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

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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.

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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