USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY05 Final Performance Report (approx. May 05 – April 06)
July 14, 2006

Cover Page

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Fiscal Year:	**2005**
FY05 ARS Agreement ID:	**59-0790-1-078**
Agreement Title:	**Study of Scab-Related Genes and Molecular Markers.**
FY05 ARS Award Amount:	**$ 53,659**

USWBSI Individual Project(s)

USWBSI Research Area*	**Project Title**	**ARS Adjusted Award Amount**
BIO	Genetic Analysis & Mapping of Major FHB Resistance QTLs in the Japanese Cultivar Tokai 66.	$ 29,269
GIE	Genetic Analysis of Major FHB Resistance QTLs in Brazilian Landrace Abura.	$ 24,390
	Total Award Amount	**$ 53,659**

Principal Investigator Date

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* 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 – FPR05)

Project 1: *Genetic Analysis & Mapping of Major FHB Resistance QTLs in the Japanese Cultivar Tokai 66.*

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

   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 the FY2005 were: 1). Continue our efforts in creating mapping populations between Tokai 66 and Y1193-6; 2) Complete preliminary SSR analysis of the F_2 populations; and 3) Screening the parents for more polymorphic SSR markers.

2. **List the most important accomplishment and its impact (how is it being used?). Complete all three sections (repeat sections for each major accomplishment):**

   Accomplishment:

   By the end of the FY05, the recombinant inbred mapping population has been advanced to $F_{2:6}$, and 98 polymorphic SSR markers have been identified between the parents. We did not do F_2 analysis of SSR marker and, instead, have decided to defer the population screening until the $F_{2:6}$ generation to get more meaningful results. SSR analysis of the $F_{2:6}$ generation is going on.

   Impact:

   The completion of the population construction has provided us the necessary materials for the goal of this project. The polymorphic SSR markers are the tools that will help us to achieve our goal. With the mapping population and the polymorphic markers, we can now start to dissect the scab resistance of Tokai 66 and identify the SSR markers for it.

   As a result of that accomplishment, what does your particular clientele, the scientific community, and agriculture as a whole have now that they didn't have before?:

   Now we have a recombinant inbred population that can be used to study the scab resistance of Tokai 66. Since Tokai 66 is known to have lower ratio of infected grains, which usually means lower DON content, than Sumai 3, we now have a chance to identify Type III/Type IV resistance QTLs.

Project 2: *Genetic Analysis of Major FHB Resistance QTLs in Brazilian Landrace Abura.*

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

Our hypothesis is that landrace Abura contains multiple novel major FHB resistance QTLs. This project aims at test this hypothesis. We are doing so by genetically analyzing the Abura/Y1193-06 and the Sumai 3/Y1193-06 segregating populations with aids by molecular assay. The population will be created, polymorphic SSR markers between the parents will be identified and used for mapping, and microarray and real-time RT-PCR will be used to profile the gene expression of both Abura and Sumai 3. Scab-related genes will be identified by comparing gene expression profiles between the scab-inoculated and the mock-inoculation control of the same geneotype.

2. List the most important accomplishment and its impact (how is it being used?). Complete all three sections (repeat sections for each major accomplishment):

Accomplishment:

The construction of the two recombinant inbred populations has been completed with the advancement of both population to the $F_{2:7}$ generation. Ninrty-nine and 97 polymorphic SSR markers have been identified, respectively, between Y1193-06 and Sumai 3 or Abura. Affymetrix Wheat Genome GeneChip has been used to profile scab-related gene expression 24 hours after scab inoculation in Abura and Sumai 3. Real-time RT-PCR was used to verify the microarray data. Of the 55,000 genes assayed, 9323 were found to be scab-related. Of these scab-related genes, 2061 differentially expressed genes were found between Abura and Sumai 3.

Impact:

The completion of the mapping population has provided a foundation for genetically verification of the novelty of the scab resistance in Abura. The polymorphic SSR markers are the resource for markers to novel scab resistance QTLs, if any, in Abura. The results of our function genomic analysis have enabled us to develop an understanding of the interaction between wheat and the fusarium fungus and the resistance mechanism of wheat to scab.

As a result of that accomplishment, what does your particular clientele, the scientific community, and agriculture as a whole have now that they didn’t have before?:

This project has provided the scientific research community two mapping populations that share a common susceptible parent, and a set of gene expression profiles of wheat under the challenge by the fusarium fungus.

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.

Weng.Y.-J. and Y. Yen. 2005. Genetic diversity among 21 elite spring wheat accessions resistant to *Fusarium* head blight assessed with SSR markers. Agronomy Abstracts.
Li, G. and Y. Yen. 2005. Profiling the expression of genes related to FHB pathogenesis in wheat with Affymetrix GeneChip Wheat Genome Array. *In*: Proceedings of the 2005 National Fusarium Head Blight Forum, Dec. 11-13, 2005, Milwaukee, WI, USA, pp 54.