Xgdm36). Three independent BAC contigs were identified and shotgun sequence from selected BACs in these contigs is being used to develop new markers for fine mapping *H13*.

Poster 45. Towards map-based cloning of Hessian fly-resistance gene H26 derived from Aegilops tauschii.

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Hessian fly (*Mayetiola destructor* (Say)) is one of the most important insect pests of wheat. Deployment of resistance genes in wheat cultivars is the most effective measure to control Hessian fly. Among the 33 *H* genes that confer resistance to Hessian fly, *H26* derived from *Aegilops tauschii*, is highly effective against several of the world's most virulent Hessian fly populations. This gene was previously mapped to the wheat chromosomal deletion bin 3DL3-0.81-1.00 in a synthetic hexaploid wheat. This study attempted to isolate *H26* through map-based cloning. In this research, we developed a mapping population of approximately 3,000 F_2 individuals derived from the cross between the *Ae. tauschii* accession CIae 25, having a resistance allele at the *H26* locus, and the *Ae. tauschii* accession AL8/78, having a susceptible allele at this locus. We conducted high-resolution mapping of *H26* in this population and developed several markers within 0.1 cM from *H26*. Using a pair of flanking markers, we identified the *Brachypodium* genomic region that is collinear with the region harboring *H26*. An *Ae. tauschii* BAC contig was identified by blasting the *Ae. tauschii* AL8/78 BAC library with the 20-kb collinear *Brachypodium* sequence. Six BAC clones in the middle of the contig were further analyzed using two flanking markers. One BAC clone that was positive for the two flanking markers was identified and it is currently being sequenced. The *H26* locus will be delimited using the markers developed based on the BAC sequence, and will be confirmed by transformation and expression analysis.

Poster 46. Introgression of crown rot resistance from hexaploid wheats into durum wheats.

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Triticum turgidum subp. *durum* (tetraploid durum) germplasm is very susceptible to crown rot, caused by the fungus *Fusarium pseudograminearum*. Partial resistance to this disease has been identified in a number of *T. aestivum* (hexaploid wheat) lines, such as 2-49 and Sunco. As these two wheat species are closely related, genes can be transferred between them. This study discusses the introgression of partial crown rot resistance from hexaploid wheat into durum wheat. Results will be presented on the cytogenetics of these crosses and the screening of the progeny for crown rot resistance. A number of different *T. aestivum* x *T. turgidum* crosses were investigated using DArT markers to determine the inheritance of parental A-, B-, and D-genome material in subsequent generations derived from these crosses. Significant variation was observed among individual crosses in the proportions of A-, B-, and D-chromosomal segments inherited from the hexaploid parent. In particular, while several early generation populations retained a significant proportion of D-genome material from the hexaploid parent, other equivalent populations from different crosses contained only tetraploid lines entirely lacking D-genome segments. Seven derived tetraploid lines showing improved resistance to crown rot over F_5, F_6, and F_7 generations were backcrossed to a range of durum parents. Results will be presented for two BCF_2 populations screened for crown rot resistance in the field during 2011.