

**USDA-ARS/  
U.S. Wheat and Barley Scab Initiative  
FY08 Final Performance Report (approx. May 08 – April 09)  
July 15, 2009**

**Cover Page**

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<b>Fiscal Year:</b>	2008
<b>USDA-ARS Agreement ID:</b>	59-0790-4-109
<b>USDA-ARS Agreement Title:</b>	Development of Markers Linked to FHB Resistance in Durum and Hexaploid Wheat.
<b>FY08 USDA-ARS Award Amount:</b>	\$ 62,002

**USWBSI Individual Project(s)**

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

July 15, 2009

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Principal Investigator

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Date

\* 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  
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?**

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 used 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. The objectives of this period were: 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; and 3) associate allelic variation with resistance loci present in FHB resistant lines.

**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:**

1. Replicated (4 replications) evaluation of FHB type II resistance of Tunisian derived line, susceptible parents/sibs, and checks in the greenhouse
2. About 10-14 SSR markers per chromosome which was roughly 10cM apart were screened for polymorphism on the parents before being applied to the derived lines
3. Marker data (SSR and DArT) analysis was used to estimate the genetic distance among the parents of various populations
4. Association mapping analysis was performed on derived lines to identify important chromosomal regions

**Impact:**

1. Replicated disease evaluation indicates that Tun7 and Tun18 have resistance comparable to that of Sumai3. Although Tun 34, Tun36 and Tun108 show better resistance levels compared to durum cultivars but statistically their level of resistance is not different from 'Lebsock' and 'Maier' (two durum cultivars). Some of the progenies derived from Tun34 × Lebsock showed better resistance

than their parents due to transgressive segregation or elimination of suppressive gene (genes) from susceptible parent.

2. SSR screening indicates about 45% polymorphism between at least two parents and about 8% polymorphism among the entire Tunisian line collection and susceptible durum cultivars. The most polymorphism was found on chromosome 5A (75%) and 3B (70%) and the least one on chromosome 6A (30%).
3. DArT analysis used 2,300 markers which showed 25% polymorphism between the parents (over 550 polymorphic loci identified). About 8% of the polymorphic markers were present in all the Tunisian lines but not the susceptible cultivars, similar to our SSR results. The cluster analysis of the polymorphic DArT markers revealed three distinct groupings of lines/cultivars. These groups consisted of: 1) all susceptible durum cultivars, 2) all Tunisian lines except for Tun7, and 3) Tun7 which was grouped by itself and separate from all other lines. This is significant as it indicates at least two varied sources of resistance among the 5 Tunisian lines.
4. Association analysis indicated 66 markers associated to FHB resistance in Tun34 pedigree. As some of these markers were linked to each other indicating about 7 different QTL regions associated to FHB resistance. These QTLs were located on Chromosomes 3B, 6B, 2A, 1B, 5B, 7A and 7B. The QTLs on 3B, 6B, 2A and 1B were strong enough to be associated to more than 5 adjacent markers in each region. We have identified two new potential QTLs for FHB located on chromosomes 5B and 7B as 3B and 6B QTLs may represent those reported previously. We have found three QTLs on 3AS, 1BL and 2AL associated to FHB resistance in the Tun7 pedigree. With Tun18 pedigree we found three QTLs on 7B, 7A and 1B. The 1B QTL were exactly in the same location as the one from Tun34 population.

Our study shows that Tun7 and Tun18 have considerable amount of resistance to FHB that has been demonstrated consistency over many disease evaluations. The cluster analysis showed the different genetic background for these Tunisian resistant lines, therefore we suggest that Tun7 and Tun18 have the potential to be used as two new sources of resistance in breeding programs. We have been able to identify potential QTL regions among the progeny in this study some of which have not been identified before in any FHB study. The results of this study are being confirmed and validated for proper application into a MAS program.

### **What would you classify as the highlight of the progress you have made thus far?**

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 of a new 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.**

R. R. Burkakoti, M. Mergoum, S. F. Kianian, and T. B. Adhikari. 2008. Characterization of Fusarium Head Blight resistance in Alsen-Frontana-derived recombinant inbred lines. Proceedings of the National Fusarium Head Blight Forum. Indianapolis, Indiana

F. Ghavami, M. Huhn, E. Elias, and S. F. Kianian. 2008. Linkage disequilibrium analysis of Fusarium Head Blight resistance in Tunisian durum wheat. Proceedings of the National Fusarium Head Blight Forum. Indianapolis, Indiana

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

**If your FY08 USDA-ARS Grant contained a VDHR-related project, 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. If this is not applicable (i.e. no VDHR-related project) to your FY08 grant, please insert ‘Not Applicable’ below.**

None to report