USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY10 Final Performance Report
One-Year No Cost Extension through FY11
July 13, 2012

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-*Fusarium* 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-*Fusarium* Interaction using NextGen Sequencing.	$ 43,902
	Total ARS Award Amount	**$ 43,902**

Fusheng Wei 7-26-2012
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: *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 need to sequence mRNA transcripts under different conditions, then quantitatively analyze the sequence reads, 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. With an upgrade of our original Illumina Genome Analyzer IIx to Illumina HiSeq 2000, we would have an 10 times increase in sequencing throughput from 50gb per run to 500gb per run. The 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. Due to the difficulty to collect samples for RNA extraction, our RNA samples were not enough for sequencing. State budget and funding issue eliminated my position. At iPlant, I didn't have the resource to continue the lab work. Although I have tried to collaborate with others, I couldn't get the needed samples. Therefore, most money didn't get spent and returned to the funding agency. However I indeed built the workflow for the RNAseq data analysis using iPlant infrastructure.

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 didn’t get enough RNA samples for sequencing. No in-depth data analysis was performed to narrow down a list of critical genes critical for the FBH resistance although we have built RNAseq workflow using iPlant infrastructure for the analysis.

   Impact: The RNAseq analysis pipeline built at the Discovery Environment if iPlant infrastructure made it possible for any large-scale RNAseq studies.

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.

Not available.