

**USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY11 Final Performance Report
July 13, 2012**

Cover Page

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Fiscal Year:	FY11
USDA-ARS Agreement ID:	59-0206-9-055
USDA-ARS Agreement Title:	Enhance Variety Development of Scab Resistant Hard Winter Wheat Varieties in Nebraska.
FY11 USDA-ARS Award Amount:	\$ 56,293

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
HWW-CP	To Enhance Variety Development of Scab Resistant Hard Winter Wheat Varieties and their Management in Nebraska to Reduce DON.	\$ 53,976
HWW-CP	Using Association Mapping to Identify and Validate New FHB Resistance QTL and Integrate the QTL into HWW.	\$ 2,317
	Total ARS Award Amount	\$ 56,293

Principal Investigator

Date

* 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
 DUR-CP – Durum Coordinated Project
 HWW-CP – Hard Winter Wheat Coordinated Project
 VDHR – Variety Development & Uniform Nurseries – Sub categories are below:
 SPR – Spring Wheat Region
 NWW – Northern Soft Winter Wheat Region
 SWW – Southern Soft Red Winter Wheat Region

Project 1: *To Enhance Variety Development of Scab Resistant Hard Winter Wheat Varieties and their Management in Nebraska to Reduce DON.*

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

The main thrust of this grant is to provide excellent new cultivars with scab tolerance. Scab remains a major disease in eastern Nebraska and one that extends into our major wheat producing regions of southwest and central Nebraska. In 2011, we made the decision that in the past we have made too many “exotic” crosses involving diverse sources of resistance. This decision was based upon research showing that *Fhb1* did not have deleterious effects in hard winter wheat backgrounds. The likelihood of finding elite lines with good scab tolerance from these exotic crosses was too low to be effective. As such, we are concentrating on crossing elite lines with native tolerance (Art, Overland, Hitch, Everest, Lyman) to backcross lines with *Fhb1* (mainly Wesley *Fhb1* created by Dr. Guihua Bai) and *Fhb3* (e.g. Jagger *Fhb3*). We are also using spring wheat lines with excellent scab resistance as they have the right end-use quality characteristics and we can easily remove spring growth habit lines by growing segregating populations in the field. We are also using BC1 instead of three way crosses to continue to focus the variation into elite backgrounds. All of our F₆ lines are screened for *Fhb1*. Of the 280 lines in this generation, 16 are homozygous or heterozygous for *Fhb1*. Of these 16 lines, four have *Sr24*, only three have rye translocations (1A.1R or 1B.1R, convey poor end-use quality), eight have the favorable Glu-D1 allele for superior end-use quality, and 13 are resistant to Soilborne Mosaic Virus. Hence the *Fhb1* lines have excellent disease resistance (scab, stem rust, and Soilborne Mosaic Virus occur in the same region) and potentially end-use quality. These lines will continue to augment our breeding efforts for scab tolerance. In addition, we are extensively evaluating *Fhb1* lines created from Dr. Bakhsh’s dissertation. We are expanding our efforts on marker based breeding because our climate is highly variable. In 2011, we lost our scab screening nursery to hail. In 2012, the earliest season in history, despite having everything set-up and used as predicted to induce a scab epidemic, the hot, dry winds appear to have reduced our scab incidence in the field screen.

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: We determined for hard winter wheat that the *Fhb1* gene or genes closely linked to it do not have deleterious effects on wheat productivity in Nebraska.

Impact: This finding has led to a reorganization of our crossing strategy and to a more efficient selection strategy. The most difficult part of breeding for scab tolerance is to have good field assays to identify native or major gene resistance in the progeny of elite crosses. We believe that we can increase the rate of gain and the development of truly scab tolerant/resistant germplasm. Our breeding program continues to develop adapted lines with *Fhb1* and other major scab tolerant/resistant major genes.

FY11 (approx. May 11 – May 12)
PI: Baenziger, P. Stephen
USDA-ARS Agreement #: 59-0206-9-055

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Accomplishment: Though not directly funded by this project, our work with lactoferrin as a transgenic approach to reducing Fusarium head blight was published (Han et al., 2012). The research was previously funded by the Initiative.

Impact: The research may lead to novel approaches for scab resistant wheat when transgenic lines are commercially acceptable.

Project 2: *Using Association Mapping to Identify and Validate New FHB Resistance QTL and Integrate the QTL into HWW.*

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

Major scab epidemics have occurred in the HWW region. Genetically improved seed coupled with appropriate management practices are the quickest and most cost effective ways to reduce DON in the grain supply. However, little is known concerning the genetic basis of native resistance in the Great Plains germplasm and how best to effectively utilize it. Using association mapping techniques, we will be able to validate reported QTLs and identify new QTLs in HWW germplasm, and move from molecular mapping to marker-assisted breeding. For this research we used selected lines from numerous sources that we have identified as being important in the creation of hard winter FHB tolerant lines. The key to this research will be to maximize the information we have already collected from our existing FHB screening nurseries, such as advanced regional lines and lines that were tested in our state variety trials. Our goal is to use 188 wheat lines including native sources of resistance (e.g. Henye, Lakin, Arapahoe, Everest, Overland, Settler CL, Lyman, Art, Hitch); DON accumulators (e.g. Harry and Trego); a series of backcross lines (Fhb1 and/or Fhb3 in Trego, Wesley, Harding, Overley, Jagger and Overland); and some accessions with various levels of FHB resistance from China and/or Japan (to look for new alleles and increase our diversity). **Phenotypic data:** All accessions are phenotyped for FHB resistance by needle inoculation in the greenhouse at KSU and SDSU, respectively and irrigated FHB winter wheat nurseries in KS, NE, and SD. Bulk samples from these phenotyping nurseries are submitted for objective FHB evaluation and DON analysis (in cooperation with Dr. Floyd Dowell). **Genotyping Using Molecular Markers:** For marker analysis, all accessions will be analyzed for structure with at least 100 genome-wide SSR markers at the USDA Genotyping Lab in Manhattan. We will also genotype the accessions using all reported markers linked to known FHB QTLs (about 50) and 9K single nucleotide polymorphism (SNP) chip for higher resolution QTL mapping. The diversity of lines should be adequate for association mapping studies and allow most important alleles to be identified, as well as some of their epistatic interactions. We believe that between the SSR and SNP markers (as well as some STS markers linked to QTLs) we will have adequate genome coverage for association mapping. **Data Analysis:** The data will be analyzed using the software developed by Dr. Dong Wang as well as others to identify major genes and epistatic gene interactions that control FHB tolerance and help reduce DON. PowerMarker software will be used to calculate values of gene diversity, and distance-based cluster analysis using the UPGMA algorithm. A database with all marker allele information will be developed for all the evaluated accessions and breeders will use them to select appropriate parents for crosses. We have chosen this approach because it directly compares our native sources of resistance (including our commercial lines), with known Asian sources of resistance at both phenotypic and genotypic levels. **Note:** the University of Nebraska role in this project is minor, mainly providing germplasm and some phenotypic data. The major project report is given by Dr. Guihua Bai.

- 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: Based upon our minor role in this effort, the accomplishments are best described by the co-PIs. Phenotypic data for FHB have been obtained from field and greenhouse experiments. About 110 SSR markers have been screened for the population. In addition, the population was also screened with 9K SNP chip from Illumina and the data scoring and analysis are in progress.

Impact: The phenotypic data of the population collected from both field and greenhouse environment will be important for breeders to better select parents for crosses because the population mainly consisted of elite breeding materials and new varieties that we use most often as parents in their crosses. The molecular data will be extremely useful to understand if our native resistance has the same or different genetic basis, hence can we incrementally increase tolerance while adding our major genes. The 9K SNP data for the population will be a useful resource for developing SNP markers linked to important QTLs in HWW.

Include below a list of 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.

In our 2010 report, we described the release of NE01481 (Husker Genetics Brand McGill) and NI04421 (Husker Genetic Brand Robidoux). No new lines were released this past year.

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.

Baenziger, P.S., R. A. Graybosch, T. Regassa, L.A. Nelson, R. N. Klein, D. K. Santra, D.D. Baltensperger, L. Xu, S. N. Wegulo, Y. Jin, J. Kolmer, Ming-shun Chen, and Guihua Bai. 2012. . Registration of ‘NE01481’ hard red winter wheat. *Journal of Plant Registrations* 6:49-53.

Baenziger, P.S., R. A. Graybosch, T. Regassa, L.A. Nelson, R. N. Klein, D. K. Santra, D.D. Baltensperger, J. M. Krall, S. N. Wegulo, Y. Jin, J. Kolmer, Ming-shun Chen, and Guihua Bai. 2012. . Registration of ‘NI04421’ hard red winter wheat. *Journal of Plant Registrations* 6:54-59.

Bakhsh, A., N. Mengistu, P.S. Baenziger, I. Dweikat, S.N. Wegulo, D. Rose, Guihua Bai, and K.M. Eskridge. Effect of Fusarium Head Blight (FHB) Resistance Gene *Fhb1* on Agronomic and End-use Quality Traits of Hard Red Winter Wheat. *Crop Science*: submitted

Bockus, W. W., Baenziger, P. S., and Berzonsky, W. 2012. Reaction of Kansas, Nebraska, and South Dakota winter wheat accessions to Fusarium head blight (FHB), 2011. (online) *Plant Disease Management Reports* 6:CF003. DOI:10.1094/PDMR06. The American Phytopathological Society, St. Paul, MN.

Han, J., K. K. Lakshman, L. C. Galvez, S. Mitra, P. S. Baenziger and A. Mitra. 2012. Transgenic expression of lactoferrin imparts enhanced resistance to head blight of wheat caused by *Fusarium graminearum*. *BMC Plant Biology* 12:33 (9 pages).

Hernandez Nopsa, J. F., P. S. Baenziger, K. M. Eskridge, K. H. S., Peiris, F. E. Dowell, S. D. Harris, and S. N. Wegulo. 2012. Differential accumulation of deoxynivalenol in two winter wheat cultivars varying in FHB phenotype response under field conditions. *Can. J. Plant Pathol.* (in press).