

WHOLE GENOME ASSOCIATION MAPPING FOR FUSARIUM HEAD BLIGHT RESISTANCE IN DURUM WHEAT

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Fusarium Head Blight (FHB) represents a worldwide threat for many grain crops leading to severe yield and quality losses and a several risk to human and animal health due to mycotoxin accumulation in harvested grain (Gorczyca et al. 2018). *Triticum turgidum ssp. durum* is the most important tetraploid wheat in the world and notoriously highly susceptible to FHB (Miedaner et al. 2017). Although breeding for resistance to FHB is one of the most promising strategies for minimizing crop damage, the attempt to detect durum wheat resistant lines have been limited so far (Hadjout et al. 2017).

With the aim to provide a most accurate inventory of Quantitative Trait Loci (QTL) for FHB present in the modern durum wheat, we performed a genetic characterization of 130 durum wheat elite accessions (Fusarium Panel) and 165 F6 RILs from the population Simeto × Levante. The Fusarium Panel was evaluated in three artificially inoculated nurseries (two locations in Bologna and one in S. Severino (MC), in three years (2015, 2016 and 2017) and inoculation was carried out with *Fusarium graminearum* and *Fusarium culmorum*, while the RIL population was evaluated in Tulln (Austria) in two years (2014 and 2015) and inoculated with *F. graminearum* in greenhouse with the same *F. graminearum* isolate.

The lme4 package (r-project) and custom R scripts were used to conduct a spatial adjustment analysis and best linear unbiased prediction (BLUP) values were used for multiple environments and years for the following traits: AUDPC incidence, AUDPC gravity, AUDPC Fusarium index, deoxynivalenol (DON) and Fusarium Damaged Kernels (FDK).

A genetic characterization of RILs and Durum 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. The tetraploid-consensus-2015 reported in Maccaferri et al. (2015) was used to cross-reference the QTLs. A remarkable number of QTL hotspots unrelated to phenology were detected in the following chromosomes: 1BL, 2AL, 3AL, 3BS, 3BL, 4AL, 5AL, 5BL and 6AL. The most interesting QTL/GWAS-QTLs were those located on 2AL, 3AL (with a valuable effect on DON content) and 5AL. Reliable and diagnostic KASP® markers were obtained to allow for marker-assisted selection for these QTL hotspots and accelerate the selection of FHB-resistant wheat cultivars.

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