

## PROGRESS IN THE POSITIONAL CLONING OF *QYLD.IDW-3B*, A MAJOR QTL FOR GRAIN YIELD IN DURUM WHEAT

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In durum wheat, a major QTL (*QYld.idw-3B*) for plant height, peduncle length, stay-green, leaf greenness, thousand kernel weight and grain yield across a broad range of soil moisture regimes was identified in a RIL population derived from Kofa and Svevo (Maccaferri et al. 2008, Genetics 178:489-511) two high-quality, elite cultivars well adapted to Mediterranean environments. The positional cloning of *QYld.idw-3B* is underway in the framework of the FP7-funded TriticeaeGenome project (<http://www.triticeaegenome.eu>). In this regard, three pairs of NILs with contrasted parental haplotypes at the target region were crossed to produce approximately 7,500 F<sub>2</sub> plants that were screened for the identification of recombinants within the 6 cM interval between *Xcft5055* and *Xgwm493*, the two markers that flanked the *QYld.idw-3B* peak. In 2011, 233 segmental isolines were phenotypically characterized for plant height and peduncle length, two traits which are supposedly influenced by *QYld.idw-3B*. In order to confirm the effect of the QTL on plant height, peduncle length, grain yield and related traits, a replicated field experiment has been carried out in 2012 with the 61 most informative segmental isolines. The data are being analyzed to determine whether pleiotropy or linkage is responsible for the phenotypes of the target traits.

Based on the sequence of chr. 3B of bread wheat cv. Chinese Spring (Paux et al. 2011, Science 322:101-104), 50 new polymorphic markers (BAC ends-derived SSR, ISBP and SNP markers) were identified, mapped and anchored to the Chinese Spring chr. 3B physical map, which allowed us to confine *QYld.idw-3B* to a 0.22 cM interval spanned by contig 954 that contains 10 genes, three of which appear as the most likely candidates. The functional characterization of these genes is underway by expression analysis. Additionally, to confirm and/or identify new candidate genes for *Qld.idw-3B* the BAC library of durum wheat cv Langdon (Cenci et al. 2004, Genome 47: 911–917), characterized by a haplotype in the target region similar to that of cv Kofa is being screened.