Poster 53. Unraveling the complexity of the net form net blotch resistance locus on barley chromosome 6H.

Jon Richards [1], Tim Friesen [1,2], Zhaohui Liu [1], and Robert Brueggeman [1].

[1] Department of Plant Pathology, North Dakota State University, Fargo, ND 58102, USA, and [2] USDA–ARS, Cereal Crops Research Unit, Red River Valley Agricultural Research Center, Fargo, ND 58102, USA.

Net form net blotch (NFNB) in barley, caused by the necrotrophic fungal pathogen *Pyrenophora teres* f. *teres* (Ptt), has a negative impact on barley production throughout the world. Resistance sources from diverse barley varieties collected around the world have been characterized and many mapped to a common locus near the centromeric region of barley chromosome 6H. The 6H locus is complex containing multiple resistance and/or susceptibility genes. Two recessive NFNB resistance genes, *rpt.r* and *rpt.k*, from the barley lines Rika and Kombar confer resistance against isolates 15A and 6A, respectively. Previous research delineated the genes to an ~3.3-cM region of barley chromosome 6H in a 'Rika/Kombar' double-haploid population consisting of 118 individuals. Utilizing genome synteny between barley chromosome 6H and *Brachypodium distachyon* chromosome 3, a ~1-Mb *Brachypodium* sequence was identified spanning the *rpt.r*/*rpt.k* region. Predicted *Brachypodium* genes were utilized to develop PCR-based molecular markers. The markers were used to saturate the *rpt.r*/*rpt.k* region in a high-resolution population developed by screening 2,973 recombinant gametes. The *rpt.r* and *rpt.k* genes were delimited to an ~0.13-cM region representing ~150 kb of *Brachypodium* sequence. Cultivar Morex BAC clones were identified using barley probes from the *rpt.r*/*rpt.k* region, and a physical map of the locus is under construction. Two orthologous barley genes with high homology to a family of *Brachypodium* leucine-rich repeat (LRR)-like genes were identified (*rpt.cg1* and *rpt.cg2*) that cosegregate with *rpt.r* and *rpt.k*, respectively, in the high-resolution map. The sequence of the *rpt.k* candidate gene (*rpt.cg2*) from Kombar has been obtained by a tailed PCR method and sequencing of the *rpt.r* candidate gene is under way. The nucleic acid sequence was determined from the full-length *rpt.k* cDNA and used to predict the protein structure. The protein contains a transmembrane domain near the N-terminus and an imperfect leucine-rich repeat region near the C-terminus. These candidate genes may support the inverse gene-for-gene model where dominant susceptibility factors interact with necrotrophic effectors that initiate cell death and necrosis resulting in susceptibility.

Poster 54. Searching via association mapping for novel sources of resistance to Ug99 and other Ethiopian stem rust races in durum wheat.

Tesfaye D. Letta [1,4], Marco Maccaferri [1], Ayele Badebo [2], Karim Ammar [3], Maria C. Sanguineti [1], Silvio Salvi [1], Jose Crossa [3], and Roberto Tuberosa [1].

[1] DiSTA, University of Bologna, Viale Fanin 44, 40127 Bologna, Italy; [2] Debre Zeit Agricultural Research Center, Debre Zeit, Ethiopia; [3] CIMMYT Int., Apdo Postal 6-641, Mexico D.F., Mexico 06600; and [4] Sinana Agricultural Research Center, Bale-Robe, Ethiopia.

Puccinia graminis f. sp. *tritici*, the causative agent of stem rust in wheat, is known to rapidly evolve new virulence to resistance genes. Although more than 50 stem rust resistance (*Sr*) loci have been identified in wheat, only a few remain effective, particularly against the highly virulent race Ug99 (TTKSK race) and a mixture of durum-specific races. Association mapping was deployed on 183 elite durum wheat accessions tested in four seasons under artificial inoculation in order to identify quantitative trait loci (QTL) for resistance to Ug99 and durum-specific races under field conditions. The panel was genotyped with 1,250 SSR and DArT markers (Mantovani et al. 2008. Mol Breed 22:629-648). Twelve QTL-tagging markers with R^2 values up to 11.3% were significantly associated with stem rust resistance across three to four seasons. Although some markers were linked to known *Sr* genes (e.g., *Sr9*, *Sr13*, and *Sr14*), other significant markers were located in chromosome regions where no *Sr* genes have been previously reported. The allelic variation identified at these novel QTL provides additional opportunities to deploy marker-assisted selection to improve resistance to stem rust in durum wheat grown under field conditions.