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

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Fiscal Year:	2007
USDA-ARS Agreement ID:	59-0790-4-116
USDA-ARS Agreement Title:	Molecular Genetic Approaches to Develop Scab Resistance.
FY07 ARS Award Amount:	$ 100,523

USWBSI Individual Project(s)

USWBSI Research Area[*]	Project Title	ARS Adjusted Award Amount
GET	Developing and Characterizing Transgenic Wheat for Scab Resistance.	$41,986
HGG	Mechanisms and Essential Genes for Resistance to Fusarium Head Blight.	$ 58,537
	Total Award Amount	**$ 100,523**

Principal Investigator Date

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[*] 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

(Form FPR07)

Project 1: *Developing and Characterizing Transgenic Wheat for Scab Resistance.*

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

Fusarium head blight (FHB or scab) is a disease that can devastate wheat. To enhance FHB resistance in wheat, we are developing transgenic wheat lines with potential resistance genes and testing these lines for scab resistance.

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:

1) We identified two wheat lines carrying a chitinase transgene that exhibited enhanced resistance in the field. A paper was published in the Journal of Experimental Botany describing the chitinase lines.
2) We also identified wheat transgenic lines carrying a ribosomal inhibitor protein (RIP), ß-1,3-glucanase/tlp, and RIP/tlp transgenes that exhibited enhanced resistance in the field.
3) We identified transgenic wheat lines carrying a glutathione-S-transferase, a lipid transfer protein, a JAMyb transcription factor, and a germin-like protein that exhibited enhanced resistance in the greenhouse.

Impact:

We identified transgenic wheat lines that exhibited enhanced resistance in the greenhouse and field.

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?:

The scientific community now has access to transgenic wheat lines that exhibit reduced FHB severity. These lines provide another source of variation for FHB resistance. In addition, the scientific community now has new information on the functional impact of a variety of genes on FHB resistance.

Project 2: *Mechanisms and Essential Genes for Resistance to Fusarium Head Blight.*

1. **What major problem or issue is being resolved and how are you resolving it?**
   Fusarium head blight (FHB or scab) is a disease that can devastate the small grains wheat and barley. The wheat and barley transformation efforts have a limited number of genes that have the potential to reduce FHB. In addition, there is a limited amount of information pertaining to the molecular genetic interaction between the small grains and *Fusarium graminearum*. Our goal is to identify the mechanisms and essential genes for wheat and barley scab resistance.

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

Accomplishments:

1) Described the impact of deoxynivalenol treatment on barley. We identified 135 barley genes that respond specifically to DON treatment. These genes encode proteins involved in trichothecene detoxification and transporter function, cell death and ubiquitination processes. A manuscript is in preparation describing this work that we plan to submit to Molecular Plant Pathology. All data will be released on the web at PLEXdb (http://www.plexdb.org/).
2) To conduct functional tests of genes potentially providing resistance, we established virus-induced gene silencing (VIGS) assays in my lab. We used VIGS to test a variety of potential FHB resistance genes that we identified in our gene expression (GeneChip) experiments. We tested four different transcription factors that have been identified in our GeneChip experiments and are involved in other plant-pathogen interactions. Our first experiments have been completed and we are evaluating the results and repeating the experiments. We also developed VIGS constructs for three other genes.
3) Reexamined data from our GeneChip experiments focused on a near-isogenic line pairs carrying resistant and susceptible alleles at FHB resistance QTL in barley and wheat. A manuscript will be submitted in July to Molecular Plant-Microbe Interactions describing the work from the wheat near-isogenic line. All data will be released on the web at PLEXdb (http://www.plexdb.org/).
4) Prepared BAC libraries for *F. graminearum* for physical mapping the genome and genome sequencing. Papers in Genome and Science were published using the BAC libraries.
5) My laboratory collaborated with Dr. Kevin Smith (University of Minnesota) to fine map a barley QTL region associated with FHB resistance, and identified a useful line and associated markers for barley breeding. A paper was published on this topic in Theoretical and Applied Genetics.

Impact:

(Accomplishment 1) Identified barley genes that respond to DON treatment. These genes potentially control a variety of cellular processes including: trichothecene detoxification and transport, cell death and ubiquitination processes.
(Accomplishments 2) We established VIGS in my laboratory to test gene function. We began to use VIGS to test the impact of four genes on FHB resistance.
(Accomplishment 3) We are identifying genes that differentiate resistant from susceptible interactions, and may be involved in providing resistance.

(Accomplishment 4) The physical map and genome sequence of *F. graminearum* is an important resource for future studies of the fungus.
(Accomplishment 5) My laboratory was involved with developing markers and a genetic line that is being used in the University of Minnesota barley-breeding program.

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?:
The scientific community has access to an unprecedented amount of expression data that defines the barley-*F. graminearum* interaction, the barley-trichothecene interaction and the wheat-*F. graminearum* interaction. In addition, candidate genes have been identified for involvement in FHB resistance. The barley line carrying the FHB resistance QTL and the development of the associated markers are useful for barley breeding. The *F. graminearum* physical map and genome sequence provided an important resource for future understanding of the fungus.

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.

Refereed Publications:

Chang, Y-L., S. Cho, H.C. Kistler, H-C. Sheng and G.J. Muehlbauer. 2007. Bacterial artificial chromosome-based physical map of *Gibberella zeae* (*Fusarium graminearum*). *Genome* 50:954-962.

Nduulu, L.M., A. Mesfin, G.J. Muehlbauer and K.P. Smith. 2007. Analysis of the chromosome 2(2H) region of barley associated with the correlated traits Fusarium head blight resistance and heading date. *Theor. Appl. Genet.* 115:561-570.

Boddu, J., S. Cho and G.J. Muehlbauer. 2007. Transcriptome analysis of trichothecene-induced gene expression in barley. Mol. Plant-Microbe Interact. 20:1364-1375.

Cuomo, C.A., U. Güldener, J-R. Xu, F. Trail, B.G. Turgeon, A. Di Pietro, J.D. Walton, L-J. Ma, S.E. Baker, M. Rep, G. Adam, J. Antoniw, T. Baldwin, S. Calvo, Y-L. Chang, D. DeCaprio, L.R. Gale, S. Gnerre, R.S. Goswami, K. Hammond-Kosack, L.J. Harris, K. Hilburn, J.C. Kennell, S. Kroken, J.K. Magnuson, G. Mannhaupt, E. Mauceli, H.-W. Mewes, R. Mitterbauer, G. Muehlbauer, M. Münsterkötter, D. Nelson, K. O'Donnell, T. Ouellet, W. Qi, H. Quesneville, M.I.G. Roncero, K-Y. Seong, I.V. Tetko, M. Urban, C. Waalwijk, T.J. Ward, J. Yao, B.W. Birren, and H.C. Kistler. 2007. The *Fusarium graminearum* genome reveals a link between localized polymorphism and pathogen specialization. *Science* 317:1400-1402.

Shin, S., C.A. Mackintosh, J. Lewis, S.J. Heinen, L. Radmer, R. Dill-Macky, G.D. Baldridge, R.J. Zeyen and G.J. Muehlbauer. 2008. Transgenic wheat expressing a barley class II chitinase gene has enhanced resistance to Fusarium Head Blight. *J. Exp. Bot.* 59:2371-2378.

Jia, H., S. Cho and G.J. Muehlbauer. Transcriptome analysis of the wheat 3BS Fusarium head blight resistance QTL during *Fusarium graminearum* infection. In preparation for submission to *Molecular Plant-Microbe Interactions*.

Gardiner, S., J. Boddu and G.J. Muehlbauer. Deoxynivalenol-induced gene expression in barley. In preparation for submission to *Molecular Plant Pathology*.

Abstracts:

Jia, H., S. Cho and G.J. Muehlbauer. 2008. Transcriptome analysis of wheat near-isogenic line pair carrying fusarium head blight resistant and susceptible alleles. Plant and Animal Genome Meeting Abstracts.

Gardiner, S.A., H. Jia, J. Boddu and G. J. Muehlbauer. 2008. Microarray analysis of deoxynivalenol-induced gene expression in susceptible (cv. Morex) barley. American Phytopathological Society Meeting Abstracts

Shin, S.H., J.M. Lewis, C.A. Mackintosh, A. Elakkad, K. Wennberg, S.J. Heinen, R. Dill-Macky, G. J. Muehlbauer. 2007. Transgenic wheat with enhanced resistance to Fusarium Head Blight. National Scab Forum Abstracts.

Boddu, J., H.C. Kistler and G.J. Muehlbauer. 2007. Role of trichothecenes in the barley-*Fusarium graminearum* interaction. National Scab Forum Abstracts.

Jia, H., B.J. Steffenson, and G.J. Muehlbauer. 2007. Effects of agronomic and morphological characters on FHB severity, deoxynivalenol and ergosterol concentration in near-isogenic line pairs of barley. National Scab Forum Abstracts.

Oral Presentations:

"The challenge for barley genomics: integrating phenotypes and genotypes" at BASF Plant Science LLC, Research Triangle Park, NC

"Genomics of the Triticeae-*Fusarium graminearum* interaction" at the Danforth Center, St. Louis, MO