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