USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY05 Final Performance Report (approx. May 05 – April 06)
July 14, 2006

Cover Page

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Fiscal Year:	**2005**
FY05 ARS Agreement ID:	**59-0790-4-110**
Agreement Title:	**Saturation Mapping of the Chromosome 2(2H)Fusarium Head Blight Resistance QTL.**
FY05 ARS Award Amount:	**$ 77,342**

USWBSI Individual Project(s)

USWBSI Research Area*	Project Title	ARS Adjusted Award Amount
BIO	Acquisition of the Haruna Nijo Bacterial Artificial Chromosome Library.	$ 16,585
BIO	Saturation Mapping of Chromosome 2(2H) Fusarium Head Blight Resistance QTL.	$ 60,757
	Total Award Amount	**$ 77,342**

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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: *Acquisition of the Haruna Nijo Bacterial Artificial Chromosome Library.*

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

The goal of this project was to acquire the Haruna Nijo Bacterial Artificial Chromosome (BAC) library and deposit at the Arizona Genomics Institute center for distribution to North American barley workers. This was accomplished. The problem addressed was the lack of adequate BAC library resources for the barley community, especially from a 2-rowed cultivar. This problem was resolved at least in part by the acquisition of this library. The library, clones and high density filters are available from Arizona Genomics Institute
`http://www.genome.arizona.edu/`

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: Acquisition and deposition of the library at the Arizona Genomics Institute makes it available for all scientists who might wish to use it.

Impact: Availability of this library will facilitate the work of scientists in developing physical contigs of important barley regions, cloning genes and comparing 2-rowed vs. 6-rowed cultivars.

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?:

They have access to an excellent BAC clone library made from a 2-rowed cultivar that supplements the existing 6-rowed cultivar Morex library.

Project 2: *Saturation Mapping of Chromosome 2(2H) Fusarium Head Blight Resistance QTL.*

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

The major problem is the difficulty to date in incorporating the CI4196 Fusarium Head Blight resistance into acceptable agronomic cultivars. To help solve this problem we are: 1) saturating the target region with molecular markers and refining the genetic map; 2) continuing development of isolines with minimal chromosome 2(2H) FHB QTL regions; 3) continuing work toward development of a physical map of the chromosome 2(2H) FHB QTL region; and 4) developing a fast neutron mutagenized population of CI4196 to isolate deletion mutants in the chromosome 2(2H) FHB QTL region.

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:

1. A molecular map of the Foster x CI4196 cross was published Horsley et al., Crop Sci. 46: 145-156 (2006). Approximately 100 additional markers have been added to the map and we are preparing for publication of a more detailed map of the chromosome 2H region containing the major Fusarium head Blight QTL.
2. Two types of isolines are partially developed, one with a Morex genotype from marker BE216598 (just proximal of the Vrs1 locus) to BF253600 distal of Vrs1 by several cM. The genotype proximal of BE216598 is CI4196. These lines are 6-rowed. This material has been back-crossed to Morex twice and was tested in China last winter. Rich Horsley has the data and he said some of the lines looked pretty good, but since it is very preliminary one should not rely on it too much. testing of these lines is continuing in North Dakota this summer (’06). The second type of isoline is based on isoline A171. It is Morex genotype from marker BE231256 to vrs1 and it is 6-rowed. The genotype from ABC306 to BE231256 and from BE519832 (just distal of vrs1) to MWG503 is CI4196. This group has been back-crossed to Morex twice and to CI4196 once. Lines are being tested in field at North Dakota this summer (’06).
3. We continue to accumulate BAC clones in the target region, but it seems to large and this will take time to complete. The cloning of the Vrs1 locus was reported by Komatsuda at the Plant and Animal Genome XIV meeting. They sequenced 4 BAC clones in the Vrs1 region and found only one gene, suggesting that at least region directly around the Vrs1 locus is gene poor. This also helps to explain why we accumulate markers around the Vrs1 region, but not very close to it.
4. A fast neutron treated CI4196 population was planted in the field summer ’05. The M2 seeds were harvested and are being studied for mutants. We are particularly interested in early, semi-dwarf, 6-rowed and FHB susceptible mutants.

Impact:

The impact of this work will be obtain 6-rowed isolines that confer resistance to FHB, develop high resolution maps and molecular markers for the major chromosome 2H FHB QTL, isolate mutants that are earlier and shorter to test the hypothesis that CI4196 is resistant due to its height and lateness, and eventually clone the genes responsible for the CI4196 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?:

The scientific community will obtain material to test some of the hypotheses generated about CI4196 resistance. Such tests are crucial because relying on inaccurate hypotheses tends to channel the research and development effort in the wrong direction. If we find mutants with increased susceptibility to FHB, these can lead directly to cloning of the genes that are responsible for the resistance. This probably sounds backwards to some, but if you want to know which gene is responsible for a tall trait you need to examine the dwarf mutant.

Some of the material may also serve as starting points for developing commercially acceptable barley cultivars that present a sufficient level of FHB resistance for use by the industry. We have already numerous lines with variable CI4196 background that are 2-rowed and have some level of FHB resistance. These are good starting points for rurther breeding work.

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.

Horsley, R. D., Schmierer, D., Maier, C., Kudrna, D., Urrea, C. A., Steffenson, B. J., Schwarz, P. B., Franckowiak, J. D., Green, M. J., Zhang, B., Kleinhofs, A. (2006) Identification of QTL associated with Fusarium Head Blight resistance in barley accession CIho 4196. Crop Sci. 46: 145-156

Maier, C., Schmierer, D., Drader, T., Horsley, R., Sushailo, S., Zhang, L., Kleinhofs, A. (2005) Fractional analysis of chromosome 2(2H) Fusarium Head Blight resistance QTL. In: Proceedings of the 2005 National Fusarium Head Blight forum. S. Canty, T. Boring, J. Wardnell, L. Silver, and R. W. Ward eds. Forum held at Milwaukee, WI Dec. 11-13, 2005. Poster 27, p57.