heptacosane formation; (2) *Iw2* inhibits fatty acid chain elongation from C_{24} to C_{26} and C_{28} and leads to accumulation of tetracosan-1-ol and absence of n-heptacosane; and (3) carbon chain length of wax species is important for glaucousness formation. Physiological studies showed that the nonglaucous NILs (*w*-NIL, *Iw1*-NIL, and *Iw2*-NIL) showed significantly higher rate of water loss and chlorophyll bleaching than S-615, suggesting the wax composition rather than wax load is important in determining cuticle permeability and glaucousness. Expression profiling of 32 genes involving cuticle biosynthesis, transport, and transcription regulation indicated that (1) *Iw1*, *Iw2*, *W1*, and *W2* employ different molecular mechanisms affecting cuticle biosynthesis are different; and (2) interactions between *W1* and *W2* are either additive or nonadditive. Combined analysis of metabolic and expression profiles suggested that several wheat homologs, including *CER4* and *WSD1*, are functionally different from their *Arabidopsis* counterparts most probably due to gene duplication and subsequent subfunctionalization.

Poster 31. Difference in vernalization duration requirement in U.S. soft winter wheat is associated with variation in VRN1 genes.

Mohammed Guedira [1], Peter Maloney [1], Paul Murphy [1], David Marshall [1,2], Jerry Johnson [3], Steve Harrison [4], and Gina Brown-Guedira [1,2].

[1] Department of Crop Science, North Carolina State University, Raleigh, NC, 27695, USA; [2] USDA–ARS Plant Science Research, Raleigh, NC 27695, USA; [3] Department of Crop and Soil Sciences, University of Georgia, Griffin, GA 30223, USA; and [4] School of Plant, Environmental and Soil Sciences, Louisiana State University, Baton Rouge, LA 70803, USA.

In winter wheat (*Triticum aestivum* L.), the timing of flowering is a crucial trait that allows the plant to fill grain during favorable conditions of spring. The timing of flowering initiation is governed by the action two main, environmentally controlled groups of genes; vernalization that defines a plant's requirement for a prolonged exposure to cold temperatures and photoperiod sensitivity defining the need for a long days to initiate floral transition. Genetic variation in both vernalization and photoperiod sensitivity allow wheat to be grown in extremely diverse environments. In the United States, winter wheat occupies more than 70% of the wheat acreage and is grown in environments with large differences in mean temperatures during winter, as well as day length at flowering. Vernalization-induced flowering is controlled by the *VERANALIZATION1* (*VRN1*) genes located on chromosomes 5A, 5B, and 5D and dominant alleles confer spring habit. Variations in *vrn-A1* were reported to be associated with early stem elongation during the floral transition. In this study, we evaluated the effect of vernalization duration (8 and 4 weeks) on flowering time of 130 recombinant inbred lines of a population generated from a cross between two soft winter wheat cultivars (carrying *vrn-A1b*, late stem elongation allele), AGS2000 and Neuse. After vernalization treatments, plants were grown in a controlled environment under long photoperiod. We identified a major locus for flowering time in the 4-week vernalization treatment in the region where *vrn-B1* resides in chromosome 5B. This region did not have a significant effect on flowering time in plants that were fully vernalized (8-week treatment). QTL for early spring growth and heading date were observed in the *vrn-B1* region when the population was evaluated in the field during 2012. Therefore, we conclude that variation in the recessive *vrn-B1* allele is important for adaptation of winter wheat to diverse environments.

Poster 32. Development of high throughput KASPar assays for the grain color loci in wheat.

K. Neelam [1], Vasu Kuraparthy [1], Mike Pumphrey [2], and Gina Brown-Guedira [1,3].

[1] Department of Crop Science, North Carolina State University, Raleigh, NC 27695, USA; [2] Department of Crop and Soil Science, Washington State University, Pullman, WA 99164, USA; and [3] USDA–ARS Plant Science Research, Raleigh, NC 27695, USA.

Grain color of is an important trait in wheat that is one of the defining characteristics of market class and end-use. Wheat seed color is controlled by three homoeologous genes, *R-A1*, *R-B1*, and *R-D1*, located on the long arms of chromosomes 3A, 3B, and 3D, respectively. The *R* loci interact epistatically with red color being dominant and increased number of red alleles leading to darker red color. White kernels result when the recessive alleles are present at all three loci. Wheat having both red and white grain is considered of mixed market class; therefore, purity of seed color is an important objective of wheat breeders and seed producers. However, it can be difficult to visually distinguish the red and white grain as seed

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.

Mohamed Mergoum [1], Vibin Harilal [1], Senay Simsek [1], Mohammed S. Alamri [2], Shahryar Kianian [1], Elias Elias [1], Ajay Kumar [1], and Filippo M. Bassi [1].

[1] Department of Plant Sciences, North Dakota State University, P.O. Box 6050, Fargo, ND 58108-6050, USA, and [2] Nutrition and Food Sciences Department, College of Food and Agricultural Sciences; King Saud University, P.O. Box 2460, Riyadh 11451, Saudi Arabia.

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).

Ajay Kumar [1], Elias M. Elias [1], Farhad Ghavami [1], Xin Xu [1], Shalu Jain [1], Frank A. Manthey [1], Mohamed Mergoum [1], Mohammed S. Alamri [2], Penny M.A. Kianian [1], and Shahryar F. Kianian [1].

[1] Department of Plant Sciences, North Dakota State University, Fargo, ND 58105, USA, and [2] Deparment of Food Sciences and Nutrition, King Saud University, Riyadh 11451, Saudi Arabia.

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-