Cover Page

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Fiscal Year:	FY11
USDA-ARS Agreement ID:	59-0206-9-086
USDA-ARS Agreement Title:	Discovering, Understanding, and Utilizing Wheat Genes for FHB Resistance in Ohio.
FY11 USDA-ARS Award Amount:	$ 141,671

USWBSI Individual Project(s)

USWBSI Research Category[*]	Project Title	ARS Award Amount
VDHR-NWW	Breeding FHB Resistant Wheat for Ohio.	$ 59,512
VDHR-NWW	Coordinated Evaluation and Utilization of Marker Assisted Selection.	$ 12,375
VDHR-NWW	Improved Breeding for FHB Resistance by Advanced Genetic and Phenotypic Characterization of Soft Winter Wheat.	$ 50,272
VDHR-NWW	Coordinated Evaluation of FHB Resistance of Advanced Soft Winter Lines and Cultivars.	$ 19,512
	Total ARS Award Amount	**$ 141,671**

7/13/2012

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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: *Breeding FHB Resistant Wheat for Ohio.*

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

   Host resistance is vital to controlling FHB. High levels of resistance are not difficult to obtain, but combing such levels with high yield is quite difficult. We are fortunate to have high levels of native resistance for FHB in soft winter wheat.   This allows us to effectively use phenotypic selection for FHB and to complement that with MAS for select QTL, mostly from exotic sources.

   The OSU program strives to phenotype as many breeding lines as possible each year in a misted and inoculated nursery. In addition we are spray inoculating 8,000 head rows each year to select against susceptibility.   These lines are all derived from crosses where at least one parent has good FHB resistance. All of our variety development crosses now involve at least one parent with strong FHB resistance.

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):**

   <u>Accomplishment:</u>

   In 2011 we screened 1270 OSU breeding line for FHB resistance in a nisted, inoculated nursery. Of these, 36% had an FHB index (% of spiklets showing symptomatic bleaching) that was ≤ the index of the most resistant check (Truman); 58% has an index ≤ the index of the moderate resistant check; 4% had an index ≥ than the index of the susceptible check. This high level of FHB resistance was generate almost exclusively by using native FHB resistance. In addition, we spray inoculated 8,000 F3:4 and F4:5 lines in an unreplicated, un-misted nursery. Symptoms were achieved and we were able to select against susceptibility.
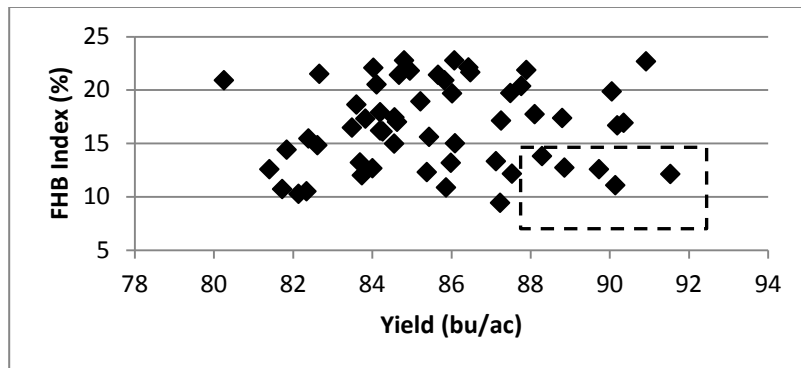
Fig. 1. Yield and FHB index of 56 lines from two years of testing. Lines in the box have greater yield than Pioneer 25R47 and lower FHB index than Truman.

Impact:

FHB resistance alone has little value as it must be combined with economically relevant levels of all other traits and especially yield. It is essential to work with breeding populations that have high levels of FHB resistance and yield to obtain the desired combination. We are having great success improving the level of FHB resistance in our population and are also having some success in combining this resistance with high yield (Fig. 1). The impact is the potential release of new cultivars with lower FHB levels and thus lower DON levels. In addition the germplasm is available for other breeders to use in crosses.

Project 2: *Coordinated Evaluation and Utilization of Marker Assisted Selection.*

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

    Phenotypic selection for FHB resistance using the native resistance in soft red winter wheat can be complemented by marker-assisted selection (MAS). This may enhance the probability of finding lines with strong FHB resistance. The genes used in MAS though need to complement our native FHB resistance genes and should have negligible impact on other key traits. Part of this work will determine the impact of MAS on FHB in SRWW and on other traits. The other part is simply using MAS in our variety development program.

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:

    In 2011 we screened 76 lines for FHB Index, *Fusarium* damaged kernels, and DON. These lines were comprised of pairs if related lines that differed for Fhb1 and the QTL on chromosome 5A. The data was sent to the PI of the project (D. Van Sanford) for analysis with data from other cooperators. We have been using MAS to backcross Fhb1, 5AS, and 2D QTL into elite lines that already have moderate FHB resistance. These lines could be released directly as new cultivars or used quickly as parents.

    Impact:

    Our data will be used with data from other cooperators in a joint analysis of the impact of MAS on multiple FHB resistance mechanisms as well as quality and yield. The results of that analysis are not yet available. More data has been collected in June of 2012.

Project 3: *Improved Breeding for FHB Resistance by Advanced Genetic and Phenotypic Characterization of Soft Winter Wheat.*

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

    Host resistance is vital for controlling FHB. Soft winter wheat contains a high level of native resistance. There have been several efforts to map QTL associated with native resistance and for the most part these efforts have discovered a few QTL with modest effect despite ample phenotypic variation. While more mapping in bi-parental populations derived from elite parents may yet uncover QTL with greater impact, association analyses (AA) may uncover these QTL more efficiently as it evaluates alleles from many parents at one time.

    Marker-assisted selection for individual genes is a useful strategy when QTL with large effects are present but is less effective when a trait is controlled by many genes with small effects. Genomic selection (GS) is a new approach to breeding that assigns value to whole genomes instead of individual genes and can hasten selection by reducing the number of years in a breeding cycle. It is possible that GS may be very useful for native FHB resistance in soft winter wheat if that resistance is controlled primarily by many genes of small effect.

    This project will conduct both AA and GS in a broad population derived from soft winter wheat with the objective of 1) doing AA to assess the presence of QTL useful in MAS, and 2) establish the feasibility of GS for FHB resistance.

    Soft winter wheat also seems to have considerable genetic variation for many types of resistance including resistance to infection and spread (type I and II).   Variation for FDK and DON are also commonly seen and not all of that variation is account for by variation for type I and II resistance. This suggests variation for resistance to kernel infection and toxin accumulation (RKI, RTA). Phenotyping of large populations for many traits may allow us to determine the coincidence of QTL for all mechanism of resistance and more detailed investigation into variation for RKI and RTA.

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):**

    <u>**Accomplishment:**</u>

    The cooperative trial involved seven breeders from MO, IL, IN, MI, KY, OH and NY. The trial consisted of evaluating 749 soft wheat lines for multiple FHB traits. Of the 749 entries, 49 were checks or parental lines and these were evaluated at all seven locations. The remaining 700 lines were RILs from the seven breeders with each evaluating their own set of 100 RILs at their location: RILs were not evaluated over environments.

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Data was collected on six FHB traits (Table 1) as well as heading date. The phenotypic data within an environment of all entries was standardized for the mean and standard deviation of the 49 checks of that environment. Heritability was high for all traits and the ratio of genetic variance to error variance was nearly one or greater for all traits (Table 1). This suggests that genotype by environment interaction (the main source of error) was not a huge source of variation after standardization. The standardization improved heritability and the ratio of genetic variance to error variance compared to raw data (Table 1).

Table 1. Summary of ratios of variances for six FHB traits from analysis of the 49 checks and RILs using raw data and standardized data.

	INC*	SEV	IND	FDK	ISK	DON
Number of Environments	6	6	7	6	6	2
Check, Raw Data: Heritability	0.82	0.81	0.78	0.85	0.90	0.62
Check, Raw Data: V_{geno}/V_{error}	0.78	0.73	0.52	0.92	1.44	0.82
RILs, Raw Data: $V_{cross}/V_{within cross}$	5.8	2.5	2.5	1.5	3.3	0.6
Check, Std Data: Heritability	0.84	0.86	0.87	0.91	0.91	0.84
Check, Std Data: V_{geno}/V_{error}	0.89	1.05	1.00	1.63	1.69	2.67
RILs, Std Data: $V_{cross}/V_{within cross}$	0.10	0.15	0.29	0.29	0.32	0.24

* INC=incidence, SEV=severity, IND=index, FDK= Fusarium damaged kernels, ISK=INC/SEV/FDK index, DON=deoxynivalenol.

Phenotypic variance was large among the 49 checks and among the RILs. For each trait, the range of the RILs exceeded that of the 49 checks. We are currently compiling the data from the second year of phenoytyping. In addition we are conducting quantitative PCR to assess the degree of kernel infection. That data will be used to determine resistance to kernel infection and toxin accumulation.

We will genotype these lines within the next 6 months and complete an association analysis using 2011 and 2012 data.

Impact:

The main impact so far is we have been able to phenotype a large population (n=749) with a high level of accuracy. Large populations are essential to accurate mapping and genomic selection but are very difficult to phenotype: no USWBSI breeder could phenotype all 749 lines for this project within their environment. We decided to split the population but this requires standardizing the data as the RILs are tested in one environment each. The use of data from a large set of checks was vital to producing the successful standardization that we employed.

This population is likely to be among largest analyzed for FHB. Genotyping costs are dropping dramatically since the project was first proposed. We have waited as long as possible to genotype so that we can use the most cost effective platform. It appears that will

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use genotyping by sequencing and that technology can now be applied and should provide 5,000 to10,000 markers for the population.

The large population size and genome-wide genotyping will provide excellent power to detect QTL and to develop accurate genomic selection models

Project 4: *Coordinated Evaluation of FHB Resistance of Advanced Soft Winter Lines and Cultivars.*

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

   Host resistance remains the foundation of controlling FHB and DON. Despite increased use of MAS, phenotyping remains the primary tool to improve host resistance. Phenotyping is difficult and ideally is conducted over multiple environments to provide robust estimates of resistance. The phenotyping is even more crucial to growers who need unbiased estimates of host resistance. This project pools all phenotyping of uniform nurseries and state official variety tests into one project. The results are distributed to all breeders and is available to all growers via extension activities and Scab Smart

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):**

   <u>Accomplishment:</u>

   This project phenotyped approximately 728 entries in the 2010-11 season (Table 1). This included 100 entries in the USWBSI uniform trials (P+NUWWSN) that are evaluated over multiple environments. In addition, the project phenotyped 208 other breeding lines at 1-2 environments: these are entries in regional cooperative yield trials. Finally, each state phenotyped all the entries in their state's official variety test. These tests contain 60-80 entries each and the evaluation in a state is conducted in one environment. Some entries are shared over states but the data is not compiled over states.

   Table 1. Summary of FHB trials screened for FHB resistance in FY11.

Test	Entries in 2011	# Environments
PNUWWSN	60	11
NUWWSN	40	7
Five State - Adv.	25	2
Five State - Pre.	25	2
Uniform Eastern	40	2
Uniform Southern	28	1

PI: Sneller, Clay
USDA-ARS Agreement #: 59-0206-9-086

Test	Entries in 2011	# Environments
Mason-Dixon	60	1
Uniform White	30	2
State Official Variety Trials	420*	1
Total	728	

* The number of entries varies over states. I assumed 60 per state and we have 7 states

The extent of disease varied by state. In the NUWWSN, 30% of the entries (18/60) displayed strong resistance while 33% of the PNUWWSN entries displayed strong resistance. A quick look at the other breeding trials indicates that about 10% of the entries had FHB resistance that was similar to Truman.

Impact:

The phenotypic screening conducted in this project is vital to improving FHB resistance in SRWW adapted to the northern US and ensuring growers are selecting the most resistant varieties. Breeders are selecting for resistance in their own programs, but these tests are essential to validate those selections. Virtually all commercial varieties currently available to growers are screened in the OVT. That information is distributed within each state via extension service. In addition the information is posted on Scab Smart.

All candidates for immediate release or release within the next 1-3 years from the public programs are screened in the eight breeding line trials.   In addition, some lines from private companies are also screened.   This allows breeders to select for resistance, and as importantly, screen against susceptibility.

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Include below a list of 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.

None in FY11

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.

1. C. Sneller, M Guttieri, P Paul, and J. Costa. "Variation for Resistance to Kernel Infection and Toxin Accumulation in Soft Winter Wheat" **In:** Proceeding of the 2011 National Fusarium Head Blight Forum. US Wheat and Barley Scab Initiative. Page 57
2. C. Sneller, J-L Jannink, A. Hoffstetter, A Cabrera. "Preliminary Evaluation of Genomic Selection for FHB Resistance and Other Traits" **In:** Proceeding of the 2011 National Fusarium Head Blight Forum. US Wheat and Barley Scab Initiative. Page 51.
3. Hoffstetter, A., C. Sneller, and A. Cabrera. "Association Analysis of Fusarium Head Blight Resistance in Soft Red Winter Wheat" **In:** Proceeding of the 2011 National Fusarium Head Blight Forum. US Wheat and Barley Scab Initiative: Page 25.
4. Hoffstetter, A., C. Sneller, and A. Cabrera. "Using association analysis to detect regions of the genome that confer resistance to Fusarium head blight in eastern U.S. soft red winter wheat". American Phytopathological Society North Central Meeting, Wooster Ohio, May 21 2012.
5. Sneller, C., P Paul, M Guttieri, L Herald, B Sugerman. "Report on the 2010-11 P+NUSSWN" **In:** Proceeding of the 2011 National Fusarium Head Blight Forum. US Wheat and Barley Scab Initiative. Pp 52-56
6. Sneller, C.; Guttieri, M.; Paul, Pierce; Broders, G.; Jackwood, R. "Variation for resistance to kernel infection and toxin accumulation in wheat lines infected with Fusarium graminearum". Phytopathology Vol. 102 no. 3:306-314.