Mapping phenotypic and gene expression QTL related to preharvest sprouting resistance in white winter wheat.

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The premature germination of seeds before harvest, known as preharvest sprouting (PHS), is a serious problem in all wheat growing regions of the world. In order to determine genetic control of PHS resistance in white winter wheat from the relatively uncharacterized United States germ plasm, a doubled-haploid population consisting of 209 lines from a cross between the PHS-resistant cultivar Cayuga and the PHS-susceptible cultivar Caledonia was used for composite interval QTL mapping (CIM) of the PHS trait and gene expression at physiological maturity. A total of 16 environments were used to detect 15 different PHS QTL including a major QTL, *QPhs.cnl-2B.1*, that was significant in all environments tested and explained from 5% to 31% of the trait variation in a given environment. Three other QTL, *QPhs.cnl-2D.1*, *QPhs.cnl-3D.1*, and *QPhs.cnl-6D.1*, were detected in six, four, and ten environments, respectively. Gene expression levels in mature embryo tissue were measured using a >17,000 feature, long-oligonucleotide microarray. Composite interval analysis revealed 2,729 eQTL from 1,700 genes distributed across the genome. Significant eQTL clusters were observed on several chromosomes. Of the 2,729 eQTL, 117 were found to overlap with the previously defined PHS QTL. The eQTL that overlapped with PHS QTL were tested for correlation with the PHS trait using the Pearson product moment correlation in R. Those genes with eQTL that collocated with PHS QTL and were significantly correlated with the PHS trait were considered good candidates for being involved in PHS and seed dormancy. This study provides valuable information for marker-assisted breeding for PHS resistance, future haplotyping studies, candidate gene analysis, and research into seed dormancy.

Poster 1. Molecular characterization of the chromosomal region harboring the Hessian fly resistance genes H32 and H26 in wheat.

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Hessian fly [*Mayetiola destructor* (Say)] is one of the most important insect pests that attack wheat. A total of 32 genes conditioning resistance to Hessian fly have been identified in wheat (*Triticum aestivum* L.) and its relatives. Two resistance genes, *H32* and *H26*, derived from *Ae. tauschii*, were mapped to the long arm of chromosome 3D and reside within the deletion bin 3DL3-0.81-1.00. The objective of this study was to determine the physical and genetic relationships between these two Hessian fly resistance genes. *H32* was previously mapped in the ITMI population and *H26* in an F_2 population. Fourteen, EST-derived, STS markers flanking the *H26* locus were assigned to the linkage map of *H32* in the ITMI population. Two of the STS markers, *Xrwgs10* and *Xrwgs11*, were found to flank the *H32* locus with a genetic distance of 0.5 cM on both sides. *Xrwgs10* is 3.2 cM distal to *H26* and *Xrwgs11* is 1.0 cM proximal to *H26* on the genetic map of *H26*. Another STS marker, *Xrwgs12*, which is 1.0 cM proximal to *H26*, co-segregated with *H32* in the ITMI population. Integrative analysis of these two genetic maps suggests that *H32* and *H26* are likely allelic or closely linked. STS markers closely linked to the Hessian fly gene (or genes) will be useful for marker-assisted selection in wheat germ plasm development and breeding.