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

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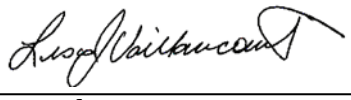
Fiscal Year:	FY11
USDA-ARS Agreement ID:	59-0206-0-062
USDA-ARS Agreement Title:	Genetics of Quantitative Pathogenic Variation in *Fusarium graminearum*.
FY11 USDA-ARS Award Amount:	$ 17,228

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
PBG	Genetics of Quantitative Pathogenic Variation in *Fusarium graminearum*.	$ 17,228
	Total ARS Award Amount	**$ 17,228**



7/13/12

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 (NA). Most NA strains reportedly belong to a single genetic lineage (lineage 7) and chemotype (15-ADON). Population genetic studies have demonstrated that the NA 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. We crossed two genetically well-characterized and phenotypically similar lineage 7 strains and obtained progeny with varying levels of aggressiveness and toxigenicity on soft red winter wheat. Our goal was to further characterize phenotypic and genetic variation among these progeny, and relate that to the pathogenicity and toxigenicity phenotypes. One objective was to produce bulk samples containing the most ten most aggressive and the ten least aggressive progeny from the cross, then to conduct Illumina sequencing of the two bulked samples, and evaluate segregation of approximately 10,000 previously published SNP markers between the two pools. Our hypothesis was that most SNP markers would segregate 1:1 while markers linked to traits with roles in aggressiveness would deviate from that ratio. A second objective was to analyze and compare the transcriptomes of florets infected with the most aggressive, and the least aggressive, progeny strains using Illumina RNAseq. The transcriptome analysis is still in progress, but the first objective was completed.

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:

Further studies demonstrated that the high and low aggressiveness and toxigenicity phenotypes of the progeny were stably inherited in their mitotic (monoconidial) progeny. It also demonstrated that toxigenicity and aggressiveness of the progeny *in planta* were correlated, although aggressiveness and *in planta* toxigenicity were not correlated with toxin production *in vitro*. Aggressiveness and toxigenicity *in planta* were also not correlated with several other traits that were examined, including asexual and sexual fecundity, and growth rate and colony morphology *in vitro*. The results of the bulk-segregant SNP analysis revealed approximately 20 genomic regions that showed a significant association with high aggressiveness versus low aggressiveness, although no region co-segregated with the phenotype 100% of the time. These regions were dispersed among the four chromosomes. Examination of gene models linked to these regions revealed a variety of predicted protein classes including hypothetical proteins, cell wall degrading enzymes, transcription factors,

and genes potentially involved in sugar metabolism and transport and in the production of secondary metabolites. Analysis of this dataset is continuing.

Impact:

Our findings are significant because they demonstrate that outcrossing in the field, even among genetically similar strains that appear similar in aggressiveness, can give rise to stable strains that are significantly more aggressive or toxigenic. Similar observations have been reported recently by other workers: however, because our work uses genetically well-characterized strains, it has been possible to identify genetic markers linked to segregating traits responsible for these changes, and thus we will be able to study exactly how these changes have occurred. Future work will be focused on this question and on the roles of linked genes in aggressiveness and toxigenicity. This could lead to development of better diagnostic assays based on linked markers, or to improved therapies targeting the products of the identified fungal genes, thus resulting in an increased 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.

Presentation:

October 24, 2011, NC1183 Mycotoxins: Biosecurity, Food Safety, and Biofuels Byproducts, Annual Meeting at the University of Kentucky. Sladana Bec, Lisa Vaillancourt. Role of mating type genes in pathogenicity of *Fusarium graminearum* (*Gibberella zeae*).

Ph.D. Dissertation:

Sladana Bec, 2011, University of Kentucky Department of Plant Pathology: Role of the Sexual Cycle in Development of Genotypic and Phenotypic Diversity in Gibberella zeae. (238 pp.)

Three papers are currently **in preparation:**

Bec, S., Farman, M., Ward, T., O'Donnell, K., Hershman, D., and Vaillancourt, L.J. Novel fingerprinting and genetic markers for studies of diversity and sexual recombination in *Gibberella zeae* (*Fusarium graminearum*).

Bec, S., Farman, M., and Vaillancourt, L. Comparative performance of the split-marker protocol for the production of deletion mutants in strain PH-1 of *Fusarium graminearum*.

Bec., S., Schwartz, S., and Vaillancourt, L. Crossing two genetically and phenotypically similar *Gibberella zeae* strains produces transgressive progeny with increased levels of aggressiveness and toxigenicity.