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.

Xiaochun Sun [1], Guihua Bai [1, 2], Brett Carver [3], and Robert Bowden[2].

[1] Department of Agronomy, Kansas State University, Manhattan KS 66502, USA; [2] ARS–USDA, Plant Science and Entomology Research Unit, Manhattan KS 66502, USA; and [3] Department of Plant and Soil Science, Oklahoma State University, Stillwater, OK, 74078, USA.

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.

Jung Hwa Do [1], Esten Mason [1], Mathew Reynolds [2], and Dirk B. Hays [1].

[1] Texas A&M University, 2474 TAMU, College Station, TX 77843, USA and [2] CIMMYT, El Batan, Mexico.

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.