

**USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY10 Preliminary Final Performance Report
July 15, 2011**

Cover Page

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Fiscal Year:	FY10
USDA-ARS Agreement ID:	59-0206-0-061
USDA-ARS Agreement Title:	Systems Biology on the Barley- <i>Fusarium</i> Interaction.
FY10 USDA-ARS Award Amount:	\$ 43,902

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
GDER	Investigation of the Barley- <i>Fusarium</i> Interaction using NextGen Sequencing.	\$ 43,902
	Total ARS Award Amount	\$ 43,902

Fusheng Wei
Principal Investigator

7-14-2011
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: *Investigation of the Barley-Fusarium Interaction using NextGen Sequencing.*

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

The objective of this proposal is to use the Illumina NextGen Sequencing platform to discover essential genes for the barley FBH resistance. To achieve this goal, we first sequence mRNA transcripts under different conditions, then quantitatively analyze the sequence read, find the differentially expressed sequences, and functionally categorize these sequences through various resistance pathways, and finalized gene set for further functional study. During the past year, we are collecting tissues and RNA samples for the RNA-seq sequencing. Now we are upgrading our original Illumina Genome Analyzer Ix to Illumina HiSeq 2000, resulting in an 10 times increase in sequencing throughput from 50gb per run to 500gb per run. We will begin sequencing the samples in the fall. This rising throughput would greatly facilitate our analysis in both rare transcript coverage and statistical sensitivity of quantitative analysis, thus narrowing down the gene list critical for FBH resistance.

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: We are in the data collection stage and just finished sample collection. Once finishing the RNA-seq, we will perform in-depth data analysis to narrow down a list of critical genes critical for the FBH resistance.

Impact: Candidate genes critical to the FBH resistance will be identified for future functional study by our increased sequence throughput which can detect rare transcript and improve the statistical sensitivity of our quantitative analysis. This systems biology study will enhance our understanding of the molecular pathway and network for FBH resistance and provide a foundation for molecular breeding to genetically control the disease.

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.

In progress