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:	**59-0790-9-48**
FY03 ARS Agreement Title:	**Development of Markers Linked to FHB Resistance in Durum and Hexaploid Wheat.**
FY03 ARS Award Amount:	**$ 100,032**

USWBSI Individual Project(s)

USWBSI Research Area*	Project Title	ARS Adjusted Award Amount
BIO	Development of markers linked to FHB resistance in hexaploid wheat.	$ 68,634
BIO	Development of markers linked to FHB resistance in durum wheat.	$ 31,398
	Total Amount Recommended	**$ 100,032**

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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: ***Development of markers linked to FHB resistance in hexaploid wheat.***

1. What major problem or issue is being resolved and how are you resolving it?

The ultimate goal of this project is to identify and develop breeder friendly markers to improve germplasm development as well as reduce the time needed to variety release in hexaploid wheat. Specific objectives of this current project are to: 1) identify QTL region(s) for FHB resistance in ND671/Wangshuibai RIL population; 2) analyze early generation lines derived from cltr9445, a Chinese source of resistance, for the presence of important FHB QTL regions; and 3) develop populations from new sources of FHB resistance for introgression of important regions into hexaploid wheat.

2. What were the most significant accomplishments?

Wangshuibai is a Chinese hexaploid line that shows a good level of resistance to the spread of the infection (Type II). In our greenhouse evaluations using single floret inoculation the spread of the infection after 21 days ranged from 7 to 11% compared to 15 to 21% range for Sumai3. A recombinant inbred line (F_6 derived) population of 88 individuals was used to construct a molecular marker linkage map with 185 loci. Quantitative trait loci (QTL) analysis revealed a major QTL on chromosome 3BS explaining 31% of the phenotypic variation at 21 days after inoculation. This locus exhibited strong epistatic interactions with other loci on chromosome 3A, 5A, 6B and 7B; individually these loci, were not significant. The best epistatic model containing the major QTL on 3BS and a locus on 3AS explained 67% of the phenotypic variation. This is the first report on the importance of epistatic interactions in FHB resistance in wheat. Validation of these results using the remaining 300 recombinant inbred lines from the same population is underway.

Cltr9445 is a Chinese landrace showing resistance to FHB. In both field and greenhouse studies at University of Missouri (Dr. Anne McKendry, USWBSI web site) Cltr9445 showed a very high level of resistance with less than 5% spread through the spike comparing to 11 and 15 for Wangshuibai and Sumai3, respectively. The goal of this study is to perform a preliminary QTL mapping work using the concept of Linkage Disequilibrium (LD). Equilibrium is assumed in natural populations after a large number of random mating generations, however disequilibrium is found in populations within families or related groups. Since selfing reduces LD, the extent of the LD is larger in early generations. Phenotypic evaluation of two populations has been accomplished for both F_3 and F_4 lines derived from Cltr9445. Tissue for DNA extractions has been collected from both populations at both generations. DNA extractions (1000+ samples) are completed and marker screening will begin immediately.

We plan to use the LD approach described above in the early generations of the populations being developed as part of this objective. As we work through and test the methodology using the Cltr9445 lines we will develop new populations from other source of resistance to FHB. Analysis of these newly developed populations would allow us to focus on those carrying new genes for FHB resistance with the goal of pyramiding as many different resistance genes in the same background as possible. Traditionally, researchers have relied on phylogenetic analysis and differences in lineage as an indication of different resistance loci. Even though these studies are valuable, they can be misleading. We believe association mapping to be a faster and more accurate method of identifying different resistance genes.

Project 2: ***Development of markers linked to FHB resistance in durum wheat.***

1. What major problem or issue is being resolved and how are you resolving it?

The ultimate goal of this project is to develop "breeder friendly" markers for FHB resistance in durum wheat to help accelerate the process of germplasm development and time to variety release. Specific objectives of the project are to 1) identify markers closely linked to FHB resistance loci; 2) develop a PCR-based marker system for screening large populations segregating for FHB; and 3) demonstrate the utility of these markers in populations developed by various breeding programs.

2. What were the most significant accomplishments?

To identify markers closely linked to FHB resistance loci we have been characterizing a number of populations and backcross derived material for introgression of valuable loci. Through this introgression we will not only be able to validate the effectiveness of various markers for FHB resistance selection but will also be able to identify and test the validity of any new markers being developed as part of various QTL analysis studies in this selection process. In this regard introgression of Sumai 3 resistance into elite durum backgrounds is continuing. A number of BC_2F_1 seeds have been harvested from various crosses carrying the markers linked to the 3BS QTL. They will now be used for advancement to BC_3F_1. We continually screen these material for FHB resistance through disease inoculation as well as marker selection.

Continuing on the same objective of introgressing valuable loci, we have been evaluating the potential of Wangshuibai as a source of resistance in durum wheat. For this a recombinant inbred line population (F_6 derived) of 140 individuals from a cross of elite durum breeding line to Wangshuibai has been evaluated in two greenhouse seasons. DNA has been extracted and the markers identified in the hexaploid population (described in the first objective of hexaploid wheat progress report) are being used to screen these lines. This will allow us to study the introgression of valuable QTLs from Wangshuibai as well as any epistatic interactions detected in a hexaploid background in a tetraploid background. Preliminary analysis indicates that the major locus on 3BS has successfully been transferred from Wangshuibai to durum wheat. Additionally, a number of the epistatic interactions described in hexaploid wheat are detectable in this tetraploid population. This study is on-going and once completed will prove highly valuable in breeding a FHB resistant durum wheat.

We have also been introgressing the 3AS FHB resistance QTL from *Triticum dicoccoides* into various durum backgrounds. We now have a number of lines in the BC_5F_1 stage that have been selected by both marker and disease inoculation. These materials will now be advanced through selfing for field evaluation possibly in the summer of 2005.

We continually screen new markers (i.e. EST derived primers or new microsatellite markers) for their use in our various introgression and mapping studies. These markers are first screened for their linkage relationship to the important FHB resistance regions. Then they are evaluated for their ease of application in a marker assisted selection scheme. This process will test the utility of these markers for screening large populations and their value in a breeding program designed for development of FHB resistance durum wheat.

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.

Berzonsky WA, Hartel KD, Kianian SF, and Leach GD. Registration of four synthetic hexaploid wheat Germplasm lines with resistance to Fusarium head blight. Crop Science 44: 1500.

Hartel KD, Berzonsky WA, Kianian SF, and Ali S. Expression of a *Triticum turgidum* L. var. dicoccoides source of Fusarium head blight resistance transferred to synthetic hexaploid wheat. Plant Breeding (in press)

Gonzalez-Hernandez JL, del Blanco A, Ali S, Berzonsky WA, and Kianian SF. Genetics of resistance to Fusarium head blight in the hexaploid wheat Wangshuibai. Genome (submitted)

Gonzalez-Hernandez JL, del Blanco A, Ali S, Berzonsky WA, and Kianian SF. Wangshuibai: a hexaploid wheat resistant to the spread of Fusarium head blight. Presented at Fusarium Head Blight Forum December 13-15, 2003.

Chen X, Hu J, Kianian SF, and Cai X. Saturation mapping of a major Fusarium head blight resistance QTL region in tetraploid wheat. Presented at Fusarium Head Blight Forum December 13-15, 2003.

Bhamidimarri S, Elias EM, Gonzalez-Hernandez JL, and Kianian SF. Comparison of marker assisted selection to phenotypic selection for FHB resistance in durum wheat. ASA annual meeting November 2-6, 2003. C01-bhamidmarri795209-oral.