

**USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY10 Final Performance Report
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Cover Page

PI:	Lisa Vaillancourt
Institution:	University of Kentucky
Address:	Department of Plant Pathology 227 Plant Science Building 0312 Lexington, KY 40546-0312
E-mail:	lisa.vaillancourt@uky.edu
Phone:	859-257-7445 x80731
Fax:	859-323-1961
Fiscal Year:	FY10
USDA-ARS Agreement ID:	59-0206-0-062
USDA-ARS Agreement Title:	Genetics of Quantitative Pathogenic Variation in <i>Fusarium graminearum</i> .
FY10 USDA-ARS Award Amount:	\$ 13,363

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
PBG	Genetics of Quantitative Pathogenic Variation in <i>Fusarium graminearum</i> .	\$ 13,363
	Total ARS Award Amount	\$ 13,363

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: *Genetics of Quantitative Pathogenic Variation in Fusarium graminearum.*

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

Fusarium graminearum (*Gibberella zeae*) is the primary causal agent of FHB in North America. Most North American strains reportedly belong to a single genetic lineage (lineage 7) and chemotype (15-ADON). Population genetic studies have demonstrated that the North American population of *G. zeae* is genetically and phenotypically diverse. The primary approach used to manage FHB is use of resistant wheat. Durability of resistance will be dependent on the ability of the pathogen population to change and adapt. Theory suggests that sexual populations change more rapidly than non-sexual populations, and that outbreeding facilitates more rapid shifts than inbreeding. *G. zeae* is a homothallic ascomycete that can outcross under laboratory conditions. Sexually produced ascospores are the primary inoculum in the field and play a critical role in the disease cycle. *G. zeae* is widely assumed to outcross in the field, though the extent to which this occurs is unknown. The issue we addressed was: what is the effect of outcrossing on the generation of genotypic and phenotypic diversity in *G. zeae*? The hypothesis we tested was that crosses of different lineage 7, 15-ADON strains of *G. zeae* would produce progeny that were more aggressive, more toxigenic, and/or more fit than either parent. The approach we took was to cross two well-characterized and phenotypically similar lineage 7 strains and evaluate pathogenically-significant traits among their progeny.

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 found that crossing the genetically and phenotypically similar lineage 7 strains Gz3639 and PH-1 resulted in some progeny strains that were significantly more aggressive, more toxigenic, and/or more sexually and asexually fecund, than either of the parental strains. We found that these phenotypes were stably inherited in single-conidial progeny. We also found, surprisingly, that some progeny of selfed perithecia were also more aggressive, toxigenic, and fit than their parents, though not to the extent seen in outcrossed perithecia. This suggested the possibility that epigenetic factors also play a role in generating diversity. In the course of doing this research, we developed a new set of fingerprinting markers for *F. graminearum* with excellent resolution for population genetic studies, as well as providing segregating markers for genetic studies of multiple strains.

Impact:

Our findings are significant because they suggest that outcrossing in the field, even among genetically similar strains that appear similar in aggressiveness, could give rise to strains that are much more aggressive or toxigenic. Surprisingly, our work suggested that even selfing

could produce strains with significant pathogenic variation, due possibly to epigenetic factors. Even more important is that we have developed tools and protocols that could be used to evaluate genes that impact these quantitative traits as well as to follow those genes in the population, which could give us much better insight into how the *F. graminearum* population might shift and adapt as new resistance sources are deployed. All of this could lead to an improved ability to predict and manage scab epidemics in the future.

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.

Presentations:

- S. Bec, D. Van Sanford, L. Vaillancourt. Crossing two closely related *Fusarium graminearum* strains generates progeny that are more aggressive than either parent. Oral Presentation. Mycological Society of America Annual Meeting, Lexington, KY 2010
- S. Bec, D. Van Sanford, L. Vaillancourt. A cross between two genetically similar *Fusarium graminearum* strains produces stable transgressive segregants for FHB pathogenicity related traits. Poster Presentation. USWBSI Conference, Milwaukee, WI 2011
- S. Bec, L. Vaillancourt. A closer look into the role of mating type genes in pathogenicity of *Gibberella zeae*. Poster Presentation. 26th Fungal Genetics Conference, Asilomar, CA 2011