USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY10 Final Performance Report
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Cover Page

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Fiscal Year:	FY10
USDA-ARS Agreement ID:	59-0206-0-060
USDA-ARS Agreement Title:	Developing More Precise Markers to FHB Resistance QTLs for Wheat.
FY10 USDA-ARS Award Amount:	$ 9,756

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
HWW-CP	Developing More Precise Markers to FHB Resistance QTLs for Wheat.	$ 9,756
	Total ARS Award Amount	**$ 9,756**

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: *Developing More Precise Markers to FHB Resistance QTLs for Wheat.*

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

The **goal** of this proposed research is to develop more precise markers for known major FHB-resistant QTLs. Genetic studies have mapped a few major FHB-resistant QTLs in wheat. However, markers developed for those QTL are of linkage indication at the best. Furthermore, little is known about what genes are associated with the mapped QTLs and how they function. In our study of the molecular mechanism of FHB pathogenesis/resistance in wheat with microarray, we have revealed 677 genes that changed expression during FHB pathogenesis/ resistance and led to our conclusion that jasmonates (JA)/ethylene (ET) signaling pathways mediate the FHB resistance in wheat. Our **hypothesis** is that, at least, some of these FHB-associated the JA/ET-signaling-related genes we discovered are associated with or regulated by the mapped FHB-resistance QTLs and thus their DNA sequence can be used as more precise markers for the QTLs they are associated with. We are testing our hypothesis in this research by associating known FHB-associated genes with known major FHB-resistant QTLs with functional study of their differential expression in a pair of near-isogenic lines for *Qfhb1* and a $F_{2:8}$ recombinant inbred population that was derived from the cross Sumai 3/Y1192-6.

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:

Of the 388 genes, seven were associated with *Qfhb1* and 17 with other QTLs in FY10. The seven *Qfhb1*-associated genes include those coding for xylanase inhibitor 8010S, peroxidase 2, LOX 2.1, Myb-like and three with unknown functions. Of them, four are up regulated and three were down regulated. The 17 other-QTL-associated genes are composed of chalcone synthase, peroxidase 1, peroxidase 4, cytochrome P450, PDR-like ABC transporter, Pathogenesis-related protein 4, zinc figure protein, etc.

Impact:

The QTL-associated genes/miRNA can be the foundation for dissecting FHB-resistance mechanism. They will also be used to develop novel, more precise, reliable markers to FHB resistance QTLs that can help increasing efficiency of individual breeding programs to develop and release FHB resistant varieties and developing new breeding technologies and germplasm to further enhance short term and long term improvement of FHB resistance and to efficiently introgress effective resistance genes into breeding germplasm.

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.