USDA-ARS / USWBSI
FY03 Final Performance Report (approx. May 03 – April 04)
July 15, 2004

Cover Page

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Year:	**FY2003 (approx. May 03 – April 04)**
FY03 ARS Agreement ID:	**NA**
FY03 ARS Agreement Title:	**Marker-assisted Characterization and Selection of Wheat Cultivars for Scab Resistance.**
FY03 ARS Award Amount:	**$ 55,387**

USWBSI Individual Project(s)

USWBSI Research Area*	Project Title	ARS Adjusted Award Amount
BIO	Molecular Characterization of QTL for Scab Resistance in Wheat Cultivar Wangshuibai.	$ 42,997
VDUN	Utilization of High-throughput Markers to Improve Scab Resistance in Wheat.	$ 12,390
	Total Amount Recommended	**$ 55,387**

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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: ***Molecular Characterization of QTL for Scab Resistance in Wheat Cultivar Wangshuibai.***

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

Effective utilization of scab resistance resources relies on understanding inheritance of wheat resistance to scab and to DON accumulation in wheat grain. Major scab resistance QTL from Sumai 3 has been mapped and widely used in breeding programs. Identification of resistance genes from different sources may enrich scab resistance gene diversity and provide new genes to enhance scab resistance level through gene pyramiding. We screening a collection of Asian wheat cultivars and landraces to identify new resistance sources different from Sumei 3, mapping scab resistance QTL from Wangshuibai, a Chinese landrace different from Sumai 3, with AFLP and microsatellite markers, and to elucidate genetic effects of these QTL by testing the mapping population for scab resistance and DON accumulation under greenhouse conditions. The results are also expected to provide breeders with selectable markers for breeding wheat cultivars with low DON and high levels of scab resistance to speed up breeding process.

2. What were the most significant accomplishments?

1. About 140 F6 RILs from Wangshuibai/Wheaton were evaluated for Type II resistance and DON content in two greenhouse cycles and about 600 AFLP primers and 800 SSR primers were screened between parents.
2. About 1000 polymorphic AFLP fragments and 150 SSR markers were analyzed in the RIL population using Li-Cor DNA Analyzer.
3. About 100 markers were identified to be associated with Type II resistance and/or low DON level with $r^2>0.05$.
4. The largest R^2 value was 0.35 for type II resistance and 0.15 for low DON content. Two QTL were detected on 3BS although SSR alleles are different from that in Sumai 3. The other possible QTLs for Type II resistance were detected on chromosomes 3A, 3D, 7A, 7B, 5B, 5A, 2B, 2A, and 6A and four of them also have significant effect on low DON content.
5. About 150 wheat accessions from China, Japan and other Asian countries were screened for Type I and Type II resistance. About 15 accessions showed a high level of resistance. Most of these accessions have different alleles from these of Sumai 3 SSR markers linked to 3BS QTL.

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.

Peer-reviewed Articles

1. Zhou W-C, Kolb F. L., Yu J-B, **Bai G-H**, Boze, L K, Domier, L.L. 2004. Molecular characterization of Fusarium head blight resistance in Wangshuibai with SSR and AFLP markers. (Accepted).
2. Zhang X, Zhou, M, Ren, L, **Bai G-H**, Ma, H, Scholten O.E., Guo P.G, Lu W-Z. 2004. Molecular characterization of *Fusarium* head blight resistance from wheat variety Wangshuibai. Euphytica (Accepted with minor revision)
3. **Bai G-H,** Shaner GE. 2004. Management and resistance in wheat and barley to Fusarium Hhead blight. Phytopathology Ann Rev. (In Press)
4. **Bai G-H**, Chen L-F and Shaner G. 2003. Breeding for resistance to head blight of wheat in China. Page 296-317 in: Wheat *Fusarium* Head Blight. Kurt Leonard (ed). APS Press.
5. **Bai G-H**, Guo P-G and Kolb FL. 2003. Genetic relationships among scab-resistant cultivars of wheat based on molecular markers. Crop Science 43: 498-507
6. Guo P-G, **Bai G-H** and Shaner G.E. 2003. AFLP and STS tagging of a major QTL for scab resistance in wheat. Theor. & Appl. Genet. 106:1011-1017
7. W-C. Zhou, F. L. Kolb, **G-H. Bai**, L. L. Domier, L. K. Boze and N. J. Smith. 2003 Validation and marker-assisted selection of a major QTL for scab resistance with SSR markers in wheat. Plant Breeding 122:40-46
8. W-C. Zhou, F. L. Kolb, **G-H. Bai**, L. L. Domier, L. K. Boze and N. J. Smith. 2003 Validation and marker-assisted selection of a major QTL for scab resistance with SSR markers in wheat. Plant Breeding 122:40-46

Meeting Abstract

1. Bernardo A.N., **Bai G-H , Ayoubi P.,** and Guenzi A. 2004. Using cDNA microarray to monitor the transcriptional response of wheat cultivars to infection by Fusarium graminearum. Genome XII Jan 10-14, San Diego. CA
2. Bernardo A.N., **Bai G-H** and Guenzi A. 2003. Microarray analysis of gene expression in wheat infected with Fusarium graminearum. Genome XI. Jan 10-16, San Diego. CA
3. Bernardo A.N., **Bai G-H , Ayoubi P.,** and Guenzi A. 2003. Using cDNA microarray to monitor the transcriptional response of wheat cultivars to infection by Fusarium graminearum. Dec. 13-15, 2003 National Fusarium Head Blight Forum, Bloomington, MN.
4. Guihua Bai. 2003. Role of USDA Regional Genotyping Centers. Dec. 13-15, 2003 National Fusarium Head Blight Forum, Bloomington, MN.

5. J-B Yu, **G-H Bai**, S-B Cai and T Ban. 2003. AFLP Analysis of Asian Wheat Cultivars Resistant to Fusarium Head Blight. November 2-6, 2003, ASA-CSSA-SSSA Annual Meetings, Denver, Colorado
6. J-B Yu, **G-H Bai**, S-B Cai and T Ban. 2003. Genetic relationship among Asian Wheat germplasm resistant to Fusarium head blight. Dec. 13-15, 2003 National Fusarium Head Blight Forum, Bloomington, MN.
7. W. C. Zhou, F. L. Kolb, **G. H. Bai**, 2003. Marker-assisted backcrossing selection of near isogenic lines for 3BS Fusarium head blight resistance QTL in hexaploid wheat. November 2-6, 2003, ASA-CSSA-SSSA Annual Meetings, Denver, Colorado
8. W. C. Zhou, F. L. Kolb, **G. H. Bai**, L. K. Boze, L. L. Domier, 2003. Molecular mapping of scab resistance QTL in Wangshuibai. November 2-6, 2003, ASA-CSSA-SSSA Annual Meetings, Denver, Colorado
9. Yang J, Bai, G-H, Yu, J-B Sood S., Bernardo A. 2003. High-throughput genotyping facility for marker-assisted breeding and molecular marker development. Dec. 13-15, 2003 National Fusarium Head Blight Forum, Bloomington, MN.

Project 2: ***Utilization of High-throughput Markers to Improve Scab Resistance in Wheat.***

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

Because large environmental variation associates with disease evaluation and the disease screening procedure is laborious, progress in breeding for resistant cultivars has been slow with conventional methods. High-throughput marker-assisted selection (MAS) can minimize environmental variation and speed up the screening processes. However, many conventional breeding programs don't have access to this type of facility due to limitation in funding. To conduct marker-assisted selection (MAS) for the major FHB resistance QTL on 3BS and other chromosomes, our lab provides marker analysis service to wheat breeding programs nationwide in order to speed up the deployment of the major QTL in the US wheat.

2. What were the most significant accomplishments?

- High throughput DNA isolation and PCR analysis protocols were established in our Genotyping Center and published on our website
- Screened two regional performance nurseries (NRPN/SRPN) with markers for 3BS major QTL
- Screened about 1000 wheat samples from three public research groups and one private company with markers for FHB resistance and generated more than 5000 datapoints

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