homoeologous A, B, and D genomes and analyze the types and rates of sequence evolution between homologous wheat genomes. Our detailed comparative sequence analyses of HMW-glutenin regions among the different wheat genomes provided molecular mechanisms underlying the rapid sequence changes among the A, B, and D genomes and revealed extensive sequence conservation between homologous HMW-glutenin genomic regions. The results from this study also provided useful knowledge on designing effective strategies to decipher the complex wheat genome.

Poster 2. Meta-analyses of QTL associated with Fusarium head blight resistance.

Shuyu Liu [1], Carl A. Griffey [1], Anne L. McKendry [2], and Marla D. Hall [1].

[1] Crop Soil Environmental Science, Virginia Polytechnic and State University, Blacksburg, VA 24061, USA and [2] Division of Plant Science, University of Missouri-Columbia, Columbia, MO 65211, USA.

Quantitative trait loci (QTL) associated with different types of Fusarium head blight (FHB) resistance have been identified from various sources. Because of differences in genetic backgrounds, experimental factors, and analysis methods, the marker loci orders on chromosomes and significance are not consistent across studies. Such discrepancies in the proposed chromosome location and the effect of putative QTL on FHB as well as differences in the amount of variation explained by markers associated with a QTL make it difficult to select common flanking markers that will be most diagnostic when applied in marker-assisted selection (MAS) and breeding. Meta-analysis has been used to estimate the confidence intervals (CI) of identified QTL in plant and animal genomes. The objective of this study is to estimate the CIs of 63 QTL associated with different types of FHB resistance and align them onto the consensus ITMI map to determine if different QTL on the same chromosomes from different studies overlap. Forty-seven QTL associated with FHB resistance types I, II, III, and IV from various sources were classified into 15 clusters on 10 chromosomes. Thirty-nine QTL are significant QTL (LOD > 4.0). Two clusters on 3BS and 5A contain confirmed QTL from Sumai 3 and Wangshuibai. Markers flanking a QTL cluster may help breeders to pyramid QTL more efficiently in marker-assisted selection.

Poster 3. Whole genome mapping and QTL analysis in a doubled-haploid population derived from the cross between a synthetic hexaploid wheat and hard red spring wheat.

Chenggen Chu [1], Steven S. Xu [2], Timothy L. Friesen [2], and Justin D. Faris [2].

[1] Department of Plant Sciences, North Dakota State University, Fargo, ND 58105, USA and [2]USDA–ARS Cereal Crops Research Unit, Northern Crop Science Laboratory, Fargo, ND 58105, USA.

Quantitative trait loci analysis allows the identification of genomic regions associated with quantitative traits, which provides an estimation of the number and chromosomal location of genes involved and leads to the identification of molecular markers suitable for marker-assisted selection. In this research, we used the 'wheat × maize' method to develop a doubled-haploid population derived from the synthetic hexaploid wheat line TA4152-60 and the North Dakota hard red spring wheat line ND495. The population consisted of 213 lines, and a subset of 120 lines was randomly selected and used to construct linkage maps of all 21 chromosomes. The maps consisted of 626 markers, including 408 SSRs and 218 TRAPs, and spanned 3,811.5 cM with an average density of one marker per 6.1 cM. Telomere, sequence-based fixed TRAP primers were used to define the ends of seven linkage groups. Novel tan spot resistance QTL were identified on chromosomes 2A, 5A, and 5B. In addition to *Tsn1* and *Snn1*, a new *Stagonospora nodorum* blotch toxin-sensitivity gene identified on chromosome 3D was found to be significantly associated with the disease. Major QTL for days to heading, plant height, coleoptile color, glume toughness, and seed threshability also were identified. The DH population and genetic map will be a useful tool for the identification of other disease resistance QTL and agronomically important loci and aid in the identification and development of markers for marker-assisted selection.