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HIGH-RESOLUTION MAPPING OF A MAJOR QTL FOR GRAIN YIELD *PER SE* IN DURUM WHEAT

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In durum wheat, two major QTL for grain yield *per se* (*QYld.idw-2B* and *QYld.idw-3B*) and related traits were identified in a recombinant population derived from Kofa and Svevo (Maccaferri *et al*. 2008, Genetics). To further investigate the genetic and physiological basis of allelic variation for this important trait, the fine mapping of *QYld.idw-3B* is underway in the framework of the FP7 TriticeaeGenome project.

In this regard, 19 pairs of near-isogenic lines (NILs) for *QYld.idw-3B* were obtained from $F_{4:5}$ heterogeneous inbred families. In order to confirm the phenotypic effect of the QTL all pairs were evaluated in field trials in 2010 and 201. Three pairs of NILs, with contrasted haplotypes at the target region, were crossed to produce a large F_2 population (ca. 7,500 plants in total) that was screened with two flanking markers for the identification of recombinants. A total of 250 homozygous $F_{4:5}$ segmental isolines were obtained and the phenotypic and genotypic characterization of these materials is underway. To increase the map resolution in the interval of *QYld.idw-3B* new polymorphic markers were identified by exploiting the sequence information produced from the assembly of the chr. 3B physical map of bread wheat. Originally, *QYld.idw-3B* was mapped on the distal region of the short arm of chr. 3B, flanked by *Xgwm389* and *Xgwm493*. A total of 44 new markers (BAC-derived SSR, ISBP and SNP markers) have been added to the target interval, with an average marker distance of 0.28 cM. All markers were anchored to the Chinese Spring physical map of chr. 3B, which allowed us to identify the BAC Contigs spanning the QTL region and to assign the QTL peak to Contig 954, most probably between *Xcfb6127* and *Xcfb6021*. Sequencing of this contig has revealed the presence of 42 genes (Choulet *et al*. 2010).

Fine mapping will be carried out by genotyping the newly developed $F_{4:5}$ recombinant segmental isolines with all the available markers. The functional characterization of the genes included in Ctg954 is being carried out in a transcriptomic experiment with NIL pairs grown in the greenhouse that are being sampled for various tissues and developmental stages. This action will aim at identifying candidate genes based on the differential transcriptional patterns and will require the development of genome-specific assays for each gene.