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.