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-