USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY12 Final Performance Report
July 16, 2013

Cover Page

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Fiscal Year:	FY12
USDA-ARS Agreement ID:	59-0206-1-119
USDA-ARS Agreement Title:	Mapping Loci Conferring Resistance to FHB and DON Accumulation in Barley.
FY12 USDA-ARS Award Amount:	$ 38,197[*]

USWBSI Individual Project(s)

USWBSI Research Category[**]	Project Title	ARS Award Amount
BAR-CP	Mapping Loci Conferring Resistance to FHB and DON Accumulation in Barley.	$ 38,197
	Total ARS Award Amount	**$ 38,197**

Brian J. Steffenson July 16, 2013

Principal Investigator Date

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[*] Partial funding for this research is under ARS agreement # 59-0206-9-070

[**] 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: *Mapping Loci Conferring Resistance to FHB and DON Accumulation in Barley.*

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

   Our primary and long-term goal is to reduce the losses caused by FHB, including quality discounts due to deoxynivalenol (DON) contamination. This can be best achieved by developing barley cultivars with the highest level of resistance possible. We identified about 20 promising accessions with partial FHB resistance through multiple years of field screening. Two of these accessions were backcrossed to the partially resistant cultivar 'Quest' to develop BC_2F_5 populations for mapping and characterizing quantitative trait locus (QTL) conferring FHB resistance and low DON accumulation. The specific objective for this proposal is to determine the number, effect, and chromosomal position of FHB resistance loci in two barley accessions (Kutahya, a two-rowed cultivar from the Netherlands and W-365, a wild barley accession from Iraq) using the advanced backcross-QTL method. The information and germplasm generated from this study will lead to the development of malting barley cultivars with FHB resistance and low DON accumulation, thereby minimizing this disease threat for producers, processors, and consumers.

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 have developed and advanced to the BC_2F_5 generation two advanced backcross populations (Kutahya/Quest with 361 lines and W-365/Quest with 378 lines) in the genetic background of moderately resistant cultivar 'Quest.' The Kutahya/Quest and W-365/Quest populations were planted at four locations for phenotyping in 2013: Nanjing, China, Crookston MN, St. Paul, MN and Brandon, Canada. FHB phenotyping at the US locations is now underway and will be completed in August. Seed of all progeny will be harvested and assayed for DON by December. DNA has been extracted from all progeny for genotyping with the 9K SNP chip.

   Impact:

   Comprehensive molecular maps will be construction for the Kutahya/Quest and W-365/Quest populations. These maps will allow us to determine the number, effect, and chromosomal position of loci conferring resistance to FHB and the accumulation of mycotoxins. Preliminary evaluations from the Nanjing nursery identified several agronomically advanced six-rowed progeny with a level of resistance greater than either of the parents. These resistant progeny lines will be given to breeders for use as parents in their FHB-resistance breeding programs. The pyramiding of new FHB resistance loci in malting barley cultivars will minimize this disease threat for producers, processors, and consumers.

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.

Huang, Y., Millett, B. P., Beaubien, K. A., Dahl, S. K., Steffenson, B. J., Smith, K. P., and Muehlbauer, G. J. 2012. Haplotype diversity and population structure in cultivated and wild barley evaluated for Fusarium head blight responses. Theor. Appl. Genet. 126:619–636.

Menke, J., Beaubien, K., Szinyei, T., Dong, Y., Chao, S., Olivera, P., Alsop, B., Dahl, S., Smith, K., and Steffenson, B. 2012. Mapping of Fusarium head blight resistance in wild barley accession PI 466423. Pages 69-73 in: Proceedings of the 2012 National Fusarium Head Blight Forum. December 4-6, Orlando, Florida.

Huang, Y., Shin, S., Millet, B. P., Li, X., Adam, G., McCormick, S., Smith, K. P., Steffenson, B. J. and Muehlbauer, G. J. 2012. Identification and characterization of barley genes that provide resistance to trichothecenes. Page 137 in: Proceedings of the 2012 National Fusarium Head Blight Forum. December 4-6, Orlando, Florida.