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

Marla Hall and Carl Griffey. Department of Crop and Soil Environmental Sciences, Virginia Polytechnic Institute and State University, Blacksburg, VA 24061, USA.

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.

Shubing Liu [1], Shibin Cai [1], Robert Graybosch [2], Cuixia Chen [1], and Guihua Bai [1,3].

[1] Department of Agronomy, Kansas State University, Manhattan, KS 66506, USA; [2] USDA–ARS, 344 Keim Hall, University of Nebraska, Lincoln, NE 68583, USA; and [3] USDA–ARS, Plant Science and Entomology Research Unit, Manhattan, KS 66506, USA.

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 .

A.N. Bernardo [1], S-W. Hu [1], P.J. Bradbury [2], R.L. Bowden [3], E.S. Buckler [2], and G-H. Bai [3].

[1] Department of Plant Pathology, Kansas State University, Manhattan KS 66506, USA; [2] ARS–USDA, Maize Genetic Diversity Laboratory, Ithaca NY 14853, USA; and [3] ARS–USDA Plant Science and Entomology Unit, Manhattan, KS 66506, USA.

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