color can be influenced by environment. We developed high-throughput, KASPar assay for genotyping the *R-A1*, *R-B1*, and *R-D1* loci. The sequence information of the *Tamyb 10-A1* gene (Genbank no. AB599721 / AB191458), *Tamyb 10-B1* gene (Genbank no. AB599722 / AB191459), and dominant *Tamyb10-D1* gene (Genbank no. AB191460) were used from NCBI for designing allele-specific primers for the KASPar assay. These assays were applied to 672 U.S. wheat cultivars and breeding lines from different market classes. Complete agreement was found when genotypes determined with the new KASP assays were compared with results of the previously reported, gel-based markers and/or visual assessment of grain color as either red or white. All white wheat cultivars were determined with the KASP markers to have recessive alleles at all three loci, and the frequency of white wheats was 32%. The frequency of one-, two-, and three-gene red alleles was calculated for the red wheat lines. The most common red allele was *R-D1b*, which was present in 43% of the lines, followed *R-A1b* and *R-B1b*, present in 35% and 28% of the lines, respectively. Only 8% of cultivars had dominant alleles at all three loci. In conclusion, this diagnostic KASPar assay for scoring one-, two-, or three-gene red seed color genotypes provides a great advantage in marker-assisted selection over gel-based PCR markers by reducing cost and time in evaluating thousands of individuals along with low error rate.

Poster 33. Quantitative trait loci mapping of transgressive agronomic and quality traits in an elite by elite wheat recombinant inbred line population.

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In this study, we investigated a population of 129 recombinant inbred lines (RIL), developed from a cross between the cultivar Steele-ND and an elite line ND 735, to identify QTL controlling several yield and quality traits. Phenotypic data were collected from four North Dakota environments for days-to-heading, plant height, spike density, spike length, grain yield, grain volume weight, 1,000-kernel weight, kernels per spike, kernel size distribution, protein, flour extraction, kernel hardness, kernel diameter, and mixograph peak time. Strong transgressive segregation was observed for all traits, with some RILs outperforming the best commercial varieties. Using a linkage map of 392 markers, composite interval mapping (CIM) identified a total of 13 environment-specific QTL. All QTL explained large phenotypic variation (R^2 = 16–44%) as expected for loci determining transgressive segregation. Two major QTL, one each on chromosome 5A and 6B, affected three yield-related traits and provided up to 252 kg/ha additional yield. Many QTL have been identified before for yield and quality, but their polygenic nature has often prevented successful marker-assisted selection. In this study, we employed directly the identified QTL for within population selection, in an extension of the concept of 'map as you go'.

Poster 34. A major QTL for gluten strength in eurum wheat (Triticum turgidum L. var. durum).

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Gluten strength is an important characteristic in determining the end product quality of durum wheat semolina. In order to identify the genetic basis of gluten strength in North Dakota durum wheat cultivars, a doubled-haploid mapping population was developed from the cross of the low-gluten cultivar Rugby and the high-gluten cultivar Maier. A framework linkage map consisting of 228 markers was constructed and used with phenotypic data on gluten strength (measured by sedimentation volume) to conduct single- and two-locus QTL analyses. Only one consistent QTL (*QGs.ndsu-1B*), contributing up to 90% of the phenotypic or 93% of the genotypic variation, was detected on 1BS. No 'QTL×QTL' or 'QTL × environment' interactions were observed. *QGs.ndsu-1B* was flanked by two DArT markers that were converted to STS markers and used along with SSR and EST–SSRs to develop a map of 1BS. QTL analysis delineated *QGs.ndsu-1B* in a 7.3-cM region flanked by an STS marker locus, *Xsts-wPt2395*, and an SSR marker locus, *Xwmc85*. The adapted back-

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