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

sensitivity to the host selective toxin SnTox1. Previous genetic and cytogenetic analysis showed that *Snn1* maps to a gene rich region on the short arm of chromosome 1B and was located distal to the 1BS-18 deletion breakpoint. We developed a saturated map of the *Snn1* region using RFLPs, SSRs, and bin-mapped ESTs, which contained 51 markers spanning a genetic distance of 64.6 cM. Markers closely linked to *Snn1* were used to develop a high-resolution map of the locus in a population of 4,255 F_2 plants. *Snn1* was delineated to a 0.46 cM interval and two ESTs were found to co-segregate with *Snn1*. Of the 44 ESTs mapped within the *Snn1* region, 20 had homology with rice sequences on nine different chromosomes. Eight of these ESTs had homology to genes on rice chromosome 5 but were not collinear due to numerous complex chromosomal rearrangements in wheat compared to rice. We initiated chromosome walking at the *Snn1* locus using the Langdon durum BAC library and assembled a 595-kb contig. BAC sequencing and annotation revealed 10 possible candidates for *Snn1*. Genetic analysis using contig-derived markers indicated variable recombination frequencies within the *Snn1* region. Functional validation of the candidate genes using virus-induced gene silencing is in progress.

Poster 22. QTL analysis of drought tolerance in a spring wheat population.

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Water availability is commonly the most limiting factor to crop production, especially in drought prone areas like the Midwest. This study mapped QTL involved in drought tolerance in wheat to enable their use for marker-assisted selection in breeding. A population of F_7-derived, recombinant inbred lines from a cross between Dharwar Dry and Sitta, spring wheat lines with contrasting drought tolerances, was analyzed using amplified fragment length polymorphism (AFLP) techniques to create a QTL map. QTL with relatively large effects or involving several traits were selected to design STS markers. Of the 256 AFLP primer combinations evaluated, 151 were found to be polymorphic on the parents and were used to screen the population. The AFLP data was combined with the SSR data and a linkage map of 32 groups was used to create a QTL map that identified QTL in 20 of these groups. A major QTL located on chromosome 4AS was found to affect eight traits, including biomass (R^2=.35) and yield (R^2=.44) under reduced irrigation. Further results will be presented.

Poster 23. Surveying expression level polymorphism and single-feature polymorphism in near-isogenic wheat lines differing for the Yr5 stripe rust resistance locus.

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DNA polymorphisms are valuable for several applications including genotyping, molecular mapping, and marker-assisted selection. The Affymetrix Wheat GeneChip was used to survey expression level polymorphisms (ELPs) and single-feature polymorphisms (SFPs) between two near-isogenic wheat genotypes (BC_7:F_4) that differ for the *Yr5* stripe rust resistance locus, with the objective of developing genetic markers linked to *Yr5*. Ninety-one ELP probe sets and 118 SFP-containing probe sets were identified between isolines, of which just nine ELP probe sets also contained SFPs. The proportion of the transcriptome estimated to be variable between isolines from this analysis was 0.30% for the ELPs and 0.39% for the SFPs, which correlated to the theoretical genome difference between isolines of ~0.39%. Using wheat–rice synteny, both ELPs and SFPs mainly clustered on long arms of rice chromosomes four and seven, which are syntenous to wheat chromosomes 2L (*Yr5* locus) and 2S, respectively. The strong physical correlation between the two types of polymorphism indicated that the ELPs may be regulated by cis-acting DNA polymorphisms. Twenty SFPs homologous to rice 4L were used to develop additional genetic markers for *Yr5*. Physical mapping of the SFP probe sets to wheat chromosomes identified nine on the target chromosome 2BL, thus, wheat–rice synteny greatly enhanced the selection of SFPs that were located on the desired wheat chromosome. Of these nine, four were converted into polymorphic cleaved amplified polymorphic sequence (CAPS) markers between the *Yr5* and *yr5* isolines, and one was mapped within 5.3 cM of the *Yr5* locus. This study represents the first array-based polymorphism survey in near-isogenic genotypes, and the results are applied to an agriculturally important trait.