USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY07 Final Performance Report (approx. May 07 – April 08)
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Cover Page

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Fiscal Year:	2007
USDA-ARS Agreement ID:	59-0790-4-109
USDA-ARS Agreement Title:	Development of Markers Linked to FHB Resistance in Durum and Hexaploid Wheat.
FY07 ARS Award Amount:	$ 39,024

USWBSI Individual Project(s)

USWBSI Research Area*	Project Title	ARS Adjusted Award Amount
HGG	Pedigree Based Association Analysis of New FHB Resistance Sources in Wheat.	$39,024
	Total Award Amount	**$ 39,024**

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
IIR – Integrated/Interdisciplinary Research
PGG – Pathogen Genetics & Genomics
VDUN – Variety Development & Uniform Nurseries

(Form FPR07)

Project 1: *Pedigree Based Association Analysis of New FHB Resistance Sources in Wheat.*

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

Sources of FHB resistance are constantly being sought to expand the number of available genes to pyramid in a single variety. However, current methods rely on developing either recombinant inbred line (RIL) or double haploid (DH) mapping populations from resistant by susceptible crosses, phenotyping in multiple replicated trials, mapping and QTL analysis. This is then followed by the transfer of desirable regions with linked markers into acceptable cultivars. This process is tedious and slows the process of cultivar development. In this study we are exploring an alternative strategy that will allow us to not only quickly map the region of interest from multiple sources but do this in breeding populations under development. Our strategy is intended to reduce the time required for QTL identification and marker assisted selection significantly. The North Dakota Durum Wheat breeding program has identified five tetraploid wheat sources of resistance from Tunisia, which were selected among a large number of lines evaluated over 55 repeated FHB trials. Since their identification these lines have been extensively used in the breeding program to derive resistant breeding lines. We plan to use this collection of backcross derived advanced resistant lines, susceptible sibs, and parental lines to identify markers that are associated with these novel sources of resistance. Again the beauty of this analysis is the integration of derived information **directly** into the breeding programs. Due to significant reduction in funding by USWBSI our objectives for this time period were: 1) evaluate the parental (resistant donor and susceptible recipient) with PCR based markers evenly spaced (10 cM intervals) throughout the wheat genome; 3) to a very limited extend analyze the derived lines (all lines in a given pedigree) for polymorphic markers; and 3) screen all advanced lines with minimal FHB screening data in the greenhouse and field nursery.

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:**__

In this study we used 184 BC1F6 and 189 BC1F7 lines derived from crossing of Tun7, Tun18, Tun34, Tun36 with durum cultivars ‘Ben’, ‘Maier’, ‘Lebsock’ and ‘Mountrail’ for association studies. As Tunisian lines pedigree shows no relation to Chinese genotypes, they probably carry different genes or alleles for resistance to FHB. We checked all the parents and RILs in the greenhouse in three seasons for type II resistance to FHB by single floret injection inoculation method. The data showed that the Tunisian lines have different amount of resistance varying from 18% to 10% infection rate through the spikes. The data also showed Maier may have some minor resistance genes because it showed a moderate resistance in our greenhouse study and the crosses between Maier and different Tunisians had more transgressive resistant progenies compare with the other crosses.

To accelerate the identification of markers associated to FHB resistance, we initially screened the parents. The amounts of recombination in wheat chromosome arms are low so we picked 10-14 SSR markers per chromosome which were roughly 10cm apart and cover the whole genome. Among the 179 SSR markers that we applied on the parents about 45% showed polymorphism for at least two parents and about 8 % showed polymorphism between the whole set of Tunisian lines and susceptible cultivars. The most polymorphism was found on chromosomes 5A and 3B and the least on chromosome 6A. About 22 SSR markers that had been mentioned in different articles to be linked to FHB resistant were also applied to the parents. Among them barc117 and gwm129 from chromosome 5A showed the same pattern in Tunisian lines but not the susceptible lines.

Impact:

This is the first time an analysis of FHB resistance in tetraploid wheat lines of Tunisian decent is being performed. This is the first step toward identification and pyramiding of FHB resistance loci from various sources. Also this is the first time a study of this type, utilizing pedigree information to identify and incorporate new genes for resistance in wheat cultivars, is being performed. Again the beauty of this analysis is the integration of derived information **directly** into the breeding programs.

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?:

New germplasm, new markers associated with novel FHB resistance regions, and new methodology to directly characterize and incorporate traits into breeding lines. These all will have a major impact on how we perform QTL analysis in the future and incorporate the results into an applied breeding program.

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.

Ghavami F., M. Huhn, E. Elias, and S.F. Kianian. 2007. Tunisian durum wheat as new sources of resistance to Fusarium head blight. Proceedings of the 2007 National Fusarium Head Blight Forum. Kansas City, MO. Pages 177-178. Poster #78.

Ghavami F., and S. F. Kianian. 2008. Pedigree based association analysis of new FHB resistance sources in durum wheat. 5th Annual Northern Plains Biological Symposium. Fargo, ND.