USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY13 Final Performance Report
July 15, 2014

Cover Page

PI:	Shahryar Kianian
Institution:	USDA-ARS
Address:	Cereal Disease Laboratory 1551 Lindig Street University of Minnesota St. Paul, MN 55108
E-mail:	Shahryar.Kianian@ARS.USDA.GOV
Phone:	612-624-4155
Fax:	
Fiscal Year:	FY13
USDA-ARS Agreement ID:	NA
USDA-ARS Agreement Title:	Pedigree Based Association Analysis of Novel Sources of FHB Resistance in Durum Wheat.
FY13 USDA-ARS Award Amount:	$ 53,107

USWBSI Individual Project(s)

USWBSI Research Category[*]	**Project Title**	**ARS Award Amount**
DUR-CP	Association Analysis of Novel Sources of Resistance and Germplasm Development.	$ 53,107
	FY13 Total ARS Award Amount	**$ 53,107**

Principal Investigator 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
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: *Association Analysis of Novel Sources of Resistance and Germplasm Development.*

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 were to:

1. complete association analysis of lines derived from Tunisian sources of resistance;
2. develop diagnostic markers for routine and effective screening of breeding populations;
3. initiate development of lines derived from popular durum cultivars missing portions of chromosome 2A region containing the FHB suppressor locus; and
4. initiate pyramiding of the FHB resistance regions on chromosomes 5BL and 3BS identified in Tunisian derived lines into a durum cultivar.

2. **List the most important accomplishments and their impact (i.e. how are they being used) to minimize the threat of Fusarium Head Blight or to reduce mycotoxins. Complete both sections; repeat sections for each major accomplishment:**

Accomplishment:

The association analysis of Tunisian sources of resistance have now been completed. Composite interval mapping of Tunisian 108xBen revealed 11 different QTL on seven different chromosomes (1A, 1B, 2B, 3B, 5A, 5B, and 7B). A novel region on chromosome 2B was identified (*Qfhb.ndsu-2B*) which provides resistance to multiple FHB components including severity, incidence, mycotoxin production and frequency of damaged kernels. Composite interval mapping of Tunisian 108xLebsock revealed 15 different QTL on seven different chromosomes (1A, 1B, 3A, 3B, 4A, 5A, and 6B). The regions on chromosomes 1A and IB were consistently significant across the experiments for type II and type I resistant respectively. We have initiated crosses to pyramid these and other previously identified QTL regions into a single durum background for further utilization by the breeding programs.

Development of deletion populations were put on hold due to recent move of the PI. We have now started that project and will initiate the necessary crosses in the next greenhouse season. A set of lines derived from some of the newest durum cultivar releases from NDSU were mutated with 5-Methyl-azacytedine that removes CG methylation. The resulting lines were advanced to the M_4 generation and tested for FHB resistance under both the greenhouse and field conditions. Among over a 1,000 lines tested we identifed 24 lines that show great promise having less than 20% infection as compared with 80-100% value for parental lines and checks, a highly significant difference. We are now evaluating these lines at the Univ. of Minnesota FHB nursery. These lines will be analyzed for the molecular basis of resistance as well as stability of mutations by crosses to durum cultivars.

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
5. Pyramiding of various regions of importance in FHB resistance into a single backgroun
6. Development and identification of lines using chemical or radiation mutagenesis, based on popular durum wheat cultivars, that have greatly improved resistance to FHB

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 FY13 grant. Please reference each item using an accepted journal format. If you need more space, continue the list on the next page.

QTL analysis of Fusarium head blight resistance in Tunisian-derived durum wheat populations. Ph.D. Dissertation thesis, North Dakota State University. Seyed Mostafa Pirseyedi, 2013. Fargo, ND.