

GWAS AND HAPLOTYPE BLOCK ANALYSIS REVEAL QTNS AND CANDIDATE GENES FOR MORPHO-PHENOLOGICAL TRAITS IN DURUM WHEAT

TARANTO F.*, ESPOSITO S.**, FANIA F.*****, SICA R.***, MARZARIO S.***, LOGOZZO G.***, GIOIA T.***, DE VITA P.**

*) Italian National Council of Research (CNR), Institute of Biosciences and Bioresources (IBBR), Via Giovanni Amendola 165/A, 70126 Bari, Italia

**) Council for Agricultural Research and Economics (CREA), Research Centre for Cereal and Industrial Crops (CREA-CI), S.S. 673, Km 25,200, 71122 Foggia, Italy

***) Department of Agriculture, Food, Natural Resources, and Engineering (DAFNE) - University of Foggia, Via Napoli, 25 71122 Foggia, Italy

****) School of Agricultural, Forestry, Food and Environmental Sciences, University of Basilicata, Viale dell 'Ateneo Lucano 10, 85100 Potenza, Italy

multi-locus GWAS, Quantitative Trait Nucleotide, haplotype blocks, plant variety protection, UPOV protocol

The rapid growth of genomic data in durum wheat (*Triticum turgidum* subsp. *durum*) deals the opportunity to disclose the effects of breeding on the genetic structures that regulate the expression of traits of agronomic interest. Furthermore, the identification of new SNP markers useful for marker-assisted selection (MAS) could also improve the consistency of technical protocols used for variety protection and registration. In our work, a collection of 123 durum wheat accessions, including landraces (LR), ancient (OC) and modern cultivars (MC), was evaluated in two locations for 34 agronomic traits, including UPOV descriptors. A panel of 4,241 SNP markers combined with six Multi-Locus models (ML-GWAS) revealed 28 reliable QTNS related to plant morphology and kernel-related traits. Some QTNS confirmed results reported in the literature, whereas those for flag leaf glaucosity (FGSGL) and yellow berry (YB) represent a novelty for durum wheat. In detail, the *Q.FGSGLs-2B.1*, identified by *RAC875_c34512_685* for FGSGL, mapped less than 1 Mb from the *EPISTATIC INHIBITORS OF GLAUCOUSNESS* (*Iw1*), thus representing a good candidate for supporting the morphological DUS traits also with molecular markers. A strong association for YB was

instead found on chromosome 6A in a region containing the *NADH-UBIQUINONE OXIDOREDUCTASE*, a gene involved in starch metabolism.

LD-based haplotype blocks were also defined to detect the impact of breeding programs on phenotypic traits. The LD haplotype survey across landraces, old and modern cultivars revealed a higher diversity, richness and length of haploblocks in MC than OC and LR (580 in LR, 585 in OC and 612 in MC), suggesting a possible effect exerted by breeding programs on genomic regions associated with the agronomic traits.

Knowledge of the genomic regions associated with key traits for durum wheat breeding and understanding the haplotype patterns across different genetic materials will be useful for exploring allelic composition in wild and domesticated germplasm to broaden their genetic variability, for selecting superior alleles and for constituting new ideotypes to use in durum wheat breeding programs.