USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY05 Final Performance Report (approx. May 05 – April 06)
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Cover Page

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Fiscal Year:	**2005**
FY05 ARS Agreement ID:	**59-0790-4-120**
Agreement Title:	**Breeding and Genetics of Fusarium Head Blight Resistance in Barley.**
FY05 ARS Award Amount:	**$ 166,018**

USWBSI Individual Project(s)

USWBSI Research Area*	Project Title	ARS Adjusted Award Amount
BIO	Developing Marker Information for Genetic Diversity and FHB Resistance in Barley.	$ 56,585
VDUN	Accelerated Development of Fusarium Resistant Barley Varieties.	$ 78,049
VDUN	Marker-Assisted Selection for FHB Resistance in Barley.	$ 31,374
	Total Award Amount	**$ 166,018**

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Principal Investigator Date

* BIO – Biotechnology
CBC – Chemical & Biological Control
EDM – Epidemiology & Disease Management
FSTU – Food Safety, Toxicology, & Utilization
GIE – Germplasm Introduction & Enhancement
VDUN – Variety Development & Uniform Nurseries

Project 1: *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) that are subsequently screened 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 characterizing these QTL regions by 1) developing near isoenic lines (NIL) for each QTL region through backcrossing and MAS; 2) using these NIL as parents to produce large segregating populations; 3) selecting recombinants from within the QTL region; 4) evaluating selected recombinants for FHB severity, DON concentration, kernel discoloration, heading date, height, and grain protein concentration.

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 identified a recombinant that carries the resistance allele from Chevron (resistance source) and the early heading allele from M69 (recurrent parent) at the tightly linked heading date QTL in the bin 8 region of chromosome 2H.

Impact:
This recombinant and the markers that flank the QTL region can be used to select for this gene using MAS. This recombinant can also be used to conduct allelism tests with other NIL for this QTL region that have been identified using other resistance sources.

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 now have a breeding line that carries a resistance gene from Chevron that is uncoupled from late heading date and are using it in crosses that will be subjected to MAS. Previously this gene was not useful for barley breeding due to undesirable linkage.

Project 2: *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 11,000 plots for FHB resistance and submitted over 2,800 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:
   We designated two new variety candidates with enhanced FHB resistance and entered them into American Malting Barley Association (AMBA) pilot malt evaluation. One of these two candidates, M122, was rated satisfactory for the 2005 crop year and will continue evaluation in 2006. Based on eleven trials conducted from 2003-2005, M122 was 8% higher in yield, an inch shorter, and similar in heading date and lodging to Robust. Based on the average of 19 FHB trials conducted from 2003-2005, M122 had 43% of the FHB severity and 48% of the DON concentration of Robust.

   Impact:
   This is the first new variety candidate with enhanced FHB resistance, lower DON, and acceptable agronomic and malting quality to come out of the University of Minnesota program. Three new variety candidates with enhanced FHB resistance were identified from 2005 data and will be evaluated this year (2006).

   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 rated satisfactory with the 2006 crop it will be eligible for plant-scale testing in 2008. Thus we are moving toward a variety that will reduce DON by half.

Project 3: *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 not been adopted by barley breeding programs for enhancing FHB resistance. Obstacles to implementing MAS include discovering good QTL target regions, identifying tightly linked markers that flank the target QTL and are polymorphic in relevant breeding populations, and establishing the laboratory capacity necessary for high through-put DNA extraction and marker screening. The Minnesota breeding program and Fargo genotyping lab initiated a project to "jump-start" MAS in barley breeding. While the target QTL are less than perfect, due to undesirable linkages and limited numbers of markers in the QTL regions, we developed populations suitable for MAS. Some of the initial crosses we made to take advantage of the Chevron resistance allele at the FHB QTL on chromosome 2H bin 8 were not subjected to MAS because we discovered that the parent used was not carrying the resistance allele at the target markers. We have since identified appropriate parents and are proceeding with new crosses. We genotyped several populations in the summer of 2005 and advanced selected lines to our winter nursery for seed increase. MAS was imposed on a total of about 2800 F2 or F3 DNA samples. These lines were segregating for the Hor211 allele at the chromosome 6H QTL. Of these about 327 lines were selected as homozygous for the resistant parent alleles and planted in the field for disease screening.

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 established a routine protocol for harvesting leaf tissue, sending and tracking samples to the Fargo lab, and utilizing genotyping facilities for marker assisted selection. In all cases, we were able to submit samples to the genotyping lab and get data back in time to to select plants prior to harvest, thus optimizing the use of our resources.

Impact: We are currently assessing the effectiveness of the particular QTL region that we were subjecting to MAS. As we move additional populations through the system, we should be able to rigorously assess the effectiveness of MAS.

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 now have a routine protocol for screening F2 and F3 barley breeding lines for SSR markers linked to FHB QTL in a high throughput system appropriate for MAS.

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.

Smith, K. P. 2005. Evaluation of breeding strategies for enhancing FHB resistance in barley. Presentation at *2005 National Fusarium Head Blight Forum*. Milwaukee, WI 12/11/05 - 12/13/05, p.85.

Brady Lee, James Anderson, Kevin Smith and Shiaoman Chao. 2005. A Cost-Effective High Throughput Genotyping Method. In *Proceedings of 2005 National Fusarium Head Blight Forum*. Milwaukee, WI 12/11/05 - 12/13/05, p. 18.

Nduulu, L.M., G.J. Muehlbauer and K.P. Smith. 2005. Fine Mapping of a QTL Region Associated with Fusarium Head Blight, Kernel Discoloration, Grain Protein Concentration, and Heading Date on Barley Chromosome 6H. In *2005 National Fusarium Head Blight Forum*. Milwaukee, WI 12/11/05 - 12/13/05, p. 75.

Beaubien, K.A. and K.P. Smith. 2005. Identifying Marker-Trait Associations for Fusarium Head Blight Using Breeding Germplasm. In *2005 National Fusarium Head Blight Forum*. Milwaukee, WI 12/11/05 - 12/13/05, p. 12.

Dill-Macky, R., B. J. Steffenson, C. Hollingsworth and K. P. Smith. 2005. Management of Barley Diseases in the Upper Midwest. In *Proceedings of the 34th Barley Improvement Conference*. Charleston, SC, Jan. 11-12, 2005, p. 1.

Horsley, R. and K. P. Smith. 2005. Development of Scab Tolerant Barley Varieties at North Dakota State University and the University of Minnesota. In *Proceedings of the 34th Barley Improvement Conference*. Charleston, SC, Jan. 11-12, 2005, p. 13.

Chao, Shiaoman, James Anderson, Karl Glover and Kevin Smith. 2006. Use of High Throughput Marker Technologies for Marker-Assisted Breeding in Wheat and Barley. In *Proceedings of Plant and Animal Genome XIV* page 17.