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# **FROM SEED TO PASTA IV**

A Sustainable Durum Wheat Chain for Food Security and Healthy Lives

## Multienvironment phenotypic evaluation and GWAS analysis on the Global Durum Resource Wheat Collection for resistance to yellow rust

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#### Introduction

Several diseases challenge bread and durum wheat productions worldwide. The importance of these cereals requires adequate protection to pathogens that can cause



strong yield and grain quality losses, also in view of the global change effects that exacerbate pathogen epidemics. *Puccinia striiformis* f.sp. *tritici*, the agent of yellow rust (Yr) on wheat, is one of the major causes of production losses worldwide. The continuous evolution of new Pst strains forces the breeder to research new sources of durable resistance in the germplasm globally. For this experiment we used the collaborative Global Durum Resource collection (https://wheat.pw.usda.gov/GG3/global\_durum\_genomic\_r esources) composed by a wide range of durum cultivars, landraces, and pre-breeding lines, to represent the genetic diversity of tetraploid wheat

#### **Materials and Methods**

- $\succ$  The collection was grown in multi-environment conducive nurseries in the Mediterranean region (Italy, Egypt, Lebanon, Morocco and Turkey) and Argentina across three years (2019-2021) for yellow rust resistance.
- > Infection Type (IT) and Severity (SEV) were scored for each environment. Infection type was scored with a 0-9 scale, while severity was recorded as the percentage of infected leaf area (0-100).
- > The collection were genotyped with the wheat highdensity Illumina iSelect 90K SNP assay.

Fig. 1: Manhattan plot chromosomal representations of GWAS-QTL significance for yellow rust resistance expressed as Infection Type (IT) in five different Mediterranean enviroments: Italy (Grosseto and Foggia), Argentina, Lebanon and Turkey. The most significant peak is highlighted with a red arrow, on chromosome 1B. The x axis shows durum chromosomes (1A - 7B). The y axis shows the  $-\log 10(p)$  values. The green line for each Manhattan is the significativity threshold, set at 4.

#### **Discussion and Conclusions**

- > The preliminary GWAS has highlighted numerous peaks that can be attributed to QTL of interest for resistance to yellow rust, potentially useful for breeding programs.
- The highest peak in 4 out of 5 environments was located on chromosome 1B (red arrow in the Manhattan plot). This locus had been identified as very effective in several environments and could therefore provide a case study for the INNOVAR objectives, that are develop advanced molecular tools to assist in DUS and VCU (Value for Cultivation and Use) plant variety registration. Complete multi-model GWAS analysis, meta-QTL analysis from the literature and candidate gene analysis is ongoing and results will be reported. The identification of new QTLs will also allow the development of additional KASP<sup>™</sup> assays to be used in MAS programs, and more in general will provide knowledge useful for informed breeding in durum wheat which is the main objective of CEREALMED project.
- > A preliminary GWAS was performed using GAPIT3 R package far the traits collected, using five different models (GLM, MLM, MLMM, BLINK, FarmCPU).

## Results

- > Preliminary GWAS identified at least 15 genomic regions harboring loci involved in YR response in the tetraploid wheat germplasm. In particular, loci in chromosome 1B, 2B, 4B, 5A, 6A, 7B showed high significance across nurseries/years.
- > The Manhattan plot below shows a comparison between the preliminary GWAS performed for 5 environments using MLM + K: Grosseto 2021, Foggia 2020, Argentina 2021, Lebanon 2019 and Turkey 2019.
- ➤ KASP<sup>™</sup> (competitive allele-specific PCR) markers have also been developed and successfully validated for 1B.
- The wide range of observed infection types and the population numerosity allowed also to perform a differential GWAS analysis for complete (IT = 0-3) or partial resistance (IT = 4-6), revealing loci with ITspecificity.

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