

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

Cover Page

PI:	Yang Yen
Institution:	South Dakota State University
Address:	Department of Biology & Microbiology 249C NPB, Box 2140D Brookings, SD 57007
E-mail:	Yang_Yen@sdstate.edu
Phone:	605-688-4567
Fax:	605-688-5624
Year:	FY2004 (approx. May 04 – April 05)
FY04 ARS Agreement ID:	59-0790-1-078
FY04 ARS Agreement Title:	Study of Scab-Related Genes and Molecular Markers.
FY04 ARS Award Amount:	\$ 57,523

USWBSI Individual Project(s)

USWBSI Research Area*	Project Title	ARS Adjusted Award Amount
BIO	Molecular Analysis & Mapping of Major FHB Resistance Genes in the Japanese Cultivar Tokai 66.	\$ 31,512
GIE	Molecular Study of the Novelty of the Newly Identified FHB Resistance Sources in Spring Wheat.	\$ 26,011
	Total ARS Award Amount	\$ 57,523

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 Analysis & Mapping of Major FHB Resistance Genes in the Japanese Cultivar Tokai 66.*

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

Sumai 3 is currently the main FHB resource used in USA and the world for breeding wheat variety with better FHB resistance. Broadening our FHB resistance sources will not only strengthen our ability to control FHB epidemics but also reduce risk of the potential disaster caused by a sudden loss of Sumai 3 derived FHB resistance. Tokai 66 is one of the newly identified FHB resistance sources showing some promise. The goal of this project is to confirm the novelty of the FHB resistance in Tokai 66 while developing SSR markers for the confirmed novel resistance QTLs. We are approaching our goal by genetically analyzing the FHB resistance of Tokai 66 with the aid of SSR markers to determine the number of FHB resistant QTLs that it may have, and compare these QTLs to their homologues in Sumai 3. Our objectives for FY2004 were: 1) Creating mapping population between Tokai 66 and Y1193-6 (a FHB-susceptible landrace); 2) Discovering polymorphic SSR markers between the parents; and 3) Initiating genetic analysis.

2. What were the most significant accomplishments and its impact (how is it being used)?

Accomplishment: Single-seed descent method has been used to achieve Objective 1. Tokai 66 was pollinated by Y1193-6 in greenhouse. Two hundred F_{2:3} plants are growing in growth chamber. To achieve Objective 2, the parents were screened for SSR polymorphism with 80 SSR primer sets, which covers every wheat chromosome arm and include all the reported that enable to generate markers to scab resistance. A total of 53 polymorphic SSR alleles were observed between the parents. These polymorphic SSR alleles will be used to screen markers for FHB resistance QTLs discovered by our genetic analysis of the segregating population. A Sumai 3/Y1193-6 F₃ population is in the field test for FHB resistance and the test results will be served as a reference for the analysis of the Tokai 66/Y1193-6 population for QTL novelty.

Impact: Our success in realizing our objectives set for FY2004 has paved a solid foundation for our research in FY2005. The outcome of this project will include the discovery of FHB resistance QTLs in Tokai 66 and the confirmation/disapproval of their novelty in comparison with those of Sumai 3. Novel resistance genes are the foundation for breeding wheat cultivars with better FHB resistance. Therefore, this project will help realize the USWBSI's goal of "To develop as quickly as possible effective control measures that minimize the threat of Fusarium head blight (scab) to the producers, processors, and consumers of wheat and barley" through achieving the following FY2004 goals set for the Biotechnology research area: "Map new and/or novel sources of resistance genes in wheat and barley germplasm" and the following USWBSI's FY2004 goal set for the Germplasm Introduction and Enhancement research area: "Genetic analyses of newly identified and/or acquired sources of resistance".

Project 2: *Molecular Study of the Novelty of the Newly Identified FHB Resistance Sources in Spring Wheat.*

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

Germplasm is the foundation of the breeding for FHB-resistant varieties. New promising FHB resistance have been selected but their novelty has yet confirmed. This project aiming at molecular confirmation of the novelty of the FHB resistance in Abura, a Brazilian landrace, that shows similar FHB resistance level as Sumai 3. Our objectives for FY2004 were: 1) Constructing subtractive FHB-resistance-related cDNA libraries for Abura and Sumai 3 for functional genomic confirmation of the novelty of the FHB resistance in Abura and 2) Developing SSR markers for the resistance QTLs. The subtractive FHB-resistance-related cDNA libraries have been successfully constructed and used to probe differentially expressed genes during FHB pathogenesis with Affymetrix GeneChip wheat microarray. We are analyzing the microarray data. To realize our second objective, we have been constructing an Abura/Y1193-6 mapping population with the single-seed-descendant method. The F_{2:3} plants are growing in growth chamber. We have also screened the two parents for SSR polymorphism with 80 SSR primer sets, which covers every wheat chromosome arm and include all the reported that enable to generate markers to scab resistance. So far 52 polymorphic SSR alleles have been observed between the parents, and these polymorphic SSR alleles will be screened for SSR markers for the FHB resistance QTLs in Abura with the mapping population.

2. What were the most significant accomplishments and its impact (how is it being used)?

Accomplishment: The subtractive FHB-resistance-related cDNA libraries have been successfully constructed and used to probe differentially expressed genes during FHB pathogenesis with Affymetrix GeneChip wheat microarray. We are analyzing the microarray data. Briefly, 890 scab-related genes are common between the two cultivars; 708 and 752 scab-related genes are unique to Suami 3 and Abura, respectively; and most of these genes belong to Fusarium. To realize our second objective, we have been constructing an Abura/Y1193-6 mapping population with the single-seed-descendant method. The F_{2:3} plants are growing in growth chamber. We have also screened the two parents for SSR polymorphism with 80 SSR primer sets, which covers every wheat chromosome arm and include all the reported that enable to generate markers to scab resistance. So far 52 polymorphic SSR alleles have been observed between the parents, and these polymorphic SSR alleles will be screened for SSR markers for the FHB resistance QTLs in Abura with the mapping population

Impact: The microarray analysis will reveal a transcriptome-wide expression profile for scab-related genes, and lead to molecular confirmation/disapproval of the novelty of the FHB resistance of Abura. It also will pave a foundation for discovery of new resistance genes and for developing a molecular understanding of FHB pathogenesis and FHB resistance. The new resistant genes will be the foundation for marker development and gene isolation. Therefore, the outcome of this project will help achieving the following USWBSI's FY2004 goal set for the Germplasm Introduction and Enhancement research area: "Genetic analyses of newly identified and/or acquired sources of resistance"; and the following FY2004 goals set for the Biotechnology research area: "Map new and/or novel sources of resistance genes in wheat and

barley germplasms" and "Characterize molecular mechanisms of host-pathogen interactions and identify potential resistance/virulence genes".

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

Liu, D., K.D. Glover and Y. Yen. 2004. MAS Efficiency in Improving Scab Resistance in Spring Wheat: A Look From the Reverse Angle. *In: Proceedings of the Second International Wheat Scab Symposium*, Dec. 11-15, 2004, Orlando, FL. USA, pp. 94-97.

Xing, D.-H., Y. Yen, Y. Jin and J. Rudd. 2004. Study of genes important to scab pathogenesis and resistance in wheat. *In: Proceedings of the Second International Wheat Scab Symposium*, Dec. 11-15, 2004, Orlando, FL. USA, pp. 534-538.

Weng, Y.-J. and Y. Yen. 2004. Quantitative assay of the expression of gene *G12* in scab resistant and susceptible wheat varieties. *In: Proceedings of the Second International Wheat Scab Symposium*, Dec. 11-15, 2004, Orlando, FL. USA, pp 201.