

Poster 15. Association analysis of wheat resistance to stem rust in U.S. winter wheat.

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Stem rust, caused by *Puccinia graminis* f. sp. *tritici*, has become a new threat for wheat production in the U.S. after the emergence and quick spread of race TTKSK from East Africa to other countries. To evaluate the current status of U.S. winter wheat resistance to stem rust, validate markers associated with known genes, and identify new loci effective against the disease, an association mapping population was assembled with 174 U.S. winter wheat cultivars and breeding lines from the 2008 regional nurseries. A total of 267 genome-wide, simple sequence repeat (SSR) markers, including those linked to reported major stem rust resistance gene/QTL, were used to genotype this population. The population was evaluated for seedling resistance to race TTKSK and both seedling and adult-plant resistance to a bulk of U.S. races. About 40% of accessions showed resistance or moderate resistance to the U.S. races in the seedling or adult stage, but only 11.5% of seedlings were resistant to the race TTKSK with an infection type (IT) of 2 or lower. The accessions carrying *Sr36* showed a high level of resistance to both U.S. races and TTKSK in the seedling stage and appeared to confer the best resistance to TTKSK in the population. *Sr38* and *Sr24* conferred a high level of resistance to the U.S. races at the adult stage, with severities lower than 10% and at least moderate resistance. *Sr24* also showed seedling resistance to TTKSK with ITs of ;2 to 2. Accessions with *Sr31* or the new SSR allele, *Xgwm334-123* on chromosome 6A, showed resistance to U.S. races in seedling and adult stages but not to TTKSK. Three additional marker alleles were associated with a low IT (2 or lower) to TTKSK and *Sr* genes linked to these alleles need further investigation. However, the frequency of all these resistance alleles for TTKSK was low in the population studied. Introducing new *Sr* genes and increasing the frequency of known effective resistance genes should be the focus of research to improve wheat resistance to stem rust.

Poster 16. A gut transcriptome of the Hessian fly (*Mayetiola destructor*), a member of the gall midges.

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Hessian fly, *Mayetiola destructor*, is a serious pest of wheat and an experimental organism for the study of gall midge-plant interactions. In addition to food digestion and detoxification, the gut of Hessian fly larvae also is an important interface for insect–host interactions. Analysis of the genes expressed in the Hessian fly larval gut will enhance our understanding of the overall gut physiology and may also lead to the identification of critical molecules for Hessian fly–host-plant interactions. Over 10,000 expressed sequence tags (ESTs) were generated and assembled into 2,007 clusters. The most striking feature of the Hessian fly larval transcriptome is the existence of a large number of transcripts coding for so-called small secretory proteins (SSP) with amino acids less than 250. Eleven of the 30 largest clusters were SSP transcripts with the largest cluster containing 11.3% of total ESTs. Microarray and qPCR analyses of representative SSP transcripts revealed that most of them were predominantly present in the gut tissue and the transcript levels of many SSP were affected by plant genotypes on which larvae feed. Transcripts coding for diverse digestive enzymes and detoxification and metabolic proteins also were identified. The putative digestive enzymes included serine proteinases (trypsin and chymotrypsin), cysteine proteases, aspartic protease, endo-oligopeptidase, aminopeptidases, carboxypeptidases, and α -amylases. Putative detoxification proteins included cytochrome P450s, glutathione S-transferases, peroxidases, ferritins, a catalase, and peroxiredoxins. This study represents the first global analysis of gut transcripts from a gall midge. The identification of a large number of SSP transcripts in the Hessian fly larval gut provides a foundation for future study on the functions of these genes.