Poster 17. Mapping adult-plant resistance to powdery mildew in soft red winter wheat.

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The soft red winter wheat cultivar USG3209 contains adult-plant resistance (APR) to powdery mildew (PM), *Blumeria graminis* (DC.) E.O. Speer f. sp. *tritici*. Because of its quantitative nature, APR to PM can be difficult to assess phenotypically, yet its durability compared to that of single, race-specific major genes makes it very desirable to wheat breeders especially in the eastern and southern U.S. soft wheat region where favorable environmental conditions create substantial PM losses. A QTL analysis for PM resistance was completed on a 'USG3209/Jaypee' recombinant inbred line mapping population in seven field environments and one greenhouse environment from 2002–07. The preliminary genetic linkage map of the 'USG3209/Jaypee' population identifies QTL for APR to PM on chromosomes 1B, 2B, and 2A. The QTL on chromosome 1B is located in the same region as the APR leaf rust gene *Lr46* near molecular marker *Xgwm259*. The QTL located on the long arm of chromosome 2A is located in the same region as the single, major PM resistance gene *Pm4*. The QTL located on chromosome 2B is located in the same region as the single, major stem rust gene *Sr36* near molecular marker *Xgwm501* and the single, major PM resistance gene *Pm6*. An updated genetic linkage map of the QTL for APR to PM contained within this population will be presented.

Poster 18. QTL for preharvest sprouting resistance in a hard white winter wheat Rio Blanco.

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Preharvest sprouting (PHS) is a major constraint for wheat production worldwide. To identify QTL for PHS resistance, a population of 170 recombinant inbred lines (RIL) from the cross between the PHS-resistant hard white wheat Rio Blanco and the PHS-susceptible line NW97S186 was evaluated for PHS under controlled moist conditions in three greenhouse experiments (2005–07) in Kansas and one field experiment (2006) in Nebraska. After 1,430 SSR primers were screened between the two parents and two bulks, 112 polymorphic markers were analyzed in the RIL population. Five QTL were detected for PHS resistance. One QTL, *QPhs.rio-3A*, with a major effect on PHS resistance was mapped in the distal region of chromosome 3AS and explained up to 38.7% of the total phenotypic variance. The second QTL on chromosome 2B, *QPhs.rio-2B.1*, explained 19.2% and 11.2% phenotypic variation in two greenhouse experiments. The third QTL also on 2B, *QPhs.rio-2B.2,* explained 15.3% and 9.8% phenotypic variation in 2006 greenhouse and field experiments, respectively. Additional two minor QTL on 1A and 5B were significant only in one experiment. The major QTL *QPhs.rio-3A* was validated in another RIL population from 'Rio Blanco/NW97S078' in all three greenhouse experiments. Because Rio Blanco is a popular parent used in many hard winter wheat breeding programs, SSR markers linked to the QTL have great potential to be used for marker-assisted selection of wheat cultivars with improved PHS resistance.

Poster 19. Using Affymetrix array to discover single nucleotide polymorphisms in wheat .

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Gene expression arrays have been used to discover single nucleotide polymorphism (SNP) in several crop species. This study was designed to explore the possibility of using the Affymetrix Wheat Genome Array for the discovery of SNP in wheat. Complementary DNAs synthesized from mRNA isolated from the seedlings of six wheat cultivars of diverse origins (Ning 7840, Clark, Jagger, Encruzilhada, Chinese Spring, and Opata 85) were hybridized to the Affymetrix Wheat Genome Array. Cluster analysis of array data selected a total of 396 genes/probe sets with a signal intensity of at least 200, p value of $< 1e^{-10}$ and overall $R^2 > 0.8$ for SNP confirmation through DNA sequencing. Sequencing results

confirmed that 87 probe sets had at least one SNP within the probe sequences. In addition, SNPs also were identified in 21 genes, but they were detected outside the probe sequences. A total of 387 SNPs were discovered from the 108 genes. One SNP was selected from each gene to design primers for SNP analysis in a mapping population using a SNaPshot kit (Applied Biosystems, Foster City, CA, USA). Forty-two SNP markers were further analyzed in 96 F_{8-12} recombinant inbred lines from the cross of 'Ning 7840/Clark', and 25 markers were integrated into the existing SSR map of the population. The result shows that Affymetrix arrays can be used to discover SNP markers in wheat.

Poster 20. Mapping rice centromere genes to wheat and Triticeae and their sequence conservation between monocots and dicots.

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Most eukaryotic centromeres consist of megabases of DNA of repetitive sequences and are generally known to be devoid of genes. However, the sequencing of centromere of rice (*Oryza sativa*) chromosome 8 revealed active genes in the centromere. These rice centromeric genes are useful to study centromere synteny between wheat and rice by comparative mapping and sequencing, and RT-PCR. The seven cDNA clones of rice centromeric genes from rice centromere 8 (*Cen8*) were directly hybridized to the genomic DNA of a set of wheat nulli-tetrasomics, ditelosomics, wheat-alien ditelosomic addition lines, and deletion lines. Four could be mapped to wheat chromosomes. One rice cDNA clone 6733.t9 located close to the end of the *Cen8* virtual contig was mapped to the distal regions of the group-3 chromosomes. However, the other three cDNA clones, 6729.t09, 6729.t10, and 6730.11, located in the kinetochore region of *Cen8*, were mapped to centromeric regions of the wheat group-7 chromosomes. Three wheat ESTs, BJ301191, BJ305475 and BJ280500 with sequences similar to those of rice centromeric genes were also mapped to the same regions as these rice clones. A possible pericentric inversion on chromosome 7D was detected by three clones, which were mapped to the long arm of chromosomes 7A and 7B but to the short arm of the chromosome 7D. The loci of four rice cDNA clones and three wheat ESTs were also detected in the corresponding homoeologous chromosomes of *Ae. speltoides*, barley, and rye using wheat-alien disomic addition lines. A pericentromeric inversion was also found in rye chromosome 7R. The PCR amplification with RT-PCR primer of 6730.t11 was conducted in the genomic DNA isolated from Triticeae species, including *T. urartu*, *T. monococcum* subsp. *monococcum* and *aegilopoides*, *Ae. speltoides*, *Ae. tauschii*, barley, rye, and *Haynaldia villosa*; the rice cultivars (*O. sativa* subsp. *Japonica*) 'Nipponbare' and (*O. sativa* subsp. *Indica*) 'IRRB7'; maize; soybean; tomato; and *Arabidopsis*. A 211-bp sequence was amplified from Nipponbare, an original source for rice genomic sequencing. Of eight plasmid clones of PCR products sequenced from IRRB7, six have the same 211-bp sequence as that in Nipponbare and two have a 202-bp sequence, which shares 100 percent and 87 percent similarity in first 38 and last 72 nucleotides with 211-bp sequence respectively. Surprisingly, the 202-bp sequence amplified from IRRB7 was found in all monocots and dicots species used in this study except Nipponbare. The sequence similarity ranges from 99% to 100% when compared to the 202-bp sequence in IRRB7. However, no sequence similar to this 202-bp sequence was found in the sequence database for the species used in this study. This sequence may be located in the centromere region, a difficult region for sequencing in most species. The RT-PCR results from CS cDNA with primers of 6729.t09, 6729.t10, and 6730.t11 indicated that the three rice centromeric genes were expressed in wheat leaf tissue. Our data demonstrate strong selection pressure for the conservation of the genes in the kinetochore region although their functional role is not clear as yet.

Poster 21. Wheat–rice collinearity and chromosome walking at the Snn1 locus in wheat.

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The wheat fungal pathogen *Stagonospora nodorum* causes Stagonospora nodorum blotch (SNB) and produces multiple host-selective toxins that interact with specific host genes to cause disease. *Snn1* is a dominant gene that confers