 stable transcripts.



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SURF
Selezione e sviluppo di materiali genetici per la resistenza alle virus del frumento
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