HOST PLANT RESISTANCE
AND
VARIETY DEVELOPMENT

DIALLEL ANALYSIS OF FUSARIUM HEAD BLIGHT RESISTANCE IN GENETICALLY DIVERSE WINTER WHEAT GERMPLASM.

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OBJECTIVE

Estimate general and specific combining ability for Fusarium head blight resistance in genetically diverse winter wheat germplasm.

INTRODUCTION

Fusarium head blight (FHB), caused by *Fusarium graminearum* Schwabe [telomorph: *Gibberella zeae* Schw. (Petch)], is a major wheat disease causing significant losses in the Midwestern U.S. and other global wheat regions where weather conditions are warm and humid. Use of FHB resistant wheat cultivars is known to be the best option to reduce damage associated with FHB. Resistant winter wheat varieties released over the past ten years including 'Ernie' (McKendry et al., 1995), 'Freedom' (Gooding et al. 1997), 'Roane' (Griffey et al. 2001), Nc-Neus (Murphy et al., 2004), Truman (McKendry et al., 2005), RCATL33 (Tamburic-Illincic et al., 2006), and Allegiance (Van Sanford et al., 2006) reflect the degree of emphasis given to FHB by wheat researchers in recent years. However, the similarities of these resistant sources with other known sources such as Frontana, Sumai 3, and its derivatives, and their genetic value as parents in breeding programs remain relatively unknown. The objective of this study was to estimate the general and specific combining ability of a number of diverse sources of FHB resistance in winter wheat backgrounds in an effort to help breeders make more informed decisions on which FHB resources to use as parents.

MATERIALS AND METHODS

Twenty genetically diverse winter wheat genotypes (Table 1) were crossed in a 20 by 20 partial diallel to generate the genetic material necessary for this study. Two hundred and ten genotypes (190 F_1 and 20 parents) were developed for analysis. Eight plants per replication per genotype were vernalized at 4°C for 8 weeks and transplanted to the greenhouse. Plants were arranged in a randomized complete block design with 2 replications. The experiment was repeated twice. At anthesis, plants were point-inoculated and scored for type II resistance according to Liu et al. (2005). Data collected included total spikelet number and the number of diseased spikelets on the inoculated head. The Fusarium head blight index (FHBI) was computed as the percentage of diseased spikelets on the inoculated head.

Mean phenotypic FHBI data for each replication as well as that for disease spread were analyzed according to Griffing's Model 1 (fixed effects), Method 2 (parents and crosses) diallel analyses (Griffing 1956). Analyses of variance and correlation analyses were done using SAS (SAS version 9.1, 2005). General combining ability (GCA) and specific combining ability (SCA) were determined using Microsoft Excel (Microsoft, Redmond, WA).

RESULTS AND DISCUSSION

Disease spread and FHBI were highly correlated ($r = 0.98$, $P<0.0001$), as FHBI is derived in part from disease spread data. Analyses were done on each trait independently because FHBI can be confounded by the number of spikelets in the inoculated head. However, results in this experiment were very similar suggesting that FHBI and disease spread could be used interchangeably to describe disease reactions in this set of genetic materials. Analyses of variance indicated no significant effect of environment in this study, thus data were combined over environments for statistical analyses. Effects of parents and crosses were highly significant for both FHBI and disease spread

(P<0.001), however, no significant differences were detected between parents and their F_1s (crosses). GCA and SCA were highly significant (P<0.0001 and P<0.001, respectively), for both FHB and disease spread. FHBI among resistant parents ranged from 6 to 21% while that for susceptible parents ranged from 33 to 70%. The top five resistant parents included Truman, Turda 95, 877-1-2, 870-1-3 and IL9624851 with mean FHBI values of 5.9, 7.7, 8.3, 9.1, and 9.2%, respectively. The most susceptible parents included Coker 9835, MO 94-317 and MO 9965-135 with FHBI values of 69.9, 63.9 and 61 %, respectively (Table 1).

General combining ability of resistant parents ranged from -13.33 to -0.52. For susceptible parents values for GCA ranged from +4.68 to +21.77. Based on GCA, the best parents for use in breeding programs included RR 243, 870-1-3, 816-3-4, Truman, and IL9624851-1 with GCA values of -13.3, -12.01, -11.46, -10.80 and - 9.94, respectively (Table 1). These data suggest that these varieties can impart their FHB resistance to any susceptible variety.

Specific combining ability was significant and estimates for resistant-by-resistant and resistant-by-susceptible crosses are given in Table 2. Low SCA values indicate enhanced levels of resistance for some specific parental combinations and suggest the existence of non-additive gene action (i.e. dominance or epistasis) conditioning FHB resistance. Low SCA values may also suggest the presence of allelic variation among wheat parents. Among the crosses that demonstrate the presence of non-additive gene action are crosses between resistant-by-susceptible parents including Coker 9835 with RR 182 (-16.1), RR 243 (-13.7), 870.1-2 (-13.4), 451.1-2 (-13.3), 816-3-4 (-12.5) (Table 2).

Based on the relative magnitudes of GCA and SCA estimates, additive genetic effects are the major gene effects conditioning FHB resistance in this set of germplasm. Other researchers have also reported significant GCA for FHB resistance in winter (Hall et al., 2003; Buerstmayr et al., 1999) and spring (Mardi et al., 2004) wheat germplasm. The results of our study indicate that the best FHB resistant parents for use in enhancing FHB resistance in U.S. winter wheat should be Truman, and IL96 24851-1 because of their high FHB resistance levels, low GCA values and adaptation in the soft red winter wheat region. A second group of lines including RR 243, 870-1-3, and 816-3-4 are less adapted to the U.S. Midwest but still would make good sources of FHB resistance for breeding programs.

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Table 1. Germplasm, pedigrees, Fusarium head blight resistance data and general combining ability data for a 20 x 20 partial diallel analysis conducted at the University of Missouri in 2006.

Germplasm designation	Cross/Pedigree	FHBI (%)	Disease spread (Spikelet no.)	GCA (FHBI)	GCA (disease spread)	FHB level	Country of origin
Truman	MO 11769/'Madison'	5.9	1.0	-10.8	-1.3	Resistant	U.S.A.
Turda 95	L99 I 1-2/T6-80-86	7.7	1.4	-0.5	0.2	Resistant	Romania
877-1-2	Yang la zi	8.3	1.1	-4.2	-0.8	Resistant	China
870-1-3	Wangshuibai	9.1	1.1	-12.0	-1.8	Resistant	China
IL9624851-1	IL90-6364//IL90-9464/Ning 7840	9.2	1.2	-9.9	-1.4	Resistant	U.S.A
P.97397E1-11	96204//Gfd/INW9824	9.3	1.1	-5.6	-0.7	Resistant	U.S.A
RR 243	Sgv/nobeokabozu/MM/Sumai 3	9.5	1.1	-13.3	-1.9	Resistant	Hungary
816-3-4	Ling Hai Mao Yang Mo	9.6	1.0	-11.5	-1.7	Resistant	China
Fundulea 201 R	F15615-2112/F2076W12-11	10.8	1.2	-1.1	-0.1	Resistant	Romania
451-1-2	Seu Seun 6	12.4	1.2	-7.4	-1.3	Resistant	S Korea
RR 182	Sgv/nobeokabozu/MM/Sumai 3	14.9	2.2	-6.6	-0.7	Resistant	Hungary
Ernie	Pike/MO 9965	20.8	2.1	-4.5	-0.9	Resistant	U.S.A.
Freedom	GR 876/OH 217	21.3	3.0	-2.8	-0.4	Resistant	U.S.A.
MO 960903	IL 85-2872/MO 10501	33.0	4.1	9.0	1.2	Susceptible	U.S.A
Patterson	P691184B8-21-1-1-2-4*2/Caldwell	35.5	4.5	4.7	0.6	Susceptible	U.S.A
Pioneer 2545	Unavailable	49.4	7.0	9.4	1.4	Susceptible	U.S.A
RR 176	Sgv/nobeokabozu/MM/Sumai 3	50.2	8.3	11.3	2.2	Susceptible	Hungary
MO 9965-135	W878//Staddard/01707	61.0	7.7	16.9	2.3	Susceptible	U.S.A
MO 94-317	AP Traveller/Pioneer 2555	63.9	7.3	17.2	2.1	Susceptible	U.S.A.
Coker 9835	Coker 85-20/Pioneer 2550	69.6	9.2	21.8	2.9	Susceptible	U.S.A
$LSD_{0.05}$		7.7	1.1	3.3	0.5		

Table 2. Specific combining ability (SCA) for the Fusarium head blight index estimated for crosses from 13 resistant-by-resistant (upper) and 13 resistant by 7 susceptible (bottom) winter wheat genotypes using partial diallel analysis. The experiment was conducted in 2006 at the University of Missouri.

Germplasm	Ernie	Truman	Freedom	PE97397E1-11	IL9624851-1	816-3-4	877-1-2	451-1-2	870-1-3	Turda 95	Fundulea 201 R	RR 182	RR 243
Ernie		-0.6	2.4	-6.2	-0.6	2.5	12.8	-1.6	2.8	-0.7	9.3	-3.7	0.6
Truman			-2.6	0.4	5.5	11.0	1.0	1.5	5.3	-6.1	10.3	-1.2	6.6
Freedom				3.9	-3.8	-2.3	-6.0	-1.7	2.2	-1.5	-5.7	0.8	-1.4
PE97397E1-11					0.0	-1.0	-2.8	-2.7	0.4	-2.6	-6.5	3.9	2.6
IL9624851-1						4.3	-3.0	5.9	4.7	-2.7	5.0	-1.4	4.6
816-3-4							1.5	9.2	7.3	-3.2	-5.3	3.1	7.6
877-1-2								-3.2	0.1	6.5	-9.1	-4.6	1.7
451-1-2									3.3	-4.1	4.3	-3.3	4.7
870-1-3										-3.1	-4.1	1.0	9.8
Turda 95											13.3	-0.7	-4.1
Fundulea 201 R												-7.5	-0.8
RR 182													2.7
RR 176	-10.0	4.8	1.9	-2.7	-1.0	-0.8	-5.9	-4.3	-5.7	12.5	6.1	-7.7	-10.1
MO 94-317	-7.9	-12.8	10.5	0.3	-6.4	-10.3	2.0	3.9	-6.3	-0.5	15.1	-2.7	-13.0
Patterson	5.9	-2.8	-10.8	4.2	-1.7	-7.8	4.9	-7.3	-4.4	3.9	-1.3	3.1	5.7
Pioneer 2545	7.1	-7.1	-3.5	2.2	-13.0	-8.7	-2.8	2.5	-5.2	1.9	10.6	12.2	-5.8
Coker 9835	7.8	-6.5	13.7	9.6	10.2	-12.5	11.0	-13.3	-13.4	13.6	-8.6	-16.1	-13.7
MO960903	-10.6	-3.8	-2.1	8.2	-12.3	-3.9	11.4	1.4	-8.6	-1.8	-4.1	8.9	-7.5
MO9965.35	-5.94	-8.75	1.35	-3.1	-3.2	-6.9	0.3	-0.3	-3.2	11.0	2.0	6.0	-13.4

LSD $_{0.05}$ ij and ik, 2.23 and LSD $_{0.05}$ ij and kl, 2.17 for comparing SCA of crosses, where i, j, k and l are parental designation.

QTL ASSOCIATED WITH LOW DEOXYNIVALENOL AND KERNEL QUALITY RETENTION IN THE FUSARIUM HEAD BLIGHT RESISTANT CULTIVAR, ERNIE.

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OBJECTIVES

To identify QTL associated with low deoxynivalenol (DON) and kernel quality retention, and determine their relationship with QTL for type II resistance in the soft red winter wheat cross Ernie/MO 94-317.

INTRODUCTION

Fusarium head blight (FHB), caused by *Fusarium graminearum* Schwabe [telomorph: *Gibberella zeae* Schw. (Petch)] reduces grain yield in wheat (*Triticum aestivum* L.) in many regions of the world. Wheat grain produced from the infected head is shriveled, with low test-weight and can have a high percentage of damaged kernels that are contaminated with the mycotoxin deoxynivalenol (DON). Deoxynivalenol is linked to feed refusal in livestock (Meronuck and Xie, 2000) and causes depression of the immune system, nausea, and vomiting in humans (Prelusky et al., 1992). Host resistance is the most cost effective method to reduce both yield and quality losses associated with FHB and DON contamination in wheat. Breeders believe that selection of lines for low FHB may result in low DON and high kernel quality retention. However, reports on the association between FHB resistance and DON are mixed with some reports suggesting the traits are independent (Somers et al., 2003) while others suggest they are interdependent (Wilde et al., 2006).

Ernie, a soft red winter wheat developed at the University of Missouri (McKendry et al., 1995) has a moderately high level of type II FHB resistance. It also has low DON content in inoculated trials with high kernel quality compared to susceptible wheat varieties. Four QTL located on chromosomes 5A, 4BL, 3B and 2B are associated with type II FHB resistance in Ernie (Liu et al., 2006). The current study was designed to identify QTL associated with low DON and kernel quality retention in Ernie and to determine their association with the 4 QTL associated with type II FHB resistance.

MATERIALS AND METHODS

A set of 243 F_3 derived F_8 recombinant inbred lines (RILs), developed at Missouri from the cross Ernie/MO 94-317 were used for this study (Liu et al., 2005; 2006). Type II resistance was determined according to protocols outlined in Liu et al. (2006) in a greenhouse experiment with plants arranged in a randomized complete block design with 3 and 4 replications in 2002 and 2003, respectively. Eight plants per RIL per replication were evaluated in each experiment.

Kernel quality evaluation: Infected heads from each replication were harvested at maturity, and hand threshed to ensure all disease kernels were collected. Kernels from each replication were bulked within line and separated into five groups (sound, slightly, moderately, highly shriveled and tombstones). The number of kernels in each group was counted to precisely determine, the proportion of Fusarium damaged kernels in the head. Kernel quality was determined as the percentage of diseased kernels (i.e. shriveled plus tombstones) to the total number of kernels in the inoculated head. Evaluated kernels were bulked and ground with coffee grinder. Deoxinivalenol was quantified by Dr. Pat Hart at Michigan State University using the mycotoxin extraction kit Veratoxin for DON 5/5 (Veratox®).

Linkage map construction: Polymorphisms between Ernie and MO 94-317 were assessed using 64 *Eco*RI/*Mse*I amplified fragment length polymorphic (AFLP) primer pairs and 420 *Xgwm* and *Xbarc* simple sequence repeat (SSR) markers (Röder et al., 1998, Song et al., 2005). Polymorphic AFLP and SSR makers were used to construct the linkage map with Mapmaker, Version 3.0 (Lander et al., 1987) using the Kosambi mapping function. Markers were grouped with a LOD value of 3.0 and distance less than 37 cM and resulted in 46 linkage groups that were used for QTL analysis.

Statistical and QTL analysis**:** Deoxynivalenol and kernel quality data were subjected to tests of normality (Proc Univariate), homogeneity of variance (Bartlett's test), combined analysis of variance (Proc Mixed), and correlation analysis (Proc Corr) using SAS (SAS version 9.1, 2005). Entry mean-based broad-sense heritability was calculated from the combined analysis of variance. The minimum number of genes was estimated using Cocherham's (1983) modification of Wright's (1968) formula. Composite interval mapping (CIM) was done using WINQTLCART (Version 2.5). One-thousand permutations were performed (Doerge and Churchill, 1996) to determine critical thresholds for significance of QTL.

RESULTS AND DISCUSSION

Both DON and kernel quality data for 2002 and 2003 were continuously distributed indicating the quantitative inheritance of the two traits, but only kernel quality was normally distributed. The DON data were log transformed and reanalyzed (Fig 1). Error variances for both traits were homogeneous (Bartlett's test, $P<0.05$). Genotypic effects among RILs were highly significant ($P<0.0001$) for DON and kernel quality for both individual year and combined data. Mean DON values for Ernie and MO 94-317 were 3.6 and 81.3 ppm, respectively while that for RILs was 37.3 ppm. Mean kernel quality data for Ernie, MO 94-317 and RILs were 27, 85 and 48 % Fusarium damaged kernels. Broad-sense heritabilities for DON and kernel quality estimated from the combined ANOVA were 72% and 77%, respectively, (Table 1) indicating the existence of sufficient genetic variance to make improvement in the two traits. The minimum number of genes conditioning low DON and kernel quality were 3 and 4, respectively. Pearson coefficient of correlation for DON and kernel quality was highly significant ($r = 0.79$, $P<0.0001$).

Three QTL associated with low DON were detected accounting for 29.6 % phenotypic variation. These QTL were located on chromosomes 5A, 4BL and 3B explaining 9.5, 6.1 and 14 % of the total phenotypic variation (Table 1). Four QTL associated with kernel quality retention were detected accounting for 40.3 % of phenotypic variation. These QTL, located on 5A, 4BL, 3B and 2B accounted for 17.2, 6.4, 12.2 and 4.1% of the phenotypic variation in kernel quality. Kernel quality QTL on chromosomes 5A, 4BL, and 3B were co-located with those for DON. Although a fourth QTL for DON was identified on 2B that was co-located with the kernel quality 2B QTL, it was below the LOD threshold for significance.

Based on the QTL position, QTL for DON and kernel quality may be the same. The 4BL QTL for both traits is located at 0.01 cM and is linked with *Xgwm495*. On 5A both QTL are linked to *Xbarc 056* with just 1 cM position difference between the DON QTL and the kernel quality QTL. On chromosome 3B the DON and kernel quality QTL are about 8 cM apart. For both DON and kernel quality, the resistance allele is derived from the resistant parent, Ernie.

In this population, DON and kernel quality were correlated with type II FHB resistance with correlation coefficients of 0.87 and 0.84 ($P<0.0001$), respectively. Liu et al. (2006) identified 4 QTL associated with type II FHB resistance on 5A, 4BL, 3B and 2B which accounted for 19.6, 8.5, 14.3 and 4.0% of the phenotypic variation, respectively. Kernel quality markers identified on 4BL, 5A and 3B were consistent with those identified for type II resistance by Liu et al. (2006). Although the marker on 2B was not the same as that for type II resistance, it was closely linked. For DON, markers on 4BL and 5A were consistent with those identified for type II resistance. Consistent with the findings of Liu et al. (2006) the DON 3B marker was centromeric; however, it may differ from

the marker identified for type II resistance. No significant 2B marker was identified for DON.

Wilde and Miedaner (2006) demonstrated the possibility of selecting wheat lines with low DON content by selecting for FHB severity in the field using spray inoculation with *Fusarium culmorum*. Our results which show associations between QTL for DON and kernel quality with those for type II resistance support their findings and suggest that breeders may select for low DON and kernel quality retention based on type II resistance.

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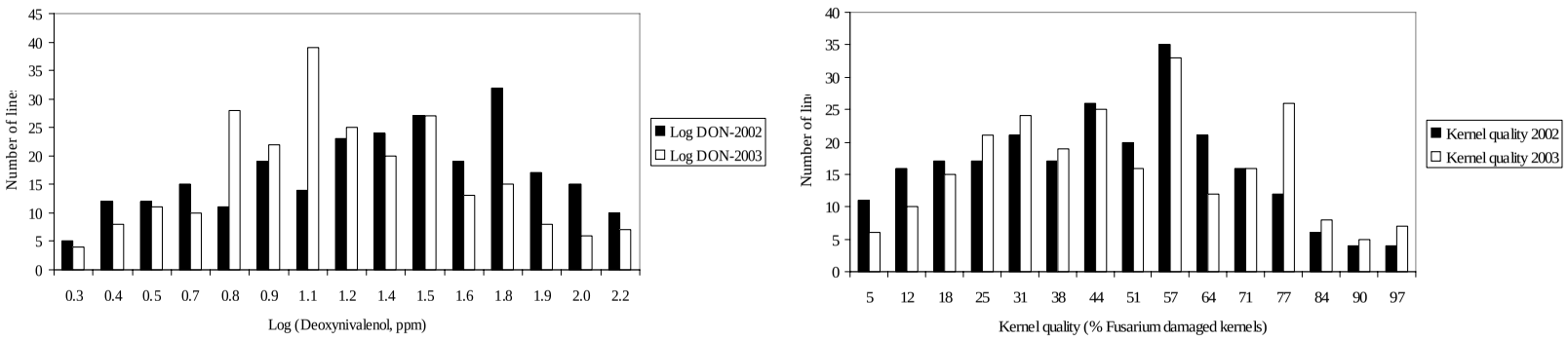

Figure 1. Frequency distributions of logarithm of deoxynivalenol (Log DON) and kernel quality (% Fusarium damaged kernels), in 2002 and 2003.

Table 1. Broad-sense heritabilities, gene number, and QTL associated with low deoxynivalenol (DON) and kernel quality retention in 243 $F_{3:8}$ and $F_{3:9}$ RILs developed from the cross, Ernie/MO 94-317. Data were collected following point-inoculation of RILs with Fusarium graminearum in the greenhouse in 2002 and 2003.

Traits	H^2_{BS} (%)	Number of genes	QTL locations	Peak QTL positions (cM)	Linked marker	LOD value	R2 (%)	Additive effects
			3B	121.70	Xe41m50_6	5.9	14.0	-0.14
			4BL	0.01	Xgwm495	4.5	6.1	-0.10
DON	72	3	5A	45.01	Xbarc056	3.8	9.5	-0.11
			2B	114.01	Xe36m50_3	3.5	4.1	-5.74
			3B	101.31	Xgwm285	8.0	12.2	-7.85
			4BL	0.01	Xgwm495	5.3	6.4	-5.92
Kernel quality	77	4	5A	44.01	Xbarc056	6.8	17.2	-8.63

TRANSFER OF A QTL FOR FHB RESISTANCE INTO HARD WINTER WHEAT USING MARKER-ASSISTED BACKCROSS.

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ABSTRACT

Epidemics of Fusarium head blight (FHB) can significantly reduce wheat grain yield and quality. Use of resistant cultivars is the most effective measure to control the disease. FHB epidemics have been severe in the central and northern Great Plains of the USA, but most hard winter wheat (HWW) cultivars currently grown in this area are highly susceptible to FHB. Some northern Great Plains HWW cultivars such as 'Darrell', 'Expedition', and 'Arapahoe' which have indigenous, unknown resistance performed better than highly susceptible cultivars in eastern South Dakota and Nebraska, but better level of performance in FHB impacted areas in Kansas, Nebraska, and South Dakota requires combining indigenous and QTL with major effect on FHB resistance into adapted HWW cultivars. Because there are large environmental variations associated with disease evaluation and the disease screening procedure is laborious, time consuming, and costly, progress in breeding for resistant HWW cultivars has been relatively slow using conventional methods. Due to the urgent need of FHB resistant cultivars in the Great Plains areas, a marker-assisted backcross project was initiated for rapid transfer of Chinese FHB-resistance QTLs into HWW grown in the region by use of the USDA high-throughput genotyping facility. Our objectives are to transfer the major QTL from Sumai 3 and other Asian sources into US HWW cultivars and to combine the major QTL with locally adapted minor FHB-resistance QTLs to develop marketable FHB resistant HWW cultivars and/or useful germplasm to minimize FHB damage in the hard HWW region. This is a collaborative project between the USDA Genotyping Center in Manhattan and three public HWW breeding programs in Nebraska, Kansas and South Dakota. The cross ND2928 (Ning 7840/ND706)/Wesley/Wesley was made at the University Nebraska and the crosses Harding/Sumai3/Harding and ND2710/Trego/Trego were made at the South Dakota State University. Using marker-assisted selection, 1000 Bc_1F_3 plants per population were screened for the 3BS QTL using 3 markers (GWM 389,GWM533, GWM493) and the 5A QTL using markers WMC705, WMC150 and Barc 180 (McCartney et al, 2004). About 40 plants per cross were recovered with at least all homozygous marker alleles for 3BS major QTL. Screening for 5AS markers was not very successful because of either non-polymorphism or a missing target band. Selected plants were subjected to AFLP analysis with 20 *EcoR*I/*Mse*I primer pairs to maximize genetic background of the recurrent parents. Five plants per population were selected based on cluster analysis of AFLP data for further backcross to the corresponding recurrent parents in the Genotyping Center. About 100 Bc_2 hybrid seeds from each backcross were harvested and advanced. About 3000 Bc_2F_2 seedlings were screened with 3BS markers early this year and 300 Bc_2F_2 plants homozygous for the 3BS QTL were selected from the three populations. The selected plants will be evaluated in the greenhouse and mist-irrigated fields for FHB resistance and other traits at three locations and by the Genotyping Center. The outputs of this research will facilitate rapid release of adapted FHB-resistant cultivars or new germplasm to help relieve FHB losses in the Great Plains.

EVALUATION OF RESISTANCE AMONG ADAPTED SPRING WHEAT GERMPLASM TO FHB INCITED BY SEVERAL *FUSARIUM* SPECIES.

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ABSTRACT

Though pathogenic races (as described by Flor) are apparently non-existent among fungal isolates able to incite Fusarium Head Blight on wheat, there are several unique species that can produce similar disease symptoms. Common resistance is a recently proposed hypothesis in which resistance levels among wheat lines are observed to be generally quite static when tested against different fungal species. Fusarium graminearum is the most prevalent FHB-causing species in the northern Great Plains; however, F culmorum, F. poae, and others are also present. The objective of this experiment was to test for the presence of common resistance in our region by inoculating several advanced experimental spring wheat breeding lines with four locally acquired Fusarium species. Results will be presented based on disease incidence, severity, and index values from tests performed in the greenhouse using a point inoculation procedure. These experiments will form the foundation by which we will explore whether the common resistance phenomenon is operative on germplasm from within our program.

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USING GENE EXPRESSION ARRAY TO DISCOVER SINGLE FEATURE POLYMORPHISMS FOR MAPPING OF FHB RESISTANCE IN WHEAT.

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ABSTRACT

Although several types of marker systems have been used for mapping of wheat resistance to Fusarium head blight (FHB), single nucleotide polymorphism (SNP) is an ideal future marker system for high-resolution maps, marker-assisted breeding and gene function study because it is the most abundant and informative marker system among all markers currently available. The abundance of SNPs increases the chances of finding markers that are tightly linked to a gene or QTL for resistance to FHB. SNPs found in intragenic regions can be used as perfect markers for selection of the gene/trait of interest. Such markers are powerful tools for marker-assisted breeding and gene isolation. Because different technologies have been available for high throughput genotyping of SNPs, the cost per data point can be very low when they are screened on a large scale. However, discovery of SNP in wheat is still in its infancy, limiting the application of SNP in wheat research. To discover potential SNPs, gene expression arrays have been successfully utilized to discover single feature polymorphisms (SFPs) in Arabidopsis and barley. To explore the possibility of using gene expression array for the discovery of SFPs in the complex wheat genome, we used Affymetrix Wheat Genome Array to screen six wheat varieties (Ning 7840, Clark, Jagger, Encruzilhada, Chinese Spring and Opata 85) of diverse origins. Among the 6 cultivars screened, Ning 7840 is highly FHB resistant and Clark is highly susceptible. A RIL mapping population is available for mapping of new SFPs that may link to FHB resistance. RNA was isolated from leaves and roots of 3-week-old seedlings and cDNAs from the six cultivars were hybridized to the wheat chips. Based on cluster analysis, a total of 396 probe sets with signal intensity of at least 200, p-value of < 1e-10 and overall R^2 >4 were selected for SFP confirmation through DNA sequencing. The result showed that the designed primers from 28 probe sets could amplify one DNA fragment from either Ning7840 or Clark in an agarose gel and these amplified fragments can be scored as dominant markers in the mapping population. To date, DNA sequencing has confirmed that 71 probe sets have SNPs within the probes that coincided with array data. The sequenced fragments were mostly 300-500 nt long and contained up to 20 additional SNPs outside the probe sequence. A total of 288 SNPs representing 90 genes have been discovered so far. Thirty-eight SNPs corresponding to different genes were further verified by SNaPshot analysis. The applicability of wheat SNP markers was demonstrated by genotyping RILs from the population of Ning/Clark. The new SNP markers will be mapped and integrated into an existing genetic linkage map derived from the population to saturate the map and to identify SNPs for high-throughput screening of FHB resistance.

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TRANSCRIPTOME ANALYSIS OF BARLEY AND WHEAT INFECTED WITH *FUSARIUM GRAMINEARUM*.

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ABSTRACT

Fusarium head blight (FHB), caused primarily by *Fusarium graminearum*, is a devastating disease of barley and wheat. The Barley1 and Wheat Affymetrix GeneChip probe arrays provide the opportunity to study in the parallel the expression patterns of 22,000 and 61,000 genes, respectively. Here, we provide a summary of the efforts being employed in our laboratory to explore the host response to *F. graminearum* infection. These analyses are primarily focused on identifying the essential genes and mechanisms involved in providing resistance. We have conducted six RNA profiling experiments including: (1) susceptible Morex barley inoculated with *F. graminearum*; (2) susceptible Morex inoculated with a trichothecene producing and non-producing strains of the fungus; (3) three near-isogenic line pairs containing resistant and susceptible alleles at QTL on barley chromosome 2H bin 8, chromosome 2H bin 13, and chromosome 3H bin 6 inoculated with *F. graminearum;* and (4) a near-isogenic line pair containing resistant and susceptible alleles at a QTL on wheat chromosome 3BS inoculated with *F. graminearum*. Overall, 4.5 million data points of transcript accumulation data have been generated. Other disease parameters such as deoxynivalenol and ergosterol concentration, *F. graminearum* infection histology and disease severity data have been or will be obtained for each of the experiments. An integrated picture of the transcript accumulation patterns along with the disease parameters in wheat and barley during *F. graminearum* infection will be presented. A comparison of the differences in transcript accumulation between the resistant and susceptible genotypes will also be presented. Finally, we will present some preliminary analyses of a comparison of wheat and barley responses to infection.

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RELATIONSHIP OF FUSARIUM HEAD BLIGHT FIELD SYMPTOMS AND KERNEL DAMAGE IN WHEAT.

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ABSTRACT

Fusarium head blight (FHB) is an important disease of small grains, causing a reduction in grain yield, shriveled *Fusarium* damaged kernels (FDK), and low test weight. The two most commonly studied types of resistance in wheat are resistance to initial infection and resistance to spread of infection. However, other types of resistance are hypothesized to exist, including resistance to kernel damage which is characterized by lines exhibiting a lower percent FDK than expected based on observed field symptoms. Twenty-four soft red winter wheat lines were chosen to study resistance to kernel damage. The lines were divided into two groups: 1) twelve lines with similar percent FDK and a range of field symptom ratings; and 2) twelve lines with similar field symptom ratings and a range of percent FDK. In 2006, the lines were grown in a mist irrigated, inoculated FHB nursery at Urbana, IL, and incidence, severity, and kernel quality were assessed for each line. An FHB index from 0 to 100 was used as an overall measure of field symptoms, where 0 is resistant and 100 is susceptible. Kernel quality was evaluated as a visual estimate of the percent FDK in a sample of grain. We observed a range of FHB index values within the set of lines where percent FDK was similar; lines in this group had percent FDK between 1% and 40% with an average of 13.4% FDK but exhibited a range of FHB index values between 3.1 and 60.9. For the second group of lines, lines with similar FHB index values tended to have similar FDK ratings. Based on our results, selection for low percentage of FDK should be possible and, in addition to field symptoms, FDK percentage should be evaluated in breeding for FHB resistance.

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GENETIC AND PHYSICAL MAPPING OF THE BARLEY CHROMOSOME 2(2H) *VRS1* REGION FUSARIUM HEAD BLIGHT RESISTANCE QTLS.

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INTRODUCTION

Developing barley with FHB resistance is problematic in that FHB severity and deoxynivalenol (DON) accumulation are negatively associated with desirable plant traits such as height and days to heading in resistant cultivar CI4196 and others (Urrea et al., 2002). We are helping to solve this problem with three converging approaches i.e. saturation genetic and physical mapping of the major FHB resistance QTLs located on barley chromosome 2H bins 8 and 10, development of isolines containing the resistance QTL in the absence of the undesirable agronomic traits such as tall and late heading, and mutagenesis to isolate variants that are agronomically acceptable such as early and semi-dwarf but retain the FHB resistance genes. In this manuscript we describe our current progress in mapping of the FHB QTL and recent mutant isolation and preliminary characterization. The isoline development is progressing, but accurate phenotyping requires extensive and repeated testing. Thus, definitive results will require another year of FHB testing.

A very strong FHB resistance QTL has been detected on barley chromosome 2(2H) bin 10, explaining 17 to 60% of the variation in Foster x CI4196 crosses (Horsley et al., 2006). A second QTL explaining 3 to 9% of the variation was detected on the same chromosome, bin 8. This general region (bins 5-10) also accounts for 25% of the variation in DON accumulation, with the highest value at the *vrs1* locus. Based on our work in collaboration with Rich Horsley we have chosen to focus on the region containing these loci flanked by the markers ABC306 and MWG882 (bins 8-10).

Horsley et al. also reported that there are two QTLs for plant height flanking the *vrs1* locus (2006). Thus a double cross-over would be required in a relatively short genetic region to isolate a normal height recombinant that still retains FHB resistance. In order to overcome this problem, we have developed backcross (BC) populations that allow us to select one recombinant at a time using molecular markers; these are Morex x FosCIA28 and Morex x FosCIA80. Preliminary results indicate that we have selected normal height 6-rowed recombinants. Testing to determine if they retain the FHB resistance is in progress.

Barley has been and continues to be one of the important species in mutagenesis studies. This is, in part, due to barley's diploid nature and seemingly extraordinary susceptibility to mutagens. Deletions are suitable for identification of the genes because they are not expressed and therefore mRNA isolated from the mutants does not hybridize to the microarray while the wild-type control does. Therefore, the genes residing in the deleted region can be visualized by differential hybridization (Zhang *et al*., 2006).

RESULTS AND DISCUSSION

The genetic and physical map in the chromosome 2H *Vrs1* region, roughly from BF263615 to MWG882, is now well saturated with molecular markers and we have identified multiple BAC clones (Fig. 1; Table 1). In order to saturate this region with markers, 29 rice

chr. 4 bacterial artificial chromosome (BAC) clones with synteny to this region were blasted against the barley expressed sequence tag (EST) database. Currently, 80 markers at 31 unique loci are associated with this region. Of these, 46 have been hybridized to the 6x cv. Morex BAC library and 37 have identified positive BAC clones giving us a physical map consisting of 200 clones (Table 1). These clones are part of 57 different contigs according to the BAC fingerprinting of the Tim Close lab at the University of California, Riverside (http://phymap.ucdavis.edu:8080/barley/index.jsp).

There remains a significant gap in the *Vrs1* distal region from marker BI955972 to MWG503. The reason for this gap is not known at this time. If it represents a region of no polymorphism between CI4196 and Morex or Foster, then it is not likely to harbor FHB resistance genes. Other explanations, however, are also possible.

To obtain additional markers, we mapped 378 DArT markers on the Foster x CI4196 map (unpublished). This map was merged with the existing Foster x CI4196 map and with other DArT barley maps developed by Andrzej Kilian's group resulting in a highly marker enriched barley genome map (Wenzl *et al.*, 2006).

The identification of candidate genes for FHB resistance and morphological characteristics has been emphasized in our studies. Results from the phenotyping of Morex x FosCIA28 and Morex x FosCIA80 suggest that the region between the *Vrs1* locus and the proximal marker ctg9802 (approximately the same location as ABG714B) is not necessary for FHB resistance. However, gene homologues of Far red impaired response, Myb transcription factors, Avr9-Cf9 elicitor, Ring Zn finger, Elicitor response gene 3, NBS-LRR-type, reductase protein, and auxin response factor 10 mapped to this region and may be involved in the undesirable morphological traits of CI4196 including increased height and late maturity.

The region distal of *Vrs1* seems to be low in gene density, based on both our mapping data and the report by Dr. Komatsuda (PAGXIV abstract) that during the cloning of *Vrs1* 4 BACs were sequenced and the only gene found was *Vrs1*. The rice syntenous region contains an AP2 domain transcription factor that is particularly interesting due to the involvement of AP2 type transcription factors in resistance to necrotrophic pathogens. However, this is a gene family and two homologs that we mapped go to chromosome 1(7H) and 7(5H).

Approximately 1 lb of CI4196 seed (from Rich Horsley) was irradiated with 4.5 Gy fast neutrons last spring and grown at Pullman WA (summer '05). Individual M1 heads and bulk M2 seed were harvested (summer '05). A bulk M2 field was grown at Pullman, WA (summer '06) and screened for morphological mutants. Jerry Franckowiak spent a few days at Pullman to help look for mutants. Some potentially useful mutants identified this year include 6-rowed, semi-dwarf, early maturity, lax spike, and upright spike. These have been confirmed as CI4196 based on molecular markers at seven unique loci and will be BCed and mapped to determine if they are from the target region. Those that are will be examined for hybridization to the Barley 1 microarray to identify deleted genes and will be phenotyped for FHB resistance.

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Table 1. All BAC clones currently associated with markers on Figure 1.

Markers	***Associated BAC Clones***
BE194244	52L22, 395n21, 475e12, 476n18, 634h22, 792h1, 792o18, 798j10
BE194424	5d23, 48l7, 67b23, 87b21, 154h7, 316l2, 352d6, 399j5, 449n22, 476f2, 478i15, 499h2, 515j23, 522f23, 601b23, 623c3, 624k7, 674d13, 675o3
BE214081	26m13, 241L2, 539k9, 535k20, 670n8, 698e15, 714c10, 804m20
BE215806	177g21, 178k22, 480c15, 526j3, 534i7, 605n2, 658h23, 771c11
BE216598	216e9, 474o3
BE455758	44b3, 55n21, 87b21, 112b5, 310o19, 352d6, 360o22, 393m6, 399j5, 457h2, 476f2, 499h2, 515j23, 648i4, 675o3, 803o17
BE558794A	385h21
BE558794B	385h21
BE602662	60e22, 183f22, 416L21, 450j21, 461d11, 542i17, 797c10
BF064573	71h20, 266g2
BF254012	287j18, 778k20, 796p6, 21i19, 813i15, 51L22, 206d10, 643h10, 675c2, 769L22
BF254076	22n22, 41j6, 397i12, 523b21
BF263615	459j1
BF267331	715o19, 736f12
BF621513	52a11, 184d13, 256n8, 536e17, 557i19, 792j23
BF622472	512L17, 712p3, 712p6, 715d12, 718g1, 721a23
BF623140	22n22, 41g17, 41j6, 184c17, 397i12, 523b21
BF625659	131n15, 485L14, 706o4, 727j5
BF628601	26h9, 48c3, 49m21, 54o20, 206L22, 236b9, 313n3, 325i12, 342o9, 345n24, 345p23, 351j8, 374k10, 375e12, 375g16, 472a20, 511d22, 523o24, 552b9, 749o7
BF628983	508o22
BG299611	286i1, 703a2
BG300704	384n8, 365e4, 536L11, 672d23
BG365406	287j18, 703a2
BG369432	10m15, 647h2, 134c3
BG369629	102p11, 384i7, 406d16
BG414848	133c13, 814d5
BG416824	112i1, 779a4
BG417014	82i4, 127d9, 559k19, 647k12, 699b21
BG418734	71h20
BI952770	145i1, 185d9, 214o16, 478a12, 606a4, 771c11, 551L22
BI955797	376j4, 465h17, 605b24
BI955972	42a11, 82i1, 116k4, 497h8, 592d23, 785d15, 152L21, 399d9, 523i16, 487f8, 785f2
BI959927	71h20
ctg37907	779a4, 346o12
MWG699	72c21, 75f19, 99m7, 108k15, 224b23, 422L15, 454a7, 559n5, 647k20, 751i5, 768n17
MWG865	485L14, 88f9, 131n15, 727j5, 436p4
myb	131j9, 143j23, 651f16, 813i15

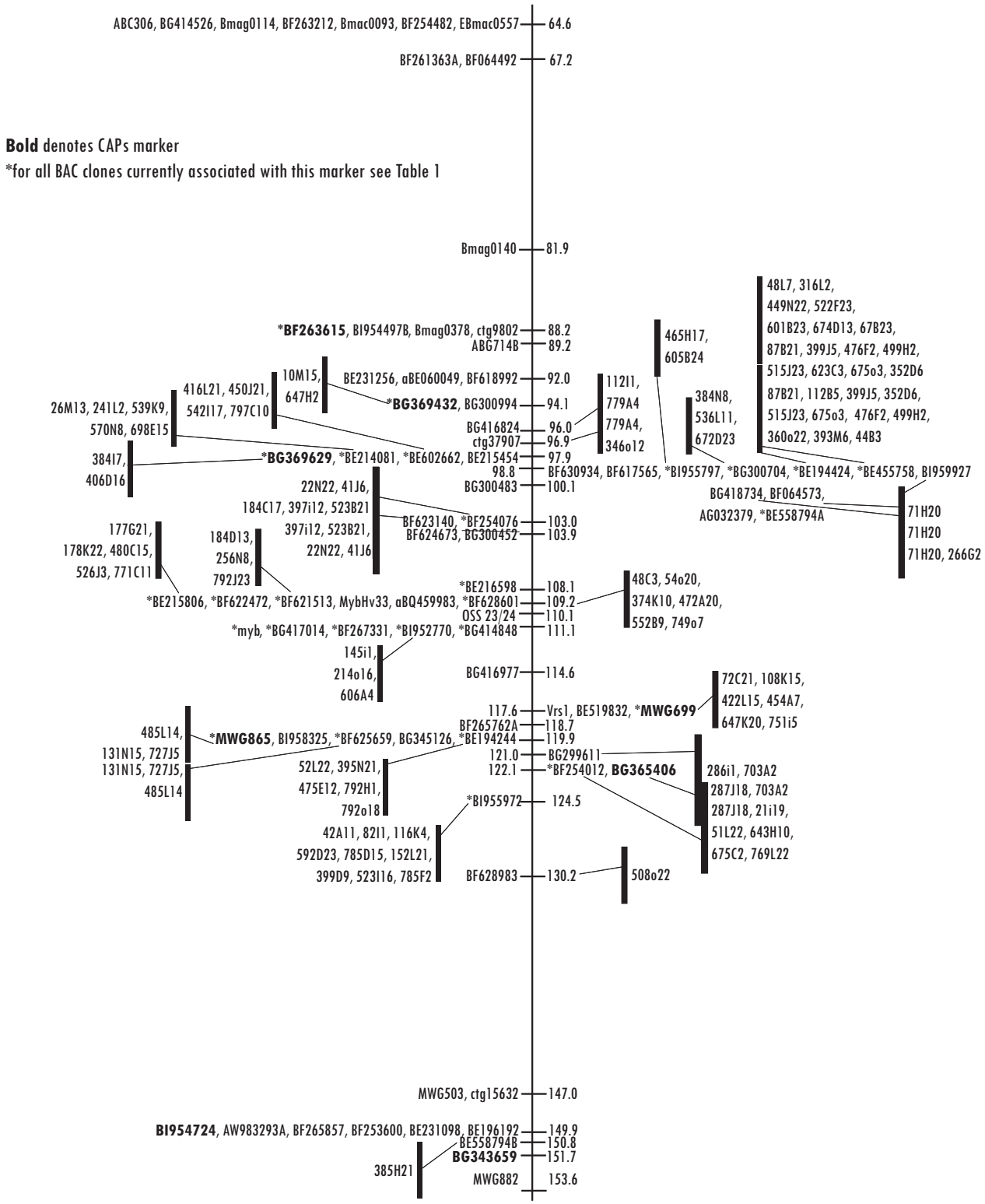

Fig. 1
Chromosome 2(2H) map for bin 8 to 10 with emphasis on the *Vrs1* region. The map was constructed from 56 recombinants selected from the Foster x CI4196 mapping population. The heavy vertical lines indicate BAC clones that have been identified with the markers and the numbers next to them indicate BAC clone addresses. Measurements are in centimorgans and so represent genetic rather than physical distances.

PROGRESS IN DEVELOPMENT AND MAS OF FHB RESISTANT WHEAT CULTIVARS AND GERMPLASM AT VIRGINIA TECH.

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ABSTRACT

To accelerate development of high yielding, FHB resistant SRW wheat lines, we have deployed a combination of top-cross, doubled haploid, backcross and marker assisted breeding methods. During the 2006 crop year, molecular markers linked to FHB resistance QTL located on wheat chromosomes 3BS, 5AS, 3AS, and 6B were used in haplotype analysis of FHB resistance in 56 wheat parents, 120 three-way F_1 progeny, 83 BC_1F_1 progeny, and 145 wheat lines in the 2006 VT FHB Advance and Preliminary Tests. Elite wheat lines having known haplotypes for target marker alleles of validated FHB QTL provide breeding programs with not only a unique source of adapted FHB resistant parents, but also knowledge of selectable markers that can be used to transfer and pyramid such QTL. Haplotyping of parental and advanced lines for known FHB QTL markers is an effective and complementary strategy to phenotypic selection for FHB resistance and, therefore, can be used to accelerate cultivar development.

VA02W-713, a top-cross (Ning7840/Pioneer2691//Roane) derived elite FHB resistant SRW wheat line, ranked 1st in grain yield (77 Bu/Ac) among 54 entries in Virginia's Advance Wheat Test over three locations in 2004. This line also performed well in Virginia's 2005 and 2006 State Variety Trials at six locations and ranked 10th out of 45 entries in the 2006 USDA-ARS Uniform Southern SRW Wheat Nursery over 21 state locations in 2006. Breeder seed of this line is being developed in anticipation of cultivar release in 2008. This line has high grain yield and good FHB resistance with target alleles for markers Xgwm493 on 3BS, Xbarc45 and Xgwm674 on 3AS, and Xgwm508 on 6BS. An additional five lines VA04W-389, VA04W-433, VA04W-474, VA04W-571, and VA04W-592 are potential germplasm releases having good FHB resistance with target marker alleles for at least two QTL on chromosomes 3BS, 5AS, 3AS, and 6B. We also identified two native sources (Massey and VA00W-38) having good FHB resistance with target marker alleles in at least two QTL regions. These and other VT FHB resistant lines are being used as parents in several breeding programs and in pyramiding multiple QTL in adapted wheat backgrounds in our breeding program.

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EVALUATION OF ELITE BREEDING LINES FOR FUSARIUM HEAD BLIGHT (FHB) RESISTANCE.

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ABSTRACT

Thirty six elite breeding lines from breeding programs in the southeast region including 8 from Arkansas, 4 from North Carolina, 6 from Virginia, and 6 from University of Georgia were evaluated with Ernie and Coker 9835 as resistant and susceptible control respectively under misted conditions in Griffin-Campus, Georgia. Ten lines showed similar level of resistance as the resistant control and 24 lines were significantly higher severity than the resistant check, Ernie. A Virginia line, VA05W-500, from a cross of Roane / PIO 2684 // OH 552 showed the best and consistent resistance among all three replications in 36 lines. VA05W-500 showed significantly higher level of resistance than other lines including the resistant control. Many crosses have been made using Sumai 3 or its derivatives as FHB resistant donors. However, FHB resistance could be enhanced significantly through combining the native resistance in soft red winter wheat germplasm. The negative yield drag associated with crosses including exotic germplasm such as Sumai3 or its derivatives could be avoided. Among the ten resistant lines, six lines, GA981621-5E34, GA98401-5E23, GA98401-5E23, AR 97124-4-3, VA05W-498, and LA98090D34-4, were from crosses of native resistant germplasm, and four lines, AR 97002-2-1, ARGE97-1064-11-5, NC03-11465, NC04-27618, were from crosses of exotic resistant germplasm. Native resistant germplasm for FHB resistance should play an important role. Study on the native resistance for FHB is needed for more efficient accumulation of native resistance into local adaptive cultivars.

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COMPLEMENTARY SCREENING TECHNIQUES FOR SELECTION OF BARLEY BREEDING LINES WITH IMPROVED REACTION TO FUSARIUM HEAD BLIGHT.

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ABSTRACT

Selecting malting barley (*Hordeum vulgare*) for resistance to Fusarium head blight (FHB), principally caused by *Fusarium graminearum*, has proven to be a difficult proposition. This can be partially attributed to limited sources of highly resistant germplasm, complex gene action of available sources of resistance and /or linkage to undesirable genes or pleotrophic effects.

These significant genetic constraints aside, we believe the major limitations on progress are related to large environmental effects on the expression of the disease, relatively large error variance associated with subjective visual ratings, and quantitative errors principally associated with sample size for deoxynivalenol (DON) content and mycelium content and the very real possibility of 'escapes'. The need to screen large numbers of breeding lines and the associated cost may limit the number of replicate samples that can be submitted for quantitative analysis from breeding programs. Even if the error variance of a given location were carefully controlled, with replications or other control measures, the large environmental effect generally renders data from a single location less valuable than initially apparent for the selection of lines with improved performance over a broader range of environments. Inoculated and misted nurseries are considered a 'necessary-evil' to ensure a higher likelihood of obtaining some results in years not favorable to disease development. The assumption that inoculated and misted nurseries are representative of natural infection conditions may not always be valid, and there are clearly subtle differences in genotype response depending on the mode of inoculation, such as infected corn spawn vs. conidial suspensions.

The best estimate of a line's reaction to Fusarium is obtained only after several location years of testing. However, it is not uncommon, particularly during preliminary screening, to have only one location of valid data.. In this circumstance, using multiple methods to quantify the variety reaction would appear to offer a better method of identifying improved lines for further screening and use in the breeding program. Beginning in 2003,we have tried to select lines for advancement using an index based on the combined response to three separate estimates of disease; FHB visual scores, grain DON content and grain mycelium content. Data analysis must be conducted with care as the results from these traits are frequently not normally distributed. DON content in particular typically fits a beta-distribution rather than a normal distribution. Correlation coefficients' between these three traits are typically in the 0.15 to 0.65 range. These moderately positive correlations show that the three traits tend to behave similarly but clearly are not equivalent, which confirms that using an index of all three traits may be more appropriate than a single evaluation method alone. This poster will examine a simulation of the ability of multiple methods of disease evaluation at a single site to predict variety performance over a range of environments by comparing the current responses of several advanced lines at the Crookston, MN evaluation nursery in 2006 with their corresponding rankings based on several prior location x years of data.

DEVELOPMENT OF SCAB RESISTANT SOFT RED WINTER WHEAT GERMPLASM USING MARKER-ASSISTED SELECTION.

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ABSTRACT

Scab of wheat, caused by *Fusarium graminearum*, is a disease that periodically strikes the US mid-Atlantic region. Breeding for resistance is an effective measure of disease control. The objective of this study was to develop scab resistant soft red winter wheat germplasm adapted to the US mid-Atlantic region using marker-assisted selection. To breed scab resistant germplasm that are adapted to the Mid-Atlantic region, a high-yielding wheat cultivar, McCormick, was used in a backcross program with the Chinese variety Ning7840. Scab resistant germplasm were bred using an accelerated backcross scheme developed to incorporate scab resistance QTLs found on chromosomes 3BS and 5A in the Chinese variety Ning7840. Two rounds of backcrossing were completed using McCormick as the female parent. Progenies from the first round of backcrossing were selected for the presence of the Ning7840 scab resistance alleles at 3BS and 5A, and then for a high background of McCormick alleles. Initially, 600 BC1F1 progenies were screened, 116 had the Ning7840 alleles at marker loci barc147 and gwm533. These loci are linked on chromosome 3BS and separated by 7.4 cM. Additionally, the 116 progenies also had the Ning7840 alleles on chromosome 5A at marker loci gwm304. All three markers showed no segregation distortion. The 116 progenies were further screened with 3BS SSR marker cfd079 and 5A SSR marker wmc705. Cfd079 was observed to be 6.2 cM from gwm533. The two marker loci on 5A, gwm304 and wmc705, were separated by 3.5 cM. Another screened marker, gwm272, was unlinked on chromosome 5DS. Furthermore, additional markers were screened to select progenies that had mostly McCormick background. Two backcross progenies had over 60% McCormick background. Using these two selected BC1F1s, 400 BC2F1s were produced in a second round of backcrossing. Additionally, the two selected BC1F1s were crossed with a wheat line with stripe rust resistance (GA96229-3A41). The BC2F1s are currently being screened with molecular markers to identify those with Ning7840 alleles (on 3BS and 5A) and most McCormick background. Selected BC2F2s populations derived from selected BC2F1 plants will be further screened with 3BS, 5AS, and 2DS markers to select those homozygous resistant (Probability: 16:1,000 for 3 loci). Additionally, we plan to derive near-isogenic lines from an F2 population to identify the effect of each QTL on scab resistance, agronomic and quality traits. We anticipate having a small amount of seed of selected BC2F3s, containing the Ning7840 alleles in the McCormick background, available for distribution to other soft red winter wheat breeders for crossing in the fall of 2008.

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EFFECT OF THE 3BS REGION OF NING 7840 ON AGRONOMIC TRAITS IN SOFT RED WINTER WHEAT.

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ABSTRACT

US Winter wheat breeders are attempting to incorporate scab resistant alleles of the Chinese cultivar Ning7840 into US wheat. The main Quantitative Trait Loci (QTL) on chromosome 3BS of the Ning7840 line that confers resistance to scab can be tracked by three Simple Sequence Repeat (SSR) markers: barc133, gwm493, and gwm533. This study was conducted to determine the effects of the 3BS region of Ning7840 on three agronomic traits: height, heading date, and powdery mildew resistance in crosses with two soft red winter wheat genotypes. In the fall of 2005, 88 F8 recombinant inbred lines of the cross Pioneer 2643/Ning7840 and 66 F8 recombinant inbred lines of the cross Pioneer 2684/Ning7840 were planted in Queenstown, MD. In the spring of 2006, the progenies were scored for heading date, plant height, and resistance to powdery mildew. Transgressive segregation was observed for all three traits, and was especially prominent in powdery mildew resistance. Seeds were set aside for DNA analysis and scored for polymorphisms for the SSR markers barc133, gwm493, and gwm533. Mapping of the SSR markers with Mapmanager software confirmed previous findings that these three markers are closely linked. For the Pioneer 2643/Ning7840 cross, gwm493 and barc133 were 11.2 cM apart and barc133 and gwm533 were 8cM apart. For the Pioneer 2684/ Ning7840 cross a distance of 10.4 cM was observed between gwm493 and barc133, and there was not enough polymorphism to map the gwm533 marker. Linear regression analysis indicated that variation in the three agronomic traits was not significantly affected by the presence of the Ning7840 alleles. Correlation analysis further indicated that the traits and the markers are unlinked. The t-tests of the mean value for each marker class and the three traits were not significant. There appears to be no linkage between the 3 SSR markers and height, heading date, or powdery mildew resistance. Thus, introducing the 3BS region of Ning7840 had no negative effect on these traits. A large number of transgressive segregants, highly resistant to powdery mildew, suggests that other unlinked alleles present on Ning7840 may be beneficial for powdery mildew resistance.

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SINGLE KERNEL SORTING TECHNOLOGY FOR ENHANCING SCAB RESISTANCE AND GRAIN QUALITY.

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ABSTRACT

We developed automated visible and near-infrared (NIR) spectroscopy procedures and instrumentation to select kernels with specific hardness, protein, and color traits to enhance the development of scab resistant hard and soft wheat varieties. The system also shows potential to sort for other characteristics such as scab damage, vomitoxin levels, ergosterol levels, vitreousness, sprout damage as measured by alpha amylase content or falling number, moisture content, selenium content, Karnal bunt-infected kernels, and waxy character. Our single kernel near-infrared system can sort single kernels based on specified properties at a rate of about one kernel/2s (500-1000g/day). We also have high-speed sorting technology that can sort visible defects at rates as high as 80,000 kernels/s (300 bu/hr). This technology is now used routinely for such applications as purifying red or white breeding lines, removing Karnal bunt-infected kernels during routine inspection for the APHIS national surveys, and selecting waxy seeds from segregating populations. While most of our work has been with wheat, we have also shown applications for proso millet, barley, rice, and sorghum. This poster will report the development of this NIR-based sorting system and our sorting accuracies.

A NOVEL APPROACH TOWARDS MOLECULAR CHARACTERIZATION AND PYRAMIDING OF NOVEL SCAB RESISTANCE SOURCES.

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ABSTRACT

Genetic studies on potentially new sources of resistance such Wangshuibai unexpectedly have not yielded novel major resistance QTL regions beside the 3BS QTL mapped in Sumai 3. These type of studies based on Recombinant Inbred Lines populations are time consuming (counting with population development, phenotypic evaluation and molecular mapping) and therefore expensive. Results from genetic diversity studies have been misleading, like in the case of Wangshuibai with no relationship with Sumai3 and completely different haplotype in the 3BS QTL region, yet containing that resistance QTL. In addition the use of unadapted germplasm as source of resistance has delayed the incorporation of resistance genes into high yielding, high quality adapted germplasm. Here, we propose the utilization of family-based genetic analysis, a 'novel' approach in plants, to study two unrelated sources of resistance (SD3942, and SD3934) adapted to the growing condition of the northern plains. This methodology will allow us to identify the genomic regions responsible for the resistance in these lines at the same time that these lines are incorporated into the HRSW breeding program at SDSU. Molecular markers identified as linked to resistance loci will be use in Marker Assisted Selection approaches expedite the development of resistance cultivars by pyramiding the resistance from SD3942 with Sumai 3 derived resistance.

The first year of the project, we will focus in adopting the procedure and the analysis of SD3942. This line has no pedigree in common with Sumai3 or Wangshuibai, yet has better resistance than Alsen or Steele-ND.

The family-based mapping approach is used frequently in human genetics, therefore the data analysis will be straight forward after adapting the methodology to wheat. This approach is based in the co transmission of marker and trait from a heterozygous parent to its progeny. The statistical test is based on a binomial distribution.

Therefore, we expect to identify the genomic region/s responsible for the resistance in SD3942, develop early generation breeding material combining this resistance source with other sources of resistance (ie. Sumai 3), and develop molecular markers linked to the resistance loci in SD3942 to aid in selection.

IS THERE VALUE IN QUANTIFYING *FUSARIUM MYCELIUM* FOR BREEDING FHB RESISTANCE?

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ABSTRACT

Previously we described a system of quantifying Fusarium Head Blight (FHB) in barley by ELISA. ELISA had lower variability (lower CV's) than visual scoring or deoxynivalenol (DON) analyses. Thus we tested ELISA, DON, and visual assessment of FHB in 1) selections from a barley doubled-haploid mapping population grown in two environments and 2) the North American barley scab evaluation nursery (NABSEN) grown at four locations. All methods of evaluation had genotype x environment interactions typically found in FHB experiments. Scattergrams of ELISA vs. DON estimates of FHB and DON vs. visual estimates of FHB suggest visual symptomology is not correlated with abundance of *Fusarium* in mature grain or the DON content following harvest. Samples low in ELISA were also low in DON. We conducted laboratory experiments to explain how environmental parameters might affect DON production by *Fusarium graminearum*. In addition we tested for abundance of the antigen specific to the monoclonal antibody used in the ELISA analysis across *Fusarium* species within the B clade (O'Donnell et al., 2004) and in mycelium grown under varying laboratory conditions. There was a temperature by osmotic potential effect on DON production in laboratory-grown cultures of *Fusarium* spp. even though growth of the fungus increased with temperature. Temperature, osmotic potential, or *Fusarium* species had no effect on abundance of antigen in mycelium of the fungi when grown *in vitro*. Therefore, ELISA is a more robust estimate of fungal infestation than FHB or DON individually, and may provide a practical alternative to dual testing for FHB and DON in plant breeding and genetic programs.

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EVALUATION OF SOFT RED WINTER WHEAT LINES FOR RESISTANCE TO MYCOTOXINS AND KERNEL INFECTION: A PROGRESS REPORT.

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OJECTIVES

The objectives of this research are to identify sources of resistance that reduce the levels of deoxynivalenol and/or nivalenol in grain, to develop techniques for efficiently selecting this type of resistance, and to determine the relationships among the different variables used to evaluate resistance to Fusarium head blight.

INTRODUCTION

Cultivars and advanced breeding lines of soft red winter wheat with resistance to Fusarium head blight (FHB) have been developed over the past ten years, but these resistant lines appear to differ in their ability to reduce the level of deoxynivalenol (DON) in the grain. Discovery in the Mid-south of *Fusarium* strains that produces nivalenol rather than DON (Gale et al. 2005) necessitates having resistance to both DON and nivalenol in wheat cultivars adapted to the Midsouth. Resistance to kernel infection and/or late-season infection may be important for achieving low levels of mycotoxins in grain.

MATERIALS AND METHODS

Thirty-five diverse lines with resistance to FHB were planted in the field in a randomized complete block design with four replications at Fayetteville, Arkansas. The experiment was inoculated with infested corn and misted daily to promote disease. Each plot was evaluated for flowering date, FHB incidence, average head severity and average plot severity. After harvest, the percentage of Fusarium-damaged kernels (FDK) was determined and level of DON in the grain was determined at Michigan State University. The percentage of kernels infected by *Fusarium graminearum* will be determined by plating 200 surface-disinfested seeds on peptone-pentachloronitrobenzene (PCNB) agar. Type II resistance (resistance to pathogen spreading in heads) was evaluated in the greenhouse on three pots per line.

RESULTS AND DISCUSSION

Of the 35 evaluated lines, a set of 12 lines (Table 1) was chosen for further evaluation based on local adaptation, level of resistance in the field and greenhouse, and diversity of resistance sources. Having similar flowering dates among lines is critical for FHB evaluations in the field, and these selected lines flowered within a 4-day period. All selected resistant lines were significantly more resistant than the susceptible check (Coker 9835) for most but not necessarily all FHB variables evaluated. Significant differences among resistant lines for some FHB variables suggest that the lines contain different genes that confer different types of resistance. Sources of FHB resistance among the selected lines include native (Freedom, Ernie, Roane, Bess), Chinese (Ning 7840, Sha 3, Ning 8026), CIMMYT (Catbird) and European (Super Zlatno) sources of resistance.

FHB incidence was the best predictor of DON level in the grain (Fig. 1A). Plot severity (Fig. 1B), FDK (Fig. 1C), and level of type II resistance (Fig 1D) were poor predictors of DON level in grain. Although Roane was significantly different from Coker 9835 for plot severity, FDK, and type II resistance, its level of DON was similar to Coker 9835. ARGE97 1047-4-2 had poor type II resistance but was among the lowest for DON level.

A greater understanding of how to select for resistance to mycotoxins is needed to develop cultivars that have low levels of mycotoxin accumulation in grain under conditions favorable for FHB. The 12 lines selected in this study appear to be suitable for identifying sources of resistance to mycotoxins, determining the relationships among different variables used to measure FHB resistance, and for developing efficient methods of selecting resistance to mycotoxins. To determine if lines resistant to DON accumulation are also resistant to nivalenol accumulation, these 12 lines will be inoculated in the greenhouse with two DON-producing isolates and two nivalenol-producing isolates. To determine if aggressive isolates capable of producing high levels of a mycotoxin can overcome resistance to mycotoxin accumulation, the DON- and nivalenol-producing isolates for the experiment will be chosen to represent low and high levels of mycotoxin production. To determine if the DON-bleached floret method is useful for selecting lines that are resistant to DON accumulation, these 12 lines will be inoculated with purified DON as described by Lemmens et al. (2005). To determine if any of these lines have resistance to late-season infection and mycotoxin accumulation, the lines will be evaluated in a separate nursery that will be inoculated and misted near physiological maturity. To determine if any of these lines have resistance to kernel infection, seed from each field experiment will be evaluated for level of kernel infection.

ACKNOWLEDGEMENTS

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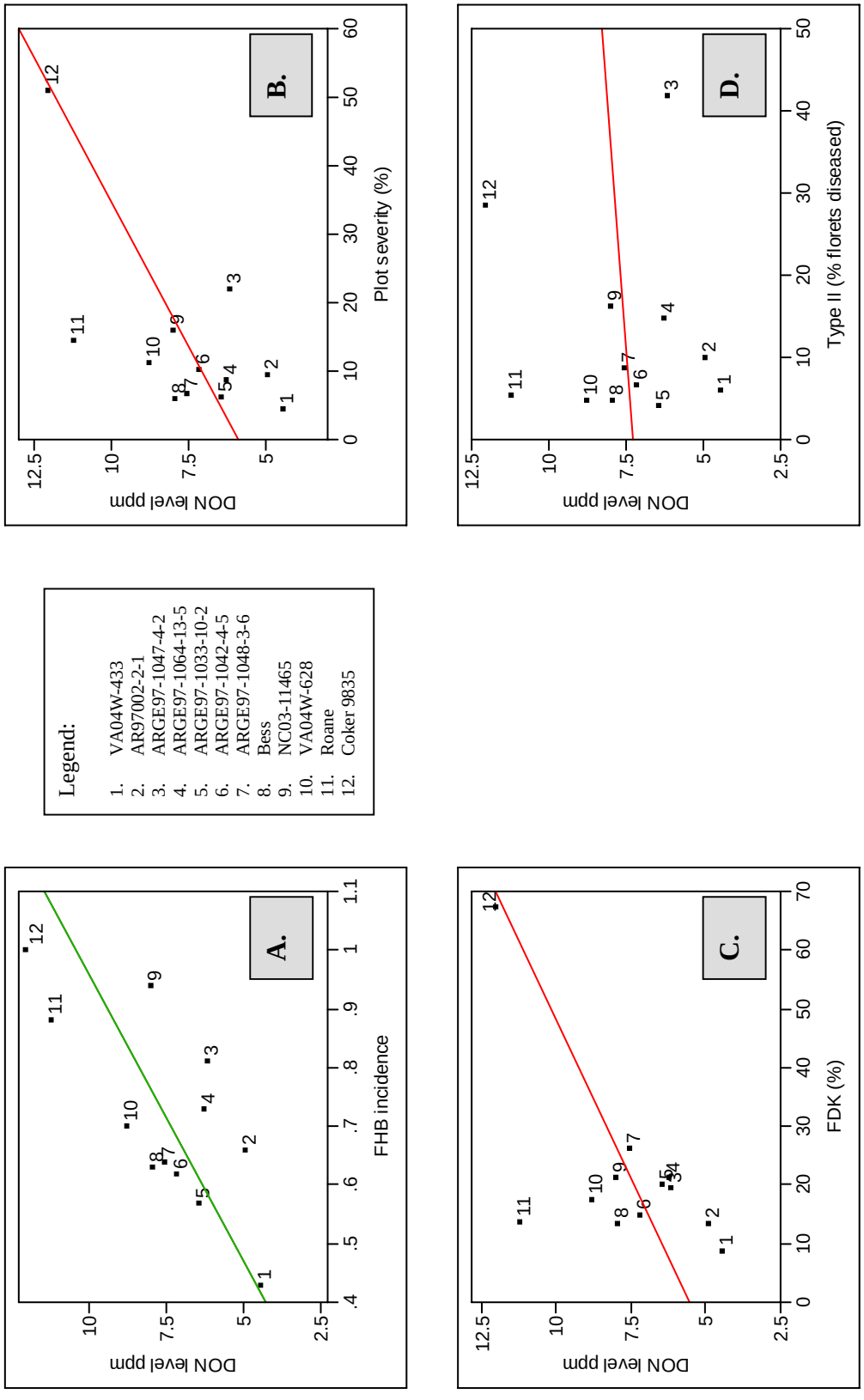

Figure 1. Relationships of DON level to other measures of Fusarium head blight resistance. A) FHB incidence, y= 10.2x + 0.2, P= 0.007, R^2= 0.54; B) Plot severity, y= 0.12x + 5.88, P= 0.019, R^2= 0.43; C) FDK, y= 0.09x + 5.53, P= 0.031, R^2= 0.39; and D) Type II resistance, y= 0.02x + 7.27, P= 0.747, R^2=0.01;

Table 1. Soft red winter wheat lines selected for further evaluation based on local adaptation, level of FHB resistance in the field and greenhouse at Fayetteville, AR, in 2006, and diversity of resistance sources.

Line	Pedigree	DON level ppm[1]	Flowering date in April[2]	FHB incidence[1]	Average head severity[1] (%)	Plot severity[1] (%)	FDK[1] (%)	Type II[3] (% florets diseased)
.04W-433	NING 7840/PION2684//96-54-244 (CK9803/FREEDOM)	4.38	11.9	0.43	9.7	4.6	8.8	6.0
.97002-2-1	AR396-4-2/NING 8026	4.88	13.4	0.66	14.0	9.6	13.5	10.0
.GE97-1047-4-2	P2643 / 3 NING 7840 // PARULA / VEERY # 6	6.13	14.5	0.81	25.2	21.9	19.5	41.8
.GE97-1064-13-5	MASON//FREEDOM/SUPER ZLATNO	6.20	14.9	0.73	12.2	8.8	21.3	14.7
.GE97-1033-10-2	FREEDOM/CATBIRD (G82)	6.38	14.8	0.57	11.3	6.3	20.0	4.2
.GE97-1042-4-5	MASON / CATBIRD	7.13	13.4	0.62	15.9	10.3	15.0	6.7
.GE97-1048-3-6	MASON // SHA 3 / CATBIRD	7.50	15.1	0.64	10.5	6.7	26.3	8.7
ss	MO 11769/Madison	7.90	14.4	0.63	8.9	5.9	13.3	4.8
03-11465	NING 7804/P2643//NC95-22426	7.93	16.1	0.94	16.9	15.9	21.3	16.2
.04W-628	ERNIE//NING7840/ERNIE	8.75	13.5	0.70	15.2	11.3	17.5	4.7
ane	VA71-54-147 (CI17449)/Coker68-15//IN65309C1-18-2-3-2	11.18	15.1	0.88	16.2	14.6	13.8	5.4
ker 9835	Susceptible check	12.00	13.8	1.00	51.1	51.1	67.5	28.6
	LSD (P= 0.05)	4.2	—	0.24	—	8.8	9.6	11.4

[1]Averaged across four replications in FHB nursery at Fayetteville.

[2]Averaged across four replications in each of two fields at Fayetteville.

[3]Averaged across 3 pots with 5 to 8 heads/pot

EVALUATION OF HARD WINTER WHEAT FOR FHB RESISTANCE IN SOUTH DAKOTA.

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ABSTRACT

South Dakota is a primary state in the US Great Plains hard winter wheat region that is threatened by Fusarium head blight (FHB) [caused by *Fusarium graminearum* Schwabe [teleomorph *Gibberella zeae* (Schwein) Petch]. A mist-irrigated field nursery consisting of 257 advanced lines, including the Northern Regional Performance Nursery (NRPN), Crop Performance Testing Variety Trial (CPT), Advanced Yield Trial (AYT), and Preliminary Yield Trial (PYT) was transplanted in May 2006 and evaluated in July 2006. The 28 CPT lines varied significantly ($P < 0.05$) for disease index (incidence percentage*severity percentage/100). Mean disease index in the CPT was 46.5%. The hard red winter wheat (HRWW) 'Darrell' had the lowest disease index (11.6%) followed by SD02279 (18.8%). On the other hand, SD01122 had the highest disease index (89.8%). Darrell was released in 2006. It has the second best FHB rating among all Great Plains HRWW varieties tested in South Dakota during the last six years, next to 'Expedition'. It ranked top for yield in the CPT in 2006 and had an exceptional three-year yield average. It had exceptional performance in the NRPN in 2003 and 2004. It has acceptable milling, good baking quality, and a good diseases package. About 3,800 head-rows and 51 Early Yield Trial (EYT) entries with tagged FHB QTL sources were planted in the '06 – '07 season. Best lines out of the head-row nursery will be included in the EYT in 2008. Resistant lines will be entered into regional nurseries to facilitate development of varieties with broad adaptation to South Dakota and the northern Great Plains.

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IDENTIFICATION OF QTLS FOR TYPE II RESISTANCE TO FHB IN THE NOVEL WHEAT GERMPLASM CJ 9306.

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OBJECTIVES

To identify the QTLs associated with Type II resistance to Fusarium head blight in the novel wheat germplasm CJ 9306.

INTRODUCTION

Fusarium head blight (FHB or scab) caused by *Fusarium* species is one of the most destructive diseases in wheat and barley worldwide. Development of resistant cultivars is the most economic, effective and environment-friendly approach to control this disease. QTL mapping and marker-assisted selection enhance the efficiency of utilizing elite germplasms and breeding resistant cultivars. CJ 9306 is a novel wheat germplasm superior to Sumai 3 in both FHB resistance and agronomic performance (Jiang et al., 2006). It was developed through multiple-parent crossing and recurrent selection combined with modified pedigree methods with the aid of a dominant male-sterile gene *Ta1* (*ms2*). The original parentage included five local superior cultivars and 15 most important resources of resistance to FHB and/or other major diseases from China and other countries (such as Sumai 3, Wangshuibai, Fanshanxiaomai, Wenzhouhongheshang, Emai 9, Zhen 7495, Ning 7840, Nobeokabuzu, Shinchunaga, Frontana, Jinzhou 1, etc.). Recurrent selection has a special advantage in accumulating multiple genes and creating desired gene combinations. Conventional genetic studies indicated that the resistance in CJ 9306 was predominantly inherited as a quantitative trait with both major and minor genes/QTLs (Jiang and Ward, 2006). Because of its excellent resistance, unique history of breeding, and complex parentage, characterization of its FHB resistance by DNA markers is very useful and significant for understanding of the underlying genetic basis and effective utilization of this novel elite germplasm.

MATERIALS AND MEHTODS

A set of 152 $F_{6:7}$ RILs derived from a wheat cross Veery/CJ 9306 and two parents were used to evaluate FHB resistance. The RILs were grown in the greenhouse at Michigan State University in a completely randomized design with two replications. For each line, six plants were planted in two pots, each having three plants per replication. The two parents were planted as the controls many times at an interval of 1 wk. The experiments were repeated three times, sown in December of 2001, January of 2002 and November of 2003, respectively, and designated as Experiment 02, 02a and 04. Single-floret inoculation was conducted immediately before or after initial anthesis. The inoculum was *F. graminearum* isolate PH-1 for Experiment 02 and 02a, and a mixture of two isolates PH-1 and WF-1 for Experiment 04. Six to eight spikes of each RIL were inoculated per replication. For each single batch of inoculation, the checks were included. The inoculated plants/pots were mist-irrigated in a misting chamber at 22-26ºC for three days. Then the pots were transferred to another greenhouse compartment. The number of scabby spikelets (NSS) on the inoculated spikes was visually counted at 5, 9, 13, 17, 21, and 25 days post-inoculation (dpi), respectively. At 25 dpi, the total spikelets were also estimated to calculate the percentage of scabby spikelets (PSS) for each observation. On the basis of PSS data, the area under disease progress curve (AUDPC) was computed.

In 2004, all the RILs and two parents were planted in greenhouse, with each having about 20 seedlings in a

pot. At Zadoks growth stage 11, the leaves were harvested and stored in a freezer at -80ºC for DNA extraction. CTAB extraction was adopted to isolate DNA. A total of about 680 SSR primer pairs were screened for polymorphism between the two parental lines. Polymorphic markers were used to genotype the mapping population with a simple and high throughput polyacrylamide gel electrophoresis system (Wang et al., 2003). The segregating data of 208 SSR markers in total were used to construct a genetic linkage map using JoinMap version 3.0 (van Oijen and Voorrips, 2001) and referring to high-density linkage maps (Shi and Ward, 2004; Somers et al., 2004).

On the basis of replication means, ANOVA was performed for single experiment and over all combination, respectively, and then broad-sense heritability on a line mean basis was estimated. QTL analysis was performed in Windows QTL Cartographer version 2.0 (Wang et al., 2001-2004), based on the genotype means. Single marker analysis (SMA), interval mapping (IM), composite interval mapping (CIM) and multiple interval mapping (MIM) were performed, respectively. A LOD value of 2.5 was set as the threshold value for declaring a QTL. The results of CIM are presented in this paper. For those QTLs/markers with a LOD value of 2.0–2.5, comparison between two groups of RILs with marker allele from Veery and CJ 9306 was conducted to verify the validation.

RESULTS AND DISCUSSION

ANOVA indicated that the differences among RILs were highly significant for both single experiment data and combined analysis over all three experiments ($P < 0.01$). The difference between environments and RIL × environment interaction were also significant

($P < 0.01$). Over all three experiments, the average AUDPC of Veery and CJ 9306 was 9.1 and 1.0, respectively. The average of AUDPC for the RIL population was 5.7 with a range of 0.8–14.2. Frequency distribution was continuous, and transgressive segregation was evident toward susceptibility (Fig. 1). The estimate of heritability in broad sense was 87.2%.

QTL analyses (CIM) indicated that four QTLs were associated with Type II resistance to FHB in CJ 9306. They all showed positive additive effects to increase the resistance (Table 1). The major QTL on 3BS explained 21–26% of phenotypic variation. The explained variation of the QTL on 2DL varied with experiments, from 9.2% to 23.1%. In comparison, the QTLs on 1AS and 7BS showed lower additive effects and explained lower variance. One QTL with negative effects on 5BL was detected by the data of Experiment 04, but not significant for other data sets. In addition, single marker analysis and group comparison of marker alleles suggested two more QTLs, which were located on 5AS and 1B, respectively. The former had positive effects on the resistance, but the latter showed negative effects (Table 2). No significant epistasis was detected.

The major QTL on 3BS has been widely validated in various investigations (Anderson et al., 2001; Mardi et al., 2005; Somers et al., 2003). In our study, comparison of alternative groups of RILs with marker alleles from Veery and CJ 9306 indicated that, on average, selection of the flanking marker Gwm533b or Gwm493 for this major QTL could lead to a decrease of 2.9 in AUDPC. Referring to NSS and PSS, the decrease was 4.0 and 22–24% (Table 2). For the markers linked to QTLs on 2DL, 1AS and 7BS, the average of RILs with allele from CJ 9306 for AUDPC, NSS and PSS was 1.8–2.1, 2.2–2.8 and 14.3–17.2% lower than that of Veery-allele RILs, respectively. The QTL on 5AS could reduce AUDPC by 1.4, or PSS by 10.3%. Chen et al. (2006) suggested that W14, a sister line of CJ 9306, had a major QTL on 5AS, especially for field resistance. In our study, its effects were smaller than the effects of most of other QTLs, and significant only for Experiment 02 and a combined analysis over all three experiments. It may be supposed that this QTL could play a more important role in Type I resistance than in Type II resistance.

In an interval (Wmc272–Barc101) on 2BL, there might be a QTL associated with FHB resistance. Based on the data of markers Barc128 and Gwm120 within this interval, for Experiment 04 and average of all three experiments, the differences in AUDPC between

Veery-allele and CJ 9306-allele RILs (1.4–2.0) were significant, although their LOD did not reach the threshold value. It is suggested that there might be some minor genes/QTLs for FHB resistance in the susceptible cultivar Veery, which are probably located on 5BL, 2BL and 1B. This may provide some underlying elaboration on the evident transgressive segregation described above, and suggest the possibility that a higher level of resistance than CJ 9306 could be achieved by pyramiding QTLs.

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DISCLAIMER

Any opinions, findings, conclusions, or recommendations expressed in this publication are those of the authors and do not necessarily reflect the view of the U.S. Department of Agriculture.

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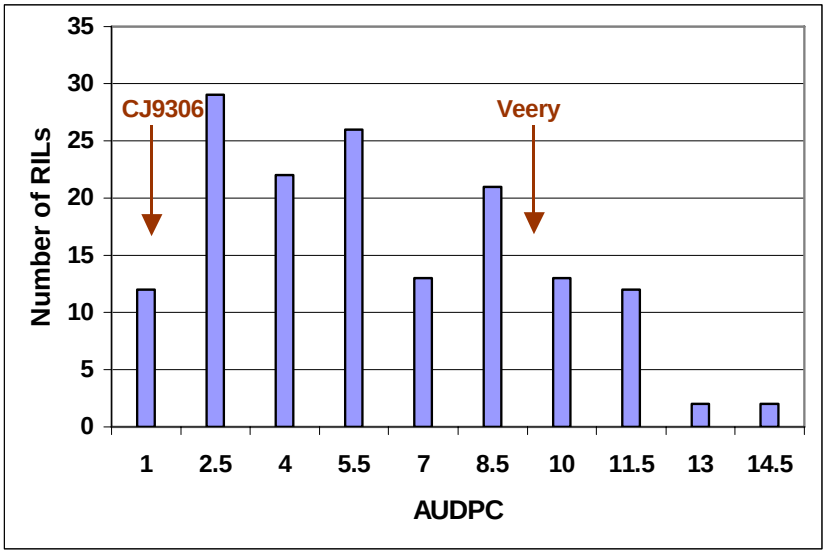

Fig. 1. Frequency distribution of 152 $F_{6:7}$ RILs derived from a wheat cross Veery/CJ 9306 for Type II resistance to FHB (AUDPC over all three experiments).

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Table 1. QTLs for Type II resistance to FHB (ADUPC) in the $F_{6:7}$ RIL population derived from the wheat cross Veery/CJ 9306 (based on CIM).

Interval	Chromosome	Region length (cM)	Experiment	LOD	Additive effects	Explained Variance (%)
Wmc291–Gwm389	3BS	40.0	2002	8.4	1.8	26.3
			2002a	7.7	1.9	20.9
			2004	11.3	2.0	25.6
			Mean overall	9.2	1.6	22.6
Gwm157–Wmc041	2DL	27.1	2002	3.0	1.0	9.2
			2002a	6.4	2.0	23.1
			2004	—	—	—
			Mean overall	3.6	1.1	10.4
Wmc024–Barc148	1AS	15.3	2002	2.6	1.0	8.4
			2002a	—	—	—
			2004	2.3	0.9	4.9
			Mean overall	3.1	1.0	8.6
Gwm400–Gwm573	7BS	29.7	2002	—	—	—
			2002a	2.7	1.2	7.8
			2004	—	—	—
			Mean overall	2.4	0.9	6.8
Barc140–Gwm371a	5BL	31.7	2004	3.3	-1.0	6.1

Table 2. Comparison of alternative SSR markers associated with Type II resistance to FHB (AUDPC) in the $F_{6:7}$ RIL population derived from the wheat cross Veery/CJ 9306 over all three experiments.

Marker	Chromosome	Veery-allele RILs		CJ 9306-allele RILs		Difference
		Number	Mean	Number	Mean	
Gmw533b	3BS	66	7.11 ± 0.42	66	4.24 ± 0.32	2.87 ****
Gwm539	2DL	82	6.58 ± 0.37	62	4.70 ± 0.38	1.87 ***
Barc148	1AS	67	6.48 ± 0.41	49	4.36 ± 0.40	2.13 ***
Gwm400	7BS	99	6.36 ± 0.33	53	4.55 ± 0.42	1.81 **
Gwm425	5AS	60	6.68 ± 0.46	71	5.29 ± 0.37	1.39 *
Barc128	2BL	45	4.54 ± 0.44	49	6.06 ± 0.47	-1.52 *
Barc1160	1B	52	4.82 ± 0.44	95	6.06 ± 0.34	-1.24 *

*, **, ***, ****: Significant at P = 5%, 1%, 0.1% and 0.01%, respectively.

FACILITATION OF INTERNATIONAL *FUSARIUM* NURSERIES AND IMPROVEMENTS OF FHB SCREENING SYSTEM AT CIMMYT.

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ABSTRACT

In March 2006 CIMMYT organized the "CIMMYT Workshop on the Global Fusarium Initiative for International Collaboration". At this workshop it was concluded that two new international spring wheat nurseries were needed for better facilitation of international exchange and evaluation of *Fusarium* relevant spring wheat materials, and the exchange of knowledge generated through the evaluation of these materials.

1. Fusarium International Elite Spring Wheat Nursery (FIESWN).

    a. The specific objective of this nursery is to enable contributors to know the performance of their entries across environments, and allow participants to identify useful sources of resistance in entries from other programs. Regional resistant and susceptible checks from each contributor are important to facilitate interpretation of the results.

    b. The nursery will include two types of entries: Elite FHB/FCR resistant spring wheats (registered or near-registered resistant cultivars) that have performed well in regional FHB/FCR nurseries; Regional FHB/FCR resistant and susceptible reference/standard checks.

2. Fusarium International Preliminary Spring Wheat Nursery (FIPSWN).

    c. The purposes of this nursery include identification of new sources of resistance, examination of stability of QTL for FHB/FCR resistance, surveillance for new and/or problematic pathogen strains, and development of knowledge or solutions in regard to other issues such as negative correlations between resistance QTL and other traits.

    d. The nursery can include: Any materials which address the objectives listed above including NILs of FHB/FCR QTL; Parents of mapping populations.

We have communicated with global communities regarding submission of entries for one or both of these Global Fusarium Initiative international spring wheat nurseries, and we are facilitating the propogation and distribution of these nurseries. The overall objective of these two nurseries is to make useful materials for Fusarium Head Blight (FHB) and Fusarium Crown Rot (FCR) available throughout the world. The current status of these nurseries will be presented.

CIMMYT has also made important changes in FHB screening methodologies for greater precision and accuracy of data collection for wheat and barley, including the relocation of the primary screening site from Toluca to El Batan, Mexico, implementation of an automated fine-misting system, and identification of new isolates for screening. An overview of these changes as well as an initial summary of results will be presented.

PLANT SIGNALING MECHANISMS ASSOCIATED WITH RESISTANCE/ SUSCEPTIBILITY TO *FUSARIUM GRAMINEARUM*.

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ABSTRACT

Fusarium graminearum is the primary agent of Fusarium head blight (FHB) disease of wheat and barley. We had previously demonstrated that constitutive expression of *Arabidopsis thaliana NPR1* gene (At*NPR1*) from the *Ubi1* promoter in transgenic wheat enhances resistance against *F. graminearum* (Makandar et al. 2006). Similarly, overexpression of At*NPR1* in arabidopsis leaves also confers enhanced resistance against *F. graminearum*. NPR1 is a key regulator of salicylic acid (SA) signaling in arabidopsis. Hence, we hypothesized that SA signaling may have a role in plant defense against *F. graminearum*. We have tested this hypothesis by monitoring SA accumulation in arabidopsis and wheat challenged with *F. graminearum*, studying the impact of SA application on growth of *F. graminearum* in arabidopsis and wheat, and monitoring *F. graminearum* growth on arabidopsis mutants deficient in SA accumulation or signaling. These studies confirm an important role of SA in plant defense against *F. graminearum*. In addition, we have also tested the involvement of ethylene and jasmonic acid (JA), two other regulators of plant defense, in plant-*F. graminearum* interaction. Our studies with ethylene and JA-insensitive arabidopsis mutants suggest that ethylene and JA signaling contribute to host susceptibility to *F. graminearum*. In addition, JA application compromises At*NPR1* expression-conferred resistance to *F. graminearum* in the *Ubi1*:At*NPR1* transgenic wheat plants. The *F. graminearum FGL1* gene, which encodes a secreted lipase, was recently shown to have a role in fungal pathogenicity (Voit et al. 2005). Our studies in arabidopsis also indicate a potential role of host lipids, or products thereof, in modulating arabidopsis-*F. graminearum* interaction.

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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.

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DIALLEL ANALYSIS OF $F_{4:5}$ POPULATIONS FOR SCAB RESISTANCE.

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ABSTRACT

Fusarium head blight (FHB), caused by *Fusarium graminearum*, is an important disease of wheat in South Dakota. This study was conducted to determine combining ability and gene effects in populations derived from mating between spring, winter and facultative wheat genotypes. Six genotypes consisting of susceptible winter wheat 'Nekota' and '2137', moderately susceptible winter wheat 'Harding', moderately resistant spring wheat 'ND2710' and 'BacUp' and resistant facultative wheat 'Ning 7840' were crossed in a partial diallel mating design. $F_{4:5}$ lines were hand transplanted in May 2006 and screened under mist-irrigated field conditions. Artificial inoculation consisted of corn spawn spread at jointing and inoculum suspension spray at flowering stages. Disease index percentage (incidence percentage * severity percentage/100) of the crosses was analyzed using Griffing's method 4 and model 1. General and specific combining abilities were highly significantl ($P < 0.01$). The result showed that both additive and non-additive gene effects were involved in the inheritance of FHB resistance. The ratio of combining ability variation components $[2\acute{o}^2_{GCA}/(2\acute{o}^2_{GCA} + \acute{o}^2_{SCA})]$ was 0.85 indicating that additive gene effects were important.

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BREEDING FOR FUSARIUM HEAD BLIGHT TOLERANCE: INCORPORATING TECHNOLOGY.

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ABSTRACT

Fusarium head blight (FHB) is an episodic disease in the hard winter wheat region of the Great Plains that is known for its diverse and highly variable climate. Fusarium head blight is most commonly found in north and eastern Nebraska, eastern South Dakota, and eastern Kansas. In eastern Nebraska, the predominant rotation is corn-soybeans, but wheat acreage is increasing as the wheat price increases, the general drought continues, and a winter annual is an important rotational crop. In west central NE, the standard rotation is wheat-corn-fallow. However, in west central Nebraska moisture is limiting and FHB rarely occurs except in irrigated production fields. Irrigated wheat is frequently sprayed with fungicide and irrigation is managed to avoid FHB. In order to ensure wheat producers have FHB tolerant varieties, the Nebraska breeding program has used over 70 sources that were previously identified as being FHB tolerant. However, many of those lines were haplotyped and contained the 3BS QTL from Sumai 3 and its derived lines. Rather than use these raw germplasm parents, a decision was made in 2005 to finish out these crosses, but in future to concentrate on using elite germplasm resources that are known to contain the 3BS QTL and often the 5AS QTL. These QTLs will be incorporated with "native" resistance that has been identified in recent releases (e.g. Husker Genetics Brand Overland (formerly NE0143)) and advanced experimental lines (e.g. NE01604, NE02584, NE03490, etc.). The majority of crosses will be relatively simple single crosses (involving elite Nebraska germplasm with the resistance QTLs by elite hard winter wheat germplasm) or three way crosses involving one to two parents with known resistance QTLs followed by marker assisted selection. However, to diversify our FHB germplasm, an alternative crossing strategy will be to cross hard spring wheat by soft winter wheat to hard winter wheat lines that all contain the 3BS QTL and where possible the 5AS QTL. Hence every progeny should minimally have the 3BS QTL and selecting with MAS is only needed for confirmation. The three-way cross will have two hard wheat parents (one soft wheat parent) and two winter wheat parents (one spring wheat parent). It will segregate for spring and winter growth habit, but the spring growth habit plants are easily killed by the Nebraska winter, leaving only winter hardy progeny. However, the population will segregate for hard and soft kernel characteristics. Using optical sorting based on near-infrared spectra, the hard and soft kernels can be readily separated so that predominantly hard kernels are retained. The advantages of using optical sorting in the F_2 or later generations are that: 1. generally large numbers of seed per population are available, 2. relatively large numbers of populations can be screened nondestructively, and 3. that other optical sorts can be run on the selected hard kernel subpopulation. The key to optical sorting is that the trait must be heritable. Preliminary research indicates that sorting for hardness and kernel color is heritable. Ideally the sorted populations could be grown in FHB inoculated fields and sorted for protein content, FHB tolerance, and possibly lower levels of DON. However the latter traits are expected to have low heritability, hence population enrichment is the expected outcome at best.

EVALUATION OF FUSARIUM HEAD BLIGHT RESISTANCE IN SOFT RED WINTER WHEAT.

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ABSTRACT

In 2006, Kentucky wheat producers harvested a record 70 bushels per acre. This made Kentucky 5th in the U.S. for wheat yield. The exceptional yield was bolstered by favorable weather conditions and low disease pressure. Only scattered fields in moderate risk areas suffered severe damage from Fusarium head blight (FHB). Epidemics were successfully created in the FHB nurseries in Lexington, KY and Princeton, KY and progressed to an adequate level for distinguishing resistant and susceptible varieties. In the Lexington FHB nursery, scabby-corn inoculum was introduced three weeks prior to heading and plots were mist-irrigated during the night and early morning. Scabby-corn inoculum was also spread in the non-irrigated Princeton FHB nursery three weeks prior to heading and plants were then treated with conidial suspensions (50,000 spores ml^{-1}) at anthesis and one week post anthesis. Detailed severity and incidence readings on select material were done only in Lexington. Readings were done 24-28 days after flowering because cool weather delayed symptom development. Material from both the Lexington and Princeton FHB nurseries was harvested and analyzed for Fusarium damaged kernels (FDK) by weight and deoxynivalenol (DON) content (ppm). Average disease severity in the Lexington FHB nursery was 41% and the ranged from 2 to 98%. Incidence ranged from 7 to 100% and the average was 38%. The range for FDK from material harvested in Lexington was 0.6 to 76% with an average of 21%. This is significantly higher ($P<0.05$) than FDK range of 0.2 to 58.8% with an average of 6.79 from Princeton FHB nursery material. DON levels were also significantly higher ($P<0.05$) in the Lexington FHB nursery, averaging 11.7 ppm, than at Princeton, where the average was 3.2 ppm. Given the variability of FHB, it is useful to have data from mulitple locations and different environmental conditions. Data from these nurseries enabled selection of breeding material for advancement or use as parents.

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THE 2005-06 UNIFORM SOUTHERN FUSARIUM HEAD BLIGHT SCREENING NURSERY.

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ABSTRACT

Phenotypic estimates of host resistance to Fusarium head blight (FHB) are greatly confounded by environmental and genotype x environment interaction effects. Thus, multiple evaluations of genotypes are necessary to determine true genetic effects. The objectives of the Uniform Southern FHB Screening Nursery are to provide breeders with a comprehensive set of resistance estimates on advanced generation breeding lines in a timely fashion, and to facilitate the sharing of the best resistant materials throughout the breeding community.

The 2005-06 nursery comprised 34 advanced generation breeding lines and two check cultivars, 'Ernie' (partially resistant) and 'Coker 9835' (susceptible). Six U.S. public programs (Univ. of Arkansas, Univ. of Georgia, Louisiana State Univ., Univ. of Maryland, N. C. State Univ., and VA Tech.), and two private companies (Syngenta, and Agripro) submitted entries. A comprehensive set of field, greenhouse and laboratory results were submitted by 11 U.S., one Romanian and one Hungarian cooperator. Copies of the full report will be available at the 2006 National Fusarium Head Blight Forum and subsequently on line at the USWBSI web site: http://www.scabusa.org/.

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Means Accross Locations 2005-06

	Cultivar/ Designation	FHB Incidence	RANK	FHB Severity	RANK	FHB Index	RANK	FDK	RANK	ISK	RANK	DON	RANK	G'hse Type II	RANK	Heading Date	RANK	Plant Height	RANK	*Fhb1* *Xcfd79* 301.5 bp	*Fhb1* *Xgwm 493* 214 bp	*Fhb1* *Xgwm533.1* 161.5 bp	*Qfhs.ifa-5A* *Xbarc 186* 227.5 bp	*Qfhs.ifa-5A* *Xgwm1304* 332.5
1	Ernie	47	7	24	9	16	9	16	1	20	2	5.7	10	26	9	116	10	33	8	.	.	.		
2	Coker 9835	80	36	50	34	43	36	52	34	58	35	9.7	28	50	19	119	26	34	13	.	.	.		
3	AR 97002-10-2	54	13	27	16	19	16	30	20	33	23	7.4	18	43	17	120	33	36	21	.	.	.		
4	AR 97002-2-1	57	19	23	5	17	11	20	8	28	12	5.4	7	14	3	116	10	33	8	X	.	.	X	X
5	AR 97007-4-1	68	31	37	27	32	29	39	26	45	29	9.6	27	50	19	118	22	35	17	.	.	.		
6	AR 97124-4-1	54	13	28	19	17	11	31	22	30	14	6.0	13	53	22	119	26	38	31	.	.	.		
7	AR 97124-4-2	55	17	30	22	19	16	26	15	31	16	7.4	18	54	25	119	26	38	31	.	.	.		
8	AR 97124-4-3	52	11	25	11	17	11	28	19	32	20	6.8	16	22	6	119	26	39	33	.	.	.		
9	ARGE97-1060-5-5	44	1	23	5	10	1	20	8	18	1	5.7	10	43	17	119	26	41	36	.	.	.		
10	ARGE97-1064-11-5	54	13	25	11	16	9	25	13	27	11	6.9	17	38	13	120	33	39	33	.	.	.		
11	B010973	45	3	25	11	12	3	20	8	24	9	5.9	12	40	15	118	22	31	1	.	.	.		
12	B011260	68	31	44	30	30	27	40	28	48	31	9.9	30	62	34	116	10	37	27	.	.	.		
13	D02-8443	58	23	33	25	22	23	39	26	38	26	9.4	26	54	25	119	26	36	21	.	.	.		
14	D02-8483	60	25	34	26	24	25	24	12	31	16	6.1	14	69	36	116	10	31	1	.	.	.		
15	D02-8486	65	28	45	31	35	30	40	28	45	29	10.4	32	61	32	114	1	33	8	.	.	.		
16	LA95135D54-2-3	76	35	47	33	40	33	51	32	56	34	14.4	36	51	21	119	26	36	21	.	.	.		
17	LA98090D34-4	54	13	24	9	19	16	25	13	26	10	7.9	21	59	29	114	1	36	21	.	.	.		
18	LA99042E-64-B	61	26	40	28	30	27	43	31	41	27	10.5	33	65	35	117	20	37	27	.	.	.		
19	MV6-82-10	57	19	32	24	23	24	31	22	32	20	5.4	7	56	27	114	1	32	4	.	.	.		
20	MV6-82-8	55	17	27	16	19	16	27	18	30	14	6.3	15	61	32	115	6	32	4	.	.	.		
21	NC03-11465	49	8	18	1	13	5	17	3	23	7	2.9	3	38	13	121	35	34	13	X	X	X		
22	NC04-27617	46	5	23	5	14	6	19	6	23	7	3.6	4	21	5	116	10	37	27	X	X	X	X	X
23	NC04-27618	44	1	23	5	15	8	17	3	22	4	2.5	1	23	7	116	10	37	27	X	X	X	X	X
24	NC04-27669	46	5	21	4	12	3	19	6	22	4	2.5	1	13	2	116	10	36	21	X	X	X	X	X
25	VA00W-38	59	24	30	22	21	21	26	15	31	16	7.9	21	11	1	118	22	33	8	X	X	.		
26	VA05W-448	61	26	28	19	21	21	22	11	31	16	5.6	9	33	12	118	22	31	1	.		.		
27	VA05W-491	53	12	26	15	17	11	26	15	28	12	7.5	20	59	29	114	1	35	17	.		.		
28	VA05W-498	50	9	18	1	14	6	16	1	20	2	4.1	5	24	8	116	10	35	17	X	X	.		
29	VA05W-500	45	3	20	3	11	2	17	3	22	4	4.7	6	16	4	115	6	34	13	X		.		
30	VA05W-633	50	9	27	16	18	15	30	20	32	20	8.4	23	60	31	117	20	36	21	.		.		
31	GA96693-4E16	66	29	42	29	35	30	36	25	42	28	10.1	31	53	24	116	10	35	17	.		.		
32	GA961171-4E21	71	33	53	36	40	33	55	36	58	35	9.2	25	29	10	114	1	32	4	.		.	X	
33	GA951231-4E26	66	29	45	31	37	32	53	35	51	33	9.8	29	40	15	115	6	33	8	.		.		
34	GA961567-4A35	71	33	51	35	41	35	51	32	50	32	10.8	34	56	27	116	10	32	4	.		.		
35	GA98401-5E23	57	19	28	19	24	25	40	28	36	25	8.9	24	53	22	115	6	34	13	X		.		
36	GA981621-5E34	57	19	25	11	19	16	31	22	33	23	13.1	35	32	11	122	36	40	35	.		.		
	Sumai 3																			X	X	X	X	X
	Mean	57		31		23		30		34		7.5		42		117		35						
	L.S.D.(0.05)	23		22		22		20		16		6.8		38		5		3						
	CV%	20		35		49.2		33.2		24.3		46.0		46.0		2.3		4.1						

INTROGRESSION AND GENETIC CHARACTERIZATION OF ALIEN FUSARIUM HEAD BLIGHT RESISTANCE IN WHEAT.

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ABSTRACT

Alien species are an important source of genetic variability in wheat (*Triticum* spp.) and carry genes for resistance to numerous pathogens, including *Fusarium graminearum* Schwabe, the causal agent of Fusarium head blight (FHB). The goal of this project was to develop breeder-friendly, FHB-resistant germplasm. Specific objectives were to identify novel sources of FHB resistance derived from relatives of wheat and transfer the resistance to adapted wheat backgrounds. Resistance to FHB was identified in four wheat-*Thinopyrum ponticum* derivatives, using the point inoculation method over three greenhouse seasons. Fluorescent genomic *in situ* hybridization indicated that the four derivatives were partial wheat-*Th. ponticum* amphiploids, each with 56 chromosomes. Conventional hybridization and use of the Ph^I system, which induces meiotic pairing and recombination between homoeologous wheat and *Th. ponticum* chromosomes, facilitated reduction of linkage drag and introgression of *Th. ponticum* chromatin into cultivated wheat. Hybridization of these amphiploids with Alsen, an FHB-resistant wheat cultivar, led to production of wheat lines with reduced amounts of *Th. ponticum* chromatin and favorable agronomic performance. Introgression lines were identified with minimal linkage drag and apparently high levels of FHB resistance. Resistance to FHB was also identified in progeny derived from hybridization of the amphiploids with Reeder, a wheat cultivar noted for FHB susceptibility. These introgression lines could provide wheat breeders access to FHB resistance genes from relatives of wheat, thus promoting development of wheat cultivars with resilient and novel resistance to this disease.

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RNA PROFILING OF SUSCEPTIBLE AND RESISTANT WHEAT VARIETIES IN THE EARLY STAGES OF FHB INFECTION.

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ABSTRACT

To gain a better understanding of the difference in response to *Fusarium graminearum* infection between susceptible and resistant varieties of wheat, gene expression profiling is being performed using the Affymetrix wheat genome array. All profiles are being compiled into a database using Acuity.

So far, we have compared the RNA profiles of three groups of wheat plants: 1) the spring wheat varieties Roblin (very susceptible), Wuhan 1 and Nuy Bay (both resistant, from Chinese and Japanese sources of resistance, respectively); 2) the spring wheat Chinese Spring (susceptible) and the introgression lines 7E and 7ES (both resistant, containing the chromosome 7 from *Thinopyrum elongatum* into Chinese Spring background); 3) the winter wheat Augusta (susceptible) and FHB148 (resistant, derived from Frontana, a Brazilian source of resistance). For group 1 and 2, florets from wheat heads at mid-anthesis were point inoculated with either *F. graminearum* spores or water (mock inoculation). Inoculated spikelets were samples after 0, 1, 2 and 4 days of infection. Two biological replicates were performed for each variety. For group 3, spray inoculation was used and sampling was done at 1, 3 and 6 days after treatment. Microarray hybridization experiments have been conducted using the wheat Affymetrix wheat genome array, comparing mock-inoculated and *Fusarium*-inoculated spikelets from the time course experiments. Northern analysis has also been performed to validate results from the microarray analysis. A preliminary analysis of the major differences observed in the response of susceptible and resistant varieties to *Fusarium* infection will be presented.

DEVELOPMENT AND CHARACTERIZATION OF A WHEAT TRANSLOCATION LINE WITH FUSARIUM HEAD BLIGHT RESISTANCE DERIVED FROM *THINOPYRUM PONTICUM*.

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ABSTRACT

A Robertsonian wheat (*Triticum aestivum*)-*Thinopyrum ponticum* translocation line KS24-2 (7DS-7EL), containing Fusarium head blight resistance QTL (*Qfhs.pur-7EL*) located on the long arm of chromosome 7E, was crossed to Chinese Spring (*ph1b*) to induce homoeologous recombination. An $F_{3:4}$ plant (275-4) was identified, by DNA marker analysis, in which the introgressed segment was reduced. The introgressed chromosome segment of 275-4 was estimated to be the distal one third of the long arm by comparison of the position of DNA markers on the wheat deletion bin map. F_5 plants from 275-4 were crossed with two wheat breeding lines with moderate Fusarium head blight resistance. Segregating populations of the two crosses were screened with DNA markers flanking *Qfhs.pur-7EL*. Analysis of variance for disease response following single-floret inoculation revealed significant differences in disease severity in different genotypes, verifying that the FHB resistance QTL was retained in the shortened chromosome segment. Transmission of the translocation segment of 275-4 was shown to be normal in female gametes, but preferentially transmitted in pollen over wheat chromosome 7D.

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DETERMINING FUSARIUM HEAD BLIGHT RESISTANCE IN SPRING MALTING BARLEY USING DON CONTENTOL OF GRAIN OVER SEVERAL YEARS.

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ABSTRACT

In 2003, researchers at the University of Minnesota Northwest Research and Outreach Center and Busch Agricultural Resources, Inc. (BARI) began collaborating yearly and have evaluated more than 1600 barley lines. Lines of experimental spring malting barley are tested for resistance to Fusarium head blight (FHB) by rating spike symptoms and measuring deoxynivalenol (DON) concentration in grain. Lines are planted into single rows in a misted, corn-spawn inoculated nursery. In 2003, 2005, and 2006, spikes were evaluated for FHB symptoms on a 0-9 scale (9 = susceptible) when symptoms were most apparent during the early dough stage (approx. Feekes 11.1 growth stage). Spikes were harvested when mature and grain samples submitted to the North Dakota State University (NDSU) DON Laboratory for analysis. Spikes were not collected in 2004 because of within field flooding. During 2005-06, both 2-row and 6-row germplasm were included in the tests. Experiments included elite lines (four or more years in yield trials) and advanced lines (two or three years in yield trials) originating from the BARI breeding program; FHB-resistant crosses from an ongoing BARI/ICARDA/CIMMYT collaboration; FHB-resistant lines directly from ICARDA/CIMMYT; as well as standard malting barley checks.

Barley lines with reduced levels of DON accumulation have been identified. Deoxynivalenol levels of 6-row germplasm ranged from 8.0 - 42.5 ppm in 2003, 0.1 - 6.6 ppm in 2005 and 2.7 – 54.6 ppm in 2006. Two rowed barley exhibited lower ranges of DON: 0.03 -2.4 ppm in 2005 and 1.0 – 22.8 ppm in 2006. These data assist in the selection and advancement of BARI advanced and elite breeding lines with reduced DON levels. A BARI/ICARDA/CIMMYT collaboration line (ADV BARI 57) continues to show lowered levels of DON and is now being used in crossing blocks with superior malting parents. Overall, this collaboration has illustrated the need for multi-year data collection and the usefulness of FHB disease nurseries for barley breeding.

CONSIDERATIONS FOR USE OF MAS IN AN APPLIED WHEAT BREEDING PROGRAM.

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ABSTRACT

Marker-assisted selection (MAS) theory focuses on improving population means while breeders are primarily interested in obtaining a new cultivar. My objective was to assess the MAS for improving quantitative traits within the context of a variety development program. A single breeding program was considered and the probability of obtaining a new cultivar was determined based on ten traits. MAS for 1 or 2 genes in early generations was considered. Given certain assumptions, MAS for one gene would require genotyping 46,496 F4 individuals to be 95% certain of releasing of a new cultivar. For two genes (two traits), 14,606 F4 individuals have to be assayed. MAS for a QTL with moderate effect did little to improve the probability of obtaining trait values required for cultivar release. Given these results, backcrossing is an attractive alternative requiring less resources and greater probability of obtaining desired quantitative trait values. Recurrent parents (RP) are often selected late in the development process such that the backcross-improved cultivar reaches commercial production five years after the RP itself. Much of this delay is due to seed increase and accelerated backcrossing has little impact while using considerable resources. A modified backcrossing scheme is proposed. Multiple RP are selected using preliminary phenotypic evaluations, backcrossing is initiated, and each backcross population is advanced or terminated based on the continued phenotypic evaluation of the RP. The backcross derived cultivar is commercially available two years after the RP, few resources are needed, and considerable genetic resources are generated.

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REPORT ON THE 2005-06 NORTHERN UNIFORM WINTER WHEAT SCAB NURSERIES.

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OBJECTIVES

This is a summary of the report on the 2005-2006 Northern Uniform Winter Wheat Scab Nursery (NUWWSN) and the Preliminary Northern Uniform Winter Wheat Scab Nursery (PNUWWSN). A full report will be available on the USWBSI web site prior to the 2006 forum. The objective of these tests is to screen winter wheat genotype adapted to the northern portion of the eastern US for scab resistance.

MATERIAL AND METHODS

The traits assessed and locations that reported data are listed in Table 1. Entries for the NUWWSN came from 14 programs while the PNUWWSN entries came from eight programs (Table 2).

RESULTS

There are eight FHB traits for each trail. Entries with means that were not significantly different than the lowest mean for six or more FHB traits are shown in Tables 3 and 4 (eg entries with at least 6 "l"s). Only two entries had DON < 2 ppm (entries 6 and 7 in the PNUWWSN, see Tables 4 and 5).

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This material is based upon work supported by the U.S. Department of Agriculture, under Agreement No. 59-0790-4-101. This is a cooperative project with the U.S. Wheat and Barley Scab Initiative. Any opinions, findings, conclusions, or recommendations expressed in this publication are those of the authors and do not necessarily reflect the view of the U.S. Department of Agriculture.

Table 1. Traits assessed in the 2005-06 PNUWWSN and NUWWSN tests

Code	Trait	Description	PNUWWSN Locations*	NUWWSN Locations*
SEV	Disease severity from field tests	% of infected spikelets in an infected head.	IL,IN1,IN2,KY,MI,MO, ON,VA	IL,IN1,IN2,KY,MD,MI,NE,NY,OH, ON, VA
INC	Disease incidence	% of heads with at least one infected spikelets	IL,IN1,IN2,KY,MI,MO, ON,VA	IL,IN1,IN2,KY,MD,MI,NE,NY,OH, ON, RO,VA
IND	Disease index	IND = (SEVxINC)/100	IL,IN1,IN2,KY,MI,MO,OH, ON,VA	IL,IN1,IN2,KS,KY,MD,MI,NE,NY, OH, ON,VA
KR	Kernel rating	A visual assessment of the percent infected kernels	IL,MO	IL,KS,MD
PSS	Percent scabby seed	Percent of scabby seed by weight	KY1,KY2	KY1,KY2,MO
ISK	Composite of head and kernel traits	ISK Index = .3 (Severity) + .3 (Incidence)+.4 (% FDK or PSS)	IL,KY,MO	IL,KY,MD,MO
DON	DON (vomitoxin)	PPM of vomitoxin in grain	IL,KY1,KY2,VA	IL,KS,KY1,KY2,MD,VA
GH	Greenhouse severity	Same as SEV except from greenhouse	IL,KY	IL,KY,MO

* ON and RO indicate Ontario Canada, and Romania, respectively

Table 2. Entries in the 2005-06 PNUWWSN and NUWWSN

NAME	**PNUWWSN** PEDIGREE
ERNIE	
TRUMAN	
FREEDOM	
PIONEER 2545	
IL00-8641	IL89-1687 // IL90-6364 / IL93-2489
IL01-16170	IL95-934 / Goldfield_
IL02-18146	Pioneer 25R26 / IL9634-24437 // IL94-1653
IL02-19463	Patton / Cardinal // IL96-2550
IL02-7735	IL94-1653 / IL96-6472
MSU E1009	MSU Line DC076/PIONEER_2555
OH01-6167	OH530/OH585/OH498/34586-20-1
OH01-7653	HOPEWELL/OH601
OH02-15978	PATTERSON/HOPEWELL
OH02-5512	OH569/OH615
OH776	OH513/OH515
P.011034A1-3	9895C1/981251E1//92145E8
P.011035A1-71	981128A1/981477A1//92145E8
P.011050A1-13	981269B1/981251E1//INW0101
P.011099A1-2	92145E8//9388A2/98133A4
P.011151B1-93	INW0101//98135C8/9672B1
MISSING	MISSING
RCAT 32/35B	Ruby/Frontana # 1/AC Ron//25R18/AC Ron
RCAT Akos2290	Zu-Rst
RCAT F13	Maringa x Akos 2196
RCAT TF174/1c	AC Ron x 25R18
VA05W-464	96W-348/P92823A1-1-4-4-5)//McCORMICK
VA05W-510	Roane / Pion 2684//OH 552
VA05W-517	Roane / Ernie//McCORMICK,F6
VA05W-673	Roane*2//W14/Roane,BC3F4
VA05W-681	Roane*2//Futai8944/Roane/3/Roane,BC3F4
M00-3904-9	89D-8096/89D*4763
M02-2152	CLEMENS//SAVANNAH/FL8643-G13-G5
M02*2518	BRADLEY/Pio2552
M03-3002	Winter/Winter FHB bulk population
KY98c-1161-03	Patterson/2540//2552
KY98c-1305-02	Shiloh/2552//2568
KY98c-1169-06	Patterson/2568//2552
KY98c-1164-04	Patterson/2540//25R26
KY98c-1470-02	VA92-51-12/Kristy//2540

NAME	**NUWWSN** PEDIGREE
ERNIE	
TRUMAN	
FREEDOM	
PIONEER 2545	
IL00-8061	P8138I1-16-5-50/Foster//IL93-2489
IL00-8109	P8138I1-16-5-50/Foster//IL93-2489
IL00-8530	IL89-1687 // IL90-6364 / IL93-2489
IL01-11445	IL87-2834-1 / IL95-678
IL01-11934	IL90-6364 / IL94-1909
MSU Line E0001	CLKS_CREAM/MSU LINE D1277
MSU Line E2017	MSU Line D3913/MSU Line D0331
MSU Line E2041	PIONEER_2555/MSU_Line D3743
MSU Line E2042	MSU Line D3743 /PIONEER_2555
MV 6-82	PIO2643/MSY*3/BALKAN//SAL
NE02465	NE95685 (=MO11785/NE87619//NE88492)
NE02584	KS92H363-2
NE03490	WI90-540W/NE93554 (=NE82419/ARAPAHOE)
NH01046	WINDSTAR
NI02425	NE94654 (ARAPAHOE 2*/ABILENE)
OH02-12678	FOSTER/HOPEWELL//OH581/OH569
OH02-12686	FOSTER/HOPEWELL//OH581/OH569
OH02-13567	OH581/IN83127E1-24-5-2-1-31//5088B-D-32-1/OH601
OH02-7217	P92118B4-2/OH561
OH904	ZM10782/FREEDOM//30584-37-2/VA91-54-219
P.0128A1-36	92829A1/Patton/3/Goldfield/X117//Roane/92145
P.0172A1-12	INW9811/Ernie//92823/Ernie/3/92829/Patton
P.0175A1-44	92807A1/92145A2//Freedom/3/INW0411
P.01931A1-5	981227A1/981518//9895/INW0304
P.01946A1-16	981477/981128//INW0304/981250A1
RCAT 202D/ 1	Freedom x Harding
RCAT 32/157	Ruby/Frontana # 1/AC Ron//25R18/AC Ron
RCAT Akos 2234	Ttj-81.F379
RCAT TF 203/2	AC Ron x 25R18
RCAT19/4c	AC Morley x 25R18
VA04W-563	Roane//FUTAI 8946/Roane,BC1F6
VA04W-592	Roane//Er-Mai 9/Roane,BC1F6
VA05W-417	ROANE/3/NING7840/CK9904//PION2552,F7
VA05W-421	ROANE/3/NING7840/CK9904//PION2552,F7
VA05W-452	IL 94-1909/SISSON"S"
M01-4377	Coker 9663/VA91-54-219
COKER 9553	89M-4035A/Pio2580
KY97c-0554-4-6	VA94-54-549/Roane//Kristy
KY97c-0540-1-2	Coker9803/L910097//2552
KY 97c-0388-5-2	2552/VA94-52-25//Pochahontas
KY97c-0304-26-10	Kristy/2628//2540
KY97c-0277-1-8	Foster/VA94-54-549//2552
KS03HW12-6-5	97HW29/97HW131//96HW100-5
KS970085-9-15	HBK0935-125-5-2/VBF0589-1//X960103
MO050101	MO11769/Madison
MO050143	MO11769/Madison
MO050132	MO11769/Madison
MO050194	MO12278/Pioneer2552
MO050207	MO11769/Madison
NY93285-9161	
NY92237-1-sp-9173	
NY94022-9093	
NY93285-9147	
NY93285-9179	

Table 3. Best entries from the 2006 NUWWSN.

ENTRY	NAME	INC	SEV	IND	KR	PSS	ISK	DON	GH	# l	# h
24	OH904	36.9 l	18.9 l	11.3 l	14.1 l	14.6 l	20.8 l	3.7 l	5.0 l	8	0
50	MO050143	45.2 l	22.0 l	11.4 l	19.0 l	9.5 l	23.7 l	6.7 l	7.2 l	8	0
13	MSU Line E2042	36.8 l	28.7 l	9.5 l	24.5 l	13.8 l	22.3 l	5.4 l	17.9	7	0
2	TRUMAN	53.7	20.5 l	12.4 l	21.5 l	5.2 l	24.1 l	6.0 l	3.3 l	7	0
21	OH02-12686	45.8 l	31.3	13.5 l	24.8 l	7.8 l	25.4 l	6.3 l	10.7 l	7	0
28	P.01931A1-5	46.4	24.0 l	13.9 l	11.8 l	4.4 l	19.3 l	3.6 l	11.9 l	7	0
33	RCAT TF 203/2	45.2 l	28.8 l	14.9 l	28.3 l	7.6 l	27.4 l	7.1 l	15.8	7	0
37	VA05W-417	46.2	26.4 l	15.3 l	26.6 l	5.5 l	22.6 l	4.9 l	12.2 l	7	0
51	MO050132	45.5 l	26.1 l	15.4 l	20.7 l	4.9 l	24.4 l	8.3	5.0 l	7	0
5	IL00-8061	44.1 l	25.7 l	15.6 l	14.4 l	5.9 l	21.4 l	5.0 l	14.7	7	0
25	P.0128A1-36	45.2 l	23.8 l	16.2 l	13.2 l	5.8 l	20.1 l	4.0 l	14.7	7	0
35	VA04W-563	50.8	26.9 l	16.5 l	13.4 l	4.2 l	20.3 l	3.3 l	10.8 l	7	0
23	OH02-7217	45.2 l	18.7 l	10.2 l	27.2 l	6.3 l	24.3 l	8.9	19.6	6	0
55	NY92237-1-sp-9173	43.0 l	22.6 l	12.7 l	26.2 l	4.8 l	26.2 l	7.3	22.1	6	0
27	P.0175A1-44	54.5	20.0 l	14.1 l	28.0 l	13.4 l	32.6	6.7 l	3.6 l	6	0
38	VA05W-421	49.2	29.0 l	15.6 l	26.6 l	4.3 l	25.8 l	6.4 l	19.5	6	0
20	OH02-12678	49.8	25.5 l	16.2 l	22.7 l	10.2 l	25.1 l	5.2 l	20.3	6	0
8	IL01-11445	46.5	30.8	16.6 l	19.8 l	1.9 l	25.9 l	6.1 l	13.4 l	6	0
52	MO050194	48.7	26.6 l	17.0 l	27.1 l	14.8 l	30.4 l	7.3	11.9 l	6	0
53	MO050207	47.3	27.2 l	17.2 l	26.3 l	5.8 l	29.9 l	8.6	7.3 l	6	0
36	VA04W-592	52.8	27.0 l	18.2	26.1 l	5.7 l	29.8 l	6.3 l	13.3 l	6	0
1	ERNIE	33.6 l	30.0 l	20.2	19.1 l	4.7 l	25.4 l	7.2 l	24.3	6	0
29	P.01946A1-16	52.3	28.6 l	22.5	25.1 l	10.6 l	30.9 l	5.9 l	7.5 l	6	0
	AVERAGE	49.6	29.0	17.4	26.2	10.8	29.5	7.1	18.9		
	# LOCATIONS	12	13	13	3	3	4	6	3		
	LSD	12.5	11.5	8.5	16.6	19.0	12.7	3.9	10.1		
	R2	0.8	0.7	0.8	0.9	0.5	0.9	0.8	0.6		
	CV	29.0	45.9	58.1	34.5	90.2	27.8	45.9	62.1		

l,h indicate a mean that is not significantly different than the lowest (l) or highest (h) mean in that column

Table 4. Best entries from the 2006 PNUWWSN.

Entry	Name	INC	SEV	IND	KR	PSS	ISK	DON	GH	# l	# h
2	TRUMAN	42.5 l	21.1 l	7.1 l	6.5 l	4.8 l	19.9 l	2.2 l	13.7 l	8	0
9	IL02-7735	40.9 l	24.5 l	9.4 l	5.0 l	1.9 l	13.6 l	2.3 l	39.8 l	8	0
38	KY98c-1164-04	44.3 l	24.3 l	11.1 l	22.5 lh	3.2 l	23.6 l	5.6 l	13.5 l	8	1
29	VA05W-673	52.3 l	25.3 l	12.5 l	7.0 l	4.5 l	17.5 l	2.8 l	2.9 l	8	0
18	P.011050A1-13	53.3 lh	23.8 l	13.1 l	11.0 l	5.0 l	17.5 l	3.9 l	12.9 l	8	1
16	P.011034A1-3	48.2 l	30.3 l	13.4 l	24.0 lh	4.9 l	21.1 l	3.2 l	36.4 l	8	1
7	IL02-18146	45.2 l	26.1 l	13.5 l	7.5 l	4.6 l	15.5 l	1.7 l	18.0 l	8	0
5	IL00-8641	51.6 l	23.8 l	13.7 l	8.0 l	8.6 l	18.6 l	4.3 l	24.6 l	8	0
1	ERNIE	50.3 l	23.0 l	14.6 l	12.5 l	3.4 l	20.3 l	5.2 l	26.5 l	8	0
25	RCAT TF174/1c	42.5 l	20.4 l	9.1 l	10.5 l	21.3	22.6 l	4.8 l	8.1 l	7	0
23	RCAT Akos2290	50.5 l	23.5 l	10.1 l	24.0 lh	23.8 h	27.7 lh	4.4 l	9.1 l	7	3
14	OH02-5512	56.5 h	23.0 l	13.1 l	16.5 l	8.3 l	22.2 l	3.4 l	12.0 l	7	1
6	IL01-16170	51.3 l	36.7 h	13.7 l	8.5 l	7.2 l	21.3 l	1.9 l	7.7 l	7	1
28	VA05W-517	52.1 l	23.4 l	14.5 l	20.0 l	2.8 l	22.8 l	3.0 l	47.3 h	7	1
3	FREEDOM	54.3 lh	34.5 lh	14.8 l	24.0 lh	7.2 l	29.2 h	4.5 l	14.4 l	7	4
30	VA05W-681	56.0 h	26.6 l	15.0 l	13.5 l	4.5 l	22.2 l	3.0 l	5.3 l	7	1
19	P.011099A1-2	51.7 l	31.6 l	15.9	17.5 l	2.6 l	22.7 l	3.0 l	26.5 l	7	0
8	IL02-19463	52.5 l	30.1 l	17.3	18.5 l	4.1 l	28.5 lh	4.7 l	32.0 l	7	1
37	KY98c-1169-06	57.0 h	22.4 l	13.2 l	21.0 l	3.4 l	24.0 l	7.4 h	32.6 l	6	2
17	P.011035A1-71	55.3 h	27.9 l	15.7	22.5 lh	9.9 l	22.2 l	4.1 l	26.1 l	6	2
	AVERAGE	54.8	31.3	16.7	22.7	8.9	26.6	5.0	29.4		
	# LOCATIONS	8	8	9	2	2	3	4	2		
	LSD	13.6	14.8	7.9	24.0	15.5	15.5	4.3	37.1		
	R2	0.8	0.5	0.7	0.8	0.7	0.9	0.7	0.7		
	CV	24.4	47.0	49.4	52.2	88.2	35.2	59.6	58.9		

l,h indicate a mean that is not significantly different than the lowest (l) or highest (h) mean in that column

Table 5. Summary of results of the 2005-2006 PNUWWSN

Ent	Name	INC		SEV		IND		KR		PSS		ISK		DON		GH		# l	# h
1	ERNIE (MR)	50.3	l	23.0	l	14.6	l	12.5	l	3.4	l	20.3	l	5.2	l	26.5	l	8	0
2	TRUMAN (R)	42.5	l	21.1	l	7.1	l	6.5	l	4.8	l	19.9	l	2.2	l	13.7	l	8	0
3	FREEDOM (MR)	54.3	lh	34.5	lh	14.8	l	24.0	lh	7.2	l	29.2	h	4.5	l	14.4	l	7	4
4	PION. 2545 (S)	62.8	h	46.8	h	27.7	h	46.5	h	15.4	l	38.8	h	8.9	h	58.4	h	1	7
5	IL00-8641	51.6	l	23.8	l	13.7	l	8.0	l	8.6	l	18.6	l	4.3	l	24.6	l	8	0
6	IL01-16170	51.3	l	36.7	h	13.7	l	8.5	l	7.2	l	21.3	l	1.9	l	7.7	l	7	1
7	IL02-18146	45.2	l	26.1	l	13.5	l	7.5	l	4.6	l	15.5	l	1.7	l	18.0	l	8	0
8	IL02-19463	52.5	l	30.1	l	17.3		18.5	l	4.1	l	28.5	lh	4.7	l	32.0	l	7	1
9	IL02-7735	40.9	l	24.5	l	9.4	l	5.0	l	1.9	l	13.6	l	2.3	l	39.8	l	8	0
10	MSU E1009	62.9	h	38.6	h	21.7	h	36.0	h	7.7	l	33.2	h	6.4	h	18.1	l	2	6
11	OH01-6167	52.4	l	36.9	h	16.6		20.0	l	11.5	l	30.4	h	5.6	l	52.3	h	4	3
12	OH01-7653	57.5	h	43.1	h	18.9		35.5	h	8.0	l	30.2	h	6.5	h	58.1	h	1	6
13	OH02-15978	56.3	h	35.1	lh	19.8	h	28.0	lh	13.7	l	30.5	h	5.8	l	47.7	h	4	6
14	OH02-5512	56.5	h	23.0	l	13.1	l	16.5	l	8.3	l	22.2	l	3.4	l	12.0	l	7	1
15	OH776	58.6	h	46.9	h	24.0	h	36.5	h	7.1	l	33.1	h	10.7	h	64.8	h	1	7
16	P.011034A1-3	48.2	l	30.3	l	13.4	l	24.0	lh	4.9	l	21.1	l	3.2	l	36.4	l	8	1
17	P.011035A1-71	55.3	h	27.9	l	15.7		22.5	lh	9.9	l	22.2	l	4.1	l	26.1	l	6	2
18	P.011050A1-13	53.3	lh	23.8	l	13.1	l	11.0	l	5.0	l	17.5	l	3.9	l	12.9	l	8	1
19	P.011099A1-2	51.7	l	31.6	l	15.9		17.5	l	2.6	l	22.7	l	3.0	l	26.5	l	7	0
20	P.011151B1-93	54.3	lh	26.5	l	16.8		18.0	l	2.4	l	21.8	l	7.2	h	45.7	h	5	3
22	RCAT 32/35B	66.9	h	39.6	h	25.4	h	26.5	lh	8.9	l	30.6	h	6.4	h	35.2	l	3	6
23	RCAT Akos2290	50.5	l	23.5	l	10.1	l	24.0	lh	23.8	h	27.7	lh	4.4	l	9.1	l	7	3
24	RCAT F13	63.2	h	29.4	l	20.1	h	40.0	h	38.5	h	43.2	h	7.3	h	23.0	l	2	6
25	RCAT TF174/1c	42.5	l	20.4	l	9.1	l	10.5	l	21.3		22.6	l	4.8	l	8.1	l	7	0
26	VA05W-464	65.9	h	29.9	l	21.9	h	22.5	lh	7.1	l	30.8	h	4.1	l	14.8	l	4	3
27	VA05W-510	61.5	h	33.4	lh	19.9	h	24.5	lh	9.8	l	28.6	lh	3.2	l	48.6	h	5	6
28	VA05W-517	52.1	l	23.4	l	14.5	l	20.0	l	2.8	l	22.8	l	3.0	l	47.3	h	7	1
29	VA05W-673	52.3	l	25.3	l	12.5	l	7.0	l	4.5	l	17.5	l	2.8	l	2.9	l	8	0
30	VA05W-681	56.0	h	26.6	l	15.0	l	13.5	l	4.5	l	22.2	l	3.0	l	5.3	l	7	1
31	M00-3904-9	62.7	h	39.6	h	23.3	h	33.5	h	4.8	l	32.9	h	7.2	h	34.2	l	2	6
32	M02-2152	56.1	h	39.0	h	21.6	h	40.5	h	12.1	l	35.5	h	7.6	h	60.2	h	1	7
33	M02*2518	63.7	h	32.9	lh	19.9	h	26.0	lh	7.1	l	31.7	h	6.8	h	17.8	l	4	6
34	M03-3002	58.2	h	34.4	lh	16.8		27.5	lh	14.5	l	35.2	h	6.0	l	15.6	l	5	4
35	KY98c-1161-03	58.0	h	37.1	h	19.0		24.0	lh	2.8	l	26.7	l	7.4	h	80.2	h	3	5
36	KY98c-1305-02	66.3	h	43.7	h	26.8	h	40.0	h	10.0	l	38.3	h	6.9	h	35.3	l	2	6
37	KY98c-1169-06	57.0	h	22.4	l	13.2	l	21.0	l	3.4	l	24.0	l	7.4	h	32.6	l	6	2
38	KY98c-1164-04	44.3	l	24.3	l	11.1	l	22.5	lh	3.2	l	23.6	l	5.6	l	13.5	l	8	1
39	KY98c-1470-02	61.1	h	42.4	h	21.4	h	36.5	h	15.5	l	38.3	h	6.4	h	60.4	h	1	7
	AVERAGE	55.2		31.5		16.9		22.7		8.8		26.9		5.2		31.0			
	# LOCATIONS	8		8		9		2		2		3		4		2			
	LSD	13.6		14.8		7.9		24.0		15.5		15.5		4.3		37.1			
	R2	0.8		0.5		0.7		0.8		0.7		0.9		0.7		0.7			
	CV	24.4		47.0		49.4		52.2		88.2		35.2		59.6		58.9			

l,h indicate a mean that is not significantly different than the lowest (l) or highest (h) mean in that column

Table 6. Summary of results of the 2005-2006 NUWWSN

ENT	NAME	INC		SEV		IND		KR		PSS		ISK		DON		GH		# l	# h
1	ERNIE (MR)	53.7		30.0	l	20.2		19.1	l	4.7	l	25.4	l	7.2	l	24.3		5	0
2	TRUMAN (R)	33.6	l	20.5	l	12.4	l	21.5	l	5.2	l	24.1	l	6.0	l	3.3	l	8	0
3	FREEDOM (MR)	55.0		29.0	l	16.4	l	35.7		17.5	l	38.4		8.8		13.3	l	4	0
4	PION. 2545 (S)	67.4	h	47.8	h	31.9	h	52.5	h	42.1	h	57.9	h	12.9	h	38.2		0	7
5	IL00-8061	44.1	l	25.7	l	15.6	l	14.4	l	5.9	l	21.4	l	5.0	l	14.7		7	0
6	IL00-8109	53.8		33.6		19.7		22.8	l	15.0	l	29.9	l	4.4	l	24.1		4	0
7	IL00-8530	55.3		33.6		22.3		15.8	l	6.7	l	27.8	l	6.1	l	22.0		4	0
8	IL01-11445	46.5		30.8		16.6	l	19.8	l	1.9	l	25.9	l	6.1	l	13.4	l	6	0
9	IL01-11934	52.7		27.7	l	18.5		20.3	l	14.5	l	25.4	l	5.1	l	17.5		5	0
10	MSU Line E0001	47.5		32.2		12.3	l	36.3	h	11.0	l	36.1		9.0		49.1	h	2	2
11	MSU Line E2017	53.3		35.4		17.3	l	35.3		7.9	l	33.1		8.4		30.3		2	0
12	MSU Line E2041	66.7	h	39.0	h	25.7	h	40.5	h	23.0		46.4	h	12.2	h	39.1		0	6
13	MSU Line E2042	36.8	l	28.7	l	9.5	l	24.5	l	13.8	l	22.3	l	5.4	l	17.9		7	0
14	MV 6-82	65.4	h	48.2	h	31.7	h	36.6	h	7.8	l	40.8		5.6	l	51.3	h	2	5
15	NE02465	60.4	h	45.1	h	26.5	h	34.6		24.2	h	43.6		9.1		48.0		0	4
16	NE02584	57.6		33.0		19.7		47.1	h	23.7	h	44.6		8.3		47.6		0	2
17	NE03490	53.6		31.7		15.6	l	34.0		17.9	l	35.0		12.7	h	30.0		2	1
18	NH01046	47.9		36.5		16.6	l	23.5	l	22.8		34.3		9.4		38.4		2	0
19	NI02425	57.5		42.7	h	23.8	h	44.6	h	25.0	h	44.0		8.2		40.8		0	4
20	OH02-12678	49.8		25.5	l	16.2	l	22.7	l	10.2	l	25.1	l	5.2	l	20.3		6	0
21	OH02-12686	45.8	l	31.3		13.5	l	24.8	l	7.8	l	25.4	l	6.3	l	10.7	l	7	0
22	OH02-13567	48.9		25.4	l	14.2	l	27.3	l	4.6	l	27.7	l	7.5		14.6		5	0
23	OH02-7217	45.2	l	18.7	l	10.2	l	27.2	l	6.3	l	24.3	l	8.9		19.6		6	0
24	OH904	36.9	l	18.9	l	11.3	l	14.1	l	14.6	l	20.8	l	3.7	l	5.0	l	8	0
25	P.0128A1-36	45.2	l	23.8	l	16.2	l	13.2	l	5.8	l	20.1	l	4.0	l	14.7		7	0
26	P.0172A1-12	54.0		32.6		21.3		15.8	l	12.0	l	31.1	l	3.7	l	12.5	l	5	0
27	P.0175A1-44	54.5		20.0	l	14.1	l	28.0	l	13.4	l	32.6		6.7	l	3.6	l	6	0
28	P.01931A1-5	46.4		24.0	l	13.9	l	11.8	l	4.4	l	19.3	l	3.6	l	11.9	l	7	0
29	P.01946A1-16	52.3		28.6	l	22.5		25.1	l	10.6	l	30.9	l	5.9	l	7.5	l	6	0
30	RCAT 202D/ 1	61.7	h	37.1		21.3		45.8	h	13.1	l	42.5		8.9		22.5		1	2
31	RCAT 32/157	49.9		33.1		14.7	l	23.6	l	16.0	l	31.6	l	9.5		55.0	h	4	1
32	RCAT Akos2234	46.8		32.6		15.9	l	29.9		21.6		28.2	l	6.4	l	21.5		3	0
33	RCAT TF 203/2	45.2	l	28.8	l	14.9	l	28.3	l	7.6	l	27.4	l	7.1	l	15.8		7	0
34	RCAT19/4c	47.0		33.0		14.8	l	30.0		27.6	h	31.0	l	6.6	l	45.5		3	1
35	VA04W-563	50.8		26.9	l	16.5	l	13.4	l	4.2	l	20.3	l	3.3	l	10.8	l	7	0
36	VA04W-592	52.8		27.0	l	18.2		26.1	l	5.7	l	29.8	l	6.3	l	13.3	l	6	0
37	VA05W-417	46.2		26.4	l	15.3	l	26.6	l	5.5	l	22.6	l	4.9	l	12.2	l	7	0
38	VA05W-421	49.2		29.0	l	15.6	l	26.6	l	4.3	l	25.8	l	6.4	l	19.5		6	0
39	VA05W-452	63.1	h	37.6		23.8	h	33.4		7.1	l	36.4		7.3		46.5		1	2
40	M01-4377	57.0		37.3		22.9		31.2		4.7	l	33.8		6.2	l	12.2	l	3	0
41	COKER 9553	64.5	h	41.4	h	29.7	h	44.8	h	9.0	l	41.4		10.4		50.5	h	1	5
42	KY97c-0554-4-6	64.2	h	33.5		22.0		23.7	l	15.6	l	33.8		5.7	l	12.5	l	4	1
43	KY97c-0540-1-2	67.6	h	35.7		23.6	h	38.1	h	10.5	l	42.2		8.4		34.6		1	3
44	KY97c-0388-5-2	67.5	h	44.4	h	30.4	h	34.1		27.2	h	46.9	h	9.0		58.6	h	0	6
45	KY97c-0304-26-10	63.0	h	42.4	h	23.5	h	48.4	h	18.0	l	47.5	h	8.6		56.1	h	1	6
46	KY97c-0277-1-8	64.9	h	38.0		25.8	h	36.3	h	23.8	h	46.1	h	8.9		22.0		0	5
47	KS03HW12-6-5	56.5		25.3	l	16.3	l	33.1		17.6	l	36.3		12.2	h	28.6		3	1
48	KS970085-9-15	70.3	h	43.7	h	30.7	h	41.0	h	17.6	l	43.4		8.5		24.1		1	4
49	MO050101	54.9		30.3		21.2		23.4	l	10.3	l	32.2		6.9	l	9.8	l	4	0
50	MO050143	45.2	l	22.0	l	11.4	l	19.0	l	9.5	l	23.7	l	6.7	l	7.2	l	8	0
51	MO050132	45.5	l	26.1	l	15.4	l	20.7	l	4.9	l	24.4	l	8.3		5.0	l	7	0
52	MO050194	48.7		26.6	l	17.0	l	27.1	l	14.8	l	30.4	l	7.3		11.9	l	6	0
53	MO050207	47.3		27.2	l	17.2	l	26.3	l	5.8	l	29.9	l	8.6		7.3	l	6	0
54	NY93285-9161	39.7	l	31.1		12.5	l	29.7		17.9	l	27.5	l	6.5	l	31.2		5	0
55	NY92237-1-sp-9173	43.0	l	22.6	l	12.7	l	26.2	l	4.8	l	26.2	l	7.3		22.1		6	0
56	NY94022-9093	59.4	h	49.7	h	28.3	h	52.5	h	19.9	l	48.4	h	16.1	h	44.4		1	6
57	NY93285-9147	40.3	l	33.9		12.6	l	37.6	h	14.6	l	30.7	l	6.7	l	27.1		5	1
58	NY93285-9179	39.3	l	36.9		14.1	l	39.2	h	10.3	l	29.4	l	6.7	l	30.7		5	1
	AVERAGE	52.4		32.1		18.7		29.4		12.9		32.5		7.4		24.9			
	# LOCATIONS	12		13		13		3		3		4		6		3			
	LSD	12.5		11.5		8.5		16.6		19.0		12.7		3.9		10.1			

PLANT BREEDING AND VARIETY DEVELOPMENT: A VITAL CAPACITY FOR U.S. NATIONAL GOALS.

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ABSTRACT

Investment in plant breeding in the U.S. is declining in the public and private sector. Many university plant breeding education programs are at risk. A factual and compelling response is needed. Significant efforts have been made; for example, the National Plant Breeding Study (NPBS) of the 1990's. However, the NPBS relied on intensive time and energy of a few individuals, who eventually were unable to continue. As a result, NPBS recommendations have seen little follow-up. Follow-up from subsequent efforts, such as the 2005 plant breeding education workshop organized by Michigan State University, faces the same risk. A sustainable effort to respond to the decline in plant breeding investment requires a means whereby multiple individuals can distribute and coordinate effort over time. To meet this need, the Plant Breeding Coordinating Committee (CC) is being established. The CC will serve as a long-term forum for leadership regarding issues, problems, and opportunities of strategic importance to the public- and private-sector U.S. national plant breeding effort. It will be the first and only regular opportunity for U.S. plant breeders from all crops and sectors to coordinate their leadership efforts. It will allow plant breeders to develop 'indigenous' leadership on strategic issues, learn from experience, and build alliances across the general society. As an initial approach, the CC will analyze the role of plant breeding in achieving widely-popular national goals:

- Excellence in science and technology.
- A competitive agricultural system in the global economy
- Competitiveness, sustainability, & quality of life in rural America
- A safe and secure food and fiber system
- A healthy, well-nourished population
- Harmony between agriculture and the environment

The work of the CC will enable plant breeders to make the value of their work more visible to the non-technical public, leading to positive outcomes for the future of plant breeding. (The start-up workshop for the Plant Breeding CC will take place in Raleigh, NC, on Feb 8-9, 2007; www.plantbreedingworkshop.ncsu.edu).

QTLS FOR THREE TYPES OF RESISTANCE TO FUSARIUM HEAD BLIGHT IN A WHEAT POPULATION OF WANGSHUIBAI/WHEATON.

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ABSTRACT

Fusarium head blight (FHB), caused by *Fusarium graminearum*, can significantly reduce both grain yield and quality of wheat. Growing FHB resistant cultivars is an effective means to reduce the losses caused by the disease. Currently used FHB resistance sources are mainly 'Sumai 3' and its derivatives. Use of FHB resistance sources other than 'Sumai 3' may enrich the genetic diversity of FHB resistance sources. 'Wangshuibai' is a FHB-resistant Chinese landrace unrelated to 'Sumai 3'. To map quantitative trait loci (QTLs) for resistance to initial infection (type I), FHB symptom spread within a spike (type II), and deoxynivalenol accumulation in infected grain (type III), 139 F_6 derived recombinant inbred lines (RILs) were developed from a cross between 'Wangshuibai' and an FHB-susceptible cultivar, 'Wheaton'. More than 1300 simple sequence repeat (SSR) and amplified fragment length polymorphism (AFLP) markers were analyzed in this population. Five QTLs for type I resistance were detected, on chromosomes 3BS, 4B, 5DL, 3AS, and 5AS; seven QTLs for type II resistance were located, on chromosomes 3BS, 1A, 5AS, 5DL, 7AL, and 3DL; and seven QTLs for low DON content were detected, on chromosomes 3BS, 5AS, 1A, 5DL, 1BL, and 7AL. These QTLs jointly explained up to 31.7%, 64%, and 52.8% of the phenotypic variation for the three types of FHB resistance, respectively. The QTLs on the distal end of 3BS, 5AS and 5DL contributed to all three types of resistance. Two QTLs, on 7AL and 1A, as well as one QTL near the centromere of 3BS (3BSc) showed effects on both resistance type II and III. The broad-sense heritabilities were low for type I resistance (0.36), but high for type II resistance (0.75), and type III (0.71). The result suggested that selection for type II resistance may simultaneously improve type I resistance and reduce DON content as well. The QTLs for FHB resistance identified in 'Wangshuibai' have potential to be used to enhance FHB resistance by pyramiding FHB resistance QTLs from different sources.

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GRAIN SHATTERING AND FHB-RESISTANCE QTLS LINKAGE IN WHEAT.

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ABSTRACT

Grain shattering can cause substantial loss in wheat (*Triticum eastivum* L.). Recently, the grain shattering problem has resurfaced with the introduction of Fusarium head blight (FHB, caused by *Fusarium graminearum* Schwabe) resistant germplasm, 'Sumai3', a susceptible wheat genotype to grain shattering. This study was designed to elucidate the relationship between grain shattering and FHB resistance based on mapping quantitative trait loci (QTL) governing resistance to the two traits. A recombinant inbred line population was developed from the cross 'Sumai3' (PI 481542)/'Stoa'(PI 520297) by single seed descent method was used to achieve the objectives of this study. Stoa, a hard red spring wheat cultivar released by North Dakota State University, is resistant to shattering but susceptible to FHB. The RILs and their parents were evaluated fro grain shattering across four North Dakota (ND) environments in 2004 and 2005. Similarly, the same material was evaluated for FHB reaction in the hard red spring wheat (HRSW) breeding scab nursery at Prosper, ND in 2004, and 2005. In order to detect QTL's for grain shattering, ten most resistant and ten most susceptible lines for grain shattering were used. Simple interval mapping analysis of the grain shattering data showed that two QTL's on chromosomes 7A and two on chromosomes 3B are involved in grain shattering. On the other hand, four QTL's were detected on chromosomes, 7A, 3B, and 2B for FHB. Among the QTL for grain shattering on chromosome 7A, one is 7.6 cM away from the one FHB QTL. Similarly, one QTL for grain shattering on chromosome 3B was located 1.5 cM away from a FHB QTL. These close positions between QTL's of grain shattering and resistance to FHB confirm the linkage between the two traits observed by breeders within the populations involving Sumai3 FHB source of resistance. However, based on the distance observed between these QTL's, the linkage can be broken if appropriate breeding method are applied. The HRSW breeding program at North Dakota State University and many other wheat breeding programs were successful to break this undesirable linkage by releasing cultivar/germplasm with resistance to both traits.

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MOLECULAR MARKER CHARACTERIZATION OF FUSARIUM HEAD BLIGHT RESISTANT GERMPLASM.

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ABSTRACT

Molecular markers linked to Fusarium head blight (FHB) resistance QTLs have been identified in the wheat genome. Marker-QTLs linkages validated in different genetic backgrounds or by different research groups can be used to postulate the presence of resistant alleles in other germplasm. The objective of this research was to postulate the presence of 3 FHB QTLs in FHB resistant germplasm using DNA markers. One hundred and sixty eight wheat lines from the USDA spring wheat germplasm collection which had moderate to high levels of FHB resistance based on field visual disease levels, visual scab kernel, and DON levels were used in this study. Marker allele type was determined for *Fhb1* (using marker STS3B-256) from Sumai 3 on chromosome 3BS; *Qfhs.ndsu-3AS* (dupw227) from Frontana; and *Qfhs.ifa-5A* (barc186) from Wuhan 3 and Sumai 3. Thirty-two accessions displayed Sumai 3 type of *Fhb1* allele of marker *STS3B-256* (Table 1). All the FHB resistance germplasm originating from Japan, except PI 81791, had the *Fhb1* allele. The second largest group of *Fhb1* Sumai 3 haplotype was from South America. Only five FHB resistant European lines and one Chinese line had the *Fhb1* haplotype. The one Chinese line with *Fhb1* was a modern cultivar. The Chinese lines without *Fhb1* were landraces originated from a spring wheat production region different from where Sumai 3 was grown, which explains the low frequency of *Fhb1* haplotype in this set of Chinese materials. Twenty-four accessions had the Frontana *dupw227* haplotype. Twelve accessions with the Frontana haplotype in the Chinese germplasm were landraces. Only four lines with the Frontana *dupw227* haplotype were of European origin, and the others were from South America. Seventeen accessions from Europe and 11 from South America displayed Wuhan 3 and Sumai 3 type of *Qfhs.ifa-5A* QTL allele using *barc186.* This allele was most common in the Japanese FHB resistant germplasm. About half of the accessions did not display any of the known QTL alleles indicating that they may have novel FHB resistance alleles. There are bound to be false positives and negatives with these data, especially dupw227 and barc186 markers, because relatively little is known about their allele diversity and the diagnostic potential of the markers. Nevertheless, accessions postulated to not contain these QTL should receive high priority for future genetic characterization, mapping, and introgression to complement the resistance genes already present in breeding populations.

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Table 1. Geographical Distribution of DNA markers alleles of three Fusarium head blight (FHB) resistance QTLs in FHB resistant germplasm.

		No. of accessions with the same marker allele as the QTL donor			
Country/ Region	No. accessions tested	*Fhb1* (STS3B-256)	*Qfhs.ndsu-3AS* (dupw227)	*Qfhs.ifa-5A* (barc186)	None
China	23	1	12	4	9
Europe	81	5	4	17	45
Japan	14	13	0	10	1
S. America	50	13	8	11	33
Total	168	32	24	42	88