USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY07 Final Performance Report (approx. May 07 – April 08)
July 15, 2008

Cover Page

PI:	Steve Scofield
Institution:	USDA-ARS
Address:	Crop Prod. & Pest Control Research 915 West State Street West Lafayette, IN 47907-2054
E-mail:	scofield@purdue.edu
Phone:	765-494-3674
Fax:	765-494-3452
Fiscal Year:	2007
USDA-ARS Agreement ID:	NA
USDA-ARS Agreement Title:	Rapid Function Identification of Genes Contributing to FHB Resistance and Susceptibility.
FY07 ARS Award Amount:	$ 55,000

USWBSI Individual Project(s)

USWBSI Research Area*	Project Title	ARS Adjusted Award Amount
HGG	Rapid Function Identification of Genes Contributing to FHB Resistance and Susceptibility.	$55,000
	Total Award Amount	**$ 55,000**

Steven R Scofield

Principal Investigator Date

* CBCC – Chemical, Biological & Cultural Control
EEDF – Etiology, Epidemiology & Disease Forecasting
FSTU – Food Safety, Toxicology, & Utilization of Mycotoxin-contaminated Grain
GET – Genetic Engineering & Transformation
HGR – Host Genetics Resources
HGG – Host Genetics & Genomics
IIR – Integrated/Interdisciplinary Research
PGG – Pathogen Genetics & Genomics
VDUN – Variety Development & Uniform Nurseries

Project 1: *Rapid Function Identification of Genes Contributing to FHB Resistance and Susceptibility.*

1. What major problem or issue is being resolved and how are you resolving it?

Fusarium head blight (FHB) is one of the major diseases that threaten US wheat and barley producers. Unfortunately, all known resistance to FHB is complex, based on multiple quantitative trait loci (QTL) that make partial contributions to resistance. Combining these QTL loci into high yielding wheat lines and eliminating the yield reducing traits linked to some of the QTLs has proven to be a slow process. Development of resistant varieties would be accelerated by knowledge of the specific genes that make essential contributions to FHB resistance.

We have developed a virus-induced gene silencing (VIGS) system based on Barley Stripe Mosaic virus (BSMV) that can switch-off, or silence, genes in hexaploid wheat so that the gene's function can be inferred by observing the effects of its silencing. Because VIGS is homology-dependent, it can silence related gene copies that encode mRNAs with >85% homology, making it ideal for creating knockouts in hexaploid wheat where at least three copies of each gene may be expressed from the A, B and D genomes.

We have demonstrated the utility of BSMV-VIGS for functionally identifying genes involve in several disease resistance systems in hexaploid wheat. In these studies a candidate gene is silenced in a plant that is normally resistant to a particular pathogen. After silencing is established, the plant is challenge with this pathogen. If the plant becomes susceptible, we have strong evidence that the candidate gene has an essential function in this resistance pathway. We have developed protocols for silencing genes in spikes of wheat plants and are now screening a list of candidate genes testing if they contribute to FHB resistance. It is very important to note, that at the start of this work, no wheat or barley gene was know that made a clear functional contribution to FHB resistance.

2. List the most important accomplishment and its impact (how is it being used?). Complete all three sections (repeat sections for each major accomplishment):

Accomplishment:

Our most important accomplishment in the work funded by the FY06 award was the discovery that wheat chitinase genes make an essential contribution to FHB resistance. This result is very important for at least two reasons.

1. It validates the ability of the VIGS assay to rapidly identify genes contributing to FHB resistance and provides confidence that continuing this approach can identify the key genes in this resistance mechanism.
2. Knowing that induction of chitinase activity makes a crucial contribution to FHB resistance gives us important insight into how the wheat and almost certainly barley defend against Fusarium.

Impact:

The FHB research community now has a powerful tool that can be used to determine which genes have essential functions in FHB resistance. These genes can then be targeted to find the best alleles in breeding strategies or employed in transgenic solutions to improving FHB resistance.

As a result of that accomplishment, what does your particular clientele, the scientific community, and agriculture as a whole have now that they didn't have before?:

The importance of this new system is evidenced by the fact that the leading labs in FHB research are adopting this technique for their own work. To this end my lab has hosted and trained scientists in the FHB-VIGS technique from Gary Muehlbauer's lab (University of Minnesota), Kim Hammond-Kosak's lab, Rothamsted, UK) and Therese Ouellet, (Agriculture and Food Canada, Ottawa, Canada)

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.

1. National Wheat Genomics Conference, held November 30 – December 2, 2007, in Kansas City.
2. US Wheat and Barley Scab Initiative National Forum, held in Kansas City from December 2 – 5, 2007.
3. The Fifth Canadian Workshop on Fusarium Head Blight, held in Winnepeg, Canada November 27-30, 2007.
4. I have been invited to speak at the 3rd International Fusarium Head Blight Symposium in Szeged, Hungary, Sept 2-7 2008.