USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY13 Final Performance Report
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Cover Page

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Fiscal Year:	FY13
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.
FY13 USDA-ARS Award Amount:	$ 8,572

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
BAR-CP	High Efficiency Method for Generating FHB-Resistant Barley: Removing Bottlenecks in the Pipeline for Deploying FHB Resistance Genes.	$ 8,572
	FY13 Total ARS Award Amount	**$ 8,572**

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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: *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?

We have employed a system, based on expression or knockout of genes in the recombinogenic plant *Physcomitrella patens*, for assaying novel genes for efficacy against FHB. The need for novel genetic sources of resistance, and for assay systems that can determine their utility, derives from the paucity of natural barley or wheat resistance genes effective against FHB. The expression or knockout of genes in Physcomitrella, has shown that a number of genes are able to decrease susceptibility and enhance resistance against FHB. Some of these genes also alter sensitivity to the mycotoxin DON while others do not and presumably function through a different cellular resistance mechanism. Our work suggests there may be multiple pathways for improving resistance against FHB in field crops. To test the if genes effective in Physcomtirella are also effective in natural FHB hosts, genic sequences have been introduced into overexpression or RNAi suppressor vectors and these have been transferred to transgenic barley (work of collaborating laboratory, Lynn Dahleen).

Introduction of these constructs into transgenic crops will allow the efficacy of these gene manipulations to be assayed in the context of other FHB-resistance factors and under field conditions of the disease. This work paves the way for the use of other genes and other approaches for enhancing resistance against FHB. These include the use of gene editing and site-specific recombination technologies, and the development of more sophisticated and physiologically appropriate assays systems.

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:

<u>Accomplishment:</u>

We have identified a number of genes effective against FHB and DON. These genes encode proteins that are involved in a number of cellular processes, including innate immunity, ER stress response, programmed cell death and hormonal regulation. We have constructed vectors and generated transgenic plants that will engineer the corresponding changes (either knock-down or overexpression) of the homologous genes in barley. After verification and assessment in the greenhouse, these plants can be tested under field conditions for altered susceptibility to FHB.

In addition to these accomplishments, our studies suggest that resistance against FHB can be engineered by manipulating multiple cellular pathways. This not only expands the toolbox of potentially useful genes, but also provides an approach for engineering more durable field

resistance that is not dependent on the presence of single disease resistance genes (classical *R*-genes).

Finally, we have developed expertise in identifying potentially useful new genes together with assay systems that allows their potential to be explored in a relatively short period of time. These accomplishments are proving useful for screening other genes, including second generation approaches for regulating gene expression in crop plants, such as the use of gene editing and inducible expression systems.

Impact:

The immediate impact of these studies is on the research community, and the longer term impact is on the community of growers and users. By developing a rapid assay system for genes effective against FHB, we have generated a tool that has proven useful for our own studies and one that can also be used by other researchers to assess the efficacy of novel genes of interest. If transgenic plants expressing gene constructs are effective against FHB it will also provide a new resource in the toolkit that can be deployed to control FHB in the field. Transgenic barley plants that show enhanced resistance can serve as the starting material in breeding programs to introduce resistance into field varieties. Alternatively, similar genes can be introduced into commercial varieties.

Genes selected for expression in transgenic plants are also experiments that directly test the contribution of a particular pathway to the expression of FHB resistance or susceptibility. In this manner, we can explore the degree to which different cellular pathways contribute to FHB resistance. This is an important outcome, as it indicates the likely cellular targets of FHB effectors (designed to undercut any plant responses) as well as the most profitable and effective pathways for us to manipulate in future work.

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 FY13 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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