**THE WHEAT GENETIC & GENOMIC RESOURCES CENTER**
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## *Notice of release of KS08WGGRC50 wheat streak mosaic virus- and Triticum mosaic virus-resistant hard red winter wheat germ plasm.*

B.S. Gill, B. Friebe, L.L. Qi, D.L. Wilson, W.J. Raupp, A.K. Fritz, D.L. Seifers, T.J. Martin, and M.O. Pumphrey.

The Agricultural Research Service, U.S. Department of Agriculture and the Kansas Agricultural Experiment Station announce the release of KS08WGGRC50 hard red winter wheat germ plasm with resistance to wheat streak mosaic virus and *Triticum* mosaic virus for breeding and experimental purposes. Scientists participating in this development were B.S. Gill, B. Friebe, L.L. Qi, D.L. Wilson, and W.J. Raupp, Department of Plant Pathology, Kansas State University, Manhattan, Kansas; A.K. Fritz, Department of Agronomy, Kansas State University, Manhattan, Kansas; D.L. Seifers and T.J. Martin, Kansas State University, Agricultural Research Center, Hays, Kansas; and M.O. Pumphrey, USDA-ARS Plant Science and Entomology Research Unit, Department of Agronomy, Kansas State University, Manhattan, Kansas.

KS08WGGRC50 is an improved derivative of KS93WGRC27 with the resistance gene *Wsm1* in the form of a wheat–*Th. intermedium* recombinant chromosome T4DL·4DS-4Ai#1S (rec213). The recombinant chromosome consists of the long arm of wheat chromosome 4D, most of the short arm of 4D, and a shortened distal segment derived from the short arm of the *Th. intermedium* chromosome 4Ai#1 harboring *Wsm1*. *Wsm1* is temperature sensitive and confers resistance to wheat streak mosaic virus and *Triticum* mosaic virus at low temperature around 18°C, whereas at higher temperatures around 24°C *Wsm1* breaks down and is no longer effective. KS08WGGRC50 is derived from the cross KS93WGRC27/2*TA3809(CSph1b)//Wichita/3/2*Overley. The $F_2$-derived families are homozygous for *Wsm1* but are segregating for other traits.

Small quantities (3 grams) of seed of KS08WGGRC50 are available upon written request. We request that the appropriate source be given when this germ plasm contributes to research or development of new cultivars. Seed stocks are maintained by the Wheat Genetic and Genomic Resources Center, Throckmorton Plant Sciences Center, Kansas State University, Manhattan, KS 66506. Genetic material of this release will be deposited in the National Plant Germplasm System where it will be available for research purposes, including the development of new cultivars.

## *Development and characterization of wheat–Leymus racemosus translocation lines with resistance to Fusarium head blight.*

B. Friebe, L.L. Qi, B.S. Gill, and P.D. Chen.

Working with scientists at Nanjing Agricultural University in China, we have identified a new source of resistance from the perennial grass relative *L. racemosus* (Lr). A chromosome segment (designated as 7Lr#1S) from this grass specifying resistance to FHB was transferred to a chromosome arm 7AL of wheat in the form of a translocation T7AL·7Lr#1S. This translocation stock was crossed twice with *ph1b* mutant stock. We screened 154 $BC_1$ plants from the cross 'T7AL·7Lr#1S / *ph1b*' using molecular markers to assay for *ph1b* and T7AL·7Lr#1S. Sixty-one plants were homozygous ph1b/ph1b and heterozygous for the translocation chromosome T7AL·7Lr#1S/7A. These plants were either backcrossed with Overley and Danby or selfed. We have developed a large, recombinant population of 1,400 $BC_2$ and more than 8,000 $BC_1F_2$ seeds. In homozygous *ph1b* genotypes, the alien 7Lr#1S arm with the gene(s) for FHB resistance is expected to recombine with homoeologous wheat arm 7AS. Meiotic pairing analysis in plants homozygous for *ph1b* and heterozygous for T7AL·7Lr#1S/7A failed to detect any metaphase I association in more than 500 PMCs, suggesting that the recovery of recombinants will be very difficult. Recently, a total of 1,150 $BC_2$ plants were screened using molecular markers, and three plants were found to be recombinants. Rec.124 is a proximal recombinant with the proximal 80% from 7Lr#1S and the distal 20% from 7AS. Two other recombinants, rec. 679 and rec.989, are distal recombinants with the proximal 80% from 7AS and the distal 20% from 7Lr#1S. These recombinants were confirmed by GISH indicating that the recovery of recombinants is possible, although at a very low frequency. These recombinants will be screened for scab resistance in the greenhouse. Our previous data indicated that a scab-resistance gene from *Ley-*

*mus* most likely resides in the distal region of the short arm of chromosome 7Lr#1. Three different recombinants provide a good opportunity to further map the FHB resistance gene to a specific chromosome region of 7Lr#1S. The FHB resistant recombinants will then be transferred to adapted wheat cultivars.

## *Stripe rust and leaf rust resistance from Ae. geniculata.*

V. Kuraparthy, P. Chhuneja, H.S. Dhaliwal, S. Kaur, and B.S. Gill.

Previously, leaf and stripe rust-resistant introgression lines were developed through induced homoeologous chromosome pairing between wheat chromosome 5D and 5Mg of *Ae. geniculata*. Genomic in situ hybridization with *Ae. comosa* DNA as probe showed three different kinds of introgressions. All three types of introgression lines showed complete and similar resistance to the most prevalent races of leaf (PRTUS25, PRTUS35, PNMQ, MCDL, and PRTUS6) and stripe rust (03 and 04) in Kansas. One resistant line (TA5602) with a cytologically undetectable introgressed segment was used for molecular characterization of leaf and stripe rust resistance. This line (TA5602), which is agronomically as good as the recipient parent (WL711), was used to transfer the leaf rust and stripe rust resistance to the Kansas winter wheat cultivars Jagger, Overley, and NewHills adapted to the Southern Great Plains (SGP), specifically to Kansas, and to advanced breeding lines (KCB35, KCB36, and KCB37) of the KSU wheat-breeding program by standard backcrossing. Cleaved Amplified Polymorphic Sequence markers were developed as diagnostic PCR-based markers for MAS of *Lr57* and *Yr40* genes into hard winter wheats. Two different CAPS markers were developed based on EST marker (XBF200555) diagnostically detecting the alien introgressed segment in T5DL·5DS-5MgS(0.95). $BC_3F_2$ plants segregating for rust resistance are being evaluated in the field at two locations in Manhattan. Homozygous $BC_3F_{2:3}$ and $BC_3F_4$ plants with rust resistant genes will be further evaluated in the field for subsequent germ plasm release.

Because most of the wheats grown in Kansas and SGP are hard winter wheats, the quality of the germ plasm lines with *Lr57* and *Yr40* genes were analyzed by molecular characterization of the Hardness (Ha) locus. Southern hybridization indicated that the *Pina-D1* and *Pinb-D1* genes were deleted in the rust-resistant introgressions, including the translocation (T5DL·5DS-5MgS(0.95)) line used for marker-assisted selection. Because the mutations and/or deletion of *Pina-D1* and *Pinb-D1* in wheat confers hard grain texture, deletion of these genes in T5DL·5DS-5MgS(0.95) suggested that germ plasm lines containing the *Ae. geniculata* segment with the *Lr57* and *Yr40* genes will give hardness to wheat. This further implied that transfer of the alien segment with *Lr57* and *Yr40* to Kansas winter wheats does not impair their quality requirements. Using genetic analysis and molecular characterization of the EMS mutants, one additional leaf rust resistance gene *LrGen* was identified in T5DL·5DS-5MgS(0.95). This suggested that the alien introgressed segment in act like a natural gene pyramid with multiple disease resistance genes for wheat improvement.

## *Leaf rust resistance from Ae. triuncialis.*

V. Kuraparthy, S. Sood, P. Chhuneja, H.S. Dhaliwal, S. Kaur, R.L. Bowden, and B.S. Gill.

One agronomically desirable, rust-resistant introgression line T2BS·2BL-2tL(0.95) was selected and advanced to BC3F11 from a cross of hexaploid wheat and *Ae. triuncialis*. The small wheat-*Ae. triuncialis* translocation T2BS·2BL-2tL(0.95) with leaf rust resistance gene *Lr58* provides a seedling resistance. The translocation line was resistant to the most prevalent races of leaf rust in Kansas. Molecular characterization suggested that the alien introgressed *Ae. triuncilais* segment with *Lr58* was less that 3.5% of the chromosome arm 2BL of wheat. Molecular markers (*XksuH16*, *XksuF11*, and *Xbg123*) diagnostically detected the alien introgressed segment in T2BS·2BL-2tL(0.95).

The rust-resistance gene *Lr58* was transferred to the HRWW cultivars Jagger and Overley by standard backcrossing. Molecular markers and/or phenotypic selection at the seedling stage for rust resistance were used to select the backcross $F_1$ and homozygous $F_2$ plants with rust resistance. Three backcrosses were made to develop $BC_3F_1$ plants and homozygous $BC_3F_2$ plants are selected based on the diagnostic DNA-marker-based assays using the SSR marker *Xcfd50* and/or RFLP marker *XksuH16*. Homozygous $BC_3F_{2:3}$ and $BC_3F_4$ plants with rust-resistance genes will be evaluated in the field for subsequent germ plasm release. CAPS based diagnostic markers are being developed for marker assisted transfer of *Lr58* for wheat improvement.

## *Chromosome specific BAC libraries, new markers for marker-assisted breeding and wheat physical mapping.*

S.K. Sehgal, W.L. Li, P. Rabinowicz, and B.S. Gill.

We are working with Dr. J. Dolezel, Czech Republic, on making chromosome-specific libraries for physically mapping the wheat genome. We grew all the double–ditelosomic stocks of Chinese Spring wheat and sent 20,000 seeds of several ditelosomic stocks (3A, 1A, 1D, 3D, and 4A) to the Dolezel laboratory. A 55,584 BAC-clone library from chromosome arm 3AS was constructed using the restriction enzyme *Hind*III and fingerprinted with the SNaPshot-based high-throughput technique. After removing clones with very small insert sizes and cross-contamination, 47,063 BAC fingerprints were used for contig assembly with FPC computer program. There are currently 1,677 contigs and 11,939 singletons. On average, there are 21 BAC clones per contig with ~235 Kb in length. The largest contig has 417 BAC clones and is ~ 2.7 Mb in length. The BAC clones in the assembly provide 75% coverage of the chromosome arm 3AS (Gill et al. 2008).

To anchor the BAC contig to genetic and deletion-bin maps, the 68 plates of the BAC library were pooled in six dimensions, 190 BAC pools distributed to the mapping labs, and 408 EST-STS primer pairs designed. A total of 145 EST–STS markers have been mapped to 3AS and 80 mapped to individual BACs using the BAC pooling strategy. Over 100 contigs have been anchored using this approach. From the BAC end sequences, we also designed primer pairs for 234 SSR and 240 genic STS markers. Polymorphisms were screened for the markers developed by this project and those previously mapped to 3AS, between the parental lines *T. monococcum* subsp. *aegilopoides* and subsp. *monococcum*, from which a mapping population of 94 recombinant inbred lines was derived. Currently, 41 (30 SSR, 5 EST-STS, and 8 genic STS) markers are polymorphic and 18 placed in a linkage map. The map is collinear with the 3A map of hexaploid wheat.

We have sequenced the ends of 9,984 BAC clones and obtained 16,795 high-quality BESs with an average read-length of 500 bp and a total length 8.3 Mb of genomic sequences. About 6.2% of the BESs are genic and 74% are repeated sequences, similar to the BES composition of the 3B library. All the BESs are submitted to GenBank. From the BESs, we identified 1,057 microsatellite markers for the 3AS arm and designed primer pairs for 234 SSR and 240 genic STS markers. We have established collaboration with Dr. Gina Brown-Guedira, USDA–ARS, for testing these markers for their utility in wheat breeding.

## *Personnel.*

Three new students joined the WGGRC laboratories in 2008, Bhanu Kalia and Shankar Rao, working toward their Ph.D. degrees, and Nolan Rothe, working toward an M.S. degree. Two new Research Associates, Calli Bi and Jia Li, are both Research Associates from the Peoples Republic of China.

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### *A rapid, small-scale method to evaluate dough viscoelastic properties*

F. Xie and B.W. Seabourn

The viscoelastic properties of dough (i.e., extensibility and resistance to extension) influence each step of the baking process, as well as the quality of the final product, and thus are important quality factors to consider in the selection of suitable lines for advancement in wheat-breeding programs. The objective of this study was to develop a rapid small-scale method to evaluate dough extensibility and resistance to extension properties. A total of 20 HRWW flour samples varying in protein content and rheological properties were studied. The standard extensigraph method and a small-scale texture analyzer (TA) method utilizing a Kieffer rig were compared and used as reference methods for a new near infrared spectroscopy (NIRS) method. Spearman rank correlation coefficient (r) between extensibility measured