# 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:** | 59-0790-8-066 |
| **USDA-ARS Agreement Title:** | Molecular Characterization and Pyramiding of Novel Scab Resistance Sources Adapted to the Northern Plains Growing Region |
| **FY11 USDA-ARS Award Amount:** | $ 56,085 |

### USWBSI Individual Project(s)

| USWBSI Research Category* | Project Title | ARS Award Amount |
|---|---|---|
| HWW-CP | Simultaneously Pyramiding and Validating Multiple FHB Resistance QTLs in Different Hard Winter Wheat Backgrounds. | $ 30,719 |
| VDHR-SPR | Simultaneously Pyramiding and Validating Multiple FHB Resistance QTLs in Different Spring Wheat Backgrounds. | $ 25,366 |
| | **Total ARS Award Amount** | **$ 56,085** |

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
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:** *Simultaneously Pyramiding and Validating Multiple FHB Resistance QTLs in Different Hard Winter Wheat Backgrounds.*

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

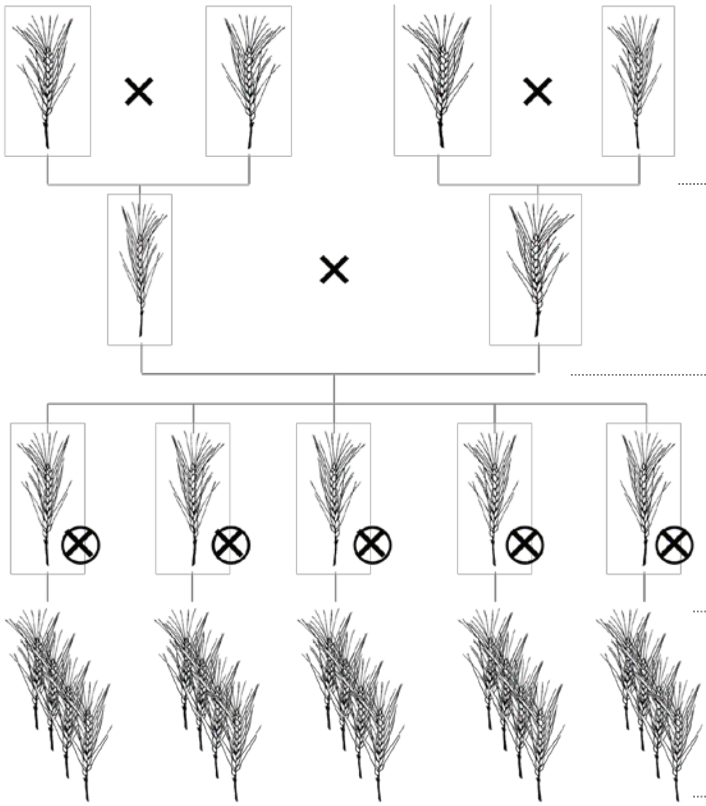
   The goal of the project was to incorporate potentially new resistance genes into the regional winter wheat breeding programs. We used a family based mapping approach to simultaneously map and incorporate multiple resistance genes into segregating early generation material.

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:** Population development and evaluation.
   *Population development (Completed):*
   Double-cross breeding populations have been developed for the purpose of pyramiding multiple FHB resistance QTL. The figure below illustrates double-cross family development, and provides detailed information on the developed populations. Founders for population development included 2 Westley-*Fhb1* backcross lines to provide *Fhb*1 in elite genetic backgrounds, as well as several other lines providing alternative sources of resistance and desirable agronomic traits (Table 1).

**Table 1.** Founder lines conferring alternative sources of resistance.

| Line | Pedigree | Resistance | Putative QTL |
|---|---|---|---|
| ERNIE | Pike/MO9965 | MR | 5A, 3B, 4BL, 2B |
| FREEDOM | GR876/OH217 | MR | 2AS |
| LYMAN | KS93U134/Arapahoe | MR | Unknown |
| OVERLAND (NE01643) | NE94482/ND8974 | MR | Unknown |
| NE06545 | KS92-946-B-15-1/Alliance | MR | Unknown |



***Founder Lines:***
*10 lines used as founders for the pedigree, including 2 Westley-Fhb1 backcross lines and lines providing alternative sources of resistance and desirable agronomic traits.*

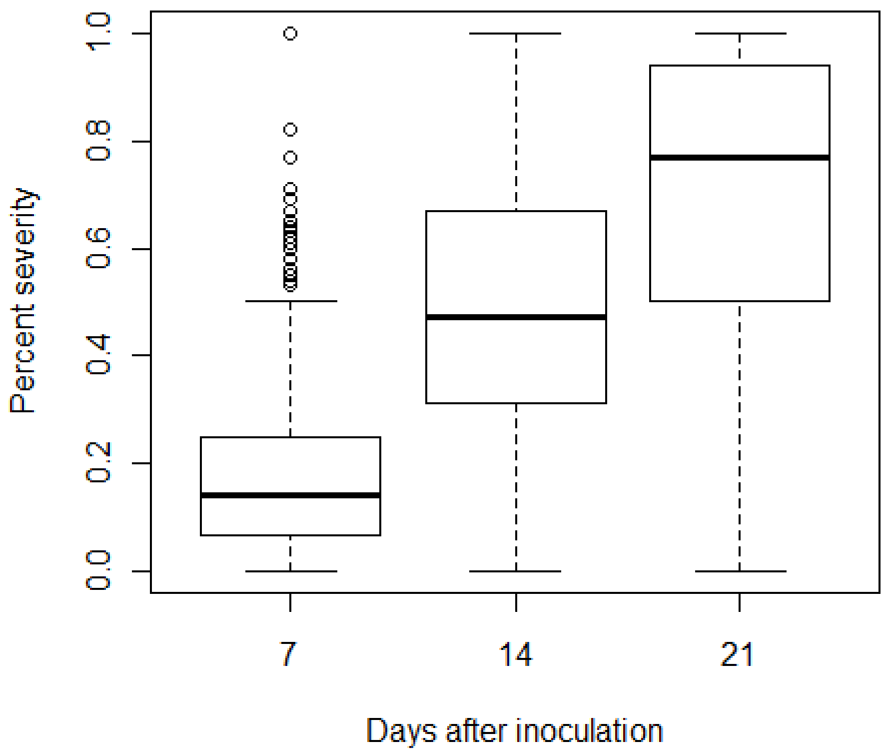
***Single-Cross F1 Hybrids:***
*28 hybrids developed from crossing founder lines were selected for intercrossing.*

***Double-Cross F1 Families:***
*28 double-cross families developed with an average family size of 30 individuals (total of 847 individuals). Individuals planted in greenhouse for selfing and evaluation.*

***$F_2$ Lines:***
*Expecting 650-700 $F_2$ lines with sufficient seed for field evaluation.*

*Greenhouse evaluations (Progress = 90%): Lines are being evaluated in the greenhouse. Inoculations are completed.*

Double-cross $F_1$ families planted in the greenhouse in April 2012 were arranged in a completely randomized design and subjected were subjected to individual head spray inoculations (25,000 spores / mL) at anthesis with the Fg4 isolate of *Fusarium graminarum*. Roughly 1000 heads were inoculated and are currently being rated for severity by counting the number of diseased spikeletes at 7, 14, and 21 days after inoculation. The raw phenotypic distributions for severity ratings obtained thus far are shown in the figure below. Greenhouse severity data will be fit to a longitudinal logistic model to obtain individual predictions for initial infection and rate of disease spread.



*Field evaluations will take place during the 2012-2013 winter wheat growing season. Arrangement are being developed with winter wheat programs in SD, ND, NE and KS.*

**Impact:** Lines are available to breeders to incorporate into their programs. During the 2012-2013 growing seasons will be able to make their own selections.

**Project 2:** *Simultaneously Pyramiding and Validating Multiple FHB Resistance QTLs in Different Spring Wheat Backgrounds.*

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

The goal of the project was to incorporate potentially new resistance genes into the HRSW breeding programs. We used a family based mapping approach to simultaneously map and incorporate multiple resistance genes into segregating early generation material.

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):**

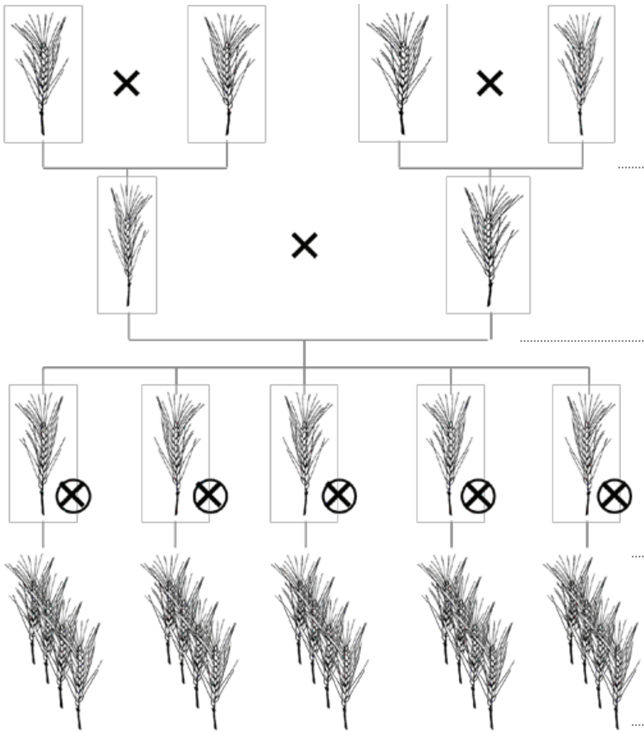
**Accomplishment:** Population development, and evaluation in field and greenhouse. Lines passed to breeding programs in the region.

*Population development (Completed):*

Double-cross breeding populations have been developed for the purpose of pyramiding and mapping multiple FHB resistance QTL. The figure below illustrates double-cross family development, and provides detailed information on the developed populations. Founder lines used for population development included 15 advanced lines from the SDSU Spring Wheat Breeding Program providing *Fhb*1 in elite genetic backgrounds, as well as 5 lines providing novel sources of FHB resistance (Table 1). Of the 15 *Fhb1* lines, 7 also potentially carry the *T. dicoccoides* derived 3AS QTL.

**Table 1.** Novel sources of resistance for pyramiding with *Fhb1*.

| Line | Pedigree | Putative QTL |
|---|---|---|
| MN99112-10-2-4 | MN93377/MN94350 | Unknown |
| MN99126-1-3-7-5 | MN94053/MN2514 | Unknown |
| RIL35 | PI 81791/Wheaton | 2B, 3B, 3D, 4D |
| RIL59 | PI 81791/Wheaton | 2B, 3B, 3D, 4D |
| MULT 757 (PI 271127) | Unknown | 7BS |



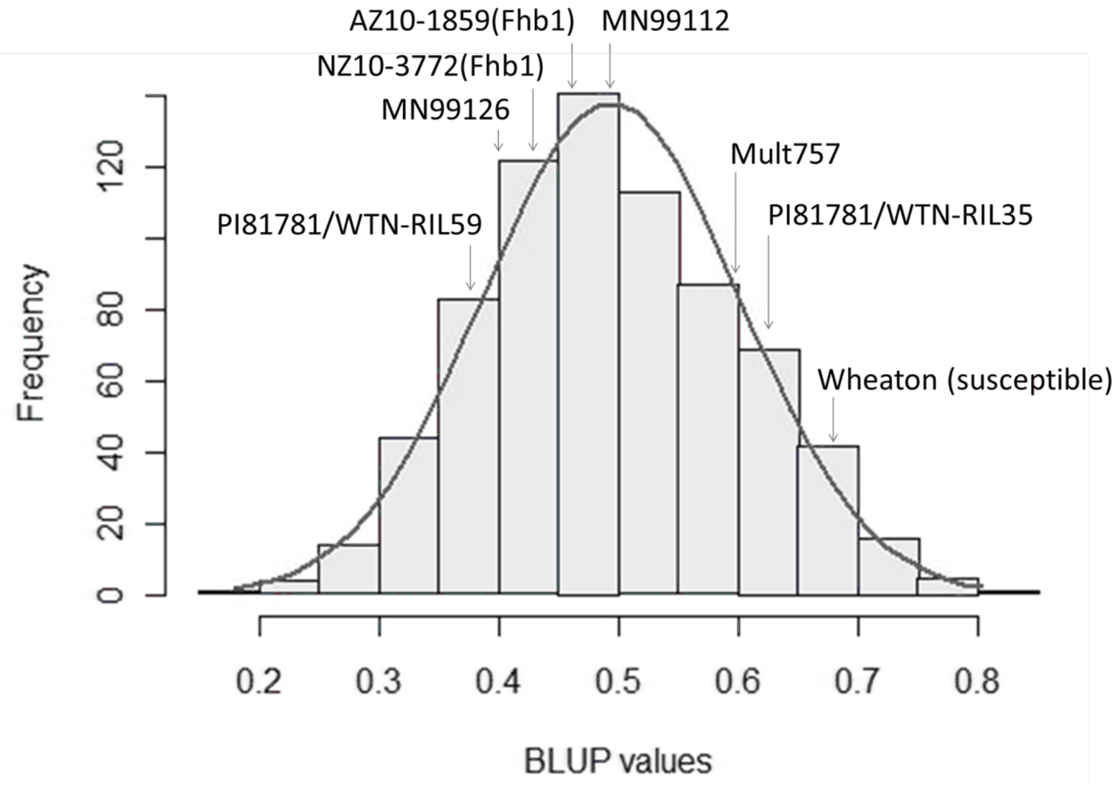
***Founder Lines:***
*20 lines used as founders for the pedigree, including 15 advanced lines from the SDSU Breeding Program providing Fhb1, and 5 lines with novel sources of resistance.*

***Single-Cross F1 Hybrids:***
*53 hybrids developed from crossing founder lines were selected for intercrossing.*

***Double-Cross F1 Families:***
*44 double-cross families developed with an average family size of 22 individuals (total of 964 individuals). Individuals planted in greenhouse for selfing and evaluation.*

***$F_2$ Lines:***
*764 $F_2$ lines developed with sufficient seed for field evaluation.*

*Greenhouse evaluations (Completed):*
Double-cross $F_1$ families planted in the greenhouse selfing in May 2011 were arranged in a completely randomized design and subjected to spray inoculations (50,000 spores / mL) with the Fg4 isolate of *Fusarium graminarum*. Roughly 1,400 heads were individually inoculated at anthesis and rated for severity by counting the number of diseased spikeletes at 14 and 21 days after inoculation. Greenhouse severity data was modeled using a logistic mixed model to provide individual plant predictions (BLUPs) for severity at 14 DAI, severity at 21 DAI, and an overall index of severity. The distribution of overall FHB severity indicates that lines carrying *Fhb1* had severity ratings between 43 to 46%, while double-cross $F_1$ individuals ranged from 18 to 80%. Thus, transgressive segregation for resistance is apparent (see figure below), suggesting enhanced resistance from pyramiding novel QTL with *Fhb*1.



*Field evaluations (Progress = 80%):* 764 $F_2$ lines were planted in roughly 1700 plots over 4 locations (Brookings SD, Volga SD, Fargo ND, and St. Paul MN) in May 2012 to provide genotypic evaluation (i.e. progeny testing) of the double-cross $F_1$ individuals. Sufficient overlap of entries (approximately 200 lines between each site) was ensured to facilitate combined analysis of the data. Plots have been inoculated and mist irrigated at all sites. Lines are currently being rated for FHB incidence and severity at 21 days after inoculation using a 0-9 visual scale on 20 heads per plot.

**Impact:** Field evaluations are being carried out in collaboration with the three regional HRSW breeding programs (SD, MN, ND). Breeders will be able to select lines from the field nurseries.

**Accomplishment:** Genotyping
DNA was extracted from leaf tissue collected from the founder lines and 955 double-cross $F_1$ individuals. Founder lines were screened for polymorphisms with 200 SSR markers, and 150 markers were selected for genotyping of the population. Genotyping is being conducted using high capacity polyacrylamide systems. Approximately 30,000 data points have been obtained thus far, initially targeting chromosomes with putative resistance QTL. Marker genotypes for chromosomes 3B, 7D, and 2A have been completed for the entire population, and the remaining chromosomes are currently being genotyped to provide a genome-wide scan for resistance QTL.

**Impact:** Once completed breeders will be able to use markers associated with each QTL in marker assisted selection schemes.

**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.**

None