Poster 43. High-density mapping of a Russian wheat aphid resistance gene: chromosome survey sequences in use.

Helena Stankova [1], Miroslav Valarik [1], Nora Lapitan [2], Paul Berkman [3], David Edwards [3], Ming-Cheng Luo [4], Jan Safar [1], Nils Stein [5], Jaroslav Dolezel [1], and Hana Simkova [1].

[1] Centre of the Region Hana for Biotechnological and Agricultural Research, Institute of Experimental Botany, Sokolovska 6, CZ-77200 Olomouc, Czech Republic; [2] Department of Soil and Crop Sciences, Colorado State University, Fort Collins, CO 80524, USA; [3] Australian Centre for Plant Functional Genomics, University of Queensland, Brisbane, QLD 4072, Australia; [4] Department of Plant Sciences, University of California, Davis, CA 95616, USA; and [5] Leibniz Institute of Plant Genetics and Crop Plant Research, Department Genebank, AG Genome Diversity, D-06466 Gatersleben, Germany.

The Russian wheat aphid (RWA), *Diuraphis noxia*, has become a serious world invasive pest of small grain cereals. Several *D. noxia* strains (biotypes) varying in virulence have spread in all wheat- and barley-growing areas with the exception of Australia. Numerous genes contributing to RWA resistance were found in various wheat lines. A dominant gene, *Dn2401*, identified in CI 2401 resistant to both *D. noxia* U.S. biotypes 1 and 2 was mapped on the short arm of the wheat chromosome 7D (7DS). Development of tightly linked markers and isolation of the resistance gene will facilitate marker-assisted breeding and/or direct gene transfer by molecular methods. To facilitate positional cloning of this gene in a complex polyploid wheat genome, we employ chromosome-based resources such as 7DS-specific BAC library, a 7DS physical map, and survey sequences of wheat group-7 chromosomes. Furthermore, a synteny-based tool GenomeZipper enabling virtual ordering of cereal genes as well as a newly constructed high-density *Ae. tauschii* linkage map assist us in a highly focused saturation of the map within a 2.5-cM interval delimited by available microsatellite markers. Moreover, annotated syntenic build of 7DS (http://www.wheatgenome.info) facilitates searching for candidate genes within the region of interest. This work has been supported by Czech Science Foundation (grant award P501/12/2554), Internal Grant Agency PrF-2012-001 and Australian Research Council (grant award LP0882095).

Poster 44. Towards fine mapping and cloning of the Hessian fly resistance gene, H13.

Anupama Joshi [1], Sunish K. Sehgal [1], Gaganpreet Kaur [1], Jeffery J. Stuart [2], Xuming Liu [3], Ming-Shun Chen [3,4], and Bikram S. Gill [1].

[1] Wheat Genetics Resource Center and Department of Plant Pathology, Kansas State University, Manhattan, KS 66506, USA; [2] Department of Entomology, Purdue University, West Lafayette, IN, USA; [3] Department of Entomology, Kansas State University, Manhattan, KS 66506, USA; and [4] Hard Winter Wheat Genetics Research Unit, USDA–ARS, Kansas State University, Manhattan, KS 66506, USA.

Wheat (*Triticum aestivum* L.) is a widely adopted crop planted all over the world and provides nearly 55% of the carbohydrates consumed. The Hessian fly, *Mayetiola destructor* (Say) (Diptera: Cecidomyiidae), is a major pest of wheat worldwide and causes 5–10% loss in wheat production. Hessian fly larvae cause damage to wheat by feeding between leaf sheath. Major symptoms include stunted growth, weak stems, reduced grain fill, and reduction in yield. Resistance genes in wheat have been the most effective and primary source for controlling Hessian fly damage. *H13* is a dominant resistance gene, which confers stable level of antibiosis against a wide range of Hessian fly biotypes. The *H13* gene is derived from KU2076 (*Aegilops tasuchii* (TA2452)). In previous studies, *H13* was mapped to the distal arm of chromosome 6DS, proximal to the breakpoint of del 6DS-6 (FL 0.99) and was found to be co-segregating with marker *Xcfd132* and flanked by *Xgdm36* at 2.7 cM (Liu et al. 2005. Theor Appl Genet 111:243-249). We have developed a high-resolution mapping population of 1,368 F_2 individuals derived from the cross between PI372129 (*Dn4*) and PI562619 (Molly, *H13*). The population was genotyped with linked co-dominant microsatellite markers *Xcfd132* and *Xgdm36* (2.7 cM distal to *H13*). Eighty-nine recombinants were observed. The F_2 plants from which the DNA was extracted for marker studies were self-pollinated to produce F_3 seeds. Around 30 F_3 seeds of each recombinant F2 plant along with Molly, Newton, *Dn4*, Karl 92, and Cladwell as controls were evaluated for phenotypic reaction following Hessian fly infestation. At the 1.5 leaf stage, seedlings were infested and 3 weeks post infestation, susceptible and resistant plants were characterized based on stunting in the compatible interactions and normal growth in the incompatible interactions respectively. *H13* was flanked by *Xcfd132* at 1.53 cM and *Xgdm36* at 2.2 cM. Three-dimensional BAC pools developed from minimal tiling path of a chromosome 1D, 4D, and 6D FPC assembly were screened for flanking markers (*Xcfd132*, *Xcfd213*, and

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.

Guotai Yu [1,6], Xiwen Cai [2], Marion O. Harris [1], Mingcheng Luo [3], Yongqiang Gu [3], and Steven S. Xu [5].

[1] Department of Entomology, North Dakota State University, Fargo, ND 58108, USA; [2] Department of Plant Sciences, North Dakota State University, Fargo, ND 58108, USA; [3] Department of Plant Sciences, University of California, Davis, CA 95616, USA; [4] USDA–ARS, Western Regional Research Center, Albany, CA, ND 94710, USA; and [5] USDA–ARS, Northern Crop Science Laboratory, P.O. Box 5677, Fargo, ND 58108, USA; [6] Present address: Department of Plant Pathology, North Dakota State University, Fargo, ND 58108, USA

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.

Anke Martin [1], Steven Simpfendorfer [2], Friederike Eberhard [1], Ray A. Hare [2,3], and Mark W. Sutherland [1].

[1] University of Southern Queensland, Centre for Systems Biology, Toowoomba, Queensland, Australia, and [2] New South Wales Department of Primary Industry, Tamworth NSW 2340, Australia; [3] Current address: Plant Breeding Institute, Cobbitty, NSW 2570, Australia.

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.