USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY08 Final Performance Report (approx. May 08 – April 09)
July 15, 2009

Cover Page

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Fiscal Year:	2008
USDA-ARS Agreement ID:	59-0790-4-116
USDA-ARS Agreement Title:	Molecular Genetic Approaches to Develop Scab Resistance.
FY08 USDA-ARS Award Amount:	$ 71,491

USWBSI Individual Project(s)

USWBSI Research Category[*]	**Project Title**	**ARS Adjusted Award Amount**
BAR-CP	Characterize and Map Barley Genes that Respond to Fusarium graminearum Infection.	$48,399
BAR-CP	Identify Barley Genes that Respond to Deoxynivalenol.	$ 23,092
	Total Award Amount	**$ 71,491**

Principal Investigator Date

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[*] MGMT – FHB Management
FSTU – Food Safety, Toxicology, & Utilization of Mycotoxin-contaminated Grain
GDER – Gene Discovery & Engineering Resistance
PBG – Pathogen Biology & Genetics
BAR-CP – Barley Coordinated Project
HWW-CP – Hard Winter Wheat Coordinated Project
VDHR – Variety Development & Uniform Nurseries – Sub categories are below:
- SPR – Spring Wheat Region
- NWW – Northern Winter Wheat Region
- SWW – Southern Sinter Wheat Region

(Form FPR08)

Project 1: *Characterize and Map Barley Genes that Respond to Fusarium graminearum Infection.*

1. **What major problem or issue is being resolved relevant to Fusarium head blight (scab) and how are you resolving it?**

Fusarium head blight (FHB or scab), caused by *Fusarium graminearum*, is a disease that can devastate the small grains wheat and barley. There is a limited amount of information pertaining to the molecular genetic interaction between barley and *F. graminearum.* Our goal is to identify and map barley genes that respond to *F. graminearum* infection.

Previously, we conducted a large set of microarray experiments in barley and wheat aimed at identifying genes that are involved in resistance or susceptibility to FHB. We also identified a large set of barley genes that respond to deoxynivalenol treatment (see below). We have carefully examined these gene lists and identified a set of genes that have the potential to play a role in the barley-*F. graminearum* interaction. We have sequenced 40 genes from a set of barley mapping population parents. Polymorphisms are being identified for mapping. These genes will be mapped in barley mapping populations. The outcomes from this work will be markers for breeding programs, potential resistance genes, and increased understanding of the barley-*F. graminearum* interaction.

In collaboration with Kevin Smith and Brian Steffenson, we identified a set of germplasm that exhibits variation for scab resistance and susceptibility. These lines were screened with DArT markers and we used that data to identify a core set of genotypes that will serve as a representative set for sequencing genes that have the potential to exhibit resistance or susceptibility.

We conducted viral induced gene silencing experiments with a set of wheat genes. We identified one gene, NFX-1, that appears to play a role in susceptibility of FHB.

2. **List the most important accomplishment and its impact (i.e. how is it being used) to minimize the threat of Fusarium head blight or to reduce mycotoxins. Complete both sections (repeat sections for each major accomplishment):**

Accomplishment (1):

We used our previous microarray studies to identify 40 genes that respond to *F. graminearum* infection and/or DON accumulation. We reexamined data from our GeneChip experiments focused on near-isogenic line pairs carrying resistant and susceptible alleles at FHB resistance QTL in barley and wheat. A manuscript is in press at Molecular Plant-Microbe Interactions describing the work from the wheat near-isogenic line pair. Two manuscripts describing the barley response to DON accumulation and *F. graminearum* are in preparation for submission to Molecular Plant-Microbe Interactions and Functional and Integrative Genomics, respectively. The data for the wheat experiment is on the web at PLEXdb (http://www.plexdb.org/) and the data for the barley experiments will be released as soon as the manuscripts are accepted.

Impact:

We have published one of our microarray studies (Jia et al., in press) that provide data for scientists working on FHB. Two additional manuscripts are in preparation for submission. We used these studies as well as previous studies to identify genes that are potential candidates for resistance/susceptibility.

Accomplishment (2):

We sequenced 40 genes that exhibit a response to *F. graminearum* infection or DON accumulation from a set of barley mapping population parents and identified polymorphisms for mapping.

Impact:

The identification of polymorphisms for genes that respond to F. graminearum infection or DON accumulation will be useful for mapping these genes.

Accomplishment (3):

We genotyped a set of 102 barley genotypes (22 susceptible and 80 resistant to FHB) with 728 DArT markers and characterized the genetic variation in a large set of barley germplasm. We selected a set of lines that represents the genetic diversity of the collection for sequencing genes that may exhibit resistance or susceptibility.

Impact:

The characterization of the germplasm set will be useful for breeders and geneticists. Breeders and geneticists will know the genetic differences between lines carrying resistance and be able to intelligently select lines for mapping and breeding. We have also used this information to select lines for gene sequencing with the goal to associate specific alleles with resistance/susceptibility.

Accomplishment (4):

We identified a wheat NFX-1 gene that may be a susceptibility factor.

Impact:

Downregulating the NFX-1 (potential susceptibility gene) gene in transgenic wheat and barley could be a strategy for controlling FHB.

Project 2: *Identify Barley Genes that Respond to Deoxynivalenol.*

1. **What major problem or issue is being resolved relevant to Fusarium head blight (scab) and how are you resolving it?**

Fusarium head blight (FHB or scab), caused by *Fusarium graminearum*, is a disease that can devastate the small grains wheat and barley. During infection, *F. graminearum* produces deoxynivalenol (DON), a trichothecene mycotoxin. There is a limited amount of information pertaining to the molecular genetic interaction between the small grains and *Fusarium graminearum* and in particular the response to DON accumulation. Our goal is to identify genes that respond to DON accumulation.

We conducted a microarray experiment to identify gene transcripts that respond to DON accumulation. We identified 255 genes that respond to DON treatment. In collaboration with Gerhard Adam we have also shown that DON is converted to the less toxic DON-3-O-glucoside in barley.

We have also cloned five genes encoding UDP-glucosyltransferases that respond to DON accumulation and sent them to Gerhard Adam for functional assays in yeast to test for the ability of these enzymes to detoxify trichothecenes. One of these UDP-glucosyltransferase genes confers resistance in yeast to DON. We developed transgenic Arabidopsis carrying this gene and it confers resistance to DON. Currently, we are developing transgenic wheat with this gene.

2. **List the most important accomplishment and its impact (i.e. how is it being used) to minimize the threat of Fusarium head blight or to reduce mycotoxins. Complete both sections (repeat sections for each major accomplishment):**

Accomplishment (1):
Described the impact of deoxynivalenol treatment on barley. We identified 255 barley genes that respond specifically to DON treatment. We also showed that barley can conjugate DON to a glucoside to create a less toxic form of the mycotoxin. A manuscript is in preparation describing this work that we plan to submit to Molecular Plant-Microbe Interactions. All data will be released on the web at PLEXdb (http://www.plexdb.org/).

Impact:
The understanding of the genes that respond to DON accumulation and how the plant detoxifies DON will be important for designing novel strategies for resistance. Data will be provided to the scientific community.

Accomplishment (2):
We identified a barley UDP-glucosyltransferase that confers DON resistance to yeast and Arabidopsis.

Impact:
The barley UDP-glucosyltransferase gene provides a proven gene that can be used to develop transgenic wheat and barley that exhibit FHB resistance.

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.

Publications:

Jia, H., S. Cho and G.J. Muehlbauer. 2009. Transcriptome analysis of the wheat 3BS Fusarium head blight resistance QTL during *Fusarium graminearum* infection. *Molecular Plant-Microbe Interactions* (In press)

Gardiner, S., J. Boddu, F. Berthiller, C. Hametner, R. Stupar, G. Adam, and G.J. Muehlbauer. Transcriptome analysis of the barley-deoxynivalenol interaction. In preparation for submission to *Molecular Plant-Microbe Interactions*.

Massman, J., B. Cooper, R. Horsley, S. Neate, R. Dill-Macky, S. Chao, Y. Dong, P. Schwarz, G.J. Muehlbauer and K.P. Smith. Genome-wide association mapping of Fusarium head blight resistance in contemporary barley breeding germplasm. In preparation for submission to *Theor. Appl. Genet*.

Jia, H., S. Cho, H. Bilgic, K.P. Smith and G.J. Muehlbauer. Transcriptome analysis of three barley near-isogenic line pairs carrying contrasting alleles for different Fusarium head blight resistance QTLs . In preparation for submission to *Functional and Integrative Genomics*.

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. Boddu, A. Cole, G. Adam, and G. J. Muehlbauer. 2008. Rapidly identify and test scab resistance genes. National Scab Forum Abstracts.

Gardiner, S.A., J. Boddu, F. Berthiller, R. Stupar, G. Adam and G.J. Muehlbauer. 2008. Barley exhibits a variety of resistance mechanisms to deoxynivalenol. National Scab Forum Abstracts.

Steiner, B., A, Limmongkon, K. Schiessl, M. Lemmens, H. Jia, G.J. Muehlbauer, and H. Buerstmayr. 2009. Gene expression analysis of related wheat lines with contrasting levels of head blight resistance after Fusarium graminearum inoculation. International Triticeae Mapping Initiative Workshop Abstracts

Schweiger, W., S. Shin, J. Boddu, B. Steiner, A. Limmongkon, M. Lemmens, H. Buerstmayr, G.J. Muehlbauer, and G. Adam. 2009. Functional testing of candidate UDP glucosyltransferases from wheat and barley for deoxynivalenol inactivation capability by expression in yeast. International Society for Mycotoxicology Abstracts.

If your FY08 USDA-ARS Grant contained a VDHR-related project, include below a list all germplasm or cultivars released with full or partial support of the USWBSI. List the release notice or publication. Briefly describe the level of FHB resistance. If this is not applicable (i.e. no VDHR-related project) to your FY08 grant, please insert 'Not Applicable' below.

Not applicable.