USDA-ARS / USWBSI
FY03 Final Performance Report (approx. May 03 – April 04)
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Cover Page

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Year:	**FY2003 (approx. May 03 – April 04)**
FY03 ARS Agreement ID:	**59-0790-9-049**
FY03 ARS Agreement Title:	**Saturation mapping of Fusarium head blight resistance QTL.**
FY03 ARS Award Amount:	**$ 69,854**

USWBSI Individual Project(s)

USWBSI Research Area*	Project Title	ARS Adjusted Award Amount
BIO	Saturation mapping of Fusarium head blight resistance QTL.	$ 69,854
	Total Amount Recommended	**$ 69,854**

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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: ***Saturation mapping of 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. There are three major approaches to fixing the problem: 1) transfer of resistance QTL from agronomicaly unsuitable barley lines to adapted cultivars 2) isolation of FHB resistance genes so that they could be manipulated in vitro to improve resistance and 3) production of transgenic cultivars carrying resistance genes from exotic species. Our research addresses the first two approaches by providing molecular markers for use in molecular marker assisted selection of FHB resistance QTL and by working towards establishing a physical map of a major FHB resistance QTL and eventual cloning of the responsible genes.

We are developing a genetic and physical map of the barley chromosome 2(2H) FHB QTL by identifying homology with sequenced rice genomic DNA from the region syntenous to the target region. This allows us to saturate the region with markers and thus facilitate their utilization for molecular marker assisted selection of specific QTL. The long term goal is to try to identify candidate genes that might be involved in the FHB resistance. Therefore, we are identifying bacterial artificial chromosome (BAC) clones for the mapped region. The BAC clones are fingerprinted and formed into contigs. Once a region identified as important in FHB resistance is covered by a physical BAC clone contig, they will be sequenced and potential candidate resistance genes identified.

2. What were the most significant accomplishments?

The 2H FHB QTL region spans ~40cM and ~30cM on the FosCI and the Steptoe/Morex (SM) genetic maps, respectively. A total of 28 rice BAC clones, comprising ~2.5Mbp, span the rice chromosome 4 region with synteny to the barley chromosome 2H QTL region. The rice chromosome 4 BACs assemble into two contigs, BAC clones OSJNBb0091E11 to OSJNBa0029H02 (~365kb) and OSJNBa0014K14 to OSJNBa0010H02 (~2.2Mbp). There is a gap of unknown distance between OSJNBa0029H02 and OSJNBa0014K14. Ninety-seven unique barley ESTs were identified from the 28 rice BACs. Fourty-seven have been tested for polymorphism against several barley cultivars. Twenty-six of these 47 have been mapped to the 2H FHB QTL region. The rest either mapped elsewhere in the genome or were non-polymorphic. These results give a 55.3% efficiency of barley ESTs identified with homology to rice that map in syntennous positions. One EST mapped to the 2H QTL region that has homology to rice chromosome 7 PAC clone P0022E03.

Wheat ESTs mapped to group 2 deletion lines were used to identify 39 homologous barley ESTs that were screened for polymorphisms. Only four of these mapped to the 2H FHB QTL region. Due to the relatively large distances between deletion line breakpoints that delimit each wheat chromosome bin, several ESTs were identified that mapped outside the FHB QTL region on 2H. Other probes were either non-polymorphic or mapped to other chromosomes.

A total of 34 probes (including genomic clones) have been mapped to the QTL region to date. Nineteen have been mapped in the FosCI population, three in SM DHLs, 10 in both FosCI and SM, one in Harrington x Morex DHLs, one in Harrington x TR306 DHLs, and one in a Chebec x Harrington population. All 34 probes have been used to screen the 6x cv. Morex barley BAC library, 17 of which have been confirmed as identifying 98 individual BAC clones. Fingerprinting of these BAC clones is in progress.

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. Horsley, and A. Kleinhofs (2003). Saturation Mapping of a Major Fusarium Head Blight QTL on Barley Chromosome 2H. 2003 National Fusarium Head Blight Forum Proceedings p36-39, Bloomington, MN, Dec. 13-15, 2003.

Schmierer, D., T. Drader, R. Horsley, and A. Kleinhofs (2003). Saturation Mapping of a Major Fusarium Head Blight QTL on Barley Chromosome 2H. Poster presented at the Plant and Animal Genome XII Poster 448, p183.