USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY09 Final Performance Report
July 15, 2010

Cover Page

PI:	Jose Gonzalez
Institution:	South Dakota State University
Address:	Plant Science Department 280 Northern Plains Biostress Building 1110 Rotunda Lane N. Brookings, SD 57007
E-mail:	jose.gonzalez@sdstate.edu
Phone:	605-688-6907
Fax:	605-688-4452
Fiscal Year:	2009
USDA-ARS Agreement ID:	59-0790-8-066
USDA-ARS Agreement Title:	Molecular Characterization and Pyramiding of Novel Scab Resistance Sources Adapted to the Northern Plains Growing Region
FY09- USDA-ARS Award Amount:	$ 19,376

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Adjusted Award Amount
VDHR-SPR	Molecular Characterization and Pyramiding of Novel Scab Resistance Sources Adapted to the Northern Plains Growing Region.	$ 19,376
	Total Award Amount	**$ 19,376**

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 Winter Wheat Region
    SWW – Southern Sinter Wheat Region

Project 1: *Molecular Characterization and Pyramiding of Novel Scab Resistance Sources Adapted to the Northern Plains Growing Region.*

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

   The major issue was to map resistance QTLs in a integrated manner with the breeding program and generating segregating breeding lines for direct use in the breeding program. For this purpose we used a family-based pedigree mapping approach.

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 #1: Validation of the family-based mapping pedigree approach using Sumai 3 derived lines.

   Impact: This novel approach can be used to quickly and simultaneously map and introgress new sources of FHB resistance into breeding material. We generated over 800 segregating lines derived from different resistant sources derived from Sumai3 in ~80 different genetic backgrounds.

   Accomplishment #2: Mapping of resistance QTL in FHB resistant line SD3934. A resistance QTL was found on chromosome 3BS.

   Impact: We corroborated that SD3934 had the 3BS QTL from ‘Norin’. We generated over 800 segregating lines derived from SD3934 in ~80 different genetic backgrounds.

   Accomplishment #3: Mapping of resistance QTL on Mult757.

   Impact: We found a resistance QTL on chromosome 7BS explaining 32% of the phenotypic variation. This location is similar to that found in other sources, however the effect is larger, suggesting that Mult757 carries a novel allele for this QTL. We generated over 800 segregating lines derived from Mult757 in ~80 different genetic backgrounds.

Include below a list all germplasm or cultivars released with full or partial support of the USWBSI. List the release notice or publication. Briefly describe the level of FHB resistance.

- We generated over 800 segregating lines derived from different resistant sources derived from Sumai3 in ~80 different genetic backgrounds.
- We generated over 800 segregating lines derived from SD3934 in ~80 different genetic backgrounds.
- We generated over 800 segregating lines derived from Mult757 in ~80 different genetic backgrounds.

All these lines were transferred to the Spring Wheat Breeding Program at South Dakota State University.

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.

Rosyara UR, **J.L Gonzalez-Hernandez**, K.D. Glover, K.R. Gedye, and J.M. Stein. 2010. Power of family-based QTL mapping: Optimizing marker density, Population Size and Structure. *In submission to Theoretical and Applied Genetics*.

Rosyara, UR, **J.L. Gonzalez-Hernandez**, K.D. Glover, K.R. Gedye and J.M. Stein 2009. Family-based mapping of quantitative trait loci in plant breeding populations with Fusarium head blight resistance in wheat as an illustration. *Theoretical and Applied Genetics. 118:1617-1631*

Umesh Rosyara, **Jose L. Gonzalez-Hernandez,** Karl D. Glover, Kristene Gedye and Jeffrey M. Stein.2009. Family Based Mapping of Quantitative Trait Loci Using Linkage and Association Approach. ASA-CSSA-SSSA Annual Meeting. November 1-5, 2009. Pittsburg, PA

U.R. Rosyara, **J.L. Gonzalez-Hernandez**, K.D. Glover, K. Gedye and J.M. Stein. 2009. Mapping and Introgression of FHB Resistant Quantitative Trait Loci from Two Spring Wheat Genotypes Using a Family-Based Approach. In: S. Canty, A. Clark, J. Mundell, E. Walton, D. Ellis and D. Van Sanford (Eds.), Proceedings of the National Fusarium Head Blight Forum; 2009 Dec 7-9; Orlando, FL. Lexington, KY: University of Kentucky.

U. Rosyara, **J.L. Gonzalez-Hernandez***, K.D. Glover, K. Gedye and J. Stein. 2008. Power of family-based QTL mapping: Optimizing Family Type, Size and Marker Density for QTLs of different magnitudes. In: Canty, S.M., E. Walton, A. Clark., D. Ellis. J. Mundell, and D.A. Van Sanford (Eds.), Proceedings of the National Fusarium Head Blight Forum; 2008 Dec 2-4; Indianapolis, IN. Lexington, KY: University of Kentucky. Page 197

U. Rosyara, **J.L. Gonzalez-Hernandez***, J. Stein, K. Gedye and K.D. Glover. 2008. Selective genotyping in Family-based Mapping of FHB resistance QTLs in Hexaploid Wheat. In:

Canty, S.M., E. Walton, A. Clark., D. Ellis. J. Mundell, and D.A. Van Sanford (Eds.), Proceedings of the National Fusarium Head Blight Forum; 2008 Dec 2-4; Indianapolis, IN. Lexington, KY: University of Kentucky. Page 198

K.D. Glover, **J.L. Gonzalez-Hernandez**, U.R. Rosyara, D. Karki, K. Gedye and J.M. Stein. 2008. Validation of a Family-based Quantitative Trait Locus Mapping Approach for Selection of Fusarium Head Blight Resistant Spring Wheat Breeding Lines. In: Canty, S.M., E. Walton, A. Clark., D. Ellis. J. Mundell, and D.A. Van Sanford (Eds.), Proceedings of the National Fusarium Head Blight Forum; 2008 Dec 2-4; Indianapolis, IN. Lexington, KY: University of Kentucky. Page 161