

MULTIENVIRONMENT ASSESSMENT AND GWAS OF THE GLOBAL DURUM GENOMIC RESOURCE FOR RESISTANCE TO YELLOW RUST

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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 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. Recently, durum wheat cultivars in Europe and in Mediterranean areas have been challenged by severe yellow rust epidemics. The collaborative Global Durum Resource collection (https://wheat.pw.usda.gov/GG3/global_durum_genomic_resources) composed by a wide range of durum cultivars, landraces, and pre-breeding lines, was assessed 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 and severity). The Global Durum Resource is provided with the Illumina wheat 90K SNP array and population structure has already been described (Maccaferri et al 2019; Mazzucotelli et al 2020). GWAS using different models (GLM, MLM, MLMM, FarmCPU and BLINK) and including the kinship matrix as covariate 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, with various patterns of GxE, hence KASP™ (competitive allele-specific PCR) markers have also been developed and successfully validated. 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 IT-specificity. Additionally, elite cultivars versus landraces differential

analysis has been carried out, revealing a differential distribution of resistance alleles on a single locus basis. This research has been supported by the project “CerealMed”- Enhancing diversity in Mediterranean cereal farming systems, funded by PRIMA2019-Section 2 and by the H2020 FP7 “INNOVAR” - Next generation variety testing for improved cropping on European farmland.