

PHENOTYPIC AND MOLECULAR CHARACTERIZATION OF QGNS.UBO2A, A MAJOR LOCUS RESPONSIBLE FOR SPIKE FERTILITY ON TRITICUM TURGIDUM SSP DURUM.

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QGns.ubo2A is a major QTL for grain number per spikelet (GNS) on chr2AS (s.i. 84.6-87.6 cM) identified in the 4-way durum wheat cross population derived from Neodur, Colosseo, Claudio and Rascon-Tarro (NCCR). The Rascon Tarro haplotype (derived from Altar84 CIMMYT founder variety) showed a 0.55 grain number increase per spikelet as compared to the other three parents. Based on the Illumina ISelect wheat 90K haplotype information, the favorable allele is present in some of the most productive CIMMYT and Italian durum wheat cultivars as well as in the Synthetic hexaploid wheat W7984 parent of the ITMI population (Mascher et al. 2013 *The Plant Journal* 76, 718–727).

Based on *Triticum turgidum* cv. Svevo reference sequence, the pericentromeric interval of 2AS contains approximately a hundred genes strongly conserved across Chinese Spring, wild emmer Zavitan and durum wheat cv. Svevo reference genomes. The genetic interval was explored pointing out possible candidate genes for the GNS trait within a 4 kbp chromosome deletion in the Altar84 and W7984 haplotype, absent in the other parents of the 4-way cross population NCCR.

Fine mapping was carried out in 2019 and 2020 by screening ca. 1000 F5 Recombinant inbred line from the cross Iride (Altar84 haplotype) x Relief population. The population was phenotyped showing a bimodal distribution and an average of 3.8 grains/spikelet for the wt haplotypes and 5.1 grains/spikelet for the Altar84 haplotypes.

Six KASP® markers developed from the 90K SNP chip were useful to tag the local Altar84 favorable haplotype.

The combined screening of the Iride x Relief population and of the ca. 2500 accessions of the Tetraploid Global Collection and Global Durum Panel (Maccaferri et al. 2019; Mazzucotelli et al. 2020) showed that

modern varieties most frequently had the low-fertility haplotype and that the causal gene is located in a 5 Mbp. Exploiting 420K Breedwheat SNP Chip, blasted against 50 durum varieties further seven KASP® markers were developed and contributed to reduce the interval to 3.9 Mbp. As to future experiment, candidate gene transcription profiling and the generation of independent knock-out mutants will be pursued to elucidate the genetic control of this interesting QTL. Additionally, physiological experiments will be set up with QGns.ubo2A QTL contrasting near isogenic stocks in growth chamber. In conclusion, we report herein the identification of a major locus for spikelet fertility and seed number per spike in tetraploid wheat, potentially valuable for improving the grain yield potential of both tetraploid and hexaploid wheat. The locus deserves a further and deep characterization towards the gene expression and fine mapping.

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