

**USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY07 Final Performance Report (approx. May 07 – April 08)
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Cover Page

PI:	Bikram Gill
Institution:	Kansas State University
Address:	Department of Plant Pathology 4024 Throckmorton Manhattan, KS 66506-5502
E-mail:	bsg@ksu.edu
Phone:	785-532-1391
Fax:	785-532-5692
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FY07 ARS Award Amount:	\$ 29,268

USWBSI Individual Project(s)

USWBSI Research Area *	Project Title	ARS Adjusted Award Amount
HGR	Alien Chromosome Engineering and the Deployment of a Novel Source of Fusarium Head Blight Resistance in Wheat.	\$29,268
	Total Award Amount	\$ 29,268

Principal Investigator

Date

* CBCC – Chemical, Biological & Cultural Control
 EEDF – Etiology, Epidemiology & Disease Forecasting
 FSTU – Food Safety, Toxicology, & Utilization of Mycotoxin-contaminated Grain
 GET – Genetic Engineering & Transformation
 HGR – Host Genetics Resources
 HGG – Host Genetics & Genomics
 IIR – Integrated/Interdisciplinary Research
 PGG – Pathogen Genetics & Genomics
 VDUN – Variety Development & Uniform Nurseries

Project 1: Alien Chromosome Engineering and the Deployment of a Novel Source of Fusarium Head Blight Resistance in Wheat.

1. What major problem or issue is being resolved and how are you resolving it?

A potential hazard to FHB resistance breeding is that only a few sources, mainly Sumai 3 and its derivatives, are now widely used around the globe. Thus, additional sources of resistance are needed to broaden the genetic basis of FHB resistance. FHB resistance was identified in the alien species *Leymus racemosus* (syn. *Elymus giganteus*). *L. racemosus* (Lr) chromosomes were isolated as single chromosome additions to bread wheat. Chromosome engineering of these lines was attempted and nine wheat-*Leymus* translocation lines were produced, five using irradiation treatment, and four using Gc gene action (Chen et al. 2005). Three lines were reported to have resistance to FHB. However, all translocations were of non-compensating type, leading to duplications/deficiencies and, hence, may not be deployed in agriculture. We further analyzed a total 58 wheat-*Leymus* introgression lines for their resistance to FHB disease. We discovered a genetically compensating translocation involving the long arm of wheat chromosome 7A and the short arm of *Leymus* chromosome 7Lr#1 (T7AL·7Lr#1S) conferring resistance to FHB. This translocation may be directly used in breeding programs. Our studies also revealed that three previously reported wheat-*Leymus* non-compensating translocations involved the same *Leymus* chromosome arm-7Lr#1S. A new FHB resistance gene located in the short arm of chromosome 7Lr#1 was named as *Fhb3*. Currently, we are using chromosome engineering to reduce linkage drag of the *Leymus* 7Lr#1S segment in wheat background.

**2. List the most important accomplishment and its impact (how is it being used?).
Complete all three sections (repeat sections for each major accomplishment):**

Accomplishment: A wheat-*Leymus* translocation line (T09) conferring FHB resistance was identified as a genetically compensating translocation involving the long arm of wheat chromosome 7A and the short arm of *Leymus* chromosome 7Lr#1 (T7AL·7Lr#1S) by C-banding, genomic in situ hybridization, and RFLP analyses. Another two resistant wheat-*Leymus* introgression lines (T01 and T14) were identified as double translocations. Lines T01 (2n = 44) and T14 (2n = 44) each had two pairs of independent translocation chromosomes. T01 had T4BS·4BL-7Lr#1S + T4BL-7Lr#1S·5Lr#1S. T14 had T6BS·6BL-7Lr#1S + T6BL·5Lr#1S. The three translocation lines, T01, T09, and T14, and the disomic addition 7Lr#1 were consistently resistant to FHB in greenhouse point-inoculation experiments, whereas the disomic addition 5Lr#1 was susceptible. The data indicated that a novel FHB resistance gene from *Leymus*, designated *Fhb3*, resides in the distal region of the short arm of chromosome 7Lr#1, because the resistant translocation lines share a common distal segment of 7Lr#1S. Three PCR-based markers, BE586744-STS, BE404728-STS, and BE586111-STS, specific for 7Lr#1S were developed to expedite marker-assisted selection in breeding programs. The compensating translocation T7AL·7Lr#1S was backcrossed twice to adapted wheat cultivars Overlay and Jagger. A total of 192 progeny homozygous for translocation T7AL·7Lr#1S were selected by molecular markers from 436 BC₁F₂ plants and they will be evaluated for FHB resistance and its effect on DON accumulation in a field nursery in Fall 2008.

Chromosome engineering was initiated to reduce genetic linkage drag associated with translocation T7AL·7Lr#1S. This line was crossed twice with the *ph1b* mutant stock. 154 BC₁ plants were screened using molecular markers to assay for *ph1b* and T7AL·7Lr#1S. Sixty-one plants were found to be homozygous *ph1b/ph1b* and heterozygous for the translocation chromosome T7AL·7Lr#1S/7A. These plants were either backcrossed with Overlay and Danby or selfed. Large recombinant populations of 1,400 BC₂ seeds and more than 8,000 BC₁F₂ seeds were developed. In homozygous *ph1b* genotypes, the alien 7Lr#1S arm with *Fhb3* is expected to recombine with homoeologous wheat arm 7AS. Work is ongoing to identify wheat-*Leymus* recombinants with smaller alien segments that still retain the FHB resistance gene *Fhb3*.

Impact: *Fhb3* is the first FHB resistance gene identified from an alien species, *Leymus racemosus*. This is a novel gene different from previously reported FHB resistance genes in *Triticum aestivum*, providing a new source for gene pyramiding in breeding programs. The advantage of the translocation T7AL·7Lr#1S is its large phenotypic effect and simple inheritance thereby facilitating its rapid deployment in wheat breeding programs. Three PCR-based markers developed will facilitate marker-assisted selection.

As a result of that accomplishment, what does your particular clientele, the scientific community, and agriculture as a whole have now that they didn't have before?:

1. Breeders have an additional source of FHB resistance carrying *Fhb3* that was not previously known or well-characterized.
2. Molecular markers to assay *Fhb3* gene in breeding programs.
3. Prebreeding of *Fhb3* with elite wheats.
4. Publication of a refereed paper describing the methodology of alien introgression.
5. The advanced germplasm will be released to plant breeders. The published data represent an important technology transfer because wheat geneticists and breeders can use the germplasm and associated markers in breeding programs.

Include below a list of the publications, presentations, peer-reviewed articles, and non-peer reviewed articles written about your work that resulted from all of the projects included in the grant. Please reference each item using an accepted journal format. If you need more space, continue the list on the next page.

L.L. Qi, M.O. Pumphrey, B. Friebe, P.D. Chen and B.S. Gill, 2008 Molecular cytogenetic characterization of alien introgressions with gene *Fhb3* for resistance to *Fusarium* head blight disease of wheat. *Theor Appl Genet* (in press)

L.L. Qi, M.O. Pumphrey, B. Friebe, P.D. Chen and B.S. Gill, 2007 Molecular characterization of a wheat-*Leymus* compensating translocation line conferring resistance to *Fusarium* head blight. *Proceeding of 2007 National Fusarium Head Blight Forum* p: 225