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

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Fiscal Year:	FY10
USDA-ARS Agreement ID:	NA
USDA-ARS Agreement Title:	Genomic Selection for FHB Resistance in Midwest Six-row Barley.
FY10 USDA-ARS Award Amount:	$ 15,000

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
BAR-CP	Genomic Selection for FHB Resistance in Midwest Six-row Barley.	$ 15,000
	Total ARS Award Amount	**$ 15,000**

Principal Investigator Date

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* 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: *Genomic Selection for FHB Resistance in Midwest Six-row Barley.*

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

   Selecting for FHB phenotypically is expensive. There are few large consistent effect QTL that might be the target of marker assisted selection. Genomic selection for FHB therefore makes sense. We collaborated with Kevin Smith in i) Selecting optimal markers to be used for genotyping. ii) Analyzing the joint marker / phenotype data to develop a GS model. iii) Applying the model to select among ~2,000 F3 barley lines, and selected individuals for advancement in the breeding program and to be used as parents in the next cycle of selection. Kevin Smith has further set up experiments to validate these selections. Thus, our goal is to both implement GS and evaluate its effectiveness for FHB resistance in barley.

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 developed a GS model that predicts FHB, DON, yield and other traits in barley. Based on cross-validation, the model accuracy is ~0.6 to 0.7. This level of accuracy coupled with a breeding cycle time, that is reduced from four years to one year, is expected to substantially increase the rate of genetic gain.

   Impact: The first breeding lines resulting from GS are in first year yield trials this year. We expect to have direct measurements of genetic gain during this current funding cycle to assess the impact.

PI: Jannink, Jean-Luc
USDA-ARS Agreement #: NA

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.

Support from this grant partially supported the following:

Presentation:
Jannink, J.-L. 2011. Methods and breeding schemes applying genomic selection to crops in the public sector. Plant and Animal Genome XIX, San Diego, CA.

Book Chapter:
Lorenz, A.J., S. Chao, F.G. Asoro, E.L. Heffner, T. Hayashi, H. Iwata, K.P. Smith, M.E. Sorrells, and **J.-L. Jannink**. 2010. Genomic Selection in Plant Breeding: Knowledge and Prospects. Adv. Agron. 110:77-123.