phloem-feeding aphid pests and cereal crop hosts using the wheat–greenbug as a model system. Recent results from our research on the following projects follow. (1) Toward map-based cloning of the *Ae. tauschii*-derived greenbug resistance gene *Gb3* in wheat. *Gb3* was mapped in the distal bin of wheat chromosome arm 7DL. Fine genetic mapping for *Gb3* is under way. Marker enrichment has identified over 30 *Gb3*-linked SSR, AFLP-, EST-, or RFLP-converted STS markers in the distal bin. Two STS markers flanking *Gb3* are being used to screen an *Ae. tauschii* BAC library to initiate chromosome walking. (2) Expression profiling of host defense responses against greenbug feeding. In a 2-genotype (bulked segregant R and S super pools), 3-time-point (0, 24, and 48 hours after infestation, hai), 3-replicate experiment, 18 Affymetrix GeneChips were used to investigate *Gb3*-mediated defense responses upon greenbug feeding. Of the 55K transcripts surveyed, 48 showed significant differences in constitutive expression between the R and S pools ($P = 0.05$). Among more than 6,000 transcripts with significant changes in expression level in both genotypes at 24hai, 165 were significantly up-regulated in the R pool as compared with those in the S pool at either 24 hai or 48 hai or both. Defense responses to greenbug feeding appear to be more similar to plant pathogens, in which the jasmonic signaling pathway seems to play important roles. (3) Development of cross-species transferable microsatellite markers for evaluation of biotypic diversity in the greenbug. Over 100 SSR markers were developed through database mining of the pea aphid and green peach aphid EST and genomic resources. Cross species transferability of these markers was high. Sixty SSRs were used to evaluate genetic diversities among six greenbug biotypes. Host-associated genotypic variation and geographical differentiation among these clones were revealed.

Poster 29. Haplotype structure and genetic diversity at Fusarium head blight resistance QTL in soft winter wheat germ plasm.

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Several quantitative trait loci for resistance to *Fusarium* head blight (FHB) have been mapped in wheat. Haplotyping strategies make use of previous QTL mapping and molecular marker information. We selected markers reported to be near FHB resistance QTL mapped in Sumai 3, Wuhan 1, and Ernie to haplotype a large set of Eastern soft winter wheat lines submitted by breeders. The objectives of this research were to (1) determine the genetic relationship among soft winter wheat lines with native and exotic sources of resistance using simple sequence repeat (SSR) marker data, (2) compare the SSR marker haplotypes of soft winter wheat lines with those of Sumai 3, Wuhan 1, and Ernie at known FHB-resistance QTL, and (3) identify lines with novel sources of FHB resistance. Reaction of the soft winter wheat entries evaluated was skewed toward resistance, with 59 lines classified as resistant, 116 moderately resistant, and 28 intermediate. Only 12 and 18 lines were considered moderately susceptible and susceptible, respectively. Of the resistant lines, 24 have exotic sources of resistance in the pedigree and the remaining resistant lines had only soft winter germ plasm in their pedigrees. Entries were grouped into 16 clusters that were generally based on breeding program or geographic origin of lines. The Chinese wheat cultivars having the *Fhb1* resistance gene were grouped separately from all other entries. The eight soft winter wheat entries in this study that have the *Fhb1*-resistance gene based on haplotype data were resistant in the field evaluation. The *Xsts3B-256* and *Xgwm533* markers can be clearly used to identify lines with the *Fhb1*-resistance gene. However, fine mapping is needed in other regions in which FHB resistance QTL have been located; particularly for resistance from Ernie, because allele sizes of Ernie for markers in the 5A and 4BL QTL intervals are common among Eastern soft wheat germ plasm. A number of soft winter wheat breeding lines did not share any haplotype at known QTL evaluated in this study. These lines likely carry novel sources of FHB resistance.