

**USDA-ARS/  
U.S. Wheat and Barley Scab Initiative  
FY12 Final Performance Report  
One-Year No Cost Extension (NCE) through FY13**

**July 15, 2014**

**Cover Page**

<b>PI:</b>	Elias Elias
<b>Institution:</b>	North Dakota State University
<b>Address:</b>	Department of Plant Sciences PO Box 6050 Fargo, ND 58108-6050
<b>E-mail:</b>	elias.elias@ndsu.edu
<b>Phone:</b>	701-231-8159
<b>Fax:</b>	701-231-8474
<b>Fiscal Year:</b>	FY12
<b>USDA-ARS Agreement ID:</b>	59-0206-9-063
<b>USDA-ARS Agreement Title:</b>	Pedigree Based Association Analysis of Novel Sources of FHB Resistance in Durum Wheat.
<b>FY12 USDA-ARS Award Amount:</b>	\$ 51,761*

**USWBSI Individual Project(s)**

<b>USWBSI Research Category**</b>	<b>Project Title</b>	<b>ARS Award Amount</b>
DUR-CP	Association Analysis of Novel Sources of Resistance and Germplasm Development.	\$ 51,761
	<b>Total ARS Award Amount</b>	<b>\$ 51,761</b>

\_\_\_\_\_  
Principal Investigator

\_\_\_\_\_  
Date

\* Part of the funding for the research was provided under ARS agreement # 59-0206-9-062

\*\* 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 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 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:**

During this period we further analyzed 171 BC<sub>1</sub>F<sub>7</sub> lines derived from Tunisian 108×Ben and 174 BC<sub>1</sub>F<sub>7</sub> lines derived from Tunisian 108×Lebsock. In total we have two field (Type I and Type II) and two greenhouse (Type II) FHB infection data for both of these populations. In addition, we have FDK and DON measurements from grain collected from 2011 field disease screening (the most severe season for FHB infection). We have generated maps for both of these populations containing over 300 marker loci. Analysis of variance showed significant effect on FHB infection rate for the genotypes and also environments, as well as G×E interactions. Broad sense heritability for FHB infection rate was calculated to be around 40.4%±0.09. The correlation between the two greenhouse seasons and also the two field scab nurseries were positive and significant while there was correlation between the one greenhouse data and the field data. Transgressive segregation for FHB severity was observed and approximately 8% of the lines performed better than the resistant parents in the field and 25% while evaluated in the greenhouse. Additionally, those 8% of the lines that showed increased resistance also had the lowest FDK score of all lines examined.

Composite interval mapping of Tunisian 108×Ben 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. Introgression of this segment can be beneficial to the development of FHB-resistant durum cultivars. A region identified on chromosome 5A in this study has been identified in other hexaploid and tetraploid material indicating a possible evolutionary significance.

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 1B were consistently significant across the experiments for type II and type I resistant respectively. At least one novel QTL was identified in this investigation on chromosome 4A (*Qfhb.ndsu-4A*) that provides type I FHB resistance.

Additionally, past attempts at transfer of resistance genes/QTLs from hexaploid sources into durum wheat have met with limited success. Various studies, including several by our groups, suggest that either the cultivated durum genome carries a suppressor of FHB resistance or is missing enhancers of resistance on D-genome chromosomes. To test these hypotheses, we treated several popular durum cultivars with a chemical that removes CG methylation. These lines were advanced and tested for FHB resistance with about 30 lines identified that show very limited infection as compared to resistant controls. In a similar project we initiated the development of deletions for portions of chromosome 2A, suggested as a possible carrier for FHB suppressor of resistance. We will further develop these lines and test homozygous derivatives for FHB response.

**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. Development and identification of lines using chemical or radiation mutagenesis, based on popular durum wheat cultivars, that have greatly improved resistance to FHB

FY12 (approx. May 12 – May 14)

FY12 Final Performance Report-NCE

PI: Elias, Elias

USDA-ARS Agreement #: 59-0206-9-063

**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.**

None