ground of this material and availability of PCR-based markers closely associated with this locus represent invaluable resources for marker-assisted introgression of gluten strength into other durum wheat varieties. A single QTL segregating in this population also makes it an ideal target for map-based cloning.

Poster 35. Towards 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, 1,000-kernel weight, and grain yield *per se* (i.e., not due to difference in flowering time) across a broad range of soil moisture regimes was identified in an 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 fine mapping of *QYld.idw-3B* is underway in the framework of the FP7 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_2 plants that were screened for the identification of recombinants within the 11-cM interval between *Xgwm389* and *Xgwm493* that flanked the *QYld.idw-3B* peak. In 2011, 233 informative, homozygous $F_{4:5}$ segmental isolines were evaluated in the field and profiled molecularly. To increase the map resolution in the target region, new polymorphic markers were identified by exploiting the sequence information produced from the assembly of the chromosome-3B physical map of bread wheat. A total of 50 new markers (BAC ends-derived SSR, ISBP, and SNP markers) have been added to the target interval. All markers were anchored to the Chinese Spring physical map of chromosome 3B, thus allowing us to identify the BAC contigs that span the QTL region. A high-resolution map has been obtained with an average marker distance of approximately 0.25 cM. *QYld.idw-3B* has been confined to a 1-cM interval spanned by contig 954 of Chinese Spring, which contains 10 genes. The functional characterization via transcriptomics of these genes is underway. The haplotype at this target region is being investigated in a collection of 189 elite genotypes suitable for association mapping studies (Maccaferri et al. 2011. J Exp Bot 62:409-438).

Poster 36. Association studies of Ppo-A1 and Ppo-D1 genes and polyphenol oxidase activity using an Argentinean hexaploid wheat panel.

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Polyphenol oxidases (PPOs) are enzymes involved in the browning of fruits, vegetables, and cereal products, which negatively influence their marketing value. These enzymes are very important to the wheat industry because they are implicated in the detrimental and time dependant browning of various products especially Asian noodles and Middle East flat breads. In this work, we determined the genetic variability of the *Ppo-A1* and *Ppo-D1* genes using functional markers and evaluated its effect on the polyphenol oxidase activity using an Association Mapping (AM) approach with a panel of 97 Argentinean bread wheat cultivars. The AM panel was grown at Marcos Juarez, Argentina (32º 41' S and 62º 09' W) in the 2009–10 and 2010–11 growing seasons using hill plots in a completely randomized block design with two replications. PPO enzymatic activity was measured in each cultivar using the L-DOPA standard assay. *Ppo-A1* and *Ppo-D1* variability was determined using functional markers previously described. To minimize spurious associations, a mixed lineal model (Q+K) was used to account for population structure and kinship relatedness of individuals among 97 entries. A genetic structure (Q) and kinship matrix (K) among the 97 cultivars was inferred using 17 nonlinked, gene-based, molecular markers and HMW-glutenin storage proteins (three loci). The genetic structure was determined using STRUCTURE-2.3 and Structure Harvester with a number of subpopulations estimated in three (Q=3). The relative