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

kinship matrix (K) was calculated using SPAGeDi-1.3c. Analysis of *Ppo-A1* and *Ppo-D1* variability showed 76.28% of cultivars carrying the *Ppo-A1a* allele and the remaining 23.71% with *Ppo-A1b*. In the case of *Ppo-D1*, 31.95% of the cultivars showed the *Ppo-D1a* allele and 68.05% presented *Ppo-D1b*. This is the first characterization of the genetic variability of *Ppo* genes in Argentinean hexaploid wheat germplasm. The association analysis showed that variation at the *Ppo-A1* locus was significantly related with PPO activity ($P = 0.0011$), with *Ppo-A1b* allele producing lower PPO activity (9.72 U) than *Ppo-A1a* (13.76 U). The *Ppo-D1* locus did not show significant association with the PPO activity in this AM panel ($P = 0.0943$). These results positioned *Ppo-A1b* allele as a valuable genetic tool to reduce PPO activity in the Argentinean bread wheat breeding programs.

Poster 37. Characterization of the effect of single and double GPC-A1 and GPC-D1 mutations in hexaploid wheat.

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Plant senescence is a tightly regulated process designated to minimize the loss of minerals by maximizing remobilization to developing organs (e.g., seeds). The individual mechanisms and regulatory networks that define senescence are still poorly understood. In wheat, most of the nitrogen accumulated in the grain was already present in the plant at anthesis and is remobilized to the grains during maturation. Therefore, attempts to understand nutrient remobilization must consider senescence as an integral part of this complex process. Recently, the existence of a close connection between these two processes was shown through the map-based cloning of a wheat *GPC* (*Grain Protein Content 1*) gene. The *GPC-B1* gene encodes a NAC transcription factor associated with earlier senescence and increased grain protein, iron and zinc content in wheat. Recombinant inbred lines (RILs) of durum wheat carrying the functional allele from wild emmer wheat senesced 4–5 days earlier and had 5–10% higher grain protein, iron and zinc concentrations. In the current research, we have identified 'loss of function' ethyl methane sulphonate (EMS) mutants for the two homeologous genes, *GPC-A1* and *GPC-D1*, in hexaploid wheat. The mutants and control lines were grown under field conditions at four locations in Israel and characterized for their senescence patterns, *GPC*, and yield components. Our results showed a delay of senescence in both *gpc-A1* and *gpc-D1* mutants and a greater effect in the double mutant, *gpc-A1*/*gpc-D1*. Complete senescence of the single *gpc-A1* and *gpc-D1* mutants was delayed 10–20 days relative to the wild type control, and the difference increased to almost 70 days in the *gpc-A1*/*gpc-D1* double mutants. Grain protein content measurements in all mutants were lower then in wildtype plants, whereas grain yield was the same for all the tested genotypes suggesting the existence of different gene regulation for the accumulation of carbohydrates and minerals in the grain.

Poster 38. Development of Thinopyrum distichum-based, hexaploid tritipyrums.

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Thinopyrum distichum (Thunb.) Löve ($2n = 28 = J_1^dJ_1^dJ_2^dJ_2^d$) is a highly salt-tolerant, perennial grass that is indigenous to the shoreline of Southern Africa where it grows within the spring high-tide zone. It is rhizomatous, exhibits facultative apomixis, and occupies highly saline coastal sands with low fertility, limited soil water, and high pH. Due to its adaptation to adverse environmental conditions, the grass has previously been targeted for gene mining and transfer to durum and common wheat, rye and triticale. It is furthermore a segmental autotetraploid and, in partial polyhaploids ($-J_1^dJ_2^d$), its two genomes show a high degree of meiotic pairing. Two lineages of plants with 2n=42 chromosomes that are presumed to have the genomic composition AABBJJ, were selected from segregating generations of crosses among primary and secondary *Triticum turdidum* subsp. *durum* / *Th. distichum* amphiploids. The J genome in each lineage is assumed to consist of seven *Thinopyrum* chromosomes. Because the plants are well developed, highly fertile, and produce well-developed seeds, their J genomes probably comprise full sets of homoeologous chromosomes, with each individual chromosome having been derived from either of the J_1^d or J_2^d genomes and altered through recombination with its homoeologue. In seedling salt-tolerance tests, the hybrids had high levels of salt tolerance comparable to those of the *Th. bessarabicum*-based tritipyrums that were developed at the John Innes Centre. One of the selections is free-threshing and without the brittle rachis trait.