USDA-ARS/
U.S. Wheat and Barley Scab Initiative
FY08 Final Performance Report (approx. May 08 – April 09)
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Cover Page

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Fiscal Year:	2008
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.
FY08 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

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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
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

(Form FPR08)

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?

DNA-based molecular markers have been used to map quantitative trait loci (QTL) with one of major objective of marker aided selection (MAS). Traditional QTL mapping techniques have some important disadvantage, most important one time requirement to accomplish; thereby the markers are not available on time to plant breeders. This limitation is very serious for devastating diseases (such as wheat scab); breeders can not wait for QTL mapping accomplished to practice MAS. In reality, as soon as breeders notice a new source of resistance and start introgression into adopted genetic backgrounds and follow classical selection techniques. Other limitation of traditional approaches identified markers may not be applicable to other genetic backgrounds then tested in mapping experiment, and mapping population development.

Moreover, the mapping populations rarely give rise to new cultivars. The mapped QTL or marker associated with it may or may not work well in genetic background of breeders' interest beside the parents involved in mapping experiment. Thus, there is requirement for a validation experiment before MAS is deployed in a whole breeding population. This will further lengthen the process. Thus, for successful and efficient application of marker in a breeding program, a single step method that can simultaneously map QTL of interest, validate the QTL / marker effectiveness in multiple genetic backgrounds of breeding interest, and practice MAS, are desirable. Using families generated at breeding program for mapping purpose can be good solution for such single step method.

We tested applicability of family-pedigree based linkage (variance component and pedigree-wide regression) and association mapping (Quantitative transmission disequilibrium test) techniques commonly used in human genetics to plant breeding populations using the well characterized QTL, *Qfhs.ndsu-3BS* in spring wheat families from SDSU wheat breeding program. The result shows the usefulness of human genetics the approach to detect relatively large effect QTLs earliest possible in breeding program and subsequent use in MAS.

Furthermore the mapping technique was further optimized for sample size requirement (family number and type) for QTLs of different magnitude using a simulated data set. Using developed method, mapping of QTLs in two resistant sources: SD3934 and Mult757 are underway. Novel QTLs, identified if any, will help in development of resistant genotypes by diversifying the resistance source other than Sumai 3. Not limited to scab resistance, the identified mapping technique might be useful in mapping sever other traits of breeders' interest in wheat and other crops.

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:

- Family based linkage and association mapping technique is validated and optimized. The method is useful for mapping other novel resistance sources (or traits of breeders' interest) with or without modification.
- Mapping of SD3934 and Mult757 are underway using the validated method. We have developed two mapping population each with ~90 families with a cross with ~40 parents. The populations are evaluated for scab resistance in greenhouse trials. Genotyping of SD3934 families is underway.

Impact:

The validated method is quick and efficient for QTL with particular interest in development of markers using breeding families. This method, if employed will help to accelerate the mapping and MAS process in entire breeding program. In addition, the mapped QTL, if novel QTLs identified, will be useful to diversify the resistance source beside dependence on Sumai 3. As the mapping population, itself is breeding families, could lead to development of cultivar after more generations of selections, yield trials, and multi-location testing.

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.

Peer-reviewed article – Published

Rosyara U.R., 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 resistance to Fusarium head blight in wheat as an illustration ***Theoretical Applied Genetics 118:1617-1631***

Peer-reviewed article – Under-preparation

Rosyara U.R., J.L. Gonzalez-Hernandez, K.D. Glover, K.R. Gedye and J.M. Stein. 2009. Power of family-based QTL mapping: Optimizing Family Type, Size and Marker Density for QTLs of different magnitudes. ***Theoretical Applied Genetics. xxx***

Poster / Oral Presentation – presented

Rosyara U.R., K.L. Maxson-Stein, K.D. Glover, J.M. Stein, and J.L. Gonzalez-Hernandez, 2008**.** Validation of variance component-based linkage analysis to map QTLs for disease resistance in wheat. Proceedings of the ***Plant and Animal Genome XVI*** January 12 - 16, 2008, Town & Country Convention Center, San Diego, California, United States

Rosyara U.R., K. Gedye, K.D. Glover, J.M. Stein, and J.L. Gonzalez-Hernandez, 2009**.** Family-based association mapping for simultaneous marker validation and marker-aided selection of scab resistance in wheat. ***Plant Science Research Day,*** May 7, 2009**,** South Dakota State University, Brookings, SD, USA

Rosyara U.R., K. Gedye, K.D. Glover, J.M. Stein, and J.L. Gonzalez-Hernandez, 2008**.** Power of family-based QTL mapping: Optimizing family type, size and marker density for QTLs of different magnitudes. Proceedings of the ***National Fusarium Head Blight Forum***. December 2-4, 2008, Crowne Plaza Hotel, Indianapolis, IN USA

Rosyara U.R., K. Gedye, K.D. Glover, J.M. Stein, and J.L. Gonzalez-Hernandez, 2008**.** Selective genotyping in Family-based Mapping of FHB resistance QTLs in Hexaploid Wheat. Proceedings of the ***National Fusarium Head Blight Forum***. December 2-4, 2008, Crowne Plaza Hotel, Indianapolis, IN USA

Glover K.D., 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. Proceedings of the ***National Fusarium Head Blight Forum***. December 2-4, 2008, Crowne Plaza Hotel, Indianapolis, IN USA

Rosyara U.R., K.L. Maxson-Stein, K.D. Glover, J.M. Stein, and J.L. Gonzalez-Hernandez, 2008. Family based mapping of FHB resistance QTLs in hexaploid wheat. Proceedings of the ***National Fusarium Head Blight Forum***. The Westin Crown Center Kansas City, Missouri 2-4 December, 2007.

Poster / Oral Presentation – scheduled in near future

Rosyara U.R., K.D. Glover, J.M. Stein, and J.L. Gonzalez-Hernandez, 2009**.** Family based mapping of Quantitative Trait Loci using linkage and association approach. ***ASA-CSSA-SSSA International Annual Meeting 2009***. Nov 1-5, Pittsburg, PA (oral presentation on Monday, November 2, 2009: 3:30 PM)

If your FY08 USDA-ARS Grant contained a VDHR-related project, 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. If this is not applicable (i.e. no VDHR-related project) to your FY08 grant, please insert 'Not Applicable' below.

Not applicable