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## GENETIC DISSECTION OF FUSARIUM HEAD BLIGHT RESISTANCE IN DURUM WHEAT (*TRITICUM TURGIDUM SSP. DURUM*)

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Fusarium Head Blight (FHB) represents a worldwide threat for many grain crops leading to severe yield and quality losses while threatening human and animal health due to mycotoxin accumulation. *Triticum turgidum* ssp. *durum*, the most important tetraploid wheat in the world, is notoriously highly susceptible to FHB.

With the aim to provide a most accurate inventory of Quantitative Trait Loci (QTLs) for FHB in durum wheat, we performed a genetic characterization of 130 elite accessions (Fusarium Panel) and 165 F6 RILs from the population Simeto × Levante. The Fusarium Panel was evaluated in three artificially inoculated nurseries and in three years while the inoculation was carried out with *Fusarium graminearum* and *Fusarium culmorum*. The RIL population was evaluated in greenhouse in Tulln (Austria) in two years and inoculated with *F. graminearum*.

Custom R scripts were used to produce best linear unbiased prediction (BLUP) values for the following traits: AUDPC incidence, AUDPC gravity, AUDPC Fusarium index, deoxynivalenol (DON) and Fusarium Damaged Kernels (FDK). A genetic characterization of RILs and Fusarium Panel was carried out using the Infinium wheat SNP 90K iSelect assay and the genotype scores were used to conduct a Genome Wide Association Study (GWAS) in Tassel v.5.2.7 (for Fusarium Panel) and a QTL analysis based on single-marker and multiple interval mapping (MIM) in Windows QTL Cartographer (for RILs). A remarkable number of QTL hotspots were detected in the following chromosomes: 1BL, 2AL, 3AL, 3BS, 3BL, 4AL, 5AL, 5BL and 6AL. Then conserved linkage blocks were investigated in major QTL/gene regions and their related effects. Tag-SNPs and haplotypes identified in this study will be used for marker-assisted selection (MAS) programs in order to accelerate new breeding strategies for FHB-resistant wheat cultivars.

## ABSTRACT