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Notice of release of KS09WGGRC51-J and KS09WGGRC51-C Hessian fly-resistant hard red winter wheat and KS09WGGRC51-P Hessian fly-resistant spring wheat germ plasm.

The Agricultural Research Service, U.S. Department of Agriculture and the Kansas Agricultural Experiment Station announce the release of KS09WGGRC51-J and KS09WGGRC51-C hard red winter wheat (*Triticum aestivum* L.) and KS09WGGRC51-P spring wheat germ plasm with resistance to Hessian fly for breeding and experimental purposes. Scientists participating in this development were B.S. Gill, B. Friebe, J.C. Cainong, D.L. Wilson, and W.J. Raupp, Department of Plant Pathology, Kansas State University, Manhattan, KS 66506; A.K. Fritz, Department of Agronomy, Kansas State University, Manhattan, KS 66506; M.S. Chen and M.O. Pumphrey, USDA–ARS Plant Science and Entomology Research Unit, Department of Agronomy, Kansas State University, Manhattan, KS 66506; J. Johnson, Griffin Campus, University of Georgia, Griffin, GA 30223; and L.E. Zavatsky and A.J. Lukaszewski, Department of Botany and Plant Sciences, Batchelor Hall, University of California, Riverside, CA 92507.

KS09WGGRC51-J, KS09WGGRC51-J, and KS09WGGRC51-P are improved derivatives of Hamlet (KS89WGRC08, PI 549276) with the resistance gene *H21* in the form of a wheat-rye (*Secale cereale*) recombinant chromosome T2BS·2BL-2R#2L. The recombinant chromosome consists of the short arm of wheat chromosome 2B, most of the long arm of 2B, and a shortened distal segment derived from the long arm of the *S. cereale* chromosome 2R#2 harboring *H21*. KS09WGGRC51-J is derived from the cross Hamlet (T2BS·2R#2L)/2B(L)+20 (T2BS·2BL-2R#5L)/2*Jagger. KS09WGGRC51-C is derived from the cross Hamlet (T2BS·2R#2L)/2B(L)+20 (T2BS·2BL-2R#5L)/2*Culver. KS09WGGRC51-P is derived from the cross Hamlet (T2BS·2R#2L)/2B(L)+20 (T2BS·2BL-2R#5L)/2*Pavon. The F_4-derived families are homozygous for *H21* but are segregating for other traits.

Small quantities (3 grams) of seed of KS09WGGRC51 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.

Lili Qi, Mike Pumphrey, Bernd Freibe, Bikram Gill, and P.D. Chen.

Fusarium head blight can be a significant disease in Kansas in a year with a wet spring. Working with scientists at Nanjing Agricultural University in China, we have identified a new source of resistance from a perennial grass relative *L. racemosis* (Lr). A chromosome segment (called 7Lr#1S) from this grass specifying resistance to FHB has been transferred to a chromosome arm of wheat (called 7AL) in the form of a translocation T7AL·7Lr#1S. Using *ph1*-induced homoeologous method, we identified three putative recombinants. Putative recombinants were confirmed by genomic in situ hybridization (GISH), and we identified one proximal recombinant (rec124) with the proximal 80% derived from 7Lr#1S and the distal 20% derived from 7AL, and two distal recombinants (rec679 and rec989) with the proximal 80% derived from 7AL and the distal 20% of the arm derived from 7Lr#1. We presently are backcrossing these recombinants with adapted Kansas winter wheats and selecting homozygous recombinant stocks. Once these have been obtained, they will be evaluated for their resistance to FHB.

Another new source of resistance is derived from the perennial relative *Elymus tsutushiense*. We identified a wheat-Elymus addition translocation stock with 42 wheat chromosomes plus a pair of translocation chromosomes in which the short arm of chromosome 1Ets#1 was transferred to an unknown wheat chromosome. This line was highly resistant to FHB in both greenhouse and under field conditions. Further chromosome engineering aimed at producing compensating translocation lines is underway.

Development of wheat–Thinopyrum intermedium recombinant lines resistant to wheat streak mosaic virus.

Bernd Friebe, Lili Qi, Duane L. Wilson, Zhijian Chang, Dallas L. Seifers, T. Joe Martin, Alan K. Fritz, and Bikram S. Gill.

Wheat streak mosaic is a devastating virus disease of bread wheat in the Great Plains of the U.S. and Canada and in most spring and winter wheat-producing areas worldwide. Only one gene conferring resistance to WSM has been designated, *Wsm1*. Previously, we released WGRC27 with resistance to WSMV controlled by *Wsm1*, a gene transferred from *Th. intermedium* to wheat in the form of a wheat–*Th. intermedium* T4Ai#2S.4D translocation, which was redesignated as T4DL·4J^{s}S. Using *ph1*-induced homoeologous pairing we identified five recombinants using molecular markers and confirmed them by GISH.

All recombinants were evaluated for their reaction to WSMV and *Triticum* mosaic virus (TMV). The distal recombinants rec45, rec64, rec87, and rec213 were free of symptoms and had low virus titers to both viruses at 18°C by ELISA. The proximal recombinant rec36 reacted susceptible to both viruses, which mapped the *Wsm1* gene in the distal 20% of the 4DS-4JsS arm.

The recombinant rec213 in the 'Overley/Amadina' background was released as a new germ plasm, KSWG-GRC50, with resistance to wheat streak and *Triticum* mosaic viruses in 2008.

A second source of WSMV resistance was mapped to the long arm of a *Th. intermedium* group-7 chromosome that is available in the form of a ditelosomic 7Ai#2L chromosome addition line. This germ plasm requires further chromosome engineering before it can be used in cultivar improvement. To speed up this process, we have developed three PCR-based STS markers that detect the 7Ai#2L-specific fragment in a wheat background, from screening 120 primer pairs designed from mapped wheat EST sequences. Five plants with a chromosome number of 2n = 40 +7D +7Ai#2L and homozygous for ph1b have been obtained. In the homozygous *ph1b* condition, the 7Ai#2L telosome is expected to pair and recombine with 7DL. Presently, we are screening these progenies using molecular markers for putative recombinants, which will be verified by GISH. Once homozygous recombinants have been obtained they will be screened for their resistance to WSMV and TMV.

Development of wheat–Elymus trachycaulus translocation lines with resistance to barley yellow dwarf virus.

Bernd Friebe and Bikram S. Gill.

Barley yellow dwarf virus is a devastating disease of bread wheat worldwide and is vectored by several aphid species. Average yield losses are between 1 and 3%, although yield losses higher than 10% have been reported. Only two genes conferring resistance to BYDV have been reported in wheat. *Bvd1* confers reduced infection to BYDV and was mapped to the short arm of wheat chromosome 7D, and *Bvd2* was derived from *Th. intermedium* and was transferred to wheat in the form of a T7DS·7DL-7Ai#1L translocation. Our previous work identified a new source of BYD resistance derived from *E. trachycaulus*, which is a tetraploid wild relative of bread wheat (2n=4x=28, S^{t}S^{t}H^{t}H^t). In 1992, we produced an alloplasmic wheat–*E. trachycaulus* translocation T7AL·7AS-1StS translocation consisting of the long arm of wheat chromosome 7A, a proximal part of 7AS and a distal segment derived from 1S^{t}S that confers resistance to BYDV. However, the 1S^{t}S segment cannot compensate for the missing 7AS segment in this translocation, causing duplications and deficiencies and, thus, is agronomically undesirable. From the cross 'CSM1B/TA5534', we have selected plants with 2n = 41 chromosomes that were monosomic for 1B and heterozygous for 7A and T7AL·7AS-1S^{t}S that were crossed

with *ph1b*. In the next growing season, we will select plants with 2n = 41 chromosomes that are homozygous for *ph1b*, monosomic for 1B, and heterozygous for chromosomes 7A and T7AL·7AS-1S^{t}S. Targeted homoeologous recombination between 1S^{t}S and 1BS can occur in these genotypes. We have also crossed the T7AL·7AS-1S^{t}S translocation stock directly with *ph1b*. The F1 was backcrossed with *ph1b* and in the next season, we will identify plants that homozygous for *ph1b* and heterozygous for chromosomes 7A and T7AL·7AS-1S^{t}S. In these genotypes, homoeologous recombination between the 1StS segment and the homoeologous short arm segments of group-1 chromosomes can occur.

Stripe rust and leaf rust resistance from Ae. geniculata.

Vasu Kuraparthy, Shilpa Sood, Deven R. See, and Bikram S. Gill.

This goatgrass is widespread in the eastern Mediterranean and southwest Asia region from western Iraq, Syria, and Jordan, through Israel and Lebanon, and the island of Cyprus. The grass is common in southern Europe and Africa north of the Sahara Desert. This species has been introduced into parts of northwest and central Europe and the United States. Aegilops geniculata has immunity to most of the diseases and pests that attack wheat, including the powdery mildew and leaf rust fungi, Hessian fly, and greenbug. WGGRC scientists have been introgressing genetic material from this grass for over 12 years. Recently, we transferred new leaf rust resistance genes *Lr57* and stripe resistance gene *Yr40* that are inherited as a single block. Cleaved amplified polymorphic sequence (CAPS) markers were developed as diagnostic PCR-based markers for marker-assisted transfer of the *Lr57* and *Yr40* genes into hard red winter wheats. Two different CAPS markers were developed based on the EST marker XBF200555 diagnostically detecting the alien introgressed segment in T5DL·5DS-5MgS(0.95). BC_3F_2 plants segregating for rust resistance were evaluated in the field at two locations in Manhattan in 2008 but were still segregating. We have now isolated homozygous $BC_3F_{2:3}$ and BC_3F_4 lines for the two rust-resistance genes and these will be further evaluated in the field in 2009 for subsequent germ plasm release.

Production of compensating Robertsonian Haynaldia villosa D-genome translocations.

Bernd Friebe, Lili Qi, Jamie J. Wilson, and Bikram S. Gill.

Haynaldia villosa is a diploid, annual wild relative of bread wheat and a promising source for agronomically important traits including disease and pest resistance and grain-quality characteristics. Resistance to powdery mildew, curl mite colonization, and spindle streak mosaic virus has been transferred from *H. villosa* and used in wheat improvement. Resistance to stem rust, an emerging threat to wheat production, also has been identified (Pumphrey MO, unpublished results). We have initiated a project aimed at producing a complete set of 14 compensating, whole-arm, Robertsonian translocations involving V- and D-genome chromosomes of wheat. The strategy involves crossing the wheat D-genome monosomic stocks (20''+D') with the disomic chromosome addition lines (DA) DA1V to DA7V (21''+V'). The F_1 plants with the chromosome constitution of 20''+D'+V', double monosomic for a D-genome and a V-genome chromosome, will be selected and allowed to self. In such plants, monosomic chromosomes frequently misdivide at the centromere and broken chromosomes fuse to form translocation chromosomes at a rate of 5 % or even higher. Progenies of such plants will be screened by molecular markers, C-banding, and GISH analyses to identify plants with compensating translocations, which will be selfed and screened for homozygous translocation stock. To date, we have produced Robertsonian translocations involving chromosomes 1D/1V (T1DL·1VS, T1DS·1VL), 4D/4V (T4DL·4VS, T4DS·4VS), 5V/5D (T5DL·5VS), 6A/6V (T6AL·6VS, T6AS·6VL), and 7D/7V (T7DS·7VL). Once complete, this set will provide a useful and efficient tool to sample the genetic variability of this species.

Chromosome specific bacterial artificial chromosome libraries for wheat physical mapping.

Sunish K. Sehgal, Wanlong Li, Pablo Rabinowicz, Jaroslav Dolezel, Ming-Cheng Luo, and Bikram S. Gill.

We are working with Dr. J. Dolezel, Czech Republic, to make chromosome-specific libraries for physically mapping the wheat genome. Twenty thousand seeds of all double ditelosomic stocks of Chinese Spring wheat and several ditelosomic stocks (3A, 1A, 1D, 3D, 4A, and 2A) were sent to the Dolezel laboratory. Using flow cytometry, we have developed two BAC libraries each for chromosome arm 3AS (110,592 clones) and 3AL (110,592 clones) and three BAC libraries (294,912 clones) for chromosomes 1D, 4D, and 6D (size fraction 1) of Chinese Spring wheat.

The BAC library for chromosome arm 3AS (55,296 clones) has been fingerprinted with a SNaPshot-based, high-throughput technique. After removing the clones with very small inserts and cross contamination, 47,063 fingerprinted BACs were used for contig assembly with the FPC computer program. There are 1,677 contigs and 11,939 singletons providing 7.5-fold coverage of 3AS. The largest contig has 417 BAC clones and is ~2.7 MB in length. We now are fingerprinting two BAC libraries, the second BAC library for 3AS (55,296 clones) and the first BAC library for chromosome arm 3AL (55,296 clones) to complete the physical map of chromosome 3A with 15x coverage. Simultaneously, fingerprinting of the first 1D, 4D, and 6D libraries (26,112 clones) also has been initiated, and a 15x physical map of these chromosomes will be developed.

Six-dimensional BAC pools were developed to integrate the genetic and physical maps in an efficient and cost-effective manner. This pooling strategy involved constructing a block of 68 (384-wells) plates in a '32x24x34' plate array creating 190 pools of BAC DNA (~6.0 chromosome arm equivalents). ESTs showing high homology with the corresponding regions in rice, Brachypodium, and barley were used to design 1,240 EST–STS markers. Nearly 400 EST–STS markers have been mapped to individual BAC clones and BAC contig(s).

Personnel.

Dr. Lili Qi joined the USDA–ARS Northern Crop Science Laboratory in November, 2008. Dr. Wanlong Li is now an assistant professor at South Dakota State University, Brookings. Two graduate students completed their thesis work in December, 2008. Shilpa Sood, Ph.D., dissertation title 'Molecular characterization of threshability genes in wheat' and Jamie J. Wilson, M.S. thesis title 'Production of wheat–*Haynaldia villosa* Robertsonian translocations'. New visiting scientists in the WGGRC laboratories include Sundeep Kumar, Sardar Vallabh Bhai Patel University of Agriculture & Technology, Meerut, India, and Cheng Liu, University of Electronic Science and Technology, Chengdu, Sichuan, PR China.

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