USDA-ARS / USWBSI
FY04 Final Performance Report
July 15, 2005

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**
Year:	**FY2004** (approx. May 04 – April 05)
FY04 ARS Agreement ID:	**59-0790-4-110**
FY04 ARS Agreement Title:	**Saturation Mapping of the Chromosome 2(2H) Fusarium Head Blight Resistance QTL.**
FY04 ARS Award Amount:	**$ 64,390**

USWBSI Individual Project(s)

USWBSI Research Area[*]	**Project Title**	**ARS Adjusted Award Amount**
BIO	Saturation Mapping of the Chromosome 2(2H) Fusarium Head Blight Resistance QTL.	$ 64,390
	Total ARS Award Amount	**$ 64,390**

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

(Form – FPR04)

Project 1: *Saturation Mapping of the Chromosome 2(2H) Fusarium Head Blight Resistance QTL.*

1. What major problem or issue is being resolved and how are you resolving it?
Fusarium head blight (FHB), incited by *Fusarium graminearum* Schwabe [telomorph *Gibberella zea* (Schwein)], adversely affects the quality of barley and wheat grown in the Upper Midwest US. The presence of blighted kernels and deoxynivalenol (DON), a mycotoxin produced by the pathogen, make barley unsuitable for malting and brewing reducing or eliminating grower profits. Barley chromosome 2H region contains genes that confer resistance to FHB. This region is also associated with undesirable traits such as late heading, tall, 2-rowed, and DON accumulation. Our work is directed at resolving these udesirable traits from the FHB resistance trait in order to facilitate incorporation of FHB resistance in commercially acceptable cultivars. To resolve this issue, we are mapping molecular markers to the region and establishing a Bacterial Artificial Chromosome (BAC) physical contig of the region. We are also developing isogenic lines containing small fragments of the resistant line CI4196 genome into a commercial, susceptible line, genomic background.

What were the most significant accomplishments?

Accomplishments: during this grant period we have focused on adding molecular markers to the region of the main FHB resistance QTL. At this time the map contains 67 markers in approximately 20 cM region containing the major FHB resistance QTL. Three of these markers were converted to CAPS markers to facilitate PCR-based selection. The physical map development is progressing. Isolines for segments of the major FHB QTL are in the final stages of development and will be available to other scientists for testing. A 6-rowed FHB resistant recombinant was identified. However, it needs further refinement because it is still late flowering and excessively tall.

Impact: Random recombination experiments have, to date, failed to separate the undesirable characteristics of CI4196 from the desirable FHB resistance trait. Our work with molecular markers is starting to make progress towards this goal. Impact to other scientists will be availability of recombinant lines more suitable for the breeding effort and also availability of multiple molecular markers for use in selection.

As a result of accomplishments, what does your clientele, the scientific community, and agriculture as a whole have that they didn’t have before?: The availability of molecular markers and recombinant lines will accelerate the rate of progress towards developing commercial barley varieties with resistance or tolerance to FHB.

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 you grant. Please reference each item using an accepted journal format. If you need more space, continue the list on the next page.

Schmierer, D., T. Drader, R. D. Horsley and A. Kleinhofs, 2004. Saturation mapping of a major fusarium head blight QTL on barley chromosome 2H. Plant and Animal Genome XII, Jan. 10-14, San Diego, CA. Abstract P448.

Wenzl, P., J. Carling, D. Kudrna, D. Jaccoud, E. Huttner, A. Kleinhofs, and A. Kilian, 2004. Diversity arrays technology (DArT) for whole-genome profiling of barley. Proc. Natl. Acad. Sci. USA 101:9915-9920.

Kleinhofs, A., 2004. Genetic and physical mapping of the barley chromosome 2H Fusarium Head Blight resistance QTL. In: Canty, S.M., Boring, T., Wardwell, J., and Ward, R.W. (Eds.), Proceedings of the 2nd international symposium on Fusarium Head Blight; incorporating the 8th European Fusarium Seminar, 2004, 11-15 December; Orlando, FL, USA Vol. 1 p 84.

Horsley, R.D., D. Schmierer, C. Maier, D. Kudrna, C.A. Urrea, B.J. Steffenson, P.B. Schwarz, J.D. Franckowiak, M.J. Green, B. Zhang, and A. Kleinhofs, 2005. Identification of QTL Associated with Fusarium Head Blight Resistance in the Barley Accession CIho4196. Submitted to Crop Science