SESSION 3:

VARIETY DEVELOPMENT AND HOST PLANT RESISTANCE

Co-Chairpersons: Fred Kolb and
Jochum Wiersma

OVERVIEW OF BREEDING FOR FHB RESISTANCE IN WHEAT – WHERE WE'VE COME FROM AND WHERE WE ARE

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ABSTRACT

The cultivation of wheat varieties resistant to Fusarium head blight (FHB) is one of the most important components to diminish losses due to this disease. Although there is no known immunity to this disease in wheat germplasm, considerable improvements in genetic resistance have been achieved in the past 20 years by concentrated breeding efforts that have relied primarily upon repeated field and greenhouse-based screening. Dedicated breeding efforts for resistance to FHB in the Upper Midwest spring wheat region date to the late 1980's when 'Sumai 3' was first introduced as a source of resistance. Since consecutive epidemics beginning in 1993, breeding for FHB has been a top priority for programs in the region. At the time of those epidemics, most cultivars available were susceptible, with only 'Pioneer 2375' rated as having an intermediate (MR-MS) level of resistance. 'Alsen', released by NDSU in 2000, was the first moderately resistant cultivar to be widely grown in the region. Today, half of the cultivars available to growers in the spring wheat region are classified as moderately resistant or better for FHB reaction and were grown on 43% of the region's spring wheat acreage in 2011. Despite these genetic gains and improved fungicides, even the most resistant materials available today can incur damage when environmental conditions are conducive for an epidemic. DNA markers have been identified for many QTL using biparental mapping populations and a few are being routinely used in marker-assisted selection (MAS). FHB resistance is a quantitative trait, and the best QTLs are able to reduce damage by 20-30%, but most QTL have far smaller effects. The *Fhb1* QTL was present in cultivars grown on 40% of the region's wheat acreage in 2011. We routinely screen with DNA markers all of our pre-yield trial F_5 lines, about 1,000 total, as well as BC_1 and TC_1 plants segregating for *Fhb1* and the 5AS QTL. Enriched populations undergo phenotypic selection for FHB resistance, and other yield, disease resistance, and end-use quality testing necessary to produce FHB resistant germplasm and variety candidates. Substantial efforts in phenotypic assessments for FHB resistance will still be necessary, even with an increase in MAS for this trait, because there are likely to be numerous genes with minor effects, which need to be combined with the major QTLs in order to obtain the desired level of resistance. We are initiating genomic selection with a primary goal of identifying and discarding susceptible lines prior to entry into yield trials, thus eliminating a major bottleneck in our breeding program.

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FINE MAPPING OF WHEAT *FHB1* USING SEQUENOM MASSARRAY SNP GENOTYPING PLATFORM

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ABSTRACT

Reduction in grain yield and quality due to Fusarium head blight (FHB) is a serious problem in bread wheat (*Triticum aestivum* L.), and the *Fhb1* QTL in chromosome 3BS provides a major source of FHB resistance. *Fhb1* has been linked to restriction fragment length polymorphisms, simple sequence repeats (SSR), amplified fragment length polymorphisms and sequence tagged site (STS) markers. In an effort to fine map the *Fhb1* QTL region using high-throughput genotyping platform, we looked at single nucleotide polymorphisms (SNPs) to saturate the region with these biallelic markers. SNPs are the most abundant form of polymorphism and are ideal for fine mapping. Fifty-five SNPs were identified between two near-isogenic lines (NILs) that were genotyped using the Illumina Infinium 9K SNP array. The NILs were derived from continuous backcross of Clark (recurrent FHB-susceptible parent) to Ning7840 (*Fhb1* donor). Two sets of multiplex SNPs representing the 55 SNPs were analyzed in 91 Ning7840/Clark BC_7F_5 lines that showed recombination in the QTL region using the Sequenom MassArray. A total of 45 SNPs showed segregation in the population and were analyzed together with known SSR, STS and SNP markers that were closely linked to *Fhb1*. Six new SNP markers were mapped between *Xgwm533* and *Xgwm493*, SSR markers flanking the *Fhb1* in 3BS. These SNPs should be useful for high resolution mapping of *Fhb1* and high-throughput marker-assisted selection in combination with other markers using Sequenom MassArray.

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GRAIN YIELD PERFORMANCE OF WESLEY BACKCROSS *FHB1* HRWW GERMPLASM

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ABSTRACT

Transferring *Fhb1*, a widely utilized and effective QTL for resistance to Fusarium head blight (FHB) from spring to winter wheat (*Triticum aestivum* L.) is important for producing more resistant winter wheat varieties. However, to release resistant winter wheat varieties with the broadest appeal to growers, the transfer and expression of resistance to FHB should also be accomplished without a significant reduction in grain yield performance. Our objective was to assess the impact of *Fhb1* on grain yield performance when the QTL was transferred to Wesley, an adapted and widely grown variety in the Northern Hard Winter Wheat (HWW) region of the US. Compared with Wesley and two other regionally grown HWW varieties, Lyman and Overland, we evaluated the grain yield performance of 20 Wesley backcross (BC) breeding lines, each of which was verified as being homozygous for *Fhb1*. The evaluated lines were produced by initially hybridizing spring wheat breeding line ND2928 as the parental source of *Fhb1* to Wesley, followed by two backcrosses to Wesley. Lines homozygous for *Fhb1* were identified and selected from among BC progeny using molecular markers STS256, Gwm533, Gwm493, and Umn10, which were applied at the various cross and BC generations. Utilizing replicated field trials; yearly grain yield evaluations were conducted from 2010 to 2012 at Mead and Lincoln, NE and at Brookings and Dakota Lakes, SD. When averaged over all years and locations, the highest yielding BC line performed at 94% of the grain yield of Wesley and at 83% of the grain yield of Overland, the highest yielding variety in the trials. Only at the Brookings location did at least one BC line exhibit a higher grain yield than Wesley in each year of the trial, and compared with 2012, approximately twice as many BC lines exhibited higher grain yield than Wesley in 2010 and 2011. Lines evaluated in 2010, 2011, and 2012 were at the BC_2F_5, BC_2F_6, and BC_2F_7 generation, respectively. In addition to the impact of seasonal and location effects on the expression of grain yield, segregation for background genes may have impacted the grain yield performance of the BC lines over years. Marker selection was applied only during the derivation of the BC lines to identify lines homozygous for *Fhb1,* and no marker background selection for the recurrent parent or within-line selection was practiced for grain yield thereafter. Consequently, background segregation for genes influencing grain yield may have been responsible for some of the differences observed between BC lines over years. Irrespective of grain yield differences due to environment, these results emphasize the importance of combining selection for grain yield performance with selection for the presence of *Fhb1* when transferring the QTL from spring wheat breeding lines to winter wheat varieties. To transfer *Fhb1* from spring wheat lines and develop high-yielding winter wheat germplasm lines, this tandem selection approach is likely to be even more important when relatively few backcrosses are made to the winter wheat parent.

ADOPTION OF WHEAT CULTIVAR EVEREST SIGNIFICANTLY LOWERED THE KANSAS STATEWIDE FUSARIUM HEAD BLIGHT PHENOTYPE

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ABSTRACT

Fusarium head blight (FHB) is a serious disease of small grains such as wheat. Significant losses can occur due to the blighting of many heads in the field. One of the best ways to manage FHB is by planting cultivars with some level of resistance. As a result of funding from the U.S. Wheat and Barley Scab Initiative, significant effort has been placed on developing cultivars adapted to Kansas with improved levels of FHB resistance. Because of this effort, the moderately-resistant cultivar Everest was released in 2009 and has gained popularity such that it now is the second most planted cultivar in Kansas and the most popular cultivar in the eastern third of the state where FHB traditionally occurs. The goal of this project was to quantify the impact that the adoption of Everest has had on the average statewide FHB phenotype and the average phenotype for the eastern third of the state. From 2003 through 2012, data were obtained from the USDA National Agricultural Statistics Service, Kansas Field Office relative to the percentage acreage planted to various wheat cultivars in Kansas. In addition, each cultivar's reaction to FHB was obtained from De Wolf et al. (2012. Wheat Variety Disease and Insect Ratings 2012. Kansas Coop. Extension Service publication MF-991. 4 pp). The above data were used to calculate a score for an average cultivar for the entire state and the eastern third of the state. The decimal equivalent of the percentage acreage planted to a cultivar in a given year was multiplied by its FHB score (1-9 scale where 1=resistant and 9=susceptible). Acreage planted to "blends" (average of 11.3% of the acres), unknown cultivars, or to cultivars where the FHB phenotype was not known was ignored. Nevertheless, the average acreage used each year was 80.5% statewide and 78.9% for the eastern third. Calculated values for all planted cultivars in a given year were added together and divided by the decimal of the total acreage for all known cultivars to obtain an average FHB phenotype. Prior to 2011, the average statewide phenotype was above 7 indicating high susceptibility. Beginning in 2009, and becoming more pronounced in 2012, there has been a noticeable decline in the statewide FHB phenotype. This has been especially evident in the eastern third of the state where the average phenotype has gone from 7.74 in 2008 to 5.73 in 2012. Although other cultivars have been recently released with improved levels of resistance (e.g. Art and Hitch), Everest has contributed the most to the observed recent improvement in FHB phenotypes. It now occupies over 23% of the acres in the eastern third of the state where FHB is especially important. Gower adoption of Everest has significantly lowered the vulnerability of the Kansas wheat crop to FHB.

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GENOTYPE BY SEQUENCING AND MARKER ASSISTED SELECTION: BREAKING THE BOTTLENECK

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ABSTRACT

Genotyping is the major resource bottleneck when developing populations to characterize disease resistance in barley or utilizing genomic selection. Until recently the Illumina Bead Express was the cheapest technology available for barley genotyping, however the cost is still prohibitive. To identify novel FHB resistance QTL in barley and the markers associated with these loci, it is essential to develop bi-parental populations and have the technology and resources available for robust genotyping and phenotyping. The Ion Torrent next generation sequencing platform presents the opportunity to overcome the resource bottleneck by generating up to ten million 400 base sequences (40 Gb of sequence) per a single run. To evaluate the potential of this technology we developed 50 barcoded adaptors with optimized restriction enzymes to reduce the complexity of the barley genome (~5,000 Mb) down to 18,243 unique sequence sites. Similarly we were able to reduce the complexity of the fungal pathogen, *Pyrenophora teres* f. *teres* (~40 Mb genome) to 14,143 unique sequence sites. Utilizing the barcoded genomic libraries, we sequenced 40 individuals from a bi-parental population of *P. teres* f. *teres* in a single Ion Torrent run. Using this data we identified >1,000 single nucleotide polymorphisms (SNPs) representing unique loci. We expect that by reducing the barley genome complexity down to 18,243 loci, we will be capable of running genotype by sequencing (GBS) on barley populations for ~$16/ line and generate ~1,000 SNP markers. The ability to genotype barley populations will allow us to characterize novel resistance sources and rapidly develop markers that can be utilized in marker-assisted selection strategies, including genomic selection. The GBS method is also being utilized to characterize virulence genes in fungal pathogens through analysis of bi-parental populations and association mapping in natural populations where crossing is not an option.

COMPARISON OF RESISTANCE OF MODERN WHEAT CUTIVARS TO THE DON PRODUCER *FUSARIUM GRAMINEARUM* AND THE T2/HT2 PRODUCER *FUSARIUM SPOROTRICHIOIDES*

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ABSTRACT

While resistance of wheat to deoxynivalenol (DON) producing Fusarium species (*e.g. F. graminearum, F. culmorum*) has been well studied, the resistance response to T2/HT2 producers (e.g. *F. sporotrichioides*) is much less investigated. Likewise, while the role of DON in the pathogenesis process has been confirmed, a potential role of T2/HT2 as aggressiveness factors is currently unknown. We therefore performed artificial inoculation trials at three locations (two in France, one in Austria) during two seasons with 48 (2011) or 96 (2012, trials in progress) wheat lines or cultivars using *F. graminearum, F. sporotrichioides* or a mix of both species. The wheat lines comprised mainly current cultivars from France and Austria and several experimental lines. We scored Fusarium head blight (FHB) visual symptoms and other morphological traits such as plant height and anther extrusion.

Based on first year results we found that 1) there was a large genetic variation in FHB resistance among current cultivars, ranging from moderately resistant to highly susceptible. 2) Experimental lines, which were selected for high FHB resistance have been confirmed. 3) Resistance to both investigated Fusarium species was highly correlated ($r>0.9$), indicating a common mechanism of resistance against DON and T2/HT2 producers. 4) The extent of anther extrusion was negatively correlated with FHB severity ($r=-0.76$). Anther extrusion may thus be a useful trait for indirect selection. Trials to re-evaluate these findings are underway.

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

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ABSTRACT

While many reports on genetic analysis of *Fusarium* resistance in bread wheat have been published, only limited information is available on Fusarium head blight (FHB) resistance derived from wheat relatives. We report about genetic analysis of FHB resistance derived from *Triticum macha* (Georgian spelt wheat). In order to introduce valuable alleles from the landrace *T. macha* into a modern genetic background we used an advanced back-cross QTL mapping scheme (Tanksley and Nelson 1996). A back-cross-two derived recombinant inbred line population of over 300 BC_2F_3 lines was developed from a cross of *T. macha* with the Austrian winter wheat cultivar Furore. The population was evaluated for Fusarium resistance in six field experiments. The population was genetically fingerprinted with > 600 markers. The obtained linkage map covered 37 linkage groups with 563 markers. Five novel FHB resistance QTL, all descending from *T. macha*, were found on four chromosomes (2A, 2B, 5A, 5B). The largest effect QTL overlapped with the *Q-locus* (spelt type) on chromosome 5A and appears therefore an interesting QTL especially for spelt wheat improvement. For details see Buerstmayr et al. (2011).

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ASSOCIATION OF THE SEMI-DWARFING ALLELES *RHT-B1A/B* OR *RHT-D1A/B* WITH FUSARIUM HEAD BLIGHT RESPONSE IN A WINTER WHEAT DOUBLED HAPLOID POPULATION AND NEAR ISOGENIC LINES

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ABSTRACT

Recent publications have shown that the widely used dwarfing genes *Rht-B1* (syn. *Rht1*) and *Rht-D1* (syn. *Rht2*) are associated with Fusarium head blight (FHB) resistance. The semi-dwarf allele *Rht-D1b* and to a lesser extent *Rht-B1b* appear to increase FHB susceptibility in wheat (Miedaner and Voss 2008, Holzapfel et al. 2008, Srinivasachary et al. 2009). In order to further evaluate the effects of these alleles we 1) developed and tested back-cross derived sister lines differing in their *Rht* alleles in a highly FHB resistant recipient line and 2) evaluated one doubled haploid population segregating at both loci.

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

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MOLECULAR MAPPING OF RESISTANCE TO FUSARIUM HEAD BLIGHT IN TETRAPLOID WHEAT

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ABSTRACT

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

In *T. dicoccum* the most consistent QTL effect mapped to chromosome 4B, and overlapped with the *Rht-B1a* allele. Further QTL mapped to 3B, 6A, 6B and 7B.

QTL for type 2 FHB resistance were detected in wild emmer (*T. dicoccoides*) mapping to chromosomes 3A and 6B. Wild and cultivated emmer wheat are promising sources for improving FHB resistance in durum wheat.

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META-ANALYSIS OF FUSARIUM HEAD BLIGHT RESISTANCE QTL IN CHINESE WHEAT LANDRACES

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ABSTRACT

Fusarium head blight (FHB) is one of the most devastating diseases in wheat. FHB not only causes significant losses in grain yield and quality, but also produces mycotoxins such as deoxynivalenol that are toxic to humans and animals. Growing resistant cultivars is one of the most effective strategies to minimize the disease damage. FHB resistance has been reported from many sources, but Chinese sources, especially Chinese landraces, such as Sumai3 and Wangshuibai, show the best resistance. Among them, Quantitative trait loci (QTL) for FHB resistance in Sumai3 have been well characterized in multiple studies, however, QTL in many other Chinese landraces are poorly characterized. Meta-analysis, a statistic method to combine QTL mapping results across independent studies, has been widely applied in human genetics research. In this study, five populations were developed from different Chinese wheat landraces (Haiyanzhong (HYZ), Wangshuibai (WSB), Baishanyuehuang (BSYH), Huangfangzhu (HFZ) and Huangcandou (HCD)). QTL have been identified in each population, however, only a selected set of markers were mapped in each population and some QTL may not be mapped due to poor coverage of markers in that population. Adding new markers to all possible QTL regions of all the five populations may recover the missing QTL. In total, after adding new markers, 12 QTL were remapped and 3 additional QTL mapped on 6 chromosomes (3A, 3BS, 3DL,5AS, 6BS, 7DL) in this study. Four QTL were identified on the consensus maps with one QTL each on chromosomes 3D and 3A, and two on chromosome 3BS. The QTL 95% confidence intervals were shortened by using a new clustering approach based on a Gaussion mixture model in MetaQTL V1.0. Thus, meta-analysis using the new maps will facilitate validation of QTL and identification of closely linked markers for marker-assisted selection.

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CHARACTERIZATION OF WHEAT MUTANTS WITH REDUCED FUSARIUM HEAD BLIGHT SYMPTOMS

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ABSTRACT

M2-derived lines with reduced Fusarium head blight symptoms have been obtained from two gamma-irradiated susceptible soft red winter wheat lines, KY93C-1238-17-1 and KY96C-0786-3-2. In 2011 and 2012 these were tested in 2 rep RCB designs in inoculated irrigated nurseries in Lexington, KY. In 2011 29 KY93C-1238-17-1 and 23 KY96C-0786-3-2 mutants were tested. In 2012 the number of mutants was reduced to 14 KY93C-1238-17-1 and 7 KY96C-0786-3-2 lines. In 2011 disease ratings (0-9), %FDK, heading date and height were collected. Additionally, in 2012 DON, incidence, severity and index were recorded. Between years there were significant overall differences ($P<0.05$) for heading date (20 days earlier in 2012), rating (1.3 in 2012 versus 1.8 in 2011) and FDK (7.6% in 2012 versus 15.1% in 2011). Nonetheless, the reduced ratings and %FDK that were seen for the mutant lines in 2011 were repeated in 2012. In 2012 we observed significant differences ($P<0.05$) among KY93-1238-17-1-derived lines for: disease rating (parental mean 2.0, mutant mean 0.6 (range 0-2.5)); severity (parental mean 31%, mutant mean 18.2% (range 8.0-35.2%) and %FDK (parental mean 10.6%, mutant mean 5.75% (range 2.9-11%)). Mean DON for KY93C-1238-17-1 was 12.6 ppm, the mutant average was 8.5 ppm (range 5.45-12.7ppm). Mean DON for Truman from neighboring tests was 8.9 ppm. Among KY96C-0786-3-2 mutants only index was significantly different at $P<0.05$ (parental mean 25.7%, mutant mean 17.9% (range 8.8-28.9%)). Reduced means for KY96C-0786-3-2 mutants were seen: DON (parental mean 22.2 ppm, mutant mean 16.7 ppm (range 12.7-20.1 ppm); FDK (parental mean 14.4%, mutant mean 9.89% (range 5.76-13.67%); disease rating (parental mean 3.5, mutant mean 2.14 (range 1-3)) and severity (parental mean 36.8%, mutant mean 31.2% (range 19.7-40.9%)).

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MAPPING RESISTANCE TO FUSARIUM HEAD BLIGHT IN A DOUBLED HAPLOID WHEAT POPULATION FROM THE CROSS MD01W233-06-1/SS8641

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ABSTRACT

Fusarium head blight (*Fusarium graminearum*) is one of the urgent fungal pathogen threats to global agriculture. It is capable of causing significant yield losses, and concomitantly lowers test weight and causes the accumulation of the mycotoxin deoxynivalenol (DON), lowering farmer incomes and potentially rendering grain unfit for human and animal consumption. Fungicides can be applied to control these fungal diseases, but there are few effective fungicides to control scab in epidemic conditions, and applying fungicides can be difficult to time correctly and can have unintended consequences for environmental and human health. Breeding for disease resistance reduces the need for fungicide application, controlling disease without the harmful side effects. The soft red winter wheat line MD01W233-06-1 is moderately resistant to FHB, without previously described sources of resistance. It was crossed with the FHB susceptible line SS8641. From this cross a doubled haploid (DH) mapping population of 124 lines was created via the maize wide cross method and evaluated in 2011 and 2012 across four field locations for FHB resistance. Phenotypic data for mapping was collected by visual estimation for scab incidence (INC) and scab severity (SEV) in the field, and seed samples were analyzed post harvest for percent *Fusarium* damaged kernel (FDK) and assayed to determine DON content. The DHs were screened with one morphological marker (red coleoptile) and 29 SSR markers and assayed on a recently developed Illumina Infinium assay with 9000 SNPs. Linkage analysis was performed with genetic markers that were polymorphic and did not show segregation distortion. The map consisted of a morphological marker, 24 polymorphic SSRs, and 1786 polymorphic SNPs. QTL IciMapping v. 3.1 was used to construct the linkage map and perform QTL analysis. Markers with previously mapped locations were anchored to chromosomes and linkage analysis produced 25 linkage groups. QTL analysis revealed 31 QTLs with LOD scores ranging from 8.0 to 3.0 on 8 chromosomes. Most QTLs were linked to markers on chromosomes 3B, 2D, and 7B. Chromosome 3B showed consistent QTLs for INC, SEV, DON, and FDK that appeared in multiple location/years. Chromosome 2D had consistent QTLs for INC, DON, and FDK across multiple location/years. Chromosome 7B had consistent QTLs for SEV and FDK across multiple location/years.

GENERALIZED LINEAR MODELS FOR GENETIC PREDICTION OF SCAB RESISTANCE FROM REGIONAL DISEASE NURSERIES

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ABSTRACT

Each year, joint efforts from the collaborators of the USWBSI generate upwards of 100,000 phenotypic data points for scab severity on promising wheat lines through the Uniform Regional Scab Nurseries, in addition to related traits such as FDK and DON concentrations. These data are quite complex, with observed responses of often being categorical or bound (proportions), and conditional variance structures being correlated and heteroscadastic. Regardless, statistical analysis of these data has primarily been limited to ANOVA (fixed effect) models to compare entry means within and among sites, which are designed for the analysis of continuous and normally distributed data with homogeneous variance. Although the ANOVA F-test is fairly robust, inference regarding the genetic differences among entries using LSD methods can be misleading when applied to categorical and bound data. Furthermore, any imbalance in the data results in different levels of precision regarding the genetic values among entries, and can greatly bias the estimates of genetic merit for the entries.

Statistical models that have less restrictive assumptions than the ANOVA method are available to model complex data. These models do not require strict distributional assumptions and can more efficiently combine the data among locations and years into a single analysis to improve the results generated from the Uniform Regional Scab Nurseries. For this project, we are evaluating and comparing different statistical methods for estimating the genetic value of entries in multi-site scab nurseries, including linear fixed-effects models (ANOVA), linear mixed-effects models (BLUP analysis), and generalized linear mixed-effects models. Simulations are being conducted to compare the accuracy and precision of the estimates for genetic merit derived from these models. The utility of the models will then be validated by application to several years of uniform regional nursery data and comparison with the existing analysis results. If more sophisticated statistical methods are capable of even marginally improving the estimation of genetic value for scab resistance from regional disease nurseries, then they provide essentially a zero cost means for improving selection for scab resistance.

MAPPING AND PYRAMIDING SCAB RESISTANCE QTL IN EARLY GENERATION SPRING AND WINTER WHEAT BREEDING POPULATIONS USING A FAMILY-BASED MAPPING APPROACH

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ABSTRACT

Resistance to Fusarium head blight in wheat is a complex trait, for which numerous QTL have been identified. While the use of *Fhb1* for development of host resistance is commonplace in wheat breeding programs, the vast genetic variation for resistance represented by smaller effect QTL has not been routinely exploited. This infrequent transition from QTL discovery to marker-assisted selection stems from disparity between mapping and breeding populations. Family-based linkage analysis developed for human pedigrees has been used successfully to identify *Fhb1* in early generation breeding populations (Rosyara et al. 2009. Theor. Appl. Genet. 118: 1617-1631), suggesting utility for integrating QTL mapping and marker-assisted selection.

This project extends the family-based mapping approach to identify and pyramid multiple scab resistance QTL in breeding populations with an *Fhb1* background. HRSW breeding populations consisting of 44 double-cross families have been developed by crossing novel sources of resistance with 16 experimental lines carrying *Fhb1* from the SDSU spring wheat breeding program. Winter wheat breeding populations consisting of 28 double-cross families have also been developed by crossing resistant varieties with 'Wesley'-Fhb1 backcross lines. Double-cross F_1 individuals were screened for resistance in the greenhouse by single head spray inoculations with *Fusarium graminearum* isolate Fg4. The heritability of individual plant severity in the greenhouse was between 0.33 and 0.39. Spring wheat F_2 lines were planted and rated for scab severity in inoculated disease nurseries by SDSU, NDSU and UMN to progeny test the F1 individuals. Winter wheat F_2 lines have been planted in disease nurseries by SDSU, NDSU, and KSU for evaluation in 2013. F_3 seed from top performing lines have been advanced to winter nurseries for further evaluation and increase.

Founder lines and double-cross F_1 individuals are being genotyped using SSR markers to provide a genome-wide scan for resistance QTL. Chromosomes 2B, 3B, 7B and 4D have already been genotyped to target previously reported QTL from the parent lines. Existing software packages MERLIN (Abecasis et al. 2002. Nat. Genet. 30(1): 97-101) and MENDEL (Lange et al. 2001. Amer J Hum Genetics 69: 504) are being used to conduct family-based linkage and association tests. Markers associated with identified resistance QTL will be used to assist selection and pyramiding of those QTL in F_4 lines for the purpose of validating the QTL and generating resistant germplasm for use in wheat breeding programs.

HISTORICAL COMPARISON OF THE NORTH AMERICAN BARLEY SCAB EVALUATION NURSERY (NABSEN)

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ABSTRACT

The North American Barley Scab Evaluation Nursery (NABSEN) was established to screen elite two-rowed and six-rowed barley germplasm for resistance to Fusarium head blight (FHB) in regional uniform nurseries in North America and China. Participants included breeding programs from North Dakota State University (NDSU), University of Minnesota (UM), Busch Ag. Resources Inc. (BARI), and Agriculture & Agri-Food Canada Research Centre (AAFC). Each year (2002-2012) seven misted inoculated sites were established in the upper Midwest of the United States and one in Canada. From 2007-2012 a site was also established in China. NABSEN participants use different criteria to select elite material for testing; NDSU submits both two-rowed and six-rowed lines, BARI and UM programs submit primarily six-rowed entries, and the Canadian breeding programs submit mostly two- rowed lines. Here we report on the resistance to FHB of entries submitted from the NDSU, UM, BARI and AAFC breeding programs. Comparisons were made with Conlon (two-rowed resistant check) and Chevron (six-rowed resistant check) for deoxynivalenol (DON) content and FHB severity. These two resistant checks have been used consistently throughout all eleven years. AAFC and NDSU had at least one two-rowed entry equal to Conlon for DON accumulation in 63.6% and 54.5% of the years, respectively. AAFC and NDSU also had at least one entry equal to Conlon for FHB severity in 90.9 % and 81.8 % of the years, respectively. AAFC, NDSU, BARI and UM, had at least one six-rowed entry equal to Chevron for DON accumulation in 18.2%, 36.7%, 18.2% and 36.7% of the years, respectively. The NDSU breeding program has had one entry equal to Chevron for FHB severity in one of the eleven years. Over the past eleven years six North American varieties that are commercially available have been included in NABSEN testing. They include Tradition, and Quest six-rowed lines and Pinnacle, CDC Mindon, Norman and Taylor two-rowed barley lines. Several of these lines have improved resistance and the collective increased resistance of materials in the NABSEN through the years and release of varieties with FHB resistance are indicators of the progress in FHB resistance and the essential role that the NABSEN has played.

GETTING FUSARIUM HEAD BLIGHT (FHB) RESISTANCE WHERE IT COUNTS, IN EXISTING COMMERCIAL CULTIVARS

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ABSTRACT

For the deployment of host genetic resistance to Fusarium head blight (FHB) to confer meaningful benefits it must preserve, or possibly enhance, the combinations of useful traits expressed by elite germplasm. In wheat, multiple genes must interact in complex ways to express FHB resistance that is sufficient to protect against losses to yield and quality. This poses a severe challenge to efforts to achieve this level of resistance while retaining all the desirable attributes of a commercial cultivar. Indeed, no contemporary cultivar has derived a high level of FHB resistance by introgression of genes from known resistance sources. An alternative approach opened with the finding that FHB-resistant 'Sumai 3' and its susceptible near-isogenic lines do not differ in the general plant defence genes that are induced in response to inoculation by *Fusarium graminearum*. With this indication that improved FHB resistance might be gained by changing the control of expression of existing genes rather than introgressing new ones, we sought to evolve heritable traits *de novo* in the descendants of germplasm subjected to systemic stresses, an approach that has already yielded new sources of resistance in wheat to wheat streak mosaic virus (WSMV) and rust infections. We chose as our starting material the contemporary Canadian hard red spring wheat cultivar 'Waskada' (intermediate FHB reaction), and subjected succeeding generations to systemic stresses including virus infection, heat and cold. In each cycle, we selected and advanced plants that differed visibly from their progenitors in a range of traits including FHB resistance, which we evaluated for the first time in the 2010 FHB nursery. The three sublines which exhibited better resistance than relevant checks became the founders of three families of sublines that were advanced in cycles of further selection in the field over the next two years before entering them in the 2012 field nursery. In this trial the original 'Waskada' progenitor had an FHB index score of 22.5, the best family of sublines had a mean score of 4.2 while the most resistant, but non-elite, checks scored 0.5-1.0. A preliminary agronomic trial, conducted in the absence of disease pressure, produced seed used to determine that the families of sublines evolved from 'Waskada' possessed quality traits similar to the cultivar progenitor.

ASSOCIATION MAPPING OF FUSARIUM HEAD BLIGHT RESISTANCE IN U.S. HARD WINTER WHEAT

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ABSTRACT

Fusarium head blight (FHB) is one of the most destructive diseases of wheat worldwide. FHB epidemics can cause severe losses in both grain yield and quality of wheat. One of the most effective approaches to reduce the disease losses is to grow FHB resistant cultivars. To characterize resistance quantitative trait loci (QTLs) in U.S. winter wheat, association mapping was conducted using 135 hard winter wheat, 66 soft winter wheat accessions and Sumai 3 as resistant control. All accessions were evaluated for FHB severity (type II) using single-point inoculation in greenhouse. Total 282 SSR, 21 other types of markers and 9000 genome-wide SNP markers were genotyped. Population structure analysis divided the population into four subgroups, including two hard winter wheat groups and two soft winter wheat groups, and Q model was the best for association mapping. In the greenhouse experiments, 4 SSR and 15 SNP markers were associated with type II resistance mainly located in chromosome of 1A, 2A, 2B, 3B, 3D, 4A, 6A, 6B, etc. Several QTL and significant markers associated with type II resistance identified in this study should be useful for improvement of FHB resistance in hard winter wheat.

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EVALUATION OF FHB RESISTANCE AND AGRONOMIC PERFORMANCE IN SOFT RED WINTER WHEAT ACROSS POPULATIONS

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ABSTRACT

Development of resistant wheat cultivars is the most efficient approach to control FHB. Local broadly adaptive cultivars have been crossed with *Fhb1* derived lines, Truman, and Jamestown to introduce FHB resistant QTL into local adaptive genetic backgrounds. Eight elite lines (GA051173W-S11, GA051173-S18, GA051173-S25, GA 051207-S19, GA 051207-S21, GAMD08-27-E9-S13 GAMD08-27-E9-S14, and GAMD08-27-E9-S15) with resistance from either Truman, IN981359C1, or Ning 7840, were evaluated in the field in 2012 for FHB resistance and agronomic performances. The closely linked markers were also used to detect the resistant QTL for FHB and other critical diseases. GAMD08-27-E9-S13, GAMD08-27-E9-S14, and GAMD08-27-E9-S15 maintained the *Fhb1* and 5A QTL from the resistant donor Ning 7840. Elite lines, GA051173-S11 and GA051173-S18, selected from the cross of Truman and AGS 2010, showed a high level of FHB resistance which was similar to the resistant controls, Bess and Jamestown. These five elite lines also included important resistant genes for Hessian fly (*H13*) and leaf rust (*Lr37/Yr17/Sr38*). GA 051207-S19 and GA 051207-S21 were the highest yielding lines with moderate resistance for FHB index and ISK index when compared to the check "AGS 2035". In addition, an elite line GA041052-11E51 evaluated in the GAWN also showed high level of FHB resistance and had very high grain yield. Several other lines with Jamestown as source of resistance will be further evaluated for FHB and grain yield.

GENETIC ANALYSIS OF FUSARIUM HEAD BLIGHT RESISTANCE IN TUNISIAN-DERIVED DURUM WHEAT POPULATIONS

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ABSTRACT

Host plant resistance is recognized as the most effective means of controlling FHB infection. Resistant FHB varieties in hexaploid wheat have been released; however, the progress toward the same goal in durum wheat (*Triticum turgidum* ssp. *durum* Desf.) wheat has been limited. Sources of resistance in durum wheat are few and transferring the resistance genes from hexaploid wheat have met with limited success. The new Tunisian resistant durum sources found recently show promising amount of resistance comparable to the hexaploid sources. We have used these sources in several studies to identify and mark genomic regions of interest for introgression into cultivated durum varieties.

In one study we used 171 BC_1F_6 and 169 BC_1F_7 lines derived from crossing of four Tunisian tetraploid sources of resistance (Tun7, Tun18, Tun34, Tun36) with durum cultivars 'Ben', 'Maier', 'Lebsock' and 'Mountrail' for association studies. The Tun18 and Tun7 FHB resistances were found to be comparable to the best hexaploid wheat sources. A new significant QTL for FHB resistance was identified on the long arm of chromosome 5B (*Qfhs.ndsu-5BL*) with both association and classical QTL mapping analysis. Linkage disequilibrium (LD) blocks extending up to 40 cM were evident in these populations. The linear mixed model considering the structure (Q or P) and the kinship matrix estimated by REML (K_T) identified as the best for association studies in a mixture of wheat populations from a breeding program. The results of association mapping analysis also demonstrated a region on the short arm of chromosome 3B as potentially linked to FHB resistance. This region is in proximity of major FHB resistance gene "*Fhb1*" reported in hexaploid wheat. A possibility of having susceptibility or suppressor of resistance gene(s) on durum wheat chromosome 2A was further confirmed in this material explaining the problem in developing resistant genotypes without counter selection against this region.

In another study, two additional Tunisian- derived advanced backcross populations, Tun 108 × Lebsock/ Lebsock and Tun 108 × Ben/Ben, were screened for FHB resistance in both greenhouse and field. A total of 171 BC_1F_7 lines derived from Tun 108 × Ben/Ben were phenotyped for their reaction to FHB in two greenhouse and two field experiments. Analysis of variance showed significant effect on FHB infection rate for the genotypes and also environments, as well as G×E interactions. Broad sense heritability for FHB infection rate was calculated to be around 40.4%±0.09. The correlation between the two greenhouse seasons and also the two field scab nurseries were positive and significant while there was correlation between only one of the greenhouse data and the field data. Transgressive segregation for FHB severity was observed and approximately 5% of the lines performed better than the resistant parents in the field and 25-30% while evaluated in the greenhouse. A total of 329 markers were mapped to 239 unique loci with coverage of 1887.6 cM, and an average of 7.89 cM between any two marker loci. QTL analysis for FHB resistance revealed six different QTL on 5 different chromosomes (1A,1B, 2B, 3B, 5A, 5B, 7A and 7B). The QTL on 5A and 7A were both effective in the field and greenhouse and

together explained ~ 9% of total phenotypic variation and 22.5% of genetic variation in Tun108×Ben/Ben population. The QTL regions on chromosomes 2B and 3B both were associated with resistance to severity, incidence, FDK and DON.

We used the same procedure for screening a population of 174 BC1 F7 individuals derived from cross between Tun 108 and Lebsock/Lebsock in 2 greenhouse and 2 field trial during 2010 to 2011. Additionally, FDK, DON, 3ADON, 15ADON and Nivalenol were measured on samples collected from 2011 field experiment. Analysis of variance indicated a significant effect on FHB infection rate for the genotypes and also environments, as well as G×E interactions. Broad sense heritability for FHB infection rate was estimated to be around 33.4%±0.09. The correlation between the two greenhouse seasons and also the two field scab nurseries were positive and significant while there was no correlation between the greenhouse data and the field data. Remarkable correlations between disease incidence and FDK ($r = 0.53$, $p < 0.0001$) was assessed, while there was no significant correlation between severity and FDK. There was no correlation between disease incidence and DON, severity and DON. Transgressive segregation for FHB severity was observed within this population. Nearly 5% of the lines with highest resistance in the field, lowest FDK and DON accumulation were selected for incorporation into the breeding program. The QTL analysis is underway and the results will be reported.

The most FHB resistant Tunisian derived backcross lines and associated markers are being employed to incorporate valuable regions into advanced durum breeding lines for cultivar improvement.

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METABOLIC PROFILING REVEALS NOVEL INSIGHTS INTO THE BIOTRANSFORMATION OF DON IN WHEAT

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ABSTRACT

In a recent study we have developed a novel approach for the untargeted screening of metabolites of xenobiotics in plants. The approach was successfully applied to wheat plants after treatment with a mixture of $^{13}C_{15}$– and non-labeled deoxynivalenol (DON) and resulted in the assignment of a total of nine different DON conjugates. Besides the well-known DON-3-*O*-glucoside, for the first time the occurrence *in planta* of DON-glutathione (GSH), DON-S-cysteinyl-glycine, DON-S-cysteine have been reported together with five other DON conjugates [1].

In the present work we have further characterized the molecular structures of the remaining five DON conjugates by liquid chromatography - tandem mass spectrometry (LC-MS/MS). Additionally, DON- and *Fusarium graminearum* treated near isogenic wheat lines, which differed in two major resistance quantitative trait loci (QTLs) against Fusarium head blight (FHB) *Qfhs.ndsu-3BS* and *Qfhs.ifa-5A*, were monitored for all nine DON conjugates.

For the two parent lines Remus (susceptible) and CM-82036 (resistant) and each NIL, wheat ears were challenged at anthesis in two inoculation variants with *F. graminearum*, and DON and harvested at 0, 14, 48 and 96h after inoculation. For each time point and inoculation variant 5 plants (1 ear per plant) were treated. After the respective inoculation period, treated ears were harvested, immediately frozen in liquid nitrogen and stored at -80°C until analysis. Frozen plant samples were homogenized in a ball mill with liquid nitrogen, extracted and analyzed by LC-high resolution-MS.

This contribution will present the putative molecular structures of the identified (novel) DON conjugates and will compare the formation of these DON biotransformation products over a time period of up to 96 hours after inoculation with either DON or *F. graminearum* strain PH-1. The results will be evaluated and discussed in view of the different combinations of resistance QTLs present in the tested near isogenic wheat lines.

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COMPARISON OF VISUAL AND DIGITAL IMAGE ANALYSIS METHODS FOR ESTIMATION OF *FUSARIUM* DAMAGED KERNELS IN WHEAT

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ABSTRACT

Fusarium head blight (FHB), or head scab, causes a reduction in grain yield and quality, as well as, the formation of shriveled, dull-grey seeds called "tombstones" or *Fusarium* damaged kernels (FDK). FDK is commonly quantified on a percentage basis by visually separating damaged kernels from the healthy kernels following harvest, a process that is both time consuming and labor intensive. The objective of this study was to evaluate an alternative method for quantifying FDK through the use of digital imagery and the digital image analysis program ImageJ. The 'NC-Neuse' x 'AGS 2000' recombinant inbred population of 172 lines and the NC-Neuse x 'Bess' double haploid population of 112 lines were used in this study. NC-Neuse and Bess were moderately resistant and AGS 2000 was susceptible to FHB. Both populations were evaluated under moderate to heavy FHB pressure in a total of five environments in North Carolina, Maryland and Missouri with two to three replications per environment. Wheat heads from each plot were harvested, dried, threshed, and cleaned by hand. Digital image analysis estimates were obtained by applying a hue, balance, saturation filter in ImageJ to images captured using a standard digital SLR camera. The filter was set to exclude the less color saturated (grey) kernels. ImageJ would then output the proportionate area of damaged kernels.

Significant genetic variation was observed using both visual and digital image analysis methods to estimated FDK. These methods' correlation values ranged from 0.72 to 0.80 over all environments. A lower correlation value of 0.54 was observed in Columbia, MO because of cracked and broken kernels in the samples. Digital image analysis was three times faster than the visual method, and was able to estimate FDK on a larger per plot sample whereas labor and time constraints limited the sample size for the visual method. Digital image analysis was consistent over different samples and appears well suited as an alternative form of FDK detection in unbroken grains samples.

PRE-BREEDING THROUGH RECURRENT MASS SELECTION

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ABSTRACT

Recurrent mass selection (RMS) is an ideal breeding strategy for the enrichment of a breeding population with respect to genes that govern complex, polygenic traits. In North Dakota, primary targets for hard red winter wheat breeding include increased winter-hardiness, high yield potential, good processing quality and effective resistance against major diseases such as Fusarium head blight, leaf and stem rust, tan spot and the septoria complex. When RMS is applied to pre-breeding, generation intervals can be shortened considerably through single seed descent. Accelerated single seed descent (SSD) inbreeding can be achieved by utilizing small soil volume, extended daylight hours, elevated temperature during growth, premature harvesting and seed drying. During SSD inbreeding, the integration of seedling screening for rust resistance or low temperature tolerance, marker aided selection for key genes and field selection for FHB resistance amid artificial epidemics can help to raise the target gene frequencies and eventually facilitate gene pyramiding. A highly diverse pre-breeding base population has been derived by making an *Ms3*- (dominant male sterility) assisted complex cross with 110 diverse lines and varieties contained within five populations. These included genotypes with native and exotic resistance and adaptation genes, primarily from spring wheat or less cold-hardy winter wheat. This base population will be subjected to recurrent selection during which F_1 female plants (1-year cycle) will be cross-pollinated with F_4-derived F_5 lines that had been field selected once during a 3-year breeding cycle.

IS THE FUSARIUM HEAD BLIGHT RESISTANCE IN TRUMAN SOFT RED WINTER WHEAT NOVEL?

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ABSTRACT

At the University of Missouri, we have been addressing losses associated with Fusarium head blight (FHB) mainly caused by *Fusarium graminearum* Schwabe [telomorph: *Gibberella zeae* Schw. (Petch)] through the identification and use of 'native' sources of resistance identified in soft red winter wheat germplasm of U.S. origin. 'Truman', developed and released by the University of Missouri has excellent, broad-based FHB resistance, coupling low incidence and severity, good kernel quality retention, and low DON with good adaptation and agronomic performance throughout the northern soft red winter wheat region. It serves as the resistant check in the Northern Uniform Scab Nursery and the Northern Preliminary Scab Nursery. Truman carries none of the known markers for FHB resistance used by the Wheat Genotyping Laboratory at Raleigh NC therefore, it may provide different FHB resistance genes that could complement other widely-used sources of resistance. Anecdotal evidence from the Missouri breeding program suggests that the source of resistance in Truman is partially dominant, and highly penetrant. Results of a diallel study of 20 winter wheat varieties confirmed that across a wide range of resistant and susceptible genotypes, Truman had very good general combining ability. A small but significant specific combining ability component was also detected which appeared to be associated with dominance gene action rather than epistasis. With funding from the USWBSI, a QTL study was undertaken on an $F_{6:8}$ recombinant inbred line mapping population developed at the Univ. of Missouri from the cross Truman x MO 94-317. Greenhouse type II phenotypic data were collected at the Univ. of Missouri while phenotypic data for field-based traits (incidence, severity, and *Fusarium* damaged kernels and DON) were collected at Missouri, Purdue, and/or the University of Kentucky. DON analyses were done at the University of Minnesota. Genetic linkage maps were constructed from 160 SSR markers, and 530 Dart markers. QTL analyses of greenhouse type II resistance combined over years identified four QTL on chromosomes 1BSc, 2BL, 2DS, and 3BSc that accounted for 10.9, 16.1, 19.9 and 7.3% of the variability respectively. QTL on 1BSc, 2BL and 3BSc do not appear to be novel. The QTL on 2DS, linked with the DArT marker wPt666223, however, may be unique to Truman. The same 2DS QTL was also detected for incidence, severity, FHBI (incidence x severity), and DON accounting for 22.9, 23.0 and 25.3, and 20.7% of the phenotypic variance, respectively as well as for incidence based on Purdue data and DON based on KY data where it accounted for 24.3 and 20.1% of the phenotypic data, respectively. Although significant for FDK the 2DS QTL had a smaller effect, accounting for 7.5% of the phenotypic variance. A second QTL on 2ASc that was also common across incidence, *FhbI*, FDK and DON accounted for 6.7, 8.2, 8.5, and 10% of the variation respectively, and may also be novel in Truman although a QTL near this region has been identified in Wangshuibai for both DON and FDK. Finally, a QTL on 3DS associated with incidence in Truman, accounting for 10% of the variance also appears to be novel. Other QTL identified in this population appear to have been reported in European, Asian or U.S. germplasm. Among the unique QTL in Truman, the region on 2D has the largest effect and providing significant reductions in DON, incidence, and disease spread within the head. Once validated, it may provide gene(s) complementary to other widely used sources that should prove valuable for marker-assisted-selection.

MAPPING OF FUSARIUM HEAD BLIGHT RESISTANCE IN WILD BARLEY ACCESSION PI 466423

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OBJECTIVE

To map loci conferring Fusarium head blight resistance in wild barley.

INTRODUCTION

The devastating Fusarium head blight (FHB) epidemics occurring over the past two decades contributed to the decline of the malting barley industry in the Red River Valley region of the USA and Canada. The best strategy for reducing disease and mycotoxin levels is an integrated approach of cultural practices, fungicide application, and host resistance. To identify resistance to FHB, over 23,000 *Hordeum* accessions were screened in field nurseries in the Midwest and China (*1, 2*). These studies showed that resistance to FHB was extremely rare as less than 2% of accessions carried useful levels of resistance for breeding. Moreover, resistance was only partial as no immune or even highly resistant accessions were identified.

Several molecular mapping studies involving cultivated barley accessions and landraces revealed that FHB resistance is controlled, in most cases, by a number of loci with relatively small effects that are scattered across the barley genome (*3, 4, 5, 6, 7*). Additionally, some agronomic (e.g. heading date and plant height) and spike architecture (e.g. row type and kernel density) traits were found to map at coincident chromosomal positions as the identified FHB resistance loci (*8*). These data raise important questions as to whether these associations are due to closely linked genes or possibly pleiotropy.

Wild barley is a very rich source of disease resistance genes, but has not been fully exploited for FHB resistance. From the extensive evaluations of *Hordeum* germplasm, we identified 27 wild barley accessions with partial resistance to FHB (*1*). One of the most resistant accessions was PI466423, which was originally collected near the village of Mehola west of the Jordan River in Israel. Our overall goal is to reduce the losses caused by FHB, especially quality discounts due to the accumulation of DON. This can be best achieved by identifying and incorporating into barley cultivars genes that confer a high level of resistance to FHB and the accumulation of mycotoxins. To increase the diversity of FHB resistance alleles in cultivated barley, we developed an advanced backcross population involving PI466423 and cultivar Rasmusson. Our specific objective was to map loci conferring FHB resistance in wild barley accession PI466423.

MATERIALS AND METHODS

Plant materials. A recombinant chromosome substitution line (RCSL) population was developed for the advanced backcross strategy of Tanksley and Nelson (*9*) using the crossing scheme of Matus et al. (*10*). The final population consisted of 258 BC_2F_4 lines

FHB phenotyping. The RCSL population was assessed for FHB severity (in percent) at St. Paul and Crookston, Minnesota in 2010, 2011 and 2012 and in Hangzhou, China in 2011. DON accumulation (in parts per million) also was assayed in all environments, except the 2012 Minnesota nurseries (pending) and 2011 China

nursery. Nurseries at Crookston and Hangzhou were inoculated using the "grain spawn" method where ascospores are the primary inoculum source (*8*). At St. Paul, a calibrated load of *Fusarium graminearum* conidia was applied to plants at the heading stage using the "spray inoculation" method. FHB and DON assessments were made according to the methods of Ma et al. (*5*) and Fuentes et al. (*11*), respectively.

Extraction of genomic DNA. Sections (5 cm) of leaf material were harvested from 2-week-old BC_2F_4 seedlings grown in a greenhouse. Tissue was flash frozen in liquid nitrogen, stored at -80˚C, and lyophilized to dryness. Leaf tissue was ground to powder using a Qiagen TissueLyser II and 3 mm tungsten carbide beads. Genomic DNA was isolated from ground tissue using a Qiagen BioSprint 96 workstation and the BioSprint 96 DNA Plant Kit. Quality and quantity of isolated genomic DNA was assessed via agarose gel electrophoresis and spectrophotometry, respectively.

Single nucleotide polymorphism (SNP) genotyping. Genotyping of parents and progeny was conducted at the USDA-ARS Cereal Crops Research Unit in Fargo, North Dakota. Samples of genomic DNA were genotyped using the Illumina Infinium assay. The Illumina genotyping array is capable of interrogating 7,863 SNPs within the barley genome simultaneously. Genotype calls for all SNP markers were visually inspected and validated using the GenomeStudio Genotyping Module. This analysis yielded 6,710 informative markers, 2,252 of which were polymorphic between the parental lines.

Genetic map construction. Genetic maps of the seven barley chromosomes were constructed using Join Map 4.0. All 2,252 polymorphic SNPs were considered for map construction, though only a single marker representing markers with greater than 98% redundancy was included in the final map. Linkage groups were determined by recombination frequency and only marker pairings with LOD > 3.0 were included in the final map. Kosambi's mapping function was used for map construction.

Marker analysis and QTL mapping. Only six-rowed RCSLs were used in the QTL analysis to eliminate the possible confounding factor of row type. Chromosome bin positions were approximated based on Munoz-Amatriain et al. (*12*). Single marker analysis to detect marker associations was conducted using QTL Cartographer 2.5_011 (*13*). Data were analyzed as a trait mean for each environment with a total of four to seven environments per trait (environments per trait are listed in Table 1). Marker-trait QTL were defined if the association was detected in two or more environments at or above LOD 3.0. QTL were defined as major if they were detected in greater than 75% of all trait environments. Allele effects at the QTL location were calculated in reference to the Rasmusson allele. Correlations for trait means were conducted using Excel.

RESULTS AND DISCUSSION

FHB and DON levels varied markedly across locations and also years (see summary data in Table 1). QTL analysis revealed a major effect QTL for FHB severity and DON concentration on chromosome 2H, bin 4 (Fig. 1). This QTL was observed in six of the seven environments, and the percentage of phenotypic variance explained ranged from 40% in 2010 to 7% in 2012 for FHB and from 25% in 2011 to 18% in 2010 for DON. Analysis of heading date and plant height revealed QTL coincident with the one for FHB and DON in the bin 4 region of chromosome 2H (Fig. 1). It is not known whether closely linked loci control these different traits or if pleiotropy may be involved. If the former case, the resistance allele may be unique and therefore useful for enhancing FHB resistance of breeding lines carrying other resistance alleles. The question of linkage vs. pleiotropy will be resolved with additional crosses as was done previously with FHB resistance loci and heading date loci by Nduulu et al. (14). In previous studies on mapping FHB resistance, QTL for heading date

(*5*,*15*), height (*15*), and DON accumulation (*3*) were identified on chromosome 2H bin 4.

The allelic effect (α) for the chromosome 2 bin 4 FHB QTL was inconsistent with four environments (Crookston 2010, 2011, and 2012 and St. Paul 2010) showing a negative α for Rasmusson, and two environments (St. Paul 2011 and 2012) showing a positive α for Rasmusson. Phenotyping barley germplasm for FHB resistance and DON accumulation is fraught with many sources of variation (*8*). Some of the variation we observed across environments may be due to the different inoculation methods employed (grain spawn spread on ground with ascospore inoculum source vs. spray inoculation directly on heading plants with conidial inoculum source), timing of disease assessments (St. Paul is taken at set intervals after inoculation whereas Crookston is not) and perhaps local climatic factors (Crookston is cooler than St. Paul and hence plants have a longer plant maturation period). Nevertheless, the same QTL was detected across different environments.

ACKNOWLEDGEMENT AND DISCLAIMER

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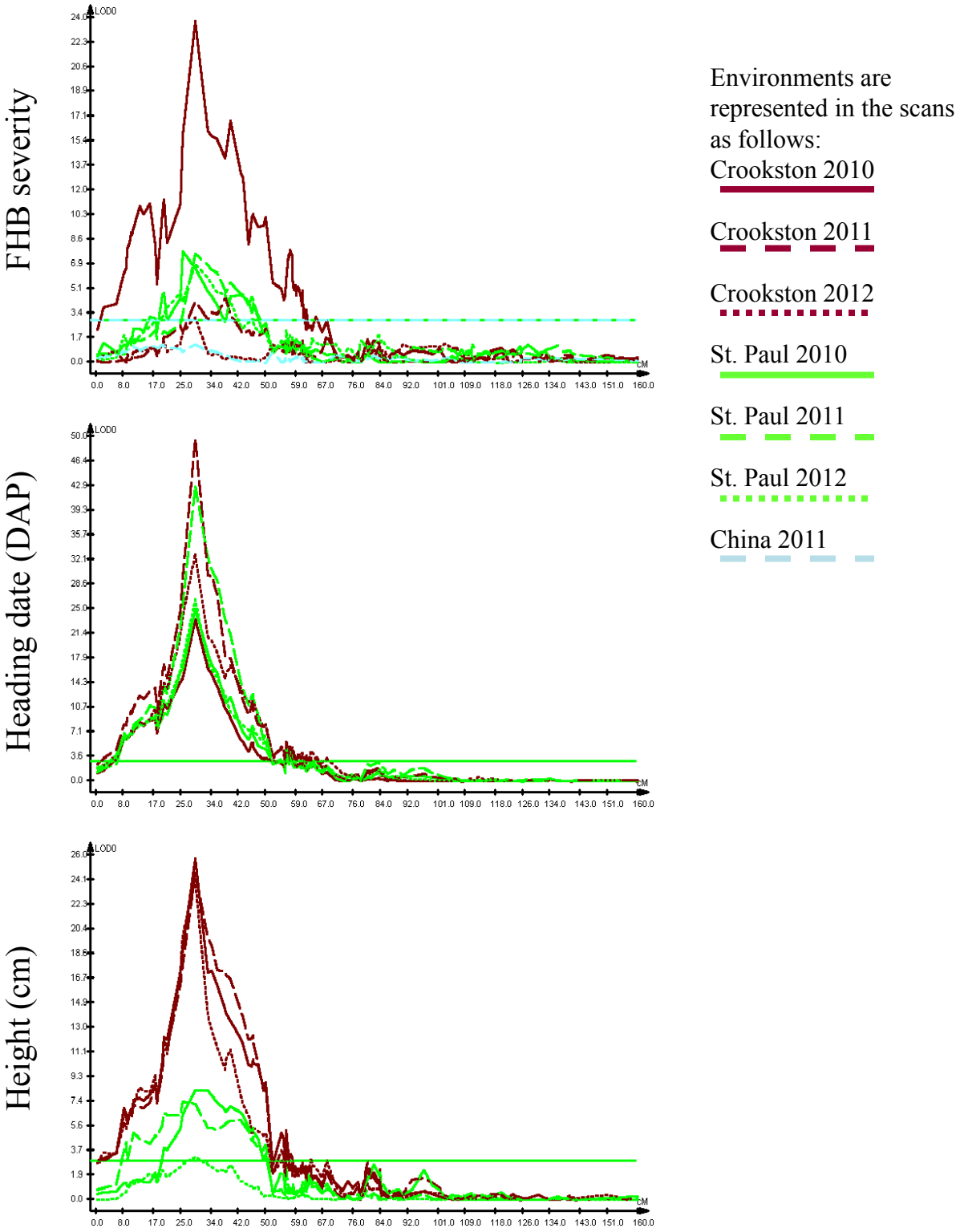

Figure 1. LOD scans for major QTL at chromosome 2 bin 4 for FHB severity, heading date and height in the PI466423/Rasmusson population. Allelic effect and R2 values for these peaks are presented in Table 1.

Table 1. Phenotypic and QTL summary for the PI466423/Rasmusson population for FHB severity, heading date, height, DON accumulation and spike angle.

Trait[§]	Environment[#]	PI466423	Rasmusson	Mean[†]	Min[†]	Max[†]	S.E.[†]	QTL Peak[£]	R^2	Alpha[‡]	QTL Peak[£]	R^2	Alpha[‡]
FHB	CR 2010	nd*	14	21	3	90	11.37	2 -- 4	0.409	-10.651			
	CR 2011	13	39	32	11	69	10.21	2 -- 4	0.090	-4.500			
	CR 2012	8	9	12	2	35	4.61	2 -- 4	0.070	-1.748			
	SP 2010	nd	9	13	1	37	6.78	2 -- 4	0.159	-3.787			
	SP2011	nd	12	11	1	34	7.30	2 -- 4	0.156	4.271			
	SP 2012	nd	nd	17	2	58	9.67	2 -- 4	0.141	5.402			
	CH 2011	1	1	1	0	4	0.42						
HD	CR 2010	58	52	51	47	56	1.86	2 -- 4	0.404	1.740			
	CR 2011	57	50	50	42	57	3.13	2 -- 4	0.661	3.739			
	CR 2012	63	59	59	50	69	4.49	2 -- 4	0.521	4.728			
	SP 2010	nd	58	55	41	69	3.70	2 -- 4	0.424	3.523			
	SP 2011	73	65	64	52	71	3.57	2 -- 4	0.608	4.094			
	SP 2012	nd	nd	57	45	75	6.04	2 -- 4	0.437	6.028			
HT	CR 2010	72	76	83	59	110	8.18	2 -- 4	0.429	7.890	3 -- 12	0.076	-3.219
	CR 2011	81	63	70	48	92	8.13	2 -- 4	0.416	7.721	3 -- 12	0.067	-3.360
	CR 2012	80	80	79	39	105	9.48	2 -- 4	0.420	8.922	3 -- 12	0.092	-4.337
	SP 2010	nd	84	83	58	114	9.29	2 -- 4	0.168	5.574	3 -- 12	0.069	-3.503
	SP 2011	nd	60	62	35	82	6.96	2 -- 4	0.155	3.819	3 -- 12	0.076	-3.042
	SP 2012	nd	66	67	39	86	7.77	2 -- 4	0.068	3.034	3 -- 12	0.067	-2.843
DON	CR 2010	3.00	23.17	15.07	1.00	56.90	8.19	2 -- 4	0.184	5.018			
	CR 2011	28.50	36.45	34.06	3.70	83.00	15.05	2 -- 4	0.255	10.621			
	SP 2010	nd	19.37	20.83	3.40	54.40	8.62	2 -- 4	0.159	4.877			
	SP 2011	nd	12.97	8.49	0.29	29.30	6.12	2 -- 4	0.162	3.631			
SA	CR 2010	1	1	1.1	1	3	0.35				5 -- 10	0.081	-0.157
	CR 2012	1.2	1	1.2	1	2.5	0.35				5 -- 10	0.044	-0.110
	SP 2010	nd	1	1.1	1	3	0.36	2 -- 6	0.141	-0.251			
	SP 2012	nd	1	1.1	1	3	0.28	2 -- 6	0.137	-0.165	5 -- 10	0.068	-0.125

[§]Trait abbreviations are FHB (FHB Severity), HD (heading date in days after planting), HT (height in cm), DON (deoxynivalenol accumulation), SA (spike angle on 1—3 scale where 1 is upright and 3 is nodding).

[#]Environments are abbreviated: CR denotes Crookston, MN, SP denotes St. Paul, MN, CH denotes Hangzhou, China.

*nd denotes no data available for parent at this environment

[†] Mean, minimum, maximum and standard error are presented for the PI466423/Rasmusson population

[£]QTL Peaks are listed by chromosome and bin position. Numbers listed are: (chromosome) – (bin)

[‡]Allelic effect of the Rasmusson allele at the QTL peak

'PROSPER': A NEW HARD RED SPRING WHEAT CULTIVAR COMBINING HIGH YIELD AND GOOD RESISTANCE TO FUSARIUM HEAD BLIGHT, LEAF DISEASES, AND QUALITY ATTRIBUTES

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OBJECTIVES

The main objective of this research project is develop new improved hard red spring wheat (HRSW) cultivar with resistance to Fusarium Head Blight (FHB) disease and superior grain yield and bread-making quality.

INTRODUCTION

For decades, scab or FHB, caused mainly by *Fusarium graminearum Schwabe* [telomorph *Gibberella zeae* (Schwein.)], has been a serious threat to wheat production throughout the world (Schroeder and Christenson, 1963; Bai and Shaner, 1994; McMullen et al., 1997; Stack, 2003). In North America and particularly in the US spring wheat region (North Dakota and neighboring states), FHB has been a major disease for HRSW produced since 1993 (Bai and Shaner, 1994; McMullen et al., 1997). Some economic reports (Nganje et al., 2004) estimate combined direct and secondary economic losses caused by FHB for all crops were at $7.7 billion. ND and MN account for about 68% ($5.2 billion) of the total dollar losses. Direct losses from 1993 through 2001 for wheat only were estimated to $2.492 billion (Nganje et al., 2004). The use of genetically resistant cultivars is believed to be the most efficient and economical method of controlling this FHB in wheat. This has been demonstrated in ND since 2002 when 'Alsen' (Frohberg et al., 2006), a moderate FHB resistance cultivar derived from the Chinese source 'Sumai 3' (PI 481542), was released by NDSU (with the support of the scab initiative funds). Sumai3, a spring wheat from China, is arguably the most used source of resistance to FHB in the world. 'Alsen' was the leading cultivar in the spring region between 2002 and 2006. Up to 2.4 million acres (37.4% of ND wheat acreages) was grown to 'Alsen' (N.D. Agricultural Statistics Service, USDA. 2006). A similar scenario was repeated with 'Glenn' (Mergoum et al., 2006a), a 2005 NDSU release which dominated the HRSW wheat region from 2007 to 2011 (N.D. Agricultural Statistics Service, USDA. 2012). The rapid increase in acreage planted to 'Alsen', Glenn, and other HRSW cultivars such 'Barlow' (Mergoum et al., 2011), indicates the desire of ND wheat growers to produce such HRSW cultivars with FHB resistance.

MATERIAL AND METHODS

The HRSW cultivar Prosper a sister line of 'Faller' (Mergoum et al., 2008) was developed using a modified bulk breeding procedure. It was selected from the "ND2857/ND2814" cross made at NDSU in the fall of 1997. ND2857 (ND2709/ ND688) is a hard red spring experimental line

that has good resistance to FHB originating from ND2709 line derived from a cross involving Sumai3. Both ND2709 and ND688 are HRSW experimental lines developed by the NDSU breeding program. ND2814 ('KITT' (PI 518818)/'AMIDON' (PI 527682)//'GRANDIN' (PI 531005) /'STOA S' (PI 520297)) is a HRSW line developed by NDSU HRSW breeding program. Kitt is HRSW cultivar released in1975 by the Minnesota Agricultural Experiment Station and the USDA-ARS while Amidon, Grandin and Stoa are HRSW cultivars released by NDAES in 1988, 1989, 1984, respectively. Prosper was selected from a bulk of one purified $F_{5:6}$ row-plot planted in 2001 at Christchurch, NZ. Prosper was tested in the breeding yield trials in many locations in ND from 2001 to 2004. Subsequently, Prosper was tested as ND 808 in the North Dakota Variety Trials (NDVT) from 2005 to 2010 and in the HRSW Uniform Regional Nursery (URN) in 2009 and 2010. The URN is conducted in various location in the US and Canadian spring wheat region. The first seed increase of Prosper was grown in Prosper, ND in the summer of 2009. Prosper was tested for its reaction to FHB and different races of tan spot, leaf and stem rusts, SNB, and STB under greenhouse and field conditions during the period of 2004 to 2010. The SNB, STB and tan spot are the major components of the leaf spotting disease complex of wheat in North America. A complex of these diseases occurs in nature. Hence managing leaf spots is difficult; however, resistant cultivars are the most effective and economical means of controlling leaf spot.

RESULTS

Prosper (ND 808) was released because it combines very high yield (Tables 1 and 2), resistance to FHB and leaf diseases (Table 3), and good end-use quality (Table 4). Prosper was named after the small town of Prosper, which is located in Cass County, ND, where the NDSU HRSW breeding program conducts its main breeding activities.

Grain yield and other agronomic traits were based on as many as 63 location-years of testing in the NDVT (Table 1). Based on data from these trials, grain yield of Prosper (4415 kg ha^{-1}) was similar to that of Barlow (4232 kg ha^{-1}), Faller (4409 kg ha^{-1}), 'Howard' (Mergoum et al., 2006b) (4214 kg ha^{-1}), and 'Steele-ND' (Mergoum et al., 2005b) (4110 kg ha^{-1}). However, Prosper yielded significantly ($p < 0.05$) more than several previously released NDSU cultivars, including 'Alsen' (3799 kg ha^{-1}), Glenn (4003 kg ha^{-1}), 'Dapps' (Mergoum et al., 2005a) (3852 kg ha^{-1}), 'Parshall' (PI 613587) (3633 kg ha^{-1}), and 'Reeder' (PI 613586) (3867 kg ha^{-1}) (Table 1). Yield data shows that Prosper is more adapted to eastern North Dakota (5389 kg ha^{-1}) compared with its yield (3897 kg ha^{-1}) in western North Dakota (Table 1). In the URN trials conducted in 2009 and 2010 (28 location-years), Prosper had a yield of 4773 kg ha^{-1}, which was significantly ($P < 0.05$) higher than all other cheeks, including 'Keene' (PI 598224) (3985 kg ha^{-1}), 'Verde' (PI 592561) (4287 kg ha^{-1}), and 'Chris' (CItr 13751) (3104 kg ha^{-1}) (Table 2). The performance of Prosper in the URN as compared to other HRSW cultivars for other agronomic traits is reported in Table 2.

Artificial inoculation with FHB disease was used to cause intense disease pressure. The average severity (Stack and Frohberg, 2000) recorded for Prosper in the field scab nursery (23%) was significantly lower than that for the very susceptible check '2398' (70%) (Table 3). In the same trials, the average FHB severity of the best FHB resistant grown checks 'Alsen' and Glenn were 22 and 25%, respectively while ND2710 (PI 633976), the most resistant elite line was 13%. Under artificial greenhouse and artificial inoculation conditions (data not shown), the average FHB severity of Prosper was 33%, which was similar to the scores of 'Alsen' (28%) and Glenn (30%); and significantly lower than the 87% and 71% registered for the susceptible checks 2398 and Reeder. Field testing and screening tests of seedlings and adult-plants conducted under greenhouse conditions from 2004 to 2010 showed that Prosper is resistant to the pathotypes of the predominant race of leaf rust in the region. Gene postulation shows that Prosper possesses Lr21, which confers resistance

to the major races of leaf rust in the spring region. Recently, however, a new race that has overcome Lr21 was observed in Minnesota and North Dakota (Table 3). Prosper is also resistant to the stem rust races TPMK, TMLK, RTQQ, QFCQ, and QTHJ under field and greenhouse conditions (Table 3). Prosper was screened for tan spot, STB, and SNB under greenhouse conditions. Prosper had an average scores of 2.2, 2.2, and 3.6 for tan spot races 2, 3, and 5, respectively, while 'Alsen' scored 3.5, 1.9, and 2.0 for the same races (Table 3). In the same screening tests, the reactions to the races 2, 3, and 5 of the check 'Salamouni' (PI 182673) were 1.4, 1.4, and 1.3 and of the check 'Glenlea' (CItr 17272) were 4.3, 2.0, and 1.9. Salamouni is considered among the best sources of resistance to tan spot, whereas Glenlea is usually used as the susceptible check to race 2. The scores for the reaction of Prosper to STB and SNB were 2.2 and 2.4, while 'Alsen' had scores of 2.7 and 4.4; Salamouni, 1.7 and 1.7; and Glenlea, 2.4 and 3.7 (Table 3).

The critical quality parameter including Falling number, Flour extraction, dough and baking parameters for Prosper and checks included in the HRSW-VT grown in North Dakota from 2004 to 2010 are reported in Table 4. The falling number of Prosper (414 s) was not significantly different than that of the most commonly grown HRSW cultivars, including Howard (422 s), Glenn (394 s), Steele-ND (432 s), 'Alsen' (414 s), and Reeder (430 s) (Table 4). Similarly, the flour extraction value (Table 4) of Prosper (709 g/kg) was similar to that of Howard (696 g/kg) and Steele-ND (692 g/kg); however, it was significantly superior to that of Glenn (680 g/kg), 'Alsen' (688 g/kg), and Reeder (684 g/kg). Mixing peak time of Prosper was 8.2 min, not significantly different from the checks, except Glenn (10 min) and 'Alsen' (10.1 min). The mixing tolerance score (14.5 min) was significantly shorter than for Glenn (20.4 min) but comparable with the scores of rest of the checks (Table 4). Bread loaf volume produced from Prosper (1000 mL) was comparable with that of all of the checks, except for Glenn (1056 mL) (Table 4). Similarly, the water absorption of Prosper (64.4%) was not significantly different from that of the checks, except for Steele-ND (66.4%) (Table 4).

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Table 1. Summary of agronomic data for Prosper and check cultivars tested in the North Dakota Hard Red Spring Wheat Variety Trials, 2005 to 2010.

	Grain yield								
Cultivar	North Dakota	Eastern North Dakota	Western North Dakota	Grain protein	1000-kernel weight	Grain volume weight	Heading date	Height	Straw strength
		kg ha^{-1}		%	g	kg m^{-3}	d after June 1st	cm	0–9†
Prosper	4415	5389	3897	14.2	33.5	763	61.6	83	1.5
Barlow	4232	4938	3857	14.8	31.6	782	58.4	85	1.5
Faller	4409	5310	3930	14.1	32.9	758	61.3	83	1.6
Glenn	4003	4630	3671	15.0	31.5	802	57.9	87	1.3
Howard	4214	5026	3783	14.5	31.7	778	59.7	85	2.0
Steele-ND	4110	4804	3742	14.8	32.2	777	59.5	85	2.2
Dapps	3852	4472	3340	16.1	29.7	756	58.2	91	1.9
Alsen	3799	4325	3577	15.2	30.5	774	59.8	81	1.3
Parshall	3633	4443	3143	15.2	27.3	774	59.4	90	1.1
Reeder	3867	4485	3671	14.9	30.9	768	60.9	81	0.8
LSD (0.05)	209	157	260	1.1	3.1	22	1.7	3.3	.9
No. of environments	63	22	41	61	29	63	98	63	35

† 0 = completely erect; 9 = completely flat at harvest.

Table 2. Summary of agronomic data for Prosper and check cultivars tested in the Hard Red Spring Wheat Uniform Regio Nursery, 2009 and 2010.

Cultivar	Grain yield	Grain volume weight	Grain protein	Heading	Height	Straw strength
	kg ha^{-1}	kg m^{-3}	g kg^{-1}	d after June 1st	cm	0–9†
Prosper	4773	770	14.3	30.5	87	1.0
Verde	4287	765	14.0	28.2	83	0.7
2375	4178	771	14.0	26.9	85	2.2
Keene	3985	776	14.3	27.5	98	2.1
Chris	3104	753	15.0	29.5	102	5.1
Marquis	3048	758	14.4	30.3	104	3.9
LSD (0.05)	432	11	0.8	1.1	3.3	1.0
No. of environments	28	28	28	28	28	28

†0 = completely erect; 9 = completely flat at harvest.

Table 3. Disease reactions of Prosper and check cultivars tested in the North Dakota Hard Red Spring Wheat Variety Trials between 2004 and 2010.

		Leaf rust		Stem rust		Tan spot				
Cultivar	FHB† Severity	Green house‡	Field	Green house§	Field	Race 2	Race 3	Race 5	Septoria blotch	Stagonospora blotch
	%						1–5¶			
Prosper	23	R/MR#	R/S	R-MR	R–MR	2.2	2.2	3.6	2.2	2.4
Alsen	22	R	MR/MS	R-MR	tR	3.5	1.9	2.0	2.7	4.4
Glenn	25	R	R	R-MR	R	–	–	–	–	–
Traverse	–	R	MR/MS	R	R	3.6	3.1	3.2	2.9	2.6
Knudson	–	–	R	R	R	1.6	1.6	1.8	2.2	1.6
Reeder	–	R	S	MR/R	5R	2.5	1.5	3.9	2.9	2.2
Steele-ND	–	R	R	R	R	2.1	2.0	4.0	2.7	4.0
2398	70	R	R	R	R	–	–	–	–	–
2710	13	R	R	R	R	–	–	–	–	–
Baart	–	–	S	–	50S	–		–	–	–
Glenlea	–	–	–	–	–	4.3	2.0	1.9	2.4	3.7
Salamouni	–	–	–	–	–	1.4	1.4	1.3	1.7	1.7
No. of environments	11	9	5	4	9	6	6	6	4	4

† FHB, Fusarium head blight ;% severity scored on 10 spikes (Stack and Frohberg (2000).
‡ Greenhouse reactions for leaf rust races MCDL and THBJ.
§ Greenhouse reactions for *P. graminis* f. sp. *tritici* races TPMK, TMLK, RTQQ, QFCQ, and QTHJ.
¶ 1 = resistant ; 5 = susceptible ; (Lamari and Bernier, 1989).
#R, resistant; MR, moderately resistant; MS, moderately susceptible; S, susceptible; TR, trace/resistant; 5R, resistant with 5% disease severity; 50MS, moderately susceptible with 50% disease severity.

Table 4. Quality parameters for Prosper and check cultivars tested in the North Dakota Hard Red Spring Wheat Variety Trials, 2005 to 2010.

Cultivar	Falling number	Flour extraction	Peak time	Mixing tolerance	Loaf volume	Water absorption
	s	g kg^{-1}		min	mL	%
Prosper	414†	709	8.2	14.5	1000	64.4
Howard	422	696	8.2	15.0	1006	66.1
Glenn	394	680	10.0	20.4	1056	65.3
Steele-ND	432	692	8.1	14.1	1015	66.4
Alsen	414	688	10.1	17.0	1018	65.3
Reeder	430	684	6.9	12.1	979	64.3
LSD (0.05)	28	19	1.7	3.7	22	1.3
No. environments	35	35	35	35	35	35

FIELD EVALUATION OF EXOTIC FUSARIUM HEAD BLIGHT RESISTANCE QTL IN SOFT RED WINTER WHEAT

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ABSTRACT

Fusarium Head Blight (FHB), caused by the fungus *Fusarium graminearum*, is a devastating disease of wheat and other cereals that colonizes the grain directly. It results in severe yield losses and accumulation of the deoxynivalenol (DON) toxin, which may leave the grain unfit for human consumption. Breeding for disease resistance is the most efficient and sustainable method of controlling FHB. Ning7840, a Chinese spring wheat cultivar, has high resistance to FHB, derived from at least three resistance QTL located on chromosomes 3B, 2D, and 5A respectively. Two of these exotic resistance QTL from Ning7840 (on 3B and 2D) were introduced into the locally-adapted soft red winter wheat cultivar McCormick by backcrossing with a final cross with the highly susceptible cultivar SS8641. F5-derived progenies were developed by self-pollination. During each selfing generation, progeny were selected based on the presence of resistance alleles on SSR markers Umn10, cfd79, and Xgm533 (on 3B) and gwm539 and cfd233 (on 2D), and for a high background of McCormick and SS8641 alleles using markers spread throughout the genome. The current population is comprised of F5-derived F6 recombinant lines with a near isogenic background and differing presence of resistance alleles flanking both QTL. The present study sought to see if there were any significant differences in phenotypic expression between lines with different combinations of QTL-flanking alleles. Disease resistance was evaluated through an FHB-inoculated and misted field study conducted in Salisbury (MD). Scab incidence (Inc), scab severity (Sev), scab index, Fusarium damaged kernels (FDK), 1000-kernel weight and deoxynivalenol (DON) were analyzed using Proc GLM in SAS. It was found that lines with resistance alleles flanking both sides of the 2D QTL and one side of the 3BS showed lower FDK than other recombinant lines as well as Ning7840 itself. This research is the first stage of a larger study which seeks to fine-map the 3B and 2D QTL by correlating phenotypic resistance to the presence/absence of a high density of molecular markers flanking the QTL.

TRENDS IN FHB RESISTANCE AMONG WHEAT CULTIVARS IN ARKANSAS AND ENTRIES IN THE USSRWWSN: 2008-2012

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ABSTRACT

Developing cultivars with resistance to FHB and evaluating existing cultivars for FHB resistance have been important objectives of wheat breeding programs funded by the Scab Initiative. Advanced breeding lines that are adapted to the southern soft red winter wheat region are evaluated in the Uniform Southern Soft Red Winter Wheat Scab Nursery (USSRWWSN) that is coordinated through the Scab Initiative. Cultivars grown on at least 5% of the acreage in states with public wheat breeding programs funded by the Scab Initiative are evaluated for FHB resistance so that the FHB reactions can be made available to growers, extension personnel, and consultants. The objective of this report is to compare the trends in FHB resistance and DON level among entries in the USSRWWSN and cultivars grown in Arkansas.

Entries in the USSRWWSN and 20 commonly-grown and promising replacement cultivars (picked by Jason Kelley, University of Arkansas Extension Wheat Agronomist) were evaluated annually in inoculated, misted FHB nurseries at two locations since 2008. The experimental design at each location was a non-randomized complete block with three replications. Coker 9835 and Bess were included in each nursery as susceptible and resistant checks, respectively. Individual plots were two 1-m-long rows. The percentage of florets blighted was estimated visually at soft dough stage as a measure of FHB severity. Both rows of all plots were harvested at maturity and threshed using low air flow to retain scabby grain. Grain samples were lightly cleaned, evaluated for the percentage of *Fusarium* damaged kernels (FDK) by comparing samples to a set of known standards, and sent to the mycotoxin lab at the University of Minnesota for DON analysis. The distribution of mean values of FHB severity, FDK and DON for USSRWWSN entries and Arkansas cultivars in each environment (year-location) were plotted using box plots to allow visual comparisons among all of the data.

For FHB severity, FDK and DON, the distributions of Arkansas cultivars and USSRWWSN entries were similar in each environment except that the distributions for USSRWWSN entries were more skewed toward greater susceptibility than the distributions for Arkansas cultivars. Arkansas cultivars almost always had lower values than Coker 9835, whereas the USSRWWSN always had entries with values greater than Coker 9835. Some entries had DON values more than double the value for Coker 9835. Only a few entries and cultivars had values that were lower than the values for Bess. The results of this study indicate there has been a consistent trend over the past 5 years for Arkansas cultivars to be slightly more resistant than entries in the USSRWWSN.

THE 2011-12 SOUTHERN UNIFORM SOFT RED WINTER WHEAT SCAB NURSERY

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ABSTRACT

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

The 2011-12 nursery comprised 47 advanced generation breeding lines and four check cultivars, 'Ernie', 'Bess', 'Jamestown' (partially resistant) and 'Coker 9835' (susceptible). Eight U.S. public programs (Univ. of Arkansas, Univ. of Georgia, Univ. of Illinois, 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 Romanian, and one Hungarian 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 genotypes based on established diagnostic markers.

Copies of the full report will be available at the 2012 National Fusarium Head Blight Forum and subsequently on line at the USWBSI web site: http://www.scabusa.org/.

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	Cultivar/ Designation	FHB Incidence	RANK	FHB Severity	RANK	FHB Index	RANK	FDK	RANK	ISK	RANK	DON	RANK
1	ERNIE	30	5	13	10	4	5	7	9	16	3	5	25
2	COKER 9835	76	50	49	49	35	49	40	49	49	49	15	49
3	BESS	21	1	12	5	2	1	4	2	11	1	3	5
4	JAMESTOWN	44	19	20	24	7	17	7	9	26	19	4	13
5	NC09-21916	34	9	24	29	5	8	6	5	23	9	3	5
6	VA08W-613	45	21	13	9	4	5	8	12	23	9	3	5
7	M08-8036#	45	22	23	27	7	17	4	2	18	5	3	5
8	IL02-18228	25	2	18	21	2	1	2	1	12	2	1	1
9	ARS07-1214	82	51	51	50	45	50	40	49	54	50	26	50
10	ARS09-173	45	26	33	43	12	35	15	34	32	36	9	42
11	ARS09-367	75	49	51	51	45	50	44	51	58	51	26	50
12	ARS09-446	57	44	38	46	22	45	27	46	48	48	11	47
13	ARS09-513	55	42	39	48	18	41	31	47	47	47	8	40
14	ARS09-595	56	43	38	45	18	41	25	45	40	43	6	32
15	ARS09-643	47	31	35	44	14	39	18	42	39	42	10	45
16	ARS09-724	46	29	27	33	11	33	8	12	29	28	4	13
17	GA 051173W-S11	39	13	28	35	9	25	13	31	27	21	9	42
18	GA 051207-S19	49	38	28	36	12	35	16	35	33	37	5	25
19	GA 051207-S21	46	28	29	38	10	28	8	12	29	28	5	25
20	GA 051173-S25	55	41	38	47	22	45	23	44	42	44	9	42
21	GA 051173-S18	36	11	22	26	5	8	11	25	25	17	4	13
22	GAMD08-27-E9-S13	47	33	25	31	8	21	12	28	30	31	4	13
23	GAMD08-27-E9-S14	47	32	13	8	6	13	8	12	23	9	4	13
24	GAMD08-27-E9-S15	45	25	11	4	8	21	11	25	28	25	4	13
25	LA'04039C-14-8	42	17	15	15	8	21	6	5	29	28	3	5
26	LA'04039C-10-6	42	15	17	18	6	13	9	17	25	17	4	13
27	LA05102C-1-2	32	7	16	16	7	17	6	5	27	21	1	1
28	LA05102C-8-8	33	8	9	3	4	5	5	4	24	14	2	3
29	LA05079D-55	57	45	25	30	25	48	17	40	45	46	7	35
30	LA05079F-P01	53	39	27	32	18	41	16	35	37	40	5	25
31	LA05079F-P03	49	37	19	22	10	28	16	35	30	31	8	40
32	LA05145D-12	58	46	30	40	16	40	16	35	35	39	7	35
33	LA05145D-24	63	48	31	42	23	47	31	48	42	44	11	47
34	MD03W61-11-2(11PW#108)	45	23	21	25	13	37	16	35	38	41	7	35
35	MD03W61-11-3(11PW#109)	46	27	17	19	10	28	9	17	28	25	5	25
36	UX0066-4-79(11PW#183)	41	14	14	12	6	13	10	22	20	6	4	13
37	MD08-22-1-6-4(11PW#189)	28	3	8	1	2	1	9	17	20	6	2	3
38	MD08-26-H2-23(11CVM-3)	35	10	12	7	5	8	7	9	22	8	3	5
39	MH07-7483	60	47	23	28	19	44	18	42	33	37	10	45
40	M09-9826#	42	16	14	14	6	13	17	40	30	31	4	13
41	NC08-23323	45	24	31	41	10	28	9	17	27	21	7	35
42	NC08-23324	54	40	28	37	9	25	12	28	30	31	7	35
43	NC09-22422 (Fhb1)	38	12	14	11	5	8	12	28	27	21	3	5
44	NC09-20986 (Fhb1)	28	4	8	2	3	4	8	12	17	4	3	5
45	NC8355-4 (Fhb1)	31	6	12	6	5	8	13	31	23	9	4	13
46	NC8452-2	47	34	14	13	7	17	10	22	23	9	6	32
47	VA09W-52	48	36	20	23	10	28	14	33	31	35	5	25
48	VA09W-73	46	30	28	34	13	37	9	17	28	25	6	32
49	VA09W-75	44	18	16	17	8	21	6	5	26	19	4	13
50	VA10W-42	47	35	17	20	9	25	10	22	24	14	5	25
51	VA10W-140	44	20	30	39	11	33	11	25	24	14	4	13
	Mean			24		12		14		30		6	
	LSD (0.05)			28		16		16		15		7	
	CV%			60.0		71.4		56.8		25.1		53.9	

	Cultivar/ Designation	Heading Date	RANK	Plant Height	RANK	Hessian Fly Biotype L	Stagon. nodorum % F'VILLE AR	Stripe Rust % N'PORT AR
1	ERNIE	108	9	30	13	0-15	7	68
2	COKER 9835	110	19	31	15	0-13	15	78
3	BESS	113	38	35	43	0-14	30	17
4	JAMESTOWN	106	3	30	8	0-16	15	0
5	NC09-21916	113	38	34	40	0-3	2	12
6	VA08W-613	108	9	32	18	0-18	2	37
7	M08-8036#	111	26	33	28	0-20	2	37
8	IL02-18228	116	43	37	49	0-16	15	7
9	ARS07-1214	116	43	33	30	0-16	15	43
10	ARS09-173	106	3	30	5	21-0	15	1
11	ARS09-367	113	38	30	14	0-17	30	48
12	ARS09-446	108	9	33	32	0-14	30	25
13	ARS09-513	110	19	32	21	0-14	15	68
14	ARS09-595	107	6	32	22	0-17	7	57
15	ARS09-643	106	3	21	1	0-15	15	0
16	ARS09-724	110	19	36	47	0-14	7	1
17	GA 051173W-S11	112	33	40	51	15-3	15	2
18	GA 051207-S19	111	26	34	38	14-0	15	15
19	GA 051207-S21	110	19	35	44	17-0	15	12
20	GA 051173-S25	112	33	34	37	13-2	15	0
21	GA 051173-S18	105	1	30	9	22-0	7	1
22	GAMD08-27-E9-S13	121	49	35	46	0-13	2	20
23	GAMD08-27-E9-S14	121	49	34	35	0-18	2	1
24	GAMD08-27-E9-S15	121	49	33	25	0-16	7	15
25	LA'04039C-14-8	107	6	30	6	0-16	2	57
26	LA'04039C-10-6	110	19	35	45	0-17	2	25
27	LA05102C-1-2	105	1	34	33	0-15	7	1
28	LA05102C-8-8	108	9	35	42	0-16	30	1
29	LA05079D-55	109	17	31	17	0-18	15	0
30	LA05079F-P01	108	9	32	23	0-16	15	0
31	LA05079F-P03	110	19	28	2	0-16	15	0
32	LA05145D-12	107	6	30	7	0-17	15	2
33	LA05145D-24	116	43	39	50	0-17	7	70
34	MD03W61-11-2(11PW#108)	111	26	30	10	0-15	7	0
35	MD03W61-11-3(11PW#109)	112	33	33	26	0-17	2	0
36	UX0066-4-79(11PW#183)	111	26	32	19	0-18	15	57
37	MD08-22-1-6-4(11PW#189)	118	48	34	39	0-19	2	80
38	MD08-26-H2-23(11CVM-3)	111	26	35	41	0-17	15	12
39	MH07-7483	116	43	36	48	0-16	30	0
40	M09-9826#	108	9	29	4	0-20	7	78
41	NC08-23323	111	26	32	20	0-13	7	89
42	NC08-23324	112	33	33	31	0-20	7	94
43	NC09-22422 (Fhb1)	111	26	30	11	20-0	7	20
44	NC09-20986 (Fhb1)	110	19	31	16	16-0	7	10
45	NC8355-4 (Fhb1)	108	9	29	3	0-20	7	6
46	NC8452-2	116	43	33	27	0-16	7	11
47	VA09W-52	109	17	30	12	0-23	30	7
48	VA09W-73	113	38	33	29	0-14	7	0
49	VA09W-75	108	9	34	34	0-17	2	3
50	VA10W-42	112	33	34	36	0-18	2	0
51	VA10W-140	113	38	33	24	0-18	15	71
	Mean	112		32			11	25
	LSD (0.05)	6		7			.	.
	CV%	2.5		10.5			.	.

	DESIGNATION	Rht-B1b	Rht-D1b	Rht8	Ppd-D1a	Vrn-A1	Lr34/Yr18	Lr37/Yr17	Sr36	Sr24/Lr24	Sr2	Lr9	Qyr.uga-2AS	Fhb1	Fhb 5A ERNIE
1	ERNIE	het	no	no	het	het	no	no	yes	no	no	no	no	no	yes
2	COKER 9835	no	yes	no	yes	vrn-A1b	no	no	yes	no	no	yes	no	no	no
3	BESS	yes	no	no	no	vrn-A1b	no	no	no	no	no	no	no	no	no
4	JAMESTOWN	no	yes	no	yes	vrn-A1a	no	no	no	no	no	no	no	no	no
5	NC09-21916	no	yes	no	yes	vrn-A1b	no	no	no	no	no	no	no	no	no
6	VA08W-613	no	yes	no	yes	vrn-A1a	no	no	no	no	no	yes	no	no	no
7	M08-8036#	no	no	no	yes	vrn-A1b	no	no	yes	no	no	yes	no	no	no
8	IL02-18228	yes	het	no	no	vrn-A1b	no	no	no	no	no	no	no	no	no
9	ARS07-1214	yes	no	no	no	vrn-A1b	no	no	no	yes	no	no	no	no	no
10	ARS09-173	yes	no	no	yes	vrn-A1b	no	yes	no	no	no	no	no	no	no
11	ARS09-367	yes	no	no	no	vrn-A1b	no	no	no	yes	no	no	no	no	no
12	ARS09-446	no	no	no	no	vrn-A1b	no	no	yes	no	no	no	no	no	no
13	ARS09-513	no	no	het	yes	vrn-A1b	no	no	het	no	no	no	no	no	no
14	ARS09-595	no	no	no	yes	vrn-A1a	no	no	yes	no	no	no	no	no	no
15	ARS09-643	no	yes	no	yes	vrn-A1b	no	het	no	no	no	no	no	no	no
16	ARS09-724	yes	no	no	yes	vrn-A1b	no	yes	no	no	no	no	no	no	no
17	GA 051173W-S11	no	yes	no	het	vrn-A1b	no	yes	no	no	no	no	no	no	no
18	GA 051207-S19	no	yes	no	yes	vrn-A1b	no	yes	no	no	no	no	no	no	no
19	GA 051207-S21	no	yes	no	yes	vrn-A1b	no	yes		no	no	no	no	no	no
20	GA 051173-S25	yes	no	no	yes	vrn-A1b	no	yes	no	no	no	no	no	no	no
21	GA 051173-S18	no	yes	no	yes	vrn-A1b	no	yes	no	no	no	no	no	no	no
22	GAMD08-27-E9-S13	no	yes	no	no	vrn-A1b	no	het	no	no	no	no	no	yes	no
23	GAMD08-27-E9-S14	no	yes	no	no	vrn-A1b	no	yes	no	no	no	no	no	yes	no
24	GAMD08-27-E9-S15	no	yes	no	no	vrn-A1b	no	het	no	no	no	no	no	yes	no
25	LA'04039C-14-8	no	no	no	het	vrn-A1b	no	no	yes	no	no	yes	no	no	no
26	LA'04039C-10-6	no	no	no	het	vrn-A1b	no	no	yes	yes	no	no	yes	no	no
27	LA05102C-1-2	no	no	no	yes	het	no	no	yes	no	no	no	yes	no	no
28	LA05102C-8-8	no	no	no	yes	vrn-A1b	no	no	yes	no	no	no	no	no	no
29	LA05079D-55	yes	no	no	no	vrn-A1b	no	no	no	no	no	no	no	no	no
30	LA05079F-P01	yes	no	no	no	vrn-A1b	no	no	no	no	no	yes	no	no	no
31	LA05079F-P03	yes	no	no	het	vrn-A1b	no	no	yes	no	no	yes	no	no	no
32	LA05145D-12	no	yes	no	yes	vrn-A1a	no	no	yes	no	no	no	no	no	no
33	LA05145D-24	no	yes	no	yes	vrn-A1a	no	no	no	no	no	yes	no	no	no
34	MD03W61-11-2(11PW	no	yes		yes	vrn-A1b	no	no	no	no	no	no	no	no	
35	MD03W61-11-3(11PW	no	yes	no	yes	vrn-A1b	no	no	yes	no	no	no	no	no	no
36	UX0066-4-79(11PW#1	no	yes	no	yes	vrn-A1b	no	no	yes	no	no	no	yes		het
37	MD08-22-1-6-4(11PW#	no	yes	no	no	vrn-A1b	no	no	no	yes	no	no	no	yes	no
38	MD08-26-H2-23(11CVI	no	yes	no	yes	vrn-A1b	no	yes	no	yes	no	no	no	yes	no
39	MH07-7483	yes	no	no	yes	vrn-A1b	no	no	no	no	no	no	no	no	no
40	M09-9826#	yes	no	no	het	vrn-A1b	no	no	yes	no	no	yes	no	no	no
41	NC08-23323	no	yes	no	yes	vrn-A1b	no	no	no	no	no	yes	no	no	no
42	NC08-23324	no	yes	no	het	vrn-A1b	no	no	no	no	no	yes	no	no	no
43	NC09-22422 (Fhb1)	het	no	no	het	vrn-A1b	no	yes	no	no	no	no	no	yes	no
44	NC09-20986 (Fhb1)	yes	no	no	het	vrn-A1b	no	yes	no	no	no	no	no	yes	no
45	NC8355-4 (Fhb1)	no	yes	no	yes	vrn-A1a	no	no	yes	no	no	no	no	yes	no
46	NC8452-2	no	yes	no	yes	vrn-A1b	no	no	het	yes	no	yes	het	no	het
47	VA09W-52	no	yes	no	yes	vrn-A1a	no	no	no	no	no	no	no	no	no
48	VA09W-73	no	het	no	no	vrn-A1b	no	no	no	no	no	yes	no	no	no
49	VA09W-75	no	yes	no	het	vrn-A1b	no	no	no	no	no	yes	no	no	no
50	VA10W-42	yes	no	no	yes	vrn-A1b	no	no	no	no	no	no	no	no	no
51	VA10W-140	no	yes	no	yes	vrn-A1b	no	no	no	no	no	yes	no	no	no

	DESIGNATION	Fhb Ernie 3Bc	Fhb 5A Ning7840	Fhb 2DL-Wuhan1/W14	1RS:1AL	1RS:1BL	H13	H9	Bdv2/3	Sbm1	Bx7 over-expressing	Glu-A1	Glu-D1	TaSus2-2B
1	ERNIE		no	no	no	no	no	no	no	no	no	Ax1 or null	het	yes
2	COKER 9835	yes	no	no	no	no	no	no	no	yes	no	Ax2*	2+12	yes
3	BESS	no	no	no	no	no	no	no	no	yes	no	Ax1 or null	2+12	no
4	JAMESTOWN	no	no	no	no	no	no	no	no	yes	no	Ax2*	2+12	no
5	NC09-21916	no	no	no	no	no	no	no	no	yes	no	Ax2*	5+10	no
6	VA08W-613	no	no	no	no	no	no	no	no	yes	no	Ax2*	2+12	no
7	M08-8036#	no	no	no	no	no	no	no	no	yes	no	Ax2*	2+12	yes
8	IL02-18228	no	no	no	no	no	no	no	no	yes	no	Ax1 or null	5+10	no
9	ARS07-1214	no	no	no	no	no	no	no	no	yes	no	Ax1 or null	2+12	no
10	ARS09-173	no	no	no	no	no	het	no	no	yes	no	Ax2*	2+12	no
11	ARS09-367	no	no	no	no	no	no	no	no	yes	no	Ax1 or null	2+12	no
12	ARS09-446	no	no	no	no	no	no	no	no	no	no	Ax2*	5+10	yes
13	ARS09-513	no	no	no	no	no	no	no	no	no	no	Ax1 or null	2+12	het
14	ARS09-595	no	no	no	no	no	no	no	no	yes	no	Ax2*	5+10	yes
15	ARS09-643	no	no	no	yes	no	no	no	no	yes	het	Ax2*	2+12	no
16	ARS09-724	no	no	no	no	no	no	no	no	no	no	Ax1 or null	2+12	no
17	GA 051173W-S11	no	no	no	no	no	yes	no	no	yes	no	het	2+12	no
18	GA 051207-S19	no	no	no	no	no	no	yes	no	yes	no	Ax2*	5+10	no
19	GA 051207-S21	no	no	no	het	no	no	yes	no	yes	no	Ax2*	5+10	no
20	GA 051173-S25	no	no	no	no	no	yes	no	no	yes	no	Ax1 or null	2+12	no
21	GA 051173-S18	no	no	no	no	no	yes	no	no	yes	no	Ax1 or null	2+12	no
22	GAMD08-27-E9-S13	no	yes	no	yes	no	no	no	no	yes	no	Ax2*	2+12	no
23	GAMD08-27-E9-S14	no	yes	no	yes	no	no	no	no	yes	no	Ax2*	2+12	no
24	GAMD08-27-E9-S15	no	yes	no	yes	no	no	no	no	yes	no	Ax2*	2+12	no
25	LA'04039C-14-8	no	no	no	no	yes	no	no	no	no	no	Ax2*	5+10	yes
26	LA'04039C-10-6	no	no	no	no	yes	no	no	no	no	no	Ax2*	5+10	yes
27	LA05102C-1-2	no	no	no	no	no	no	no	no	yes	no	Ax2*	2+12	yes
28	LA05102C-8-8	no	no	no	no	no	no	no	no	yes	no	Ax2*	2+12	yes
29	LA05079D-55	no	no	no	no	no	no	no	no	yes	no	Ax1 or null	2+12	no
30	LA05079F-P01	no	no	no	no	no	no	no	no	yes	no	Ax1 or null	2+12	no
31	LA05079F-P03	no	no	no	no	no	no	no	no	het	yes	Ax2*	5+10	yes
32	LA05145D-12	no		no	no	yes	no	no	no	yes	het	Ax2*	5+10	yes
33	LA05145D-24	no	no	no	no	no	no	no	no	yes	no	Ax2*	2+12	no
34	MD03W61-11-2(11PW#108)	no		no	no	no	no	no		yes	no	Ax2*	2+12	het
35	MD03W61-11-3(11PW#109)		no	no	no	no	no	no	no	yes	no	Ax2*	2+12	yes
36	UX0066-4-79(11PW#183)	no	no	no	no	no	no	no	no	yes	no	Ax2*	2+12	yes
37	MD08-22-1-6-4(11PW#189)	no	yes	no	yes	no	no	no	no	yes	no	Ax2*	2+12	no
38	MD08-26-H2-23(11CVM-3)	no	het	no	no	no	no	no	no	yes	no	Ax2*	2+12	no
39	MH07-7483	no	no	no	no	yes	no	no	no	yes	no	Ax1 or null	het	no
40	M09-9826#	no	no	no	no	no	no	no	no	yes	no	Ax2*	het	yes
41	NC08-23323	het?	no	no	het	no	no	no	no	yes	no	Ax1 or null	2+12	no
42	NC08-23324	no	no	no	yes	no	no	no	no	yes	no	Ax1 or null	2+12	no
43	NC09-22422 (Fhb1)	no	no	no	no	no	yes	no	no	yes	no	Ax2*	nknow	no
44	NC09-20986 (Fhb1)	no	no	no	no	no	het	no	no	yes	no	Ax2*	het	no
45	NC8355-4 (Fhb1)	no	no	no	no	no	no	no	no	yes	no	Ax1 or null	5+10	yes
46	NC8452-2	no	no	no	het	no	no	no	no	yes	no	Ax2*	2+12	het
47	VA09W-52	no	no	no	het	no	no	no	no	yes	no	Ax1 or null	2+12	no
48	VA09W-73	no	no	no	no	no	no	no	no	no	no	Ax2*	2+12	no
49	VA09W-75	no	no	no	yes	no	no	no	no	no	no	Ax2*	2+12	no
50	VA10W-42	no	no	no		no	no	no	no	yes	no	Ax2*	2+12	no
51	VA10W-140	no	no	no	no	no	no	no	no	no	no	Ax2*	5+10	no

BREEDING FOR FUSARIUM HEAD BLIGHT (FHB), RUST AND BARLEY YELLOW DWARF (BYD) RESISTANCE IN PURDUE SOFT WINTER WHEAT LINES 05247 AND 02444

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ABSTRACT

Fusarium head blight (FHB) of wheat, caused mainly by *Fusarium graminearum* Schwabe (telemorph *Gibberella zeae*), results in serious yield loss and vomitoxin (DON) contamination in wheat grain. In addition to FHB, other diseases such as rust and barley yellow dwarf (BYD) all cause reduced yield and lowered grain quality. Stacking various disease resistance genes in wheat cultivars is an important strategy to reduce production losses. The wheat breeding program at Purdue University aims at developing soft winter wheat lines with FHB resistance and other various disease resistances. Both 05247 and 02444 have high yield potential, producing 16317 kg ha^{-1} and 14536 kg ha^{-1}, respectively (compared with 13505 kg ha^{-1} for Branson) averaged two years (2011 and 2012) at Lafayette, IN. Both lines also have various disease resistances, such as FHB, BYD, HF and rust. As indicated by the FHB inoculation data from year 2010 and 2011, line 05247 and 02444 have good FHB type II resistance, with an average of 2.75 and 2.50 spikelets for disease spread, respectively. In year 2012, due to a dry and early season, no FHB disease had developed and a disease score of 0.5 for Type II resistance was seen for almost all of the lines. However, the environment was optimum for rust development. With disease readings of one for both stripe rust and leaf rust, line 05247 shows excellent rust resistance.

HIGH SPEED SORTING OF *FUSARIUM* DAMAGED WHEAT KERNELS

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OBJECTIVES

To demonstrate feasibility of removing *Fusarium*-damaged wheat kernels from breeder samples using a low-cost, high-speed, sorting machine capable of measuring several visible and near infrared (NIR) spectral bands.

INTRODUCTION

Use of visible and NIR light for phenotypic sorting of single wheat kernels has been shown to be a useful tool to improve several quality traits (Dowell et al., 2009). One such application is to use NIR to distinguish single wheat kernels with high levels of deoxynivalenol (DON) from kernels having low DON levels using chemometric models implemented on the automated Perten single kernel NIR system (SKNIR). Additionally, the SKNIR has proven to be a useful tool to objectively separate kernels having low, intermediate, and high levels of *Fusarium* damaged kernels (FDK) (Peiris et al., 2010). This is important for breeding programs as it has been shown that resistance to Fusarium head blight (FHB) and accumulation of DON can be inherited (Buerstmayr et al., 1999, Miedaner et al., 2003). However, instrumentation for automatically and rapidly segregating single wheat kernels on the basis of NIR characteristics is expensive and no longer readily available. To fill this void, a simple light emitting diode (LED) based sorting machine was developed to rapidly measure light reflection within a limited number of visible and NIR spectral bands and sort kernels at a rate of about 20 kernels/s or 2.3 Kg/hr (Pearson et al., 2012). Compared with the SKNIR, the LED system is potentially much lower cost, ~$3000 vs ~$100,000, and the throughput is much higher, 20 kernels/s vs 0.5 kernels/s. The only significant drawback is that the LED sorter could have lower accuracy in some applications due to the limited number of spectral bands used.

MATERIALS AND METHODS

IIn the LED based sorting instrument developed by Pearson et al. (2012), visible and NIR reflectance data was acquired by rapidly blinking six different LEDs one at a time. For this study, the number of LEDs were increased to nine with peak emission wavelengths at: 1070nm, 1050nm, 970nm, 940nm, 880nm, 850nm, 624nm (red), 527nm (green), and 470nm (blue). Selection of LEDs was limited to those with a peak emission wavelength less than 1100nm due to the silicon based sensor used. An image of the LED circuit board illuminating a wheat kernel exiting the end of a chute is shown in Figure 1. Reflected light from the kernel is projected by the lens onto a photo-diode. The photo-diode signal is amplified and input to a micro-controller on the same circuit board which also controls the LEDs, performs all computations, classifies kernels based on reflected light from several of the LEDs, and outputs a digital signal to activate an air valve to divert kernels based on the classification.

Ten different samples of hard red spring (HRS) wheat and soft red winter (SRW) wheat were used to test the sorter. The varieties of HRS used were: Altona, Clearwater, Crystal, Cypress River, Grandin, Fairfax, Hollsus, Kane, Plum and Westroc. The incidence of FDK averaged 21.2% and ranged from 12.4% to 30.5%. Sorter performance can be affected by kernel size variation; the 1000 kernel weights of undamaged kernels averaged 32.7g and

ranged between 27.7g to 42.2g so these samples encompass a fairly broad range of sizes. The ten SRW samples were comprised of breeding population samples supplied by the University of Kentucky. The incidence of FDK averaged 11.8%, ranging from 6.3% to 19.6%. The 1000 kernel weights of undamaged SRW kernels averaged 37.7g, ranging between 32.6g to 39.3g.

While separate calibrations for the LED sorter were developed and used for SRW and HRS, the calibration procedure was the same. Two hundred undamaged kernels and 200 kernels classified as having an intermediate level of FDK were separated by the SKNIR instrument using the calibration developed by Peiris et al. (2010) and these kernels were used for calibrating the LED instrument. KY07C-1056 breeding population SRW and Clearwater variety HRS were used for the calibration samples. These calibration samples were then fed through the LED instrument and the responses from the nine LEDs for all kernels were saved to a personal computer. Letting each of the nine LED responses be represented by $\lambda 1 ... \lambda 9$, every possible unique combination of $(\lambda x - \lambda y)/\lambda z$ were computed except for cases where $\lambda x = \lambda y$. These difference ratios have the benefit of cancelling out background noise, fluctuations in illumination levels, and help characterize where differences in spectra occur. Stepwise discriminant analysis (Hintze, 2001) was then used to select a small subset of these ratios to be used in sorting after they were programmed back into the micro-controller for sorting.

The nine HRS and SRW wheat samples not used in the calibration were sorted by the LED sorter into three groups: (a) undamaged, (b) intermediate, and (3) FDK. While this sorter is only capable of performing two way classifications, the three groups were created by passing all kernels through the sorter twice and grouping the samples based on the number of times they were accepted or rejected. Samples that were accepted twice were called "undamaged", samples rejected once and accepted once comprised the "intermediate" group, and samples rejected twice were classified as "FDK"..

To determine the sorting accuracy of the LED sorter, the SKNIR was used to sort each of the three LED sorted groups. The SKNIR instrument sorted 1,000 kernels of each LED sort stream into three categories per the Peiris et al. (2010) calibration: (a) undamaged – Bin 1; (b) Intermediate – Bin 2, and (c) FDK – Bins 3 and 4. After completion, the kernel distribution was recorded and compared with the LED sorted classification.

RESULTS AND DISCUSSION

Table 1 displays the average agreement between the LED and SKNIR sorters for classifying HRS samples into the three FDK categories. Overall, after sorting HRS in the LED sorter twice, FDK concentration was reduced from an unsorted average of 21.2% to 4.8% in the undamaged group, a 77% reduction, while the false positive reject rate for undamaged kernels was 12%. The false positive error rate was computed by combining the weight percent of the LED sorted samples (Table 1) with the percentage of undamaged kernels in the intermediate and FDK categories. Of the HRS kernels that the LED sorter classified as undamaged, the SKNIR found that 4.8% were FDK (range: 2.5 to 6.5%). However, visual inspection of these indicated that less than 1/10 of these kernels show visual symptoms of severe FDK such the "tombstone" appearance. The LED sorter is able to distinguish many kernels with minor symptoms of FDK as 61% of the kernels classified as intermediate by the LED sorter were also classified as intermediate or FDK by the SKNIR. Undamaged kernels that were lighter in color, possibly due to weathering, tended to be classified as FDK or intermediate by the LED sorter but were classified as undamaged by the SKNIR. Therefore, results may vary depending on other environmental effects during the growing season.

As shown in Table 2, the LED sorter removed a greater percentage of FDK from SRW while maintaining similar false positive rates. Two passes through the LED sorter resulted in an 87% reduction of FDK compared the original unsorted

FDK concentration (11.8% unsorted to 1.5% sorted) with a false positive rate of 14.7%. Only 1.5% of the kernels classified as undamaged by the LED sorter were considered FDK by the SKNIR and none of these had the "tombstone" appearance. The fact that nearly half of the kernels classified as intermediate by the LED sorter were classified as intermediate or FDK by the SKNIR indicates that, as with HRS, the LED sorter was able to separate many kernels with minor symptoms of FDK from undamaged kernels.

The spectral band difference ratios selected during the calibration procedure for HRS were: (blue-green)/1070nm, (green-850nm)/970nm, and (red-850nm)/1070nm, (1050nm-1070nm)/1070nm; and for SRW: (blue-red)/red, (850nm-970nmnm)/970nm, and (blue-1070nm)/red. An additional study is currently underway to build and test a similar LED sorter circuit board that uses an InGaAs sensor so that LEDs in the range of 900 to 1700nm can be used. Delwiche and Harland (2004) showed that FDK could be detected with high accuracy using a few spectral bands in this region. Nevertheless, the results indicate that the sorter in its current form is able to remove FDK from breeder samples, making it a viable tool for use in developing Fusarium resistant wheat varieties. The LED sorter has also proven effective for separating red and white wheat as well as sorting kernels on the basis of protein content (Pearson et al., 2012), attesting to the versatility of this instrument.

ACKNOWLEDGEMENT AND DISCLAIMER

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Mention of trade names or commercial products in this publication is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the U.S. Department of Agriculture. USDA is an equal opportunity provider and employer.

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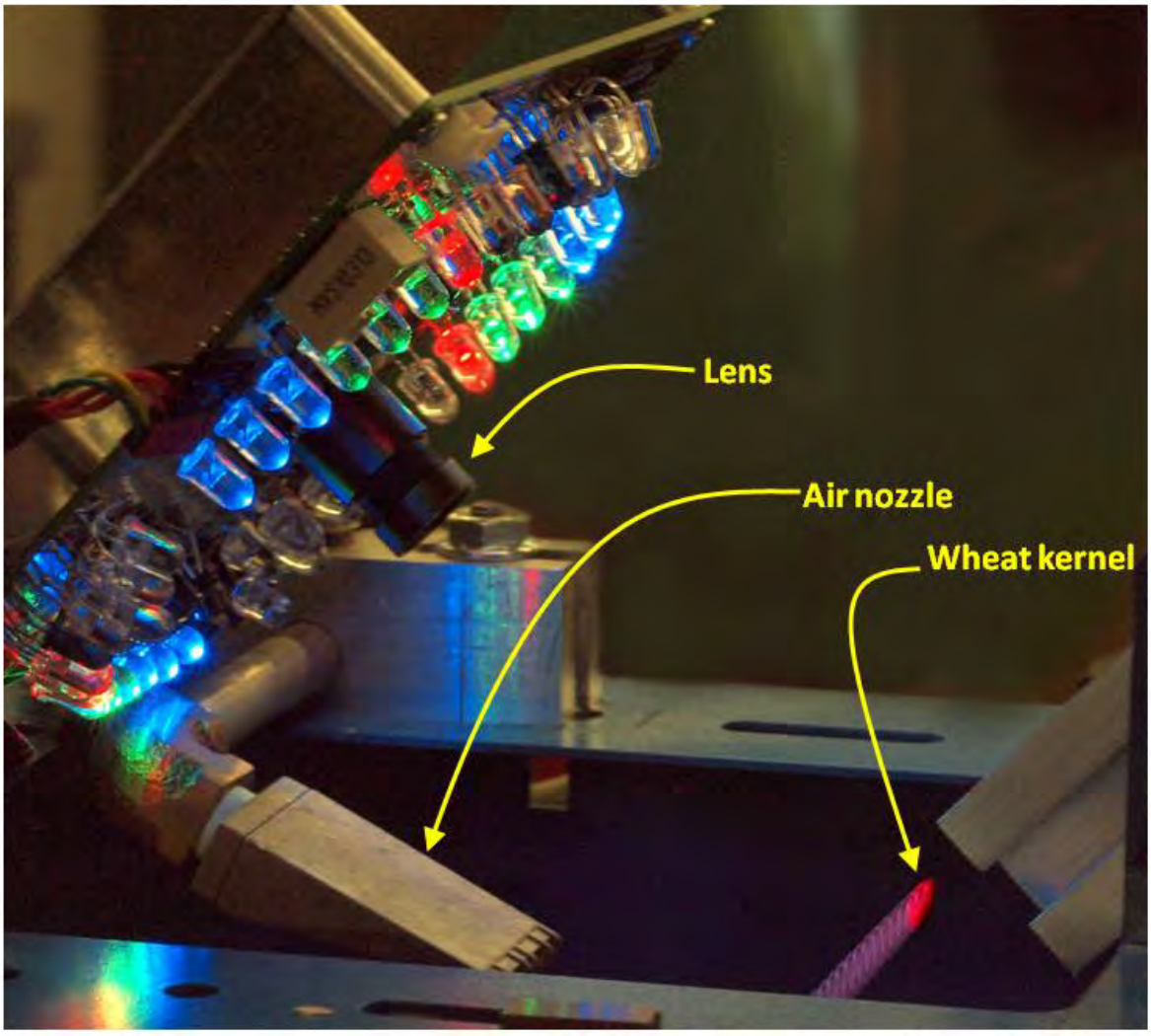

Figure 1. LEDs illuminating a wheat kernel as it falls off of the chute. The air nozzle can be activated to re-direct the falling kernel if the light reflected from the kernel indicates it is FDK. Note that even though several LEDs appear to be on at the same time, they actually blink much more rapidly than the camera exposure time; so at any given time, only one type of LED is energized. The pattern in the streak ahead of the kernel represents the distance the kernel travels in the time for all nine LEDs to blink.

Table 1. Average agreement (± std. dev.) of HRS between LED and SKNIR instruments.

LED Sorter classification	% Number of kernels sorted into groups using Perten SKNIR sorter			weight % of original sample
	undamaged	Intermediate	FDK	
undamaged	83.2 ±5.4	12.0 ±4.8	4.8 ±1.7	54.8 ±7.3
Intermediate	38.7 ±19.5	38.9 ±18.9	22.4 ±7.8	23.5 ±4.6
FDK	14.4 ±10.5	19.4 ±10.4	66.1 ±20.2	21.6 ±5.1

Table 2. Average agreement (± std. dev.) of SRW between LED and SKNIR instruments.

LED Sorter classification	% Number of kernels sorted into groups using Perten SKNIR sorter			weight % of original sample
	undamaged	Intermediate	FDK	
undamaged	94.3 ±2.0	4.2±1.7	1.5 ±0.6	66.3 ±8.7
Intermediate	56.5 ±13.0	26.4 ±7.7	17.2 ±6.5	21.1 ±5.0
FDK	21.7 ±11.3	23.6 ±5.3	54.7 ±9.6	12.6 ±3.9

QTL ASSOCIATED WITH FUSARIUM HEAD BLIGHT RESISTANCE IN THE NC-NEUSE X AGS 2000 RECOMBINANT INBRED POPULATION

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ABSTRACT

Breeding for resistance to Fusarium Head Blight is of major importance, as the disease can have serious negative impacts on wheat production in warm and humid regions of the world, including the state of North Carolina. Fusarium Head Blight can cause significant grain yield reduction, but also severely affect the grain quality due to accumulation of mycotoxins produced by the pathogen. The importance of finding native sources of resistance in U.S. soft red winter wheat lines has been emphasized in recent years. 'NC-Neuse' is a North Carolina soft red winter wheat cultivar, released in 2003, which is moderately FHB resistant.

A population of 179 random F_5-derived recombinant inbred lines derived from a cross between 'NC-Neuse' and the FHB susceptible line 'AGS 2000' was evaluated for FHB resistance at one field location (3 reps) in the 2010-11 field season, and at two field locations (2 reps/loc) in the 2011-12 season. The FHB related traits evaluated included disease incidence (INC), severity (SEV), *Fusarium* damaged kernels (FDK), and accumulation of the mycotoxin deoxynivalenol (DON). A linkage map developed prior to this QTL mapping study with a total of 1536 polymorphic SSR, DArT and SNP markers across 31 linkage groups was utilized for mapping of QTL (with additional 345 polymorphic unlinked markers). QTL analysis for individual environments and across environments was conducted using Multiple Interval Mapping (MIM) with WinQTLCart v. 2.5. The critical LOD value to declare QTL significance was 3.2, based on 1000 permutations.

QTL associated with one or more FHB resistance traits were identified on chromosomes 1A, 1B, 2AL, 4A, 5A, 5B, 6AL, and 7B. Their LOD score values ranged from 3.2 to 4.38 with R^2 values of 5.5% to 13.3%.

Incidence data from Salisbury, MD 2012 were used for analysis. One QTL associated with decreased disease incidence (type I resistance) was identified on chromosome 1B explaining 7.4% of the phenotypic variation, and one QTL associated with increased incidence (and later heading date) was identified on chromosome 5B explaining 10.3% of the phenotypic variation.

Severity data from Kinston, NC 2011 and Salisbury, MD 2012 were analyzed. Two QTL associated with decreased severity (type II resistance) were identified on chromosomes 4A and 6AL that explained 13.3 and 11.1% of the phenotypic variation, respectively.

Fusarium damaged kernel data from Kinston, NC 2011 and 2012, as well as Salisbury, MD 2012 were analyzed. A total of three QTL associated with decreased proportion of FDK was found. Two QTL were found on chromosome 1A explaining 8.6 and 9.4% of the phenotypic variation, as well as one QTL on chromosome 7B explaining 12.4% of the phenotypic variation.

Deoxynivalenol data from Kinston, NC 2011 and 2012 were used for analysis. Four QTL associated with decreased DON content were found on chromosomes 2AL, 4A, 5A and 6AL explaining between 5.5 and 10.1% of the phenotypic variation.

The evaluations are continuing in the 2012-13 season where we will test the consistency of these tentative QTL.

SOFT WINTER WHEAT RESPONSES TO *FHB1* AND *QFHS.NAU-2DL* QTL FOR FUSARIUM HEAD BLIGHT RESISTANCE IN F_2 DERIVED POPULATIONS

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ABSTRACT

Fusarium Head Blight (FHB), caused by *Fusarium graminearum* Schwabe [teleomorph: *Giberella zeae* Schein. (Petch)] is recognized as one of the most destructive diseases of wheat (*Triticum aestivum* L. and *T. durum* L.) and barley (*Hordeum vulgare* L.). Breeding for FHB resistance is one of the most efficient approaches to reducing this damage. Disease resistance must be accompanied by selection for desirable agronomic traits. Donor parents with two FHB resistance quantitative trait loci (QTL) *Fhb1* (chromosome 3BS) and *QFhs.nau-2DL* (chromosome 2DL) were crossed to four adapted SRW wheat lines to generate backcross and forward-cross progeny. F_2 individuals were genotyped and assigned to 4 different groups according to presence/ absence of resistance alleles at both QTL. The effectiveness of these QTL in reducing FHB in F_2 derived lines was assessed in a misted, inoculated scab nursery for 2 years. Backcross-derived progeny from four genetic backgrounds were planted in replicated plots and in the scab nursery at Lexington, KY in 2011 and 2012. Traits measured included rating (1-9), severity, incidence, FHB index (severity * incidence), FDK (*Fusarium* damaged kernels) and DON (deoxynivalenol). FDK and DON were predicted with Near Infrared Reflectance (NIR) and compared with actual values. One of our objectives was to explore the utility of F_2 populations as indicators of expression levels of QTL prior to extensive backcrossing. The *Fhb1* + 2DL combination showed higher resistance and lower FDK than other QTL classes in most of the populations. FDK was reduced by resistance alleles at one or both QTLs in all four populations. Rating values were significantly ($P \leq 0.05$) reduced by the presence of resistance alleles. In some cases where the average QTL effect was not significant, there was significant ($P \leq 0.05$) variation among $F_{2:4}$ lines within QTL class for FDK, Rating and FHB index. Significant QTL effects on FDK were also detected using NIR. Correlations between FDKNIR and actual FDK ranged from 0.53 to 0.77 across the four populations. Correlations between DONNIR and FDK ranged from 0.55 to 0.74 among populations. BC_1F_3 lines revealed that one backcross had restored yield potential, in that there were lines with yields not significantly different from commercial checks. In population 7, almost 58% of the lines showed competitive yield that did not significantly differ ($P \leq 0.05$) from the commercial checks. Preliminary results indicated that BC1 populations may be a useful source of breeding lines. F_2 populations should be used for genotyping, ensuring QTL are effective before extensive backcrossing.

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QTL MAPPING TO INVESTIGATE POSSIBLE INHIBITION OF *FHB1*

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ABSTRACT

Fhb1 is the major Fusarium head blight resistance gene in wheat, and its lineage traces back to introgression from the Chinese cultivar Sumai 3. This gene is most strongly associated with Type II resistance (resistance to fungal spread within the wheat head), but also contributes to other forms of resistance. While investigating *Fhb1* candidate genes as part of our ongoing efforts to clone this gene, we discovered that the recipient genotype, 'Bobwhite' failed to consistently express the effect of *Fhb1*. In addition to this particular gene, there have been other QTL mapping studies published in which a source of resistance is contributed by the susceptible parent in the cross. The failure of *Fhb1* to express in Bobwhite, supported by these other findings, seems to indicate either the interaction of a gene inhibitor with *Fhb1*, or the presence of multiple segregating QTL regions in the resistant parent that confer the segregating response. In order to investigate these hypotheses, we generated a recombinant inbred mapping population of 129 $F_{5:7}$ lines from the cross between '260-2' and 'Bobwhite' where all lines were homozygous positive for the *Fhb1* resistance allele. Bobwhite is negative for the *Fhb1* resistance allele, while 260-2 is a near isogenic line containing *Fhb1* from a Sumai3/Stoa//MN97448 background. Two seasons of Type II resistance screening were undertaken in the greenhouse. Inoculations were conducted using the single-floret (point) inoculation method, and the phenotype assessed as the percent spread of symptoms from the inoculated spikelet. Replicated field trials were conducted in St. Paul, MN in 2011 and 2012 and Crookston, MN in 2012 using both the mapping population and a population of 114 $F_{5:7}$ RILs from the same cross that were homozygous negative for *Fhb1*. Symptomatic spikelet counts (20 heads/plot)were taken at approximately 21 dai to estimate FHB severity (FHBS). Thirty head weights, the percentage of visually scabby kernels (VSK) and the deoxynivalenol content of grain (DON) were assessed on the harvested grain. Phenotypes for all traits analyzed indicate multiple gene segregation. The population was genotyped using the Illumina 9K SNP Infinium assay. The traits examined have now been mapped and 11 QTL regions contributing to FHB resistance have thus far been identified.

DEVELOPMENT OF INTERNATIONAL FUSARIUM HEAD BLIGHT SCREENING NURSERIES OF WHEAT AT CIMMYT, MEXICO

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ABSTRACT

Fusarium head blight (FHB) or head scab, is a fungal disease of small grain cereals that has become a major threat to wheat production globally. *Fusarium graminearum*, the predominant species causing FHB worldwide, is known to produce two important mycotoxins, deoxynivalenol (DON) and zearalenone, which can contaminate the diseased grain. FHB disease causes yield loss, low test weights, low seed germination and contamination of grain with mycotoxins which makes it unfit for human and animal consumption. Changes in agricultural practices including more maize-wheat rotation and adaptation of conservation agriculture practices and global warming have contributed to enhanced incidence and severity of FHB globally. Fungicide application, biological control and adoption of specific agronomic practices have shown limited success in FHB control, increase cost of production, pollution concerns and pose practical constrains in their large scale adaptation. The most effective, economical and environmentally friendly means of managing FHB involves incorporation of genetic resistance into commercial cultivars. FHB research began at the International Maize and Wheat Improvement Center (CIMMYT), Mexico in the early 1980's, and since then, large-scale FHB screening has been conducted to identify and incorporate new resistance genes into elite CIMMYT germplasm. To develop FHB resistant germplasm, large scale FHB screening work has been performed on the promising breeding lines from different CIMMYT breeding programs, genbank accessions and other resources, and crosses have been made between parents with complimentary disease resistance and agronomic traits. The screening field at El Batan, Mexico covers 2 hectares with a yearly screening capacity of up to 10,000 plots, and a programmable misting system is equipped to provide uniform humidity conditions favourable to FHB development. Spray inoculation is being used in the field to assess the combined effect of Type I and Type II resistance, and DON contamination is assayed in the laboratory for promising lines. Furthermore, a haplotyping system has also been established to diagnose well known FHB QTL. Promising lines with good FHB resistance based on multiple years of screening are regularly compiled as a Fusarium Head Blight Screening Nursery (FHBSN) and distributed worldwide. In 2012, the 20 entries comprising the 14th FHBSN were tested at El Batan, Mexico and distributed to 94 institutes in 26 countries. The FHBSN comprise agronomically superior breeding lines possessing Sumai3 and/or non-Sumai3 resistance.

EVALUATING GENOMIC SELECTION FOR DON IN A COLLABORATIVE BARLEY BREEDING EFFORT

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ABSTRACT

Accelerating the development of new varieties with low deoxynivalenol (DON) is a critical component of the USWBSI mission to reduce the risk of Fusarium head blight (FHB). To meet this goal, we have established a project that couples 1) a collaborative breeding effort between three Midwest barley breeding programs to exploit elite FHB germplasm and 2) genomic selection (GS) breeding methods to reduce the breeding cycle time and increase the rate of gain from selection. Using a large marker and trait database assembled through the Barley Coordinated Agricultural Project (CAP), we constructed several training populations with elite breeding lines from the Midwest breeding programs and trained a ridge regression model to calculate genomic estimated breeding values (GEBVs) for DON. Model accuracy was calculated as the correlation between GEBV and the observed phenotype divided by the square root of the heritability. Models trained with breeding lines from a single breeding program were better predictors of lines from that same program. Pooling lines from several breeding programs produced a single model that gave accurate predictions for all lines from all breeding programs, but did not increase accuracy over the other models. The results of this validation study prompted us to implement GS and then evaluate model accuracy on actual breeding progenies. A collaborative breeding population was established by crossing among elite breeding lines with enhanced FHB resistance from the University of Minnesota (M), North Dakota State University (N) and Busch Agriculture (B) breeding programs to generate 1440 F3 progeny. These lines were genotyped with a custom 384 SNP assay and predictions were made using models trained with the Barley CAP marker and trait data. Three breeding progeny populations (MxM, NxN, MxN) of 100 randomly selected lines were evaluated in field trials for DON. As predicted by the results of the prior validation study, models trained with M breeding lines were more accurate for MxM progenies (r=0.58) then for NxN progenies (r=0.07). Likewise the N model was more accurate for NxN (r=0.48) then for MxM progenies (r=0.26). The M+N training population produced accuracies of 0.56 for MxM, 0.40 for NxN, and 0.35 for MxN progenies. This suggests that pooling lines from the two breeding programs will be important for predicting progenies that result from crosses between the programs.

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PHENOTYPIC ANALYSIS OF A SOFT WHEAT POPULATION THAT WILL BE USED FOR ASSOCIATION ANALYSIS AND GENOMIC SELECTION

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ABSTRACT

Soft winter wheat (SWW) from the Eastern US has considerable resistance to FHB. Our objectives are to use a large SWW population to i) elucidate the genetics of resistance using association analyses and ii) to develop genomic selection models. This poster presents analysis of the 2011 and 2012 phenotypic data from the population. The population is comprised of 49 checks and 700 RILs. The population will be phenotyped by seven co-PIs in 2011, 2012, and 2013. Each co-PI phenotyped 149 entries comprised of the 49 checks and 100 RILs from their program: a RIL was only tested at one location each year. The traits are incidence, severity, index, *Fusarium* damaged kernels (FDK), and DON. The mean and standard deviation of the 49 checks from an environment were used to standardize data from all entries from that environment.

Over all trait/entry combinations, 31% of the combinations had lower trait values than Truman (R check), 76% were less than Freedom (MR check) and only 5% were greater than Pioneer 2545 (S check). The 700 RILs come from 76 crosses with 41 crosses having ≥ six entries. Over the 222 trait/cross combinations involving these 41 crosses, 73% showed evidence of segregation while in 27% of the combinations all RILs from the cross were at least moderately resistant for the trait: none of these crosses produced only susceptible RILs for any trait.

Resistance to toxin accumulation (RTA) was assessed by regressing DON on estimates of grain infection (FDK or fungal biomass assessed by qPCR) within in each environment using 2011 data. Entries with negative residuals have less DON than predicted based in grain infection and may have high RTA. Several entries had negative residuals in all environments indicating they consistently resist toxin accumulation despite grain infection. Other entries repeatedly had positive residuals indicating they have low RTA.

In conclusion, data standardization eliminated environment effects and minimized entry by environment effects. The population shows good segregation for all traits both overall and within most individual crosses and should be well suited for future association analyses and genomic selection. There is evidence for genetic variation for RTA.

REPORT ON THE 2011-2012 NORTHERN UNIFORM WINTER WHEAT SCAB NURSERIES (NUWWSN AND PNUWWSN)

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OBJECTIVES

This is a summary of the report on the 2011-2012 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 2012 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 56 (+ 4 checks) entries in the NUWWSN came from 14 programs while the 46 (+ 4 checks) entries in the PNUWWSN entries came from nine programs (Table 2).

RESULTS

Many entries in the PNUWWSN and the NUWWSN showed very good resistance to FHB. In the NUWWSN 22% were not significantly different from the most resistant entry for all seven FHB traits. Only 9% of the entries were susceptible for four or more traits. Over 31% of the entries had DON levels < 4 ppm from these inoculated and listed nurseries where the average DON was 6.5 ppm. In the PNUWWSN, over 43% were not significantly different from the most resistant entry for all seven FHB traits, though 26% of the entries were susceptible for four or more traits. Over 47% of the entries had DON levels < 4 ppm from these inoculated and listed nurseries where the average DON was 5.3 ppm.

Table 1. Traits assessed in the 2011-12 PNUWWSN and NUWWSN tests.

Code	Trait	Description	PNUWWSN Locations*	NUWWSN Locations*
INC	Disease incidence	% of heads with at least one infected spikelets	MI,VA,KY,MO	MI,MD,VA,NY,KY,NE,MO
SEV	Disease severity from field tests	% of infected spikelets in an infected head.	MI,VA,KY,MO	MI,MD,VA,NY,KY,NE,MO
IND	Disease index	IND = (SEVxINC)/100	MI,VA,KY,MO,OH	MI,MD,VA,NY,KY,NE,MO,OH
FDK	Fusarium damaged kernels	Percentage of grain ishowing sypmotoms of Fusarium infection	KY,MO	MD,OH,NY,KY,NE,MO
ISK	Composite of head and kernel traits	ISK Index = 0.3 (Severity) +0 .3 (Incidence)+ 0.4 FDK)	KY,MO	MD,OH,NY,KY,NE,MO
DON	DON (vomitoxin)	PPM of vomitoxin in grain	VA,KY	OH,VA,KY
GH	Greenhouse severity	Same as SEV except from greenhouse	IL,MO	IL,MO
HD	Heading date	Julian date when 50% of heads have emerged	MI,OH,VA,KY	MI,MD,OH,VA,NY,KY

Table 2. Entries in the 2011-12 PNUWWSN (PNU) and NUWWSN (NU)

NU	ERNIE	
NU	FREEDOM	
NU	TRUMAN	
NU	PIONEER2545	
NU	NY103-208-7263	Cayuga/Caled.
NU	NY94052-3329	Pioneer2737w/Harus
NU	NY05072&75-1	Superior*6/Pinb-a
NU	KWS007	IL87-2834-1 / 960314
NU	KWS001	TOTEM / M98-2152
NU	KWS002	TWO44-094 / HONEY
NU	KWS003	95-3245/ Ernie
NU	LCS19214	T814/L900819
NU	LCS19209	Goldfield//IL84-3010/T812
NU	LCS19231	VA99W-200/Patton
NU	LCS19103	IL84-3010/T812
NU	LCS19104	Auburn/T812
NU	E9021R	Pioneer 2552/D8006
NU	OH05-200-74	OH629/HOPEWELL
NU	OH06-159-6	P.92145E8-7-7-1-9-1 / OH728
NU	F0065	Pioneer 25R37/D6234
NU	OH08-133-25	HONEY / COKER 9663
NU	OH06-180-57	KY90C-042-37-1/OH687
NU	OH07-166-41	OH708 / OH684
NU	OH07-263-3	OH748 / BRAVO
NU	04606RA1-1-7-1-6	Truman/INW0316
NU	P0537A1-3-12	IN0411/2754//IN0412/98134
NU	P0566A1-3-1-67	INW0412/992060
NU	P05222A1-1-2-7	99840/INW0304//INW0304/INW0316
NU	MH07-7483	M95-2994-1/P 25R57
NU	MH07-7474	M97-1048/ELKHART
NU	M08-8036#	COKER 9511/BRANSON
NU	M08-8214	COOPER/PIO2552
NU	DH1-46	Superior x D8006W
NU	DH1-62	Superior x D8006W
NU	DH2-4	25R47 x ADV Dyno
NU	DH2-45	25R47 x ADV Dyno
NU	DH5-56	25R56 X Emmit
NU	IL06-13721	IL00-8530 / IL97-3632
NU	IL06-23571	IL96-6472/ Pioneer 25W33 // 94-1653
NU	IL07-4415	P96169RE2-3-6-4 / IL01-34159
NU	IL07-19334	IL01-36115 / IL79-008T-B-B
NU	KY04C-2004-1-1-3	Roane/Allegiance
NU	KY03C-1224-10-12-3	25R18/VA87W-375ws//KY96C-0767-1
NU	KY03C-1195-10-8-5	KY92-0010-17//25R18/KY92C0017-17
NU	KY04C-2031-29-7-3	Truman/VA97W-375ws
NU	MD08-22-1-6-2	Ning7840/McCormick*3
NU	MD08-22-32	Ning7840/McCormick*3
NU	MO090932	980829/Ernie
NU	MO081320	980525//981020/AP Patton
NU	MO090478	980429/Ernie
NU	MO091068	Ernie/Colorben 4
NU	NE10514	NE99533-3/NE99464
NU	NE10449	NI03418/Camelot
NU	NW03666	N94S097KS/NE93459
NU	NW10401	SHARK/F4105W2.1//NI02425
NU	NE10418	OK99212/Overland
NU	VA09W-52	GF921221E16 / McCormick"S" // VA99W-200
NU	VA09W-73	SS 520 (VA96W-158) / VA99W-188 // TRIBUTE
NU	VA10W-21	Z00-5018 / VA01W-158
NU	VA09W-75	SS 520 (VA96W-158) / VA99W-188 // TRIBUTE
PNU	ERNIE	
PNU	FREEDOM	
PNU	TRUMAN	
PNU	PIONEER2545	
PNU	KWS006	PUR 89118 / RINGO
PNU	KWS004	RAVEN / ATLAS
PNU	KWS005	HARVARD / DINGO
PNU	F0051R	Gold./CJ9306//Caled/CJ9403/3/Caled/4/Caled
PNU	F0014	Pioneer 2552 / E0029
PNU	F0038	D8006 / CJ9306 // Caled. /3/ Caled. /4/ Caled.
PNU	F0036R	D6234/W14/E0038-1/3/E0038-1
PNU	OH08-172-42	DOUGLAS / JEKYL
PNU	7x831-1-I-03Ser (2)	Malabar*4/Karl
PNU	OH08-172-42	DOUGLAS / JEKYL
PNU	OH08-180-48	DOUGLAS / MCCORMICK
PNU	OH08-269-58	P.92226E2-5-3 / OH708
PNU	OH07-254-11	OH728 / VA97W-361WS
PNU	05247A1-7-7-3-1	99840*2/03726//99794
PNU	P0566A1-3-1-65	INW0412/992060
PNU	P05247A1-7-3-27	99840*2/03726//99794
PNU	P05247A1-7-3-120	99840*2/03726//99794
PNU	P0762A1-2-8	981129/99793//INW0301/92145/3/981477/981312//INW0316
PNU	P07287RA1-14	INW0304/INW0316//97462/3/Truman
PNU	M09-9811#	TRUMAN/CK9511
PNU	M09-9826#	CK9511/M03-3002
PNU	IL07-21847	IL99-2536/ IL97-3632// IL00-8061
PNU	IL08-8844	IL00-8109 / IL02-24251
PNU	IL08-22206	IL00-8530 / VA01-476 // IL79-002DH
PNU	IL08-33373	IL79-005T-B-B / IL00-8530
PNU	IL07-20728	McCormick/IL97-1828// IL00-8061
PNU	IL07-20743	McCormick/IL97-1828// IL00-8061
PNU	KY04C-2031-29-6-1	Truman/VA97W-375ws
PNU	KY03C-2022-16-18-1	KY93C-0876-66/25R18
PNU	KY04C-2006-45-5-1	Roane/KY93C-1238-17-1
PNU	KY04C-2150-66-16-5	25R18/KY93C-1238-17-1
PNU	KY04C-2150-64-16-1	25R18/KY93C-1238-17-1
PNU	KY04C-2150-64-17-1	25R18/KY93C-1238-17-1
PNU	MO100295	981020/010895
PNU	MO101235	001164/IL 96-6472
PNU	MO100532	000925//980525/433-1-2
PNU	MO100314	010708/AP Patton
PNU	MO100410	980829/IL 96-346
PNU	MO101259	002409/980525
PNU	MO081765	L910097/MO 92-599
PNU	VA08W-613	FREEDOM / NEUSE"S" // VA98W-688
PNU	VA09W-608	P97397B1-4-5 / McCORMICK // COKER 9511
PNU	VA10W-663	P97397B1-4-5 / McCORMICK // COKER 9511
PNU	VA10W-28	SS-MPV57 (VA97W-24) / M99*3098
PNU	VA09W-654	VA98W-749 / IL96-3073 // P9793A1-5
PNU	VA10W-617	VA98W-749 / IL96-3073 // COKER 9474

Table 3. Most resistant entries from the 2011-12 NUWWSN (top of table) and PNUWWSN (bottom of table).

NAME	INC	SEV	IND	FDK	ISK	DON	GHSEV	HD	#l	#h
MD08-22-1-6-2	20.4 l	7.4 l	1.9 l	5.7 l	10.0 l	1.2 l	13.9 l	136	7	0
MD08-22-32	21.5 l	8.1 l	2.0 l	9.7 l	11.4 l	1.4 l	10.0 l	134	7	0
IL07-4415	22.2 l	5.1 l	2.1 l	9.6 l	12.8 l	1.6 l	11.7 l	130 l	7	0
IL07-19334	25.2 l	6.5 l	2.5 l	5.3 l	11.5 l	3.0 l	8.3 l	134	7	0
MO091068	19.3 l	10.0 l	2.9 l	11.0 l	13.9 l	2.2 l	8.2 l	133	7	0
M08-8214	28.2 l	7.2 l	3.0 l	6.5 l	13.8 l	3.1 l	24.3 l	131 l	7	0
IL06-13721	21.3 l	9.5 l	3.5 l	11.1 l	15.9 l	2.3 l	19.0 l	129 l	7	0
LCS19103	23.1 l	9.5 l	3.8 l	11.2 l	16.3 l	2.5 l	17.9 l	131 l	7	0
IL06-23571	33.0 l	11.3 l	5.2 l	7.0 l	16.6 l	2.6 l	11.8 l	129 l	7	0
M08-8036#	35.9 l	13.1 l	5.3 l	9.1 l	18.7 l	2.6 l	21.0 l	130 l	7	0
LCS19214	34.2 l	11.1 l	5.7 l	7.7 l	18.5 l	2.9 l	38.0 hl	131 l	7	1
MO090478	24.9 l	13.0 l	6.3 l	13.8 l	18.2 l	3.5 l	19.0 l	129 l	7	0
MO090932	21.7 l	8.4 l	3.1 l	7.5 l	10.4 l	6.4	6.0 l	139	6	0
TRUMAN	21.2 l	6.0 l	3.8 l	8.5 l	12.8 l	6.3	8.5 l	139	6	0
NW10401	25.9 l	14.0 l	5.0 l	10.5 l	15.9 l	3.9 l	63.0 h	131 l	6	1
LCS19209	33.9 l	11.0 l	6.1 l	8.8 l	19.3	2.2 l	24.8 l	131 l	6	0
MO081320	24.6 l	7.2 l	6.3 l	10.3 l	17.8 l	3.6 l	34.3 hl	131 l	6	0
LCS19104	27.1 l	16.7	6.6 l	12.7 l	18.0 l	3.5 l	15.8 l	132	6	0
OH07-166-41	28.3 l	15.2 l	6.7 l	7.5 l	18.0 l	3.9 l	57.9 h	134	6	1
LCS19231	34.6 l	18.5	7.5 l	10.1 l	19.0 l	4.2 l	33.8 hl	133	6	1
KY03C-1224-10-12-3	29.1 l	15.4 l	7.9 l	10.5 l	17.3 l	7.7	8.5 l	134	6	0
NE10514	28.8 l	12.5 l	5.6 l	17.8	18.6 l	9.9	23.3 l	138	5	0
ERNIE	26.5 l	9.6 l	6.4 l	14.2 l	19.7	6.7	17.8 l	129 l	5	0
VA09W-52	36.5	13.1 l	8.2 l	8.3 l	20.1	2.7 l	24.6 l	130 l	5	0
P0762A1-2-8	23.7 l	4.0 l	2.2 l	8.3 l	20.0 l	3.2 l	11.4 l	135 l	7	0
MO101259	30.0 l	7.9 l	2.6 l	11.1 hl	17.2 l	5.2 l	16.8 l	140 h	7	1
KY04C-2150-66-16-5	33.7 l	6.4 l	3.1 l	7.6 l	22.2 l	2.9 l	17.1 l	139 h	7	0
MO100295	29.0 l	12.3 l	3.9 l	4.5 l	18.6 l	3.7 l	30.6 hl	136	7	1
MO100314	33.9 l	8.8 l	4.0 l	5.9 l	18.6 l	2.3 l	6.9 l	138	7	0
MO081765	32.3 l	9.7 l	4.2 l	7.7 l	22.8 l	1.7 l	9.8 l	136	7	0
MO100532	32.6 l	11.5 l	4.5 l	3.7 l	20.1 l	2.2 l	24.8 l	134 l	7	0
VA10W-617	26.4 l	11.2 l	5.0 l	3.7 l	19.0 l	2.5 l	22.8 l	134 l	7	0
KY04C-2150-64-16-1	42.4 l	10.6 l	5.2 l	8.7 l	24.8 l	3.6 l	13.4 l	138	7	0
IL07-20743	34.4 l	9.1 l	5.3 l	7.5 l	22.8 l	4.5 l	26.4 l	137	7	0
MO101235	32.4 l	13.7 l	5.5 l	5.1 l	19.2 l	4.8 l	14.5 l	136	7	0
IL07-21847	32.5 l	9.7 l	5.8 l	13.5 hl	22.6 l	2.3 l	21.5 l	134 l	7	1
P05247A1-7-3-27	39.8 l	8.4 l	5.9 l	17.4 hl	28.1 l	5.2 l	35.4 hl	134 l	7	2
VA09W-608	31.7 l	12.4 l	5.9 l	9.6 l	23.0 l	1.6 l	10.3 l	134 l	7	0
IL08-33373	39.4 l	6.6 l	6.1 l	15.2 hl	24.8 l	2.7 l	10.6 l	140 h	7	1
TRUMAN	42.4 l	15.8 l	6.2 l	4.8 l	23.7 l	6.5 l	7.9 l	142 h	7	0
IL07-20728	40.5 l	14.8 l	6.3 l	3.4 l	20.4 l	2.0 l	30.0 hl	137	7	1
IL08-22206	35.6 l	8.1 l	6.6 l	4.8 l	24.3 l	1.8 l	23.8 l	134 l	7	0
MO100410	33.7 l	7.8 l	6.9 l	7.4 l	21.3 l	5.3 l	6.9 l	142 h	7	0
IL08-8844	35.3 l	17.5 l	7.1 l	9.0 l	22.2 l	3.3 l	19.0 l	134 l	7	0
VA09W-654	28.6 l	14.0 l	7.7 l	4.7 l	18.3 l	2.1 l	33.0 hl	139	7	1
VA08W-613	33.6 l	9.0 l	8.0 l	18.2 hl	30.0 l	4.7 l	13.3 l	132 l	7	1
P07287RA1-14	29.9 l	11.9 l	5.3 l	17.4 hl	27.4 l	3.5 l	47.0 h	133 l	6	2
M09-9811#	36.8 l	20.8 h	6.2 l	8.1 l	23.4 l	3.1 l	21.4 l	135	6	1
KY04C-2150-64-17-1	48.7 h	9.2 l	6.8 l	5.3 l	28.5 l	4.8 l	15.5 l	139	6	1
ERNIE	36.3 l	7.6 l	8.8 l	11.7 hl	27.7 l	5.3 l	16.9 l	133 l	6	0

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

Table 4. Summary of results of the 2011-12 NUWWSN.

NAME	INC		SEV		IND		FDK		ISK		DON		GHSEV		HD		HGT		#l	#h
ERNIE	26.5	l	9.6	l	6.4	l	14.2	l	19.7		6.7		17.8	l	129	l	34		5	0
FREEDOM	46.0	h	20.5		14.2		13.3	l	27.4		3.9	l	7.6	l	134		38		3	1
TRUMAN	21.2	l	6.0	l	3.8	l	8.5	l	12.8	l	6.3		8.5	l	139		41		6	0
PIONEER2545	54.4	h	32.6	h	28.1	h	23.2	h	40.7	h	11.2		58.7	h	135		38		0	6
NY103-208-7263	43.1	h	24.9	h	13.6		16.9		26.4		10.7		14.8	l	143	h	43		1	2
NY94052-3329	49.2	h	25.5	h	16.9		21.5	h	31.3		17.1	h	21.3	l	142	h	39		1	4
NY05072&75-1	39.2	h	22.7	h	12.1		20.7	h	25.3		6.2		25.8	l	143	h	47	h	1	3
KWS007	45.4	h	25.1	h	14.8		16.4		29.4		9.0		44.5	h	136		38		0	3
KWS001	39.1	h	19.7		11.9		18.5		28.0		10.7		33.8	hl	135		34		1	2
KWS002	42.1	h	19.3		9.1	l	15.7		24.9		7.4		9.9	l	136		39		2	1
KWS003	41.0	h	17.4		8.1	l	13.2	l	22.5		4.1	l	23.6	l	136		34		4	1
LCS19214	34.2	l	11.1	l	5.7	l	7.7	l	18.5	l	2.9	l	38.0	hl	131	l	35		7	1
LCS19209	33.9	l	11.0	l	6.1	l	8.8	l	19.3		2.2	l	24.8	l	131	l	35		6	0
LCS19231	34.6	l	18.5		7.5	l	10.1	l	19.0	l	4.2	l	33.8	hl	133		43		6	1
LCS19103	23.1	l	9.5	l	3.8	l	11.2	l	16.3	l	2.5	l	17.9	l	131	l	40		7	0
LCS19104	27.1	l	16.7		6.6	l	12.7	l	18.0	l	3.5	l	15.8	l	132		40		6	0
E9021R	42.7	h	27.7	h	13.7		10.0	l	25.7		7.1		45.3	h	133		39		1	3
OH05-200-74	31.9	l	7.3	l	5.7	l	15.9		20.2		6.3		15.4	l	136		38		4	0
OH06-159-6	29.7	l	10.4	l	5.2	l	18.6		20.8		7.6		62.3	h	130	l	35		3	1
F0065	46.3	h	33.6	h	20.5		14.9	l	33.6	h	10.1		55.7	h	134		37		1	4
OH08-133-25	43.0	h	26.1	h	15.1		21.7	h	31.9	h	5.4	l	51.4	h	132		37		1	5
OH06-180-57	38.4	h	21.6		15.0		12.3	l	27.0		8.0		56.9	h	134		37		1	2
OH07-166-41	28.3	l	15.2	l	6.7	l	7.5	l	18.0	l	3.9	l	57.9	h	134		38		6	1
OH07-263-3	40.9	h	17.7		11.6		8.7	l	22.5		4.9	l	47.1	h	131	l	38		2	2
P04606RA1-1-7-1-6	45.9	h	12.1	l	10.0		16.5		26.3		15.3	h	5.3	l	136		41		2	2
P0537A1-3-12	34.5	l	17.4		8.4	l	15.6	l	23.3		7.2		21.2	l	132		35		4	0
P0566A1-3-1-67	38.0	h	11.5	l	7.1	l	20.3	h	25.1		4.2	l	8.6	l	130	l	33		4	2
P05222A1-1-2-7	39.2	h	11.3	l	7.5	l	18.2		24.5		8.6		30.1	hl	130	l	29	l	3	2
MH07-7483	40.4	h	18.1		9.9		20.6	h	27.3		9.9		27.1	l	134		36		1	2
MH07-7474	34.3	l	19.7		8.4	l	14.0	l	21.5		8.0		35.3	hl	134		36		4	1
M08-8036#	35.9	l	13.1	l	5.3	l	9.1	l	18.7	l	2.6	l	21.0	l	130	l	35		7	0
M08-8214	28.2	l	7.2	l	3.0	l	6.5	l	13.8	l	3.1	l	24.3	l	131	l	40		7	0
DH1-46	33.6	l	15.4	l	10.4		23.4	h	25.4		10.3		53.8	h	141		42		2	2
DH1-62	43.7	h	26.1	h	13.6		25.6	h	29.4		13.0	h	13.0	l	143	h	42		1	4
DH2-4	34.5	l	18.8		7.9	l	29.0	h	24.0		12.2		7.7	l	141	h	38		3	1
DH2-45	44.7	h	22.2		13.7		22.7	h	29.8		11.0		37.3	hl	134		36		1	3
DH5-56	37.8	h	26.0	h	12.9		19.9	h	30.0		7.2		34.2	hl	136		38		1	4
IL06-13721	21.3	l	9.5	l	3.5	l	11.1	l	15.9	l	2.3	l	19.0	l	129	l	35		7	0
IL06-23571	33.0	l	11.3	l	5.2	l	7.0	l	16.6	l	2.6	l	11.8	l	129	l	37		7	0
IL07-4415	22.2	l	5.1	l	2.1	l	9.6	l	12.8	l	1.6	l	11.7	l	130	l	35		7	0
IL07-19334	25.2	l	6.5	l	2.5	l	5.3	l	11.5	l	3.0	l	8.3	l	134		38		7	0
KY04C-2004-1-1-3	37.3		18.6		8.4	l	20.0	h	24.5		8.3		9.8	l	135		37		2	1
KY03C-1224-10-12-3	29.1	l	15.4	l	7.9	l	10.5	l	17.3	l	7.7		8.5	l	134		32	l	6	0
KY03C-1195-10-8-5	50.2	h	12.7	l	10.6		15.2	l	26.3		8.5		9.8	l	136		35		3	1
KY04C-2031-29-7-3	36.8		20.9		10.9		9.7	l	22.5		6.6		39.4	h	133		33		1	1
MD08-22-1-6-2	20.4	l	7.4	l	1.9	l	5.7	l	10.0	l	1.2	l	13.9	l	136		34		7	0
MD08-22-32	21.5	l	8.1	l	2.0	l	9.7	l	11.4	l	1.4	l	10.0	l	134		35		7	0
MO090932	21.7	l	8.4	l	3.1	l	7.5	l	10.4	l	6.4		6.0	l	139		41		6	0
MO081320	24.6	l	7.2	l	6.3	l	10.3	l	17.8	l	3.6	l	34.3	hl	131	l	37		6	0
MO090478	24.9	l	13.0	l	6.3	l	13.8	l	18.2	l	3.5	l	19.0	l	129	l	33		7	0
MO091068	19.3	l	10.0	l	2.9	l	11.0	l	13.9	l	2.2	l	8.2	l	133		35		7	0
NE10514	28.8	l	12.5	l	5.6	l	17.8		18.6	l	9.9		23.3	l	138		38		5	0
NE10449	32.2	l	16.3		7.8	l	26.2	h	25.9		8.3		33.3	hl	138		41		3	2
NW03666	38.0	h	15.1	l	8.0	l	18.3		22.9		10.6		27.0	l	136		40		3	1
NW10401	25.9	l	14.0	l	5.0	l	10.5	l	15.9	l	3.9	l	63.0	h	131	l	38		6	1
NE10418	36.4		17.7		7.0	l	17.1		22.7		5.3	l	26.2	l	130	l	40		3	0
VA09W-52	36.5		13.1	l	8.2	l	8.3	l	20.1		2.7	l	24.6	l	130	l	34		5	0
VA09W-73	41.3	h	22.5	h	10.2		16.7		24.6		3.8	l	25.0	l	131	l	35		2	2
VA10W-21	34.3	l	17.1		8.3	l	12.5	l	21.2		5.3	l	42.3	h	131	l	34		4	1
VA09W-75	42.8	h	22.8	h	10.7		17.8		25.4		5.6	l	32.1	hl	133		36		2	3
AVERAGE	34.9		16.2		8.7		14.6		22.1		6.5		26.9		134		37			
MINUMUM	19.3		5.1		1.9		5.3		10.0		1.2		5.3		129		29			
MAXIMUM	54.4		33.6		28.1		29.0		40.7		17.1		63.0		143		47			
LSD(0.05)	16.9		11.1		7.3		10.3		9.3		4.5		34.1		3		3			
# LOCATIONS	7		7		8		6		6		3		2		6		2			

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 2011-12 NUWWSN.

NAME	INC		SEV		IND		FDK		ISK		DON		GH		HG		HGT	#l	#h
ERNIE	36.3	l	7.6	l	8.8	l	11.7	hl	27.7	l	5.3	l	16.9	l	133	l	35	6	0
FREEDOM	53.7	h	25.6	h	20.0	h	23.8	h	38.6	h	6.2	l	13.2	l	139		38	2	5
TRUMAN	42.4	l	15.8	l	6.2	l	4.8	l	23.7	l	6.5	l	7.9	l	142	h	41	7	0
PIONEER2545	67.7	h	25.0	h	26.6	h	25.9	h	45.3	h	12.8	h	22.6	l	138		39	1	6
KWS006	39.2	l	8.0	l	12.1		26.3	h	28.2	l	8.8		9.6	l	136		38	4	1
KWS004	36.6	l	25.9	h	11.2	l	26.0	h	32.0	hl	4.0	l	60.6	h	136		41	4	4
KWS005	48.4		24.6	h	10.6	l	28.4	h	39.1	h	4.9	l	30.1	hl	140	h	40	3	4
F0051R	57.5	h	20.0	h	11.1	l	12.5	hl	37.5	h	6.9	l	14.6	l	140	h	38	4	4
F0014	61.0	h	33.2	h	28.0	h	25.3	h	45.3	h	15.3	h	22.9	l	137		35	1	6
F0038	56.7	h	29.1	h	20.2	h	15.3	hl	36.3	h	13.1	h	30.3	hl	139		38	1	6
F0036R	52.6	h	28.2	h	17.4		16.3	hl	36.4	h	10.5	h	22.9	l	137		35	1	4
OH08-172-42	51.1	h	16.6	l	12.3		16.2	hl	31.9	hl	7.2		15.3	l	137		39	4	3
7x831-1-l-03Ser (2)	45.5		15.2	l	9.0	l	14.6	hl	31.7	hl	8.1		40.3	h	141	h	47	4	2
OH08-172-42	52.5	h	20.6	h	12.7		20.2	hl	34.2	h	7.8		36.4	hl	137		41	2	5
OH08-180-48	52.5	h	14.1	l	13.8		19.9	hl	39.6	h	11.2	h	37.8	hl	138		35	3	5
OH08-269-58	46.0		17.9	l	15.6		14.5	hl	28.9	l	7.5		43.3	h	137		41	3	2
OH07-254-11	50.3	h	28.6	h	12.9		24.4	h	36.3	h	12.8	h	26.5	l	135		37	1	5
P05247A1-7-7-3-1	54.8	h	18.0	l	11.3	l	10.9	hl	34.4	h	5.4	l	34.6	hl	140	h	38	5	3
P0566A1-3-1-65	48.9	h	18.2	l	9.6	l	5.3	l	32.8	h	5.5	l	13.6	l	133	l	36	5	2
P05247A1-7-3-27	39.8	l	8.4	l	5.9	l	17.4	hl	28.1	l	5.2	l	35.4	hl	134	l	34	7	2
P05247A1-7-3-120	48.6	h	16.0	l	10.2	l	16.2	hl	34.3	h	5.8	l	46.7	h	134	l	34	4	4
P0762A1-2-8	23.7	l	4.0	l	2.2	l	8.3	l	20.0	l	3.2	l	11.4	l	135	l	34	7	0
P07287RA1-14	29.9	l	11.9	l	5.3	l	17.4	hl	27.4	l	3.5	l	47.0	h	133	l	34	6	2
M09-9811#	36.8	l	20.8	h	6.2	l	8.1	l	23.4	l	3.1	l	21.4	l	135		40	6	1
M09-9826#	46.1		9.7	l	8.6	l	25.5	h	34.9	h	4.8	l	16.0	l	134	l	34	4	2
IL07-21847	32.5	l	9.7	l	5.8	l	13.5	hl	22.6	l	2.3	l	21.5	l	134	l	38	7	1
IL08-8844	35.3	l	17.5	l	7.1	l	9.0	l	22.2	l	3.3	l	19.0	l	134	l	39	7	0
IL08-22206	35.6	l	8.1	l	6.6	l	4.8	l	24.3	l	1.8	l	23.8	l	134	l	37	7	0
IL08-33373	39.4	l	6.6	l	6.1	l	15.2	hl	24.8	l	2.7	l	10.6	l	140	h	40	7	1
IL07-20728	40.5	l	14.8	l	6.3	l	3.4	l	20.4	l	2.0	l	30.0	hl	137		38	7	1
IL07-20743	34.4	l	9.1	l	5.3	l	7.5	l	22.8	l	4.5	l	26.4	l	137		39	7	0
KY04C-2031-29-6-1	58.9	h	27.8	h	10.9	l	22.1	h	37.5	h	5.4	l	25.8	l	140	h	41	3	4
KY03C-2022-16-18-1	61.2	h	25.6	h	10.7	l	13.2	hl	36.8	h	3.7	l	18.4	l	140	h	36	4	4
KY04C-2006-45-5-1	55.4	h	21.0	h	9.7	l	9.5	l	32.8	h	4.0	l	11.0	l	138		40	4	3
KY04C-2150-66-16-5	33.7	l	6.4	l	3.1	l	7.6	l	22.2	l	2.9	l	17.1	l	139	h	35	7	0
KY04C-2150-64-16-1	42.4	l	10.6	l	5.2	l	8.7	l	24.8	l	3.6	l	13.4	l	138		38	7	0
KY04C-2150-64-17-1	48.7	h	9.2	l	6.8	l	5.3	l	28.5	l	4.8	l	15.5	l	139		36	6	1
MO100295	29.0	l	12.3	l	3.9	l	4.5	l	18.6	l	3.7	l	30.6	hl	136		43	7	1
MO101235	32.4	l	13.7	l	5.5	l	5.1	l	19.2	l	4.8	l	14.5	l	136		40	7	0
MO100532	32.6	l	11.5	l	4.5	l	3.7	l	20.1	l	2.2	l	24.8	l	134	l	41	7	0
MO100314	33.9	l	8.8	l	4.0	l	5.9	l	18.6	l	2.3	l	6.9	l	138		50	7	0
MO100410	33.7	l	7.8	l	6.9	l	7.4	l	21.3	l	5.3	l	6.9	l	142	h	51	7	0
MO101259	30.0	l	7.9	l	2.6	l	11.1	hl	17.2	l	5.2	l	16.8	l	140	h	42	7	1
MO081765	32.3	l	9.7	l	4.2	l	7.7	l	22.8	l	1.7	l	9.8	l	136		37	7	0
VA08W-613	33.6	l	9.0	l	8.0	l	18.2	hl	30.0	l	4.7	l	13.3	l	132	l	35	7	1
VA09W-608	31.7	l	12.4	l	5.9	l	9.6	l	23.0	l	1.6	l	10.3	l	134	l	35	7	0
VA10W-663	45.7		28.0	h	13.8		4.0	l	32.1	h	1.8	l	18.2	l	132	l	27	3	2
VA10W-28	44.5		26.9	h	11.2	l	3.4	l	30.2	l	2.0	l	22.0	l	133	l	34	5	1
VA09W-654	28.6	l	14.0	l	7.7	l	4.7	l	18.3	l	2.1	l	33.0	hl	139		43	7	1
VA10W-617	26.4	l	11.2	l	5.0	l	3.7	l	19.0	l	2.5	l	22.8	l	134	l	37	7	0
AVERAGE	42.6		16.1		9.5		12.9		28.7		5.3		22.8		137		38		
MINUMUM	23.7		4.0		2.2		3.4		17.2		1.6		6.9		132		27		
MAXIMUM	67.7		33.2		28.0		28.4		45.3		15.3		60.6		142		51		
LSD(0.05)	19.2		14.7		9.3		17.8		14.8		5.3		32.6		3		.		
# LOCATIONS	4		4		5		2		2		2		2		4		1		

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

SSR MARKER HAPLOTYPES CONFIRM FIVE NOVEL FHB RESISTANCE SOURCES FROM THE CIMMYT SCAB RESISTANCE SCREENING NURSERY

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ABSTRACT

Wheat production in South Africa under irrigation is periodically under threat from fungal diseases. Fusarium head blight (FHB) caused predominantly by *Fusarium graminearium*, has become the most prevalent disease on wheat in different irrigation production areas. Under severe disease pressure, in combination with the planting of highly susceptible cultivars, maize-wheat crop rotation and no-tilling practices, yield losses of up to 40% are possible. A secondary concern is the FHB infected grain contaminated with mycotoxins, such as Deoxynivalenol (DON), which are harmful to humans and animals after consumption. Currently in South Africa there is very little enforcement of mycotoxin monitoring regulations within contaminated wheat grain. Additionally, there is no officially registered fungicide to control Fusarium head blight in South Africa to date. The most environment friendly and efficient FHB control method is host plant resistance. There are different forms of FHB resistance documented that make up the FHB disease complex: Type I- resistance to initial infection, Type II- resistance to the spread of disease symptoms within the spike and Type III- resistance to the accumulation of mycotoxins in infected grain. To date there are no moderately tolerant or moderate-highly FHB resistant wheat cultivars available in South Africa for commercial use. Seven sources of resistance were used for targeted SSR haplotype comparison namely, Sumai 3 (*3B-Fhb1, 5A, 6B-Fhb2 & Fhb7AC*), Frontana (*3A*), Asozaria III (QTL?), Baisanyuehuang (*3BSc* & *Fhb1*), Huangcandou (*Fhb1, 3Bsc & 2D*), Huangfangzhu (*7A* & *3B*), Haiyanzhong (*7D*) and Wangshuibai (*Fhb4 & Fhb5*). For a number of years the well documented FHB resistant QTL (*3B-Fhb1, 5A, 6B-Fhb2 & Fhb7AC*) in Sumai 3 have been used throughout the world primarily transferring the *Fhb1* gene into different wheat varieties. However, it is important to further diversify FHB resistance gene pool available and continually search for new novel, FHB resistant sources to prevent total dependence on the existing well characterised sources which are predominantly of Asian origin. In this study, five resistant lines identified during a two year phenotypic screening process were further genotyped and characterised with the use of 22 Simple sequence repeat (SSR) markers associated with a number of different FHB QTL/genes from the seven known FHB resistant sources listed. The lines originated from the Wheat germplasm nurseries (Scab Resistant Screening Nursery - SRSN) imported from CIMMYT, Mexico and were tested with the South African FHB complex isolates. Pedigree analysis of selected lines showed no related kinship to any of the seven known resistance sources. A number of the SSR markers showed clear allelic differences between the five CIMMYT lines and the seven known resistance sources tested. These findings indicate the true novelty of the resistance in these five sources from the CIMMYT SRSN. Mapping populations of these sources will need to be developed to attempt to map and identify the different QTL/genes present and regulating FHB resistance expression. This will be an important step in improving and further diversifying FHB resistant levels available in South African wheat, as we look into the future.

FHB SYMPTOMS AND DON ACCUMULATION IN WINTER DURUM CULTIVARS AND DOUBLE HAPLOID LINES

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ABSTRACT

Fusarium graminearum (FG) Schwabe [teleomorph *Gibberella zeae* Schwein. Petch] is the predominant *Fusarium* species pathogenic to cereals in North America. The most important mycotoxin produced by FG is deoxynivalenol (DON). In general, durum (*Triticum turgidum* subsp *durum* L) is more susceptible to FHB than common wheat (*Triticum aestivum* L.). The most practical way to control FHB is through the development of resistant cultivars. OAC Amber is the only winter durum registered in Canada. The objective of this study was to investigate the level of resistance to FHB in several winter durum cultivars and double haploid (DH) lines. Fifteen winter durum cultivars from Italy and 73 DH lines (cross OAC Amber x NSD 11/00) were screened for FHB resistance. The plots were spray inoculated with a mixture of *F. graminearum* isolates at 50% anthesis. FHB symptoms were recorded as a product of incidence and severity. Deoxynivalenol was quantified in harvested grain by ELISA (EZ-Quant® www.diagnostix.ca). Mean FHB index and DON level across durum cultivars from Italy were 55.7 % and 9.5 ppm, respectively, with the lowest FHB index (23.8%) and DON level (2.6 ppm) detected in the cv Arna Coris. FHB index and DON level in OAC Amber were 44.9% and 11.2 ppm, respectively, while mean DON across the DH population was 30.1 ppm, ranging from 10.5 ppm to 68.6 ppm. A number of winter durum genotypes with lower DON levels than OAC Amber have been identified. If found to be phenotypically stable in coming years, they would be considered as FHB donor parents for future crosses. In general, higher DON levels were detected in winter durum compared with common wheat lines grown in the same FHB nursery in Ridgetown, Ontario, Canada in 2012. These results indicate that breeding for FHB resistance and lower DON accumulation in winter durum grain is a realistic and promising goal.

COORDINATED EVALUATION AND UTILIZATION OF MARKER ASSISTED SELECTION FOR FHB RESISTANCE

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ABSTRACT

The objectives of this project were to 1) evaluate the effectiveness of use of FHB-resistance QTL in the NWW breeding programs through marker assisted selection (MAS); 2) quantify the effects of these QTL in reducing FHB and DON, and 3) measure their impact on other important traits such as yield and milling and baking quality. Soft winter wheat breeding programs in NY, MI, OH, IN, IL, MO and KY each identified ~10 lines from their programs for inclusion in the study. All lines had shown FHB resistance in individual program FHB nurseries. Based on pedigree, it was assumed that in some lines the resistance derived from exotic QTL such as *Fhb1* and in other cases, resistance was considered to be native. The lines were genotyped at the USDA-ARS Eastern Regional Small Grain Genotyping Lab in Raleigh, NC. Two resistant check cultivars were included in the study: Truman and Pioneer Brand 25R32. Yield trials were grown in 2011 and 2012 in MI and KY; FHB nurseries were grown both years in OH, IL, IN, and MO. Due to extremely dry conditions in 2012, FHB data was recorded at only two locations: MO and OH. Samples from the MI yield trial were submitted both years to the USDA-ARS Soft Wheat Quality Lab in Wooster, OH for milling and baking quality evaluation.

For incidence, severity, index, FDK (2011-2012), and DON (2011) the mean score for the QTL based resistance class was numerically lower than that of the native class but the difference was rarely significant at $P < 0.05$. QTL based resistance had no measurable effect on yield or test weight; the difference between classes for these traits was non-significant and the top yielding lines were from both classes of resistance. Milling and baking quality of this group of lines was not great, based on 2011 samples from MI. In general, the two classes of resistance differed very little for quality traits. Numerically, QTL - derived resistance was associated with higher flour yield, softer kernels and stronger gluten than was native resistance.

Other soft winter wheat studies have reported successful use of resistance QTL without a negative effect on milling and baking quality. The picture from this study should be clarified when the 2012 quality data become available.

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MAPPING OF FHB RESISTANCE IN SRW WHEAT CULTIVAR JAMESTOWN

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ABSTRACT

A major pathogen of wheat (*Triticum aestivum* L.), Fusarium Head Blight (FHB), is caused by the pathogen *Fusarium graminearum* Schwabe. Infection of wheat with FHB results in yield loss, reduced seed quality, and accumulation of mycotoxins such as deoxynivalenol (DON) and nivalenol (NIV). An important strategy for FHB control is pyramiding multiple resistance genes to provide a broad range of resistance, Type I (resistance to initial infection) and Type II (resistance to spread in wheat spike). The objective of this study is to identify quantitative trait loci (QTL) for FHB resistance in the native soft red winter (SRW) wheat cultivar Jamestown. A total of 77 Jamestown/LA97113UC-124 (JT/LA) $F_{4:6}$ recombinant inbred lines (RILs) lines and 186 Pioneer 25R47/Jamestown (P47/JT) $F_{5:7}$ RILs were evaluated for FHB incidence, severity, index, and concentrations of DON and NIV in three environments (JT/LA:Arkansas, Georgia, Louisiana, and Virginia ; P47/JT: Maryland, North Carolina, and Virginia). Both public and proprietary single nucleotide polymorphism (SNP) markers were used to genotype all of the JT/LA RILs and 42 of the P47/JT RILs at Monsanto Company. A 9k SNP platform was used and about 2,000 polymorphic markers were identified in the JT/LA population and about 250 markers in the P47/JT population. The linkage map was constructed using Map Manager QTX, based on the consensus map provided by the Monsanto Company. Windows Cartographer (WinQTLCart version 2.5) was used to identify possible QTLs. For the Jamestown/LA97113UC-124 population evaluated for FHB in 2011, 108 QTLs were detected on all wheat chromosomes except for 4D, 5D, 6B, 6D, and 7D. There were eight, six, four, and nine QTLs associated with FHB incidence, severity, and DON and NIV content, respectively. Among the 108 QTLs, 13 were consistent in that a given QTL controlled multiple FHB traits and 4 of these QTL were observed across environments. These consistent QTL were located on chromosomes 1A, 1B, 1D, 2A, 3B, 4A, 5A, 5B, 6B, 6D, 7A, and 7B. In 2012, nine QTLs for FHB were detected on chromosomes 1A, 2B, 2D, 3B, 6A, 7A, and 7B in the JT/LA population. For the Pioneer 25R47/Jamestown population, six and four QTLs were identified in 2011 and 2012, respectively, and the QTLs were located on chromosomes 1B, 2B, 3A, and 6A in 2011 and 2A, 3A, 3B, and 6A in 2012. Among the ten QTLs identified, two were found to be consistent across multiple environments and multiple traits. The consistent QTLs were located on chromosome 3A and 6A. In these populations, the RIL genotypes are being further characterized using SSR markers. More informative linkage map and QTL results will be reported with the addition of SSR markers in these populations.

QTL MAPPING IN A DOUBLED HAPLOID POPULATION OF WHEAT TO EXPLORE THE RELATIONSHIP BETWEEN PLANT MORPHOLOGICAL TRAITS AND FUSARIUM HEAD BLIGHT RESISTANCE

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ABSTRACT

Fusarium head blight (FHB) is a serious wheat disease in major wheat growing regions all over the world. Many reports have been published on genetic analysis of FHB resistance, which is a quantitative trait governed by polygenes. Plant height, spike length, leaf length and leaf width are crucial morphological traits that have been reported to contribute to plant architecture and indirectly affect host FHB resistance and grain yield. In this study, we are interested in the plant morphological QTLs that are coincident with or closely linked to FHB resistance loci and will conduct QTL mapping based on a wheat doubled haploid (DH) population of 124 lines derived from the cross between MD01W233-06-1 and SS8641. MD01W233-06-1, a soft winter wheat germplasm released in 2010, shows resistance to powdery mildew, leaf rust and FHB. SS8641 is a commercial cultivar with broad spectrum rust and mildew resistance but is susceptible to FHB. The DH lines were tested for grain yield, plant height, spike length, flag leaf length and flag leaf width in 2012. The DH population showed a very wide range of variation for these morphological traits in addition to scab resistance. A genetic linkage map with ~1800 SSR and SNP markers was constructed. Data from 2012 was analyzed using Inclusive Composite Interval Mapping (ICIM) methods, which detected 16 potential QTLs explaining 8.2 to 55.8% of the corresponding phenotypic variance with LOD scores greater than 3.0. Three QTLs were detected for flag leaf length and flag leaf width, respectively, with LOD scores ranging from 3.0 to 4.2, 4.5 to 5.6 and corresponding R^2 ranging from 14.1 to 55.8%, 12.0 to 15.9%. One QTL for spike length with LOD=3.4 and R^2=12.1%, six QTLs for plant height with LOD scores ranging from 3.7 to 8.3 and R^2 ranging from 8.2 to 22.7% and three QTLs for grain yield with LOD scores ranging from 3.1 to 3.5 and R^2 ranging from 9.9 to 21.7% were also identified. Detected QTLs for morphological traits will be examined with FHB resistance loci (study in progress) to provide insight into their relationship. Furthermore, the DH population will be evaluated in 2013 at three field locations: Upper Marlboro (MD), Queenstown (MD), and Clarksville (MD) as well as at a research greenhouse at the University of Maryland.

FUSARIUM HEAD BLIGHT REACTIONS OF LANGDON DURUM D-GENOME DISOMIC SUBSTITUTION LINES

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ABSTRACT

An effective source of resistance to Fusarium Head Blight (FHB) like Sumai 3 has not been found in durum wheat. Limited progress has been made in the improvement of FHB resistance in durum by utilizing resistance sources derived from hexaploid wheat and tetraploid relatives of durum. We have observed that FHB resistance QTL exhibited less effectiveness of resistance in durum than hexaploid wheat. It has been anticipated that D-genome chromosomes of hexaploid wheat might play a role in the expression of FHB resistance genes in wheat. Here we report the FHB reaction of a complete set of Langdon (LDN) durum D-genome disomic substitution lines (DSLs), where one pair of A- or B-genome chromosomes of LDN were replaced by one pair of homoeologous D-genome chromosomes from common wheat 'Chinese Spring (CS)'. The 14 DSLs were evaluated for Type II resistance with point inoculation method under three greenhouse environments in two seasons (Fall 2011 and Spring 2012). Homogeneity test indicated there was no significant difference among three greenhouse environments ($p<0.05$). So combined statistical analyses were performed with the DSLs. LDN exhibited a mean FHB severity of 57.47%. The mean FHB severity for each of the DSLs over the three environments ranged from 27.75% for the DSL LDN5D(5A) to 84.42% for LDN6D(6A). FHB severity of LDN5D(5A) was significantly lower than LDN and other DSLs. In addition, LDN5D(5A) had long and slim spikes due to the absence of *Q* gene on chromosome 5A. This modified spike structure might constrain the infection and/or spreading processes of the fungal pathogen and then reduce FHB disease in LDN5D(5A). Additional studies are under way to further determine the effect of this 5D(5A) chromosome substitution on FHB resistance. On the other hand, two DSLs, including LDN6D(6A) and LDN2D(2B), exhibited significantly higher severity than LDN. These results suggest that chromosome 6A and 2B might contain genes enhancing FHB resistance in LDN or chromosome 6D and 2D contain the genes for FHB susceptibility and/or suppression of FHB resistance in LDN background. A better understanding of the effects of these chromosome substitutions on FHB resistance/susceptibility will facilitate the development of durum varieties and germplasm with improved resistance to FHB.