USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY09 Final Performance Report
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Cover Page

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Fiscal Year:	2009
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.
FY09- USDA-ARS Award Amount:	$ 62,002

USWBSI Individual Project(s)

USWBSI Research Category[*]	**Project Title**	**ARS Adjusted Award Amount**
DUR-CP	Pedigree Based Association Analysis of Novel Sources of FHB Resistance in Durum Wheat.	$ 62,002
	Total Award Amount	**$ 62,002**

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 Winter Wheat Region
  - SWW – Southern Sinter 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):**

Accomplishment:

In this study we used 171 BC_1F_6 and 169 BC_1F_7 lines derived from crossing of Tun7, Tun18, Tun34, Tun36 with durum cultivars ‘Ben’, ‘Maier’, ‘Lebsock’ and ‘Mountrail’ for association studies. We found Tun18 and Tun7 as additional sources of resistance to FHB comparable to hexaploid wheat sources like sumai3. A new significant QTL for FHB on chromosome arm 5BL with both association mapping analysis and classical QTL mapping analysis in durum wheat was confirmed. Of the 10 different association mapping models compared, the linear mixed model considering the structure (Q or P) and the kinship matrix estimated by REML (K_T) would be the best for association studies in a mixture of wheat populations coming from different breeding programs. The results of association mapping analysis also demonstrated another genomic region on chromosome arm 3BS which can be potentially linked to FHB resistance. This region is approximately located on the genomic region where major resistance gene “*fhb1*” reported in hexaploid wheat. We also observed the potential of having a susceptibility gene on durum wheat from 2A chromosome reported by other scientists.

During this granting period we further analyzed two backcross F_6 population (BC_1F_6) derived from cross between Tun 108 × Lebsock/Lebsock and Tun 108 × Ben/Ben (184 lines in each population). They were evaluated for their FHB reaction in the greenhouse (2 replications, Spring 2010) and are currently being evaluated in the field nursery (2 replications, Summer 2010). The scoring data from the greenhouse was collected 14 and 21 days after inoculation according to the percent of spike infection. All lines in two populations were genotyped using approximately eighth thousand DArT markers. Initial investigation revealed that, there are remarkable numbers of resistant line in these two populations which can be used as main sources of resistance in further breeding program. A third FHB screening is planned for Winter 2010 greenhouse is planned and upon completion of that study genome-wide association analysis for identification of important regions will begin.

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 all germplasm or cultivars released with full or partial support of the USWBSI. List the release notice or publication. Briefly describe the level of FHB resistance.

Not Applicable

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, Mamidi S, Sargolzaei M, Elias EM, Kianian SF. 2009. Mixed model association analysis for FHB resistance in Tunisian durum wheat populations. In: S. Canty, A. Clark, J. Mundell, E. Walton, D. Ellis and D. Van Sanford (Eds.), Proceedings of the National Fusarium Head Blight Forum; 2009 Dec 7-9; Orlando, FL. Lexington, KY: University of Kentucky. pp. 119-120.

Zhu X, Chao S, Elias EM, Kianian SF, Cai X. 2009. Comparative mapping of the chromosomal region harboring the Fusarium head blight resistance QTL *QFHS.NDSU-3AS* in durum wheat. In: S. Canty, A. Clark, J. Mundell, E. Walton, D. Ellis and D. Van Sanford (Eds.), Proceedings of the National Fusarium Head Blight Forum; 2009 Dec 7-9; Orlando, FL. Lexington, KY: University of Kentucky. pp. 165.

Ansari O, Ghavami F, Elias EM, Kianian SF. 2009. Quantitative trait loci mapping of Fusarium head blight resistance in advanced back cross population (BC1F6) derived from Tun 34 X Lebsock tetraploid wheat. In: S. Canty, A. Clark, J. Mundell, E. Walton, D. Ellis and D. Van Sanford (Eds.), Proceedings of the National Fusarium Head Blight Forum; 2009 Dec 7-9; Orlando, FL. Lexington, KY: University of Kentucky. pp. 187-188.