USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY11 Preliminary Final Performance Report
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Cover Page

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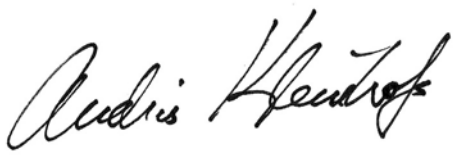
Fiscal Year:	FY11
USDA-ARS Agreement ID:	59-0206-9-075
USDA-ARS Agreement Title:	Mapping and Sequencing of CHR. 2H Bin 10 FHB Resistance QTL for Gene Discovery.
FY11 USDA-ARS Award Amount:	$ 61,095

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
BAR-CP	Genetic and Physical Mapping of the chr. 2H Bin 10 FHB Resistance QTL.	$ 61,095
	Total ARS Award Amount	**$ 61,095**



7/11/12

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 Soft Winter Wheat Region
SWW – Southern Soft Red Winter Wheat Region

Project 1: *Genetic and Physical Mapping of the chr. 2H Bin 10 FHB Resistance QTL.*

1. **What major problem or issue is being resolved relevant to Fusarium head blight (scab) and how are you resolving it?**

   Breeding for resistance to a hemi-biotrophic disease organism, such as Fusarium Head Blight (FHB), is a slow incremental process. To develop new genetic modification approaches, we need to understand the resistance genes and mechanisms involved. There are no single strong resistance genes known for FHB. The Chromosome 2H bin 10 QTL identified in hoCI4196 is one of the strongest FHB resistance QTL known and therefore presents a target for cloning and characterization. Cloning QTL is difficult. In order to facilitate the process we sequenced 36 Bacterial Artificial Chromosome (BAC) clones from the target region in order to identify potential candidate genes and develop improved molecular markers. The candidate genes will be useful as molecular markers in Molecular Marker Assisted Selection (MMAS) and will facilitate identification and validation of resistance QTL from other sources. They should also facilitate understanding of the FHB resistance mechanism.

   Line CIho4196 carries good to excellent FHB resistance, but it is a poor breeding parent.

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:

   We sequenced 36 BAC clones from the bin 10 region, 12 from each region. The region 1 sequences were assembled in 110 contigs ranging in size from 84.37 kb to 101 bp. Of the 110 contigs, 32 were 10 kb or more representing a total sequence of 870 kb. The FGENESH gene finder program (http://linux1.softberry.com) identified 139 putative genes from region 1. This is the region of bin 10 that we believe is most likely to hold the FHB resistance QTL. Putative gene sequence were blasted against the non-redundant protein sequence database using Blastp resulting in only 22 genes with probable known function. The majority of the remaining sequences were due to probable retrotransposons although there were considerable number of “no hit” sequences. To facilitate further development of the physical map, the gene order developed in this study is being compared to the databases available at IPK-Gatersleben (http://webblast.ipk-gatersleben.de/barley/viroblast.php) and Havest barley genome version 0.05 (www.harvest-blast.org).

   Regions 2 and 3 were analyzed in a similar manner

   Impact:

   Sequence data and gene order information will facilitate development of new and better positioned molecular markers to facilitate Molecular Marker based selection of the resistance trait.

Accomplishment:

To rapidly facilitate the breeding effort, we identified a mutant that converted the 2-rowed CIho4196 plant to 6-rowed type while retaining the same level of resistance as CIho4196. This line has been widely distributed to breeders. An improved set of primers that facilitate selection of the mutant type *vrs1* gene (6-rowed) were developed. A male sterile mutant was developed and distributed to facilitate crossing. The early and semi-dwarf mutants have not shown good agronomic potential so far.

Impact:

The 6-rowed mutant has been widely distributed to barley breeders. The male sterile mutant also has been distributed and should facilitate crossing with the FHB resistant parent. It is expected that these mutants will positively impact the development of 6-rowed FHB resistant cultivars suitable for US barley growers.

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.

None