USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY06 Final Performance Report (approx. May 06 – April 07)
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Cover Page

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Fiscal Year:	2006
USDA-ARS Agreement ID:	59-0790-4-109
USDA-ARS Agreement Title:	Development of Markers Linked to FHB Resistance in Durum and Hexaploid Wheat.
FY06 ARS Award Amount:	$ 83,189

USWBSI Individual Project(s)

USWBSI Research Area[*]	Project Title	ARS Award Amount
HGG	Development of Markers Linked to FHB Resistance in Durum Wheat.	$ 35,380
HGG	Development of Markers Linked to FHB Resistance in Hexaploid Wheat.	$ 47,810
	Total Award Amount	**$ 83,189**

Principal Investigator Date

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[*] CBCC – Chemical, Biological & Cultural Control
EEDF – Etiology, Epidemiology & Disease Forecasting
FSTU – Food Safety, Toxicology, & Utilization of Mycotoxin-contaminated Grain
GET – Genetic Engineering & Transformation
HGR – Host Genetics Resources
HGG – Host Genetics & Genomics
PGG – Pathogen Genetics & Genomics
VDUN – Variety Development & Uniform Nurseries

(Form – FPR06)

Project 1: *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?

Markers linked to resistance genes can accelerate selection, germplasm development and time to variety release expediting this process and providing diverse germplasm for durum breeding. The specific objectives of this project are to:

1) identify QTL region(s) for FHB resistance in Wangshuibai derived RIL populations of durum wheat;
2) develop the populations and methodology to quickly screen number of tetraploid FHB resistant sources from Tunisia; and
3) demonstrate the utility of the work by analysis of populations developed for breeding programs.

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:

- We developed 140 F5 derived RIL population of durum cultivar Ben crossed with FHB resistant source Wangshuibai. This population was evaluated for FHB resistance in two seasons at two replications each in the greenhouse. Broad sense heritability estimate for FHB was 0.74 ± 0.11 for this trait. Total of 215 SSR and STS markers were screened on the parental lines with 122 showing polymorphism (56%). These generated a 23 linkage group map covering 1008 cM or about 37% of the reference ITMI map. QTL analysis indicated a major locus on chromosome 3BS (same location as the Sumai 3 locus) explaining at the most 15% of the phenotypic variation or about 20% of the genotypic variation. Obviously there are other regions of importance that are not yet marked. We plan to add additional markers to this map possibly identifying other important regions.
- We are currently in the process of evaluating a number of Tunisan derived durum lines for their potential value in contributing to FHB resistance by pedigree based association mapping. These lines have been evaluated for two greenhouse seasons at two replications each for disease severity. To date the parental lines have been evaluated for 180 SSR markers showing a 45% level of polymorphism. The progeny is currently being mapped with polymorphic loci as well as evaluation of parental lines for additional polymorphism.
- We evaluated the effectiveness of various 3BS markers and phenotypic selection on deriving FHB resistant durum lines from Sumai 3 derived sources. Analysis indicates that markers will be valuable in removing majority of the susceptible lines from future consideration.

Impact:

- From our Wangshuibai population we identified a number of lines showing FHB scores of 5% severity or lower in repeated measurements. These lines are currently being used in the breeding program.
- Our study is the first time QTL analysis of FHB resistance from Wangshuibai has been conducted in durum wheat

- We have developed a number of excellent advanced breeding lines from our Sumai3 selection project. They are currently being evaluated by the durum breeding program.

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?

More FHB resistant lines from various sources in durum wheat.
Markers that can be used to augment phenotypic selection in the breeding program.

Project 2: *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?**

We have developed lines from various sources (Cltr9445 a Chinese accession, PI478472 and PI48121 *T. dicoccoides* accessions) that show significant reduction in FHB infection (in certain cases they are almost tolerant). Thus, the specific objectives of this project are:

1. complete analysis of early generation lines derived from CItr 9445 for the presence of important FHB QTL regions;
2. identify chromosomal regions introgressed into HRS wheat associated with FHB resistance derived from two *Triticum dicoccoides* accessions (PI478472 and PI48121); and
3. develop the populations for early generation analysis of lines derived from five different sources (PI 192863, PI 349478, PI 382154, PI 382161, PI 382167) of FHB resistance.

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:

- We analyzed over 100 F_3 families derived from Cltr9445 for FHB resistance in two greenhouse seasons. Advanced these lines to the F_4 generation and again screened them in the greenhouse for disease reaction. Both sets of populations were evaluated for nearly 190 SSR markers with 55 showing polymorphism and being mapped on the populations. Early analysis of the F_3 families indicated that markers GWM160 (4A) and GWM131 (1B) are significantly associated (GWM160 $P=3.8 \times 10^{-12}$ and GWM131 $P= 8.2 \times 10^{-14}$) with FHB resistance regions derived from the donor parent. However, F4 results did not confirm this finding. We are currently evaluating the possibility of using either DART or SNP markers to expand our genome coverage on these populations to help identify the important region(s).
- Our results of the T. dicoccoides accessions has so far been inconclusive. The issue is the same as in the previous study, need for additional markers to expand the portion of genome coverage. We are again looking at DART and/or SNP markers to greatly expand our map coverage.
- Populations from various PI lines are currently at the F_2 generation. We plan to advance these lines to F_3 families, evaluate them for FHB resistance and possibly develop BC2 lines for marker analysis.

Impact:

- Number of FHB resistant lines developed from various accessions in good HRS backgrounds have developed and are being incorporated into cultivar development programs.
- Number of early generation lines carrying multiple sources of FHB resistance are being developed that can be used in early generation association studies and incorporated into breeding programs for cultivar development.

<u>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?</u>
Number of advance FHB resistant lines carrying resistance from varied sources.

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.

None to report at this time, some are in review and expected shortly..