USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY07 Final Performance Report (approx. May 07 – April 08)
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Cover Page

PI:	Kevin Smith
Institution:	University of Minnesota
Address:	Department of Agronomy and Plant Genetics 411 Borlaug Hall 1991 Upper Buford Circle St. Paul, MN 55108
E-mail:	smith376@umn.edu
Phone:	612-625-1211
Fax:	612-625-1268
Fiscal Year:	2007
USDA-ARS Agreement ID:	59-0790-4-120
USDA-ARS Agreement Title:	Breeding and Genetics of Fusarium Head Blight Resistance in Barley.
FY07 ARS Award Amount:	$ 154,654

USWBSI Individual Project(s)

USWBSI Research Area*	Project Title	ARS Adjusted Award Amount
HGR	Marker Assisted Selection for FHB Resistance in Barley.	$17,581
HGG	Developing Marker Information for Genetic Diversity and FHB Resistance in Barley.	$ 53,171
VDUN	Accelerated Development of Fusarium Resistant Barley Varieties.	$ 83,902
	Total Award Amount	**$ 154,654**

Principal Investigator Date

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* CBCC – Chemical, Biological & Cultural Control
EEDF – Etiology, Epidemiology & Disease Forecasting
FSTU – Food Safety, Toxicology, & Utilization of Mycotoxin-contaminated Grain
GET – Genetic Engineering & Transformation
HGR – Host Genetics Resources
HGG – Host Genetics & Genomics
IIR – Integrated/Interdisciplinary Research
PGG – Pathogen Genetics & Genomics
VDUN – Variety Development & Uniform Nurseries

(Form FPR07)

Project 1: *Marker Assisted Selection for FHB Resistance in Barley.*

1. **What major problem or issue is being resolved and how are you resolving it?**

Marker assisted selection (MAS) has only recently been adopted on a small scale by barley breeding programs for enhancing FHB resistance. We are working with the USDA Genotyping Center at Fargo to implement MAS with the best available markers to improve FHB resistance in barley. In the summer of 2007, we evaluated three breeding populations that were subjected to MAS for a chromosome 6H QTL in replicated FHB nurseries in Minnesota. In one of those three population, we saw a modestly significant effect of MAS ($P=0.07$) resulting in a 19% reduction in FHB severity. This QTL region (6H) has been inconsistently detected in the past in both mapping and MAS experiments. We are conducting additional fine mapping in this region and will initiate new MAS populations after we have better genetic information and more informative markers. This summer, we have three new populations that were subjected to MAS for the chromosome 2H bin 8 QTL planted in two FHB nurseries. Last fall we made 12 new crosses for the 2H QTL involving susceptible elite parents as well as new FHB variety candidates. The F2 generation is growing this summer and MAS will commence in the fall.

2. **List the most important accomplishment and its impact (how is it being used?). Complete all three sections (repeat sections for each major accomplishment):**

Accomplishment:

Tested MAS on three breeding populations with Chevron allele at 6H QTL.

Impact:

Variable effectiveness means that MAS using this QTL will need to wait until additional mapping work is complete.

As a result of that accomplishment, what does your particular clientele, the scientific community, and agriculture as a whole have now that they didn't have before?:

While the MAS results are not terribly impressive yet, we are advancing any promising lines in our breeding program.

Project 2: *Developing Marker Information for Genetic Diversity and FHB Resistance in Barley.*

1. What major problem or issue is being resolved and how are you resolving it?

Progress in breeding for FHB resistance in barley to date has relied entirely on field-based phenotypic selection for disease severity and DON concentration of grain samples. Use of marker assisted selection (MAS) in early generations could provide a valuable tool to enrich breeding populations for resistance alleles at quantitative trait loci (QTL) prior to screening in the field. A major hurdle to using currently available QTL information for MAS is linkage of the resistance alleles to several undesirable traits (late heading, high grain protein concentration, tall plant height). Our project is focused on characterizing several important QTL regions in barley and resolving undesirable linkages. This information will lead to the implementation of MAS for FHB resistance in barley to complement ongoing traditional breeding efforts. We are currently involved in fine mapping three QTL regions (chromosomes 2H, 3H, and 6H). We are also using association mapping with breeding germplasm to identify new QTL that have not been discovered in traditional bi-parental mapping populations and that are presumably free of undesirable linkages due to selection in the breeding programs. This work is collaborative with the Busch Agriculture and North Dakota State University breeding and pathology programs and is primarily supported by the USDA Barley Coordinated Agricultural Project (CAP). This study is using data from 768 breeding lines evaluated in 5 trials for FHB and DON in 2006 and 2007 and screened with 3,000 SNP markers to identify QTL via genome-wide association mapping.

2. List the most important accomplishment and its impact (how is it being used?). Complete all three sections (repeat sections for each major accomplishment):

Accomplishment:

We have generated large F2 populations for three QTL regions (2H, 3H, and 6H). We have used markers to select recombinants within the target region. We have planted recombinants from the 2H and 6H populations in FHB nurseries this summer. The data we collect this summer and in subsequent nurseries will help elucidate the position of FHB and DON resistance and help distinguish them from QTL for other linked traits. The 3H recombinants were evaluated in the greenhouse and we are still processing those samples and data. Preliminary data from the association mapping work indicates that there are ~8 QTL that were identified. All have relatively small effects with the largest having an R^2 value of 0.12. We are currently investigating these QTL regions and developing MAS strategies that could be used to exploit them.

Impact:

Too early to assess the impact of these projects.

As a result of that accomplishment, what does your particular clientele, the scientific community, and agriculture as a whole have now that they didn't have before?:

We will soon be able to reveal the QTL that were detected in the association mapping study giving the Midwest barley breeders some potential new targets for MAS.

Project 3: *Accelerated Development of Fusarium Resistant Barley Varieties.*

1. **What major problem or issue is being resolved and how are you resolving it?**

None of the currently grown malting barley varieties are more resistant than the variety Robust which has dominated the barley acreage in the Midwest since 1986. We are conducting a comprehensive field-based breeding effort to develop new barley varieties with enhanced FHB resistance. In order for these new varieties to be adopted by growers they must also be agronomically competitive with current varieties and meet the quality standards of the malting and brewing industries. We conduct extensive field evaluation of FHB resistance in inoculated and mist-irrigated nurseries in three locations in Minnesota. Last year we evaluated over 12,000 plots for FHB resistance and submitted over 3,000 grain samples for DON analysis.

2. **List the most important accomplishment and its impact (how is it being used?). Complete all three sections (repeat sections for each major accomplishment):**

Accomplishment:

One of our variety candidates, M122, was entered into AMBA plant-scale brewing evaluations. If this variety is rated satisfactory in its first year, we would anticipate releasing it as a variety in January 2010. M122 accumulates about half the level of DON compared to Robust.

Two other variety candidates, M128 and M129, were rated satisfactory in their second year of AMBA pilot testing. These lines reduce DON by about 30%. We are currently evaluating their entrance into plant-scale brewing evaluation.

This year we have four first-year entries into AMBA pilot-scale malt testing that all have enhanced FHB resistance. We have reached a point in our breeding program where the pipeline is full of FHB material and all our submissions to AMBA will have enhanced FHB resistance.

Impact:

The impact of this work will be felt after our first release with enhanced resistance to FHB.

As a result of that accomplishment, what does your particular clientele, the scientific community, and agriculture as a whole have now that they didn't have before?:

If M122 is approved by AMBA, this would be the first malting variety with enhanced resistance to M122 available to farmers in the Midwest. This line reduces DON by half compared to the currently grown varieties which is the current short term goal for the

USWBSI. In addition, M122 has been made available to other scientists that are evaluating integrated disease managements strategies to determine the effectiveness of combining genetic resistance with other FHB management strategies.

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.

Nduulu L. M., A. Mesfin, G. J. Muehlbauer, and K. P. Smith. 2007. Analysis of the chromosome 2(2H) region of barley associated with the correlated traits Fusarium head blight resistance and heading date. Theor. Appl. Genet. 115:561–570.

Smith, K. P. The search for QTL to employ in marker assisted selection for FHB resistance in barley. Invited talk at the 5th Canadian Workshop on Fusarium Head Blight Nov 27-29.

Massman, J and K. P. Smith. 2007. Prospects for Identifying Fusarium Head Blight Resistance QTL by Association Mapping using Breeding Germplasm. Proceedings of the 2007 National Fusarium Head Blight Forum, The Westin Crown Center, Kansas City, Missouri, Dec. 2-4, 2007, p. 203.

Smith, K. P., E. Schiefelbein and G. Velasquez. 2007. Development of Barley Variety Candidate M122 with Enhanced Resistance to FHB. Proceedings of the 2007 National Fusarium Head Blight Forum, The Westin Crown Center, Kansas City, Missouri, Dec. 2-4, 2007, p. 232

Massman, J. M. and K. P. Smith. 2008. Investigating The Suitability Of Contemporary Breeding Populations For Association Mapping Of Fusarium Head Blight Resistance In Barley. Plant & Animal Genomes XVI Conference, January 12-16, 2008, Town & Country Convention Center, San Diego, CA. P329.