USDA-ARS/

U.S. Wheat and Barley Scab Initiative FY06 Final Performance Report (approx. May 06 – April 07) July 16, 2007

Cover Page

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Fiscal Year:	2006
USDA-ARS Agreement ID:	59-0790-4-094
USDA-ARS Agreement	Hastening the Development of Speciality Spring Wheats with
Title:	Resistance to Fusarium Head Blight.
FY06 ARS Award Amount:	\$ 38,248

USWBSI Individual Project(s)

USWBSI Research Area*	Project Title	ARS Award Amount
VDUN	Pyramiding Sources of Scab Resistance in Spring Wheat.	\$ 38,248
	Total Award Amount	\$ 38,248

Principal Investigator	Date

^{*} CBCC – Chemical, Biological & Cultural Control

EEDF - Etiology, Epidemiology & Disease Forecasting

FSTU – Food Safety, Toxicology, & Utilization of Mycotoxin-contaminated Grain

GET – Genetic Engineering & Transformation

HGR – Host Genetics Resources

 $HGG-Host\ Genetics\ \&\ Genomics$

PGG – Pathogen Genetics & Genomics

VDUN – Variety Development & Uniform Nurseries

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Project 1: Pyramiding Sources of Scab Resistance in Spring Wheat.

1. What major problem or issue is being resolved and how are you resolving it?

Despite the fact that growers are using more resistant spring wheat varieties, wheat producers and end-users continue to experience significant economic losses due to Fusarium head blight (FHB). This underscores the need for a higher level of expressed resistance and a more durable type of resistance. We are using molecular markers to genes for resistance and marker-assisted selection to 1) combine or pyramid three different sources of FHB resistance originating from Sumai 3, *T. dicoccoides*, and Frontana spring wheat, 2) assess the level of resistance conferred by pyramiding different gene sources and 3) rapidly advance genotypes with pyramided sources of resistance for release as germplasm lines or varieties.

2. List the most important accomplishment and its impact (how is it being used?). Complete all three sections (repeat sections for each major accomplishment):

Accomplishment:

We combined two different sources of FHB resistance, one source originally from Sumai 3 and the other from *T. dicoccoides*. Two genetically similar doubled-haploid (DH) spring wheat lines, one with only the Sumai 3 source of resistance and the other with both sources were compared for FHB resistance. The DH lines were produced by first hybridizing Alsen to a synthetic hexaploid wheat, expressing the *T. dicoccoides* resistance. Progeny were backcrossed twice to Alsen, and the resulting backcrossed lines were pollinated with maize to produce the DH lines. Molecular markers were used to select the DH lines and confirm the presence of the resistance QTL from Sumai 3 and *T. dicoccoides*. The two lines were evaluated for FHB resistance in two greenhouse experiments. The DH line with only Sumai 3 exhibited a mean FHB severity of 14%, while the line with both sources of FHB resistance exhibited a mean of 7%. Mean DON content of the single-source line was 6.4 ppm, while the DON content of the two-source line was 1.6 ppm. Results of this greenhouse experiments suggest that pyramiding the two sources enhanced the level of resistance to FHB.

We completed a study to determine the genetic nature of the type I resistance to FHB exhibited by 'Frontana' spring wheat. A backcross reciprocal monosomic analysis was conducted to identify Frontana chromosomes with resistance. Disomic lines, one set containing critical chromosomes from Frontana and the other containing chromosomes from susceptible Chris, were spray-inoculated and evaluated in separate greenhouse experiments. In one experiment, reciprocal chromosome lines 5B for visually diseased kernels, lines 7B for kernels/g, and lines 4B and 6A for DON content were significantly different. Lines with Frontana chromosomes 3A, 6A and 4D reduced visually diseased kernels, kernels/g and DON content in both studies, while Frontana chromosomes 2A, 2B, 4B and 7B increased susceptibility, as indicated by an increase in these same measurements in both experiments. Genes carried on Frontana chromosomes 3A, 6A and 4D could be useful for diversifying and pyramiding sources of FHB resistance in spring wheat.

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Impact:

Our studies represent important steps toward improving resistance to FHB and particularly lowering DON content through the use of resistant wheat genotypes. Combining or pyramiding genes for resistance appears to be one way to enhance the expression of resistance and perhaps the durability of existing resistance genes. Also, identifying the Frontana chromosomes involved in the type I resistance to FHB is a first step in determining how a type I resistance functions compared with a type II resistance. It has been difficult to identify new and useful sources of FHB resistance, so pyramiding existing genes and utilizing a type I resistance in combination with a type II resistance can help improve the level of expressed resistance and perhaps extend the useful lifetime of existing genes for FHB resistance.

As a result of that accomplishment, what does your particular clientele, the scientific community, and agriculture as a whole have now that they didn't have before?

As a result of the experiments analyzing lines where we combined two sources of resistance, wheat breeders now know that pyramiding different sources of FHB genes can be an effective approach to enhancing host plant resistance and lowering the production of DON in grain. Furthermore, we demonstrated that molecular markers for resistance genes can be effectively used to pyramid different sources of FHB resistance. Ultimately, the release of the line with the two sources of resistance will provide plant breeders with a valuable genetic resource to use in enhancing the FHB resistance of breeding lines they target for release as varieties.

The published results from the reciprocal backcross monosomic study involving Frontana are important for two reasons. First we identified individual Frontana chromosomes which are involved in increasing the type I resistance and increasing susceptibility to FHB. The scientific community can use this information to focus on these chromosomes, which should help in the mapping of specific resistance genes and possibly the eventual cloning of these genes. Second, the development of these lines provides the scientific community with valuable genetic material to use in additional studies into the genetic nature of a type I compared to a type II resistance to FHB. For example, other scientists are already using the reciprocal backcross monosomic Frontana lines to test whether chromosomes putatively involved in resistance carry genes which act to exclude fungal invasion of leaf tissue. Breeders might eventually be able to release wheat varieties which combine both type I and II sources of resistance to lower the expression of FHB symptoms and the development of DON in the grain.

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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.

- Berzonsky, W.A., B.L. Gebhard, E. Gamotin, G.D. Leach, and S. Ali. 2007. A reciprocal backcross monosomic analysis of the scab resistant spring wheat (*Triticum aestivum* L.) cultivar, `Frontana'. Plant Breeding 126:234-239.
- Gamotin E.L., W.A. Berzonsky, S. Ali, T. Adhikari, and G.D. Leach. Pyramiding different sources of fusarium head blight Resistance into spring wheat. Plant and Animal Genome conference XVI. January 2007, San Diego, CA (poster presentation).
- Berzonsky, W.A. Stepping out of the primary gene pool: A breeders perspective on using alien germplasm. USWBSI Alien Introgression Workshop, August 2006. Fargo, ND. (invited oral presentation).