

**USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY13 Final Performance Report
July 15, 2014**

Cover Page

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Fiscal Year:	FY13
USDA-ARS Agreement ID:	59-0200-3-005
USDA-ARS Agreement Title:	Molecular Characterization and Pyramiding of Novel Scab Resistance Sources Adapted to the Northern Plains Growing Region.
FY13 USDA-ARS Award Amount:	\$ 24,109

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
HWW-CP	Pyramiding and Validating Multiple FHB Resistance QTLs in Different Winter Wheat Backgrounds.	\$ 12,170
VDHR-SPR	Pyramiding and Validating Multiple FHB Resistance QTLs in Different Spring Wheat Backgrounds.	\$ 11,939
	FY13 Total ARS Award Amount	\$ 24,109

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: Pyramiding and Validating Multiple FHB Resistance QTLs in Different 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 main issue we are addressing is the need to find additional resistance genes and combine them with *Fhb1* to potentially increase the level of resistance in the HWW breeding germplasm. While a more traditional approach calls for mapping individually each potential new source and later pyramid the genes one by one, we are using an identical-by-descent approach to simultaneously combine and map multiple resistance sources. In the case of HWW we are using backcrosses on ‘Wesley’ carrying the *Fhb1* locus as the backbone of multiple 4 way crosses derived families, plus elite lines previously described as moderately resistant; some of these lines are ‘Lyman’ and ‘Overland’, two of the top performers in the region. The early generations of multiple 4way crosses derived families are evaluated in greenhouse and multi-location field trials in collaboration with breeding programs and plant pathologist in the HWW region. The collaborating breeding programs are free to make selections from this material. Additionally from the most resistant segregating families we have developed over 200 double haploid lines that will be shared and evaluated by all the breeding programs in the region. Our approach is a good complement to other ongoing efforts in the region following a step-by-step approach.

2. List the most important accomplishments and their impact (i.e. how are they being used) to minimize the threat of Fusarium Head Blight or to reduce mycotoxins. Complete both sections; repeat sections for each major accomplishment:

Accomplishment: Development of more than 500 lines segregating for multiple FHB resistance QTLs.

Impact: Pyramiding QTL from multiple sources for FHB resistance presents an opportunity to enhance the FHB resistance of elite wheat germplasm. Mapping FHB resistance QTL directly in wheat breeding populations would eliminate the need for purpose built mapping population, and thus accelerating marker-assisted pyramiding efforts. In this study we demonstrate that multiple QTL for FHB resistance can be mapped directly in early generation breeding populations by application of identical-by-descent (IBD)-based linkage mapping. IBD-based linkage analysis was conducted using 565 segregating F₁ progeny derived from 28 four-way crosses among *Fhb1* donor lines and multiple native sources of resistance including Lyman, Overland, Ernie and Freedom. These lines have been shared across the CP allowing breeders to make their own selections. This should help to increase the presence of resistance alleles in the germplasm pool across the region.

Accomplishment: Identification of several QTL regions associated with FHB resistance.

Impact: A total of 15 QTL for FHB resistance were mapped on chromosomes 1A, 1B, 2A, 3A, 3B, 4A, 4B, 4D, 5A, 6A, 6D and 7D, including known loci *Fhb1*, *Fhb5*, and *Rht-B1*.

QTL conferring native resistance in the cultivars Lyman and Overland are mapped for the first time in this study, including a QTL on chromosome 1AS (*Qfhb.sdsu-1A*) explaining between 4.5 to 9.9% of the phenotypic variance in all evaluations. Marker haplotypes for these QTL regions can be used to conduct marker assisted selection and fixation of resistance alleles in subsequent generations of these and other breeding populations derived from Lyman and Overland

Project 2: 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 main issue that this project address is the need to add additional resistance sources in the HRSw germplasm that can be combined with *Fhb1*. Pyramiding QTL from multiple sources for FHB resistance presents an opportunity to enhance the *Fhb1* derived resistance of elite spring wheat germplasm. Conventionally, pyramiding QTL using a marker assisted-selection approach would require preliminary mapping studies to identify the resistance QTL from each parental line and validation studies to assess the QTL effects in multiple genetic backgrounds. This study evaluates identity-by-descent (IBD)-based linkage analysis for the purpose of mapping and marker-assisted pyramiding of resistance QTL simultaneously in breeding populations.

2. List the most important accomplishments and their impact (i.e. how are they being used) to minimize the threat of Fusarium Head Blight or to reduce mycotoxins. Complete both sections; repeat sections for each major accomplishment:

Accomplishment: Development of over 800 HRSW lines segregating for at least 4 resistance QTL each.

Impact: A total of 829 segregating F₁ progeny from 43 four-way crosses among multiple sources of resistance were evaluated in the greenhouse and in field-based progeny tests. IBD-based linkage analysis was conducted using a mixed model extension of Haseman-Elston sib-pair regression. These lines have been shared across the CP allowing breeders to make their own selections. This should help to increase the presence of resistance alleles in the germplasm pool across the region.

Accomplishment: Identification of several QTL regions associated with FHB resistance.

Impact: QTL for FHB resistance were identified on chromosomes 2A, 2B, 3B and 7B, explaining between 18 to 21% of the variance for FHB severity in different evaluations. The QTL on chromosome 3B corresponded with *Fhb1*, and the QTL on chromosomes 2B and 7B are corroborated by previous mapping studies. The QTL mapped to chromosome 2A represents a novel source of resistance derived from elite North American spring wheat

germplasm. Marker haplotypes for these QTL regions can be used for marker assisted selection and fixation of resistance alleles in subsequent generations of these breeding populations.

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 FY13 grant. Please reference each item using an accepted journal format. If you need more space, continue the list on the next page.

J.T. Eckard, J.L. Gonzalez-Hernandez, S. Chao, P. St Amand, G. Bai. 2014. Construction of dense linkage maps “on the fly” using early generation wheat breeding populations. *Accepted in Molecular Breeding*. Available online (doi:10.1007/s11032-014-0116-1)

Jonathan T. Eckard, Melanie Caffé, William Berzonsky, William W. Bockus, G. Francois Marais, P. Stephen Baenziger and Jose L. Gonzalez-Hernandez. (2014) Native Fusarium head blight resistance from winter wheat cultivars ‘Lyman’, ‘Overland’, ‘Ernie’, and ‘Freedom’ mapped and pyramided onto ‘Wesley’-*Fhb1* backgrounds. *Under review in Molecular Breeding*

Jonathan T. Eckard, Karl D. Glover, Mohamed Mergoum, James A. Anderson and Jose L. Gonzalez-Hernandez. (2014). Multiple Fusarium head blight resistance loci mapped and pyramided onto elite spring wheat *Fhb1* backgrounds using an IBD-based linkage approach. *Under Review in Euphytica*.

J.T. Eckard, J.L. Gonzalez-Hernandez, S. Chao, P. St. Amand and G. Bai Construction Of Dense Linkage Maps “On The Fly” Using Early Generation Plant Breeding Populations To Facilitate Mapping Of Fusarium Head Blight Resistance QTL. In: S. Canty, A. Clark, Y. Salat and D. Van Sanford (Eds.), Proceedings of the 2013 National Fusarium Head Blight Forum (pp. 15). East Lansing, MI/Lexington, KY: U.S. Wheat & Barley Scab Initiative.

J.T. Eckard, J.L. Gonzalez-Hernandez, K.D. Glover, J. Anderson And M. Mergoum Multiple Fusarium Head Blight Resistance QTL Pyramided Onto Elite Spring Wheat *Fhb1* Backgrounds Using A Family-Based Mapping Approach.. In: S. Canty, A. Clark, Y. Salat and D. Van Sanford (Eds.), Proceedings of the 2013 National Fusarium Head Blight Forum (pp. 16). East Lansing, MI/Lexington, KY: U.S. Wheat & Barley Scab Initiative.

J.T. Eckard, J.L. Gonzalez-Hernandez, W.A. Berzonsky, W. Bockus And G.F. Marais Native Fusarium Head Blight Resistance From ‘Lyman’, ‘Overland’, ‘Ernie’ And ‘Freedom’ Wheat Cultivars Pyramided Onto Wesley-*Fhb1* Backgrounds Using A Family-Based Mapping Approach. In: S. Canty, A. Clark, Y. Salat and D. Van Sanford (Eds.), Proceedings of the 2013 National Fusarium Head Blight Forum (pp. 17). East Lansing, MI/Lexington, KY: U.S. Wheat & Barley Scab Initiative.