race 1. The QTL region is located in the most distal bin of chromosome 3AS in a 2.2-cM marker interval. Flanking markers *Xbarc45* and *Xbarc86* are suitable for marker-assisted selection for tan spot resistance.

Poster 15. Computer tools for high-throughput wheat genome data analysis.

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The GrainGenes (graingenes.org) database project has worked alongside many Triticeae research projects over the years, and has developed several computer tools which have assisted in wheat genome research. Initial applications have dealt mainly with sequence processing and archiving (e.g., SQPR), and clone identification and selection (e.g., Hybsweeper). These software were important toward generating EST collections and assisting in clone picking methods for furthering genetic research within the laboratory. Other applications have been applied toward extracting high information content fingerprint traces (e.g., GenoProfiler) used for constructing physical mapping scaffolds of and viewing (e.g., FPC WebViewer) the wheat genome. These tools have been useful in determining the linear order of cloned genes and have helped to build a linear order of clones along a chromosome. Additional applications have been developed for sequence data analysis used for generating genome primers (e.g., BatchPrimer3) and reporting sequence alignments (e.g., SNPreporter) to distinguish germ plasm differences. This collection of tools has been useful in the development of genome-specific primers and new molecular markers. Other applications serve to report analysis in a database format (e.g., WheatDB and SNPdb). These resources have proven useful as a starting point for the design of many genetic experiments and surveys. Other projects under development attempt to assist gene discovery using gene-mining algorithms (e.g., CCV). For these and other examples, please visit the GrainGenes demonstration page at wheat.pw.usda.gov/demos. These and other tools from community resources can assist in the study of the wheat genome.

Poster 16. Structural characterization of the model Brachypodium genome and the observation of synteny conservation with wheat.

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Because of its small genome size (~350 Mb) and several desirable attributes, *Brachypodium distachyon* is emerging as a model system for temperate grasses, including important crops like wheat and barley. Analysis of 10.9% of the *Brachypodium* genome based on 64,696 BAC end sequences (BES) revealed that the genome consists of ~18.4% repetitive elements (TEs), with 11% known TEs and 7.4% unique *Brachypodium* TEs. Sequence analysis indicated that approximately 21.2% of the *Brachypodium* genome represents coding sequence. The BESs were integrated into the BAC-based physical maps of the *Brachypodium* genome, which allows for comparison of gene order and contents with that of another grass model genome, *Oryza sativa* (rice), at a genome-wide level. Large, conserved genomic regions were readily identified between the two small grass genomes. We also analyzed the sequence conservation at the microcolinearity level by comparing sequenced *Brachypodium* BACs with the orthologous regions from rice. Genomic rearrangements, differential gene amplification, and deletion appeared to be the common evolutionary events that caused variations of microcolinearity at different orthologous genomic regions. Our conclusions also were supported by a preliminary analysis of the 4X whole-genome sequence produced by the *Brachypodium* sequencing project at the DOE Joint Genome Institute. In addition, several annotated genes in *Brachypodium* BACs have matches to the wheat deletion bin-mapped ESTs. In some cases, genes in the same BACs matched to wheat ESTs that were mapped to the same wheat deletion bins, suggesting that the *Brachypodium* genome will provide useful information in placing the order of mapped wheat ESTs within the deletion bins and developing specific markers in the targeted regions of wheat chromosomes.