Poster 4. Development of markers from BAC-end sequences (BESs) for anchoring 3AS BAC contigs in wheat.

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In an effort to develop wheat resources for genomics studies, we are constructing a BAC-based physical map for the chromosome arm 3AS of hexaploid wheat cultivar Chinese Spring. In total, 16,795 high-quality BAC-end sequences showing an average read-length of 500 bp with a total of 8.3 Mb of genomic sequence were obtained from 9,984 clones. To accelerate the integration of the bacterial clone resources with the genetic map for the International Wheat Genome Sequencing Project, we searched all available markers from these sequence data. A total of 1,057 simple sequence repeats (SSR) were identified out of which 189 had more than nine repeats. Microsatellite primers were successfully developed from 598 SSRs, and a subset was screened for polymorphism in both *T. monococcum* and *T. turgidum* species. On average, 20 and 11 % of the markers were polymorphic in *T. monococcum* and *T. turgidum*, respectively. Most of the primers showed simple amplification patterns indicating their utility in genetic mapping. Efforts are underway to map these markers for physical anchoring the BACs to the genetic map. Another 504 genic sequences were identified from the BES and were screened in the 3AS BAC fingerprint database. Primers were developed from 249 genic sequences that were present in contigs and will be used for anchoring BAC contigs to genetic map.

Poster 5. Validation of six QTL associated with Fusarium head blight resistance in adapted soft red winter wheat.

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This study was conducted to validate molecular markers linked to six FHB resistance QTL previously identified in different biparental populations using elite breeding lines with incorporated FHB resistance to initial infection, spread, and DON accumulation in different genetic backgrounds. A total of 129 SSRs were characterized in the 145 breeding lines. Forty-four unrelated SSRs (four SSRs/chromosome) were used in background selection and the remaining 85 SSRs were used to validate the target QTL. The 145 wheat lines also were evaluated in yield performance trials at two locations, Blacksburg and Warsaw, VA, and for type I, type II, and DON resistance in a scab nursery at Blacksburg, VA, in 2005 and 2006. Molecular markers linked to scab resistance genes located on wheat chromosomes 2BS, 2DS, 3AS, 3BS, 5AS, and 6BS were confirmed and the allelic effect of associated marker loci was analyzed. Adapted, resistant lines with novel alleles different from known exotic sources were characterized. Renwood 3260 and its derived lines have good overall resistance and high yield potential. These lines have unique resistance with alleles differing from those of known resistance sources W14 and Sumai 3 at marker loci GWM429, GWM120, GWM261, BARC33, and GWM186 in the chromosome 2BS, 2DS, 3BS, and 5AS QTL regions, respectively. Ernie and its derived lines also have good overall resistance but did not produce promising grain yields in Virginia. These lines have unique resistance comprised of same resistance alleles as Renwood 3260 at loci GWM429, GWM120, and GWM261 in the 2BS and 2DS QTL regions. Both the Ernie and Renwood 3260 derivatives contain the same resistance alleles as the donor parent W14 at loci WMC264, BARC133, and BARC117 in 3AS, 3BS, and 5AS QTL regions, respectively. In addition, these lines have unique resistance alleles in their background at GWM493 and WMC152 in 3BS and 6BS QTL regions. This is the first study to validate six FHB QTL in elite breeding lines. QTL markers validated in the current study have been used widely in parental selection, gene pyramiding, and in postulating and selection of FHB resistance of progeny derived from such newly developed FHB-resistant lines. This also is the first study evaluating the effects of allelic differences and genetic backgrounds on FHB resistance. Newly developed, FHB-resistant lines with unique QTL/allele combinations have been used as parental lines in most Eastern U.S. wheat-breeding programs. Some of these lines will be released as cultivars and/or adapted germ plasm. The newly developed FHB-resistant lines and unique QTL/marker allele profiles identified

in this study will set the stage for using MAS not only for FHB resistance but also in combining FHB resistance with other important agronomic traits.

Poster 6. Molecular mapping of leaf rust resistance genes Lr41 and Lr42 in wheat.

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Leaf rust, caused by *Puccinia triticina* Erikss., is an important foliar disease of wheat worldwide. Pyramiding of major rust-resistance genes into a single cultivar by aid of molecular markers is an effective strategy to control the disease. Two leaf rust resistance genes, *Lr41* and *Lr42*, have been widely transferred from *Ae. tauschii* into wheat germ plasm lines. Recent mapping work located *L41* on 2DS, but markers for *Lr42* have not been reported to date. In this study, two sets of NILs were developed by backcrossing the two *Ae. tauschii* accessions TA2460 (*Lr41*) and TA2450 (*Lr42*) to the leaf rust-susceptible hard winter wheat cultivar Century. To identify new markers for *Lr42* and verify the markers for *Lr41*, two populations of 95 $BC_3F_{2:6}$ lines were analyzed with microsatellite markers. Four markers from chromosome 2DS were linked to *Lr41*, and two markers on chromosome 1DS were tightly linked to *Lr42*. The marker *Xbarc124* on 2DS was located 0.3 cM proximal to *Lr41*, and marker *Xwmc432* on 1DS was located 0.6 cM proximal to *Lr42*. Physical mapping of the markers using Chinese Spring nulli-tetrasomic and ditelosomic genetic stocks confirmed that markers linked to *Lr41* and *Lr42* were on 1DS and 2DS, respectively. Closely linked markers to *Lr41* and *Lr42* genes are new markers for these genes identified in this study and can be used for marker-assisted gene pyramiding in breeding programs.

Poster 7. Mapping of QTL for heat tolerance of wheat in response to high temperature.

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In cereals, heat stress during seed formation is critical factor in lowering yield. This study identified and mapped QTL for heat tolerance in wheat in response to two heat treatments (short and long term) during seed formation using recombinant inbred lines derived from the cross '7C'(heat resistant)/SERI M 82(heat susceptible)'. Yield components, such as kernel number, kernel weight, and grain filling duration were used as indicators of heat susceptibility. The phenotypic variation of individual yield components was normally distributed in response to heat stress suggesting that they have quantitative heritability. Transgressive segregation compared to the parents also was observed, suggesting that genetic variation from an optimal recombination of favorable loci from both parents occurred in the progeny population. One hundred thirteen SSR markers out of 320 were polymorphic between the 7C and SERI M 82 parental lines with a linkage coverage of 2,609 cM and average interval map distance of 25 cM throughout the whole genome. QTL for heat tolerance and their genetic effects were analyzed by association of percent reduction of each phenotypic trait of yield components with polymorphism in the 62 RILs. Eleven and 22 QTL for heat tolerance under short-term and long-term heat stress, respectively, were detected for each yield component phenotypic trait. Phenotypic variation was 93% for short-term and 86% under long-term heat stress.