

heptacosane formation; (2) *Iw2* inhibits fatty acid chain elongation from C₂₄ to C₂₆ and C₂₈ 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 nonglauous 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.

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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 *VERNALIZATION1* (*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.

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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