USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY09 Final Performance Report
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Cover Page

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Fiscal Year:	2009
USDA-ARS Agreement ID:	59-0206-9-075
USDA-ARS Agreement Title:	Mapping and Sequencing of CHR. 2H Bin 10 FHB Resistance QTL for Gene Discovery.
FY09- USDA-ARS Award Amount:	$ 77,452

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Adjusted Award Amount
BAR-CP	Genetic and Physical Mapping of the chr. 2H Bin 10 FHB Resistance QTL and Development of Recombinant Lines and Mutants to Facilitate Breeding.	$ 48,397
GDER	Sequencing BAC Clones from Chr2(H) FHB Resistance QTL for Gene Discovery.	$ 29,055
	Total Award Amount	**$ 77,452**

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Principal Investigator Date

* 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 Winter Wheat Region
SWW – Southern Sinter Wheat Region

Project 1: *Genetic and Physical Mapping of the chr. 2H Bin 10 FHB Resistance QTL and Development of Recombinant Lines and Mutants to Facilitate Breeding.*

1. **What major problem or issue is being resolved relevant to Fusarium head blight (scab) and how are you resolving it?** There are two major problems that our research is addressing. 1) the lack of suitable molecular markers to facilitate breeding and lack of knowledge about the gene(s) that control FHB resistance. 2) lack of parent material with suitable agronomic qualities for breeding.
   (1) In order to facilitate molecular marker development and gain an understanding of the genes involved in FHB resistance, we are developing a saturated genetic and physical map of the chromosome 2H bin 10 region. Last year we focused on developing and mapping additional markers based on synteny with the recently sequenced *Brachypodium* genome. This work is continuing, but we have also sequenced a number of BAC clones from the region and identified putative genes that were previously not present among our markers. These will be placed on the genetic map and used to isolate new BAC clones to extend and refine the physical map. This work goes hand in hand with our other project**:** *Sequencing BAC Clones from Chr2(H) FHB Resistance QTL for Gene Discovery*, described in more detail below. This work resulted in the identification of 35 new putative genes that are available from our cDNA libraries. The mapping work was initiated with these because they are the most easily available to us. Other putative genes present in other barley EST libraries will be used to develop molecular markers based on the published sequences in the NCBI database. Because these markers will be closely linked to already mapped markers, we are developing high resolution genetic mapping populations. Towards this end two crosses were made and the F2 developed this past year. They are now being screened for recombinants in a circa 5 cM region from Vrs1 to Uni9735. Additional crosses were made this summer to select additional recombinants as needed.
   (2) The FHB resistant line CIho4196 is 2-rowed, late and tall, all undesirable parental traits for breeding FHB resistant 6-rowed Mid-Western barley cultivars. To assist in corecting this problem, we have taken a mutagenesis approach to select 6-rowed, early and semi-dwarf CI4196 lines that still retain the FHB resistance comparable to CIho4196. To date we have selected 6-rowed mutants, some early lines and potential semi-dwarfs. These are being characterized and submited for FHB evaluation as they become available. One 6-rowed mutant, designated *vrs1.u*, has been characterized and submited to breeders for use (Boyd et al., 2008). Another potential 6-rowed mutant is being evaluated. A very early line (γ08−109) was selected along with two additional early lines. These lines were selected as early at the Pullman agronomy farm. However, in China the γ08−109 line did not appear to be significantly earlier than CIho4196 according to data submited to us by Rich Horsley (a maturity rating of 4 & 5 vs. 5 for CIho4196 and 3 for Foster and Morex). We await the evaluation of these lines for their heading dates under US Mid-Western conditions. In the meantime we are intercrossing all early lines in order to develop an early CIho4196 line suitable for use as a parent for breeding FHB resistant cultivars. The semi-dwarf lines are problematic because they are even later than CIho4196. They are being intercrossed with early lines. Our goal is to develop a CIho4196 line that is 6-rowed, semi-dwarf and of suitable maturity while maintaining FHB resistance. A male sterile CIho4196 line was developed to facilitate this process. This line may also be useful in breeding programs.

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: An improved genetic and physical map of the chromosome 2H region has been developed. The BAC clone contigs from the chr. 2H bin 10 region were sequenced and are being analyzed to develop additional molecular markers. Agronomically improved CIho4196 mutants were developed. These are being characterized and provided to breeders. Thirty-four CAPS markers were developed and sequences published. These are available for use by breeders.

Impact: BAC clone sequences obtained will facilitate improvement of the chromosome 2H bin 10 FHB resistance genetic and physical map that will result in development of new and improved molecular markers for use in selection by breeders. Development of mutants selected to improve the agronomic qualities of CIho4196 will facilitate breeding for FHB resistance by providing a better FHB resistant parent to breeders.

Project 2: *Sequencing BAC Clones from Chr2(H) FHB Resistance QTL for Gene Discovery.*

1. **What major problem or issue is being resolved relevant to Fusarium head blight (scab) and how are you resolving it?** The major problem is that we do not have sufficient molecular markers that are suitable for breeding or for the development of a complete physical map of the chromosome 2H bin 10 FHB resistance QTL region. We are resolving this problem by sequencing the BAC contigs developed so far and by using that sequence for additional marker development and extension of the physical map. The sequence data will also allow us to search for FHB resistance candidate genes.

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: Thirty six BAC clones were sequenced in groups of 12. This resulted in the identification of 2002 sequence contigs. The contigs were analyzed for predicted genes and identified 133 genes. These are being analyzed for function. The genes are being developed into molecular markers and placed on the genetic and physical map under the auspices of our other project: *Genetic and Physical Mapping of the chr. 2H Bin 10 FHB Resistance QTL and Development of Recombinant Lines and Mutants to Facilitate Breeding.*

   Impact: The availability of the BAC sequences will greatly facilitate identification of new molecular markers, development of an improved physical map and identification of candidate FHB resistance genes.

Include below a list all germplasm or cultivars released with full or partial support of the USWBSI. List the release notice or publication. Briefly describe the level of FHB resistance.

A six-rowed CIho4196 mutant designated *vrs1.u*. Described in BGNL 38:7-9.

A group of other CIho4196 mutants not yet published, but available to the barley community. All mutants, including *vrs1.u* show comparable resistance to CIho4196 in China tests.

γ06–002 – male sterile line to facilitate crossing
g08-109 – showing much earlier flowering and maturity at the WSU agronomy farm compared to the parent
g07-038 (early 13) – somewhat earlier than parent
g07-033 (early 8) – somewhat earlier than parent
g07-92 – semi-dwarf, but also very late
g07-070 (dwarf 1) – semi-dwarf, but also very late

other mutants are being evaluated; descriptions will be published as more data is accumulated.

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.

Boyd, C.N., Horsley, R., and Kleinhofs, A. 2008. A six-rowed *vrs1* mutant in Fusarium Head Blight resistant line CIho4196. USWB SCAB Newsletter, Fusarium Focus 8(2) p6.

Boyd, C.N., Horsley, R., and Kleinhofs, A. 2009. Sequence Analysis for Gene Discovery in Barley Chr. 2H Bin 10 Region. Presented at the 2009 National Fusarium Head Blight Forum; Dec. 7-9, 2009; Hyatt Regency Milwaukee, Orlando, Florida. http://scabusa.org/forum.html#forum09 Poster 40, p112

Boyd, C.N., Horsley, R., and Kleinhofs, A. Saturation genetic and physical mapping of the barley 2H bin 10 Fusarium Head Blight resistance QTL. In preparation for Genome.