Poster 12. Molecular detection of QTL associated with adult-plant resistance to powdery mildew in two soft red winter wheat populations.

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The soft red winter wheat cultivars Massey and USG3209 contain adult-plant resistance (APR) to powdery mildew (PM), which is caused by the fungual pathogen *Blumeria graminis* f. sp. *tritici*. Quantitative trait loci (QTL) analyses were completed using composite interval mapping on two different recombinant inbred line populations, 'Becker/Massey' (B/M) and 'USG3209/Jaypee' (U/J). Genotypic data were collected using 589 diversity-arrary technology (DArT) markers and 10 microsatellite markers on 152 individuals from the B/M population and 363 DArT markers, three single-nucleotide polymorphism, and 225 microsatellite markers on 130 individuals from the U/J population. Powdery mildew phenotypic data were collected in 16 environments for the U/J population and in four environments for the B/M population. Significant QTL conferring APR to PM were identified on chromosomes 2A, 2B, and 1B in both populations. Additional data including yield, leaf rust resistance, milling and baking quality, height, and heading date have been collected on the U/J population for use in the Wheat CAP project. Several significant QTL have been identified for these additional traits in the U/J population. Updated genetic linkage maps from both populations have been produced.

Poster 13. Moving Bdv2, conferring resistance to yellow dwarf disease, from chromosome 7D to chromosome 7A or 7B in wheat.

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Yellow dwarf (YD) disease caused by the luteoviruses BYDV and CYDV is one of the most prevalent and devastating viral diseases affecting wheat yields. The viruses are transmitted to wheat plants by aphids (*Rhopalosiphum padi*). Partial resistance to YD occurs in wheat (*Triticum aestivum* L.). The highly effective resistance genes *Bdv2* and *Bdv3* have been transferred to wheat from a related grass species, *Thinopyrum intermedium*. *Bdv2*, from chromosome 7ST, and *Bdv3*, from chromosome 7E, were, respectively, introgressed into wheat on a chromosome segment that replaced the distal half of chromosome arm 7DL. In order to combine *Bdv2* and *Bdv3* in wheat, one of the two genes must be moved to another homoeologous chromosome, 7A or 7B. The objective of this research is to move *Bdv2* to chromosome 7A or 7B in wheat. A wheat line containing *Bdv2* was crossed with the Chinese Spring lines N7D–T7A and N7D–T7B. The resulting F_1 plants were then crossed with the Chinese Spring *Ph1b* deletion line to encourage homoeologous chromosome pairing between T7DS·7DL-7ST and 7A or between T7DS·7DL-7ST and 7B. F_2 plants identified by DNA marker genotyping as homozygous for the *Ph1b* deletion and heterozygous for *Bdv2* were harvested. The F_3 seedlings were exposed to viruliferous *R. padi* aphids, and an ELISA test was performed to determine the virus titer. Plants with low virus titer are being screened with markers associated with *Bdv2* and markers mapped to chromosome 7AL or 7BL. Plants in which *Bdv2* is present and markers on 7AL or 7BL are absent are likely recombinants in which *Bdv2* was moved to 7A or 7B.