USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY10 Final Performance Report
July 15, 2011

Cover Page

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Fiscal Year:	FY10
USDA-ARS Agreement ID:	59-0206-9-063
USDA-ARS Agreement Title:	Pedigree Based Association Analysis of Novel Sources of FHB Resistance in Durum Wheat.
FY10- USDA-ARS Award Amount:	$ 55,553

USWBSI Individual Project(s)

USWBSI Research Category*	**Project Title**	**ARS Award Amount**
DUR-CP	Pedigree Based Association Analysis of Novel Sources of FHB Resistance in Durum Wheat.	$ 55,553
	Total ARS Award Amount	**$ 55,553**

Principal Investigator Date

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* MGMT – FHB Management
FSTU – Food Safety, Toxicology, & Utilization of Mycotoxin-contaminated Grain
GDER – Gene Discovery & Engineering Resistance
PBG – Pathogen Biology & Genetics
BAR-CP – Barley Coordinated Project
DUR-CP – Durum Coordinated Project
HWW-CP – Hard Winter Wheat Coordinated Project
VDHR – Variety Development & Uniform Nurseries – Sub categories are below:
    SPR – Spring Wheat Region
    NWW – Northern Soft Winter Wheat Region
    SWW – Southern Soft Red Winter Wheat Region

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

1. What major problem or issue is being resolved relevant to Fusarium head blight (scab) and how are you resolving it?

The objectives of this project are:

1) Characterize a collection of advanced durum wheat breeding lines with known pedigrees for allelic variation in markers distributed throughout the genome;
2) Characterize the same collection of lines in the same environment for reaction to FHB;
3) Associate allelic variation with resistance loci present in FHB resistant lines;
4) Validate marker-FHB resistance loci association; and
5) Develop diagnostic markers for routine and effective screening of breeding populations.

2. List the most important accomplishment and its impact (i.e. how is it being used) to minimize the threat of Fusarium head blight or to reduce mycotoxins. Complete both sections (repeat sections for each major accomplishment):

<u>Accomplishment:</u>

During this granting period we further analyzed two backcross backcross F_6 populations (BC_1F_6) derived from cross between Tun 108 × Lebsock/Lebsock and Tun 108 × Ben/Ben in greenhouse (for type II resistance) and field (for type I and type II resistance). To date we have three greenhouse screening data for Tun108/Lebsock population (Winter 2010, Fall 2010, and Winter 2011) and three greenhouse seasons for Tun108/Ben (Winter 2010, Fall 2010, Spring 2011). The Fall 2010 greenhouse evaluation was not successful due to high level of humidity and powdery mildew outbreak. Nearly 10% of the lines in this greenhouse showed excellent level of resistant and were similar to the tolerant lines in other screening. Thus this greenhouse experiment was not a complete failure. In summer 2010 all of the lines were evaluated in the field nursery and they are again planted in the summer of 2011. Although there are obvious discrepancies between the data sets due to environmental effect, on the average, 53 of 173 (30.6%) lines in Tun108/Lebsock and 57 of 170 (33.5%) lines in Tun108/Ben showed less than 20 percent infection. Second greenhouse and field evaluation is currently underway. DArT (DNA Array Technology) analysis detected 553 polymorphic loci that located on the A and B genome chromosomes. Testing 310 SSR marker on the parental lines revealed 96 polymorphic loci (~31%) between Tunisian background and locally adapted cultivars. Upon completion of our phenotypic analysis association mapping will begin in earnest in an effort to identify the genomic regions significantly associated with resistance that can be transferred to durum wheat.

Impact:

1. Genetic characterization of a collection of advanced durum wheat breeding lines derived from new sources of FHB resistance from Tunisia for allelic variation in markers distributed throughout the genome
2. Phenotypic characterization of the same collection of lines for reaction to FHB
3. Development and application of a methodology for analysis of important genomic regions associated with FHB resistance in advanced breeding lines based on pedigree, phenotypic, and marker data
4. Identification of possible genomic regions associated with FHB resistance in these same collection of lines

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.

F. Ghavami, E.M. Elias, S. Mamidi, O. Ansari, M. Sargolzaei, T. Adhikari, M. Mergoum and S.F. 2011. Kianian. Mixed model association mapping for Fusarium head blight resistance in Tunisian derived durum wheat populations. Genes, Genomes, Genetics (in press)

S.M. Pirseyedi, F. Ghavami, O. Ansari, E.M. Elias, and S.F. Kianian. 2010. Association analysis of FHB resistance derived from Tunisian 108 in durum wheat. National Fusarium Head Blight Forum Dec. 2010.