USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY11 Final Performance Report
One-Year No Cost Extension (NCE) through FY12
July 16, 2013

Cover Page

PI:	Andris Kleinhofs
Institution:	Washington State University
Address:	Department of Crop and Soil Science P.O. Box 6420 201 Johnson Hall Pullman, WA 99164-6420
E-mail:	andyk@wsu.edu
Phone:	509-335-4389
Fax:	509-335-8674
Fiscal Year:	FY11 (NCE for FY12)
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**

Andris Kleinhofs 7/9/13
Principal Investigator Date

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[*] 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?**

   We conducted genetic and physical mapping of the barley chromosome 2H bin 10 FHB QTL. This work strives to provide detailed knowledge of this QTL and identify candidate genes that contribute to the FHB resistance. The candidate genes will be useful as molecular markers in MAS and facilitate identification and validation of resistance QTL in other sources. They should also facilitate understanding of the FHB resistance mechanism.
   We developed mutants derived from CIho4196 with 6-rowed head type, early maturity and reduced height while maintaining FHB resistance and DON levels comparable to CIho4196.

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 in three groups of 12. The sequence was analyzed and identified 132 predicted genes. Of these, only 32 were previously mapped and used to identify BAC clones. The recent sequencing of the barley genome now enables the analysis of all the putative genes in the chromosome 2H bin 10 FHB resistance region. Unfortunately we have not been able to complete this work due to funding and ability to hire qualified persons to carry out the work.

   Thirty-two CAPS markers were developed for mapping the chr. 2H bin 10 region. Information about these has been made available to barley scientists for use in MAS selection and mapping.

   Mutants of the FHB resistant line for 6-rowed head type, early maturity and reduced height have been identified and intercrossing is in progress to combine these traits in commercially useful parent germplasm. The mutants have retained the CIho4196 FHB resistance and low DON levels. A male sterile mutant was developed to facilitate crossing. These lines are available to barley scientists for use in breeding.

   Impact:
   The development of a 6-rowed CIho4196 line and its distribution to breeders is probably the major impact. Exactly how significant it will be remains to be seen from the breeding efforts. The development of the CIho4196 male sterile mutant also constitutes a potential significant impact. The other mutants do not appear to be useful for practical breeding.
   Our sequencing effort is now mute with the release of the whole barley genome sequence. The CAPS markers we developed have potential impact, but remain to be confirmed as useful or not by the plant breeders.

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