SESSION 5:

VARIETY DEVELOPMENT AND HOST RESISTANCE

Co-Chairpersons: Bill Berzonsky
and Jose Costa

VALIDATION OF *FHB1* AND *QFHS.NAU-2DL* IN SEVERAL SRW WHEAT BREEDING POPULATIONS

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ABSTRACT

Fhb1 is the most widely used exotic Fusarium Head Blight (FHB) resistance quantitative trait locus (QTL). Located on the short arm of chromosome 3B, this QTL is derived from Sumai-3. *QFhs.nau-2DL* is a non-Sumai-3 QTL that has been suggested as a complement to *Fhb1* in conferring FHB resistance, specifically by reducing deoxynivalenol (DON) concentrations. To validate the effects of both QTLs, five populations were evaluated in the Lexington scab nursery in 2010: Cross 12 (26R58/VA01W-476//KY97C-0574-01), Cross 17 (25R54/VA01W-476//KY97C-0574-01), Cross 19 (25R54/VA01W-476//KY97C-0554-02), Cross 40 (25R78/Cumberland//VA01W-476) and Cross 42 (25R23/KY93C-1238-17-1//VA01W-476). Traits measured included incidence, severity, FHB index, Fusarium damaged kernels (FDK) and deoxynivalenol (DON) concentration. It is expensive and time consuming to quantify FDK and DON. Thus, rapid and non-destructive methods for predicting these traits are of great interest. Near infrared (NIR) calibrations to predict FDK and DON have been recently developed at the University of Kentucky. The objectives of this study are (i) to investigate the impact of *Fhb1* and *QFhs.nau-2DL* on FHB resistance and (ii) to improve current NIR calibrations to predict FDK and DON. FDK was significantly reduced between 37 and 41 % due to the effect of *Fhb1* in all five populations. *Fhb1* also reduced FHB index between 18 and 49 % in four of five populations and it reduced DON 23 % in Cross 19 and 33 % in Cross 42. *QFhs.nau-2DL* reduced severity 31 % in Cross 19 and FDK 35 % in Cross 40. The correlation between FDK measured using air separation and using NIR spectroscopy was 0.66 and 0.73 for Crosses 19 and 42, respectively.

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ASSOCIATION ANALYSIS OF MARKERS FOR BREEDING SCAB RESISTANCE IN WINTER WHEAT

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ABSTRACT

Marker assisted breeding is suited for low heritability traits and QTL of moderate to small effect. In order for markers to be applied, they must exhibit a trait association and be able to differentiate the target allele in a variety of germplasm. Bi-parental mapping is the conventional approach to identify marker-trait associations, although LD is maximized and polymorphism is limited to the parental alleles contributed. Association analysis is an approach that can determine the diagnostic ability of markers in a wide collection of material, in addition to determining or validating marker-trait association. An association analysis in wheat is needed because over 250 QTL for FHB resistance have been reported in bi-parental maps; few of which have been validated in alternate market class germplasm.

We report the results of an association study with advanced breeding lines from 19 Eastern United States breeding programs in relation to Fusarium Head blight resistance. Our analysis combined the phenotypic results of 258 lines from three uniform disease nurseries over three years. These advanced breeding lines were genotyped with 112 SSR and 2072 DArT markers. The population stratification and marker-trait associations were analyzed with TASSEL (v3.0.46). The results of the genome wide association study will be presented.

PHENOTYPIC CHARACTERIZATION OF FUSARIUM HEAD BLIGHT (FHB) RESISTANCE IN HULLED AND HULLESS WINTER BARLEY GROWN IN THE MID-ATLANTIC REGION

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ABSTRACT

Interest in use of winter barley (*Hordeum vulgare*) for ethanol production has heightened research focusing on its improvement, production, grain composition, utilization, and high value byproducts. Fusarium head blight (FHB), caused by *Fusarium graminearum*, is a serious fungal pathogen that produces the mycotoxin deoxynivalenol (DON), which is known to accumulate in barley grain and can become concentrated in dried distiller's grain with solubles (DDGS). These high value DDGS produced as a byproduct of ethanol production are used in animal feeds and have potential for use in human foods. High DON concentration in DDGS can render them unmarketable. Information is needed regarding the accumulation, fate and changes in DON concentration in barley grain and during ethanol production. Potential ways to reduce DON concentration in grain and/or to degrade it during ethanol production include use of FHB resistant cultivars, milling or pearling to remove hulls where DON is concentrated, and development of yeast strains having the capability to degrade DON. Currently, little is known about FHB resistance in hulled and hulless winter barley grown in Virginia. Nine winter (hulled and hulless) barley genotypes including three putatively resistant, moderately resistant, and susceptible lines were selected from the Virginia Tech barley breeding program to further characterize FHB resistance. Genotypes were planted in a randomized complete block with two replications in mist-irrigated nurseries at Blacksburg and Mt. Holly, VA. Plots were 1.5 m x 13.4 m to produce sufficient grain for analysis of DON concentration in barley grain, during ethanol fermentation, and in DDGS. *Fusarium graminearum* colonized corn (*Zea mays*) kernels were applied to plots at the boot stage at both locations, and the test at Blacksburg was spray inoculated using conidia (1×10^4) applied at 50% flowering stage. Plots were rated for FHB incidence, proportion of 30 heads infected with FHB per plot, and FHB severity, number of infected spikelets divided by the total number of spikelets for thirty heads per plot. Additional data collected included grain yield, test weight, 1000 kernel weight, Fusarium damaged kernels (FDK), and DON concentration. Analysis of variance showed significant differences ($P \leq 0.05$) among genotypes for all traits. A significant ($P \leq 0.05$) genotype x environment interaction occurred for yield, test weight, and incidence. All FHB measurement parameters were significantly ($P \leq 0.0001$) correlated with each other. Pearson correlation coefficients ranged from r = 0.43 to 0.91. All FHB parameters had a significant ($P \leq 0.05$) negative effect on yield, test weight, and 1000 kernel weight, except for incidence, which did not have a significant effect on yield. Correlation coefficients ranged from r = -0.24 to -0.73. Results indicate that a range in resistance exists among both hulled and hulless winter barley lines and cultivars grown in the Mid-Atlantic region. FHB has a significant negative effect on important agronomic traits. Additional research is underway to track DON concentration in barley grain, during ethanol fermentation, and in DDGS.

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COMPARISON OF TWO METHODS FOR ESTIMATING FUSARIUM DAMAGED KERNELS IN SOFT RED WINTER WHEAT

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ABSTRACT

Evaluating seed samples for Fusarium damaged kernels (FDK) by visual estimates is a tedious, highly subjective task. High-tech devices, such as spectral imaging and optical sorters, and low-tech machines, such as gravity tables, are available for detecting and/or separating FDK from healthy kernels, but are cost prohibitive or do not work well with our small sample sizes. A low-cost specific gravity separation device, developed at the University of Kentucky, uses a vacuum and air column to separate the FDK from the healthy kernels. Both portions of the seeds are weighed, and a percentage (W/W) is calculated. Our objective was to see how well visual estimates and air separation percentages correlated to known FDK scores.

The test was a completely randomized design of 80 lines grown in three replications in the 2009 Fusarium head blight (FHB) disease nursery in Urbana, IL. Two samples of each line were scored for FDK by three methods: 100 seed count, visual estimate, and air separation. Seed from each line were then sent to the University of Minnesota DON testing lab for deoxynivalenol quantification. Data were analyzed using PROC CORR in SAS 9.2. We used Spearman's rank correlation to compare the methods. All methods had highly significant correlations ($P < 0.001$). Both visual estimates and air separation percentages had strong correlations to the actual FDK count ($r = 0.81$ and 0.73, respectively). DON levels were not as closely correlated to the 100 seed count ($r = 0.59$), visual estimate ($r = 0.58$), or air separation ($r = 0.51$) method, but correlations were similar among methods.

These data support the use of an air column separation device or visual estimates for evaluating FDK. While a single air column separation device may not hasten the evaluation of FDK samples, it provides objective and reproducible data, and can be operated by hourly employees. Operating several separation devices would speed up the process and allow for evaluation of more samples. Obtaining the DON data was ancillary to the main objective of the study, but the moderate correlations between DON level and visual kernel damage serve are a reminder that visual kernel damage may not always be a good indicator of DON content in the grain.

CURRENT KNOWLEDGE ON THE GENETICS OF FUSARIUM HEAD BLIGHT RESISTANCE IN WHEAT - IMPLICATIONS FOR RESISTANCE BREEDING

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INTRODUCTION

In the wheat gene pool significant variation for resistance to Fusarium head blight has been discovered and documented for several decades. Resistance to Fusarium head blight is a quantitative trait controlled by polygenes and modulated by the environment. Numerous studies were performed to decipher the inheritance of Fusarium head blight resistance in wheat. Quantitative trait loci (QTL) mapping became the standard method for genetic analyses of FHB resistance. Most of the published studies were based on 'classical' QTL mapping using segregating populations from bi-parental crosses of a resistant with a susceptible parental line (Tanksley 1993). More recently, methods of association mapping have to been proposed for genetic analysis of quantitative traits. In this case sets of genotypes, which may be cultivars, breeding lines, or introduced germplasm collections, with or without pedigree and kinship information, are used for genetic analysis. This approach aims to associate the occurrence of certain marker haplotypes with trait expression (Gupta et al. 2005, Rostoks et al. 2006). Initial studies applying association mapping for FHB resistance in winter wheat were recently published by Zwart et al. (2008) and Miedaner et al. (2010).

MAPPED QTL FOR FUSARIUM HEAD BLIGHT RESISTANCE

A detailed review on FHB resistance QTL was recently compiled by Buerstmayr et al. (2009). In this article we summarized the relevant findings from 51 quantitative trait loci (QTL) mapping studies and included 9 research articles on marker assisted selection and 7 on marker assisted germplasm evaluation. Up to now QTL for FHB resistance were reported on almost all wheat chromosomes. Some QTL were found in several independent mapping studies indicating that such QTL are stable and appear therefore useful in breeding programs. We summarize and update current knowledge on the genetics of Fusarium head blight resistance in wheat and review breeding strategies based on the available information and DNA markers. Two independent meta-QTL studies were published recently (Löffler et al. 2009, Liu et al. 2009), which to a large extent agree with each other and with the review by Buerstmayr et al. (2009)

Obviously, the most repeatable QTL are those on chromosomes 3BS (*Fhb1*), 5AS (*Qfhs.ifa-5A*), and 6BS (*Fhb2*) all based on resistance sources from Asia (Buerstmayr et al. 2009). In addition, *Fhb4* (*Qfhi.nau-4B*) has been fine mapped by Xue et al. (2010). Recently several QTL from European winter wheat have been mapped and validated, *e.g.* on chromosomes 6AL and 7BS (Häberle et al. 2007, Wilde et al. 2008) and on 1BL (Häberle et al. 2009). For further details on FHB resistance QTL see Buerstmayr et al. (2009), Löffler et al. (2009) and Liu et al. (2009).

MOLECULAR BREEDING FOR FHB RESISTANCE

For the purpose of marker assisted selection, diagnostic markers are currently available for only *Fhb1*. Other FHB QTL have also been used in MAS programs, especially in cases where breeders are familiar with marker allele types of the QTL donors and the recipient germplasm. More diagnostic markers should be developed for QTL to be easily adopted by breeders. Therefore, the emphasis of future research

activities should be to discover '*perfect*' markers for the most repeatable QTL.

While in hexaploid wheat both conventional and marker assisted breeding for improving FHB resistance has made significant progress, in tetraploid durum wheat good sources of resistance are still sparse and more work is needed to identify resistant germplasm and to decipher its FHB resistance.

Marker assisted selection for major QTL has proven very efficient. For example marker assisted incorporation of *Fhb1* and *Qfhs.ifa-5A* in winter wheat cultivars resulted in an average reduction of the disease severity in the range 20-40%, relative to lines without the resistance QTL alleles (Salameh et al. 2010, von der Ohe et al. 2010). Currently, for practical cultivar improvement a skilful combination of marker assisted selection for relatively large effect QTL with phenotypic selection is a very useful strategy. Because of the quantitative nature of FHB resistance in the different wheat gene pools, the adoption of novel 'genomic selection' methods appears a very valuable research field and could increase the gain by selection.

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ADVANCED BACK-CROSS QTL MAPPING OF RESISTANCE TO FUSARIUM HEAD BLIGHT DERIVED FROM *TRITICUM MACHA* (GEORGIAN SPELT WHEAT)

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ABSTRACT

While many reports on genetic analysis of Fusarium resistance in bread wheat have been published during the past decade, only limited information is available on FHB resistance derived from wheat relatives. In this contribution we report about genetic analysis of FHB resistance derived from *Triticum macha* (Georgian spelt wheat). As the origin of *T. macha* is in the Caucasian region it is supposed, that its FHB resistance differs from other well investigated resistance sources. In order to introduce valuable alleles from the landrace *T. macha* into a modern genetic background we adopted an advanced back-cross QTL mapping scheme (Tanksley and Nelson 1996).

A large back-cross-two derived recombinant inbred line population of over 300 BC_2F_3 lines was developed from a cross of *T. macha* with the Austrian winter wheat cultivar 'Furore'. The population was evaluated for Fusarium resistance in six field experiments during three seasons using spray inoculations. The population was genetically fingerprinted using SSR and AFLP markers.

Map construction was done with an updated version of *CarthaGène* (De Givry et al. 2005). For QTL mapping *QGene* (Nelson 1997) was used. The obtained linkage map covered 37 linkage groups with 563 markers. Five novel FHB resistance QTL, all descending from *T. macha*, were found on four chromosomes (2A, 2B, 5A, 5B). The largest effect QTL overlapped with the *Q-locus* (spelt type) on chromosome 5A and appears therefore an interesting QTL especially for spelt wheat improvement.

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EVALUATION OF BACK-CROSS-TWO DERIVED SISTER LINES CARRYING *RHT-B1A/B* OR *RHT-D1A/B* IN A HIGHLY FUSARIUM RESISTANT DONOR BACKGROUND

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ABSTRACT

Recent publications have shown that the widely used dwarfing genes *Rht-B1* (syn. *Rht1*) and *Rht-D1* (syn. *Rht2*) are associated with Fusarium head blight (FHB) resistance. The semi-dwarf allele *Rht-D1b* and to a lesser extent *Rht-B1b* appear to increase FHB susceptibility in wheat (Miedaner and Voss 2008, Holzapfel et al. 2008, Srinivasachary et al. 2009). In order to further evaluate the effects of these alleles we developed and tested back-cross derived sister lines differing in their *Rht* alleles.

As donor line we used the highly FHB resistant breeding line '20812.2.2' derived from the cross 'Capo' x 'Sumai-3', which possesses the tall alleles *Rht-B1a* and *Rht-D1a*. As donors for the semi-dwarf alleles we used 'Hermann' (*Rht-B1b*, *Rht-D1a*), 'Toras' (*Rht-B1a*, *Rht-D1b*) and 'Courtot' (*Rht-B1b*, *Rht-D1b*). Using diagnostic PCR markers for the *Rht* alleles, we generated back-cross-two derived sister lines ($BC_2F_{2:3}$ lines) which were homozygous for contrasting *Rht* alleles and tested these in one field trial at IFA-Tulln using spray inoculations.

On average across seven NIL-pairs for *Rht-B1* we found that lines with the semi-dwarf allele *Rht-B1b* showed about 90% increased FHB severity compared to their sister lines which had the tall allele *Rht-B1a*. The difference was even more pronounced for *Rht-D1*, where on average across six NIL-pairs lines with the semi-dwarf allele *Rht-D1b* had about 160% higher FHB severity compared to lines with the *Rht-D1a* allele. Our data are in agreement with previous findings that semi-dwarfing alleles reduce FHB resistance and that *Rht-B1b* is less damaging than *Rht-D1b*. However, the negative effect of the semi-dwarf alleles can be balanced by selecting lines with other known or unknown FHB resistance QTL in their genome. Therefore, selection of semi-dwarf cultivars with good FHB resistance is quite difficult but feasible.

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DEVELOPMENT OF ADVANCED SPRING WHEAT LINES WITH FHB RESISTANCE THROUGH ALIEN INTROGRESSION

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ABSTRACT

One hundred and fourteen advanced spring wheat lines with various levels of FHB resistance were developed from crosses of adapted hard red spring wheat varieties with different wheat-alien species derivatives. These advanced breeding lines were evaluated for FHB resistance in multiple greenhouse seasons and at three field locations (Jianyang, Fujian Province, China; Prosper, ND; and Langdon, ND). Thirty-six of them exhibited good agronomic characteristics, such as maturity, test weight, and yield, in addition to FHB resistance in the 2009 field trial at Prosper, ND. One of the advanced lines showed significantly higher yield than the corresponding wheat parents when grown at Prosper, ND. The 36 advanced lines were further evaluated for FHB resistance and agronomic performance in a replicated yield trial at Langdon, ND in 2010. Most of the lines consistently showed FHB resistance and yield advantage when grown at Langdon, ND. Genotyping of these lines at *umn10* locus, a molecular marker tagging Sumai 3-derived FHB resistance gene *Fhb1*, indicated some of the advanced lines did not contain the "Sumai 3" allele at this marker locus. Deoxynivalenol (DON) content was measured in seed samples that were collected from146 alien introgression lines in a field experiment with three replicates. Some of the lines had significantly lower DON content than corresponding wheat parents. In addition, some of the advanced spring wheat lines exhibited advantages over wheat parents on some of the end-use quality characteristics. FHB resistance of these lines will be further verified in a replicated field experiment at Jianyang, China in 2011. Some of the lines have been provided to wheat breeding programs to be used for variety development. We anticipate releasing several spring wheat germplasm with FHB resistance and good agronomic characteristics in 2011.

EVALUATION OF SCAB RESISTANCE QTLS ON AGRONOMIC AND QUALITY TRAITS OF SOFT RED WINTER WHEAT

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ABSTRACT

Fusarium head blight (FHB) is a devastating fungal disease which affects wheat crops worldwide. While many quantitative trait loci (QTL) responsible for FHB resistance have been reported, some of the most widely used sources are from exotic varieties. Ning 7840, a Chinese hard red spring wheat, contains a major QTL on the 3BS chromosome, as well as two minor QTL on the 5A and 2DL chromosomes. Ning 7840 was crossed with Pioneer 2643, a soft red winter wheat, and a recombinant inbred line population was derived. The effect of the Ning7840 alleles on agronomic traits and milling and baking quality was examined over three growing seasons in Maryland. In 2009 and 2010, height was reduced by the 3BS QTL, incidence was decreased by the 5A QTL, and seed weight was decreased by both the 2DL QTL and the 5A QTL. These results suggest that the introduction of FHB resistance QTLs into soft red winter wheat may have consequences on agronomic and quality traits.

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MAPPING SCAB RESISTANCE IN THE WINTER WHEAT LINE MD01W233-06-1

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OBJECTIVE

To map resistance to scab in a doubled haploid population derived from the resistant soft winter wheat genotype MD01W233-06-1 and the susceptible genotype SS8641 under field conditions.

INTRODUCTION

Fusarium head blight (FHB), caused by *Fusarium graminearum*, is a devastating disease of wheat (*Triticum aestivum* L.) in the United States and around the world that affects grain yield and quality. High levels of the toxin deoxynivalenol (DON) in the grain are often associated with this disease (Bai and Shaner, 1994). Infection of wheat spikes may cause significant grain yield and quality losses due to poor grain fill, high percentage of Fusarium damaged kernels (FDK), and low test weights. Development of resistant cultivars is an important means of controlling FHB. Sources of resistance to FHB are limited to a few wheat cultivars, such as 'Sumai 3' (Anderson et al., 2001) and 'Frontana' (Steiner et al., 2004), which hinders the development of improved cultivars. New resistance sources are needed for breeding wheat with FHB resistance. 'MD01W233-06-1', a soft red winter wheat (SRWW) (*Triticum aestivum* L.) germplasm, is a US native source of FHB resistance that does not carry Sumai 3 alleles (Costa et al., 2010). Here, we make an initial evaluation of a doubled haploid population derived from the cross of MD01W233-06-1 with SS8641, a scab susceptible cultivar.

MATERIALS AND METHODS

Plant material and experimental design - A doubled haploid (DH) population that consisted of 90 DH lines obtained via the maize method (Laurie and Bennett, 1988) from an F1 resulting from a cross between: 'SS8641', a FHB scab susceptible cultivar, and the SRWW scab resistant MD01W233-06-1 cultivar. Field plots were established in Salisbury (MD) in a conventionally tilled field, previously planted with corn. A total of 184 plots (5-ft long) were planted on October 13, 2009. The experimental design was a randomized complete block, with two replications. The experiment was inoculated with Fusarium colonized corn (*Zea mays*) kernels prior to anthesis and was mist-irrigated from late April through May and early June 2010.

Trait analysis - Heading date (HD) and plant height (HT) were measured by hand in the field. Incidence (I) and severity (S) were visually estimated in two groups of 20 spikes randomly chosen within each plot from which FHB index (IND) was calculated. *Fusarium* damaged kernels (FDK) were based on counting 200 seeds (%). ISK was calculated by estimating incidence and severity and FDK. DON extraction and analysis were as described in Mirocha et al. (1998). Statistical analysis of phenotypic data was carried out using SAS version 9.2 (SAS Institute, Cary, NC) where block were considered as random effects and genotype and environment as fixed effects. Coleoptiles (red or white color) were visually scored in the greenhouse.

Genetic map construction and QTL analysis - Extraction of genomic DNA, PCR amplification, PCR screening and genotyping data was performed as previously described by Somers et al. (2004). One phenotypic and 29 SSR markers were scored. A genetic map was constructed with MAPMANAGER QTXb20. The mapping function was used to convert recombination fractions into centiMorgans (cM) as map distance. (Kosambi, 1944)

RESULTS AND DISCUSSION

Phenotypic variation of parental lines and DH population - In the 2009-2010 growing season, SS8641 had similar heading date, was taller, had higher incidence, severity, index, *Fusarium* damaged kernels, ISK, and DON than MD01W233-06-1 (Table 1). In the DH population, measured traits varied over a wide range and were normally distributed (Table 1). Significant differences were found among DHs. For most of the traits analyzed, positive and negative transgressive segregants were observed in the DH population, which suggest that positive and negative alleles may be found in both parental lines. Correlation coefficients among the average values of measured traits are presented in Table 2. Heading date had a positive correlation with INC, FDK and DON. Height was not correlated with other traits. INC exhibited a strong correlation with SEV, Index and ISK. SEV showed a positive correlation with Index and ISK. Index had a strong positive correlation with ISK. Another strong positive correlation was observed between FDK and DON. Additionally, there was a positive correlation between ISK and DON.

QTL mapping - Twenty nine SSR markers, and one morphological marker (red coleoptile) were used for linkage analysis and mapping of the quality traits for scab resistance. Seven linkage groups with 2 to 3 markers and one group of unlinked 15 markers were found. A total of 26 QTLs were detected by Map manager analysis (Table 3). The QTL with the highest effect was for ISK, FDK, and DON on 1A near SSR marker wmc278Fd (for ISK) and wmc496Nd (for FDK and DON) near the 1AL.1RS translocation. Oliver et al. (2005) similarly suggested that the 1AL.1RS translocation may be responsible for FHB resistance in the wheat line Amigo.

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Table 1. Mean, range, CV, LSD of heading date (HD), height (HT), incidence (I), severity (S), *Fusarium* damaged kernels (FDK) and DON from an inoculated and misted study in Salisbury (MD) in 2010.

	PARENTAL LINES		DHs(90)		WHOLE POPULATION		
	MD01W 233-06-1	SS8641	AVERAGE	RANGE	MEAN	CV	LSD
HD(d)	123	123	123	120-129	123	0.9	2.1
HT(inches)	33.0	34.5	30.4	23.0-36.5	30.4	6.0	3.6
I (%)	8.0	10.0	15.2	2.5-67.5	15.4	66.8	20.4
S (%)	10.0	30.0	19.9	5.0-60.0	20.2	55.5	22.3
IND	1.2	2.8	4.3	0.1-38.0	4.4	126.1	11
FDK (%)	3.8	15.0	29.4	2.8-53.0	14.7	43.9	12.9
ISK	0.3	1.5	3.8	0.0-71.8	3.7	192.2	14.2
DON (ppm)	2.5	8.8	8.3	0.5-40.3	8.2	65.0	10.6

Table 2. Correlation coefficients among the traits measured.

	Height	INC	SEV	Index	FDK	ISK	DON
Julian	0.01^{NS}	0.39**	0.17*	0.26**	0.59**	0.30**	0.63**
Height		0.06^{NS}	0.14^{NS}	0.02^{NS}	-0.07^{NS}	-0.01^{NS}	-0.07^{NS}
INC			0.65**	0.89**	0.55**	0.78**	0.35**
SEV				0.78**	0.36**	0.58**	0.23**
Index					0.48**	0.90**	0.26**
FDK						0.59**	0.81**
ISK							0.36**

**Correlation significantly different from zero at the 0.01 level, *Correlation significantly different from zero at the 0.05, NS: non significantly different from zero.

INC: incidence, SEV: severity, FDK: *Fusarium* Damaged Kernels.

Table 3. Quantitative trait loci detected in the MD01W233-06-1×SS8641 wheat population by composite cumulative mapping.

Trait	Chromosome	Position	Flanking markers	R^2	LRS
Julian	1A	61.7	wmc278Fd	5	4.9
	1A		wmc496Nd	9	8.6
	1A	58.2	barc28Fd	9	7.9
Height	1A	61.7	wmc278Fd	3	2.8
			wmc471Vd	5	4.6
	7D		Red coleoptile	2	2.0
Incidence	1A	61.7	wmc278Fd	5	4.9
	1A		wmc496Nd	5	4.9
	1A	58.2	barc28Fd	5	4.7
	4B	30.9	gwm149Fd	4	3.7
Severity	4B	30.9	gwm149Fd	5	4.4
			wmc471Vd	5	4.5
Index	1A	61.7	wmc278Fd	4	4.0
	4B	30.9	gwm149Fd	6	5.1
ISK	1A	61.7	wmc278Fd	12	11.4
	1A		wmc496Nd	4	3.9
	1A	58.2	barc28Fd	4	3.5
	4B	30.9	gwm149Fd	5	5.1
FDK	1A	61.7	wmc278Fd	9	7.9
	1A		wmc496Nd	11	11.0
	1A	58.2	barc28Fd	10	9.4
	4B	30.9	gwm149Fd	4	3.3
DON	1A	61.7	wmc278Fd	6	5.6
	1A		wmc496Nd	8	7.0
	1A	58.2	barc28Fd	7	5.8
	4B	30.9	gwm149Fd	3	2.5

A NOVEL GENOME MUTATION IN WHEAT INCREASES FUSARIUM HEAD BLIGHT RESISTANCE

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ABSTRACT

We sought to validate an FHB resistance QTL reported to be on chromosome 2A in the soft red winter wheat cultivar Freedom, by introducing it into the highly susceptible rapid maturing dwarf wheat Apogee. Marker-assisted backcrossing with an SSR marker reported to be associated with this QTL was undertaken. One backcross four-derived Apogee near-isogenic line (NIL), designated A30, exhibited improved type II FHB resistance. Other independently derived NILs harboring the introgressed Freedom SSR marker did not exhibit improved FHB resistance, suggesting that the FHB resistance of A30 could be due to the presence of an unlinked major FHB resistance QTL from Freedom. A project was undertaken to identify marker loci for this putative new FHB resistance QTL. Ninety F2:3 families derived from the cross Apogee x A30 were evaluated for type II FHB resistance in two greenhouse evaluations. SSR marker polymorphisms between A30 and an FHB susceptible sib line, A31, were identified to provide targets for mapping the putative new QTL in the Apogee x A30 population. Sampling of markers in major intervals of A30 deriving from Freedom did not reveal an association with FHB resistance in the mapping population. However, when a set of segregating SSR markers present in Apogee (and A31) but null in A30 was examined, a significant relationship with FHB resistance was detected, with a positive effect associated with the null allele state. On average, F2:3 families homozygous for the null alleles were approximately 50% more resistant than Apogee in the greenhouse evaluations. Aneuploid analysis with Chinese Spring cytogenetic stocks mapped the null markers to chromosome arm 3DL. Evaluation of other markers previously mapped to this chromosome arm identified a new set that were null in A30 and present in Apogee. The null marker loci in A30 were localized to bin 3 of the Chinese Spring chromosome arm 3DL segmental deletion line series. Interestingly, Freedom is not null for these same SSR markers. We conclude that during the course of our backcrossing efforts between Apogee and Freedom, a segment of the terminal end of chromosome arm 3DL of Apogee was deleted. Deletion of this chromosome segment has a significant positive effect on type II FHB resistance. The gain of FHB resistance associated with the loss of a chromosome segment suggests that the region contains either a suppressor of FHB resistance or a gene that promotes virulence of *F. graminearum*. We are now examining whether this effect occurs in other genetic backgrounds.

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FUSARIUM HEAD BLIGHT IN BARLEY: IDENTIFICATION OF THE CAUSAL FUSARIUM SPECIES IN EUROPE AND TESTING OF FHB RESISTANCE USING ARTIFICIAL INOCULATION

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ABSTRACT

Fusarium head blight (FHB) in barley can be caused by different *Fusarium spp.* producing various mycotoxins. Breeding for resistance requires 1) resistance sources and 2) a reliable screening technique. Syngenta wanted to investigate FHB resistance of a barley nursery as a basis for future breeding programs. We also compared different inoculation methods and the resistance to DON/NIV and T2/HT2-producing *Fusarium spp.* We started with the isolation, purification and identification of *Fusarium* isolates from infected barley kernels originating from France, Germany and UK. In total 63 isolates were identified belonging to 8 different *Fusarium spp.* Most frequently detected isolates in Germany were *F. poae*, in France *F. cerealis* and *F. graminearum* and in the UK *F. avenaceum*. FHB resistance was tested with spray inoculation and with the kernel spawn method. Five different *Fusarium spp.* were used for inoculation. Scored was disease incidence and severity. ANOVA analyses showed highly significant differences between genotypes and treatments. Resistance data obtained with both inoculation techniques and with most *Fusarium spp.* were significantly related (r = 0.57-0.81). Correlation coefficients between disease incidence and severity data were highly significant (r=0.93-0.99). We could not find any evidence for specific plant resistance against a particular type of toxin producer.

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MOLECULAR MAPPING OF RESISTANCE TO FUSARIUM HEAD BLIGHT IN TETRAPLOID WHEAT

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ABSTRACT

While many reports on genetic analysis of Fusarium resistance in bread wheat have been published, only limited information is available on FHB resistance derived from tetraploid wheats. In this contribution we report about genetic analysis of FHB resistance derived from two tetraploid *Triticum* sources: 1) *Triticum dicoccum* (cultivated emmer) and 2) *Triticum dicoccoides* (wild emmer). Back-cross-one derived recombinant inbred line populations were developed from crosses of the resistance donors with adapted Austrian durum wheat cultivars. The populations were evaluated for Fusarium resistance in well replicated experiments with artificial inoculation. The *T. dicoccum* derived populations were tested in field trials using spray inoculations and the *T. dicoccoides* derived mapping population was greenhouse tested using single-floret inoculations. The same lines were genetically analysed using SSR and AFLP markers. Map construction based on the back-cross derived RIL populations was done with *CarthaGène* (De Givry et al. 2005) and QTL mapping in *Qgene* (Nelson 1997). In *T. dicoccum* the most consistent QTL mapped to chromosome 4B, associated with the *Rht-B1a* allele. A second consistent QTL mapped to chromosome 6B. Significant QTL for type 2 FHB resistance were detected in wild emmer (*T. dicoccoides*) mapping to chromosomes 3A and 6B. Wild and cultivated emmer wheat are promising sources for improving FHB resistance in durum wheat.

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PRELIMINARY QTL ANALYSIS OF FUSARIUM HEAD BLIGHT RESISTANCE IN THE SOFT RED WINTER WHEAT, 'TRUMAN'

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ABSTRACT

Fusarium graminearum Schwabe (teleomorph *Gibberella zeae* (Schwein.), the pathogen known to cause Fusarium head blight (FHB) or scab, is an increasingly important problem for wheat production in warm and humid regions of the world. To date, most advances in FHB-resistance breeding have been made through selection for type II resistance largely because this type of resistance is durable, reliably estimated, and less sensitive to non-genetic factors than other types of resistance. Combining type II resistance from various sources of resistance to FHB is expected to generate lines with higher levels of resistance, more effective resistance under high inoculum loads, and/or varieties in which resistance is more stable over broad geographic areas but is limited by a lack of highly effective, genetically different sources of type II resistance. 'Truman' soft red winter wheat was developed and released by the University of Missouri. Its resistance is broadly based combining good levels of types I and II resistance with low DON and good kernel quality retention under disease pressure. The type II resistance in Truman is comparable to that in Sumai 3 but appears to be conditioned by different genes and is also unique in that it appears to be highly penetrant with good breeding value. This research was conducted to identify QTL associated with type II resistances in a set of F_9 recombinant inbred lines developed from the cross Truman/MO 94-317. MO 94-317 is a highly susceptible inbred line developed in the University of Missouri's wheat breeding program. Two years (5 replications) of greenhouse type II phenotypic data were collected for this study. A Missouri isolate of *F. graminearum* previously tested for pathogenicity was used for all inoculations. Each plant was inoculated at first anthesis with 10 µL of a macroconidial suspension of this isolate concentrated to 50, 000 mL^{-1}. Inoculum was placed in the basal floret of a central spikelet. Plants were incubated in a mist chamber at 100% relative humidity for 72 h post-inoculation to initiate disease development and then returned to the greenhouse bench to enable the disease to progress in the head. Ratings for type II resistance were taken at 21 d post-inoculation. Fusarium head blight severity was determined as the ratio of disease spread to the total number of spikelets on the inoculated head expressed as percentage. Molecular marker analysis was conducted using SSR and DArT [Diversity Arrays Technology Pty Ltd, (Triticarte) Yarralumla, Australia] markers. Genetic linkage maps were constructed using MapMaker 3.0. QTL analysis for individual replications and across reps was conducted using composite interval mapping (CIM) with WinQTLCart 4.0. Preliminary data suggest QTL for type II resistance on chromosomes 1B, 2B, and 6B at the 0.05 significance level.

ENHANCEMENT OF FUSARIUM HEAD BLIGHT RESISTANCE IN SOFT RED WINTER WHEAT USING MARKER ASSISTED SELECTION

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ABSTRACT

Both exotic and native resistant sources have been employed in our breeding program to improve the local adaptive soft red winter wheat (*Triticum aestivum* L.) varieties for Fusarium head blight (FHB) resistance. Progenies of F_3 lines with desired agronomic traits were genotyped with molecular markers on chromosome 2A, 2DL, 3BS, 3BSc, and 5A. Elite lines with FHB QTL from Sumai3, Roane, and Truman3BS were identified and advanced into the next generation for further evaluations for FHB and pest resistance in the field and agronomic traits.

IDENTIFYING QTL FOR FUSARIUM HEAD BLIGHT RESISTANCE IN A RIL POPULATION DERIVED FROM A THREE-WAY CROSS INVOLVING THREE RESISTANT PARENTS

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ABSTRACT

Fusarium head blight (FHB) of wheat has become an increasingly important disease over the past 25 years. Significant yield losses due to FHB can be observed when there is a favorable environment for disease development. Grain quality is also of great concern. Fusarium graminearum, the primary fungal pathogen that causes FHB produces deoxynivalenol, a mycotoxin that can cause serious health problems for both humans and livestock when consumed in FHB infected grain. While cultural practices and fungicide treatments can suppress FHB, the use of resistant varieties is the most effective method for control of FHB. Breeding for resistance to FHB has become a very large part of wheat and barley breeding programs in temperate climates. Various sources of resistance have been used to develop new varieties that have high levels of resistance. The primary objective of this study was to combine multiple sources of resistance using a recombinant inbred line (RIL) population derived from three FHB-resistant University of Illinois breeding lines (IL96-6472, IL97-6755 and IL97-1828) to obtain transgressive segregants that are significantly better than the three parents. The RIL population, consisting of 266 lines, was evaluated for FHB resistance in the greenhouse and in a mist irrigated, inoculated disease nursery. Forty-three simple sequence repeat (SSR) and 250 Diversity Arrays Technology (DArT) polymorphic markers were used to create a linkage map using Joinmap 3.0. PlabQTL was used for composite interval mapping and detection of significant QTL. QTL were found for all measured traits except formean severity in the 2008 and 2009 greenhouse evaluation. QTL on the short arm of chromosome 3B were identified for all measured traits and accounted for 6.8% to 10.1% of the phenotypic variation, depending on the trait. We believe that these markers are associated with Fhb1 or QTL tightly linked to Fhb1. Minor QTL were also found on chromosomes 7B and 1Aexplaining a smaller amount of phenotypic variation (between 5.3% and 8.2%). A total of 13 transgressive segregants were found that were significantly better than the mean of the three FHB-resistant parents for more than one trait. These thirteen lines were found to carry many of the resistance alleles associated with the QTL found in the study. Although the population was derived from three FHB-resistant parents, and there were likely QTL that were not detected due to a lack of polymorphism, we believe that multiple genes for resistance were combined in the transgressive segregants observed in the recombinant inbred line population.

A TRANSCRIPTOMIC APPROACH TO ELUCIDATE THE POSSIBLE ROLES OF BRASSINOSTEROIDS IN EARLY PLANT DEFENSE RESPONSES

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ABSTRACT

Brassinosteroids (BRs) are a class of plant hormones that have received great attention for their growth-promoting activities. They have pleotropic effects and can induce a broad spectrum of cellular processes. It has been demonstrated that BRs function in mediating an enhanced broad disease resistance in tobacco and rice. We investigated the effect of BR signalling on *Fusarium* seedling blight disease of barley. Results obtained using BR-insensitive mutant, isogenic wild type barley and brassinosteroid treatment in seedling blight disease trials indicated that this hormonal pathway influences cereal defense against *Fusarium culmorum*. The exact mechanism of BRs mediated plant defense responses is not yet elucidated. Using both microarray analyses and real time RT-PCR analyses, we investigated the effect of BR treatment and BR insensitivity on the transcriptome of healthy and *Fusarium*-inoculated barley stem base tissue (24 and 48 h post-treatment). The most striking result was the pronounced effect that both the BR-insensitive mutation and BR treatment had on defense gene expression.

EFFECT OF ISOLATED MICROSPORE CULTURE AND SILVER NITRATE PRE-TREATMENT ON IMPROVING *IN VITRO* SELECTION TO REDUCE DEOXYNIVALENOL ACCUMULATION IN BARLEY

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ABSTRACT

Fusarium head blight (FHB) incited by *Fusarium graminearum* Schwabe is presently the most damaging disease of barley in Canada, primarily due to grain contamination by mycotoxins. As resistance from exotic landraces has been difficult to incorporate in barley (*Hordeum vulgare* L.), *in vitro* selection (IVS) was applied in concurrence with doubled haploid production as an alternative to traditional breeding methods in attempt to reduce deoxynivalenol (DON) accumulation. A large FHB screening nursery at Brandon, MB was used to evaluate DON content in harvested grains of experimental lines. Previous attempts to include trichothecenes in anther culture culture media, had proven to be largely unsuccessful at selecting breeding lines with reduced DON content. A novel "bridge" method was developed to incorporate DON in liquid media during isolated microspore culture (IMC) which typically uses solid media. Barley cultivar Newdale and F_1 plants from the BM0332 (Svansota/Newdale) and BMO270 (TR04282/Newdale) crosses, were used as donors. Contrasts between selected lines and respective controls indicated that IVS was not effective in IMC using the new method. Barley cultivar Newdale and F_1 plants from the BM0362 (HDE84194-622-1/Newdale) and BM0525 (HB382/Newdale) crosses were used to investigate the effect of anther pre-treatment with silver nitrate on improving FHB resistance. Although the addition of DON to the silver nitrate pre-treatment mixture did not appear to lower DON content in the resulting DH plants, a trend was observed for silver nitrate pre-treated lines from Newdale and both F_1 populations with or without DON in the culture media to accumulate less DON than controls. Four of the Newdale DH lines subjected to silver nitrate pre-treatment will be evaluated further by the breeding program, and one of them may be advanced to registration trials in 2011.

EFFICACY OF NEAR-INFRARED REFLECTANCE SPECTROSCOPY TO PREDICT *FUSARIUM* DAMAGED KERNELS AND DEOXYNIVELANOL IN RED AND WHITE WHEAT IN MICHIGAN

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ABSTRACT

Michigan State University annually evaluates the Michigan State Performance Trial (MSPT) entries for Fusarium head blight (FHB) resistance. The MSPT consists of both red and white genotypes that vary in visual field symptoms of FHB, *Fusarium* Damaged Kernels (FDK) and deoxynivalenol (DON) levels. It has been previously reported that white wheat accumulates higher amounts of DON than red wheat (Knott, Van Sanford et al. 2008). In addition, near-infrared spectroscopy (NIRS) predictions for DON levels have been investigated, in general. However, the effect of grain color (red vs. white) in NIRS predictions of FDK and DON have not, to our knowledge, been investigated. In this poster we will present data of visual field symptoms of FHB (incidence, severity, index), FDK, DON and NIRS predictions of both FDK and DON when grain color is considered for the 2009 MSPT.

REFERENCE

Knott, C. A., D. A. Van Sanford, et al. (2008). "Comparison of selection methods for the development of white-seeded lines from red x white soft winter wheat crosses." Crop Science **48**(5): 1807-1816.

EFFICIENT SELECTION FOR LOW DON LEVELS IN WHEAT

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ABSTRACT

Deoxynivalenol (DON) is the most common mycotoxin associated with wheat grain from fields affected by Fusarium head blight (FHB). Growing cultivars that are resistant to FHB is believed to be the key component for reducing DON levels in grain. Wheat breeding programs have been successful at reducing the levels of DON in some recently released cultivars relative to the DON levels in susceptible cultivars and are continuing efforts to reduce DON to even lower levels. Given that reducing DON levels in wheat grain is a high priority for breeders, millers, and consumers and that screening lines for DON level is expensive, becoming more efficient at selecting wheat lines with low DON levels should be a priority for breeding programs in the USWBSI. The objective of this study is to determine how to most efficiently select wheat lines that have low levels of DON in harvested grain. Twenty cultivars representative of those being grown in Arkansas in 2010 and 58 lines from the 2010 Southern Uniform Winter Wheat Scab Nursery (SUWWSN) were grown in early-planted and late-planted FHB nurseries at Fayetteville. Plots were two rows x 1 m long and replicated three times in each nursery. Plots were inoculated using infested corn kernels and misted to promote ascospore development and infection. Lines were evaluated for FHB severity at soft dough stage and harvested at maturity. A 50-g sample of grain was visually rated for percentage of scabby kernels by comparing samples to a set of standards, and this same sample was ground to determine DON level. A 4-g subsample of ground grain was sent to the mycotoxin lab at the University of Minnesota for DON analysis. To determine the relationships among FHB severity, percentage of scabby kernels and DON level, Pearson correlation coefficients were calculated for each pair of variables for the cultivars and the SUWWSN in the early- and late-planted FHB nurseries. The percentage of scabby kernels was positively correlated with FHB severity (range 0.68-0.85, mean 0.77), and DON level was positively correlated with FHB severity (range 0.61-0.82, mean 0.72) and Percentage of scabby kernels (range 0.84-0.91, mean 0.88). These results indicate that lines with high FHB severities do not need to be harvested and that harvested lines with high percentages of scabby kernels do not need to be assayed for DON level in order to identify lines with low DON level. Thresholds for deciding which lines should be harvested and sent for DON analysis should be based on values for resistant checks. Considerable savings can be realized by not harvesting or analyzing lines with a low probability for low DON level.

USEFULNESS OF GREENHOUSE EVALUATIONS AS A PREDICTOR OF WHEAT HEAD BLIGHT RESISTANCE IN THE FIELD

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ABSTRACT

Five types of resistance to Fusarium head blight (FHB) of wheat have been hypothesized. A new method for conducting greenhouse evaluations generates data on four of these types: resistance to initial infection, resistance of spread within a spike, tolerance (i.e. ability to yield when affected by FHB), and resistance to deoxynivalenol (DON) accumulation. The objective of this study is to determine how well the results from greenhouse evaluations predict results from evaluations in inoculated, misted field nurseries that are commonly used by breeding programs to select resistant lines. Two sets of wheat lines (20 cultivars commonly grown in Arkansas and 58 lines in the 2010 Southern Uniform Winter Wheat Scab Nursery (SUWWSN)) were evaluated in greenhouse/growth chambers and in early- and late-planted inoculated, misted nurseries at Fayetteville. Briefly, plants with spikes at flowering stage were spray-inoculated, bagged, and incubated at constant 23°C. Bags were removed after 48 h, and plants were moved to a greenhouse 5 days after inoculation (dai). The percentage of blighted primary florets was determined at 5, 14 and 21 dai, and the area under the disease progress curve (AUDPC) was calculated between 5 and 21 dai. The percentage of blighted florets at 5 dai estimates resistance to initial infection, and the AUDPC estimates resistance to spread. Grain was harvested at maturity, bulked across six reps, weighed to determine tolerance to FHB, ground, and sent for DON analysis. Three reps of two-row wide x 1-m long field plots were rated for percentage of blighted florets at soft dough stage, harvested at maturity, weighed, and a sample sent for DON analysis. Pearson and Spearman correlations were calculated to determine how well greenhouse/growth chamber results predicted field results for the 20 cultivars and 58 SUWWSN lines in each field nursery, except yield data from the early-planted nursery were not useable because of erratic stands. Pearson correlation coefficients were similar for the four correlations between field FHB severity and AUDPC, averaging 0.71, and for the two correlations between field yield and greenhouse yield, averaging 0.70. For comparing field DON to greenhouse DON, Pearson correlation coefficients were similar for the two correlations involving the SUWWSN lines, averaging 0.63, and for the two correlations involving the cultivars, only averaging 0.34. Spearman correlations gave similar results, and coefficients for both Pearson and Spearman correlations averaged 0.62 across all ten correlations. These results indicate that the new method for conducting greenhouse evaluations predicted field results moderately well and may be useful for quantifying four types of resistance. However, evaluations in inoculated, misted field nurseries can accommodate a large number of lines at less expense per line, and field evaluations across multiple locations and years may be the most efficient way to select resistant lines in breeding programs.

COMPARISON OF DIFFERENT INOCULATION METHODS FOR EVALUATION OF FHB RESISTANCE IN WHEAT VARIETIES

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ABSTRACT

Fusarium head blight (FHB) in wheat is caused by the fungus *Fusarium graminearum*, which infects wheat heads at anthesis. Weather conditions such as humidity and temperature play an important role in the extent of infection. Several mechanisms have been proposed for host resistance, including resistance to the incidence of disease (Type I) and resistance to spread of infection (Type II). Several screening methods have been researched for successful prediction of resistance to FHB infection; the most prominent being spray and point inoculation which measure Type I and Type II resistance respectively.

The objective of this study was to compare the efficiency of the following methods for evaluating resistance to FHB: spray inoculation in the greenhouse followed by bagging, spray inoculation in the field followed by bagging, and traditional field method using grain spawn inoculum. The study includes 16 varieties adapted to Michigan, which includes both soft red and soft white winter wheat lines with varying levels of resistance to FHB. Comparisons are made on % incidence, % severity and Fusarium damaged kernels (FDK).

THE 2009-10 SOUTHERN UNIFORM WINTER WHEAT SCAB NURSERY

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ABSTRACT

The Southern Uniform Winter Wheat Scab Nursery provides breeders in the public and private sectors with an opportunity for multi-environment, independent evaluations of FHB resistance in advanced generation breeding lines compared with the current most resistant check varieties Ernie, Bess and Jamestown. Valuable data are provided on resistance to other important fungal and viral diseases, milling and baking quality and agronomic characteristics. In addition, genotypic analyses identify alleles present at numerous important loci. The nursery is the primary method to facilitate the sharing of the best resistant materials throughout the breeding community.

The 2009-10 nursery comprised 54 advanced generation breeding lines and four check cultivars, 'Ernie', 'Bess', 'Jamestown' (partially resistant) and 'Coker 9835' (susceptible). Seven U.S. public programs (Univ. of Arkansas, Univ. of Georgia, Louisiana State University, Univ. of Maryland, N.C. State Univ., VA Tech., and USDA-ARS, and one private company, Agripro-Coker, submitted entries. The nursery was distributed to 11 U.S., and one Romanian cooperator for field, and / or greenhouse evaluations. In addition, three USDA-ARS laboratories conducted evaluations for Hessian fly resistance, milling and baking quality and marker genoypes based on established diagnostic markers.

Copies of the full report will be available at the 2010 National Fusarium Head Blight Forum and subsequently on line at the USWBSI web site: http://www.scabusa.org/.

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Table 1. Mean performance of the 58 entries in the 2009-10 Southern Uniform Winter Wheat Scab Nursery evaluated at up to 11 locations for components of FHB resistance.

	Cultivar/ Designation	FHB Incidence	RANK	FHB Severity	RANK	FHB Index	RANK	FDK	RANK	ISK	RANK	G'hse Severity	RANK	DON	RANK
1	ERNIE	39	1	20	4	9	1	18	12	25	3	16	14	11	6
2	COKER 9835	63	51	57	53	39	53	40	48	55	49	68	54	25	50
3	BESS	43	3	23	8	12	3	8	1	22	1	7	1	13	17
4	JAMESTOWN	47	6	22	5	13	4	14	5	28	9	18	19	11	6
5	LA01164D-94-2	54	31	34	37	23	34	28	33	37	27	23	29	14	21
6	03M1539#031	57	39	31	26	24	38	13	4	31	13	32	37	23	45
7	AR 99054-4-1	52	22	33	34	21	30	24	25	40	37	33	40	27	53
8	ARS03-4736	55	32	32	31	20	29	24	25	35	21	18	18	23	45
9	ARS05-1234	49	9	37	40	24	38	30	38	38	31	17	15	39	57
10	LA01141D-98-6-2	61	48	40	43	30	44	42	49	52	46	21	26	18	39
11	03M1539#019	53	29	32	31	19	23	24	25	37	27	23	30	16	29
12	AR99092-4-1	51	17	27	13	15	9	23	23	32	14	14	10	20	42
13	AR99102-4-1	53	29	40	43	27	42	34	44	47	43	47	47	16	29
14	AR99160-1-1-B	47	6	28	17	14	6	15	8	28	9	10	5	32	55
15	AR99264-8-1	56	35	31	26	21	30	15	8	34	17	18	20	18	39
16	AR99311-12-1	58	42	33	34	23	34	24	25	39	34	20	25	11	6
17	ARGE97-1042-4-5-20	39	1	17	1	10	2	22	18	25	3	15	11	11	6
18	ARGE97-1047-4-2-9	45	4	17	1	13	4	14	5	23	2	9	3	9	2
19	ARGE97-1048-3-6-7	52	22	26	11	16	16	22	18	34	17	23	31	8	1
20	ARS04-1267	49	9	30	22	15	9	17	11	27	6	14	7	16	29
21	ARS05-0005	58	42	48	48	34	49	38	46	52	46	48	48	15	26
22	ARS05-0043	50	13	27	13	19	23	33	43	39	34	18	21	15	26
23	ARS05-0277	64	53	51	49	38	52	28	33	48	44	62	53	21	44
24	ARS07 0095	62	50	45	47	29	43	30	38	46	42	35	41	26	51
25	ARS07-0203	59	45	53	50	35	51	38	46	55	49	40	44	16	29
26	GA031188-O15	69	58	64	55	45	57	58	57	68	57	88	58	24	49
27	GA031188-O16	65	55	64	55	43	54	47	52	63	55	68	55	23	45
28	GA031188-O17	65	55	66	58	44	56	51	53	63	55	77	56	23	45
29	GA041243-LE36	64	53	35	39	25	40	42	49	49	45	50	49	16	29
30	GA041260-Q19	59	45	56	52	31	47	53	55	58	52	59	52	26	51
31	GA041271-PL49	61	48	56	51	34	49	59	58	59	53	39	43	60	58
32	GA041271-Q23	63	51	65	57	47	58	56	56	69	58	78	57	35	56
33	GA041271-Q24	67	57	61	54	43	54	52	54	61	54	57	51	29	54
34	LA01141D-98-6-3	59	45	38	41	30	44	46	51	56	51	39	42	17	37
35	LA02058E63	49	9	34	37	18	18	30	38	38	31	23	28	14	21
36	LA02058E97	58	42	40	43	25	40	32	41	44	39	31	36	17	37
37	LA03130E68	51	17	22	5	15	9	24	25	36	23	14	9	15	26
38	LA03186E2	56	35	39	42	30	44	36	45	52	46	19	24	16	29
39	LA04142C-P5	57	39	31	26	23	34	29	36	44	39	44	46	14	21
40	M08*8005#	52	22	28	17	15	9	12	3	27	6	31	35	11	6
41	MD01W233-07-1	55	32	32	31	23	34	25	30	40	37	25	33	11	6
42	MD02W135-08-9	52	22	31	26	18	18	19	16	34	17	27	34	12	13
43	MD03W61-09-1	50	13	19	3	14	6	16	10	30	11	14	8	13	17
44	MD03W91-09-7	45	4	22	5	15	9	11	2	25	3	9	2	11	6
45	NC07-21036	51	17	30	22	19	23	22	18	37	27	17	17	13	17
46	NC07-23081	50	13	24	10	18	18	22	18	34	17	19	22	12	13
47	NC07-23126	50	13	28	17	15	9	23	23	35	21	41	45	16	29
48	NC07-23771	51	17	33	34	19	23	32	41	38	31	25	32	14	21
49	NC07-24445	55	32	41	46	31	47	26	32	44	39	52	50	13	17
50	VA06W-580	51	17	26	11	16	16	14	5	27	6	33	39	12	13
51	VA07W-569	52	22	30	22	18	18	25	30	37	27	19	23	14	21
52	VA08W-622	56	35	27	13	18	18	18	12	33	15	32	38	10	4
53	VA08W-630	57	39	31	26	22	33	28	33	39	34	10	4	16	29
54	VA08W-653	56	35	28	17	21	30	22	18	36	23	16	13	19	41
55	VA08W-709	48	8	27	13	15	9	18	12	30	11	15	12	12	13
56	VA09W-641	52	22	23	8	14	6	21	17	33	15	13	6	10	4
57	VA09W-654	52	22	28	17	19	23	18	12	36	23	21	27	9	2
58	W1104	49	9	30	22	19	23	29	36	36	23	17	16	20	42
	Mean	54		35		23		28		41		31		18	
	LSD (0.05)	23.9		24		22		25		19		29		15	
	CV%	22.4		35.4		48.6		45.5		23.7		43.2		41.9	

	Cultivar/ Designation	Heading Date	RANK	Plant Height	RANK	Spindle Streak 0-9	Hessian Fly Biotype L	MILLING QUALITY SCORE		BAKING QUALITY SCORE		SOFT. EQUIV. SCORE		Stripe Rust (0-9) F'VILLE (1) AR	Stripe Rust (0-9) F'VILLE (2) AR	Stem Rust % F'VILLE AR
1	ERNIE	127	6	33	20	4.0	0-14	56	D	51	D	60	C	63	15	2
2	COKER 9835	130	41	32	13	5.0	0-15	64	C	65	C	80	B	54	63	0
3	BESS	129	28	35	33	4.5	0-19	66	C	61	C	66	C	1	0	2
4	JAMESTOWN	125	2	31	9	4.5	0-12	62	C	52	D	64	C	0	0	2
5	LA01164D-94-2	129	28	37	50	5.5	0-16	74	B	53	D	49	E	23	43	0
6	03M1539#031	128	11	36	43	5.5	15-4	73	B	88	A	81	A	7	6	70
7	AR 99054-4-1	131	49	39	55	2.5	0-14	67	C	55	D	57	D	1	0	15
8	ARS03-4736	128	11	36	45	2.0	11-5	62	C	25	F	24	F	1	1	7
9	ARS05-1234	132	57	36	41	2.0	0-19	70	C	43	E	38	F	3	57	0
10	LA01141D-98-6-2	129	28	32	11	7.5	0-13	72	B	65	C	68	C	2	0	30
11	03M1539#019	129	28	36	46	6.5	14-0	62	C	75	B	78	B	10	68	2
12	AR99092-4-1	130	41	42	58	5.0	0-16	59	D	61	C	54	D	0	2	2
13	AR99102-4-1	130	41	36	44	3.5	0-18	67	C	50	E	49	E	1	5	0
14	AR99160-1-1-B	131	49	42	57	6.0	0-17	79	B	68	C	43	E	0	0	2
15	AR99264-8-1	130	41	42	56	4.5	0-12	69	C	70	B	68	C	0	0	30
16	AR99311-12-1	128	11	32	10	4.5	0-14	63	C	55	D	64	C	0	0	2
17	ARGE97-1042-4-5-20	128	11	35	34	7.5	0-16	59	D	35	F	23	F	0	0	2
18	ARGE97-1047-4-2-9	126	3	38	51	6.0	0-18	63	C	52	D	19	F	1	0	0
19	ARGE97-1048-3-6-7	127	6	38	53	6.5	0-16	52	D	38	F	44	E	3	1	7
20	ARS04-1267	128	11	33	23	2.0	0-15	62	C	25	F	15	F	0	0	2
21	ARS05-0005	129	28	34	28	4.5	0-14	57	D	44	E	30	F	1	0	2
22	ARS05-0043	128	11	34	27	4.0	0-17	57	D	43	E	31	F	0	0	7
23	ARS05-0277	129	28	32	12	4.5	0-15	64	C	62	C	54	D	1	0	0
24	ARS07 0095	131	49	34	29	3.0	0-14	66	C	64	C	62	C	1	0	2
25	ARS07-0203	131	49	33	16	4.5	0-17	76	B	65	C	60	C	0	0	2
26	GA031188-O15	128	11	36	49	2.5	0-15	76	B	72	B	57	D	1	0	0
27	GA031188-O16	128	11	34	31	3.0	0-14	72	B	64	C	55	D	1	0	0
28	GA031188-O17	129	28	34	24	3.0	0-15	73	B	69	C	56	D	1	0	0
29	GA041243-LE36	128	11	36	40	5.0	16-0	56	D	58	D	55	D	1	0	0
30	GA041260-Q19	129	28	33	17	6.5	0-19	70	B	63	C	63	C	10	0	0
31	GA041271-PL49	136	58	38	52	5.5	0-16	66	C	46	E	65	C	15	11	0
32	GA041271-Q23	131	49	36	48	4.5	0-19	65	C	44	E	57	D	49	29	7
33	GA041271-Q24	131	49	36	47	5.0	0-17	67	C	50	E	55	D	45	36	2
34	LA01141D-98-6-3	128	11	33	22	7.5	0-17	71	B	56	D	59	D	1	0	15
35	LA02058E63	127	6	33	19	5.5	0-17	67	C	34	F	44	E	2	1	0
36	LA02058E97	128	11	35	38	5.5	0-19	69	C	38	F	49	E	17	1	0
37	LA03130E68	124	1	35	36	4.0	0-18	69	C	58	D	51	D	11	0	0
38	LA03186E2	130	41	38	54	3.5	0-17	66	C	54	D	50	E	1	1	50
39	LA04142C-P5	128	11	36	42	4.0	0-15	62	C	51	D	54	D	1	0	2
40	M08*8005#	126	3	34	30	4.0	0-17	69	C	77	B	65	C	2	0	2
41	MD01W233-07-1	131	49	31	8	3.5	0-12	65	C	60	C	61	C	6	1	15
42	MD02W135-08-9	129	28	30	4	2.0	0-14	51	D	49	E	73	B	80	75	7
43	MD03W61-09-1	128	11	34	26	2.5	0-17	55	D	47	E	55	D	8	13	2
44	MD03W91-09-7	127	6	35	37	6.5	0-17	54	D	46	E	46	E	0	0	0
45	NC07-21036	130	41	30	5	5.0	16-0	63	C	56	D	62	C	1	0	7
46	NC07-23081	128	11	33	18	5.0	0-18	53	D	41	E	46	E	21	63	2
47	NC07-23126	129	28	32	15	5.5	0-17	58	D	49	E	56	D	6	5	0
48	NC07-23771	129	28	32	14	6.0	0-18	63	C	59	D	53	D	16	1	0
49	NC07-24445	127	6	31	7	5.0	0-19	62	C	59	D	56	D	1	0	0
50	VA06W-580	128	11	28	2	4.5	0-17	66	C	61	C	59	D	0	2	0
51	VA07W-569	129	28	36	39	5.0	0-16	57	D	51	D	59	D	0	1	30
52	VA08W-622	128	11	34	32	5.0	0-17	70	C	68	C	58	D	10	17	2
53	VA08W-630	129	28	29	3	4.0	0-16	64	C	62	C	68	C	17	19	30
54	VA08W-653	130	41	27	1	6.0	16-0	55	D	59	D	69	C	0	0	30
55	VA08W-709	128	11	34	25	5.0	0-18	62	C	79	B	72	B	5	0	15
56	VA09W-641	126	3	33	21	5.5	0-20	61	C	54	D	60	D	37	24	7
57	VA09W-654	131	49	35	35	2.5	0-15	66	C	51	D	65	C	11	0	30
58	W1104	130	41	31	6	3	0-17	59	D	84	A	65	C	0	0	7
	Mean	129		34		.	.	64		56		55		.	.	54
	LSD (0.05)	3		5		.	.	.		.		.		.	.	13
	CV%	1.1		7.2		.	.	.		.		.		.	.	12

	CULTIVAR/ DESIGNATION	Fhb1	Wuh-1 2DL	Ning 5AS	Ernie 3BSc	Ernie 5AS	H9	H13	1RS tran	Lr34/Yr18	Lr24/Sr24
1	ERNIE	.	.	.	yes	yes	.	.	.	.	.
2	COKER 9835	.	.	.	.	.	.	.	.	.	.
3	BESS	.	.	.	.	.	.	.	.	.	.
4	JAMESTOWN	.	.	.	.	.	.	.	.	.	.
5	LA01164D-94-2	yes	.	.	.	.	.	.	.	.	.
6	03M1539#031	.		.	.	.	yes	.	.	.	.
7	AR 99054-4-1	.	.	.	.	.	.	.	.	.	.
8	ARS03-4736	.	.	.	.	.	.	.	1RS:1AL	.	.
9	ARS05-1234	.	.	.	.	.	.	.	.	.	.
10	LA01141D-98-6-2	.	.	.	.	.	.	.	.	yes	.
11	03M1539#019	.	.	.	.	.	yes	.	1RS:1BL	.	.
12	AR99092-4-1	.	.	.	.	.	.	.	.	.	.
13	AR99102-4-1	.	.	.	.	.	.	.	.	.	.
14	AR99160-1-1-B	.	.	.	yes	.	.	.	.	.	.
15	AR99264-8-1	.	.	.	.	.	.	.	.	.	.
16	AR99311-12-1	.	.	.	.	.	.	.	.	.	.
17	ARGE97-1042-4-5-	.	.	.	.	.	.	.	1RS:1BL	.	.
18	ARGE97-1047-4-2-	het?	.	.	.	.	.	.	1RS:1BL	.	.
19	ARGE97-1048-3-6-	.	yes	.	.	.	.	.	.	.	.
20	ARS04-1267	.	.	.	.	.	.	.	1RS:1AL	.	.
21	ARS05-0005	.	.	.	.	.	.	.	.	.	yes
22	ARS05-0043	.	.	.	.	.	.	.	.	.	yes
23	ARS05-0277	.	.	.	.	.	.	.	1RS:1AL	.	.
24	ARS07 0095	.	.	.	.	het	.	.	1RS:1AL	.	yes
25	ARS07-0203	.	.	.	.	.	.	.	.	.	.
26	GA031188-O15	.	.	.	.	.	.	.	.	.	.
27	GA031188-O16	.	.	.	.	.	.	.	.	.	.
28	GA031188-O17	.	.	.	.	.	.	.	.	.	.
29	GA041243-LE36	.	.	.	.	.	.	yes	.	.	.
30	GA041260-Q19	.	.	.	.	.	.	.	.	.	.
31	GA041271-PL49	.	.	.	.	.	.	.	.	.	.
32	GA041271-Q23	.	.	.	.	.	.	.	.	.	.
33	GA041271-Q24	.	.	.	.	.	.	.	.	.	.
34	LA01141D-98-6-3	.	.	.	.	.	.	.	.	yes	.
35	LA02058E63	yes	yes	.	het?	.	.	.	1RS:1BL	.	.
36	LA02058E97	yes	yes	.	.	.	.	.	1RS:1BL	.	.
37	LA03130E68	.	.	.	.	.	.	.	.	yes	.
38	LA03186E2	.	yes	.	.	.	.	.	.	.	.
39	LA04142C-P5	.	.	.	.	.	.	.	.	.	.
40	M08*8005#	.	.	.	.	.	.	.	.	.	.
41	MD01W233-07-1	.	.	.	.	.	.	.	1RS:1AL	.	yes
42	MD02W135-08-9	.	.	.	.	.	.	.	1RS:1BL, 1RS:1AL	.	.
43	MD03W61-09-1	?	.	.	.	.	.	.	1RS:1BL	.	.
44	MD03W91-09-7	.	.	.	.	.	.	.	1RS:1AL	.	.
45	NC07-21036	.	.	.	.	.	.	.	1RS:1AL	.	yes
46	NC07-23081	.	.	.	.	.	yes	.	1RS:1AL	.	.
47	NC07-23126	.	.	.	.	.	.	.	1RS:1AL	.	yes
48	NC07-23771	.	.	.	.	.	.	.	.	.	.
49	NC07-24445	.	.	.	yes	.	.	.	.	.	.
50	VA06W-580	.	.	.	.	.	.	.	.	.	.
51	VA07W-569	.	.	.	yes?	.	.	.	1RS:1AL	.	.
52	VA08W-622	.	.	.	.	.	.	.	non-1RS	.	.
53	VA08W-630	.	.	.	.	.	.	.	1RS:1AL	.	.
54	VA08W-653	.	.	.	.	.	yes	.		.	.
55	VA08W-709	.	.	.	.	.	.	.	1RS:1BL, 1RS:1AL	.	yes
56	VA09W-641	.	.	.	.	yes	.	.	1RS:1AL	.	.
57	VA09W-654	.	.	.	.	.	.	.	.	.	.
58	W1104	.	.	.	.	yes	.	.	1RS:1BL	.	.

	CULTIVAR/ DESIGNATION	Sr2	Sr36	Lr37/Yr17/Sr28	BVD2/3	Rht-B1b (Rht1)	Rht-D1b (Rht2)	Rht8	Ppd-D1a Insen.	Bx7 OE	Glu-D1	Glu-A1
1	ERNIE	.	het	.	.	yes	.	.	.	.	2+12	Ax1 or null
2	COKER 9835	.	yes	.	.	.	yes	.	yes	.	2+12	Ax2*
3	BESS	.	.	.	.	yes	.	.	het	.	2+12	Ax1 or null
4	JAMESTOWN	.	.	.	.	.	Negative	.	yes	.	2+12	Ax2*
5	LA01164D-94-2	.	het	yes	.	.	yes	.	.	yes	2+12	het
6	03M1539#031	.	.	.	.	yes	het	.	yes	.	2+12	het
7	AR 99054-4-1	.	.	.	.	.	.	.	.	.	2+12	Ax2*
8	ARS03-4736	.	.	.	.	yes	.	.	nd	.	2+12	Ax2*
9	ARS05-1234	.	.	yes	.	yes	.	.	.	.	2+12	Ax1 or null
10	LA01141D-98-6-2	.	.	yes	.	.	yes	.	yes	het	2+12	Ax2*
11	03M1539#019	.	.	yes	.	yes	.	.	.	.	2+12	Ax2*
12	AR99092-4-1	.	.	.	.	.	.	.	yes	.	2+12	Ax2*
13	AR99102-4-1	.	.	.	.	het	.	het	yes	.	5+10	Ax1 or null
14	AR99160-1-1-B	.	.	.	.	.	.	.	.	.	2+12	Ax1 or null
15	AR99264-8-1	.	.	.	.	.	.	.	yes	.	2+12	Ax2*
16	AR99311-12-1	.	.	.	.	.	yes	.	yes	.	2+12	Ax2*
17	ARGE97-1042-4-5-	.	.	.	.	yes	.	.	.	.	2+12	Ax2*
18	ARGE97-1047-4-2-	.	.	.	.	het	.	.	yes	.	het?	Ax2*
19	ARGE97-1048-3-6-	.	.	.	.	yes	.	.	yes	.	2+12	Ax1 or null
20	ARS04-1267	.	.	yes	.	yes	.	.	.	.	5+10	Ax2*
21	ARS05-0005	.	.	.	.	yes	.	.	yes	.	2+12	Ax2*
22	ARS05-0043	.	.	.	.	yes	.	.	yes	.	2+12	Ax1 or null
23	ARS05-0277	.	het	.	.	yes	.	.	.	.	5+10	Ax2*
24	ARS07 0095	.	.	.	.	Unknown	Unknown	.	.	.	5+10	het
25	ARS07-0203	.	yes	yes	.	.	yes	.	yes	.	2+12	Ax1 or null
26	GA031188-O15	.	.	yes	.	.	yes	.	yes	.	2+12	Ax2*
27	GA031188-O16	.	.	yes	.	.	yes	.	yes	.	2+12	Ax2*
28	GA031188-O17	.	.	yes	.	.	yes	.	yes	.	2+12	Ax2*
29	GA041243-LE36	.	.	yes	.	yes	.	.	yes	.	2+12	Ax1 or null
30	GA041260-Q19	.	.	yes	.	.	yes	.	yes	.	2+12	Ax1 or null
31	GA041271-PL49	.	.	yes	.	.	yes	.	.	.	5+10	Ax2*
32	GA041271-Q23	.	.	yes	.	Unknown	Unknown	.	.	.	5+10	Ax2*
33	GA041271-Q24	.	.	yes	.	.	yes	.	.	.	5+10	Ax2*
34	LA01141D-98-6-3	.	.	yes	.	.	yes	.	yes	.	2+12	Ax2*
35	LA02058E63	.	.	yes	.	.	yes	yes	yes	.	het?	Ax1 or null
36	LA02058E97	.	.	yes	.	.	yes	yes	yes	.	het	Ax1 or null
37	LA03130E68	.	yes	.	.	yes	.	.	yes	.	2+12	Ax2*
38	LA03186E2	.	.	.	.	yes	.	.	.	.	2+12	Ax1 or null
39	LA04142C-P5	.	.	.	.	.	.	.	.	.	2+12	Ax2*
40	M08*8005#	.	.	.	.	yes	Unknown	.	yes	.	5+10	Ax2*
41	MD01W233-07-1	.	.	.	.	.	yes	.	.	.	2+12	Ax2*
42	MD02W135-08-9	.	.	.	.	.	yes	.	.	.	2+12	Ax2*
43	MD03W61-09-1	.	.	.	.	.	yes	.	yes	.	2+12	Ax1 or null
44	MD03W91-09-7	.	yes	.	.	.	het	.	yes	.	5+10	Ax2*
45	NC07-21036	.	.	.	.	.	yes	.	.	.	2+12	Ax2*
46	NC07-23081	.	yes	.	.	yes	.	.	yes	.	2+12	Ax2*
47	NC07-23126	.	yes	.	.	yes	.	.	.	.	5+10	Ax2*
48	NC07-23771	.	yes	.	.	.	Unknown	.	.	.	2+12	Ax1 or null
49	NC07-24445	.	yes	.	.	.	yes	yes	yes	.	5+10	Ax1 or null
50	VA06W-580	.	yes	.	.	.	yes	.	yes	.	2+12	Ax2*
51	VA07W-569	.	.	.	.	.	yes	.	.	.	2+12	Ax2*
52	VA08W-622	.	yes	.	.	.	.	.	.	.	2+12	Ax1 or null
53	VA08W-630	.	.	.	.	.	yes	.	.	.	2+12	Ax2*
54	VA08W-653	.	het	.	.	.	yes	.	.	.	2+12	Ax1 or null
55	VA08W-709	.	.	.	.	.	yes	.	.	.	het?	Ax2*
56	VA09W-641	.	.	.	.	.	yes	.	.	.	2+12	het
57	VA09W-654	.	.	.	.	.	.	.	.	.	5+10	Ax1 or null
58	W1104	.	.	.	.	yes	.	.	yes	yes	2+12	Ax2*

APPLICATION OF SINGLE KERNEL NIR TECHNOLOGY FOR EVALUATION OF WHEAT CULTIVARS AND FUNGICIDES FOR FHB MANAGEMENT

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ABSTRACT

DON value of grains and percentage of *Fusarium* damaged kernels (FDK) are often used for the evaluation of cultivars for FHB resistance and also for evaluation of the efficacy of fungicides for control of FHB disease in wheat. The ability of the Single Kernel Near Infra Red (SKNIR) instrument to estimate DON and FDK levels of small bulk samples as a rapid, non-destructive and economical method was tested using 80 wheat samples from a nested trial established to evaluate eight wheat cultivars and five fungicides.

About 50 g of kernels were loaded into SKNIR grain feeder and programmed to estimate single kernel DON levels in 500-kernels per sample. Each sample was sorted into four groups based on estimated DON value and the number of kernels and weight of each group was recorded. The bulk DON level of the 500-kernel sample was computed by using single kernel DON concentration and average weight of kernels in each group. The FDK levels were computed by calculating the number of kernels having DON in 500-kernel sample. The SKNIR estimated bulk DON and FDK values were compared with the visually estimated FDK levels and DON values of representative samples estimated by the standard gas chromatography - electron capture (GC-EC) analytical method.

Compared with the DON values estimated by the standard method, SKNIR estimated the bulk DON level of samples with a mean difference of 4.3 ppm. The DON values of 80% of the samples were estimated within standard DON value ± 5.9 ppm with a mean difference of 2.5 ppm. Likewise, the SKNIR estimated FDK% had a mean difference of 4.9% compared to visual FDK estimates and FDK levels of 80% of the samples were estimated within ± 7.4% with a mean difference of 3.0%.

To assess the sampling error in bulk DON estimation, 3000 kernels from a sample with a DON value of 8.0 ppm was sorted and from this 50 random 500-kernel samples were drawn and DON values were computed. The estimated DON values ranged from 5.4 - 15.8 ppm with a mean of 9.7 ppm and standard deviation of 1.7 ppm. When sampling errors are also taken into account, it seems that SKNIR can estimate the bulk DON value of grain samples fairly well. The SKNIR estimated bulk DON and FDK levels for evaluation of cultivars and fungicide treatments are quite comparable to that of evaluation with visual FDK estimates and standard DON measurements. Ranked single kernel DON values from the SKNIR method also provide additional information on the composition of the bulk DON level and this may be used to assess types of FHB resistance in cultivars. Therefore, the SKNIR technique could be used as a low cost, rapid and nondestructive method for evaluation of cultivars or fungicide treatments for FHB management.

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DEVELOPMENT OF SINGLE KERNEL NIR TECHNOLOGY FOR EVALUATION OF FHB RESISTANCE AND FOR IDENTIFICATION OF REDUCED DON IN HARVESTED WHEAT GRAIN

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ABSTRACT

We have developed a calibration for our Single Kernel Near Infrared (SKNIR) sorter to estimate the DON concentration in single wheat kernels. We used this calibration to estimate DON levels in 500-kernel bulk samples by using estimated DON concentration and weight of single kernels. A preliminary study to evaluate four wheat cultivars with diverse FHB resistance levels using SKNIR DON estimation in 500-kernel bulk samples showed promising results. Using SKNIR, sample DON levels were fairly accurately estimated. The distribution pattern of DON levels in kernel samples among varieties could help geneticists better understand the expression of resistance in varieties. Studies are currently underway to further test this technique, and use it to estimate DON levels to evaluate varieties for resistance and to evaluate the efficacy of fungicides for FHB control in wheat.

We have developed a calibration for the SKNIR to estimate single kernel moisture content, water mass, and weight from samples having sound and *Fusarium* damaged kernels to enable an estimate of certain kernel characteristics on a mass/kernel basis instead of percentage basis. This will be helpful to non-destructively estimate DON and other characteristics of single kernels on a constant moisture basis and to estimate these characteristics in small bulk grain samples more accurately.

We showed that the distribution pattern of DON levels in kernels within artificially inoculated spikes can differ depending on the genotype. Additional experiments are ongoing to estimate DON levels in kernels within artificially inoculated spikes. Use of the SKNIR technique to evaluate disease progression within spikes may help in evaluating for differences in Type II and Type III resistance mechanisms between genotypes.

In a preliminary test, pearl milling and the SKNIR technique was used to evaluate DON levels in kernel bran derived from red and white wheat. Additional tests are planned to develop the SKNIR technique as a method to determine potential differences in the levels of DON accumulation when comparing the bran from near-isogenic red and white seeded lines.

We also plan to study FHB infected kernels and DON using Fourier-transformed mid-infrared spectroscopy and micro-spectroscopy. Such studies are expected to contribute to a better understanding of NIR absorption bands for DON and the distribution of DON within kernels infected with Fusarium.

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MAPPING WHEAT HEAD SCAB RESISTANCE QTL IN MULT757 USING FAMILY-BASED LINKAGE AND ASSOCIATION APPROACH

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ABSTRACT

Breeding for Fusarium head blight (FHB) resistance in wheat is an important objective in breeding programs. Regardless of the number of mapping studies done in the past, progress in finding large effect quantitative trait loci (QTL) is limited. The 3B QTL from 'Sumai 3' is likely the most widely used resistance source in the US. As with other traits in experimental mapping populations, FHB resistance QTL mapping is typically done with specifically designed biparental populations. Some important restrictions associated such an approach include the fact that mapping populations rarely give rise to new cultivars, the time required for population development, and extra steps necessary for validation in multiple genetic backgrounds of interest. Our previous studies have validated the application of using breeding families as mapping populations to solve limitations associated with biparental populations based QTL mapping. The current experiment was conducted to map FHB resistance QTL in wheat genotype *Mult757* (PI 271127) using the family-based linkage and association approach. Eighty-three families of three- or four-way crosses were developed using *Mult757* with 37 susceptible spring wheat genotypes. Previously, validated family-based linkage (pedigree-wide regression and variance component method), as well as association (quantitative transmission disequilibrium), tests were used. A single QTL on chromosome 7B that explained 27 to 32% of total phenotypic variation was identified. This further demonstrates application of family-based approach in plants (does it also demonstrate that a new qtl was found?).

FINE MAPPING OF A REGION ON CHROMOSOME 6H ASSOCIATED WITH DON IN BARLEY

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ABSTRACT

The centromeric region of chromosome 6H has been associated with resistance to Fusarium head blight (FHB), deoxynivalenol (DON) accumulation, kernel discoloration (KD), and grain protein concentration (GPC). Fine mapping this region is important to determine if these QTLs are closely linked or controlled by a single locus and to develop strategies for exploiting genetic resistance. A BC_5 line carrying 17 cM segment encompassing this region, derived from Chevron (resistant with high GPC), in a Lacey (susceptible with moderate GPC) background was used to generate a set of recombinant NILs which were in turn used to fine map this region. To develop the NILs, 1968 F_2 plants generated from a cross between Lacey and the BC_5 line were genotyped with SSR markers and recombinants were advanced to the next generation. Informative recombinants in the F_3 were selected and advanced to produce 269 F_4 plants. We then selected 78 recombinant NILs that represented 20 different recombination classes. These 78 NILs were phenotyped for FHB, DON, KD, and GPC in a total of four field and one greenhouse environments. A fine map for chromosome 6H at this region was constructed using ten simple sequence repeat (SSR) and three single nucleotide polymorphism (SNP) markers. Using these lines we narrowed the region containing the locus associated with DON, KD, and GPC to about 1 cM. We believe this locus is homologous to the *Gpc-B1* locus in wheat which is associated with GPC and senescence. Similar to wheat, we observe that higher GPC is associated with earlier senescence. Our hypothesis is that early senescence shortens the window of time for FHB infection and toxin production by the pathogen resulting in a lower DON.

DEVELOPMENT AND DISTRIBUTION OF MALE-STERILE FACILITATED RECURRENT SELECTION POPULATIONS

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ABSTRACT

Recurrent selection is a breeding procedure with the objective of increasing the frequency of desirable alleles for one or more traits while maintaining a high level of variability in the population. Intermating among selected parents each generation allows recombination to occur thus combining genes from different sources. Male sterility in a self-pollinated species provides a mechanism to easily produce many crosses. Male-sterile recurrent selection in wheat derives its power from recombination of sources of genetic variation for a specific trait and intensity of selection due to large population size that results from many crosses. Progress from selection when recombining genetic sources of FHB resistance is directly related to the amount of genetic variation for the trait in the population and the identification of parents with a high level of expression of the desired trait.

The dominant male-sterile gene was utilized to create recurrent selection populations segregating for FHB resistance because the progenies of the male-sterile plants always segregate 1:1 for sterility and a generation of selfing is not required to obtain true-breeding fertile genotypes. Our objective is to create four populations with FHB resistance adapted to different regions of the eastern U.S.

The male-sterile populations derive from the Idaho Intensive Management Male-Sterile population (PI 573190). They were developed in Wooster, OH beginning in 2006, using elite soft red winter and soft white winter wheat varieties as pollinators. Some were included as sources of FHB resistance and others as sources of adaptation and genes for high yield potential.

Pollinators were planted as mixtures in rows that alternated with rows of male-sterile plants. Seed from the sterile heads are planted, and their sterile offspring are tagged for harvest to repeat the process. Sterile plants are selected; those highly susceptible to FHB are discarded.

In 2009, male-sterile populations were grown in the field at Wooster, OH. From this, four populations were developed in 2009-2010:

1. The early maturity selections from the male-sterile population were planted with pollinator parents for a southern-mid-Atlantic soft red wheat population.

2. Two-thirds of the seed from the mid-maturity selections from the male-sterile population were planted with pollinator parents for an early Midwest soft red wheat population.

3. One-third of the seed from mid-maturity selections from the male-sterile population and some from the late selections were planted with pollinator parents for a late Midwest soft red wheat population.

4. Late maturity selections from the male-sterile population were planted with pollinator parents for a late soft winter wheat population, including white winter wheat genotypes.

In summer 2010, sterile heads were identified and tagged at four different maturity dates. Sterile heads that were very susceptible to *Fusarium graminearium* (Figure 3) were removed on June 14 (early Midwest and mid-Atl.) and June 17 (late Midwest and white). After being harvested and threshed, *Fusarium* damaged kernels were removed by aspiration, removing approximately 50% of the kernels.

A bulk from each population was distributed to cooperating breeding programs in Fall 2010. Cooperating breeding programs have been provided educational materials to assist them in utilizing the populations in their individual breeding programs, continuing cycles of mating and selection for FHB resistance within their target environments.

REPORT ON THE 2009-2010 NORTHERN UNIFORM WINTER WHEAT SCAB NURSERIES

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ABSTRACT

The USWBSI funds the uniform testing of soft winter wheat lines in two tests: the Northern Uniform Winter Wheat Scab Nurseries (NUWWSN and the preliminary NUWWSN (PNUWWSN). In the 2009-2010 season the NUWWSN had 56 entries (plus four checks) from 13 breeders and obtained phenotypic data from 13 locations. The PNUWWSN had 47entries (plus four checks) from nine breeders and obtained phenotypic data from eight locations. The FHB Index valued ranged from 8.1 to 38% in the NUWWSN: 12 entries had an Index value that were not significantly less than the lowest Index value in the test and all 12 had a lower Index value than Truman (the most MR check). The FHB Index valued ranged from 8.0 to 41.5% in the PNUWWSN: 23 entries had an Index value that were not significantly less than the lowest Index value in the test though only two had a lower Index value than Truman. More detailed analysis of the 2009-2010 trials will be presented at the 2010 Forum and a full report will be available on line at http://www.scabusa.org. In addition, we will do analysis of FHB data from past NUWWSN and PNUWWSN to assess trends over time and the prevalence of soft winter wheat lines with good FHB resistance.

GENOMIC SELECTION FOR FUSARIUM HEAD BLIGHT RESISTANCE IN WHEAT

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ABSTRACT

Resistance to Fusarium Head Blight (FHB) in wheat is a low-heritability trait that is strongly influenced by environment and difficult to evaluate. Although there have been resistance QTL identified in Chinese germplasm that explain up to 30% of the phenotypic variation, there are several native sources of resistance that are currently being mapped and are likely to be controlled by several QTL. Marker-assisted selection (MAS) is an effective approach to pyramiding multiple large-effect genes in a single genotype, however most important agronomic traits are controlled by many genes with effects below levels of statistical significance. The complementary application of MAS for qualitative traits and genomic selection (GS) for quantitative traits, such as FHB resistance, is a promising strategy for increasing the annual rate of genetic gain in breeding programs. This study utilizes data for 252 entries from the 2008-1010 Northern Uniform Winter Wheat Scab Screening Nursery (11-13 locations), Preliminary Northern Uniform Winter Wheat Scab Screening Nursery (8-10 locations), and Uniform Southern FHB Screening Nursery (13 locations) to evaluate GS models for predicting FHB phenotypes. Cross validation of genomic estimated breeding values compared to phenotypic values resulted in correlations ranging from 0.3 to 0.7. Breeding programs are rapidly transitioning to whole genome genotyping and models used to analyze these data will be valuable for selecting FHB resistant genotypes prior to testing. The Northern Cooperative FHB Project has two multi-PI subprojects that will contribute directly to implementing GS in wheat breeding programs. Multi-PI project #4 has as a goal of developing models to implement GS for multiple FHB traits. Multi-PI project #5 has developed male-sterile facilitated recurrent selection populations using FHB resistant germplasm. These projects, combined with the information in this study, set the stage for greatly enhancing the rate of genetic gain from selection for FHB resistance. This material is based upon work supported by the U.S. Department of Agriculture. This is a cooperative project with the U.S. Wheat & Barley Scab Initiative. Any opinions, findings, conclusions, or recommendations expressed in this publication are those of the author(s) and do not necessarily reflect the view of the U.S. Department of Agriculture.

MILLING AND FLOUR ANALYSIS OF WINTER WHEAT GENOTYPES IN REGIONAL FUSARIUM NURSERIES

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ABSTRACT

We evaluated the milling and flour quality of 117 grain samples from wheat entries in the Northern and Southern Uniform Winter Wheat Scab Nurseries. Samples were provided from uninocculated trials in Warsaw, VA (courtesy of Carl Griffey) for the Southern Nursery and West Lafayette, IN (Courtesy of Herb Ohm) for the Northern Nursery. Data evaluated included grain protein, grain hardness, flour yield, softness equivalent, sucrose solvent retention capacity test and lactic acid solvent retention capacity test. Sequentially selecting for flour yield, softness equivalent and sucrose SRC should identify the best quality genotypes in this study. In the Northern Nursery the best quality genotypes were with better than average ratings for both Fusarium index and FDK were: 03M1539#031, IL06-7550, IL06-14262, and MO071522. In the Southern Nursery, the best quality genotypes (without considering disease ratings) were 03M1539#031, ARS07-0203, GA031188-O15, GA031188-O17, M08*8005#, and VA08W-622. The full report will provide both summaries with disease resistance ratings and soft wheat quality ratings.

COMPARISON OF TWO FUSARIUM HEAD BLIGHT INOCULATION METHODS IN WHEAT

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ABSTRACT

Fusarium head blight (FHB) is a destructive fungal disease of wheat and barley, causing significant reduction in yield and test weight. Grain may also be contaminated with mycotoxins, posing serious health risks to end users. Developing host plant resistance, a primary control method for FHB, relies on the evaluation of breeding lines using inoculation methods. Various inoculation methods are employed to evaluate wheat breeding lines. The use of an infected grain spawn coupled with irrigation is likely the most common method to screen large numbers of breeding lines. The objective of our study was to evaluate a spray and bag inoculation method by comparing it to a grain spawn mist irrigated method. In the spray and bag method, a macroconidial suspension was used to inoculate a small group of wheat heads in yield plots, and a 1.1L WhirlPak™ bag with six air holes punched in the top of the bag was placed over inoculated heads for 48 h to maintain high relative humidity. If data from the two methods are well correlated, the spray and bag method could be used to evaluate breeding lines for FHB resistance at multiple locations without the establishment of mist irrigation at all sites. These two methods were compared previously in 2008, and results between the two methods were well correlated. In 2010, the spray and bag method was used at two locations in Illinois on a total of 120 lines with two replications. The grain spawn method was evaluated at a single location. Spearman rank order correlation coefficients were obtained using the PROC CORR procedure of SAS 9.2. In 2010, while significant, correlations between the two methods were not as high as observed in 2008. Correlations ranged from 0.22 for incidence to 0.54 for FHB index between the two methods. Of concern were low correlations between locations of the spray and bag method. Correlations with incidence were not significant, and severity (r=.25) and FHB index (r=0.31) were poorly correlated between methods. Incidence was extremely high in one location (X=97.6%) possibly overwhelming genetic resistance and contributing to the weaker correlations between locations. Correlations between the two methods for the most resistant and susceptible lines (determined as the top and bottom 20% of breeding lines for FHB index in the grain spawn method) improved in most cases. Correlation between the two methods for FHB index improved to 0.64. These results indicate that this method is able to determine the most resistant and susceptible lines better than the moderately resistant or moderately susceptible lines. A comparison of breeding lines shared between the top and bottom 10, 20, and 30% of the two methods also supports this conclusion, as half the lines in the top third of each method were shared. Also, only a few lines that were in the bottom third or top third of one method rose or fell to the top or bottom third of the other method. The results of this study indicate the spray and bag method could be used to obtain FHB resistance data in multiple environments. Further work is planned to determine a more suitable inoculum concentration so that genetic resistance is not overwhelmed and a better distinction between resistant and susceptible lines is achieved.

IDENTIFICATION OF QUANTITATIVE TRAIT LOCI FOR FUSARIUM HEAD BLIGHT RESISTANCE IN A WINTER WHEAT POPULATION

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ABSTRACT

Wheat scab, or Fusarium head blight (FHB), causes devastating losses in wheat worldwide. Host plant resistance is a primary method to reduce the impact of this disease. Obtaining an adequate level of host resistance for this quantitatively inherited trait requires the combination of resistance alleles from different sources. Additionally, to obtain resistance capable of withstanding a disease epidemic it is necessary for a cultivar to possess multiple types of resistance to FHB. Our objective in this study was to identify quantitative trait loci (QTL) for FHB resistance in the soft red winter wheat line IL97-1828. IL97-1828 consistently produces low disease symptoms and low percentage of Fusarium damaged kernels (FDK) under high disease pressure in the field. The resistance within IL97-1828 is considered to be native and independent of widely used resistance sources from Asia and Europe. A population, consisting of 242 recombinant inbred lines, was developed from a cross between IL97-1828 and the FHB susceptible parent Clark. The RIL population was evaluated for disease incidence, severity, FDK percentage, and DON concentration in the field in Urbana, IL in 2009 and 2010, and Wooster, OH in 2010. FHB index and ISK index were also calculated. The population was genotyped using DArT markers by Triticarte Pty. Ltd. and a small set of simple sequence repeat (SSR) markers. A linkage map for the population was constructed using JoinMap 3.0, and composite interval mapping was performed using PLABQTL. Distributions for phenotypic disease measurements were broad and continuous for all measured disease traits. Disease incidence in 2009 was significantly less than that observed for both locations in 2010. Also, FDK percentage was higher in Urbana than in Wooster, OH in 2010. Correlations between environments, while significant, were relatively low ($0.20 < r < 0.54$). Averaged across environments disease measurements were significantly correlated in all cases ($0.31 < r < 0.96$). QTL for resistance to FHB were identified on seven linkage groups that mapped to six different chromosomes (1A, 1B, 1D, 2B, 3B, and 4A). In all cases QTL were minor explaining between 2.9% and 8.7% of the phenotypic variance, respectively. No QTL were detected across all environments, and only three QTL were identified in a single environment. A single region on chromosome 1B was identified for reduction in disease incidence ($0.034 < R^2 < 0.062$). A QTL on 2B was significant for reduction in severity, FHB index, FDK percentage, and ISK index. The QTL on 2B was also identified for DON reduction in both years in Urbana, IL ($0.045 < R^2 < 0.065$). Two QTL on chromosome 3B were not near the 3BS region, and one was likely close to 3BSc and the other near 3BL. A QTL on the long arm of chromosome 3B explained approximately 8% of the phenotypic variance for ISK index at Urbana in 2009. None of these QTL appear to be novel as previous reports have indicated QTL in these regions; however, it is not clear whether they are different alleles at the same loci or different genes in the same region. Our results indicate several regions contributing small effects are important for FHB resistance in IL97-1828.

INTROGRESSION OF TWO MAJOR FHB-RESISTANCE QTLS INTO DURUM AND HARD RED SPRING WHEAT

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ABSTRACT

Identification and deployment of novel sources of resistance to Fusarium head blight (FHB) are crucial in the current effort in fighting against this serious disease in durum and bread wheat. Recently, we identified and mapped a novel major FHB resistance QTL on chromosome arm 5AL and another major QTL on 5AS in the hexaploid wheat accession PI 277012. This accession has been misclassified as cultivated emmer wheat (*Triticum turgidum* subsp. *dicoccum*) in the National Small Grain Collection. PI 277012 is a spring wheat with non-free threshing spikes as well as being morphologically similar to synthetic hexaploid wheat. Thus it is not suitable for direct uses in wheat breeding. The objective of this study was to transfer the two QTLs into durum and hard red spring wheat cultivars adapted to the Northern Great Plains. The accession PI 277012 was crossed with three hard red spring cultivars ('Grandin', 'Reeder', and 'Russ') and three durum cultivars ('Ben', 'Lebsock', and 'Divide'), and the F_1 hybrids were then backcrossed with those cultivars to produce BC_1 seeds. The BC_1F_1 plants were advanced to the BC_1F_4 generation through greenhouse evaluation and selection. The BC_1F_5-derived lines with putative FHB resistance and good agronomic performance were evaluated in field disease nurseries at two locations (Fargo and Langdon, ND). Through this process, a number of hard red spring wheat lines with high levels of FHB resistance and several durum lines with improved levels of FHB resistance were identified. Molecular marker analysis showed that these resistant lines carry at least one of the two major QTLs from PI 277012, indicating that the high level of FHB resistance in PI 277012 can be steadily expressed in different genetic backgrounds.

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OTHER PAPERS

THE U.S. WHEAT AND BARLEY SCAB INITIATIVE'S FHB ALERT SYSTEM

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ABSTRACT

The United States Wheat and Barley Scab Initiative and the curators of the FHB Risk Assessment Tool (based at Penn State University and Kansas State University) have collaborated to provide growers with a live notification system for Fusarium Head Blight (FHB) conditions throughout growing regions in the United States. Users can access maps using the Fusarium Head Blight Risk Assessment Tool (http://www.wheatscab.psu.edu/riskTool_2010.html) to find FHB related field observations and information posted by state specialists in regions of interest. Updates posted to the Fusarium Head Blight Risk Assessment Tool are automatically sent out to the community using various electronic communication methods. These methods include the USWBSI blog (http://scabusa.org/modules/wordpress/), the various subscriber mailing lists hosted by the USWBSI, and a subscription service to receive text messages on cell phones each time new information is posted. The email and/or text message subscription form, as well as additional information about the service, can be found on the USWBSI site at http://scabusa.org/fhb_alert.php.

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2010 FUSARIUM HEAD BLIGHT EPIDEMIC IN OHIO: OUR ROLE IN EXTENSION AND OUTREACH

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ABSTRACT

During the 2010 wheat-growing season, researchers at The Ohio State University continued ongoing efforts to educate growers and others in the wheat industry about the tools and information available to help them assess the risk of a Fusarium head blight (FHB) epidemic in their area of the state and the importance of making informed FHB management decisions. Accomplishing these goals was made easy by the fact that multiple resources are currently in place to provide timely information to our clientele. The available resources include the FHB prediction center, the Crop Observation and Recommendation Network (CORN) Newsletter (a weekly publication by the Ohio State Agronomic Crops Team and Ohio State Extension), and professional relationships with county educators, millers, grain buyers, crop consultants, and local growers. In the early spring, we began promoting use of the FHB prediction center, and prepared a factsheet with detailed information on how to navigate the FHB Risk Assessment Tool and interpret the results. Throughout the anthesis period, we prepared updates for the commentary section of the FHB Risk Assessment Tool and released newsletters that provided interpretations of the risk predictions, information about new tools such as SCAB SMART and SCAB ALERT, and management options and recommendations. The anthesis period lasts approximately 2 to 3 weeks in Ohio where wheat in southern parts of the state reaches this critical growth stage before wheat in northern Ohio. To evaluate the FHB Risk Assessment Tool and provide a quick assessment of FHB levels within selected counties, a field survey was conducted approximately three weeks after anthesis. This coordinated survey has been completed in a fairly uniform manner for the past 9 years. Each year, between 67 and 159 fields were surveyed in 12 to 32 Ohio counties. Within each field, the surveyor (extension educators and graduate students) walked a diagonal through the field and identified ten sites that were approximately 30m apart to assess disease incidence. Each site consists of 0.3m of one row of wheat. Incidence was assessed as the proportion of diseased spikes at each site relative to the total number of spikes examined. In 2010, 145 fields in 32 counties were surveyed and average county incidence ranged from 1.17 to 50.37%. Counties with the highest levels of scab were clustered in the central northwestern part of the state. The FHB Risk Assessment Tool did indicate that these counties were at moderate to high risk for an FHB epidemic during their anthesis periods. The survey results clearly showed that during the 2010 FHB outbreak, the more serious and aggressive managers generally had the best wheat crop. Even in areas where FHB levels were high, some fields with the lowest levels of vomitoxin and highest yields and test weights were those planted with a resistant variety and sprayed with a fungicide application at flowering. Towards the end of the growing season, several newsletters were prepared to provide growers with information on how to harvest and handle grain from FHB-infected fields, sample and test for DON, feed or dispose of contaminated grain, and select moderately resistant varieties for the 2010/2011 growing season.

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