SESSION 3:

VARIETY DEVELOPMENT AND HOST RESISTANCE

Co-Chairpersons: Anne McKendry and

Kevin Smith

MAPPING QTL FOR FHB RESISTANCE AND DON ACCUMULATION IN BARLEY POPULATION COMP351 X M98-102

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ABSTRACT

Many previous studies have identified QTL for FHB resistance in barley, but most of these QTL co-locate to the same regions. To continue making progress in enhancing the FHB resistance of barley, additional unique sources of resistance must be identified. As an alternative means for identifying FHB resistance in barley, bulked seed of Composite Cross XXX-G was evaluated in China and over 350 early maturing, six-rowed lines with low (<5%) infection were selected for further evaluation in the Midwest. In subsequent screening tests, two selections (COMP 351 and COMP 355) consistently exhibited low levels of FHB and deoxynivalenol (DON). Crosses were made between COMP 351 and breeding line M98-102 to identify and map QTL loci conferring resistance to FHB and the accumulation of DON. A population of 137 $F_{4:5}$ lines derived from COMP351 x M98-102 was evaluated in seven field trials for FHB severity. Deoxynivalenol (DON) concentration, days to heading, spike angle, height, and spike density were evaluated in most, but not all of the environments. Lines were genotyped by Triticarte Pty. Ltd. using Diversity Arrays Technology (DArT) markers. Six hundred and fifty DArT markers were polymorphic between the parents and met the quality standards recommended by Triticarte for mapping. Joinmap 4.0 was used to construct the genetic maps, and QTL Cartographer (2.5) was used for single marker analysis and composite interval mapping. Six QTL for FHB severity and four QTL for DON accumulation were significant in two or more environments. The six QTL for FHB resistance were identified on chromosome 2H and 4H and four on chromosome 7H (0.21>R2>0.04). The four DON QTL were identified on chromosome 2H, 3H, 5H and 7H (0.22>R2 >0.05). QTL conferring heading date (0.37>R2>0.02) and height (0.24>R2>0.05) also were identified. Two QTL regions were coincident for FHB resistance and DON accumulation on chromosome 2H and chromosome 7H. The 2H QTL region was also associated with heading date and height in this study and has been described in other studies. Two of the four FHB QTL on chromosome 7H were associated with other traits. One was associated with DON and height and the other was associated with heading date. One major effect QTL for spike angle was identified on chromosome 5H (0.20>R2>0.12) and was not associated with FHB severity or DON accumulation. At least two of the FHB QTL on chromosome 7H appear to be novel and could be exploited for marker assisted selection.

ASSOCIATION ANALYSIS OF FHB RESISTANCE IN SOFT WINTER WHEAT

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ABSTRACT

Resistance to Fusarium head blight (FHB) has been identified in soft winter wheat (SWW) cultivars from the Eastern United States, although little information has been available about the genetic basis of resistance. Recently, QTL mapping has been done in bi-parental crosses involving SWW sources of resistance, but mapped QTL need to be validated in diverse genetic backgrounds. Conducting a genome-wide association analysis on SSW lines grown in uniform regional scab screening nurseries will enable breeders to identify and validate QTL associated with FHB resistance. Association analysis is amenable for analyzing multiple diverse populations for FHB resistance. The approach can offer greater power and precision to test QTL effects and associated markers for their diagnostic capacity. The Northern Uniform Winter Wheat Scab Nursery (NUWWSN) and Uniform Southern Fusarium Head Blight Nursery (USFHBN), grown at a total of 16 locations during 2008 and 2009, were rated for several phenotypic traits associated with the disease (INC, SEV, INDEX, FDK and DON). Nursery entries were genotyped with SSR markers targeted to regions previously associated with FHB resistance QTL and genome-wide DArT markers. Unlinked markers were used to assess the relatedness of lines using STRUCTURE 2.3.1, Principal Component Analysis (SASv9.1.3), and Kinship (TASSLE v2.1). Results of associations identified using mixed model analysis in TASSLE and SAS will be presented.

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DEVELOPMENT, MAPPING AND HAPLOTYPE ANALYSIS OF EST-BASED SNPS IN THE WHEAT *FHB1* REGION

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ABSTRACT

Fusarium head blight (FHB) is a destructive disease that reduces wheat grain yield and quality. The Chinese variety Sumai 3 and its derivatives such as Ning 7840 have a high level of resistance to FHB symptom spread within a spike (Type II resistance) and have been widely used as resistant parents in breeding programs worldwide. The quantitative trait locus (QTL) in chromosome 3BS (*Fhb1)* from Sumai 3 source has been identified to have the largest effect on FHB resistance to date. This QTL has been linked to restriction fragment length polymorphisms, simple sequence repeats (SSR), amplified fragment length polymorphisms and sequence tagged site (STS) markers. Single nucleotide polymorphism (SNP) is the most common form of genetic variation and will be the next generation marker system for mapping and marker-assisted selection (MAS). In this study, we developed SNP markers based on wheat expressed sequence tags (ESTs) associated with *Fhb1*. A total of 131 SNPs were identified between Ning 7840 (FHB-resistant) and Clark (susceptible) based on sequences of ten ESTs. SNPs were analyzed in a BC_7F_7 population derived from Ning 7840/Clark using the single base extension method. Six SNP markers mapped between *Xgwm533* and *Xgwm493*, SSR markers flanking the *Fhb1*. Four of these SNP markers clustered with five other SSR/STS markers and covered a 7.4 cM interval. This marker-dense region gave the highest R^2 (40-54%) and LOD values (9.16-11.80) and is the most likely location of *Fhb1*. Haplotype analysis of 63 wheat accessions from eight countries based on EST sequence (SNP), SSR and STS markers associated with *Fhb1* identified four major groups: (1) US-Clark, (2) Asian, (3) US-Ernie and (4) Chinese Spring cluster. The Asian cluster consisted of Chinese and Japanese lines that carry *Fhb1* and a marker *Xumn10* haplotype could differentiate these accessions from accessions in all other groups. All Sumai3-related accessions formed a sub-cluster within the Asian group and can be sorted out by the marker *Xsnp3BS-8* from all other accessions. The SNP markers identified in this study should be good for fine-mapping and MAS of *Fhb1*.

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SEQUENCE ANALYSIS FOR GENE DISCOVERY IN BARLEY CHR. 2H BIN 10 REGION

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ABSTRACT

Efficiently identifying candidate genes for FHB resistance is an important yet challenging goal. Without sequence data, gene discovery in barley must depend on syntenous organisms such as rice and the newly sequenced *Brachypodium distachyon*. The genetic map of barley chromosome (chr.) 2H bin 10 is well-saturated with only one gap over 2.2 cM and the syntenous region in rice has been mined for markers. *Brachypodium* synteny has already added seven markers to the region and provided further probes for creating a physical map. From probes throughout bin 10, we have created a minimum tiling path of 36 BACs covering nearly 3 Mb that are currently being sequenced at WSU in order to increase gene identification efficiency. Candidate genes will be identified by bioinformatic data analyses. The candidate genes will be used to further saturate the chr. 2H bin 10 genetic and physical maps. We now have two years of phenotyping data from our recombinant lines but though we have separated height and head type from FHB resistance, we still do not have markers that segregate with the disease. Mutagenesis of CIho4196 has provided us with FHB resistant lines that are 6-rowed, early, sterile and hence potentially promising as breeding parents. We are working to combine these traits in a single line.

SCAB RESISTANCE QTLS HAVE AN EFFECT ON AGRONOMIC AND QUALITY TRAITS OF SOFT RED WINTER WHEAT

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ABSTRACT

Fusarium head blight (FHB) is a disease that affects wheat world-wide. However, most of the quantitative trait loci (QTLs) in wheat which are responsible for resistance to FHB are derived from exotic spring wheat cultivars originating in Asia. The purpose of this research was to determine whether the introduction of exotic FHB resistance QTLs has an effect on the quality and agronomic traits of soft red winter wheat. Eighty-six F2 derived recombinant inbred lines were developed by crossing Ning 7840, a Chinese spring wheat with FHB resistance QTLs, with Pioneer 2643, an FHB susceptible soft red winter wheat. Using a complete block design, the recombinant inbred lines were evaluated for the presence of FHB resistance QTLs, agronomic performance and grain quality in 2009. Height was reduced by the 3BS QTL, lodging was increased by the 5A QTL, and seed weight was reduced by the 2DL QTL. The softness equivalent score was lowered by the presence of the 5A QTL. These results suggest that the introduction of FHB resistance QTLs into soft red winter wheat can have consequences on agronomic and quality traits.

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EXPLORATION, IDENTIFICATION, TRANSFERRING AND UTILIZATION OF NEW SCAB RESISTANCE IN WHEAT IMPROVEMENT

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ABSTRACT

It is widely considered that scab resistance is controlled by two or three major genes and several minor genes (QTL's). Recombination and convergence of different resistant components has been successfully used in wheat breeding for scab resistance worldwide. *Roegneria kamoji, Roegneria ciliaris* and *Leymus racemosus* have been identified with high scab resistance. They are new genetic resources and would be helpful for broadening the genetic basis of scab resistance. Three *Triticum aestivum-Leymus racemosus* disomic addition lines 5Lr.#1, 7Lr.#1 and Lr.7, one *T.aestivum-Roegneria kamoji* addition line 1Rk#1 and one *T.aestivum-R.ciliaris* addition line $2S^c$ with scab resistance have been developed in Nanjing Agricultural University. Similar as in common wheat, scab resistance of *Leymus racemosus* is controlled by at least three loci on different chromosomes. More than thirty wheat-*L.racemosus* translocation lines involving in chromosomes 5Lr.#1, 7Lr.#1 and Lr.7 with different chromosome segments have been developed by irradiation and gametocidal gene effect and characterized by chromosome C-banding, *in situ* hybridization, and molecular marker analysis. Their scab resistance was evaluated both in the greenhouse and field in multiple locations and multiple years. Three *T.aestivum-L. racemosus* translocation lines, NAU601 (T4BS·4BL-7Lr#1S), NAU617 (T6AL·7Lr#1S) and NAU635 (T1BL·7Lr.#1S), and several introgression lines with high scab resistance and good fertility were selected. A wheat-*R. kamoji* translocation line with scab resistance involving the short arm of 1Rk#1 was obtained. Intercrosses between different alien translocation lines with scab resistance and between alien chromosome lines and common wheat were made to pyramid different scab resistance genes. Varieties or elite lines were used as recurrent parents to improve agronomic characters of these resistant lines. A multiple translocation line with both scab and powdery mildew resistance and several advanced lines with scab resistance and good agronomic characters have been developed. These new genetic resources are being used as parents in wheat breeding program for scab resistance.

VALIDATION OF *FHB*1 IN SEVERAL SOFT RED WINTER WHEAT BREEDING POPULATIONS

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ABSTRACT

Marker assisted selection offers one potential strategy for developing wheat varieties resistant to Fusarium head blight (FHB). By incorporating resistance alleles at major quantitative trait loci, such as *Fhb*1, into genetic backgrounds with improved agronomic and quality characteristics, breeding lines with cultivar release potential should result. To quantify and validate the effect of *Fhb*1, we evaluated five different populations: 26R58/VA01W-476//KY97C-0574-01, 25R54/VA01W-476//KY97C-0574-01, 25R54/VA01W-476//KY97C-0554-02, 25R78/Cumberland//VA01W-476 and 25R23/KY93C-1238-17-1//VA01W-476. These three-way crosses were considered typical of those used in the University of Kentucky FHB resistance - breeding program. F_2 individuals were genotyped for the presence of resistance alleles at *Fhb*1. A total of 185 homozygous resistant and susceptible $F_{2:4}$ lines were rated for disease symptoms in the Lexington scab nursery in 2009. Grain was analyzed for percentage *Fusarium* damaged kernels (FDK) using air separation. In four populations, mean disease ratings (0-9) of lines containing *Fhb*1 were reduced from 3.3 to 1.7. Mean FDK was reduced from 24.7 to 15.5, despite the early generation of genotyping.

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EVALUATION OF *HORDEUM* ACCESSIONS FOR RESISTANCE TO FUSARIUM HEAD BLIGHT

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ABSTRACT

Fusarium head blight (FHB), caused by *Fusarium graminearum*, has devastated the malting barley industry in the Upper Midwest. The deployment of cultivars with resistance to *F. graminearum* and its associated mycotoxins is the best means for combating the disease. Over the past decade, 21,487 cultivated barley and 1,768 wild barley (*Hordeum vulgare* subsp. *spontaneum*) accessions were screened for FHB resistance in Hangzhou, China and/or St. Paul and Crookston, Minnesota. The diverse *Hordeum* germplasm was provided by the USDA National Small Grains Collection, Aberdeen, ID USA; N. I. Vavilov All-Russian Scientific Research Institute of Plant Industry [VIR] in St. Petersburg, Russia; Station federale de recherches en production vegetale de Changins [SFRSPP] in Nyon, Switzerland; Nordic Gene Bank [NGB] in Alnarp, Sweden; Institute for Cereal Crops Improvement [ICCI] in Tel Aviv, Israel; International Center for Agricultural Research in the Dry Areas [ICARDA] in Aleppo, Syria; and Plant Gene Resources of Canada (Agriculture and Agri-Food Canada) in Saskatoon, Canada. Using the six-rowed cultivar Chevron as the standard for resistance, only 279 cultivated (1.3%) and 26 wild (1.5%) barley accessions were selected as possessing a useful level of partial resistance to FHB. Seventy-seven of the 279 selected cultivated barleys have been evaluated for resistance in three or more years. Of these 77 accessions, 15 (19.5%) were six-rowed, 58 (75.3%) were two-rowed, and 4 (5.2%) were of unknown type. Within the group of 77 selected barleys, the highest frequency of resistance found was in accessions from Ethiopia (11.7%), Switzerland (10.4%), Japan (7.8%), Finland (6.5%), and Czech Republic and Ukraine (each with 5.2%). For wild barley, the highest frequency of resistance found was in accessions from Israel (65.4%), Iran (19.2%), and Azerbaijan, Iraq, Jordan, and Syria (each with 3.8%). These selected *Hordeum* accessions should provide diverse alleles for enhancing the level of FHB resistance in barley breeding programs.

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CHROMOSOME ENGINEERING OF T7A·7LR#1S FOR THE ISOLATION OF NEW RECOMBINANTS AND FIELD EVALUATION OF T7A·7LR#1S CHROMOSOME INTROGRESSION HARD WINTER WHEAT LINES FOR RESISTANCE TO FHB AND DON

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ABSTRACT

T7AL·7Lr#1S is a genetically compensating wheat-*Leymus* translocation line (T09) involving wheat chromosome 7AL arm and *Leymus racemosus* (Lr) chromosome 7Lr#1S arm in CS (Chinese Spring) and was consistently resistant to FHB in greenhouse point-inoculation experiments. The novel FHB resistance gene was designated *Fhb3* and resides in the distal region of the short arm of chromosome 7Lr#1. T7AL·7Lr#1S was backcrossed twice to Overley and Jagger and ten lines homozygous for T7AL.7Lr#1S, three in Overley and seven in Jagger background, were evaluated for FHB resistance in a field nursery in Manhattan. All of the translocation lines except 08-183 had significantly lower mean disease ratings compared to their susceptible parent Overley. Unfortunately, the other backcross parent Jagger was not included in the test; however, three of the translocation lines (08-193, 08-189, and 08-184) had significantly lower ratings than Jagalene, which is known to be identical to Jagger in its reaction to FHB. It appears that *Fhb3* increased resistance in these entries. Similarly, the same three translocation entries had significantly lower DON levels than those of Overley and Jagalene and were statistically similar to moderately-resistant Truman.

Simultaneously, chromosome engineering was initiated to reduce the genetic linkage drag associated with T7AL·7Lr#1S. Three PCR-based markers, BE586744-STS, BE404728-STS, and BE586111-STS, specific for 7Lr#1S, were developed to expedite marker-assisted selection of recombinants. Upon analysis of 1,118 progeny, three wheat-*Leymus* recombinants, one proximal (#124) and two distal (#679 and #989), have been isolated in homozygous condition. These lines along with resistant and susceptible controls, as well as 08-193, 08-189, and 08-184, will be evaluated for FHB resistance by single point inoculation method in the greenhouses.

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DEVELOPMENT AND EVALUATION OF HARD RED SPRING WHEAT QTL-NILS FROM DIVERSE FHB RESISTANCE SOURCES

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ABSTRACT

Fusarium head blight (FHB) resistance has been identified in many diverse wheat genotypes from around the world, and a multitude of FHB resistance QTLs has been reported. One challenge that wheat breeders face is deciding which QTLs reported in unadapted or exotic backgrounds will be worth the time and resource investment associated with their introgression into regionally adapted germplasm. Over the course of several years, we used backcrossing coupled to marker assisted selection to develop near isoline sets of the FHB-susceptible hard red spring wheat cultivars Norm, Wheaton, and Apogee that possess one of five reported FHB resistance QTLs from a range of unadapted and exotic wheat sources. The FHB resistance of these near-isoline series has been evaluated in multiple greenhouse and field studies. Results of these studies and future research directions based on the findings will be presented.

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MIXED MODEL ASSOCIATION ANALYSIS FOR FHB RESISTANCE IN TUNISIAN DURUM WHEAT POPULATIONS

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ABSTRACT

There are limited sources of resistance to Fusarium head blight (FHB) predominantly derived from Chinese hexaploid genotypes like Sumai3 and Wangshuibai. Therefore, there is a need to use more diverse sources of resistance to expand the number of genes that may be used in gene pyramiding. In this study we used 184 BC_1F_6 and 189 BC_1F_7 lines derived from crossing Tun7, Tun18, Tun34, and Tun36 with durum cultivars 'Ben', 'Maier', 'Lebsock' and 'Mountrail' for association studies. We evaluated all the parents and RILs in the greenhouse in two seasons for type II resistance to FHB using the single floret injection inoculation method. The data showed the Tunisian lines have good level of resistance varying from 22% to 10% infection rate through the spikes.

To have a full coverage of the genome for association analysis lines were genotyped utilizing the 2,300 Diversity Array Technology (DArT) markers showing 25% polymorphism between the parents. The cluster analysis of the polymorphic markers revealed three distinct groups. The major groups were the North Dakota derived durum cultivars and majority of Tunisian lines except for Tun7 that was in a separate group far from the others. As both Tun7 and Tun18 are resistance to FHB and have different genetic backgrounds, both could be considered as potential candidates for new sources of resistance.

Different association mapping strategies were performed and the best models were used to find the associated markers to FHB resistance. In total 537 polymorphic markers had allelic frequencies more than 5% and used in the analysis. Ten different models (Naïve, K, K_T, Pedigree, Q, PCA, QK, QK_T, PK and PK_T) were compared and best models were selected by considering the lowest mean of squared difference (MSD) between observed and expected p-values of all marker loci and percentage of observations below 0.05 in P (expected)-P (observed) plot. MSD values for the $K_{T(0.65)}$ and $QK_{T(0.7)}$ was the lowest among all other models. These two models had an MSD 50 times lower than the naïve model. The P-P plot also showed the mixed model performs better than the Naïve model.

A union output of the two different models showed 20 markers from 2A, 3B, 4A, 5B and 6B, and 15 markers with unknown locations are associated ($p<0.05$) with FHB resistance when analyzing the whole population derived from nine different crosses. Of these 35 markers, association of five markers was significant after correcting for multiple testing using positive false discovery rate (pFDR) criterion. All of these markers were from the same QTL located on 5BL. The other QTL found in this study were not confirmed by pFDR<0.1 although the QTL from 3BS seems promising as the pFDR criterion is very close to being significant. Tun 18 and Tun 7 which have both QTLs are the parents which show a good level of resistance in our study. We could also hypothesize the potential of having a suppressive gene(s) coming from susceptible cultivars that masks the effect of the resistance genes in the population. All

the susceptible cultivars are sensitive to FHB infection although they carry the 5BL QTL.

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AN ALTERNATIVE PATH TO FUSARIUM HEAD BLIGHT (FHB) RESISTANT WHEAT CULTIVARS: EXPRESSION RATHER THAN INTROGRESSION

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ABSTRACT

Decades of sustained effort attest to the difficulty of generating FHB-resistant spring wheat cultivars. The common assumption underlying these efforts is that discrete genes conditioning superior FHB resistance must be introgressed from sources such as Sumai 3 into elite germplasm. An alternative path could start from a very different assumption. FHB-susceptible near-isogenic lines of Sumai 3, like Sumai 3 itself, carry pathogenesis-related genes that are induced by *Fusarium graminearum* Schwabe. This suggests that the key to FHB resistance is the control of expression of critical genes that are already present. A scheme that might generate variation in expression was suggested when we observed that progeny derived by selfing of plants under pressure from systemic virus infection could vary visibly from type. We devised an iterative protocol which, even within small populations, selects such variants and identifies by their expression in subsequent generations those whose altered traits are heritable. Promising individuals are then advanced as founders of lines for testing. Within three years we have thus derived lines from the doubled haploid cultivar 'McKenzie' that express traits not seen in their progenitor: short stature, near-immunity to wheat streak mosaic virus, and improved resistance to leaf spot diseases and FHB. These new characteristics have been stably expressed over multiple generations.

LEVEL OF *FUSARIUM* MYCOTOXINS IN WHEAT GRAIN HIGHLY ASSOCIATED WITH PERCENTAGE OF SCABBY KERNELS

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ABSTRACT

Resistance to head blight of winter wheat is believed to be essential for managing the disease and achieving low levels of associated mycotoxins in grain. Resistance to mycotoxin accumulation has been hypothesized as one of the five types of head blight resistance. Relative to our understanding of resistance to initial infection and spread within a spike, little is known about resistance to mycotoxin accumulation, and there has been no definitive data on how best to select for low mycotoxin accumulation in grain. The objectives of this research were to develop an efficient method for selecting lines with low levels of mycotoxin accumulation in grain and to determine if resistance to mycotoxin accumulation is a separate, independent resistance component or simply a pleiotropic effect of other resistance mechanisms. A susceptible cultivar (Coker 9835) and 15 winter wheat lines with diverse sources of head blight resistance were evaluated in a series of field and greenhouse experiments. Lines were inoculated with deoxynivalenol (DON) and nivalenol (NIV) chemotype isolates of *Fusarium graminearum* and characterized for head blight severity, percentage of scabby grain, and level of mycotoxins in the grain. Correlation analyses were performed to determine the relationships of severity and percentage of scabby grain with the levels of mycotoxins in grain. Compared to the susceptible check, all resistant lines had significantly lower levels of DON and NIV in grain. In the greenhouse tests, DON and NIV levels in grain were positively correlated with the percentage of florets blighted 21 days after inoculation ($r = 0.87$ and 0.96, respectively) and with the percentage by weight of the scabby grain ($r = 0.96$ and 0.88, respectively). Furthermore, most of the mycotoxins were associated with the scabby grain, and healthy grain had low levels of mycotoxins. In the field experiments, DON levels in the grain were positively correlated with head blight severity at soft dough stage ($r = 0.83$ to 0.93) and with percentage of scabby grain ($r = 0.96$ to 0.97). Compared to DON levels for the susceptible check, DON levels for the most resistant lines were reduced up to 94%. The results of this study indicate that selecting wheat lines for lower disease severity, or more importantly for lower levels of scabby grain, also will select lines with lower levels of *Fusarium* mycotoxins in harvested grain. Furthermore, reduced mycotoxin accumulation in grain appears to be a pleiotropic effect of other resistance mechanisms rather than an independent mechanism. These findings should simplify the process of developing cultivars with lower levels of mycotoxin accumulation in grain, and the resistances in these lines would have a significant impact on *Fusarium* mycotoxin levels in grain if the resistances were incorporated into cultivars that replaced existing susceptible cultivars.

MAPPING QTL FOR FUSARIUM HEAD BLIGHT RESISTANCE IN WHEAT CHROMOSOME 7A

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OBJECTIVES

1) Characterize QTLs for type II FHB resistance in Wheat chromosome 7A using Chinese Spring – Sumai3 7A chromosome recombinant inbred lines. 2) Identify SSR markers associated with the QTL to be used in marker-assisted selection (MAS).

INTRODUCTION

Fusarium head blight (FHB), caused by *Fusarium graminearum*, has been an important cereal disease in tropical and sub tropical regions of the world for a century. Its epidemics not only reduce yield and quality, but also produce mycotoxins that result in a potential health hazard to humans and animals (Bai and Shaner, 2004).

FHB resistance is a quantitative trait (Grausgruber et al., 1999) therefore its expression is heavily influenced by the existing environmental conditions. Currently no single measure can completely control its epidemics. Integration of cultural practices, chemical applications and use of resistant cultivars have proven to be the most promising approach to reduce the losses caused by FHB. Among different types of resistance against FHB, resistance to disease spread within a spike (type II) is the most stable type of resistance (Bai and Shaner, 2004). QTL mapping discovered many QTLs associated with type II resistance in wheat (Chen et al., 2006; Ma et al., 2006b; Mardi et al., 2006; Yu et al., 2008). Pyramiding these QTLs into cultivars by marker-assisted selection will enhance cultivar resistance under FHB epidemics (Bai and Shaner, 2004).

Chinese landrace Sumai3 and its derivatives are excellent sources for type II FHB resistance. Sumai3 has been used as the resistant parent in many breeding programs worldwide (Bai and Shaner, 2004). QTLs with Sumai3 origin are reported in chromosome 3BS, 5AS, 6A, 6BS, 2D and 4D (Anderson et al., 2001; Ma et al., 2006b; Waldron et al., 1999), but never on chromosome 7A. However, QTLs for type II FHB resistance was reported in 7A chromosome of Wangshuibai and Frontana (Mardi et al., 2006; Yu et al., 2008). A previous study revealed a high level of type II resistance in Chinese Spring-Sumai3 chromosome 7A substitution lines (Zhou et al. 2002a), but mapping work did not find any QTL on the chromosome (Ma et al., 2006b). In this study, we developed 7A chromosome recombinant inbred lines to investigate the effect of QTL on 7A chromosome of Sumai3 origin.

MATERIALS AND METHODS

Planting Materials

An F_5 population of 191 Chinese Spring-Sumai3-7A chromosome recombinant inbred lines (CRIL) was derived from the cross between Chinese Spring and Chinese Spring-Sumai3-7A disomic substitution lines by single seed descent.

Planting, Inoculation, Disease Evaluation and Phenotypic Data Analysis

Disease evaluation was carried out in spring 2009 in a greenhouse at Kansas State University, Manhattan, KS. Experimental lines consisted of 191 Chinese Spring-Sumai3-7A CRILs and their parents. Fifteen seeds from each CRIL along with

the parents were planted in trays containing soil (Sungrow Metro-mix 360® growing medium) and vernalized in a growth chamber at 4°C for one month. The seedlings of each experimental line were divided into three replicates and transplanted in plastic pots containing soil. The pots were arranged in the greenhouse in a randomized complete block design. Greenhouse temperature was maintained at 20°C. Plants were watered and fertilized with Miracle-grow® as necessary throughout the season.

Fusarium graminearum inoculum was prepared by growing the Kansas strain GZ3639 in mung bean liquid medium (Bai and Shaner, 1996). The spore density was evaluated by counting them using a hemocytometer under a microscope. Inoculum concentration was adjusted to 100,000 conidial spores per ml. At anthesis, a single spikelet residing in the center of the spike was inoculated by dispersing 10 µl/spikelet using a syringe. Five to six heads were inoculated in each pot. The plants were placed in a humid chamber, and sealed by polythene sheets to facilitate disease development. After 48 hours the plants were moved back to a greenhouse bench. Watering was done as necessary. Disease was evaluated at 21 days after inoculation by counting the number of infected spikelets and the total number of spikelets/inoculated spike. Any spikelet with a dark brown water-soaked spot to a completely bleached spikelet was recorded as a diseased spikelet (Figure 1). Proportion of symptomatic spikelets (PSS) for each CRIL was calculated for QTL analysis.

DNA Extraction and Genotyping

Three-weeks-old seedlings of population F_6 were used for DNA extraction. Leaf tissues were collected into 1.1 ml strip tubes. The tissue samples were dried in a freeze dryer for three days. A 3.2 mm stainless steel bead was loaded into each strip tube and the Mixer Mill was used to ground the dry tissue to a fine powder by shaking the tubes for 6 minutes at a speed of 1200 rpm. DNA was extracted using a modified Cetyltrimethyl ammonium bromide method (Saghai-Maroof et al., 1984).

Parents were screened using 60 SSR markers (Somers et al., 2004) mapped on 7A chromosome and 28 polymorphic markers were used to screen the CRIL population. Polymerase chain reaction (PCR) was done with 14 µl of PCR mix containing a final concentration of 10X ASB buffer, 2.5 mM of $MgCl_2$, 200 µM of dNTP, 100 nM each of forward M13-tailed primer and M13-fluorescent-dye labeled primer, 200 nM of reverse primer, 1 U of *Taq* DNA polymerase and 50 ng template DNA. PCR was carried out in a GeneAmp® 9700 PCR system using a touchdown program with initial denaturing at 95°C for 5 min, 5 cycles of 96°C for 1 min, 68°C for 3 min with a reduction of 2°C in each following cycle and 72°C for 1 min, followed by 4 cycles again with a modified annealing temperature of 58°C for 2 min. The final step consisted of 40 cycles of 96°C for 20 sec., 50°C for 20 sec., 72°C for 30 sec. and ended with a final extension step of 72°C for 5 min.

PCR products with four M13-florescent dyes (FAM, VIC, NED and PET) were pooled using the Bechman Coulter 96-channels Biomek NXp Liquid Handling System and the pooled PCR products were analyzed in an ABI PRISM 3730 DNA Analyzer. Data were analyzed using GeneMarker v1.75 and CRILs were scored for the polymorphic alleles between the two parents.

QTL Mapping

Linkage maps were developed using JoinMap v3.0 using a LOD score of 4.00 and Kosambi mapping function. QTL maps were analyzed by composite interval mapping feature of QTL Cartographer v2.5 at a walking speed of 2.0 cM and a window size of 2.0 cM. Threshold value to claim a significant QTL was set using 1000 permutation at a significance level of 0.05.

RESULTS AND DISCUSSION

A population of CRIL created by crossing a susceptible cultivar to the same cultivars with one chromosome substituted by a chromosome from a resistant cultivar is an ideal mapping population

to study the QTL effects of individual chromosomes (Garvin et al., 2009; Kumar et al., 2007). Previous studies showed that Chinese Spring is a wheat line that is moderately resistant to FHB (Grausgruber et al., 1999) and Chinese Spring-Sumai3-chromosome-7A disomic substitution line is highly resistant to FHB (Ma et al., 2006a; Ma et al., 2006b; Zhou et al., 2002a). The same results were obtained for the parents in this study. Segregation for FHB was observed among F_5 CRIL with average proportions of symptomatic spikelets (PSS) ranging from 5% to 97%. The frequency distribution of PSS was bimodal (Figure 2). This suggests an existence of few QTLs with a major effect on type II FHB resistance in the population.

QTL mapping using polymorphic markers on chromosome 7A detected a major putative QTL for type II FHB resistance on the short arm of chromosome 7A with a LOD score of 5, flanked by markers *Xbarc174* and *Xwmc17* (Figure 3). The QTL explained 12% of the phenotypic variation in the population.

Ma et al. (2006b) used a recombinant inbred line population derived by crossing Chinese Spring-Sumai3-chromosome-7A disomic substitution line to a Chinese cultivar Annong 8455 and did not find any QTL associated with type II FHB resistance on chromosome 7A. Lack of marker polymorphism between the parents in the QTL region could have been one of the factors (Ma et al., 2006b; Zhou et al., 2002b).

To validate the findings from this study, the mapping population will be repeatedly evaluated for two more seasons under greenhouse conditions. Deoxynivalenol (DON) content in infected kernels will be measured to evaluate the effect of the QTL on reducing DON content. Comparative mapping will be conducted between the QTL region and the corresponding rice chromosome region to map functional ESTs and develop SNP markers in the region for further improvement of the linkage map resolution.

ACKNOWLEDGEMENT AND DISCLAIMER

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Figure 1: a) Susceptible spike of chromosome recombinant inbred line 57 b) Resistant spike of chromosome recombinant inbred line 119 after needle inoculation in the center spikelet of a spike

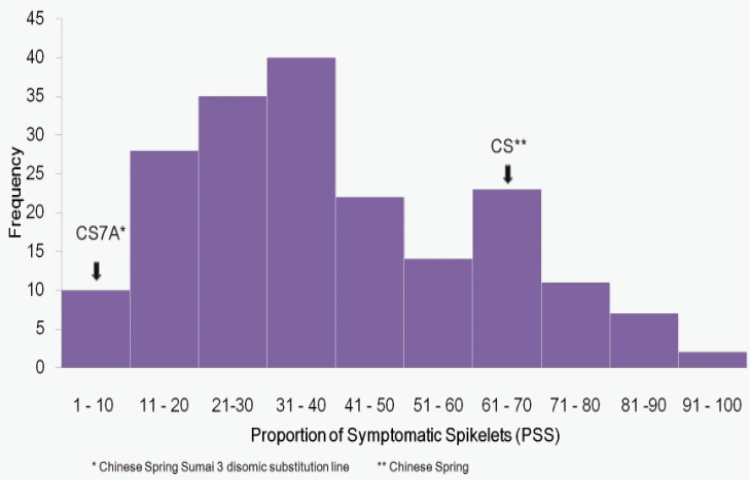

Figure 2: Frequency distribution of proportion of symptomatic spikelets in CS-Sumai3 7A chromosome recombinant inbred population.

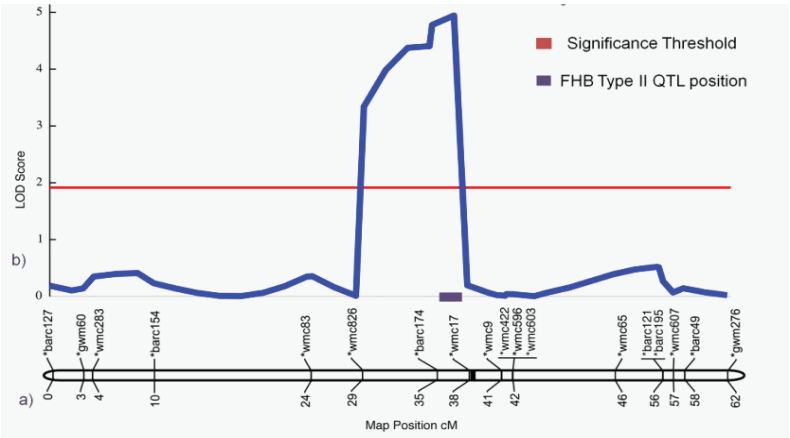

Figure 3: A genetic linkage map of Chromosome 7A (a) and a LOD score map to show possible QTL position in the map (b)

MARKER ASSISTED TRANSFERRING OF FUSARIUM HEAD BLIGHT RESISTANCE QTLS INTO LOCAL ADAPTIVESOFT RED WINTER WHEAT

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ABSTRACT

Fusarium head blight (FHB), also known as scab, is a potentially devastating winter wheat disease in southeast region where persistent rainfall could happen during the spring season. FHB can cause significant reduction in seed yields and quality. Infested seeds are often contaminated with trichothecene and estrogenic mycotoxins, which is a serious threat to animal health and food safety. Effect of chemical control of FHB was limited by the narrow window of application and cost increase. Development of resistant cultivars is the most efficient option to control FHB. Top crosses were made to introduce FHB resistance QTLs from VA04W-433, VA01-476, Sumai 3 derivatives, from Virginia and IN97397 from Indiana into our local adapted soft red winter wheat elite lines. Massive selections with molecular markers were carried out from the early generations to prevent the loss of FHD resistant QTLs which could happen if selection were carried out for economical and agricultural important traits in the early generations without marker assisted selection for FHB QTLs.

EVALUATION OF EXOTIC SCAB RESISTANCE QUANTITATIVE TRAIT LOCI (QTL) EFFECTS ON SOFT RED WINTER WHEAT

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ABSTRACT

Fusarium Head blight (FHB) of wheat, caused by *Fusarium graminearum*, is a disease that periodically strikes the mid-Atlantic region of the USA. Breeding for resistant wheat varieties is an effective method of disease control. The objective of this study was to evaluate the effects of exotic FHB resistance QTL, singly and in combination, on FHB resistance in soft red winter wheat. McCormick, a soft red winter wheat (SRWW) genotype adapted to the mid-Atlantic region, was used in a backcross program with the Chinese variety Ning7840. Eight Near-Isogenic Lines (NILs) were developed by marker-assisted backcrossing. Three FHB resistance QTLs on chromosomes 3BS, 2DL, and 5A were introgressed from non-adapted Ning7840 into the elite SRWW McCormick. The 3BS+2DL NIL showed higher resistance and lower deoxynivalenol (DON) content than other NILs in one greenhouse study conducted in College Park (MD) and also in two field studies conducted in Salisbury (MD) in 2008 and 2009 and in one field study conducted in 2009 in Lexington (KY). These results indicate that the 3BS+2DL NIL could be used in the mid-Atlantic region to breed for improved FHB resistance in soft red winter wheat.

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EVALUATION OF HOST PLANT RESISTANCE AND FUNGICIDE TREATMENT FOR SUPPRESSION OF FUSARIUM HEAD BLIGHT

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ABSTRACT

Fusarium head blight (FHB), caused by *Fusarium graminearum* has become a formidable opponent to wheat production in the United States over the past 25 years. A favorable climate, as well as high levels of inoculum has caused FHB to become a major disease of wheat that can cause significant economic losses. Until recently, there were few fungicides labeled for suppression of FHB. Numerous studies have shown that fungicides containing the active ingredient tebuconazole are very effective in reducing losses caused by FHB. While fungicides can be a useful tool for FHB suppression, they do not provide complete control, and their efficacy is greatly affected by timing. Planting varieties that are resistant to FHB infection provides farmers with continual protection against the disease. Our objective in this study was to examine the effectiveness of two foliar applied fungicide products on Fusarium head blight, and assess fungicide performance on varieties with varying levels of resistance. The experiment was set up as a split plot design, and conducted in both 2008 and 2009. The plots were grown in a grain spawn inoculated/ mist irrigated nursery in Urbana, IL with four replications. The main plots consisted of the fungicide treatment where the following were applied: an untreated check, Folicur® (tebuconazole), or Prosaro® (tebuconazole + prothioconazole). The sub plots consisted of twelve wheat cultivars with a range of FHB resistance, from very susceptible to resistant. Data were collected on incidence, severity, FHB index, *Fusarium* damaged kernels (FDK), ISK index (incidence/ severity/kernel quality index), deoxynivalenol (DON) concentration, yield, and test weight. Data from each year were combined when the year variance was homogeneous. Transformations were performed to correct for non-homogeneous year variance, as well as non-normally distributed residuals when possible. Data were analyzed and contrasts were made using the Proc Mixed procedure in SAS9.2. Both fungicide treatment and cultivar had a significant effect on all measures ($P<.05$). We found significant interactions between fungicide treatment and variety for *Fusarium* damaged kernels and yield. A high level of disease pressure was observed in both 2008 and 2009 with a wide range in incidence and severity. Also, we observed a broad range in yield for both years from 73 to 121 bu/A in 2008 and 64 to 114 bu/A in 2009. When split into two groups (6 resistant and 6 susceptible) and averaged over all treatments, the resistant cultivars significantly ($P<.05$) outperformed susceptible cultivars for all measured values; this was also the case when the resistant cultivars were compared to the susceptible cultivars with no fungicide applied. The resistant cultivars reduced mean incidence by 26 percent and mean severity by 17 percent while increasing yield by 12.7 bu/A. Both Folicur® and Prosaro® provided a significant benefit for all measures when compared to untreated checks. Mean incidence was reduced by an average of 32 percent when Prosaro® was applied and by 20 percent when Folicur® was applied. Prosaro® increased yield by an average of 12.4 bu/A while Folicur® increased yield by an average of 9.0 bu/A when compared to the untreated plots. Prosaro® and Folicur® significantly improved test weight. Prosaro® consistently provided more improvement in the measured variables than Folicur®; however, the Prosaro® treatment was not significantly ($P<.05$) different than Folicur® application for test weight, mean incidence, or yield. When the six susceptible cultivars treated with Prosaro® and Folicur® were compared to the six resistant cultivars with no fungicide treatment, the fungicide treated

cultivars provided significantly better results for most disease measures; however, the untreated resistant cultivars did not exhibit a significant response in yield due to fungicide application. While there were slightly lower yields when the resistant varieties were untreated, the resistant varieties were still able to provide acceptable yields and DON concentrations under heavy disease pressure. Based on the data from these two years, suppression of FHB can be achieved by planting resistant varieties and applying a fungicide such as Folicur® or Prosaro®. The results confirm the importance of planting a resistant variety. In some cases, fungicide application may not be possible or the timing may not be optimal; therefore, it is imperative for farmers to plant resistant cultivars.

SUCCESSES IN DEVELOPMENT OF FUSARIUM HEAD BLIGHT RESISTANT SOFT RED WINTER WHEAT VARIETIES USING PHENOTYPIC EVALUATION

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ABSTRACT

Development of high-yielding, well-adapted Fusarium head blight (FHB) resistant wheat varieties is essential for reducing the damage and substantial economic losses due to FHB when conditions favor infection. FHB resistance has been an important breeding objective of my program since about 1995. We have been evaluating FHB resistance in a mist-irrigated, inoculated FHB nursery since 1997. Each year we make at least 200 two-way and 200 three-way or four-way crosses involving one or more sources of FHB resistance. In 2009 we made 433 crosses, and 93.7 % had at least one FHB resistant parent. Many of the resistance sources we are now using are breeding lines from our program or other soft red winter wheat programs, and many crosses now involve more than one source of FHB resistance. Although we are using marker assisted selection to enrich F_2 populations in some crosses, for most populations we use phenotypic selection to select FHB resistant lines derived from F_3 or F_4 bulk populations. In addition to evaluation of lines in six cooperative nurseries and the Illinois Wheat Variety Trial, we evaluate all University of Illinois breeding lines in the misted, inoculated FHB field nursery each year. Approximately 2500 rows are evaluated each year in the replicated FHB nursery. Grain spawn (corn kernels cultured with 6-10 FHB isolates) is used to inoculate the nursery. Experiments have either two or three replications. Data are collected on incidence, severity and percent *Fusarium* damaged kernels (FDK). Data on incidence are based on visual assessment of the percentage of heads in a row that show symptoms. Severity is assessed by counting, or estimating, the number of infected spikelets per head on 7 to 10 heads per row. Percentage of FDK is determined by visual assessment compared to standards with known FDK percentages. FHB and ISK indexes are calculated. Grain samples are harvested sent to the University of Minnesota for DON evaluation. Data are analyzed with Agrobase and SAS software. In addition, about 1850 breeding lines (first year after headrows) are evaluated in a single row in the misted, inoculated field nursery. A single observation for FHB resistance is performed on each of these rows to identify the susceptible lines for discard at an early stage of evaluation. Producers will not adopt FHB resistant breeding lines unless they are yield competitive; therefore, breeding lines are evaluated for an array of traits at multiple locations. Advanced breeding lines are evaluated in three replication performance tests at four locations. Preliminary breeding lines are also evaluated at four locations but with fewer replicates. The first year after a line is selected in a headrow it is evaluated in single plot nurseries at two locations. In 2010 we will have 1944 entries in the single plot nursery excluding checks (Total plot number at both locations with checks = 4320). We will have 3960 plots in 2010 in replicated performance trials, and will evaluate 428 Illinois breeding lines in replicated tests. Breeding lines from the University of Illinois program have regularly been among the most resistant lines in the NUWWSN and the PNUWWSN. There are currently at least eight University of Illinois breeding lines with FHB resistance in commercial production or in various stages of advanced or regional evaluation and seed increase.

RECENT PROGRESS IN BREEDING FOR FHB RESISTANCE IN CANADIAN BARLEY

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ABSTRACT

Fusarium head blight (FHB) caused by *Fusarium graminearum* continues to be the most destructive disease of barley in Canada. Good progress has been made over the past decade by Canadian barley breeding programs in developing FHB resistant cultivars and germplasm with low deoxynivalenol (DON) accumulation, particularly in two-row classes which occupy the largest acreage in Canada. Progress has generally been lagging in six-row germplasm. The two-row feed barley cultivar CDC Mindon, developed by the Crop Development Centre (CDC), University of Saskatchewan, Saskatoon, SK, was registered in 2007, and has set the standard with about 40 to 50% lower DON content than AC Metcalfe over many years of testing. Two new cultivars, Norman (TR05915) and HB705, resulting from *in vitro* selection (IVS) using *Fusarium* mycotoxins during doubled haploid (DH) production at the Agriculture and Agri-Food Canada (AAFC) Brandon Research Centre, were registered in 2009. Norman, developed jointly by AAFC-Brandon and the CDC, is a two-row malting cultivar selected from CDC Kendall with 25-30% lower DON content than its parent, while maintaining CDC Kendall's desirable quality profile. HB705, a two-row hulless cultivar with malting quality potential selected from the CDC Freedom/Rivers cross at AAFC-Brandon, combines reduced DON content relative to other hulless cultivars with high malt extract, which may be attractive to the malting and brewing industry. Most programs are in the second or third breeding cycle, and have better parents available for crossing purposes to enhance FHB resistance. Use of exotic parents, such as the two-row Chinese accession Harbin, has been attempted with limited success. TR08203, a promising two-row malting line developed at AAFC Brandon that traces back to Harbin, has DON levels intermediate between AC Metcalfe and CDC Mindon and was advanced to a second year in the 2009 Western Cooperative Two-row Barley Registration Test. Numerous breeding lines with promising FHB resistance at various stages of development are being evaluated. In 2009, the FHB project in western Canada will replace selection based on visual symptoms for most advanced breeding lines in the FHB nursery with preliminary selection for DON content using near infrared reflectance (NIR) spectrometry to identify lines for further DON testing with standard methods. Although funding constraints may affect future progress, more new cultivars with low DON accumulation should be released over the next few years.

ASSOCIATION ANALYSES OF SNP MARKERS WITH SCAB RESISTANCE IN WINTER FEED BARLEY

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ABSTRACT

Two Barley OPAs, consisting of 3,072 SNPs, were used to genotype 284 barley breeding lines from Virginia Tech evaluated in the Barley CAP project. Among them 102 lines were screened for scab resistance in a mist-irrigated nursery inoculated with scabby corn seed and a conidial suspension spray from 2006 to 2009. Scab incidence, severity, and DON toxin concentration were determined in each year. FHB index was calculated using incidence and severity data. Association analysis was conducted to identify SNP markers linked to scab resistance. Each set of barley CAP lines from 2006, 2007 and 2008 were analyzed separately based on two sets of SNP data. Scab data collected from the field were averaged over two or three years for each set of barley CAP lines including the maximum number of common lines. The following preliminary results are from the analyses of 46 lines from barley CAP 2006 based on scab data averaged over three years from 2006 to 2008. Nine chromosome regions were associated with at least one type of scab resistance using OPA1. Among these nine regions, five regions were also identified from analyses using OPA2 SNP data. Important SNPs were identified on chromosomes 2H, 3H, 5H, and 7H and explained a range of variation in scab resistance. Of particular interest is a region on chromosome 5H at 151 cM which explained 9% of DON toxin levels, 11% of FHB incidence, and 15% of FHB severity. Another region on chromosome 7H explained 15% of DON toxin levels and 18% of FHB index. Barley CAP lines in 2007 and 2008 will be analyzed in a similar way and overlapping or common regions will provide barley breeders with useful information regarding putative FHB resistance QTL. SNP markers will be validated in breeding populations and can be applied in marker-assisted selection.

ACKNOWLEDGEMENT AND DISCLAIMER

This material is based upon work supported by the U.S. Department of Agriculture, under Agreement No. 59-0790-4-102. This is a cooperative project with the U.S. Wheat & Barley Scab Initiative, and the USDA-CSREES Barley Coordinated Agricultural Project. 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.

SATURATION MAPPING OF SCAB RESISTANCE QTL IN ERNIE AND IDENTIFICATION OF DIAGNOSTIC MARKERS FOR BREEDING SCAB RESISTANCE

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ABSTRACT

Fusarium head blight (FHB) has decreased wheat yields and quality significantly under epidemic conditions in the eastern and southern U.S.. Many QTL for scab resistance have been mapped in exotic and native sources. However, only a few QTL have been widely deployed in breeding programs using marker-assisted selection (MAS) due to the lack of diagnostic and tightly linked markers for most QTL. Four major QTL for type II resistance were mapped on chromosomes 5A, 4B, 3BSc and 2B of Ernie. A set of 243 RILs were evaluated in inoculated, mist-irrigated scab nurseries at Columbia, MO and Blacksburg, VA in 2008 and at Blacksburg and Warsaw, VA in 2009. Phenotypic data were obtained for FHB infection and severity, DON toxin accumulation, and *Fusarium* damaged kernels. Forty-seven new microsatellite markers were mapped to saturate these four QTL target regions and other regions based on field scab resistance. Overlapping and distinct QTL were identified for different types of resistance in Ernie. Markers linked to QTL on chromosome 4B are associated with greenhouse and field severity, and grain weight with R^2 values at 12%, 5%, and 12% over years. The awn suppressor gene on chromosome 5AL, B_1, explained variation in field incidence, severity, and grain weight at 6%, 8% and 5% over years. Tightly linked markers were tested in a wide range of Chinese, European and America sources. The most diagnostic markers were used in marker-assisted selection to pyramid various QTL.

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SATURATION MAPPING QTL FOR SCAB RESISTANCE IN A VIRGINIA WHEAT CULTIVAR MASSEY

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ABSTRACT

Fusarium Head Blight (FHB) or scab is a serious disease which reduces yield and quality of wheat in warm and humid areas worldwide. Planting resistant varieties is an economically beneficial and environmentally sound way to manage this disease. Identifying new sources of resistance and characterizing native sources of resistance are both major components in developing scab resistant wheat varieties. Massey, a cultivar released by Virginia Tech in 1985, has adult plant resistance to powdery mildew as well as being moderately resistant to scab. A set of 589 Diversity Array Technology (DArT) markers were mapped onto all 21 chromosomes in a Becker/Massey mapping population comprised of 152 recombinant inbred lines. Phenotypic data for FHB severity were obtained from a greenhouse test conducted in Virginia. Data for FHB incidence and severity, *Fusarium* damaged kernels (FDK) and DON toxin concentration were collected in field tests conducted in Virginia (2007, 2008, 2009), Missouri (2008), and Kentucky (2008). Within each test, FHB incidence was significantly correlated to FHB severity ($P < 0.001$). A set of fifty-eight simple sequence repeat markers were mapped to target regions. Three major QTLs conferring resistance to FHB in Massey were located on chromosomes 3B, 4B, 4D on the basis of field data. The QTL on chromosome 3BSc was associated with greenhouse severity, field severity, and FDK with R^2 ranging from 7.1% to 16.6%. The QTL on chromosomes 4B, close to *Rht1* gene, explained 9.5% of field index based on three year data, 22% of grain weight, and 26% of FDK based on data from 2008. The QTL on chromosome 4D, close to *Rht2* gene, explained 9% to 35% of field incidence, severity, FDK and grain weight. However, the R^2 might be overestimated due to the low marker density at this target region. More markers derived from wheat EST or rice synteny regions will be mapped to the target regions. Diagnostic markers will be validated and applied in marker-assisted selection.

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INTEGRATION OF 3BS (*FHB1*) FHB QTL USING MARKER-ASSISTED BREEDING INTO HARD RED WINTER WHEAT (*TRITICUM AESTIVUM* L.) OF NEBRASKA

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ABSTRACT

Fusarium head blight (FHB), also known as scab, is a prevalent disease of wheat (*Triticum aestivum* L.) in warm, humid regions where flowering coincides with rainy periods. Natural epidemics of the disease may result in severe yield losses, reduction in quality, and contamination of the harvested grain by mycotoxin. The use of host resistance has long been considered the most practical and effective means to control FHB. The objectives of this study were to evaluate FHB severity under visual based (phenotypic) and marker based (genotypic) selection procedures. In order to supplement the existing native tolerance to FHB, spring wheat cultivar 'Alsen' was crossed with two elite adapted hard winter Nebraska lines through a three way cross [(spring x winter) x winter]. In this study a population of 116 $F_{3:4}$ lines were genotyped for the 3BS QTL using 5 diagnostic molecular markers and also field evaluated under mist irrigation at two sites in Nebraska (Lincoln and Mead) during the 2008 and 2009 cropping seasons. Out of the 116 $F_{3:4}$ lines 42 of them showed at least four 3BS markers from Alsen. The population showed significant differences for the measured phenotypic traits that included incidence, severity, and index in all the individual testing environments and for the combined analysis. Lines with and without the 3BS allele were compared for their field resistance. Generally, the lines identified with the 3BS QTL have good field FHB resistance and can be used as adapted resistance sources in the future hard winter wheat breeding program.

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EVALUATION OF DIFFERENT GREENHOUSE INOCULATION MODELS FOR PREDICTION OF FHB INFECTION RATES IN FIELD

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ABSTRACT

Fusarium Head Blight is a fungal disease in wheat, caused by *Fusarium graminearum*. It causes severe losses in yield and grain quality and is responsible for considerable economic losses. Susceptible wheat heads are infected at the time of anthesis, and late infections can also occur. Varieties are known to exhibit varying levels of resistance to the initiation of infection (Type 1 resistance) and the spread of infection (Type 2 resistance). There have been questions on the ability of greenhouse evaluation of FHB to effectively predict field performance (which is due to an interaction of both type 1 and type 2 resistance). We have examined four greenhouse inoculation protocols- 1) Point inoculation at anthesis, 2) Point inoculation at 7 days post anthesis, 3) Spray inoculation at anthesis and 4) Spray inoculation 7 days post anthesis for their correlation with field symptoms. The study was conducted on 26 varieties adapted to Michigan; which included both soft red and soft white winter wheat lines with varying levels of resistance to FHB. The infection observed was measured as the number of infected spikelets per total number of spikelets in an individual head, and observations were recorded at two time points in both the greenhouse and the field. This poster presents visually observed infection levels. Further work will involve studying the correlation of toxin accumulation in the field vs. greenhouse, and validation of the most effect greenhouse method identified here.

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THE 2008-09 SOUTHERN UNIFORM WINTER WHEAT SCAB NURSERY

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ABSTRACT

Most components of Fusarium Head Blight (FHB) resistance are greatly influenced by genotype by environment interaction which limits the heritability of resistance estimated by a single program in any given year. The Southern Uniform Winter Wheat Scab Nursery provides breeders in the public and private sectors with an opportunity for multi-environment, independent evaluations of FHB resistance in advanced generation breeding lines compared with the current most resistant check varieties Ernie, Bess and Jamestown. Valuable data are provided on milling and baking quality of entries, and genotypic analyses identify alleles present at numerous important loci. In addition, the nursery facilitates the sharing of the best resistant materials throughout the breeding community.

The 2008-09 nursery comprised 54 advanced generation breeding lines and four check cultivars, 'Ernie', 'Bess', 'Jamestown' (partially resistant) and 'Coker 9835' (susceptible). Seven U.S. public programs (Univ. of Arkansas, Univ. of Georgia, Louisiana State University, Univ. of Maryland, N.C. State Univ., VA Tech., and USDA-ARS, and one private company, Agripro-Coker, submitted entries. The nursery was distributed to 11 U.S., one Hungarian, and one Romanian cooperator for field, and / or greenhouse evaluations. In addition, three USDA-ARS laboratories conducted evaluations for Hessian fly resistance, milling and baking quality and marker genoypes based on established diagnostic markers.

Mean performance results are shown in Table 1. Copies of the full report will be available at the 2009 National Fusarium Head Blight Forum and subsequently on line at the USWBSI web site: http://www.scabusa.org

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Table 1. Mean performance of the 57 entries in the 2008-09 Southern Uniform Winter Wheat Scab Nursery evaluated at up to 11 locations for components of FHB resistance.

	Cultivar/ Designation	FHB ncidence		FHB Severity		FHB Index		FDK		ISK		DON		G'hse # Florets		Heading Date		Plant Height		*Fhb1*
			RANK		*RANK*		*RANK*		*RANK*		*RANK*		*RANK*		*RANK*		*RANK*		*RANK*	*3BS*
1	ERNIE	45	*16*	25	*4*	17	*6*	17	*6*	39	*17*	16	*46*	2	*10*	129	*1*	33	*8*	*no*
2	COKER 9835	65	*57*	56	*56*	50	*57*	47	*57*	65	*56*	15	*42*	11	*43*	133	*43*	32	*1*	*no*
3	BESS	40	*4*	18	*1*	12	*1*	12	*1*	29	*2*	8	*4*	2	*10*	131	*17*	36	*39*	*no*
4	JAMESTOWN	44	*9*	27	*10*	20	*14*	22	*21*	30	*3*	8	*4*	12	*45*	129	*1*	32	*1*	*no*
5	AR 97002-2-1	41	*5*	26	*6*	16	*5*	20	*15*	36	*8*	6	*1*	1	*2*	130	*6*	34	*20*	*no*
6	AR99039-5-2	49	*36*	36	*32*	30	*45*	35	*45*	49	*40*	17	*49*	25	*56*	136	*56*	35	*29*	*no*
7	AR 99263-7-1	46	*23*	25	*4*	19	*10*	19	*12*	40	*20*	12	*25*	9	*34*	133	*43*	39	*55*	*no*
8	VA05W-510	48	*30*	28	*11*	22	*22*	19	*12*	42	*26*	11	*19*	7	*28*	130	*6*	34	*20*	*no*
9	B030543	46	*23*	28	*11*	21	*18*	16	*4*	41	*22*	7	*2*	9	*34*	131	*17*	35	*29*	*no*
10	LA01164D-94-2	48	*30*	29	*18*	24	*28*	18	*10*	45	*33*	11	*19*	4	*19*	132	*34*	34	*20*	*yes*
11	LA01162D-131-8	44	*9*	29	*18*	21	*18*	21	*19*	33	*4*	11	*19*	5	*22*	131	*17*	35	*29*	*yes*
12	LA01162D-136-8	50	*38*	37	*34*	29	*42*	29	*36*	41	*22*	12	*25*	18	*52*	133	*43*	33	*8*	*yes*
13	GA 031454-DH7	53	*44*	44	*48*	32	*48*	31	*38*	50	*43*	10	*17*	1	*2*	131	*17*	38	*50*	*no*
14	GA 031307-DH14	59	*52*	46	*50*	30	*45*	31	*38*	54	*51*	14	*35*	9	*34*	130	*6*	32	*1*	*no*
15	NC05-21090	50	*38*	37	*34*	27	*35*	23	*22*	47	*36*	15	*42*	22	*55*	131	*17*	33	*8*	*no*
16	AR 99254-7-1	46	*23*	28	*11*	22	*22*	19	*12*	39	*17*	19	*51*	2	*10*	134	*52*	38	*50*	*no*
17	AR 99054-4-1	41	*5*	35	*28*	19	*10*	16	*4*	33	*4*	14	*35*	7	*28*	133	*43*	38	*50*	*no*
18	AR 99071-7-2	49	*36*	33	*25*	27	*35*	31	*38*	48	*38*	16	*46*	20	*53*	132	*34*	36	*39*	*no*
19	MD02W81-08-6	44	*9*	31	*21*	23	*25*	35	*45*	43	*29*	11	*19*	15	*49*	133	*43*	36	*39*	*no*
20	MD01W255-08-1	45	*16*	34	*26*	23	*25*	24	*27*	41	*22*	11	*19*	11	*43*	132	*34*	35	*29*	*no*
21	M05-1531	45	*16*	28	*11*	20	*14*	20	*15*	36	*8*	9	*9*	9	*34*	130	*6*	36	*39*	*no*
22	B0390207	54	*45*	44	*48*	29	*42*	27	*33*	48	*38*	13	*31*	3	*14*	129	*1*	34	*20*	*no*
23	03M1539#031	45	*16*	35	*28*	23	*25*	18	*10*	33	*4*	13	*31*	6	*25*	130	*6*	35	*29*	*no*
24	03M1599#0007	54	*45*	50	*52*	35	*50*	42	*53*	51	*46*	12	*25*	10	*41*	130	*6*	34	*20*	*no*
25	MH06-2370	44	*9*	31	*21*	20	*14*	21	*19*	39	*17*	9	*9*	9	*34*	131	*17*	35	*29*	*no*
26	ML07*7571	46	*23*	26	*6*	18	*9*	17	*6*	38	*14*	13	*31*	3	*14*	131	*17*	34	*20*	*no*
27	ML07-7758	43	*8*	24	*3*	17	*6*	20	*15*	36	*8*	7	*2*	1	*2*	131	*17*	39	*55*	*het*
28	VA04W-90	48	*30*	35	*28*	28	*38*	24	*27*	43	*29*	9	*9*	6	*25*	131	*17*	35	*29*	*no*
29	VA05W-534	37	*1*	28	*11*	14	*2*	14	*2*	28	*1*	9	*9*	8	*33*	130	*6*	35	*29*	*no*
30	VA06W-575	48	*30*	38	*37*	26	*31*	23	*22*	41	*22*	12	*25*	3	*14*	130	*6*	32	*1*	*no*
31	VA06W-587	44	*9*	31	*21*	19	*10*	17	*6*	38	*14*	8	*4*	1	*2*	129	*1*	34	*20*	*no*
32	VA07W-568	44	*9*	30	*20*	17	*6*	15	*3*	37	*12*	8	*4*	1	*2*	131	*17*	35	*29*	*no*
33	VA07W-607	45	*16*	28	*11*	20	*14*	17	*6*	44	*31*	8	*4*	12	*45*	131	*17*	33	*8*	*no*
34	VA05W-640	46	*23*	38	*37*	24	*28*	33	*42*	49	*40*	14	*35*	4	*19*	130	*6*	34	*20*	*no*
35	LA01141D-98-6-2	64	*56*	53	*54*	43	*55*	43	*54*	66	*57*	14	*35*	1	*2*	133	*43*	32	*1*	*yes*
36	LA03187C-2	48	*30*	48	*51*	34	*49*	39	*51*	56	*52*	14	*35*	4	*19*	132	*34*	36	*39*	*no*
37	LA01164D-43-7-B	38	*2*	34	*26*	19	*10*	25	*30*	36	*8*	12	*25*	3	*14*	131	*17*	37	*48*	*no*
38	ARGE97-1048-6	60	*54*	52	*53*	35	*50*	35	*45*	49	*40*	20	*54*	3	*14*	131	*17*	36	*39*	*no*
39	GA 991209-6E33	61	*55*	54	*55*	35	*50*	38	*50*	53	*48*	15	*42*	1	*2*	130	*6*	36	*39*	*no*
40	GA 031454-DH38-7	45	*16*	31	*21*	21	*18*	20	*15*	42	*26*	9	*9*	6	*25*	132	*34*	33	*8*	*no*
41	GA 031454-DH38-8 (11?)-	46	*23*	28	*11*	21	*18*	28	*34*	45	*33*	10	*17*	5	*22*	131	*17*	34	*20*	*no*
42	GA 991109-1-G1	54	*45*	40	*41*	26	*31*	23	*22*	42	*26*	14	*35*	1	*2*	129	*1*	33	*8*	*no*
43	GA 991109-1-G2	58	*50*	43	*45*	28	*38*	28	*34*	50	*43*	11	*19*	0	*1*	130	*6*	35	*29*	*no*
44	ARS03-5358	51	*40*	43	*45*	28	*38*	39	*51*	53	*48*	23	*56*	9	*34*	134	*52*	41	*57*	*no*
45	ARS03-3806	39	*3*	22	*2*	15	*3*	23	*22*	37	*12*	9	*9*	2	*10*	132	*34*	36	*39*	*no*
46	ARS03-4736	58	*50*	37	*34*	28	*38*	32	*41*	52	*47*	15	*42*	9	*34*	132	*34*	37	*48*	*no*
47	ARS04-1249	46	*23*	35	*28*	29	*42*	36	*48*	50	*43*	23	*56*	16	*50*	135	*54*	36	*39*	*no*
48	ARS05-0443	45	*16*	40	*41*	24	*28*	43	*54*	40	*20*	18	*50*	12	*45*	133	*43*	33	*8*	*no*
49	ARS05-0242	55	*48*	58	*57*	43	*55*	44	*56*	61	*55*	19	*51*	10	*41*	133	*43*	33	*8*	*no*
50	ARS05-1044	44	*9*	26	*6*	15	*3*	24	*27*	38	*14*	20	*54*	5	*22*	131	*17*	38	50	*no*
51	ARS05-1234	48	*30*	42	*44*	35	*50*	34	*44*	57	*54*	19	*51*	14	*48*	135	54	38	50	*no*
52	NC05-23015	51	*40*	39	*40*	26	*31*	25	*30*	45	*33*	14	*35*	20	*53*	131	17	32	1	*no*
53	NC05-20671	52	*43*	40	*41*	27	*35*	29	*36*	47	*36*	9	*9*	7	*28*	131	17	32	1	*no*
54	NC05-21937	59	*52*	43	*45*	40	*54*	36	*48*	56	*52*	16	*46*	29	*57*	133	43	33	8	*yes*
55	NC06-20288	55	*48*	38	*37*	30	*45*	33	*42*	53	*48*	9	*9*	7	*28*	132	34	33	8	*no*
56	NC07-23170	51	*40*	36	*32*	26	*31*	23	*22*	44	*31*	13	*31*	17	*51*	132	34	33	8	*no*
57	NC07-22927	41	*5*	26	*6*	22	*22*	26	*32*	35	*7*	12	*25*	7	*28*	136	57	33	8	*het*
	Mean	48.5		36		25		27		44		13		34		131		35		
	LSD (0.05)	21.0		26		20		24		17		10		35		3		3		
	CV%	22.0		37.1		40.8		44.9		19.3		40.5		50.7		1.3		4.0		

ASSOCIATION MAPPING QTL FOR FHB RESISTANCE IN SIX-ROW BARLEY BREEDING LINES

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ABSTRACT

Association mapping is a strategy to identify significant associations between markers and quantitative trait loci (QTL) that does not rely on bi-parental mapping populations. We used association mapping to identify QTL for FHB resistance using six-row spring barley breeding lines from North Dakota State University and the University of Minnesota six-rowed breeding programs. Lines were evaluated in mist-irrigated and inoculated field nurseries. FHB severity, rated as a percentage of diseased kernels, and deoxynivalenol concentration in harvested grain was collected over two years in several environments. The software TASSEL v. 2.1 was used to identify associations between two sets of 1536 barley Oligo Pool Assay (BOPA I and II) single nucleotide polymorphism (SNP) markers and disease data. Markers were evaluated in two sets in each breeding program; BOPA I alone and BOPA I/BOPA II combined. Three models, naïve association, structure matrix (using principal component analysis), and structure plus kinship matrix were used to detect significant associations. We will report analyses that examine the effect of marker number on detection of QTL and compare QTL identified in the two breeding programs.

PROGRESS ON DEVELOPMENT AND APPLICATION OF SINGLE KERNEL NIR SORTING TECHNOLOGY FOR ASSESSMENT OF FHB RESISTANCE IN WHEAT GERMPLASM

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ABSTRACT

We are developing Near Infrared (NIR) spectroscopic methods to sort *Fusarium* damaged wheat kernels (FDK) from sound kernels and to nondestructively determine deoxynivalenol (DON) levels of FDK. Our objective is to facilitate the rapid and objective evaluation of varieties for *Fusarium* resistance. We herein report progress and highlight research results in the development and use of our single kernel NIR (SKNIR) scab sorting and DON estimation techniques and other scab related studies.

Since December 2008 we have sorted 216 kernel samples for *Fusarium* damage from North Dakota State University (NDSU) and 216 samples from University of Nebraska, Lincoln (UNL) wheat breeders. DON analysis of sorted FDK fractions of NDSU samples for two seasons confirmed that SKNIR sorted FDK fractions had significantly higher DON levels. Therefore, this technique may be employed to obtain a more detailed characterization of host plant resistance mechanisms compared to characterizations that are based on DON analyses of composite samples.

We investigated the NIR absorbance characteristics of DON and that of sound and *Fusarium* damaged wheat kernels and showed that DON has NIR absorption bands with peaks at 1408, 1904 and 1919 nm. Therefore NIR may be absorbed by DON in *Fusarium* damaged wheat kernels indicating the suitability of NIR spectroscopic technique for objective evaluation of *Fusarium* damage on the basis of kernel DON levels. In collaboration with UNL, we have also completed a study to assess the accuracy of SKNIR to sort kernels based on scab and DON levels using our scab and DON calibrations.

We studied the distribution of DON levels among single kernels in artificially inoculated wheat spikes. The concentration of DON among single kernels above and below the point of inoculation varied between two varieties studied. Results indicated the existence of asymptomatic kernels with high DON levels as well as scabby kernels without DON in infected spikes. This may in part explain the failure to observe a consistent relationship between the intensity of scab infestation and DON levels.

We have developed a NIR moisture calibration for the SKNIR to estimate single kernel moisture content in samples having sound and *Fusarium* damaged kernels. This will be helpful to non-destructively estimate DON and other constituent levels of single kernels at a constant moisture basis.

We have initiated work on using Raman Spectroscopy to detect *Fusarium* damage in wheat kernels. Raman spectroscopy has the advantage of being insensitive to water, whereas NIR detection of DON is very sensitive to interference from strong NIR water absorption bands found adjacent to NIR absorption bands of DON. Our preliminary work to study the Raman spectra of pure DON using a 785 nm Raman system showed that DON is a Raman active compound. However, due to heavy fluorescence interference, 785 nm Raman system was not suitable for scanning intact single kernels. Therefore, we expect to use a 1064 nm Raman system for scanning single kernels in the future.

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QTL MAPPING OF FHB RESISTANCE TRAITS IN THE JAPANESE WHEAT LANDRACE, PI 81791

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ABSTRACT

The Japanese wheat landrace, PI 81791 (Sapporo Haru Komungi Jugo), has consistent resistance to FHB in field and greenhouse studies. A population of 150 recombinant inbred lines was developed from a cross between this genotype and the susceptible spring wheat variety, Wheaton. Phenotypic data for resistance to initial infection (type 1), and resistance to the spread of infection (type 2) was collected in four field environments. Post-harvest resistance traits, including grain weight, visually scabby kernels (VSK), and DON accumulation were analyzed from grain harvested from these same field experiments. Type 2 data also was collected from two greenhouse-based point inoculation experiments. Approximately 500 SSR markers were used to construct linkage maps for all chromosomes. Composite interval mapping was used to identify QTL for resistance and single marker analysis was used to identify markers associated with these QTL. Markers with $P < 0.01$ for grand averages for each trait and $P < 0.05$ for at least 3 out of 4 environments were considered significant and explored for marker assisted selection. These analyses identified QTL on chromosomes 2B, 2D, 3A, 3B, 3D, 4A, 4D, 5A, 5B, and 6B. Two QTL on both 3BL and 5AL and a single QTL on 4D were associated with several different resistance traits, including type 1 and 2 field resistance, post harvest grain traits, and greenhouse type 2 resistance. The QTL on the distal end of 5AL is near marker Xwmc727 (R^2=2-6.6%), and may represent, or lie adjacent to, a QTL identified in the winter wheat varieties Apache, Pirat and Arina (Holzapfel *et al*., *Theor Appl Genet*, 2008). The QTL on the proximal end of 5AL is near marker Xwmc415 (R^2=3.1-6.8%), and maps at or near a QTL for DON accumulation identified in Nyubai. The QTL on 3BL are both located in the central region. One is near Xgpw94037 (R^2=3.0-8.6%) and a QTL for type 2 resistance identified in Ernie, and the other appears to be a novel QTL near Xgwm108 (R^2=3.2-10.9%). The QTL on 4D may be problematic to utilize as the resistance QTL is flanked by QTL for plant height and heading date (morphological traits that can influence resistance). However, selection with marker Xgwm192 (R^2=3.1-9.0%) may help avoid confluence of resistance and morphological traits, as this marker is significantly associated with resistance traits, but not with morphological characters. Major QTL for type 2 greenhouse resistance were identified on chromosomes 2B (Xgwm120, R^2=1.1-5.7%) and 3A (Xbarc1057, R^2=12.4-15.8%; Xgwm30, R^2=12.2-16.0%). The 2B QTL also was significant for field and grain resistance. These QTL map in regions previously identified for type 2 resistance in Ning7840 and Strongfield. The QTL on 3A, however, did not provide field-related resistance in our population even though it is in a region associated with FHB resistance QTL in other wheat varieties. Overall, markers Xgwm120 (2B), Xbarc1057 and Xgwm30 (3A), Xgpw94037, Xbarc229, and Xgwm108 (3B), Xbarc98 and/or Xgwm192 (4D), Xwmc415 and Xwmc727 (5A) represent QTL for a variety of resistance traits and can be used for validation purposes as well as marker assisted selection. The markers Xwmc111 (2D, adjacent to heading date QTL), Xwmc656 (3D), Xbarc233 (4A), Xbarc156 (5B), and Xgwm219 (6B) can be used in addition to the markers listed above to select on minor QTL for field, greenhouse, and grain resistance traits.

MAPPING AND INTROGRESSION OF FHB RESISTANT QUANTITATIVE TRAIT LOCI FROM TWO SPRING WHEAT GENOTYPES USING A FAMILY-BASED APPROACH

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ABSTRACT

Finding new quantitative trait loci (QTL), and introgressing them into adopted genetic backgrounds is a very important objective in the development of wheat cultivars resistant to the Fusarium head blight (FHB). We previously reported the use of a family-based method for QTL mapping in plant breeding families that allows for simultaneous mapping, marker validation, and marker-aided selection. We are applying this method to map QTLs in two resistant genotypes "SD3934" and "Mult 757". Three- and four-way crosses were made to develop families and each family had one of the resistant genotypes as a parent. The SD3934 based population consisted of 90 families with an average size of 13. Similarly, the Mult 757 population consisted on 86 families with an average size of 10. Genotyping was performed using simple sequence repeat (SSR) and sequence tagged sites (STS) markers elucidated on an ABI 3031*xl* genetic analyzer. Phenotyping F_1 plants for FHB resistance was performed in the greenhouse through artificial inoculation of a mixture of isolates collected from South Dakota. Mapping was performed using both family-based linkage (variance component linkage and pedigree-wide regression) and association (quantitative transmission disequilibrium test) approaches. Results from SD3934 suggest the presence of a QTL on chromosome 3BS. Selected individuals carrying the resistance allele were further advanced to the F_2 generation. Similar procedures will be followed with Multi 757 families. Results of this experiment further document the usefulness of a family-based method for simultaneous mapping, marker validation, and marker-assisted selection, within adapted genetic backgrounds.

RESULTS FROM THE SECOND *FUSARIUM* INTERNATIONAL SPRING WHEAT NURSERY (FIEPSN)

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ABSTRACT

The *Fusarium* International Elite and Preliminary Spring Wheat Nursery (FIEPSN) was assembled after merging the *Fusarium* International Elite Spring Wheat Nursery (FIESWN) and *Fusarium* International Preliminary Spring Wheat Nursery (FIPSWN) and distributed in 2009. Entries were tested for Type-I resistance and DON content at CIMMYT in Mexico, both in 2008 and 2009. Plants were inoculated artificially using precision CO_2 backpack sprayers equipped with flat fan nozzles at a defined pressure of 40 psi. Inoculum concentration was adjusted to 50,000 conidia ml^{-1} and 39 ml of inoculum per meter were applied. The inoculum consisted of a mixture of 5 different *F. graminearum* strains collected during the preceding year in naturally infected fields. Haplotyping was conducted at USDA-ARS (Fargo, ND) to determine the presence or abscence of different QTLs: 3B, 5A and 6B (Sumai #3), 3A and 5A (Frontana), 2D and 4B (Wuhan 1), 2D (CJ9306) and 3A and 7A (*T. dicoccoides*). Sumai #3 (resistant) and Flycatcher (Ocoroni F 86) and Gamenya (both susceptible checks) were used as controls.

The FHB index ranged from 0.87% (Sumai #3) to 68.95% (Gamenya) in 2008 and from 0.06% (Sumai #3) to 93.7% (Gamenya) in 2009, respectively. Drought stress in July 2009 resulted in lower FHB indices for most genotypes in comparison to 2008 in spite of a higher FHB severity observed in Gamenya. The drought conditions seemed not to influence the DON content. No correlation could be observed between FHB index and DON content in both years: r = 0.27 in 2008 and r = 0.05 in 2009, respectively, This observation may result from two explanations. (i) Mostly tolerant and nearly resistant material have been tested and showed low FHB indices in most cases whereas Type-I resistance does not necessarily offer protection against high DON contamination. (ii) The materials were tested under high artificial inoculation pressure which can lead to much higher DON contamination than natural infection. The haplotyping showed the diversity of sources of resistance within the FIEPSN. Only 4 lines of the nursery had the QTLs from Sumai #3 which suggest that new sources of resistance to FHB have become available.

SCREENING FOR NEW SOURCES OF FUSARIUM HEAD BLIGHT RESISTANCE IN CHINESE WHEATS FROM CIMMYT GERMPLASM BANK

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ABSTRACT

The evaluation of 583 Chinese wheat genotypes from CIMMYT germplasm bank was initiated in 2009 to identify new sources of Fusarium Head Blight resistance. This preliminary trial was not replicated due to the small amount of seed available.

Plants were tested in hill plots for Type-I resistance at CIMMYT in El Batan (Mexico) under artificial inoculation using precision CO_2 backpack sprayers equipped with flat fan nozzles at a defined pressure of 40 psi. The inoculum concentration was adjusted to 50,000 conidia ml^{-1} and 39 ml of inoculum per meter was applied. The inoculum consisted of a mixture of 5 different *F. graminearum* strains collected during the preceding year in naturally infected fields. Five tillers that flowered at the same time were scored 30 days after inoculation. A total of 491 entries out of 583 genotypes could be evaluated. Of these 491 lines, 13 genotypes (2.9%) showed a FHB index of 0%, a level of severity similar or lower than resistant check Sumai #3 which had a FHB index of 0.05%. The susceptible check Gamenya showed the highest FHB index (96.6%). Of the 491 lines 313 genotypes (63.7%) showed a FHB index below 7% whereas 134 lines (27.3%) scored below 1%.

Genotypes with a FHB index lower than 7% will be planted in hillplots at CIMMYT's field station in Ciudad Obregón for seed increase to allow the confirmation of preliminary results under FHB artificial epidemic using larger plots in 2010 at El Batan. In Ciudad Obregón, genotypes will also be selected for leaf rust resistance and agronomic type.

FAMILY-BASED ASSOCIATION ANALYSIS FOR PLANT POPULATIONS

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ABSTRACT

Association analyses (AA) test the association between marker loci and phenotypic variation. Plant geneticists have generally used a population-based AA (PBAA) where a single statistic is computed across all levels of population structure and then tested for significance. PBAA models must model the structure (subgroups, lineages, etc) of a population and adjust for its effect on type I error, a process that can be inadequate in small highly structure populations. In family-based AA (FBAA), statistics are computed within lineages of related individuals, then compiled over the lineages and tested for significance. As such, population structure does not lead to type I error and significance in a FBAA requires linkage between marker loci and QTL.

FBAA and PBAA were first developed in mammalian genetics where FBAA has been used extensively. Only recently have human geneticists started to use PBAA, motivated by reasons that are not applicable to plants genetics. First, family data is expensive to generate in humans whereas it is cheap in plants due to the extensive phenotyping conducted by large breeding programs. Second, human populations used in human genetics have little structure due to experimental design and careful *apriori* sampling of case/controls from all levels of a population's structure. This minimizes the impact of the structure on type I error from PBAA. In contrast, plant populations used in PBAA so far are very structured and perhaps poorly suited for PBAA despite their success. Uses of simple FBAA approaches in plant breeding populations for QTL discovery and QTL validation will be discussed.

REPORT ON THE 2008-09 NORTHERN UNIFORM WINTER WHEAT SCAB NURSERIES (NUWWSN AND PNUWWSN)

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OBJECTIVES

This is a summary of the report on the 2008-2009 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 after the 2009 forum. The objective of these tests is to screen winter wheat genotypes 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. The 60 entries in the NUWWSN came from 13 programs while the 46 entries in the PNUWWSN entries came from nine programs (Table 2).

RESULTS

Many entries in the NUWWSN showed very good resistance to FHB (Table 3). Over 33.3% (21/60) were not significantly different from the most resistant entry for all seven FHB traits: seven of these were also more resistant than the most susceptible entry for all seven traits. Only three entries had DON levels < 5 ppm from these inoculated and listed nurseries. FHB resistance was lower in the PNUWWSN (Tables 4,5) than in the NUWWSN (Table 6) as only 6.5% (3/46) of the entries were not significantly different that the most resistant entry for all six traits and none had DON levels < 5 ppm.

Table 1. Traits assessed in the 2008-09 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,IN,IN,KY,MI,MO,ON,VA	IL,IN,IN,KY,MD,MI,MO,NE,NY,OH ON,VA
INC	Disease incidence	% of heads with at least one infected spikelets	IL,IN,IN,KY,MI,MO,ON,VA	IL,IN,IN,KY,MD,MI,MO,NE,NY,OH ON,VA
IND	Disease index	IND = (SEVxINC)/100	IL,IN,KY,MI,MO,OH,ON,VA	IL,IN,KY,MD,MI,MO,NE,NY,OH ON,VA
FDK	Fusarium damaged kernels	Percentage of grain ishowing sypmotoms of Fusarium infection	IL,IN,KY,MO,RO	IL,IN,IN,KY,MD, MO,NE,RO
ISK	Composite of head and kernel traits	ISK Index = .3 (Severity) + .3 (Incidence)+.4 (FDK)	IL,IN,KY,MO	IL,IN,KY,MD,MO,NE
DON	DON (vomitoxin)	PPM of vomitoxin in grain	KY,VA	KY,MD,NE,VA
GH	Greenhouse severity	Same as SEV except from greenhouse	IL	IL,MO

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

Table 2. Entries in the 2008-09 PNUWWSN and NUWWSN.

NUWWSN NAME	NUWWSN PEDIGREE
ERNIE	CHECK
TRUMAN	CHECK
FREEDOM	CHECK
PIONEER 2545	CHECK
P.03615A1-4-4	Ernie/INW0316//981358/97462
P.04704A1-2-1-1	INW0316*2//Ernie/9346
P.053A1-6-7	2754/INW0412/Truman/INW0303
P.0537A1-7-12	INW0411/2754//INW0412/98134
P.0128A1-22-22	L4/Foster/4/Gfd/X117/3/VA54-429//92145
MOCHA	OH489/OH490
SHAVER	NASW84-345/Coker9835//0H419/OH389
RUBIN	MO800071-56/PION2545//KY88C
ARENA	NASW84-345/Coker9835//0H419/OH389
CANON	MV 17/RUBY
NE06469	Unknown
NI04420	NE96644//PAVON/*3SCOUT66/3/WAHOO SIB
NI04427	KS98HW22//W95-615W/N94L189
NE05459	IN92823A1-1-4-5/NE92458
NE06471	W95-610W/WAHOO//NE98574
NY03179FHB-10	NY7387/Caledonia//Caledonia-2///Caledonia
NY03180FHB-10	NY7387/Caledonia//Caledonia-2///Caledonia
NY03179FHB-12	NY7387/Caledonia//Caledonia-2///Caledonia
NYW103-21-9183	Cayuga/ Caledonia
NYW103-102-9103	Cayuga/ Caledonia
IL02-18228	Pio25R26/9634-24437//95-4162
IL04-7874	G65201/ IL98-12212
IL04-7942	G65201/ IL98-12212
IL04-10721	IL95-4162/ IL97-7010
IL04-10741	IL95-4162/ IL97-7010
MD02W81-08-2	Freedom/Ning7840//VA97W533
MD02W81-08-4	Freedom/Ning7840//VA97W533
ACF213003B	
ACF126103	
ACF12004	
RCUOGTr34	
RCUOGTr35	
M05-1531	LA87167-D8-/P92118B4-2
B0390207	BL931167/Pioneer 2643
03M1539#031	GIBSON/92226E2-5-3
03M1599#0007	M99*3038/Pioneer 25R49
MO 050101	Bess reselection
MO 050921	Ernie/980521
MO 041020	MO 960429/960112
MO 050219	MO 010708 RS
MO 050144	MO 010708 RS
KY00C-2059-19	KY91C-170-3/2552
KY00C-2515-02	SS 550/KY93C-0721-34
KY00C-2059-24	KY91C-170-3/2552
KY00C-2567-01	SS 520/25W33
KY00C-2143-08	KY90C-048-59/KY90C-160-14
MSU Line E6003	VA96W-403-WS / W14
MSU Line E7035R	MSU Line D6234 / W14
OH04-264-58	OH645/HOPEWELL
OH04-268-39	HOPEWELL/VA96-54-372
OH05-248-38	OH685/OH686

NUWWSN	(continued)
VA07W-580	Goldfield /TRIBUTE//IL4162
VA07W-600	OH 552/SS550//RC-STRATEGY,F8
VA07W-672	REN3260*2//W14/ REN3260 /3/ REN3260
VA06W-558	96W-348/P92823A1-1-4-4-5 //McCORMICK
VA06W-615	ROANE/OH 552//RC STRATEGY

PNUWWS NAME	PNUWWSN PEDIGREE
ERNIE	CHECK
TRUMAN	CHECK
FREEDOM	CHECK
PIONEER 2545	CHECK
P.0513A1-2-3	Truman/INW0731//Fdm/F201R
P.0527A1-9-15	99751/2754//97462/INW0412
P.0558A1-5-5	INW0412/L3//F201R/97462
P.0570A1-7-6	9017/92823//F201R/04302
P.05218A1-6-31	INW0304/9346//97395/INW0411
OH02-12686	FOSTER/HOPEWELL//OH581/OH569
SILAS	OH546/SE1694-12
LINUS	5-TIEGANMAI/PION 25R26
OKIE	F285N3-111/65343(spelt)
PENZO	5-TIEGANMAI/PION 25R26
AJAX	T63/PION2737W
IL04-11003	IL96-3073/ Roane
IL04-17762	IL97-3578/ IL97-7010
IL05-15079	NEL-1538/ KY93C-38-17-1
IL05-27333	IL96-24851-1/ IL97-3574// IL97-3950
IL05-27522	IL96-24851-1/ IL97-3574// IL99-2536
MH06-2370	COOPER/SS550
MH06-2410	M98-1660//PATTON/Pioneer 2552
ML07*7571	VA98W-586/HONEY
ML07-7758	COKER 9025/Pioneer 25R57
MO 050771	MO 960120/MO 960304
MO 041687	MO 960304/MO 960815
MO 071411	MO 980429/P86958RC4-2-1-1-10
MO 071722	MO 980429/Ernie
MO 071522	MO 003013/MO 980525
KY02C-3007-41	25R18/Allegiance
KY02C-3005-25	25R18/McCormick
KY03C-2170-24	VA01W-476/Roane
KY03C-2170-06	VA01W-476/Roane
KY02C-3007-45	25R18/Allegiance
MSU Line E5024	MSU Line D6234 / Pio25W33
VA07W-643	COKER 9474/ McCormick"S"
VA06W-580	Roane / Pion 2684//OH 552
VA07W-591	FREEDM/NC96-13374 // RC-STRATEGY
VA06W-578	Roane / Pion 2684//OH 552
VA04W-90	SS 520/PION2552//ROANE
OH05-101-1	HOPEWELL/PIONEER 25R26
OH05-72-6	PIONEER 25R18/VA97W-375
OH05-249-32	OH685/OH686
OH05-152-68	OH685/PATTON
OH05-164-76	PIONEER 25R18/OH686
OH05-200-74	OH629/HOPEWELL

Table 3. Best (top) and worst (bottom) entries from the 2008-09 NUWWSN. Summary statistics are for all entries.

NAME	INC		SEV		IND		FDK		ISK		DON		GHSEV		#l	#h
MSU Line E6003	40.0	l	10.3	l	6.2	l	7.9	l	23.9	l	5.2	l	19.6	l	7	0
MD02W81-08-4	43.6	l	14.2	l	9.1	l	18.9	l	27.6	l	3.5	l	14.1	l	7	0
MD02W81-08-2	47.3	l	17.9	l	12.1	l	17.0	l	29.6	l	7.0	l	11.3	l	7	0
IL02-18228	35.4	l	19.0	l	12.3	l	9.9	l	25.1	l	2.3	l	35.0	l	7	0
RCUOGTr34	42.3	l	19.7	l	12.8	l	19.6	l	33.3	l	5.8	l	28.4	l	7	0
MO050101	48.0	l	18.2	l	12.9	l	9.1	l	31.3	l	6.6	l	6.8	l	7	0
NYW103-102-9103	40.6	l	22.7	l	13.7	l	16.2	l	29.4	l	6.1	l	10.0	l	7	0
TRUMAN	41.3	l	15.4	l	9.4	l	12.9	l	28.1	l	9.0	hl	4.4	l	7	1
MO050921	42.9	l	19.3	l	11.3	l	14.8	l	27.7	l	12.8	hl	10.5	l	7	1
P.0128A1-22-22	52.4	hl	22.3	l	12.0	l	11.1	l	33.8	l	4.3	l	15.9	l	7	1
IL04-10741	43.4	l	24.5	hl	15.3	l	18.0	l	32.1	l	7.0	l	23.5	l	7	1
RCUOGTr35	47.3	l	26.1	hl	15.4	l	23.9	l	36.9	l	4.3	l	32.0	l	7	1
MO041020	52.2	hl	18.9	l	13.5	l	15.8	l	34.9	l	13.2	hl	10.9	l	7	2
MO050144	56.2	hl	17.7	l	13.5	l	17.3	l	32.4	l	7.7	hl	12.1	l	7	2
VA07W-600	53.0	hl	20.2	l	14.4	l	15.5	l	34.9	l	12.4	hl	14.3	l	7	2
ERNIE	50.8	hl	22.5	l	14.9	l	20.5	l	33.3	l	11.6	hl	19.8	l	7	2
P.0537A1-7-12	58.0	hl	22.8	l	16.1	l	17.0	l	38.5	l	9.2	hl	27.9	l	7	2
VA06W-558	52.9	hl	24.5	hl	16.9	l	21.0	l	33.4	l	5.4	l	17.3	l	7	2
MO050219	55.1	hl	22.2	l	17.1	l	15.5	l	37.6	l	12.6	hl	27.0	l	7	2
IL04-7942	46.2	l	24.8	hl	17.3	l	19.4	l	32.3	l	8.7	hl	16.5	l	7	2
M05-1531	53.9	hl	25.5	hl	17.9	l	23.0	l	38.2	l	4.6	l	12.3	l	7	2
RUBIN	59.3	hl	37.9	h	27.4	h	35.4	h	49.0	h	9.0	hl	60.8		2	6
CANON	69.4	h	35.9	h	28.5	h	31.1	h	50.4	h	7.4	hl	24.6	l	2	6
MOCHA	68.2	h	38.8	h	31.4	h	39.8	h	52.5	h	10.7	hl	21.9	l	2	6
SHAVER	72.0	h	42.3	h	32.7	h	36.4	h	53.0	h	8.9	hl	32.1	l	2	6
P.03615A1-4-4	67.5	h	35.7	h	26.0	h	29.5	h	51.4	h	14.2	h	11.5	l	1	6
NE05459	67.9	h	33.9	h	26.9	h	35.9	h	50.4	h	9.4	hl	40.0		1	6
KY00C-2059-24	68.4	h	34.0	h	26.9	h	26.9	hl	48.7	h	17.9	h	66.5		1	6
P.053A1-6-7	63.3	h	36.3	h	29.8	h	27.4	h	51.0	h	13.8	h	21.5	l	1	6
NI04420	69.9	h	35.8	h	29.9	h	38.9	h	52.7	h	15.7	h	28.2	l	1	6
03M1599#0007	70.4	h	44.2	h	34.6	h	33.4	h	52.3	h	7.5	hl	67.3		1	6
KY00C-2059-19	70.4	h	32.3	h	25.4	h	27.9	h	45.5	h	18.4	h	42.8		0	6
KY00C-2515-02	64.0	h	37.2	h	27.4	h	35.6	h	50.8	h	13.6	h	67.4		0	6
OH05-248-38	69.0	h	40.0	h	30.4	h	36.0	h	51.3	h	14.3	h	84.6		0	6
ARENA	73.9	h	37.3	h	30.9	h	36.6	h	51.4	h	14.9	h	47.1		0	6
B0390207	62.3	h	40.7	h	30.9	h	30.2	h	50.7	h	14.7	h	80.4		0	6
PIONEER 2545	72.4	h	43.7	h	37.4	h	44.2	h	58.6	h	14.0	h	53.1		0	6

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

Table 4. Best (top) and worst (bottom) entries from the 2008-09 PNUWWSN. Summary statistics are for all entries.

NAME	INC		SEV		IND		FDK		ISK		DON		GHSEV	#l	#h
KY02C-3005-25	47.8	l	15.9	l	8.2	l	8.6	l	28.7	l	8.4	l	6.2	6	0
IL05-27522	49.6	l	18.0	l	11.0	l	23.5	l	24.6	l	13.2	hl	13.7	6	1
TRUMAN	35.3	l	20.1	l	11.3	l	18.1	l	29.5	l	8.9	l	3.5	6	0
KY02C-3007-45	52.3		16.2	l	10.3	l	19.1	l	35.6	l	12.3	hl	6.2	5	1
KY02C-3007-41	53.6		17.1	l	10.6	l	20.5	l	36.3	l	13.4	hl	3.4	5	1
MO 050771	50.1		20.7	l	10.9	l	22.0	l	33.4	l	20.9	hl	17.0	5	1
MO 071411	54.4		19.1	l	11.0	l	24.5	l	31.4	l	15.4	hl	37.8	5	1
IL04-17762	54.3		22.6	l	12.3	l	24.5	l	37.2	l	11.9	hl	43.2	5	1
ML07-7758	56.3		22.9	l	12.9	l	30.3	hl	33.8	l	9.7	l	2.7	5	1
OH05-101-1	61.9		22.4	l	13.3	l	28.4	hl	36.2	l	8.9	l	23.3	5	1
VA06W-580	54.2		26.9	l	14.3	l	22.0	l	38.7	l	12.9	hl	2.6	5	1
KY03C-2170-06	60.3		25.9	l	14.8	l	14.1	l	39.2	l	6.7	l	7.7	5	0
IL05-27333	60.3		22.4	l	15.7	l	22.7	l	38.1	l	12.1	hl	9.2	5	1
PIONEER 2545	77.3	h	46.3		36.9	h	46.8	hl	63.0	h	31.0	hl	82.4	2	5
AJAX	70.1	h	49.1	h	36.4	h	51.0	h	63.1	h	37.1	h	45.7	0	6
PENZO	75.0	h	55.5	h	41.8	h	46.8	hl	66.9	h	21.5	hl	41.5	2	6
LINUS	82.1	h	59.2	h	46.5	h	65.2	h	75.8	h	20.7	hl	81.4	1	6

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 2008-09 PNUWWSN.

ENTRY	NAME	INC	SEV	IND	FDK	ISK	DON	GHSEV	#l	#h
1	ERNIE	53.4	23.9 l	14.1 l	21.6 l	34.6 l	21.7 hl	27.3	4	1
2	TRUMAN	35.3 l	20.1 l	11.3 l	18.1 l	29.5 l	8.9 l	3.5	6	0
3	FREEDOM	62.0	27.1 l	18.8	34.6 hl	45.8	21.3 hl	5.7	3	2
4	PIONEER 2545	77.3 h	46.3	36.9 h	46.8 hl	63.0 h	31.0 hl	82.4	2	5
5	P.0513A1-2-3	57.8	25.7 l	16.7 l	26.6 hl	41.5	12.5 hl	57.3	4	2
6	P.0527A1-9-15	72.1 h	35.4	28.5	44.6 hl	61.4 h	21.4 hl	34.0	2	4
7	P.0558A1-5-5	69.2 h	31.9	23.2	35.0 hl	51.5	19.6 hl	8.5	2	3
8	P.0570A1-7-6	68.7 h	39.6	29.6	33.7 hl	55.4	20.3 hl	59.3	2	3
9	P.05218A1-6-31	63.3	27.7 l	17.7 l	36.4 hl	41.7	21.4 hl	9.2	4	2
10	OH02-12686	60.5	34.6	26.1	42.5 hl	56.4	11.2 l	5.0	2	1
11	SILAS	61.6	38.4	24.0	29.9 hl	50.9	21.6 hl	4.5	2	2
12	LINUS	82.1 h	59.2 h	46.5 h	65.2 h	75.8 h	20.7 hl	81.4	1	6
13	OKIE	57.8	40.0	23.2	45.7 hl	48.4	14.8 hl	80.6	2	2
14	PENZO	75.0 h	55.5 h	41.8 h	46.8 hl	66.9 h	21.5 hl	41.5	2	6
15	AJAX	70.1 h	49.1 h	36.4 h	51.0 h	63.1 h	37.1 h	45.7	0	6
16	IL04-11003	55.4	25.3 l	14.5 l	34.5 hl	42.2	11.6 hl	15.2	4	2
17	IL04-17762	54.3	22.6 l	12.3 l	24.5 l	37.2 l	11.9 hl	43.2	5	1
18	IL05-15079	63.5	28.8	19.1	20.1 l	42.5	15.5 hl	10.2	2	1
19	IL05-27333	60.3	22.4 l	15.7 l	22.7 l	38.1 l	12.1 hl	9.2	5	1
20	IL05-27522	49.6 l	18.0 l	11.0 l	23.5 l	24.6 l	13.2 hl	13.7	6	1
21	MH06-2370	62.3	32.6	22.0	43.6 hl	47.7	12.6 hl	30.7	2	2
22	MH06-2410	53.9	21.2 l	14.3 l	25.0 l	41.3	16.6 hl	13.7	4	1
23	ML07*7571	64.3	24.2 l	16.7 l	40.6 hl	43.4	20.6 hl	7.6	4	2
24	ML07-7758	56.3	22.9 l	12.9 l	30.3 hl	33.8 l	9.7 l	2.7	5	1
25	MO 050771	50.1	20.7 l	10.9 l	22.0 l	33.4 l	20.9 hl	17.0	5	1
26	MO 041687	62.7	35.2	23.0	24.9 l	46.6	20.2 hl	42.8	2	1
27	MO 071411	54.4	19.1 l	11.0 l	24.5 l	31.4 l	15.4 hl	37.8	5	1
28	MO 071722	66.0	35.7	22.7	26.9 hl	45.0	13.8 hl	33.2	2	2
29	MO 071522	49.5 l	28.8	20.8	17.2 l	47.3	7.0 l	5.3	3	0
30	KY02C-3007-41	53.6	17.1 l	10.6 l	20.5 l	36.3 l	13.4 hl	3.4	5	1
31	KY02C-3005-25	47.8 l	15.9 l	8.2 l	8.6 l	28.7 l	8.4 l	6.2	6	0
32	KY03C-2170-24	58.1	28.3 l	14.3 l	35.1 hl	35.0 l	13.4 hl	24.2	5	2
33	KY03C-2170-06	60.3	25.9 l	14.8 l	14.1 l	39.2 l	6.7 l	7.7	5	0
34	KY02C-3007-45	52.3	16.2 l	10.3 l	19.1 l	35.6 l	12.3 hl	6.2	5	1
35	MSU Line E5024	59.0	25.1 l	18.5 l	30.0 hl	40.9	36.9 h	75.3	3	1
36	VA07W-643	66.4	23.8 l	17.4 l	24.8 l	43.4	10.8 l	3.3	4	0
37	VA06W-580	54.2	26.9 l	14.3 l	22.0 l	38.7 l	12.9 hl	2.6	5	1
38	VA07W-591	73.3 h	31.5	21.8	36.1 hl	46.9	24.7 hl	28.2	2	3
39	VA06W-578	69.5 h	32.6	24.0	36.9 hl	49.8	22.7 hl	25.2	2	3
40	VA04W-90	57.2	28.8	17.5 l	27.0 hl	42.2	16.9 hl	10.0	3	2
41	OH05-101-1	61.9	22.4 l	13.3 l	28.4 hl	36.2 l	8.9 l	23.3	6	2
42	OH05-72-6	59.3	28.5 l	14.5 l	36.8 hl	40.7	15.0 hl	23.5	4	2
43	OH05-249-32	53.2	25.7 l	15.6 l	37.6 hl	36.4 l	13.7 hl	97.2	5	2
44	OH05-152-68	56.4	32.1	20.1	41.6 hl	46.6	16.5 hl	28.0	2	2
45	OH05-164-76	63.3	24.2 l	16.3 l	29.2 hl	44.2	16.5 hl	5.4	4	2
46	OH05-200-74	57.5	22.0 l	13.8 l	36.9 hl	40.1	15.0 hl	3.3	4	2
	AVERAGE	60.3	29.1	19.3	31.4	43.9	16.8	26.1		
	MINUMUM	35.3	15.9	8.2	8.6	24.6	6.7	2.6		
	MAXIMUM	82.1	59.2	46.5	65.2	75.8	37.1	97.2		
	LSD(0.05)	14.6	12.8	10.4	38.9	14.8	25.8	.		
	# ENVIRONS	8	7	8	5	4	2	1		

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 2008-09 NUWWSN.

NAME	INC		SEV		IND		FDK		ISK		DON		GHSEV		#l	#h
ERNIE	50.8	hl	22.5	l	14.9	l	20.5	l	33.3	l	11.6	hl	19.8	l	7	2
TRUMAN	41.3	l	15.4	l	9.4	l	12.9	l	28.1	l	9.0	hl	4.4	l	7	1
FREEDOM	56.9	hl	20.3	l	14.6	l	29.6	h	38.5	l	10.7	hl	8.2	l	6	3
PIONEER 2545	72.4	h	43.7	h	37.4	h	44.2	h	58.6	h	14.0	h	53.1		0	6
P.03615A1-4-4	67.5	h	35.7	h	26.0	h	29.5	h	51.4	h	14.2	h	11.5	l	1	6
P.04704A1-2-1-1	63.2	h	41.0	h	31.3	h	24.3	l	48.7	h	11.5	hl	28.4	l	3	5
P.053A1-6-7	63.3	h	36.3	h	29.8	h	27.4	h	51.0	h	13.8	h	21.5	l	1	6
P.0537A1-7-12	58.0	hl	22.8	l	16.1	l	17.0	l	38.5	l	9.2	hl	27.9	l	7	2
P.0128A1-22-22	52.4	hl	22.3	l	12.0	l	11.1	l	33.8	l	4.3	l	15.9	l	7	1
MOCHA	68.2	h	38.8	h	31.4	h	39.8	h	52.5	h	10.7	hl	21.9	l	2	6
SHAVER	72.0	h	42.3	h	32.7	h	36.4	h	53.0	h	8.9	hl	32.1	l	2	6
RUBIN	59.3	hl	37.9	h	27.4	h	35.4	h	49.0	h	9.0	hl	60.8		2	6
ARENA	73.9	h	37.3	h	30.9	h	36.6	h	51.4	h	14.9	h	47.1		0	6
CANON	69.4	h	35.9	h	28.5	h	31.1	h	50.4	h	7.4	hl	24.6	l	2	6
NE06469	57.8	hl	25.7	hl	18.5	l	34.4	h	41.6	h	17.1	h	50.1		3	5
NI04420	69.9	h	35.8	h	29.9	h	38.9	h	52.7	h	15.7	h	28.2	l	1	6
NI04427	70.4	h	33.8	h	27.3	h	34.9	h	49.7	h	9.4	hl	27.7	l	1	5
NE05459	67.9	h	33.9	h	26.9	h	35.9	h	50.4	h	9.4	hl	40.0		1	6
NE06471	62.0	h	30.7	h	23.8	hl	30.0	h	49.2	h	7.8	hl	28.0	l	3	6
NY03179FHB-10	55.8	hl	25.3	hl	20.5	hl	23.1	l	40.5	l	13.2	hl	31.8	l	7	4
NY03180FHB-10	52.1	hl	29.0	hl	20.0	hl	23.4	l	39.3	l	6.5	l	24.8	l	7	3
NY03179FHB-12	61.6	h	34.0	h	26.9	h	25.1	hl	47.5	h	11.8	hl	32.3	l	3	6
NYW103-21-9183	57.3	hl	31.6	h	22.4	hl	23.7	l	44.0	h	5.4	l	20.8	l	5	4
NYW103-102-9103	40.6	l	22.7	l	13.7	l	16.2	l	29.4	l	6.1	l	10.0	l	7	0
IL02-18228	35.4	l	19.0	l	12.3	l	9.9	l	25.1	l	2.3	l	35.0	l	7	0
IL04-7874	50.0	hl	25.9	hl	19.1	l	16.3	l	32.4	l	12.2	hl	25.6	l	7	3
IL04-7942	46.2	l	24.8	hl	17.3	l	19.4	l	32.3	l	8.7	hl	16.5	l	7	2
IL04-10721	52.8	hl	25.8	hl	19.0	l	16.5	l	34.9	l	7.3	hl	20.1	l	7	3
IL04-10741	43.4	l	24.5	hl	15.3	l	18.0	l	32.1	l	7.0	l	23.5	l	7	1
MD02W81-08-2	47.3	l	17.9	l	12.1	l	17.0	l	29.6	l	7.0	l	11.3	l	7	0
MD02W81-08-4	43.6	l	14.2	l	9.1	l	18.9	l	27.6	l	3.5	l	14.1	l	7	0
ACF213003B	60.1	hl	30.3	hl	22.3	hl	30.2	h	40.5	l	11.2	hl	35.0	l	6	5
ACF126103	62.1	h	29.9	hl	23.2	hl	26.7	hl	43.2	h	17.7	h	29.5	l	4	7
ACF12004	64.8	h	31.1	h	23.5	hl	35.8	h	43.9	h	8.8	hl	45.5		2	6
RCUOGTr34	42.3	l	19.7	l	12.8	l	19.6	l	33.3	l	5.8	l	28.4	l	7	0
RCUOGTr35	47.3	l	26.1	hl	15.4	l	23.9	l	36.9	l	4.3	l	32.0	l	7	1
M05-1531	53.9	hl	25.5	hl	17.9	l	23.0	l	38.2	l	4.6	l	12.3	l	7	2
B0390207	62.3	h	40.7	h	30.9	h	30.2	h	50.7	h	14.7	h	80.4		0	6
03M1539#031	49.2	hl	30.2	hl	18.6	l	17.4	l	38.3	l	9.2	hl	41.6		6	3
03M1599#0007	70.4	h	44.2	h	34.6	h	33.4	h	52.3	h	7.5	hl	67.3		1	6
MO050101	48.0	l	18.2	l	12.9	l	9.1	l	31.3	l	6.6	l	6.8	l	7	0
MO050921	42.9	l	19.3	l	11.3	l	14.8	l	27.7	l	12.8	hl	10.5	l	7	1
MO041020	52.2	hl	18.9	l	13.5	l	15.8	l	34.9	l	13.2	hl	10.9	l	7	2
MO050219	55.1	hl	22.2	l	17.1	l	15.5	l	37.6	l	12.6	hl	27.0	l	7	2
MO050144	56.2	hl	17.7	l	13.5	l	17.3	l	32.4	l	7.7	hl	12.1	l	7	2
KY00C-2059-19	70.4	h	32.3	h	25.4	h	27.9	h	45.5	h	18.4	h	42.8		0	6
KY00C-2515-02	64.0	h	37.2	h	27.4	h	35.6	h	50.8	h	13.6	h	67.4		0	6
KY00C-2059-24	68.4	h	34.0	h	26.9	h	26.9	hl	48.7	h	17.9	h	66.5		1	6
KY00C-2567-01	61.9	h	32.3	h	23.3	hl	25.1	hl	44.0	h	15.1	h	35.5	l	3	6
KY00C-2143-08	62.2	h	32.7	h	22.4	hl	27.6	h	40.9	l	9.3	hl	61.5		3	5
MSU Line E6003	40.0	l	10.3	l	6.2	l	7.9	l	23.9	l	5.2	l	19.6	l	7	0
MSU Line E7035R	67.7	h	23.0	l	18.5	l	18.7	l	40.6	l	6.1	l	12.6	l	6	1
OH04-264-58	65.1	h	28.4	hl	22.7	hl	21.0	l	42.1	h	10.0	hl	40.8		4	5
OH04-268-39	52.7	hl	27.9	hl	21.3	hl	27.6	h	40.9	l	10.5	hl	11.1	l	6	5
OH05-248-38	69.0	h	40.0	h	30.4	h	36.0	h	51.3	h	14.3	h	84.6		0	6
VA07W-580	51.7	hl	22.4	l	15.3	l	22.9	l	35.6	l	11.5	hl	55.8		6	2
VA07W-600	53.0	hl	20.2	l	14.4	l	15.5	l	34.9	l	12.4	hl	14.3	l	7	2
VA07W-672	51.2	hl	35.3	h	21.8	hl	24.3	l	44.8	h	9.7	hl	128.0	h	4	6
VA06W-558	52.9	hl	24.5	hl	16.9	l	21.0	l	33.4	l	5.4	l	17.3	l	7	2
VA06W-615	59.6	hl	26.0	hl	18.6	l	22.4	l	38.1	l	8.2	hl	14.3	l	7	3
AVERAGE	57.3		28.5		20.9		24.5		40.9		10.1		32.1			
LSD(0.05)	25.6		20.2		18.0		19.2		17.5		11.2		34.5			
# environs	8		11		11		8		6		4		2			

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

CAN HOST PLANT RESISTANCE PROTECT THE QUALITY OF WHEAT FROM FUSARIUM HEAD BLIGHT?

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ABSTRACT

Fusarium head blight (FHB) infection reduces the amount of millable grain from an infected field, reduces mill yields, and generally degrades end-use quality. In 2009, the Logan County, KY, wheat trial had extended conditions for infection with FHB resulting in extensive and uniform infection within the trial. FHB disease incidence and field grain yield were recorded. The trials were harvested and evaluated for percent of millable grain, milling yield and soft wheat quality using standard methods of the American Association of Cereal Chemistry. Four field replications of samples were weighed before and after aspiration; after aspiration the four replications were combined to form two replications for milling and baking evaluation. Cultivars differed for the amount of grain aspirated during cleaning (Cultivar F-value > 22) with Coker 9511 having the smallest loss due to aspiration (3.4% removed) and SS 8641 having the greatest aspiration removal (74.4% removed). Generally the results correlated to known resistance levels with resistant cultivars having fewer scabby or shriveled grains. The percent of aspirated seed was negatively correlated to field yield ($r > -0.25^{*}$) and test weight ($r > -0.87^{***}$), and was positively correlated to field infection ($r > 0.63^{***}$). Effects of infection on end-use quality varied for the cultivars and will be discussed in greater detail.

ACKNOWLEDGEMENT AND DISCLAIMER

This material is based upon work supported by the U.S. Department of Agriculture. This is a cooperative project with the U.S. Wheat & Barley Scab Initiative. Any opinions, findings, conclusions, or recommendations expressed in this publication are those of the author(s) and do not necessarily reflect the view of the U.S. Department of Agriculture.

EFFECT OF TOLERANT VARIETIES AND FUNGICIDE TREATMENT ON FHB RATING, DON CONTENT AND YIELD UNDER HIGH INFECTION PRESSURE

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OBJECTIVES

To assess Fusarium Head Blight (FHB) impact on yield reduction and deoxynivalenol (DON) accumulation in winter wheat varieties with different resistance level and different fungicide treatment. To find out if medium tolerant varieties and fungicide treatment are sufficient to reach acceptable FHB rating and keep DON content below hygienic limit.

INTRODUCTION

Food safety is nowadays priority for cereal producers and grain-processing industry. FHB causes severe yield losses and decreases baking and food quality (Mesterházy, 2003). Natural occurrence of FHB in the Czech Republic varies between years and locations. Increasing of FHB was recorded during last years in consequence of higher ratio of corn in crop rotations and frequent using of no tillage system of soil processing. A survey of *Fusarium* mycotoxin deoxynivalenol in cereals intended for human consumption was carried out in Czech Republic for eight-year period (2000-2007). Wheat samples were collected directly from farmers so as to represent most of regions in the Czech Republic. 82% of 444 wheat samples were positive for DON content and maximum levels for DON according to Commission Regulation (EC) 1881/2006 were exceeded in 3.6% of wheat samples (Stockova et al., 2008).

Breeding for resistance to FHB has a more than twenty year tradition in breeding company Selgen. Number of resistance sources was used in breeding program (in the first place Sumai3 and Nobeoca Bozu). However, high FHB resistance level was lost during selection for other important agronomic traits. Also transfer of resistance from spring wheat to winter wheat type (80 % of wheat area in the Czech Republic) could be a complication.

Similarly, the results of many research studies shows us that it is difficult to reach high resistance level and simultaneously high yield and necessary bread-making quality (Mesterházy, 2003). Our results from tests of F_4 generation randomly founded number of tolerant types with desirable other agronomic traits. Two lines were managed to new winter wheat varieties, line SG-S1800 (Sakura) (Horcicka et al., 2007) and line SG-S1875 (Simila) (Horcicka and Hanisova, 2006).

Whether this level of FHB tolerance is sufficient under high pathogen impact and how important is contribution of variety and fungicide on pathogen development, DON content and yield reduction were focused in this work.

MATERIALS AND METHODS

Nine winter wheat varieties differed into 3 groups were used: R - tolerant group (with medium resistant varieties – Sakura, Simila, Petrus), M – medium susceptible (Bohemia, Raduza, Rheia) and S - susceptible group (Darwin, Mladka, Sulamit). Varieties were sown in 3 replications each of 4 variants of treatment: 1) control – without artificial infection and fungicidal treatment, 2) infection – with artificial *Fusarium* infection, without fungicide, 3) infection + common fungicide for leaf diseases (Tango Super), 4) infection + common leaf fungicide and targeted fungicide for spike diseases (Swing Top). Variant with Tango Super (1.0 l.ha-

^{1}, active substances: epoxiconazole 84 g.ha^{-1} and fenpropimorph 250 g.ha^{-1}) was sprayed in growing stage DC 37 – 39; variant with Swing Top (1.5 l.ha^{-1}, active substances: dimoxystrobin 250 g.ha^{-1} and epoxiconazole 84 g.ha^{-1}) was sprayed 24 hours before *Fusarium* infection. The experiment was planted by small parcel sowing machine type Hege. Final parcel area was 10 square meters. Experiment was done in three years (2007-2009) and at two locations.

Inoculum with spore concentrations of 6-7x10^{6} spores/ml was prepared and each parcel was infected with 1 liter of inoculum. Inoculum contained mix of pathotypes collected in whole area of the Czech Republic by State Phytosanitary Administration and multiplied by Research Institute of Crop Production in Prague. Infections run up in full flowering period according to each variety term. Symptomatic evaluation was carried in 21st day after the infection. The experiment was harvested by small plot harvester. Yield and DON content were evaluated. Data was statistically analyzed using ANOVA (Statgraphics XV.II).

RESULTS AND DISCUSSION

Basic Statistic ANOVA - The significant effects of genotype (variety), spike fungicide treatment, environment and interaction of genotype with the environment were found on DON content, FHB rating and yield from the ANOVA results. Analysis of the share of individual sources of variability on overall variability in the trial showed a highly predominant role of year and location. A significant source of variability was also the genotype (about 18% of variability for DON content, 55% for FHB rating and 13% for relative yield reduction). The effect of basic fungicide treatment (Tango Super) was not significant for DON content and FHB rating and results are not included. Treatment combination of Tango Super and Swing Top had also significantly positive effect on these traits but represented lower source of variation than genotype.

The role of tolerant varieties - Tolerant varieties have with strong infectious pressure significantly lower occurrence of pathogen, DON content and percentage of yield reduction in comparison with susceptible varieties (Table 1). Tolerant varieties not exceed in average hygienic limit for DON content at infection variant, however variety Simila reached boundary value of medium susceptible group. Absolute values passed beyond hygienic limit (1.25 ppm) in some samples of each tolerant variety. Medium tolerant varieties contributed to lover DON content than in susceptible ones (approximately 7 ppm). However, tolerant varieties were standalone insufficient for safety production in high infection pressure and favorable weather conditions. FHB rating below 1.3 (approximately less than 13% of spikes with visible symptoms) could leads to safe grain production although this relation can not run properly in every condition. Important is also 6-15% yield effect of tolerant varieties in compare with susceptible.

The effect of fungicide treatment – Fungicide treatment on spikes led to reduced occurence of symptoms (the evaluation was about 1 point better) and lower DON content (Table 2). Yield reduction of fungicide treated infected variant was compared with only control variant of experiment without infection and fungicide treatment. Therefore such evaluation is not exact. Impact of fungicide on DON content and FHB rating was lower than effect of genotype, but sufficient to keep the most of tolerant varieties samples under hygienic limit. Only five samples of this group were over. These results agree with Mielke and Weinert (1996) work, who found FHB rating near zero when moderately tolerant varieties were treated by fungicide. Susceptible group was over limit in spite of fungicide treatment.

Conclusions – These results showed importance of tolerant varieties as basic FHB-prevention. Medium tolerant varieties (Petrus, Sakura, Simila) could be sufficient prevention of over-limit mycotoxins production at common growing condition in the Czech Republic. Fungicide treatment into spikes could be useful when wheat growth follow corn and at no tillage technology. However type of application and environmental effects also play

very important role. Optimal timing of fungicide application should be taken into account in this experiment. Medium susceptible varieties are suitable to use together with fungicide treatment. Epidemic severity of FHB causes unacceptable mycotoxins content when these varieties are used. Additional separation of harvested grains by specific weight is the only possible means of reducing monitory levels below the hygienic limit, but this brings higher costs of wheat production. FHB susceptible varieties represent risk of production with high DON content and should be excluded from food and feed production.

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Table 1: Variety means of inoculated plots (I) and plots treated with fungicide (IF) for DON content, FHB (disease severity) and relative yield reduction (% to uninfected control) in 2007-2009 experiments at two locations.

		DON (ppm)				FHB rating (1-9)*				Rel. yield (%)			
Variety		**I**		**IF**		**I**		**IF**		**I**		**IF**	
Sakura	R	0,75	a	0,44	a	1,2	a	0,5	a	98	a	104	ab
Petrus	R	0,84	a	0,38	a	1,3	a	0,9	a	98	a	98	bc
Simila	R	1,18	ab	0,74	ab	1,6	ab	1,1	ab	95	ab	99	bc
Bohemia	M	2,36	b	1,50	ab	2,4	c	1,7	bc	94	ab	100	abc
Raduza	M	2,41	b	1,60	ab	2,2	bc	1,8	cd	92	abc	99	bc
Rheia	M	3,04	b	1,75	ab	3,1	d	2,4	de	90	bcd	95	c
Sulamit	S	4,44	bc	2,71	bc	4,0	e	2,9	ef	92	abc	108	a
Darwin	S	7,70	c	4,09	c	4,4	e	3,4	fg	87	cd	98	bc
Mladka	S	11,31	d	4,21	c	5,2	f	3,7	g	83	d	97	bc
Average		**3,78**		**1,94**		**2,8**		**2,1**		**92**		**100**	

* 1= no symptoms visible

Means in the columns followed by the same letter are not significantly different from each other at P<0.05 of LSD test

Table 2: Variety group (R, M, S) means of inoculated plots (I) and plots treated with fungicide (IF) for DON content, FHB (disease severity) and relative yield reduction (% to uninfected control) in 2007-2009 experiments at two locations.

	DON (ppm)		FHB rating (1-9)*		Rel. yield (%)	
Variety group**	**IF**	**I**	**IF**	**I**	**IF**	**I**
R	0,52	0,92	0,8	1,4	100	97
M	1,62	2,60	2,0	2,6	98	92
S	3,67	7,82	3,3	4,5	101	87

* 1= no symptoms visible

** R- medium tolerant; M-medium susceptible; S-susceptible

PLANT ORGAN SPECIFIC GLYCOSYLATION OF DON IN THREE WINTER WHEAT CULTIVARS AFTER STEM BASE INFECTION WITH TOXIGENIC *FUSARIUM* SPECIES

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ABSTRACT

The ability of wheat (*Triticum aestivum* L.) to transform the *Fusarium* trichothecene B mycotoxin deoxynivalenol (DON) into non-phytotoxic DON glucosides is suggested to contribute to fusarium head blight (FHB) resistance. Recently, we found that following stem base infection with toxigenic *Fusarium* species, *Fusarium graminearum* and *F. culmorum*, DON is translocated in all plant parts including ears and grains. Mechanisms to convert DON into non-phytotoxic derivatives could also reduce damage through stem base infections with *Fusarium* spp., because DON is considered a virulence factor. Three winter wheat cultivars differing in resistance to FHB (highly, moderately susceptible and resistant) were tested for responses to soil-borne infection of the stem base with *F. graminearum* and *F. culmorum.* DON and its degradation product DON-3-glucoside (D3G) were found in the stem base, ear rachis and corresponding grains. HPLC-MS analysis of stem base, grain and corresponding ear rachis samples showed lowest levels of DON and D3G in the highly resistant cultivar, but levels did not correlate with susceptibility levels of the two sensitive cultivars. Transcript accumulation studies with real-time RT-PCR of genes associated with DON degradation and transport activities illustrated distinct differences between the wheat cultivars and between stem base and ears. Highest levels of D3G were always found in the ear rachis, in which however gene expression levels were significantly lower than in the stem base, indicating that DON degradation takes place already in the stem base and D3G is also transported within the plant. The level of D3G in stem base samples corresponded with expression levels of a gene coding for DON glucoside forming uridine diphosphate-glucosyltransferase (UGT). This study elucidates the role of DON glycosylation in cultivar resistance with regards to *Fusarium* stem base infection and translocation of mycotoxins to the ears.

DEVELOPMENT OF DURUM WHEAT GERMPLASM WITH ENHANCED RESISTANCE TO FUSARIUM HEAD BLIGHT DERIVED FROM EMMER WHEAT

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ABSTRACT

Durum wheat (*Tirticum turgidum* L. subsp. *durum*) is a unique class of commercial wheat specifically for making pasta products. Durum production has been seriously challenged by the Fusarium head blight (FHB) disease in the United States in the past decade. Although utilization of resistant cultivars is considered as an effective measure to control the FHB, the progress in development of resistant durum cultivars is limited due to the unavailability of high levels of FHB resistance in durum germplasm. We previously identified a number of cultivated emmer (*T. dicoccum*) and Persian wheat (*T. carthlicum*) accessions with increased levels of FHB resistance. These resistant tetraploid wheat accessions are currently utilized for developing durum wheat germplasm resistant to FHB. In this research, we selected five *T. carthlicum* and four *T. dicoccum* for introgression of the resistance into leading ND durum cultivars through double haploid (DH) and backcross methods. Over the past four years, we have developed 551 DH lines and 559 BC_1-derived advanced (BC_1F_5 - BC_1F_8) lines from crosses with four leading ND durum cultivars Lebsock, Ben, Maier, and Mountrail. One DH line and five BC_1-derived advanced lines have exhibited significantly improved resistance to FHB in the greenhouse and field evaluation for two years compared to their durum parents. Theses resistant lines are currently being used in a 2nd round of introgression and breeding for FHB resistance.

CHROMOSOME LOCATION OF FUSARIUM HEAD BLIGHT RESISTANCE IN 'FRONTANA' SPRING WHEAT

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OBJECTIVE

To determine which chromosomes bear resistance genes to Fusarium head blight (FHB) incidence, severity, and spread.

INTRODUCTION

Substantial resources including monetary, have been lost over the last two decades in attempts to control FHB, also known as scab, a fungal disease caused by *Fusarium* ssp in wheat (*Triticum aestivum* L.) and other small grains. The main causal agent of FHB is *Fusarium graminearum* Schwabe teleomorph *Gibberella zeae* (Schwein). The pathogen causes losses in yield, poor kernel quality, and reduced market value of the kernels due to discolored and shrunken kernels on infected plants. Kernels are also contaminated with mycotoxins, primarily deoxynivalenol (DON) that make kernels not only unpalatable but also noxious to both human and animals (McMullen et al., 1997).

Integrated disease management (IDM) is the best tool to control the disease with use of resistant cultivars as the pivotal aspect of the IDM. Schroeder and Christensen (1963) described resistance to initial infection as Type I and resistance to spread of disease within the spike as Type II.

Identifying and understanding how resistance genes work against FHB are vital for breeding endeavors. Studies to map genes for FHB resistance have been carried out in wheat. Steiner et al. (2004) and Mardi et al. (2006) mapped FHB resistance genes to 3A chromosome. Berzonsky et al. (2007) used reciprocal backcross monosomic lines (RBCM) and established that chromosomes 3A, 6A and 4D reduced *Fusarium* damaged kernels. Breeding against FHB is laborious and time consuming because FHB resistance is governed by many genes and expression is affected by the environmental conditions.

MATERIALS AND METHODS

Plant Material

Frontana and 'Chris' RBCM comprising of chromosomes 3A, 6A and 4D were employed in this study. Previously, Berzonsky et al. (2007) found that RBCM lines originating from Frontana expressed resistance to FHB while RBCM lines with a Chris background were susceptible. 'Alsen' (Frohbreg et al., 2006) and 'Choteau' were used as medium resistant and susceptible checks, respectively. The parental lines used to develop the RBCM were also included in the study (Table 1). The study was conducted under greenhouse conditions at North Dakota State University campus (46° N and 96° W) with a 16h photoperiod and temperatures were maintained between 16 and 21°C.

Inoculum and inoculation

A field isolate of *Fusarium graminearum* provided by the Plant Pathology group was used to prepare inoculum that was cultured in petri dishes on a mung bean media at 4°C for 7 days. The macroconidia were suspended in autoclaved double distilled water and a haemacytometer was used to determine the spore concentration. Point and spray inoculation techniques were used to introduce the pathogen to the plants. This was done when 50% of the spikes per plot were at anthesis.

Data Collection

Evaluations of FHB incidence, severity, and spread percentages were collected 21days after inoculation. Disease incidence and severity were determined on spray inoculated spikes using the scale proposed by Stack and McMullen (1995). Disease spread was expressed as a percentage of the number of spikelets that developed FHB symptoms beyond the initial inoculation point following a SFI to the total number of spikelets on the spike.

Experimental Design and Data analysis

The experiment was laid out in randomized as a nested block arrangement where genotypes were nested with in three chromosome groups (CG), namely 3A (CG1), 6A (CG2), and 4D (CG3). Each treatment had three replicates with eight plants per replicates. The experiment was conducted in four greenhouse seasons during 2007-2009.

Data were analyzed using a mixed model (PROC-MIX) of SAS 9.1 program (Cary, NC), and experiment-wise error was set at $p \leq 0.05$. Genotypes, chromosome groups, and inoculation method effects were considered fixed. Replicates and seasons were considered as random effects. Homogeneity test across seasons using Bartlett method ($p \leq 0.001$).

RESULTS AND DISCUSSION

Data on FHB disease incidence, severity, and spread are reported in Table 2. Using the assessment method as described by Steiner et al., (2004), type I resistance evaluation data suggest that Frontana's chromosomes 3A and 4D have genomic regions that may play a major role in governing Type I resistance. Chromosome 6A, though showed some Type I resistance level to FHB, the difference between Frontana 6A and Chris 6A was not significant. However, Frontana had much lower disease scores than all Frontana RBCM. This is probably because genes on 3A and 4D interact with genes on other chromosomes to confer resistance in Frontana.

Frontana 3A expressed reduced disease severity in CG1 following spray inoculation. This implies that chromosome 3A is involved in reducing disease severity (Table 2). Steiner et al. (2004) indicated that 3A from Frontana was associated with FHB severity explaining 16% of the phenotypic variance. Similarly to FHB incidence, Frontana had much lower disease scores than Frontana 3A. This may results from interaction (epistasis) between FHB resistance genes on 3A and genes on other chromosomes to confer resistance in Frontana. Results for CG2 illustrate that Frontana's 6A chromosome might not be involved in reducing disease severity. However, Frontana 4D (CG3) also plays a role in reducing FHB severity (Table 2). This is consistent with findings by Loffler et al. (2009); and Berzonsky et al. (2007).

In terms of disease spread, results of RBCM of the three groups (Table 2) show that Frontana 3A, 6A, and 4D had reduced FHB spread beyond the initial inoculation point. This suggests that Frontana chromosomes3A, 6A, and 4D have genes that restrict disease spread. Alsen has Type II resistance (Mergoum et al., 2007) and CG2 results between Alsen and Frontana 6A are not significantly different. Similarly, disease spread scores for Frontana 4D and Alsen in CG3 are similar. These observations suggest that 6A and 4D might be remotely involved in reducing disease spread as previously discussed by Buerstmayr et al. (1999) using a backcross reciprocal monosomic analysis involving 'Hobbit/U-136.1'.

Relationships among the above FHB resistance parameters were performed. A strong relationship between FHB severity and incidence [r^2=0.94 and a Pearson Correlation of r=0.97, P<.0001] was observed. Disease spread and severity were also highly correlated (r=0.91) and so were the disease severity and *Fusarium* damaged kernels (FDK). An analysis of the association between FHB incidence and spread revealed a strong correlation (r=0.93, P<.0001). These strong relationships suggest that FHB incidence, severity and spread are under similar genetic control as indicated by some previous works (Steiner et al., 2004; Groth

et al., 1999). A negative correlation between FHB severity and plant height was observed. However, the relationship was weak [r^2=0.098 and r=0.31, P<.005)]. Therefore, tall genotypes reported to have better FHB resistance than short genotypes (Buerstmayr et al., 2000) were not confirmed by our results which indicate no relationship between FHB and plant height.

In conclusion, the results from this study indicate that 3A in Frontana is the major genomic region not only for FHB incidence (Type I) and severity but also spread (Type II). The results show also that chromosomes 4D and, to a lesser extent, 6A, play a significant role in FHB resistance types I and II.

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DISCLAIMER

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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Table 1. List of genotypes used in the study, their description, and known reaction to FHB.

ID	Genotype	Description	FHB Reaction
1	Frontana(3A)	RBCM†	Resistant
2	Frontana(6A)	RBCM	Resistant
3	Frontana (4D)	RBCM	Resistant
4	Chris(3A)	RBCM	Susceptible
5	Chris(6A)	RBCM	Susceptible
6	Chris(4D)	RBCM	Susceptible
	Euploid controls:		
7	Frontana	Parent (Euploid)	Resistant
8	Chris	Parent (Euploid)	Susceptible
9	Alsen	Control (Euploid)	Resistant
10	Choteau	Control (Euploid)	Susceptible

†RBCM=Reciprocal backcross monosomic line.

Table 2. Means of FHB disease incidence, severity, and spread of wheat genotypes grown under greenhouse conditions using spray inoculation method.

		FHB Incidence		FHB Severity		FHB Spread	
Genotype	CG†	Mean (%)		Mean (%)		Mean (%)	
Alsen	1	28.63	ab‡	10.82	a	20.83	b
Choteau	1	62.17	d	53.50	d	50.07	d
Chris	1	60.25	d	41.62	cd	46.12	d
Chris 3A	1	51.83	cd	40.69	cd	43.31	cd
Frontana 3A	1	27.67	a	17.70	ab	12.62	ab
Frontana	1	12.50	a	5.45	a	5.37	a
Alsen	2	17.67	a	7.76	a	27.78	bc
Choteau	2	55.83	d	41.50	cd	41.93	c
Chris	2	52.33	cd	36.24	c	38.68	c
Chris 6A	2	43.83	bcd	43.23	cd	38.26	c
Frontana 6A	2	32.92	bc	26.81	bc	26.71	b
Frontana	2	16.67	a	6.80	a	8.55	a
Alsen	3	15.50	a	8.73	a	24.61	b
Choteau	3	59.98	d	43.51	d	58.92	d
Chris	3	55.08	d	42.97	cd	44.03	cd
Chris 4D	3	53.14	cd	41.87	cd	47.99	d
Frontana 4D	3	29.08	ab	18.89	ab	23.09	b
Frontana	3	11.67	a	4.81	a	7.72	a

†CG = Chromosome group

‡Means followed by the same letter within column are not significantly different at $p<.05$

COMPARATIVE MAPPING OF THE CHROMOSOMAL REGION HARBORING THE FUSARIUM HEAD BLIGHT RESISTANCE QTL *QFHS.NDSU-3AS* IN DURUM WHEAT

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ABSTRACT

Fusarium head blight (FHB), caused mainly by *Fusarium graminearum*, has been one of the major threats to durum wheat production worldwide. A source of resistance comparable to "Sumai 3" and others in bread wheat has not been found in durum. A major FHB resistance QTL derived from *Triticum turgidum* ssp. *dicoccoides*, designated *Qfhs.ndsu-3AS*, was identified and mapped to the short arm of chromosome 3A (3AS) in our previous studies. We have saturated the chromosomal region harboring the QTL with wheat EST-derived STS (sequence tagged site) and SSR (simple sequence repeat) markers. A large portion of wheat ESTs have not been mapped to individual chromosomes. We have identified genomic regions on rice chromosome 1 and in *Brachypodium distachyon*, which are collinear with the QTL region on 3AS, using the wheat ESTs previously mapped to the QTL region. The genomic sequences of the collinear regions in rice and *Brachypodium* have been used to BLAST wheat EST pool and to identify ESTs/genes within the QTL region. A total of 813 pairs of STS primers and 42 pairs of SSR primers have been designed from tentative consensus sequences (TCs) and singletons of the ESTs identified. As a result, 56 polymorphic STS and SSR markers have been developed and 45 of them mapped to a genomic region of 232 cM on chromosome 3A. Of the 45 markers, 23 mapped to a chromosomal interval of 14.9 cM harboring *Qfhs.ndsu-3AS* in the population of 83 recombinant inbred chromosome lines (RICLs). The average map distance between maker loci was reduced from 4.9 cM in the previous study to 1.24 cM in the QTL region. Five co-segregating markers were 0.6 cM proximal to *Xgwm2*, a SSR locus closely linked to the QTL peak. Comparative analysis has identified several chromosomal intervals in the distal region of the short arm of rice chromosome 1 and a few *Brachypodium* genomic regions collinear with the chromosomal region harboring *Qfhs.ndsu-3AS* on wheat 3AS. In addition, we have been constructing a genetic map of the QTL region with a higher resolution in a large segregating population with over 1,800 F_2 individuals. This will provide a better understanding of this chromosomal region and position the FHB resistance QTL *Qfhs.ndsu-3AS* more precisely within the region. User-friendly molecular markers tagging this resistance QTL have been developed and utilized in wheat breeding and germplasm development.