USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY06 Final Performance Report (approx. May 06 – April 07)
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Cover Page

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Fiscal Year:	2006
USDA-ARS Agreement ID:	59-0790-4-120
USDA-ARS Agreement Title:	Breeding and Genetics of Fusarium Head Blight Resistance in Barley.
FY06 ARS Award Amount:	$ 164,481

USWBSI Individual Project(s)

USWBSI Research Area*	Project Title	ARS Award Amount
EC/HQ	Multi-State Barley Winter Nursery - FY06 (05/06).	$ 4,781
HGR	Marker Assisted Selection for FHB Resistance in Barley.	$ 25,067
HGG	Developing Marker Information for Genetic Diversity and FHB Resistance in Barley.	$ 54,503
VDUN	Accelerated Development of Fusarium Resistant Barley Varieties.	$ 54,503
	Total Award Amount	**$ 164,481**

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Principal Investigator Date

* 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
PGG – Pathogen Genetics & Genomics
VDUN – Variety Development & Uniform Nurseries

Project 1: *Multi-State Barley Winter Nursery - FY06 (05/06).*

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

Reliable evaluation of early generation breeding lines for FHB requires sufficient seed for replicated multi-location trials. This winter nursery provides seed from single F4 plants sufficient to plant 2 location – 2 rep trials for FHB in the summer in St. Paul and Crookston. This increased efficiency will result in faster development of FHB resistant barley varieties.

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 harvested sufficient seed from approximately 2,000 F4 plants that was used to plant FHB nurseries in Morris, St. Paul, and Crookston, MN.

Impact:
This has allowed us to collect better quality data for FHB and make better decisions regarding selection for resistance and the advancement of breeding lines in our program.

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?
Our breeding program can collect replicated data at an earlier stage of breeding which will improve our ability to select for resistance and speed the development of FHB resistant barley varieties.

Project 2: *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. 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 USDA 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. Selected lines from these populations were planted in the summer of 2007 and are currently being evaluated for FHB.

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 initiated MAS in our program and are in the process of collecting data to determine the effect of MAS for FHB.

Impact:
We are determining the effect of selection so that we can determine the impact.

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 have breeding lines that are currently being evaluated for disease and agronomics that were identified using MAS. If these the markers that we use perform well, they can be used by other breeding programs and may eventually contribute to the development of new varieties.

Project 3: *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 isogenic 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 separated the linkage between a resistance QTL for FHB and heading date on chromosome 2 (Nduulu et al., 2007).

   Impact:
   We are now using MAS to exploit this resistance QTL in our breeding program.

   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?
   A breeding line and marker information is now available to other breeding programs to utilize this resistance gene.

Project 4: *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 rated satisfactory in its second year in AMBA pilot-scale malting evaluations. It is now scheduled to be evaluated in plant scale brewing evaluations with the 2008 crop. 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 2003-2006, M122 had 42% of the FHB severity and 50% of the DON concentration of Robust.
Two newer variety candidates, M128 and M129, were rated satisfactory in their first year of AMBA pilot testing. These lines reduce DON by about 30%.

Impact:
If M122 is rated satisfactory with the 2008 crop, we would release it as a variety in January of 2010. This would be the first variety release from the UM with enhanced FHB resistance.

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 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.

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., Mesfin, A., Muehlbauer, G. and Smith, K. P. 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. (in press)

Steffenson, B. J and Smith, K. P. 2006. Breeding Barley for Multiple Disease Resistance in the Upper Midwest Region of the USA. Czech J. Genet. Plant Breed. 41: 79–85.

Beaubien, K. A. and K. P. Smith. 2006. Identifying Marker-Trait Associations In Contemporary Midwest Breeding Germplasm. In: *Plant and Animal Genome XIV Abstracts*, San Diego, CA. Jan 14 – 18, 2005, P317

Shiaoman Chao, S., J. Anderson, K. Glover, K.P. Smith. 2006. Use Of High Throughput Marker Technologies For Marker-Assisted Breeding In Wheat And Barley. In: *Plant and Animal Genome XIV Abstracts*, San Diego, CA. Jan 14 – 18, 2005, W43

Bilgic, H., S. Cho, L. Nduulu, K. P. Smith, and G. J. Muehlbauer. 2006. Microarray Analysis of Gene Expression in Barley During *Fusarium graminearum* Infection. In: *Proceedings of the In Vitro Biology Meeting*, Minneapolis, MN, June 3-7, 2006