

FINE MAPPING AND CHARACTERIZATION OF GRAIN NUMBER INCREASE-2 LOCUS (GNI-A2) IN DURUM WHEAT

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spike fertility, KASP markers, HIF-derived near-isogenic lines, sink-source interplay.

Exploring the genetic basis of grain yield and its components is an important objective for cereal agricultural genetics and genomics. This objective is even more important in durum wheat, the most relevant cereal crop for Italian agriculture, which is mostly cultivated under rainfed conditions ranging from semi-arid to favorable conditions. Thus, fine-tuning yield potential genetic determinants is crucial for a successful durum wheat variety. An initial explorative mapping study was conducted based on 338 RILs derived from a four-way cross among diverse elite highly differentiated grain yield components (Milner et al. PBJ, 2016). Parents were cultivars Neodur (French cv), Claudio (Italian cv), Colosseo (Italian cv), and Rascon/2*Tarro (CIMMYT cv) (NCCR Population). RIL and the parental lines had been previously genotyped with the 90K Illumina iSelect SNP array and were characterized for a range of agronomic traits over two consecutive years in two locations of the Po Valley, Italy. A highly significant genomic region with a phenotypic variance explained (PVE) around 39% underlying the number of kernels per central spikelet (KNSL) and the number of kernels per spike (KNS) was detected on chromosome 2A, named GNI-2A. The

favorable allele (+ 0.56 grain per central spikelet) was identified in the CIMMYT parent Rascon/2*Tarro.

Subsequently, a population of 1,500 F4 lines from Relief (GNI-2A -) X Iride (GNI-2A +) was used for fine mapping and developing congenic stocks. Both Illumina 90K SNP and the Affymetrix Axiom TaBW280K SNP sequence info were used to develop a series of KASP® markers flanking the GNI-2A interval. Based on recombinants, GNI-2A interval was narrowed down to 4Mb, including 11 High Confidence (HC) genes and 16 Low confidence genes (LC). Candidate genes included transcription factors that could have a role in wheat development.

As a follow-up, we also obtained three pairs of congenic lines (HIF-NILs) from heterogeneous inbred families (HIFs) that were selected by MAS, seed increased, and validated for the GNI-2A effect. These lines will be used for RNA-seq assa

ys to obtain a transcriptome profiling of the gene network controlled by the investigated genomic region at target developmental stages: green anther, GA, tipping stage (TP), heading stage (HD), anthesis (Fwt). Additionally, the HIF-NILs will be used to conduct physiological studies on the effects of the increased sink demand driven by the plus allele as well as measuring other physiological-related traits (Stem elongation period, heading date, Stay green index, and chlorophyll content). In conclusion, the GNI-2A + is a locus relevant for wheat improvement, found in the elite durum wheat germplasm.

The tools for deploying the alleles at the breeding level have been developed and the locus characterization is underway.