USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY11 Final Performance Report
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Cover Page

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Fiscal Year:	FY11
USDA-ARS Agreement ID:	59-0206-1-112
USDA-ARS Agreement Title:	A Rapid Assay System for Transgenes that Confer Resistance to DON and FHB.
FY11 USDA-ARS Award Amount:	$ 54,975

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
GDER	A Rapid Assay System for Transgenes that Confer Resistance to DON and FHB.	$ 45,219
BAR-CP	High Efficiency Method for Generating FHB-Resistant Barley: Removing Bottlenecks in the Pipeline for Deploying FHB Resistance Genes.	$ 9,756
	Total ARS Award Amount	**$ 54,975**

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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: *A Rapid Assay System for Transgenes that Confer Resistance to DON and FHB.*

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

   There are few useful natural genetic sources of FHB resistance among collected wheat and barley accessions. Transgenic plants allow additional genetic resources to be accessed and introduced into grain crops. The goal of this project is to screen and identify genes the confer resistance to FHB that can be introduced into wheat and barley by transgenesis. To facilitate this process, we have employed the recombinogenic plant *Physcomitrella patens*, which allows the contribution of genes to FHB resistant or susceptibility to be rapidly assessed via the creation of gene knockouts or gene overexpression. This assay system has been used to identify genes that confer resistance to treatment with DON and to infection with FHB. These assays have identified a number of genes, operating through distinct molecular pathways, which are able to alter susceptibility to FHB when overexpressed or suppressed (via gene knockout or RNAi) in transgenic lines. These assays provide an early test for gene function and utility, prior to their introduction into crop species. This project addresses the GDER goal to efficiently identify candidate genes for resistance against FHB and reduced DON accumulation through high-throughput functional screening assays.

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 have used *Physcomitrella patens* to identify genes effective against FHB that operate through a variety of molecular and cellular mechanisms. These genes are associated with Programmed Cell Death, ER stress and induced immunity. Previous studies defined the importance of conserved genes involved in the perception and signaling of induced immunity pathway in mounting a similar response to FHB in Physcomitrella. Our studies indicate that this pathway is functionally conserved in Physcomitrella and in barley. We have constructed transgenic lines that overexpress components of induced immune signaling and these are being tested for altered sensitivity to FHB. In parallel we isolated barley homologs of these genes so that a similar approach can be tested in transgenic barley.

   Impact:
   Our studies provide a functional test of whether increased resistance to FHB can be conferred by overexpressing signaling components of the induced immune response. If so, then the structural and functional conservation of this pathway may similarly allow its manipulation in crop plants. The advantage of this approach is that is makes use of conserved plant genes and mechanisms and takes advantage of the natural immunity of the plants.

Project 2: *High Efficiency Method for Generating FHB-Resistant Barley: Removing Bottlenecks in the Pipeline for Deploying FHB Resistance Genes.*

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

   These studies address whether genes identified from rapid heterologous assay systems are able to confer resistance to FHB in barley. They constitute the downstream components of a pipeline for generating and assessing transgenic FHB-resistance crops. These studies address Objectives 4 and 6 of the Barley Coordinated Project to develop barley varieties with enhanced resistance to FHB and to evaluate promising transgenes in adapted genetic backgrounds.

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 have defined a group of barley homologs of Physcomitrella genes previously shown to be effective against FHB in Physcomitrella. We have introduced constructs for several of these genes into plasmid vectors suitable for Agrobacterium-mediated transformation of barley plants by our colleagues in the USWBSI.

   Impact:
   The generation of transgenic plants expressing novel genes provides a formal test of the validity of the rapid assay system for selecting and screening genes for introduction into barley. Comparison of gene performance in barley and Physcomitrella will also allow us to evaluate which resistance mechanisms are conserved. The generation of transgenic plants will also provide new germplasm for introduction into regionally adapted varieties of barley.

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.

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