SESSION 1:

VARIETY DEVELOPMENT AND HOST PLANT RESISTANCE

Co-Chairpersons: Rich Horsley and Steven Xu

SUCCESSFUL ADOPTION OF SPRING WHEAT CULTIVARS WITH MODERATE RESISTANCE TO FHB BY GROWERS IN THE NORTH CENTRAL REGION

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ABSTRACT

More than $1 billion in direct economic losses in the spring wheat region were attributed to Fusarium head blight (FHB) from 1993-2000. Growers continue to incur losses when susceptible cultivars are grown and environmental conditions are conducive to disease. Dedicated breeding efforts for resistance to FHB in the region date to the late 1980's when 'Sumai 3' was first introduced as a source of resistance. Since the epidemics of the 1990's, 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. Alsen contains the *Fhb1* QTL for FHB resistance, as well as other QTL, inherited from Sumai 3. Alsen has been grown on nearly 12 million acres in North Dakota since its release and was the most popular cultivar in North Dakota from 2002 to 2006. Today, nearly half of the cultivars available to growers in the spring wheat region are classified as moderately resistant or better for FHB reaction. Moderately resistant cultivars were grown on 43% of the region's spring wheat acreage in 2011, compared with 0, 20, 19, and 36% in 1999, 2002, 2005, and 2008, respectively. The proportion of the region's acreage occupied by moderately susceptible or worse cultivars dropped from 76% in 1999 to 31% in 2011. The *Fhb1* QTL was present in cultivars grown on 40% of the region's wheat acreage in 2011.

BREEDING FOR SCAB RESISTANT HARD WINTER WHEAT: THE THRILL OF VICTORY AND THE AGONY OF DEFEAT

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ABSTRACT

Of all the traits that we breed for in the Great Plains, breeding for Fusarium head blight (FHB, incited by *Fusarium* spp.) is certainly among the most difficult. A major reason for this difficulty is the highly variable climate of the Great Plains where the east to west gradients in many states range from relatively high rainfall (>75 cm/year) to very low rainfall (~25 cm/year). However even in the driest parts of our states, we can find major FHB outbreaks in years of high rainfall. Part of this seeming anomaly may be due to much of the annual rainfall occurring at flowering, the continued expansion of corn (*Zeae mays* L.) into the western Great Plains where the major wheat (*Triticum aestivum* L.) producing region is, and that most of our rotations involve minimum or reduced tillage, thus having high levels of inoculum on the soil surface. Selecting for FHB tolerant lines is difficult because much of the Great Plains has winds during the night and early morning which dry the wheat tissue before infection can occur even under mist irrigation nurseries. Our best screening nurseries tend to be on sheltered farms in areas where wind is low during the night and early morning (e.g. Manhattan, KS).

Despite these difficulties with our screening nurseries, excellent progress has been made with identifying and deploying native resistance. Among those cultivars which have a lower level of FHB than other cultivars are: Everest (KSU), Overland (UNL), Lyman (SDSU), Art (Syngenta), and Hitch (Westbred). The cultivars span the region (thus providing growers with choices in managing FHB) and are particularly well adapted to the most scab prone regions of the Great Plains. Fusarium head blight tolerant lines, such as Overland, are the most popularly grown cultivars in their state of origin (in this case NE) and are popular throughout the region. Hence significant progress has been made in reducing the impact of FHB. This is the thrill of victory.

However, in bad FHB years, native resistance can be overwhelmed and gene pyramiding or an integrated approach involving fungicides are needed to further reduce the effects of FHB. Though we have worked for 10 or more years with parent lines containing *Fhb1*, there is currently no released line and few advanced experimental lines with *Fhb1* or other major known QTLs (the agony of defeat). The lack of success with incorporating *Fhb1* into elite germplasm, led us to wonder if *Fhb1* or closely linked genes had a detrimental effect on agronomic performance. In studies involving Wesley and Wesley backcross (BC_2) lines with *Fhb1*, many of the Wesley *Fhb1* lines were lower yielding than Wesley, however some of the backcross lines yielded very similarly to Wesley, the recurrent parent. These lines are being retested and are are under increase. Furthermore, using a population approach, we compared 20 derived lines with *Fhb1* to 20 lines for non-*Fhb1* lines and no detrimental effects were associated with *Fhb1*. We interpret these results as our previous efforts were using *Fhb1* in too much unadapted germplasm and the rare *Fhb1* derived progeny

was due to the low number of lines with good agronomic performance (*Fhb1* or non-*Fhb1* derived lines). Hence we have changed our strategy to ensure that FHB QTLs are first put into adapted backgrounds through backcrossing and then forward breeding can occur. We are currently using the Wesley BC *Fhb1* lines, as well the advanced lines with *Fhb1* from our population approaches and the recently developed BC lines for *Fhb3* as parents for gene pyramiding, especially into backgrounds such as Overland with good native resistance. By pyramiding two or more QTLs into a background with native resistance and with the use of a fungicide, we hope to reduce the chance for high levels of DON to a minimum in the Great Plains. We now have sufficient elite germplasm to really make progress in creating lines with excellent FHB tolerance. The use of molecular markers is critical and more efficient because in many years the phenotypic assay is difficult and requires many location-year tests to get reliable data. One surprise in this effort is that we have identified lines with phenotypically low FHB scores that have elevated DON (e.g. Harry). We have no explanation for this discovery, but it highlights the need for DON testing and phenotyping for low disease does not always indicate low DON.

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USING MAKER-ASSISTED SELECTION TO IMPROVE FUSARIUM HEAD BLIGHT (FHB) RESISTANCE IN HARD WINTER WHEAT

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ABSTRACT

Epidemics of wheat Fusarium head blight (FHB, incited by *Fusarium graminearum*) usually occur in the northern part of the Great Plains. However, in the last several years, FHB have moved south to most of Kansas and Oklahoma where FHB was not seen before, partially due to reduced tillage and the continued expansion of corn (*Zea mays* L.) into the major wheat (*Triticum aestivum* L.) producing region in the Great Plains. Thus, breeding for FHB resistance has become one of major breeding objectives in most HWW breeding programs in the Great Plains. Among all QTLs reported for FHB resistance to date, *Fhb1* is still the one with the largest effect on FHB resistance and the QTL of FHB resistance widely used in breeding programs worldwide. Although work to move *Fhb1* from Chinese sources into US hard winter wheat (HWW) has been initiated for more than 10 years, there is no released cultivar and only few advanced breeding lines with *Fhb1* in HWW due to poor adaptation traits associated with *Fhb1* containing parents. More recently, we successfully transferred *Fhb1* to several US adapted HWW backgrounds using marker-assisted backcrossing. The resulting near-isogenic lines (NILs) with *Fhb1* showed a high level of type II FHB resistance in several US winter wheat backgrounds. However, the levels of FHB resistance among NILs varied with recurrent parents. Yield testing of NILs contrasting in *Fhb1* showed that most of NILs had lower yield than recurrent parents, but some NILs with *Fhb1* demonstrated a high level of resistance with similar yield as recurrent parents. Wesley*Fhb1* NILs have been evaluated in yield trials of NE and SD and some lines can be released as cultivars or germplasm. To date, *Fhb1* was transferred into seven US winter wheat cultivars (6 HWW) and they are ideal parents for incorporation of *Fhb1* into US wheat. For marker-assisted selection, we developed single nucleotide polymorphism (SNP) markers for *Fhb1*. Currently we are converting markers for FHB resistance and other traits into SNP. A set of 50 SNP associated with FHB resistance and other traits will be available for MAS using Sequenom MassArray.

Using QTL mapping, we also characterized FHB resistance in five Chinese landraces. Most of these accessions carry the *Fhb1* allele, but the effect of the QTL on type II resistance appeared to be smaller than that in Ning 7840. Besides *Fhb1*, QTLs were identified on chromosomes 7A, 3A, 7D and 3BS near the centromere region. These germplasm and QTLs will be useful sources of resistance for pyramiding of different QTLs in a new cultivar and will diversify the sources of FHB resistance in US breeding programs.

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EFFECTS OF *FHB1* AND *QFHS.NAU-2DL* ON FUSARIUM HEAD BLIGHT AND AGRONOMIC TRAITS IN SRW WHEAT

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ABSTRACT

The use of exotic resistance quantitative trait loci (QTL) provides one strategy for breeding wheat cultivars resistant to Fusarium Head Blight (FHB). The success of this approach depends on 1) effectiveness of the QTL in diverse genetic backgrounds, and 2) the effects of the QTL on agronomic and quality traits. In this study, we evaluated two QTL, *Fhb1* (chromosome 3B) and *QFhs.nau-2DL* (chromosome 2D) in this context. To validate both QTL in diverse genetic backgrounds, we measured FHB index, *Fusarium* damaged kernels (FDK) and deoxynivalenol (DON) concentration in inbred lines from five crosses in the scab nursery at Lexington, KY in 2010 and 2011: population 1 (26R58/VA01W-476//KY97C-0574-01), 2 (25R54/VA01W-476//KY97C-0574-01), 3 (25R54/VA01W-476//KY97C-0554-02), 4 (25R78/VA01W-476) and 5 (KY93C-1238-17-1/VA01W-476). The populations were also grown in yield trials at Lexington (2010 and 2011) and Princeton (2011), KY, for measurement of agronomic and quality traits. In addition to assessing FHB levels by traditional methods, we also used whole kernel NIR. On average, *Fhb1*-derived resistance significantly reduced FDK by 32% and DON by 20 % in 5 and 4 populations, respectively. On average, *QFhs.nau-2DL* significantly reduced FDK by 21 % and DON by 23 % in 3 populations, respectively. Both QTL significantly affected yield and test weight in a positive manner but small in absolute values. Milling and baking quality traits were affected but not in a consistent direction or in all populations. Correlation of NIR values with FDK and DON in 2011 was r = 0.78 and 0.60, respectively. Both QTL can reduce FHB in soft red winter wheat without significant negative impacts on agronomic and quality traits. However, expression levels of the QTL can be expected to vary according to genetic background.

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FUSARIUM HEAD BLIGHT RESISTANCE AND DEOXYNIVALENOL ACCUMULATION IN HULLED AND HULLESS WINTER BARLEY AND DISTILLER'S DRIED GRAIN

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ABSTRACT

Interest in use of winter barley (*Hordeum vulgare*) for ethanol production has prompted additional research on barley improvement, production, use, grain composition, and high value byproducts. *Fusarium graminearum*, causal agent of Fusarium head blight (FHB), is a serious fungal pathogen that produces the mycotoxin deoxynivalenol (DON), which is known to accumulate in barley grain and can become concentrated in distiller's dried grain with solubles (DDGS). These high value DDGS produced as a byproduct of ethanol production are used in animal feeds and have potential for use in human foods. High DON concentration in DDGS can render them unmarketable. Information is needed regarding the accumulation, fate and changes in DON concentration in barley grain and during ethanol production. Potential ways to reduce DON concentration in grain and/or to degrade it during ethanol production include use of FHB resistant cultivars, milling or pearling to remove hulls where DON is concentrated, and development of yeast strains having the capability to degrade DON. Currently, little is known about FHB resistance in winter barley grown in Virginia. Nine hulled and hulless winter barley genotypes including three putatively resistant, moderately resistant, and susceptible lines were selected from the Virginia Tech barley breeding program to further characterize FHB resistance. Genotypes were planted in a randomized complete block with two replications in mist-irrigated nurseries at Blacksburg and Mt. Holly, VA during the 2009-10 and 2010-11 growing seasons. Plots were 1.5 m x 13.4 m to produce sufficient grain for analysis of DON concentration in barley grain, during ethanol fermentation, and in DDGS. *Fusarium graminearum* colonized corn (*Zea mays*) kernels were applied to plots at the boot stage at both locations, and tests at Blacksburg were spray inoculated using conidia (5×10^4) applied at 50% flowering stage. Genotypes were rated for FHB incidence (proportion of 30 heads infected with FHB per plot), FHB severity (number of infected spikelets divided by the total number of spikelets for thirty heads per plot), *Fusarium* damaged kernels (FDK), and DON concentration. Analysis of variance showed significant differences ($P \leq 0.05$) among genotypes for all traits. Significant ($P \leq 0.05$) genotype x environment interaction occurred for FHB incidence, FHB severity, FHB index (incidence x severity/100), and DON concentration. Concomitantly, a significant ($P \leq 0.05$) genotype x environment x year interaction occurred for FHB severity. Deoxynivalenol concentration correlated most significantly with FHB Index in both environments. Pearson correlation values for DON accumulation and FHB index were r = 0.31 ($P \leq 0.008$) for Blacksburg and r = 0.76 ($P \leq 0.001$) for Mt. Holly. Significant ($P \leq 0.05$) interactions can be attributed to changes in rank among susceptible lines when averaged across years for a given environment for FHB Incidence and FHB Index. A change in magnitude of values for DON concentration contributed to both the change in rank among lines across environments and the significant ($P \leq 0.05$) genotype x environment interaction. Fusarium head blight incidence values ranged from 42.5% to 82.5% in Blacksburg and 32.5% to 95.8% in Mt. Holly. Fusarium head blight index values ranged from 8.6 to 42.6 for Blacksburg and 3.5 to 49.5 in Mt. Holly. Deoxynivalenol concentrations ranged

from 0.3 to 3.3 ppm in Blacksburg and 5.6 to 45.6 ppm in Mt. Holly. Two hulless genotypes, VA06H-48 and Eve, and the hulled cultivar Nomini exhibited consistent resistance to FHB and DON accumulation in this study. Initial fermentation studies with seven select lines indicated that DON was concentrated at a rate ranging from 2x to 8x in DDGS. The resistant genotype Eve had a DON concentration of 3 ppm in the grain sample and a final concentration of 26 ppm in the DDGS sample. The susceptible line VA06H-25 had a DON concentration of 130 ppm in the grain sample and a final concentration of 244 ppm in the DDGS sample. Deoxynivalenol increased 12% in the DDGS sample of Eve and 60% in the DDGS sample of VA06H-25. Additional fermentations using grain harvested during the 2010-11 growing seasons will be completed this coming spring. Results indicate that a range in FHB resistance exists among both hulled and hulless winter barley lines and cultivars grown in the Mid-Atlantic region.

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CLARK NEAR-ISOGENIC LINES CONTRASTING IN *FHB1* FOR FHB RESISTANCE DID NOT SHOW SIGNIFICANT REDUCTION IN GRAIN YIELD

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ABSTRACT

Fusarium head blight (FHB) is a devastating disease that leads to severe losses in wheat grain yield and quality. The most consistent quantitative trait loci (QTL) for resistance to FHB symptom spread within a spike, *Fhb1*, has been mapped on chromosome 3BS of the Chinese variety Sumai3 and its derivatives, which include Ning7840. *Fhb1* in Ning7840 explained up to 53% of the phenotypic variation in FHB resistance and this variety has been widely used as resistant parent in breeding programs worldwide. The use of an exotic variety as resistant parent in US breeding programs may potentially involve reduction in grain yield due to the transfer of undesirable genes linked to the QTL (linkage drag). The objective of this study was to assess linkage drag at *Fhb1* by evaluating grain yield in near-isogenic lines (NILs) developed by backcrossing Clark (recurrent parent) with Ning7840 (*Fhb1* donor). Clark is a soft winter wheat variety released from Purdue University, Indiana, and has high yield potential, but is susceptible to FHB (Ohm et al., 1988). Approximately 2000 BC_7F_2 plants were screened with SSR markers (*Xgwm533 and Xgwm493*) for *Fhb1* and 200 BC_7F_3 families were selected for FHB evaluation in greenhouses experiments. Five NILs were selected at BC_7F_7 and validated for presence and absence of markers for *Fhb1*. Repeated experiments were conducted to evaluate FHB resistance for the set of NILs in the greenhouse and field using the single-floret inoculation method. Among them were four NILs with a proportion of scabbed spikelet (PSS) rating of 0.05-0.3 and one susceptible NIL (PSS=0.42-0.95). The five NILs were evaluated for yield difference in three field trials, two in 2010 and 2011 at Manhattan, KS and one in 2011 in Urbana, IL. Resistant NILs with yields not significantly different from that of Clark were identified. Deoxynivalenol (DON) analysis showed that all resistant NILs have lower DON content compared to the susceptible controls. Marker-assisted backcross efficiently removed undesired traits associated with *Fhb1* in a Chinese source and the NILs with *Fhb1* should be useful parents for transferring *Fhb1* into US wheat cultivars.

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MAPPING QTL FOR FUSARIUM HEAD BLIGHT RESISTANCE TO CHINESE WHEAT LANDRACE HUANGCANDOU (HCD)

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ABSTRACT

Fusarium Head blight (FHB) is a devastative disease that can cause severe reduction in grain yield and quality, especially in humid and semi-humid wheat growing regions. Growing resistant cultivars is one of the most effective strategies to minimize the disease damage. Currently, the widely used source of resistance in most breeding programs worldwide is mainly Sumai 3 or its derivatives. Exploring new sources of resistance can diversify sources of FHB resistance used in wheat breeding programs. A Chinese wheat landrace Huangcandou (HCD) was identified to show a high level of FHB type II resistance (Yu et al. 2006). To identify quantitative trait loci (QTL) responsible for type II resistance in HCD, a population of 190 recombinant inbred lines (RIL) was developed from a cross between HCD and Jagger, a susceptible hard winter wheat from the U.S.A. The population was evaluated for type II resistance as reflected by percentage of symptomatic spikelets (PSS) per spike in greenhouse at Kansas State University spring 2010 and 2011, fall 2010. Plants were inoculated using single floret inoculation and arranged on greenhouse benches in a randomized complete block design (RCBD). Five plants per pot were inoculated with two replications (block) per experiment. PSS was recorded 18th day after inoculation and used for QTL analysis. Initial marker screening identified 252 polymorphic simple-sequence repeats (SSR) between parents. Analysis of the RIL population with those markers identified three QTL. Among them, two were on the short arm of chromosome 3B (3BS) with one major QTL on the distal arm of 3BS (3BSd) and one near the centromere of 3BS (3BSc). The QTL 3BSd showed the largest effect on type II resistance, which coincided with a formerly reported QTL *Fhb1*, and explained 10.80% to 36.86% of phenotypic variation for FHB resistance. The QTL 3BSc had a smaller effect than 3BSd. The third one was on chromosome 2D and explained 6.49% of phenotypic variations for type II resistance. Resistance alleles for two QTL on chromosome 3BS were from HCD, while the allele for QTL on 2D was from Jagger. Allelic substitution effect analysis using the closest marker to each QTL revealed that substitution of two alleles on 3BS from Jagger with those from HCD significantly reduced the PSS. HCD shows a high level of type II resistance and contains both QTL on 3BS, therefore is a potential alternative FHB resistance source for improving FHB type II resistance in wheat.

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FUSARIUM HEAD BLIGHT RESISTANCE IN DURUM WHEAT – PROGRESS AND CHALLENGE

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ABSTRACT

Several sources of FHB resistance have been identified in tetraploid wheat, including durum (*Triticum turgidum* ssp. *durum*, genome AABB), emmer (*T. turgidum* ssp. *dicoccum*, genome AABB), wild emmer (*T. turgidum* ssp. *dicoccoides*, genome AABB), Persian wheat (*T. turgidum* ssp. *carthlicum*, genome AABB) and timopheevii wheat (*T. timopheevii*, genome AAGG). None of these resistance sources is comparable to 'Sumai 3', a major source of resistance found in hexaploid wheat (*T. aestivum* L., genome AABBDD). We have identified and mapped several novel FHB resistance QTL from the tetraploid sources, including *Qfhs.ndsu-3AS* from wild emmer, *Qfhs.ndsu-5BL* from durum, and *Qfhb.rwg-5A.1* and *Qfhb.rwg-5A.2* possibly from timopheevii. Molecular markers have been developed to tag these resistance QTL and used to assist selection of the QTL in the germplasm/cultivar development. Significant efforts have been made to introgress FHB resistance from the tetraploid and hexaploid sources into adapted durum backgrounds. Durum cultivars with improved FHB resistance, such as Divide, have been released and widely grown in ND. In addition, a large number of durum germplasm lines with various levels of resistance have been developed. However, the durum lines with resistance QTL from the tetraploid and hexaploid sources have always exhibited lower levels of resistance than the original sources or no resistance at all especially under field conditions. This has been a big puzzle and challenge for durum researchers to develop durum cultivars and germplasm with high levels of resistance to FHB. Recently, we have identified FHB resistance QTL on chromosome 5A and 5B of a moderately resistant synthetic hexaploid wheat line (genome AABBDD) derived from the cross of the susceptible durum cultivar 'Scoop 1' (genome AABB) and *Aegilops tauschii* (genome DD). These results suggest that D genome might have the capacity to boost expression of FHB resistance genes in A and B genomes. Further studies are being performed on the role of the D-genome chromosomes in the expression of FHB resistance QTL derived from A and B genomes. Additionally, a possible susceptibility or suppressor of resistance locus on durum chromosome 2A has been identified. Efforts are underway to remove or mutate this locus to characterize its effect and increase the resistance in adapted cultivars.

APPLICATION OF MAS FOR DEVELOPMENT OF WHITE SEEDED WHEAT RESISTANT TO FUSARIUM HEAD BLIGHT

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ABSTRACT

Fusarium head blight (FHB) is an important disease of wheat, and Sumai 3, a Chinese wheat cultivar, has been used as a source of resistance to FHB in almost all wheat breeding programs. We are attempting to develop a white seeded wheat with a high level of FHB resistance using marker assisted selection (MAS). Snowbird, a FHB susceptible white hard white seeded wheat registered by the C. R.C. in Winnipeg, was crossed to Sumai 3 as a female parent. Twenty thousand F_2 plants were produced and grown in the greenhouse. One thousand and five hundred white seeds were visually selected from the F_2 population. This population was advanced to F_5 by single seed descent. At the seedling stage of F5, a MAS was performed for three FHB QTLs on chromosome 5A, 3B and 6B. Two hundred and fifty F_5 lines were selected with two or three resistance QTLs and grown in a FHB nursery in 2008. Fifteen F_6 lines were selected based on FHB resistance and agronomic performance. Seed of the 15 lines was increased in the greenhouse in the winter of 2009. These 15 lines and two parents Sumai 3 and Snowbird, plus AC Vista as a check were planted in the FHB nursery with three replications and in a preliminary yield trial with two reps in the summers of 2009, 2010 and 2011. The results showed that the 15 lines had either 2 or 3 of the FHB QTLs. The range in DON values for the 15 lines was from 1.5 ppm to 9.4 ppm compared to the checks Snowbird, AC Vista, Snowstar, AC Barrie and Sumai 3 at 19.2, 18.8, 19.0, 4.4 and 2.2 ppm, respectively. Most of lines were earlier in maturity than Sumai 3. The quality of the lines was significantly improved over Sumai 3, based on the Glutomatic test. The yields of these lines were also improved compared to Sumai 3. The lines WS-131A, WS-321 and WS-481 are currently being used in a spring wheat breeding program for development of a hard white wheat with FHB resistance.

MUTATION BREEDING FOR FUSARIUM HEAD BLIGHT RESISTANCE

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ABSTRACT

Mutation breeding has been a successful way of producing lines where variability for a trait of interest is limited. We conducted a pilot study to improve resistance to Fusarium head blight (FHB) in soft red winter wheat. Following production of kill curves, to determine appropriate doses of radiation, 1kg samples of susceptible breeding lines KY93C-1238-17-1 and KY96C-0786-3-2 seed (approximately 35,000 and 29,000 seeds, respectively) that had absorbed 100 and 300Gy of gamma radiation (M1) respectively were increased in plots and M2 seed harvested in bulk. An estimated 37,000 and 27,000 of randomly sampled M2 seed for KY93C-1238-17-1 and KY96C-0786-3-2 was seeded in 240 and 204 rows in an inoculated irrigated scab nursery in Lexington, KY in 2009. Seventy eight and 60 asymptomatic heads were tagged, harvested and seeded as head rows in a similar nursery in 2010. Twenty nine (KY93C-1238-17-1) and 23 (KY96C-0786-3-2) rows were selected based on spike symptoms and seeded in a 2 rep RCB design in the Lexington scab nursery in 2011. We observed significant ($P<0.05$) differences, among KY93C-1238-17-1 derived lines for scab rating (0-9). Ratings of mutant lines ranged from 0 to 5.5; the mean rating for KY93C-1238-17-1 was 5.0. Significant ($P<0.05$) differences among lines were also observed for % FDK (w/w). FDK ranged from 9.2 to 28.1%; mean % FDK for KY93C-1238-17-1 was 18.9. Analysis of scab rating of the KY96C-0786-3-2 derived material showed a similar pattern. Significant ($P<0.05$) differences among mutant lines were observed; entry means ranged from 1.5 to 4.5. Mean FHB rating for KY96C-0786-3-2 was 4.5. Significant differences for %FDK among KY96C-0786-3-2 derived lines were not seen. Mutagenesis and selection for reduced visual symptoms produced lines with significantly reduced FHB ratings from both parents. However, FDK was reduced following selection for spike symptoms in only one of two genetic backgrounds.

ACKNOWLEDGEMENT AND DISCLAIMER

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

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ABSTRACT

Wheat scab or Fusarium head blight (FHB) is caused by the fungus *Fusarium graminearum*. This is a wide spread disease of wheat (*Triticum aestivum* L.) and other cereals in the United States and around the world that affects grain yield and quality. The fungus also produces the mycotoxin vomitoxin or deoxynivalenol (DON), which accumulates in seed. This can lower the value of grain and pose health risks to humans and livestock. The soft winter wheat MD01W233-06-1 ('McCormick'/'Choptank') has been shown to have FHB resistance, without Sumai-3 alleles—a common source of scab resistance in many breeding programs. The objective of this research is to map resistance to scab in a population of 131 doubled haploids (DH) derived from a cross of the resistant soft winter wheat genotype MD01W233-06-1 and the susceptible genotype SS8641 under Maryland field conditions and in the greenhouse. A total of 125 DH lines were evaluated in the field in the spring of 2011 for heading date, leaf length, susceptibility to powdery mildew, and incidence and severity of FHB. After threshing the percentage of *Fusarium* damaged kernels (FDK), 1000 kernel weight and DON concentration were measured for each DH. The FHB index and ISK were calculated from the field data. In the winter of 2010-2011, 128 lines were grown in the greenhouse and evaluated for FHB resistance by single floret injection. Severity and spread of FHB, FDK, and DON were measured in each line. In both greenhouse and field evaluations, there were significant negative correlations between all measures of FHB (incidence, severity, FDK, FHB index, ISK) and the 1000 kernel weight. Twenty nine simple sequence repeat (SSR) markers, and one morphological marker (red coleoptile) were used for linkage analysis and mapping of scab resistance traits. Nine linkage groups with 2 to 3 markers and 10 unlinked markers were found, using Map Manager QTX. QTLs with the highest for DON, FHB, and ISK were linked to markers on chromosomes 1A, 3A, and 3B.

IMPROVEMENT OF FUSARIUM HEAD BLIGHT RESISTANCE IN SOUTH AFRICAN WHEAT GERMPLASM

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ABSTRACT

In South Africa wheat is planted in different production areas where diseases are often an important production constraint. One of the most important diseases is Fusarium head blight (FHB), which occurs mainly under irrigation on small grains such as wheat, barley and oat. The predominant *Fusarium* species that cause head blight worldwide are *F. graminearum*, *F. culmorum* and *F. avenaceum*. The causal species in a specific region depends on factors such as environmental conditions, crop rotation, tillage practices and the amount of inoculum present. Yield losses of up to 40% have been reported in infected fields and grain may contain mycotoxins that are harmful to humans and animals. Currently, all wheat cultivars grown under irrigation in South Africa are susceptible to FHB. In addition, control options for FHB are limited, since no fungicides are registered against this disease. It is therefore important to utilize genetic resistance which may provide viable and cost effective control of this disease. This paper discusses the evaluation of wheat germplasm for resistance to the South African complex of FHB. Wheat germplasm nurseries (Scab Resistant Screening Nursery - SRSN) were imported from CIMMYT, Mexico and planted in a honeycomb design at Bethlehem. Trials were inoculated with a cocktail of single spore isolates, prepared by using the bubble breeding method, and sprayed using a Stihl mist blower during flowering stage since optimum disease pressure is needed for infection. Two hundred and nine lines were evaluated three weeks after inoculation for Type II resistance and five lines were selected over a two year period for FHB resistance and quality characteristics. Selected lines were incorporated in a crossing block using the South African cultivars (Baviaans, Buffels and Duzi) which are well adapted and widely utilized in the irrigation areas of South Africa. The progeny of the back crossed material is currently being tested under field conditions where FHB response in the field, adaptation, yield and quality are factors being considered during selection.

Key words: Fusarium head blight, South African germplasm, Scab, *Fusarium graminearum*, Yield loss, *Gibberella zeae*.

SIMULTANEOUS MAPPING AND PYRAMIDING OF SCAB RESISTANCE QTL BY FAMILY-BASED MAPPING IN EARLY GENERATION WHEAT BREEDING POPULATIONS

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ABSTRACT

QTL mapping for scab resistance has relied on specifically designed populations derived from biparental inbred line crosses. Such mapping populations have important practical limitations for plant breeding programs: 1) the number of detectable QTL is limited, 2) estimated QTL and marker effects cannot be extrapolated to the diverse genetic backgrounds in breeding populations, and 3) mapping efforts are disjointed from breeding efforts to introgress QTL. Family-based linkage analysis developed for human and animal populations may facilitate mapping QTL directly in early generation breeding populations (Rosyara et al. 2009), thus integrating QTL mapping and marker-assisted breeding efforts. Therefore, this project applies a family-based mapping approach to early generation spring and winter wheat breeding populations to simultaneously map and pyramid scab resistance QTL, while concomitantly developing scab resistant germplasm lines for inclusion in contributing breeding programs. Spring wheat breeding populations consisting of 44 related double-cross families (964 individuals) have been developed for mapping and pyramiding of resistance QTL. A separate set of winter wheat populations are currently being developed. Founders for the spring wheat populations consist of 17 experimental lines from the SDSU spring wheat breeding program carrying the *Fhb1* (3BS) QTL, 2 experimental lines from the UMN spring wheat breeding program with unknown source of resistance, 2 recombinant inbred lines from the cross PI81791/Wheaton with putative resistance QTL located on 2B, 3B, 3D and 4D, and Mult757 with putative resistance QTL located on 7BS. Double-cross F1 individuals were selfed and evaluated in the greenhouse for scab resistance by spray inoculation. Predictions from combined mixed model analysis of severity (% infected spikelets) at 14 and 21 DAI ranged from 18 to 80% for double-cross individuals, 43 to 46% for founder lines carrying *Fhb1*, and 36 to 60% for all resistant founder lines. Thus, substantial transgressive segregation for resistance was evident, supporting the segregation of multiple disparate QTL from the founder lines. Double-cross individuals are to be progeny tested using F2 head rows in replicated field trials by contributing programs. Founder lines and double-cross individuals are currently being genotyped using SSR markers to provide a genome-wide scan for resistance QTL. Family-based linkage methods developed for human and animal populations (Jannink et al. 2011) will be adapted to map resistance QTL. Existing software packages (e.g. Abecasis et al. 2002) will be used accommodate the complex pedigree structures.

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PHENOTYPIC EVALUATION OF CIMMYT WHEAT GERMPLASM FOR FHB AND YR RESISTANCE

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ABSTRACT

Fusarium Head Blight (FHB), mainly caused by *Fusarium graminearum*, and Yellow Rust (YR), caused by *Puccinia striiformis*, are two of the most important wheat diseases around the world. These diseases can cause severe yield reduction and grain quality deterioration in wheat. In the case of FHB, there is an additional concern related with the accumulation of mycotoxins in the kernel. Breeding for resistance has been considered as the most practical strategy for control of each of these diseases. The current study is part of a collaborative project between Michigan State University (USA), CIMMYT (Mexico), and INIAP (Ecuador) to identify QTLs for FHB and YR resistance in spring wheat germplasm using an Association Mapping (AM) approach. An AM population of 297 advanced lines of bread wheat was planted in Mexico (Toluca and El Batan) in 2011 and phenotyped for FHB and stripe rust. Preliminary results of the most important phenotypic variables will be shown and discussed. The variables evaluated in Toluca were 'YR severity' and 'Disease reaction type'; meanwhile, the variables collected in El Batan were 'FHB severity', 'FHB incidence', 'DON concentration', '*Fusarium* Damaged Kernels (FDK)', 'Plant height', 'Days to flowering' and 'days to harvest'. To ensure high inoculum pressure at the YR experiment in Toluca, the susceptible cultivar 'Morocco' was planted around the experiment. Meanwhile, direct inoculation with *Fusarium graminearum* at flowering time was performed in the FHB experiment in El Batan. The genotypes in the FHB experiment showed a wide variation in the severity. More than 30% of genotypes of the population were susceptible to *Fusarium graminearum*, having a severity greater than 20%. The susceptible control (Gamenya) showed high susceptibility (51.7%). ELISA tests were performed to quantify DON concentration and showed a range from 0.23 ppm – 16.3 ppm. In the YR study, 30% of the genotypes were without symptoms of the disease. The YR severity in the AM population ranged from 0% to 70%. The average was 8.37%. It has been planned to conduct a seedling test to confirm the presence of major genes and also the identification of genotypes with Adult Plant Resistance. Preliminary results showed a significant correlation between 'percentage of severity' vs. 'DON concentration', however, the correlation between 'Percentage of severity' vs. 'FDK' or 'FDK' vs. 'DON' were not significant. A second field evaluation will be conducted in Mexico along with evaluations in Ecuador. The phenotypic data will allow us to conduct an association analysis to identify QTLs for FHB and YR resistance in this population. We gratefully acknowledge the support of INIAP and the Monsanto Beachell-Borlaug International Scholars Program for funding this project.

NEW SOURCES OF RESISTANCE TO FUSARIUM HEAD BLIGHT AND THEIR MODE OF ACTION

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Fusarium head blight continues to be a serious problem in all temperate grain growing regions of the world. Sumai3 and to a lesser extent Frontana, NyuBay, Wuhan1 and Maringa continue to be used primarily for breeding for FHB resistance.

QTL for FHB resistance have now been mapped to every wheat chromosome (Buerstmayr et al., 2009). High levels of FHB resistance have also been found in an array of alien species (Oliver et al., 2005; Cao et al., 2009; Fedak et al., 2000, 2004).

Breeding efforts are continuing in FHB problem areas and incremental improvements in FHB resistance are being made with each new cultivar. Despite these efforts no one has yet produced a variety equal to Sumai3 in FHB resistance. However, these studies have revealed several issues involved in enhancement of FHB resistance.

There can be unexpected and unexplained interactions between mapped QTLs (McCartney et al., 2007), so that gene pyramiding may not always be predictable or effective. Many researchers are now realizing that minor QTLs are necessary to enhance the disease resistance levels of the major QTL. Thus there is a justification in searching for additional major and minor QTL to supplement those already available.

Our approaches involve screening of hundreds of accessions of alien species or existing cytogenetic stocks. The transfer procedures involve crossing followed by embryo rescue to establish the hybrids then backcrossing and screening to restore fertility. Screening for type I resistance was conducted in field epiphytotic nurseries and for type II resistance by point inoculation. Testing for DON content was carried out by an ELISA type method (Sinha et al., 1995) on extracts from one gram grain samples.

In our studies we largely concentrated on species that have not been studied in other laboratories. The ongoing studies are at various stages in terms of introgression, development of mapping populations and marker assignments

A. FHB resistance in alien species

a. *Triticum mococcum* (A genome) - After screening about 200 accessions, line 10-1 was found to have the best FHB resistance. After crossing and backcrossing to AC Superb, line M321 was isolated. A unique QTL for this resistance was discovered on chromosome 5A. This line also has a unique gene for leaf rust resistance.

b. *Aegilops speltoides* (B genome) - The *Ae. speltoides* accession selected for FHB resistance produced an F1 hybrid with high chromosome pairing when crossed to AC Superb. Marker analysis detected 8 introgressions into the B genome of wheat.

c.*Triticum timopheevi* (AG genome) - Accession PI343447 was crossed onto the variety Crocus. After the first backcross, the population was advanced to F7 by SSD. Out of 535 lines evaluated for FHB resistance and agronomics, line TC67 was selected as the best. Its DON level was at approximately 7.7 ppm under conditions where Sumai3 was at 6.6,

Roblin at 35.0 and HY644 at 25.3ppm. The major QTL for this resistance was found on chromosome 5A, along with a weaker one on 5B. This line has been released as germplasm (Cao et al., 2009).

d. *Ae.cylindrica* (CD genome) - A number of resistant lines were selected out of hybrids with this species and crossed to Canadian cultivars. The most resistant lines have come from hybrids with Superb and Alsen. The DON levels of those lines ranged from 5.0 to 13.0 compared to the check cultivar Roblin at 11.0 ppm (the DON levels were very low in this test). The genomic constitution of *Ae. cylindrica* is CD. It is anticipated that unique resistance QTL(s) will be derived from this combination. Early indications are that resistance QTLs are present on chromosomes 3D, 4D, 5D & 6D.

e. *Triticale miguschovae* (AGD genome) - The resistant lines (F7) coming from crosses to AC Superb had a range in DON content of 3.5 to 8.2 ppm compared to the check cultivar Sumai3 at 2.7 and Roblin at 17.2. The construction of a mapping population is in progress.

f. *Elymus repens* (StStH genome) - A strain of *E. repens* was crossed onto the wheat variety Crocus and backcrossed once. The BC1 progeny were advanced to F7 by SSD. Sixteen lines were evaluated in the epiphytotic nursery for FHB resistance and agronomics. Ten lines with enhanced FHB resistance were selected. The F9 population contained some unusual segregates with chromosome numbers ranging from 42 to 52, 54 & 56. GISH analysis revealed various combinations of wheat and *Elymus* chromosomes and various translocations. The most promising line contained 42 chromosomes with a small terminal translocation at both ends of one chromosome pair.

B. Tetraploid wheat

a. *Triticum carthlicum* - A strain with FHB resistance also had black awns hence the same Blackbird. A mapping population was developed from a hybrid with Strongfield. The Type II resistance was mapping to chromosome 6B; to the same location as the 6B QTL in hexaploid wheat (Somers et al., 2006.). Another FHB resistance QTL was discovered in Strongfield that was mapping to chromosome 2A. A QTL for Type I resistance was also detected in this population, on chromosome 1A (Singh et al., 2008).

b. *Tritordeum* (ABH) - In our initial screening, it was difficult to find any FHB resistance among tetraploid wheats or their tetraploid relatives. A screening of available *Tritordeum* lines identified some with fair FHB resistance. One of these lines was crossed and backcrossed to durum cultivar Strong field. Three lines were selected out of F6 progeny. DON values for these lines ranged from 3.3 to 27.7 ppm compared to check varieties Strongfield at 14.1 and Roblin at 17.2 ppm.

C. *Thinopyrum elongatum* (E genome) as a source of FHB resistance

a.We have found, as have others, a high level of FHB resistance in the diploid species *Th. elongatum*. This resistance has been manifest in both durum and spring wheat backgrounds as amphiploids or addition lines. A high level of resistance was observed in an ABE amphiploid derived from crossing *Th. elongatum* onto durum wheat. We are in the process of producing E genome additions in a durum background. Our efforts at producing additions in the variety Strongfield were unsuccessful as all derivatives were totally sterile. However early generation progeny of hybrids between the ABE amphiploid and Langdon durum have fair fertility and are thus more promising. E chromosome additions are being identified by chromosome specific SSR markers. E genome substitution lines and disomic additions (as whole chromosomes or telocentrics) have been produced in a Chinese Spring background (Dvorak and Knott, 1974). Chromosome 7E as a disomic addition or substitution is the critical one with FHB resistance, more specifically; ditelo 7EL which carries the resistance gene(s). In our tests the FHB index levels in the various aneuploids are as follows. The FHB index in the ditelo addition was 9.6 compared to the parental cultivar CS at 57.5 and 7ES at 86.5 (unpublished data).Populations of recombinants are being produced.

b. GFP studies- QTL responsible for FHB resistance are generally scattered over many chromosomes (e.g. 3B, 5A, 6B, 2D etc.) so it was amazing that the ditelo addition 7EL had such a high level of resistance. To examine the infection process, a *F. graminearum* strain transformed with green fluorescent protein was used to inoculate ditelo addition 7EL and its parent cultivar Chinese Spring (CS) (Miller et al., 2011). The infection rapidly spread from the inoculated spikelet into the node and adjacent spikelets in CS. However, in the ditelo addition line, the infection was localized to the infected spikelet and infection totally blocked by the nodal tissue. The blockage was related to the deposition of an as yet unknown substance in the nodal tissue. It was also observed that the internodal segments were longer in the aneuploid. Thus it appears that the nodal tissue offers chemical and physical barriers to fungal growth.

c. RT-qPCR studies - In a parallel study, a reverse transcription quantitative polymerase chain reaction (RT-qPCR) was employed to examine expression levels of genes involved in plant defence responses in the 7EL addition line (Wang et al., 2010; Miller et al., 2011). Genes such as PR4 (pathogenesis related protein 4) and PAL (phenylalanine lyase) were up-regulated in the 7EL addition line while other genes such as EDS5 (enhanced disease susceptibility 5 positive regulator) and BLG-2 (beta-1, 3 glucanase), that are associated with the salicylic acid-induced defence mechanisms, were down regulated. It appears that the nodal tissues of 7EL are responsible for physical and chemical factors that restrict the spread of the fungal mycelia from the point of inoculation.

D. Biofungicides for control of FHB and DON in wheat

A formulated product of *Clonostachys rosea* strain ACM941-CLO-1 was found to control FHB symptoms and DON content in wheat in greenhouse and field trials (Xue et al., 2009). In greenhouse trials it reduced the AUDPC by 65.4-83.2%, FDK by 67.8-91.6% and DON content by 51.4-95.1%. Under field conditions the bioagent reduced the FHB index by 30.1-46.3%, FDK by 30.7-38.5% and DON content by 21.6-32.5%. The effects were lower than, but not statistically significantly different from those induced by the fungicide Folicur. CLO-1 was more effective on moderately resistant cultivars than on resistant or susceptible cultivars.

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CHANGING EXPRESSION TO MAKE SUSCEPTIBLE BREAD WHEAT RESISTANT TO FUSARIUM HEAD BLIGHT

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ABSTRACT

Fusarium head blight (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*. If altered expression, as much as genetic differences, account for the range of host response to *Fusarium* infection, changing the expression of existing genes may offer a useful alternative approach. Heritable traits have recently been shown to be capable of being evolved *de novo* in the descendants of germplasm subjected to systemic stresses. We took sublines (plants grown from seed of a single head) of the susceptible cultivar Roblin, 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 2009 FHB nursery. The two sublines which exhibited better resistance than relevant checks were advanced in cycles of further selection indoors in winter, and yielded families of sublines that were then tested in the 2010 FHB nursery. Among a wide range of responses, those sublines which performed well, and that were also members of families whose FHB index scores substantially bettered those of relevant checks, were subjected indoors to cycles of further selection, yielding sublines that were then entered in the 2011 field nursery. While the original Roblin progenitor scored 45, the best sublines scored between 0.5 and 6.0 which compares favourably with FHB index scores of between 0.5 and 1.0 for the most resistant checks. Roblin, widely used as a spring wheat 'susceptible check', thus appears to already contain genes which, suitably expressed, confer improved resistance that is both heritable and stable.

REVISITING AN EVOLUTIONARY APPROACH TO DERIVING FUSARIUM HEAD BLIGHT-RESISTANT LINES FROM ELITE DURUM GERMPLASM

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ABSTRACT

In 2007 we presented a new approach to improving the Fusarium head blight (FHB) resistance of durum wheat (*Triticum turgidum* L. var *durum*), a class without well-characterized sources of genetic resistance. The expression of genes in resistance pathways induced by *Fusarium graminearum* inoculation does not differ significantly among FHB-resistant Sumai 3 and its susceptible near-isogenic lines. Durum wheat lines might similarly already contain resistance genes induced by *F. graminearum* but remain susceptible because, unlike Sumai 3, they fail to express these genes effectively.

We had recently shown that growing successive generations of virus-susceptible wheat plants under pressure from seedling infection with wheat streak mosaic virus (WSMV) gave rise to lines with heritable variation in traits such as height, maturity and resistance to WSMV. Initially, we introgressed hexaploid sources of virus resistance; derived backcross generations were tetraploid and resembled durum wheat in all morphological and developmental traits. Selected individual BC_3F_5 lines (recurrent durum parent was Strongfield) had FHB index scores as low as 2.0 (compared with 43.1 for Strongfield) but this level of resistance was not consistently expressed in descendant generations.

To avoid possible effects of gene re-assortment we modified our methods to select for improved FHB resistance in generations of selfed descendants, and applied milder virus infection pressure in early cycles. Generations of sublines (plants grown from seed of a single head) that descended from breeding lines DT802 and DT809, as well as recently-registered Transcend were subjected to systemic stresses that included virus infection, heat and cold. In each cycle, we advanced the seed of individual plants that differed visibly from their progenitors in a range of traits including FHB resistance, which we evaluated for the first time in the 2009 FHB nursery. Following cycles of further selection indoors in winter, we advanced families of sublines to the 2010 FHB nursery and observed a wide range of responses. Sublines which performed well, and that were also members of families whose FHB index scores substantially bettered those of relevant checks, were subjected indoors to further cycles of selection, then entered in the 2011 FHB nursery. While Transcend, DT802 and DT809 scored 20, 22 and 25, respectively, the best sublines scored between 1.0 and 3.0. This compares with FHB index scores between 15 and 25 for the checks of the durum class, and 0.5 to 1.0 for the most resistant hexaploid checks. Durum germplasm appears to contain genetic information which, suitably expressed, confers improved FHB resistance that is both heritable and stable.

ASSOCIATION ANALYSIS OF FUSARIUM HEAD BLIGHT RESISTANCE IN RED SOFT WINTER WHEAT

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ABSTRACT

Fusarium head blight (FHB, caused by *Fusarium graminearum)* is a serious disease of wheat and barley with infection occurring during flowering and grain filling in wet weather. Infection is accompanied by production of the mycotoxin deoxynivalenol (DON), which can cause adverse effects in humans and livestock. Our objective was to detect QTL that control host resistance to FHB. We used a population of 449 soft winter wheat (*Triticum aestivum*) lines from the Ohio State University wheat breeding program that was genotyped with 1,820 DArT markers in an association analysis. Phenotypes were obtained from three rep RCBD trials conducted in inoculated misted FHB nursery in Wooster Ohio in 2010 and 2011. Resistance was assessed as a visual estimate of the percentage of symptomatic spikelets. This estimate was obtained at three areas of a plot. There was significantly greater disease pressure and heritability in 2010 than 2011. Thus we analyzed the data by year and overall. Significant ($P<0.01$) QTLs were detected in the population with more detected in the 2010 data than the 2011. The analysis over years was similar to the analysis using 2010 data only. There were 17 regions with evidence of QTL in the 2010 and overall analysis. These were located on chromosomes 1B, 2B, 3B, 3D, 4A, 4B, 5A, 5B, 6A, and 7A. The absolute value of the genetic value (a) for these significant regions ranged from 1.15 to 3.2 over years and thus the QTL had small effects. The largest effect QTL were located on chromosomes 1B, 2B, 3B, 4A, 4B, 5B. The frequency of the resistant allele at these regions was 0.82, 0.11, 0.91, 0.92, 0.94, and 0.06, respectively. We conclude that FHB resistance in this population is conferred by many QTL with small effects. Many of the notable alleles for resistance are already at a high frequency in this population. Marker-assisted selection could significantly impact FHB resistance by increasing the frequency of resistant alleles at regions such as those on chromosomes 2B and 5B. The results suggest that genomic selection may be well suited to improve FHB resistance in this population.

RESISTANCE TO DON APPLIED INTO WHEAT FLORETS AND TOLERANCE TO EFFECTS ON YIELD

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ABSTRACT

Deoxynivalenol (DON) is the most prevalent mycotoxin associated with wheat head blight caused by *Fusarium graminearum*. Because DON is toxic to plants and enhances the ability of the pathogen to spread within a spike, wheat lines with resistance to DON should be more resistant to head blight. Resistance to DON has been associated with resistance gene *Fhb1* that has been hypothesized to encode for or regulate the expression of a DON-glucosyl-transferase enzyme that converts DON to DON-3-O-glucoside and thereby slows the spread of head blight symptoms in wheat spikes (type II resistance).The objectives of this study were to determine if wheat lines resistant to head blight also were resistant to DON, if genes other than *Fhb1* confer resistance to DON, and to identify lines able to fill grain in the presence of DON. Susceptible checks and diverse American and European winter wheat lines with resistance to head blight were screened for molecular markers linked to known head blight resistance genes and were evaluated in a greenhouse for resistance to DON and for relative yield after application of DON to spikes at flowering. As measured by the number of DON-bleached primary florets, only wheat lines with *Fhb1* had resistance to DON, and *Fhb1* appeared to have the unique ability to confer resistance to DON. Given that *Fhb1* likely functions by converting DON to the masked mycotoxin, DON-3-O-glucocide, it is important to note that other unknown genes conferring high levels of resistance to spread within a spike have a different mode of action and are less likely to result in the accumulation of DON-3-O-glucocide in harvested grain. Based on the relative yield of treated spikes compared to non-treated spikes, *Fhb1* did not protect plants from the phytotoxic effects of DON on kernel formation, but several European wheat lines had significantly higher relative yields that may be associated with tolerance to FHB. Measuring the relative yield loss following DON application may be useful for identifying lines with tolerance to head blight.

QTL ASSOCIATED WITH FUSARIUM HEAD BLIGHT INCIDENCE AND SEVERITY IN TRUMAN SOFT RED WINTER WHEAT

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ABSTRACT

Fusarium graminearum Schwabe (teleomorph *Gibberella zeae* (Schwein.), the pathogen known to cause Fusarium head blight (FHB) or scab, is an increasingly important problem for wheat production in the north-central U.S. Host-plant resistance provides the best hope for reducing economic losses but sources of resistance are limited. 'Truman' soft red winter wheat has very good levels of each of the four components of FHB resistance including types I and II resistance, low DON and good kernel quality retention under disease pressure. Although haplotype data suggests that the resistance in Truman is genetically different from other known sources, it has not been genetically characterized. This research was conducted to identify QTL associated FHB resistance in Truman including: i) reduced initial infection; and ii) reduced disease severity in infected heads using a set of F_8 recombinant inbred lines (RILs) developed from the cross Truman/MO 94-317. Two years, (2 replications/location/year) of phenotypic data were collected for this study at Missouri, Purdue, and Kentucky. At Missouri, a macroconidial suspension concentrated 70,000 mL^{-1} was sprayed on each RIL at 75% flowering while grain spawn and/or corn residue provided inoculum at Kentucky and Purdue. Incidence and severity data were collected (from 10 heads/replication/RIL) at 10 and 21 days after inoculation as the number of heads and the number of spikelets in each diseased spike showing symptoms, respectively. For molecular marker analyses, genetic linkage maps were constructed from 161 SSR and 458 DArT markers using Joinmap 2.0. QTL analysis for individual replications and across replications was conducted using multiple interval mapping (MIM) with WinQTLCart 2.5. The critical LOD value to declare QTL significance was 3.2, based on 1000 permutations. Incidence data from Missouri and Purdue and severity data from Kentucky and Missouri were used for analyses. For FHB incidence, three QTL were identified on chromosomes 2AL, 2DLc, and 5DL from Missouri data that explained 9.8, 5.8 and 10.9 % of the phenotypic variation, respectively, while four QTL on chromosomes 3BLc, 5DL, 6DS, and 7DL were identified from Purdue data that accounted for 6.7, 9.1, 21.4, and 9.4 % of phenotypic variation, respectively. For FHB severity, three QTL on chromosomes 2DLc, 3BSc and 5DL were identified from Missouri data that accounted for 10.1, 9.5 and 7.3 of the phenotypic variation, respectively, while two QTL on chromosomes 2AL, and 3BSc explaining 7.2, and 7.9 % of the phenotypic variation, respectively, were identified from Kentucky data. All QTL were from Truman and were associated with reduced incidence and severity. The QTL on chromosomes 7DL, 5DL, and 6DS appear to be novel and should be valuable for marker-assisted pyramiding of FHB resistance alleles for incidence and severity.

QTL ASSOCIATED WITH KERNEL QUALITY RETENTION AND DON IN TRUMAN SOFT RED WINTER WHEAT

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ABSTRACT

Fusarium graminearum Schwabe (teleomorph *Gibberella zeae* (Schwein.), the pathogen known to cause Fusarium head blight (FHB) or scab, continues to impact wheat production in the north-central U.S. 'Truman' soft red winter wheat, developed and released by the University of Missouri combines very good levels of type I and II resistance with low DON and good kernel quality retention under disease pressure and thus is a valuable parent for soft red winter wheat breeding programs. Although haplotype data suggests that the resistance in Truman is genetically different from other known sources, it has not been genetically characterized. This research was conducted to identify QTL associated with kernel quality retention and low DON in Truman using a set of F_8 recombinant inbred lines (RILs) developed from the cross Truman/MO 94-317. Phenotypic data were collected over two years (2 replications/year) at three Midwestern locations including inoculated, misted nurseries at the University of Missouri, Purdue, and the University of Kentucky. Kernel quality was assessed as the percentage of *Fusarium* damaged kernels (FDK) from field inoculated, carefully threshed samples of seed from each RIL while the level of deoxynivalenol (DON) in seed of each RIL was determined at the University of Minnesota's DON testing laboratory under the direction of Dr. Yanhong Dong. For molecular marker analysis genetic linkage maps were constructed with 161 SSR and 458 DArT using Joinmap 2.0. QTL analysis for individual replications and across reps was conducted using multiple interval mapping (MIM) with WinQTLCart 2.5. The critical LOD value to declare QTL significance was 3.2, based on 1000 permutations. Four QTL associated with FDK were identified on chromosomes 1AL, 2AL, 2DLc, and 6BSc from Missouri data that explained 6.4, 6.9, 8.4 and 11.8 % of the phenotypic variation, respectively, while three QTL were identified from Kentucky and Purdue data. From Kentucky data, QTL on chromosomes 1Bc, 2ASc, and 6BSc accounted for 24.3, 8.8, 9.5 % of the phenotypic variation while from Purdue data three QTL on 2DL, 3BSc, and 7DL accounted 8.2, 8.2, 15.5 % of total phenotypic variation. For DON, four QTL on 2AL, 3BSc, 5DL, 6DS were identified from Missouri data that accounted for 13.5, 7.5, 15.9 and 20.9 % of the phenotypic variation in DON, respectively, while two QTL associated with DON reduction were identified from data from Purdue and Kentucky. From Kentucky data, QTL on 2ASc, 5DL accounted for 10.5 and 16 % of the variation while QTL on 2ASc, 3BL accounted 6.5, 45.3 % of the variation in DON based on Purdue data. All QTL were from Truman and were associated with reduced FDK and DON. Common QTL on 5DL, 6DS and 7DL appear to be unique and once further investigated, may provide breeders with novel genes associated with reductions in FDK and DON.

QTL ASSOCIATED WITH TYPE II FUSARIUM HEAD BLIGHT RESISTANCE IN TRUMAN SOFT RED WINTER WHEAT

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ABSTRACT

Fusarium graminearum Schwabe (teleomorph *Gibberella zeae* (Schwein.), the pathogen known to cause Fusarium head blight (FHB) or scab, is an increasingly important problem for wheat production in warm and humid regions of the world. To date, most advances in FHB-resistance breeding have been made through selection for type II resistance largely because this type of resistance is durable, reliably estimated, and less sensitive to non-genetic factors than other types of resistance. Combining type II FHB resistance from genetically different sources of resistance is expected to generate lines with higher levels of resistance, more effective resistance under high inoculum loads, and/or varieties in which resistance is more stable over broad geographic areas. This approach, however, is limited by a lack of highly effective, genetically different sources of type II resistance. 'Truman' soft red winter wheat has excellent type II resistance that, based on haplotype data, appears to be genetically different from other known sources of resistance. This research was conducted to identify QTL associated with type II resistances in a set of F_8 recombinant inbred lines developed from the cross Truman/MO 94-317. Two years (5 replications) of greenhouse type II phenotypic data were collected at the University of Missouri for this study. A Missouri isolate of *F. graminearum* previously tested for pathogenicity was used for all inoculations. Each plant was inoculated at first anthesis with 10 µL of a macroconidial suspension of this isolate concentrated to 50, 000 mL^{-1}. Inoculum was placed in the basal floret of a central spikelet. Plants were incubated in a mist chamber at 100% relative humidity for 72 h post-inoculation to initiate disease development and then returned to the greenhouse bench to enable disease development in the head. Ratings for type II resistance were taken at 21 d post-inoculation. Fusarium head blight severity was determined as the ratio of diseased spikelets to the total number of spikelets on the inoculated head expressed as percentage. Molecular marker analysis was conducted using SSR and DArT [Diversity Arrays Technology Pty Ltd, (Triticarte) Yarralumla, Australia] markers. Genetic linkage maps were constructed with 161 SSR and 458 DArT using Joinmap 2.0. QTL analysis for individual replications and across reps was conducted using multiple interval mapping (MIM) with WinQTLCart 2.5. The critical LOD value to declare QTL significance was 3.2, based on 1000 permutations. Type II resistance in Truman was highly heritable (75%) and appears to be conditioned by a minimum of 5 genes. Six QTL associated with type II resistance were identified on chromosomes 1AL, 1BC, 2BL, 2DS, 5DL, 6BSC that explained 12.6, 8.1, 9.8, 10.6, 8.3 and 7.0% of total phenotypic variation, respectively. All QTL were from Truman and were associated with reduced disease spread following point inoculation. QTL on 1AL and 5DL appear to be novel and therefore should be valuable for marker-assisted gene pyramiding for type II resistance.

FUSARIUM HEAD BLIGHT RESISTANCE IN US HARD WINTER WHEAT

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ABSTRACT

Fusarium head blight (FHB) is one of the most destructive diseases of wheat in humid and semi-humid wheat grown areas 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. Unfortunately, most hard winter wheat (HWW) cultivars grown in the Great Plains are susceptible to FHB, and FHB resistance in US HWW germplasm has not been well characterized. In this study, a collection of 364 US winter wheat elite breeding lines and cultivars, including 295 HWW and 69 soft winter wheat lines, was evaluated for FHB resistance in three greenhouse experiments and 207 of them were also evaluated in three field experiments from 2009 to 2011. In both conditions, about 1000 conidia were injected into a central spikelet of a spike at anthesis and the inoculated plants were misted by either keeping them in a moist chamber for 48 h after inoculation or misting the plots using sprinklers from heading to late dough stages. In field, Fusarium-infected corn kernels were scattered on the ground to facilitate natural infection. Number of symptomatic spikelets and total spikelets in an inoculated spike were counted to calculate percentage of symptomatic spikelets (PSS) at 18th day after inoculation in the greenhouse experiments and 21th day in the field experiments. The correlation coefficients of PSS among experiments were significant for both greenhouse and field experiments. Sumai3, SD06069 and Duster were designated as resistant (R), moderately resistant (MR), and susceptible (S) controls, respectively. All the accessions were classified into four classes (R, MR, MS, S) based on their PSS means and the 95% confidence intervals of each controls. Moderate resistance genotypes were estimated based on difference between MR and S. Only about one fourth of accessions tested showed either resistance (8%) or moderate resistantce (18%) to FHB in greenhouse experiments, indicating that most of the breeding lines or cultivars tested are susceptible or moderately susceptible. In HWW 20 showed a similar level of resistance to Sumai 3 in greenhouse experiments. Those accessions included some cultivars that were previously reported to have FHB resistance, such as Heyne, and newly identified resistant cultivars or breeding lines such as OK05134, T154, Century, Atlas66, etc. Those accessions can be useful sources for type II resistance in FHB resistance breeding. Forty-eight HWW accessions displayed moderate resistance to FHB and also can be useful parents for adding other exotic resistance genes. Among the 207 wheat accessions tested in field, 10% demonstrated a similar level of FHB resistance to Sumai 3, including 6 HWW. Some accessions showed contrasting reactions to FHB between greenhouse and field experiments. However, 8 accessions (OK05143, T154, T153, SD05210, KS970093-8-9-#1, Endurance, AP05T2413, HV9W02-942R) were identified to have resistance or moderate resistance both in greenhouse and field experiments. These accessions with consistent resistance in both field and greenhouse may have both type I and type II resistance and have potential to be released as FHB resistant germplasm or cultivars.

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PYRAMIDING QTLS IN SOFT RED WINTER WHEAT FOR ENHANCING FHB RESISTANCE IN SOUTH EAST US

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ABSTRACT

Severe epidemics of FHB have caused significant economic losses to Georgia's wheat producers for both grain yield and quality with high DON concentration. Development of resistant soft red winter wheat cultivars is the most efficient option to control FHB. Crosses have been made between local broadly adaptive cultivars AGS2000 or its derivatives and both exotic (derivatives of Sumai 3) and native resistant sources (Truman) to introduce FHB resistant QTLs into our widely local adaptive genetic background. Eight elite lines, GA04496-S6, GA041273-S14, GA041273-S15, GA04496-S5, GA04496-S8, GA051173W-S11, GA051173W-S12, GA051173W-S13, were evaluated in the field in 2011 for FHB resistance and agronomic performances with Ernie, Bess, Jamestown as resistant control and Coker 9835 susceptible control. SSR markers were also used to detect the resistant QTLs for FHB and other critical diseases. GA04496-S5, GA04496-S6, and GA04496-S8 maintained the Fhb1 from the resistant donor, VA01W476. However, the performance of scab resistance was not as reliable with only one QTL detected. Elite lines, GA051173W-S11, GA051173W-S12, and GA051173W-S13, which were 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 three elite lines also included two important resistant genes for Hessian fly (H13) and leaf rust (Lr37/Yr17/Sr38). GA051173W-S11 produced higher yield and test weight than the check AGS2035. Yield reduction of 42-53% was observed in exotic *Fhb1* carrying lines. *Fhb1* in the presence of the semi-dwarf gene, Rht-D1, did not provide a high level of resistance. Pyramiding QTLs will be necessary with the presence of Rht-D1. The native source provided good resistance for soft red winter wheat improvement in the presence of the Rht-D1 gene.

CHARACTERIZATION OF FUSARIUM HEAD BLIGHT RESISTANCE IN SOFT RED WINTER WHEAT LINE VA00W-38

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ABSTRACT

Many quantitative trait loci (QTL) in wheat (*Triticum aestivum*) conferring resistance to Fusarium head blight (FHB), caused by the pathogen *Fusarium graminearium* Schwabe [telomorph: *Gibberella zeae* Schw. (Petch)], have been mapped in diverse genetic backgrounds. Most of the FHB resistant wheat sources are either spring types such as 'Sumai 3' and its derivatives or European wheat lines. Use of these non-adapted FHB resistance sources by breeding programs in the soft red winter (SRW) wheat region of the U.S. has not been very successful in improving FHB resistance. Native sources of FHB resistance are used predominantly in the SRW wheat breeding programs as cultivars with FHB resistance have been identified and/or validated in uniform FHB screening nurseries in diverse environments. The Virginia Tech breeding line VA00W-38 has moderate FHB resistance and does not possess any previously identified exotic sources of resistance in its parentage. A set of 182 recombinant inbred lines (RILs) were developed and tested in field scab nurseries at Blacksburg and Warsaw, VA. The FHB related traits evaluated in the study were disease incidence (INC), severity (SEV), index (IND), *Fusarium* damaged kernels (FDK), thousand kernel weight (TKW), and deoxynivalenol (DON). Six consistent QTL were identified on chromosomes 1BL, 1D, 2B, 3BS, 6A and 6BS and explained 6.6% to 15.8% of the phenotypic variation. Eleven other tentative QTL were detected in one environment and explained 7.8% to 20.2% of trait variation with favorable alleles of VA00W-38 associated with lower FHB and higher TKW. Tightly linked markers identified for these consistent and tentative QTL can be used to select for favorable alleles associated with FHB resistance in breeding populations.

MAPPING FUSARIUM HEAD BLIGHT RESISTANCE IN WHEAT CULTIVARS ERNIE AND MASSEY

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ABSTRACT

Many quantitative trait loci (QTL) for resistance to Fusarium Head Blight (FHB), caused by *Fusarium graminearum* Schwabe, in wheat (*Triticum aestivum* L.) have been identified in diverse sources worldwide. However, most research has been conducted in spring wheat sources, such as the Chinese cultivar Sumai 3, which has been widely used in spring wheat regions. In the soft red winter (SRW) wheat regions of the U.S., FHB resistance derived from locally adapted germplasm has been used predominantly in breeding programs. Two SRW wheat cultivars, Massey and Ernie, have moderate resistance to FHB. A set of 152 $F_{7:14}$ recombinant inbred lines (RILs), derived from the cross 'Becker'/Massey (BM) and 231 RILs from Ernie/MO 94-317 (EM), were evaluated for FHB resistance in nine environments during three years. A total of 32 QTL associated with FHB resistance and other related traits were identified in the BM and EM populations. Six common QTL associated with FHB resistance among the two populations are located on chromosomes 2BL, 2DS, 3BL, 4BS, 4DS, and 5AS. Their LOD scores ranged from 2.6 to 31.3 with R^2 values of 3.3% to 36.5%. Eight QTL in BM and four QTL in EM populations were consistently associated with more than two FHB resistance traits or with one trait in multiple environments. QTL associated with higher thousand kernel weight in both populations were identified on chromosomes 2BL, 4BS, 4DS, and 5AS, and another common QTL on chromosome 4DS was associated with a lower number of *Fusarium* damaged kernels (FDK). Favorable alleles for these common QTL can be enriched in breeding populations via marker assisted selection (MAS) to enhance the FHB resistance in winter wheat.

GENETIC CONTROL OF FUSARIUM HEAD BLIGHT IN THE NC-NEUSE X AGS2000 RECOMBINANT INBRED POPULATION

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ABSTRACT

Fusarium Head Blight (FHB) infests North Carolina wheat fields annually. Severe epidemics of FHB can result in substantial reductions in grain yield, test weight and end-use quality. Resistance to FHB is quantitatively inherited and phenotyping is labor intensive. The North Carolina cultivar NC-Neuse has consistently exhibited moderate levels of resistance to FHB and the cultivar AGS2000 has consistently exhibited susceptibility to FHB. A recombinant inbred population consisting of 182 $F_{5:6}$ lines from the cross of NC-Neuse x AGS2000 was genotyped using DArT and SSR markers, and assessed at one field location in the 2010-2011 field season for FHB infection severity (Type II resistance) as well as *Fusarium* damaged kernels (Type IV resistance) and deoxynivalenol toxin (DON) (Type III resistance). An update of pertinent results will be presented.

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MAPPING OF THE WUHAN-1 CHROMOSOME 2DL FHB QTL IN A UNIFORM GENETIC BACKGROUND

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ABSTRACT

Fusarium head blight (FHB) resistance is a key breeding objective for wheat breeding programs globally. Breeding FHB resistance is difficult because of complex genetics and random variability in phenotyping, which results in experiment error. Marker-assisted selection promises to improve selection efficiency but requires markers known to be tightly linked to the gene(s) of interest. The Wuhan-1 FHB resistance QTL on chromosome 2DL was mapped in a uniform genetic background to improve the resolution of QTL location and identify additional SSRs that will be useful in Canadian germplasm. An F_2 population was developed from a single BC_2F_1 plant (pedigree: CDC Alsask*3/HC374) that was fixed with FHB susceptibility alleles at 3BS (*Fhb1*), 6BS (*Fhb2*), 4B, and 5A. HC374 is a DH line from the cross Wuhan-1/Nyubai, which carries the 2DL QTL. The F_2 population was genotyped with the SSRs wmc144 and gwm608, which flank the 2D QTL. Fifty-eight fixed recombinants were identified and subsequently genotyped and evaluated for FHB incidence, severity, and *Fusarium*-damaged kernels (FDK) in five field FHB tests. A linkage map was developed consisting of 17 SSRs. QTL analyses identified the location of the QTL on the genetic map and confirmed the significance of the QTL based upon FHB incidence, FHB severity, FHB index, and FDK. In the original mapping population, the 2D QTL was detected by single-floret injection only and not detected in FHB field tests or DON accumulation in harvested grain. These results indicate that a near-isogenic background is critical for map-based cloning efforts of FHB QTL.

THE 2010-11 UNIFORM 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 2010-11 nursery comprised 56 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 2011 National Fusarium Head Blight Forum and subsequently on line at the USWBSI web site: http://www.scabusa.org/.

ACKNOWLEDGEMENT AND DISCLAIMER

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

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

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

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

VALIDATING DEOXYNIVALENOL QTL PREVIOUSLY IDENTIFIED THROUGH ASSOCIATION MAPPING USING NEAR ISOGENIC BARLEY

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ABSTRACT

Association mapping (AM) is a powerful tool for utilizing diverse genotypic and phenotype data for marker-trait associations. AM's ability to dissect complex polygenic traits including resistance to Fusarium head blight (FHB) and deoxynivalenol (DON) accumulation in barley makes it a promising QTL identification strategy. Despite its potential, few studies have tested the approach; even fewer results have been confirmed. Validation of potential QTL is especially important due to the inherent need to account for population structure when drawing from diverse germplasm resources, potentially resulting in spurious associations if not properly accounted for. The size of allelic effects further complicates analysis, as few large effects QTL are more likely to be detected than the likely many with small effects. Avoiding the deployment of false positive QTL in breeding populations, and identifying as many regions of the genome that contribute to resistance as possible will enable researchers to concentrate on true associations, and subsequently release better varieties for farmers.

A previous AM study by Massman et al. (2011) identified 4 and 8 major QTL for FHB and DON accumulation, respectively from a diverse barley Coordinated Agricultural Project (CAP) breeding population. This study aims to validate those major (and several other minor) DON QTL in 6 row spring barley using near isogenic lines (NILs) derived from the same AM population. 48 informative barley SNPs from a pool of 3,072 barley OPA markers were selected to genotype the progenies of 30 barley CAP lines from the University of Minnesota and North Dakota State University breeding programs. These lines were selected based on heterozygous loci within the QTL regions of interest. After genotyping, 18 out of 30 informative NIL pairs with contrasting alleles were used to evaluate 10 DON QTL regions. The lines, planted in summer 2011 in St. Paul MN, Crookston MN, and Osnabrock ND, were inoculated with several isolates of *F. graminearum* followed with mist irrigation to facilitate disease development. Seed from the trials was harvested, processed, and analyzed for toxin concentration. Comparing lines with contrasting alleles in an essentially fixed genetic background will localize the observed effects to one region of the barley genome. If differences in DON accumulation are detected between NIL pairs, it is probable the QTL from the original AM study is involved in disease severity. FHB results from the summer 2011 disease nurseries will be reported, as well as preliminary DON analysis from Saint Paul.

REFERENCES

Massman J, Cooper B, Horsley R, Neate S, Dill-Macky R, Chao S, Dong Y, Schwarz P, Muehlbauer GJ, and Smith KP (2011) Genome-wide association mapping of Fusarium head blight resistance in contemporary barley breeding germplasm. Molecular Breeding 27(4): 439-454

A SINGLE KERNEL NEAR-INFRARED (SKNIR) TECHNIQUE FOR COMPREHENSIVE EVALUATION OF FUSARIUM HEAD BLIGHT (FHB) RESISTANCE IN WHEAT GERMPLASM AND FOR EVALUATION OF FUNGICIDE TREATMENTS FOR MANAGING FHB IN WHEAT

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ABSTRACT

Deoxynivalenol (DON) content and percentage *Fusarium* Damaged Kernel (FDK) are often used for evaluation of FHB damage in wheat. Single kernel analysis of DON levels in a bulk sample can provide more detailed information on the concentration and distribution of DON levels among kernels in the sample. We describe a NIR spectroscopic method to estimate bulk DON content based on single kernel DON levels in small grain samples for evaluation of the effect of varieties and/or fungicides for FHB disease management.

This method is demonstrated using two wheat varieties (FHB moderately resistant Everest and FHB susceptible Tomahawk) grown in 2009/2010 (2010) and 2010/2011 (2011) with or without fungicide "Prosaro" application to control FHB. Each variety-fungicide treatment combination had four replicates. A subsample of grains of about 80-90 g, enough to fill a petridish, was drawn from the harvested grain and cleaned to remove chaff and other debris besides scabby kernels. About 50 g of those cleaned kernels were loaded to the single-kernel near infrared (SKNIR) instrument for automatic selection, analysis of DON concentration, and sorting of 500 randomly selected kernels into four bins. Kernels without any detectable DON sorted into Bin 1 were regarded as sound. Those kernels with increasing levels of DON sorted into Bins 2 - 4 were regarded as DON containing kernels (DCK). The number and weight of kernels sorted into each bin were recorded. The average weight of kernels in each bin was used to estimate the DON content in single kernels in μg/kernel. The DON contents in kernels were plotted against percentage of kernels to visualize the single kernel DON distribution among kernels in the sample.

Overall DON levels were lower in 2011 compared to 2010. Variety Tomahawk contained a higher percentage of DCK than variety Everest in both years. Application of fungicide Prosaro in 2010 notably reduced DCK in variety Tomahawk from 32.3% to 19.6% while the change in variety Everest was from 6.4% – 5.7%. Fungicide application in 2011 brought down DCK in variety Tomahawk from 7.0% to 4.0% while that for variety Everest was lowered from 1.8% to 1.4%. These results show that the effects of fungicide on reducing the percentage of DCK and the effects of fungicide was more pronounced in FHB susceptible variety Tomahawk when FHB disease pressure was high in 2010.

The above SKNIR method to estimate bulk DON content was further validated by comparing the SKNIR estimated DON content in 160 bulk kernel samples with the DON levels of subsamples determined by the

standard GC-MS method. The SKNIR method predicted the bulk DON content with Root Mean Squared Error of Prediction (RMSEP) = 4.98 ppm, bias= -1.04 ppm and R^2=0.35 (P-value < 0.001). Removal of 5 outliers reduced RMSEP to 3.69 ppm with bias = -1.62 ppm and R^2 = 0.43 (P-value < 0.001).

Above results show that bulk DON levels of small kernel samples can be estimated fairly well by the SKNIR method. Single kernel DON distribution among kernels can provide more insight into how DCK contribute to the final DON levels of harvested grain. Two samples having the same DCK and bulk DON levels can also be distinguished based on DON distribution patterns among kernels.

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STUDY OF INFRARED SPECTRAL PROPERTIES OF GERM, BRAN AND ENDOSPERM SECTIONS OF SOUND AND FUSARIUM DAMAGED WHEAT KERNELS

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ABSTRACT

Spectroscopic methods for estimating deoxynivalenol (DON) levels in single kernels of wheat should be able to see *Fusarium* mycotoxin DON in infected grains. Experiments were conducted to study the mid infrared (MIR) spectra of wheat kernel parts of sound and *Fusarium* damaged kernels (FDK). The objective of this study was to identify spectral differences of sound and FDK kernel parts.

Wheat germ, bran and endosperm sections from three different kernels each of sound and FDKs of wheat varieties Everest (FHB resistant) and Tomahawk (FHB susceptible) were dissected under a microscope. The dissected sections were immediately scanned using the Universal Attenuated Total Reflectance accessory of the Perkin Elmer Spectrum 400 FTIR/FTNIR spectrometer in the 4000-380 cm^{-1}spectral region. The spectrometer conditions used were resolution = 2 cm^{-1}, data interval= 0.5 cm^{-1}, mirror speed = 0.1 cm/s and 10 scans were averaged to get the final spectrum for each kernel section.

The MIR spectra showed that bran of FDKs were considerably different from the bran of sound kernels and the differences were more pronounced in FHB susceptible variety Tomahawk compared to the FHB resistant variety Everest. Likewise, some changes were also noted in the spectra of wheat germ from FDK and sound kernels. In contrast, the spectra of endosperm of sound and FDK of both varieties did not have noticeable differences. Probably the endosperm is not greatly altered by the actions of fungi or fungal metabolites due to *Fusarium* infection on the surface of the kernel.

The observed spectral differences in bran and germ of FDK and sound kernels may be caused by *Fusarium* fungi and DON. Therefore, as the next step these observed spectral differences should be studied in comparison with the MIR spectra of *Fusarium* mycelia and DON to see which of those observed differences are brought about by DON.

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FUSARIUM HEAD BLIGHT RESISTANCE IN TWO DURUM WHEAT BACKCROSS DERIVED INBRED LINE POPULATIONS

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ABSTRACT

Fusarium head blight (FHB) causes extensive losses in wheat and barley estimated to be ~3 billion dollars in 1990s across the United States. 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 (*Triticum turgidum* ssp. *Durum* (Desf.) MacKey) 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 showed promising amounts of resistance comparable to the hexaploid sources. They have shown consistent Type II resistance to FHB in the field and greenhouses during several years of experiments and have been used by the NDSU durum wheat breeding program. To incorporate the new sources of FHB resistance two populations of 174, and 171 backcross derived inbred lines (BC1F6) were developed by crossing Tun108 with durum wheat cultivars "Ben" and "Lebsock". Using single-spikelet inoculations and corn kernel infection methods, both populations were evaluated for type II FHB resistance for two seasons in the greenhouse and two seasons in the field nursery. Disease incidence and severity were assessed by visual scoring. The analysis of variance for type II FHB resistance showed significant effects for different environments, different genotypes and also genotype and environment interactions (GxE). There was a significant positive correlation between the FHB infection rates of the lines in the greenhouse and field seasons while there was no correlation between the field and greenhouse data. We observed transgressive segregation for FHB resistance genes in both populations. The parents of crosses had the infection rate of 50-80% while some progenies (~15% of the population) were even better than resistant parents and some were better than well-known resistant hexaploid wheat "sumai 3".

DArT (Diversity Array Technology®) analysis resulted in 308 polymorphic loci in Tun108×Lebsock and 280 polymorphic markers in Tun108×Ben. The markers mapped across the genome with higher density on chromosomes 3B, 4A and 1A. We are in the process of analyzing the data for the detection of main effect quantitative trait loci (QTL) involved in the genetic control of FHB in these two populations. As we had a significant GxE interaction, multi-location data will also be used to identify the QTL involved in epistatic and environmental interactions using QTLNetwork which is based on mixed model composite interval mapping. Comprehensive data will be presented in FHB forum in near future.

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EVALUATION OF GENOMIC PREDICTION METHODS FOR FUSARIUM HEAD BLIGHT RESISTANCE IN WHEAT

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ABSTRACT

Breeding for resistance to Fusarium Head Blight (FHB) is slow and costly because it is quantitatively inherited and difficult to evaluate accurately. A new marker assisted breeding method, genomic selection (GS), is suited for quantitative traits, and could potentially accelerate breeding for FHB resistance. GS involves predicting breeding values based on genome-wide markers using a model trained with phenotypic and genotypic data. In this paper we used data from the cooperative Fusarium head blight (FHB) nurseries across the United States to evaluate prediction accuracies for FHB resistance traits: severity (SEV), incidence (INC), *Fusarium* damaged kernels (FDK), and incidence/severity/kernel quality index (ISK), as well as deoxynivalenol levels (DON) and days to heading (HD). For all traits we compared prediction accuracies of four different GS models: Ridge-Regression (RR), Bayesian-Lassso (BL), Reproduction Kernel Hilbert Spaces Regression (RKHS), Random Forest Regression (RF), and one multiple linear regression model (MLR). In addition, we compared prediction accuracies using three different marker sets: genome-wide markers, FHB QTL targeted markers only, and both sets combined. GS accuracies were always higher than MLR accuracies, and except for DON, using QTL targeted markers alone always led to significantly lower accuracies. For DON we also evaluated prediction accuracies achieved from using phenotypes for correlated traits: SEV, INC, FDK, and ISK, as well as a RF model combining markers and ISK as predictors. Using markers targeted to QTL and ISK in a RF model, we achieved a mean accuracy of 0.641 for DON. Our results showed that we can expect genetic gain from implementing GS for FHB resistance in this germplasm, and for DON, we can expect equal genetic gain per cycle and greater genetic gain per unit time with GS compared to selection based on correlated traits.

EVALUATION OF FHB RESISTANCE AND AGRONOMIC PERFORMANCE IN BACKCROSS AND FORWARD-CROSS POPULATIONS

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ABSTRACT

Breeding for Fusarium Head Blight (FHB) resistance is one of the most efficient approaches to reducing FHB damage in wheat and barley. 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. F2 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 F2 derived lines was assessed in a misted, inoculated scab nursery. Backcross-derived progeny from four genetic backgrounds were planted in replicated plots and in the scab nursery at Lexington, KY in 2011. Traits measured included rating (1-9), severity, incidence, FHB index (severity * incidence) and FDK (*Fusarium* damaged kernels). FDK and DON (deoxynivalenol) were predicted with Near Infrared Reflectance (NIR) and compared with actual values. One of our objectives was to explore the utility of F2 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 by 17%, 24%, 33% and 39% in the four populations. Severity and rating were significantly ($P \leq 0.05$) reduced by the presence of resistance alleles, except in one population. In some cases where the average QTL effect was not significant, there was significant ($P \leq 0.05$) variation among F2:4 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 0.31 to 0.69 across the four populations. Correlations between DONNIR and FDK ranged from 0.41 to 0.62 among populations. BC1F3 lines revealed that one backcross had restored yield potential. In each population there were lines with yields not significantly different from the commercial checks used in the experiment. In population 2, almost 44% 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. F2 populations should be used for genotyping, ensuring QTL are effective before extensive backcrossing.

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INVESTIGATION OF A POTENTIAL INHIBITOR OF *FHB1* IN HEXAPLOID WHEAT

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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), but also contributes to other types of resistance. While investigating *Fhb1* candidate genes as part of our ongoing efforts to clone this gene, we discovered that the recipient genotype, 'Bobwhite' inhibited 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 case of *Fhb1*, supported by these other findings, seems to indicate the interaction of either a gene inhibitor or susceptibility factor with the major resistance gene, conferring the segregating response. In order to uncover the locus or loci responsible for this, we generated a recombinant inbred mapping population of 129 $F_{5:6}$ lines from the cross between '260-2' (near isogenic line containing *Fhb1* from the Sumai3/Stoa//MN97448 background) and 'Bobwhite' (negative for *Fhb1* resistance allele) that are homozygous positive for the *Fhb1* resistance allele. Two seasons of Type II resistance screening were undertaken in the greenhouse using single-floret (point) inoculations, with the percent spread used as the phenotypic trait. Replicated field trials were conducted in 2011, in St. Paul, MN, using both the mapping population and a population of 114 $F_{5:6}$ RIL's from the same cross that were homozygous negative for *Fhb1*. Symptomatic spikelet counts were taken at 14 and 21 dai to estimate FHB severity and fungal spread. Visually scabby kernel assessments and thousand grain weights on the harvested grain were recorded, and deoxynivalenol content will be quantified. Phenotypic segregation patterns indicate 1-2 genes likely controlling inhibition of *Fhb1*. These data will be used for QTL mapping to see if the resistance types identified in the field are coincident with the QTL identified for Type II resistance in the greenhouse. Genotyping is underway using the 9K SNP Infinium assay, and QTL mapping will subsequently be used to identify genomic regions controlling FHB resistance. Even if these field data are uninformative for mapping purposes, they should enable us to better postulate whether the loci identified are acting as inhibitors of *Fhb1*, or as susceptibility factors.

GENOMIC SELECTION FOR FUSARIUM HEAD BLIGHT RESISTANCE IN BARLEY

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ABSTRACT

Fusarium head blight (FHB) resistance in barley has relatively low heritability, is difficult and expensive to phenotype in the field, and is correlated with unfavorable traits such as late flowering, tall plant height, and high grain protein concentration. Phenotypic breeding efforts have produced advanced breeding lines and one new variety with improved resistance. However, these efforts required a minimum of three breeding cycles from the exotic source of resistance to produce an acceptable variety. Several large effect QTL that are coincident with morphological traits as well as many small effect QTL that are not detected consistently across environments or mapping populations have been identified. Association mapping studies with elite breeding germplasm indicate multiple QTL with relatively small effects are segregating in breeding populations and thus suggest that genomic selection (GS) may be more effective than traditional MAS. In addition, inexpensive and high-throughput genotyping platforms has made GS more feasible. While traditional MAS requires QTL identification and subsequent marker-based selection of few targeted QTL, GS uses large sets of markers to estimate breeding values of individuals for complex traits. The primary advantage of GS is selecting parents much sooner in the breeding process, and therefore, drastically reducing the length of the breeding cycle and increasing gain per unit time. The key to success of GS is training accurate models using marker and phenotype data sets to predict breeding values. We have evaluated various parameters of training data sets including population size, composition, and marker number to examine their effects on accuracy. Using cross validation, we find model accuracy for FHB severity is about 0.6. We also find that training populations of as few as 200 individuals and marker sets of 384 SNPs can be used to generate accurate predicted breeding values. We have implemented GS in a barley breeding population that was generated by crossing elite parents from three Midwest breeding programs to enhance FHB resistance. Our first cycle of GS was conducted in the fall of 2010 with 384 markers on ~1400 F3 breeding lines. Data collected in 2011 is being used to assess the effectiveness of selection and genetic gains.

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PRELIMINARY EVALUATION OF GENOMIC SELECTION FOR FHB RESISTANCE AND OTHER TRAITS

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ABSTRACT

Resistance to Fusarium Head Blight is a complex trait. While a few major genes for resistance have been identified in Asian varieties, the majority of the genetic variation appears to be controlled by genes with small effects and thus not amenable to manipulation by traditional marker-assisted selection (MAS). Genomic selection (GS) is a form of MAS that has applications to traits controlled by many genes of small effect. In GS individuals are genotyped with markers that cover the entire genome. All markers are included in a model that predicts the breeding value of the individuals. Our objective was to assess the ability of GS to predict the genetic value of individuals for FHB resistance as well as yield and two quality traits. We phenotyped and genotyped 449 soft red winter wheat breeding lines from the Ohio State University wheat breeding program. The lines were genotyped with 1820 DArT markers. They were phenotyped for FHB in a total of two environments, yield in six environments, and quality in two environments over the 2009-2010 and 2010-2011 seasons. Predicted breeding values were modeled using ridge regression and Bayes-B. Results will be presented.

REPORT ON THE 2010-11 NORTHERN UNIFORM WINTER WHEAT SCAB NURSERIES (NUWWSN AND PNUWWSN)

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OBJECTIVES

This is a summary of the report on the 2010-11 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 2011 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 are listed in Table 1. The 60 entries in the NUWWSN came from 12 programs while the 40 entries in the PNUWWSN entries came from eight programs (Table 2).

RESULTS

Many entries in the NUWWSN showed very good resistance to FHB. Nearly 27% (16/60) of the NUWWSN entries were not significantly different from the most resistant entry for six of seven FHB traits while 35% of the PNUWWSN were not significantly different from the most resistant entry for six of seven FHB traits. Over 78% of the entries in both tests had an FHB Index that was < than that of the moderate resistant check (Freedom), though none had a lower index than Truman. In the NUWWSN, 28% of the entries had less DON than Truman while 40% of the PNUWWSN entries had less DON than Truman.

Table 1. Traits assessed in the 2010-11 PNUWWSN and NUWWSN tests.

Code	Trait	Description
SEV	Disease severity from field tests	% of infected spikelets in an infected head.
INC	Disease incidence	% of heads with at least one infected spikelets
IND	Disease index	IND = (SEVxINC)/100
FDK	Fusarium damaged kernels	Percentage of grain ishowing sypmotoms of Fusarium infection
ISK	Composite of head and kernel traits	ISK Index = .3 (Severity) + .3 (Incidence)+.4 FDK)
DON	DON (vomitoxin)	PPM of vomitoxin in grain
GH	Greenhouse severity	Same as SEV except from greenhouse

Table 2. Entries in the 2010-11 PNUWWSN and NUWWSN.

	NUWWSN	
1	ERNIE	
2	TRUMAN	
3	FREEDOM	
4	PIONEER2545	
5	NY99066-3025	NY87048W-7387/Mendon
6	OH751	10584-08-01 / Coker9663
7	NY99068-383	NY87048W-7387/P25W33
8	NY93246SP-6093	Harus/3/92145:91009(Geneva/U1273-5-18-8)/NY73116-4W
9	E6012	Caledonia / Pioneer Brand 25W33
10	E6032	Pioneer Brand 25W33 / Pioneer Brand 2552
11	E9022R	Pioneer Brand 2552/D8006
12	E9024R	Pioneer Brand 2552/Pioneer Brand 25R18
13	OH05-200-74	OH629/HOPEWELL
14	OH06-150-57	P.92201D5-2-29/OH708
15	OH06-180-57	KY90C-042-37-1/OH687
16	OH07-98-21	FOSTER / IL95-947
17	OH07-166-49	OH708 / OH684
18	03633A1--5	992059/INW0316//981358/97462
19	04704A1--1	INW0316/INW0304//9346/INW0301
20	04606A1--7	Truman/INW0316
21	05247A1--3	99840*2/03726//99794
22	05264A1--2	INW0304*2/03727/5/96169/3/Tadinia/BH1146//Geneva/4/INW0316
23	M05-1526	FFR502/P931765C-H21
24	M08*8005#	BRANSON/M99*3098
25	M08-8036#	COKER 9511/BRANSON
26	M08-8214	COOPER/PIO2552
27	M08-8349	M99-2418/PATTON
28	RCUOG1	Vienna x AC F1 19/4C
29	RCUOG2	RCL33xRCS 115
30	RCUOG3	Bezostaja x DH TF 203/2
31	RCUOG4	23/3 X Amigo
32	RCUOG5	TF174 x SD97060
33	IL06-14262	IL00-8530 /IL97-1828
34	IL06-14325	IL 00-8530 / IL97-1828
35	IL06-13721	IL00-8530 / IL97-3632
36	IL06-13708	IL00-8530 / IL97-3632
37	IL04-24668	IL98-13404 / IL97-3578
38	KY02C-1002-06	KY93C-0876-66-1//Tribute /KY92C-0168-95
39	KY03C-1237-32	25R18/92C-0017-17//KY96C-0767-1
40	KY02C-2216-05	Tribute/25W60
41	KY03C-1075-04	25R44/Tribute//KY96C-0769-3
42	KY-03C-2047-06	Roane/McCormick
43	MD03W485-10-9	USG3209/TRIBUTE//MD71-5(USG3342"S")
44	MD03W61-10-2	25R42/CHESAPEAKE
45	MD03W69-15	McCormick/25R42
46	MD03W61-09-7	25R42/CHESAPEAKE
47	MO080104	L910097/MO 92-599
48	MO081652	Pioneer 2552/MO 980829
49	MO080589	KY 90C-383-18-1/IL 94-1653
50	MO081777	Pioneer 2552/MO 980829
51	MO080789	MO 980525//MO 981020/IL95-4162
52	NE01481	
53	NE02558	
54	NE05548	
55	NE06469	
56	NE07444	
57	VA08W-176	KY96C-0079-5 / McCORMICK,F9
58	VA08W-294	SS 520/ VA99W-188 //TRIBUTE
59	VA09W-657	NEUSE/ VA99W-200 //McCORMICK,F10
60	VA09W-659	NEUSE/ VA99W-200 //McCORMICK,F10

	PNUWWSN	
1	ERNIE	
2	TRUMAN	
3	FREEDOM	
4	PIONEER2545	
5	E9020R	Pioneer Brand 2552/D8006
6	E9021R	Pioneer Brand 2552/D8006
7	E9009	D6234/E0029
8	M09-9804#	TRUMAN/COKER 9511
9	OH07-166-41	OH708 / OH684
10	OH07-254-11	OH728 / VA97W-361WS
11	OH07-263-3	OH748 / BRAVO
12	OH08-133-25	HONEY / COKER 9663
13	OH08-269-58	P.92226E2-5-3 / OH708
14	05251A1--5	INW0412*2/03705//981312
15	05269A1--1	INW0316*2//INW0304/9346/3/Arina/INW0301//M-6synthStb8/981004
16	06497A1--3	INW0412/B990081//0128
17	0711A1--1	92829/A941048/3/Gfd/X117//Roane/92145
18	0724B1--13	INW0731/OH904
19	M08-8352	M99-2418/PATTON
20	IL07-4348	P96169RE2-3-6-4 / IL01-34159
21	IL07-4415	P96169RE2-3-6-4 / IL01-34159
22	IL07-7525	IL97-1828 / IL99-12976
23	IL07-14547	IL01-5642 / IL01-3570
24	IL07-19334	IL01-36115 / IL79-008T-B-B
25	KY03C-2047-07	Roane/McCormick
26	KY04C-2023-18	VA97W-375WS/Truman
27	KY04C-2034-2	Truman/KY93C-1238-17-5
28	KY04C-2034-3	Truman/KY93C-1238-17-5
29	KY04C-2034-4	Truman/KY93C-1238-17-5
30	MO080241	MO 980521/MO 971215
31	MO090862	MO 980725/Sumai 3
32	MO090577	L910097/MO 92-599
33	MO090812	MO 980829//MO 980725/IL95-4162
34	MO091122	Ernie/Colorben 4
35	VA08W-632	OH 552/SS550//RC STRATEGY
36	VA09W-608	97397B1-4-5/McCORMICK// B980582
37	VA09W-635	COKER 9474/ McCormick "S" // ERNIE,F10
38	VA09W-636	ERNIE/ NC96-13374(SCAB RES) //McCORMICK
39	VA09W-644	ERNIE/ NC96-13374(SCAB RES) //McCORMICK
40	VA09W-654	VA98W-749/IL96-3073(SCAB RES) //9793A1-5

Table 3. Best (top) and worst (bottom) entries from the 2010-11 NUWWSN.

ENTRY	NAME	INC	SEV	IND	FDK	ISK	DON	GHSEV	#l	#h
2	TRUMAN	36.6 l	16.5 l	6.7 l	8.7 l	22.5 l	3.6 l	6.4 l	7	0
48	MO081652	40.0 l	13.8 l	6.8 l	11.9 l	27.0 l	1.7 l	3.8 l	7	0
51	MO080789	37.6 l	18.4 l	6.8 l	10.7 l	25.8 l	2.7 l	11.3 l	7	0
47	MO080104	43.0 l	15.3 l	7.5 l	13.2 l	24.6 l	2.2 l	13.9 l	7	0
50	MO081777	45.0 l	15.2 l	7.7 l	13.3 l	25.7 l	2.0 l	5.7 l	7	0
49	MO080589	36.4 l	14.3 l	7.8 l	12.5 l	23.8 l	3.7 l	15.7 l	7	0
25	M08-8036#	44.0 l	17.8 l	8.7 l	13.5 l	26.5 l	1.6 l	15.1 l	7	0
26	M08-8214	45.3 l	16.3 l	9.3 l	13.3 l	27.0 l	3.7 l	12.3 l	7	0
35	IL06-13721	40.5 l	21.7 l	9.3 l	6.2 l	23.2 l	2.1 l	37.2 l	7	0
33	IL06-14262	44.7 l	21.1 l	12.8 l	13.4 l	29.5 l	2.7 l	8.8 l	7	0
7	NY99068-383	47.3	16.1 l	7.5 l	15.3 l	28.3 l	4.7 l	14.5 l	6	0
36	IL06-13708	48.3	18.6 l	9.5 l	12.5 l	25.8 l	2.1 l	36.5 l	6	0
20	04606A1--7	43.5 l	16.6 l	9.9 l	13.0 l	25.0 l	7.0	4.6 l	6	0
60	VA09W-659	45.6 l	16.7 l	9.9 l	14.0 l	30.8	3.6 l	10.9 l	6	0
45	MD03W69-15	44.7 l	15.5 l	10.1 l	16.4	30.1 l	2.3 l	3.1 l	6	0
44	MD03W61-10-2	53.5	15.3 l	10.5 l	12.1 l	29.4 l	2.7 l	4.3 l	6	0
18	03633A1--5	47.9	16.0 l	9.8 l	14.9 l	27.7 l	5.4	15.1 l	5	0
24	M08*8005#	43.7 l	20.0 l	10.4 l	18.3	29.3 l	3.1 l	65.3 h	5	1
37	IL04-24668	47.7	23.6	12.1 l	12.6 l	28.6 l	3.3 l	29.4 l	5	0
11	E9022R	66.8 h	37.2 h	25.1 h	25.2	40.6 h	6.3	63.1 h	0	5
4	PIONEER2545	60.9 h	38.9 h	27.0 h	39.1 h	46.8 h	11.2 h	46.1 h	0	7

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

Table 4. Best (top) and worst (bottom) entries from the 2010-11 PNUWWSN.

ENTRY	NAME	INC	SEV	IND	FDK	ISK	DON	GHSEV	#l	#h
2	TRUMAN	35.6 h	12.1 l	5.8 l	8.6 l	22.6 l	6.6 l	3.1 l	7	1
24	IL07-19334	38.0 h	14.9 l	6.7 l	12.3 l	25.6 l	3.9 l	30.0 hl	7	2
26	KY04C-2023-18	44.9 h	14.4 l	6.7 l	9.8 l	27.1 l	6.6 l	6.5 l	7	1
30	MO080241	37.5 h	15.6 l	7.1 l	14.7 l	25.3 l	5.3 l	17.6 l	7	1
36	VA09W-608	42.0 h	17.8 l	8.3 l	18.4 l	29.5 l	3.9 l	20.2 l	7	1
23	IL07-14547	41.9 h	18.1 l	9.1 l	15.7 l	28.5 l	2.4 l	28.7 hl	7	2
39	VA09W-644	45.5 h	20.5 l	9.6 l	16.2 l	31.5 l	5.8 l	35.2 hl	7	1
16	06497A1--3	40.8 h	19.8 l	10.7 l	18.7 l	32.2 l	7.7 l	15.6 l	7	1
32	MO090577	50.1	13.5 l	7.9 l	14.6 l	30.2 l	4.4 l	6.8 l	6	0
18	0724B1--13	50.1	16.0 l	9.4 l	16.1 l	31.0 l	4.7 l	9.6 l	6	0
33	MO090812	43.6 h	20.4 l	10.0 l	17.1 l	32.4	8.1 l	6.5 l	6	1
20	IL07-4348	49.2	14.7 l	10.2 l	13.6 l	30.3 l	4.5 l	7.2 l	6	0
40	VA09W-654	49.8	19.0 l	10.8 l	14.0 l	30.9 l	4.4 l	40.8 hl	6	1
21	IL07-4415	51.1	17.4 l	11.3 l	15.1 l	31.0 l	3.6 l	7.0 l	6	0
22	IL07-7525	50.2	21.0 l	11.6 l	17.7 l	33.7	5.6 l	36.3 hl	5	1
8	M09-9804#	50.7	21.5 l	12.0 l	15.5 l	34.2	5.9 l	14.6 l	5	0
25	KY03C-2047-07	50.5	21.8 l	14.1 l	15.6 l	34.8	5.9 l	12.3 l	5	0
5	E9020R	52.7	41.4 h	23.5 h	30.9 h	44.8 h	10.4 l	47.2 h	1	5
12	OH08-133-25	52.0	39.7 h	23.3 h	31.4 h	44.4 h	12.4 h	47.2 h	0	6
15	05269A1--1	64.4 h	36.6 h	25.3 h	36.2 h	47.3 h	16.1 h	54.2 h	0	6
4	PIONEER2545	57.6 h	44.0 h	29.3 h	38.7 h	47.6 h	19.5 h	66.5 h	0	6

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

Table 5. Summary of results of the 2010-11 PNUWWSN.

ENTRY	NAME	INC	SEV	IND	FDK	ISK	DON	GHSEV	#l	#h
1	ERNIE	45.0 h	25.2	15.1	20.7	35.2	8.7 l	20.9 l	3	1
2	TRUMAN	35.6 h	12.1 l	5.8 l	8.6 l	22.6 l	6.6 l	3.1 l	7	1
3	FREEDOM	54.0	30.0	20.7	30.4 h	40.9 h	11.7 h	20.0 l	1	3
4	PIONEER2545	57.6 h	44.0 h	29.3 h	38.7 h	47.6 h	19.5 h	66.5 h	0	6
5	E9020R	52.7	41.4 h	23.5 h	30.9 h	44.8 h	10.4 l	47.2 h	1	5
6	E9021R	57.8 h	39.3 h	23.9 h	26.6	42.9 h	8.7 l	44.9 h	1	4
7	E9009	53.7	38.8 h	23.0 h	23.2	41.7 h	12.3 h	13.6 l	1	4
8	M09-9804#	50.7	21.5 l	12.0 l	15.5 l	34.2	5.9 l	14.6 l	5	0
9	OH07-166-41	49.4	32.4	17.5	24.0	37.9	8.6 l	53.2 h	1	1
10	OH07-254-11	47.7	30.5	16.8	30.3 h	42.0 h	16.8 h	50.9 h	0	4
11	OH07-263-3	53.7	28.0	15.1	20.9	37.5	8.1 l	56.6 h	1	1
12	OH08-133-25	52.0	39.7 h	23.3 h	31.4 h	44.4 h	12.4 h	47.2 h	0	6
13	OH08-269-58	59.9 h	41.2 h	24.4 h	27.4	40.5 h	7.8 l	32.9 hl	2	4
14	05251A1--5	55.9 h	30.3	18.6	25.1	41.0 h	11.3 h	12.1 l	1	2
15	05269A1--1	64.4 h	36.6 h	25.3 h	36.2 h	47.3 h	16.1 h	54.2 h	0	6
16	06497A1--3	40.8 h	19.8 l	10.7 l	18.7 l	32.2 l	7.7 l	15.6 l	7	1
17	0711A1--1	49.9	24.5	14.8	21.7	37.3	6 l	41.7 h	1	1
18	0724B1--13	50.1	16.0 l	9.4 l	16.1 l	31.0 l	4.7 l	9.6 l	6	0
19	M08-8352	45.8 h	25.4	13.2 l	25.7	36.3	7.4 l	27.1 l	4	1
20	IL07-4348	49.2	14.7 l	10.2 l	13.6 l	30.3 l	4.5 l	7.2 l	6	0
21	IL07-4415	51.1	17.4 l	11.3 l	15.1 l	31.0 l	3.6 l	7.0 l	6	0
22	IL07-7525	50.2	21.0 l	11.6 l	17.7 l	33.7	5.6 l	36.3 hl	5	1
23	IL07-14547	41.9 h	18.1 l	9.1 l	15.7 l	28.5 l	2.4 l	28.7 hl	7	2
24	IL07-19334	38.0 h	14.9 l	6.7 l	12.3 l	25.6 l	3.9 l	30.0 hl	7	2
25	KY03C-2047-07	50.5	21.8 l	14.1 l	15.6 l	34.8	5.9 l	12.3 l	5	0
26	KY04C-2023-18	44.9 h	14.4 l	6.7 l	9.8 l	27.1 l	6.6 l	6.5 l	7	1
27	KY04C-2034-2	50.0	32.2	18.4	18.9 l	35.7	9.6 l	21.4 l	3	0
28	KY04C-2034-3	50.4	25.8	13.4 l	18.3 l	34.9	8.8 l	9.9 l	4	0
29	KY04C-2034-4	50.8	23.6	14.0 l	22.0	36.1	6.3 l	17.3 l	3	0
30	MO080241	37.5 h	15.6 l	7.1 l	14.7 l	25.3 l	5.3 l	17.6 l	7	1
31	MO090862	49.0	25.0	14.5	13.7 l	33.3	4.5 l	32.8 hl	3	1
32	MO090577	50.1	13.5 l	7.9 l	14.6 l	30.2 l	4.4 l	6.8 l	6	0
33	MO090812	43.6 h	20.4 l	10.0 l	17.1 l	32.4	8.1 l	6.5 l	6	1
34	MO091122	43.0 h	29.2	12.6 l	25.1	36.7	9.4 l	23.8 l	4	1
35	VA08W-632	56.5 h	29.6	18.2	28.3 h	41.6 h	6.9 l	11.9 l	2	2
36	VA09W-608	42.0 h	17.8 l	8.3 l	18.4 l	29.5 l	3.9 l	20.2 l	7	1
37	VA09W-635	53.2	26.6	17.1	28.3 h	40.7 h	8.1 l	18.5 l	2	2
38	VA09W-636	45.1 h	31.4	13.5 l	21.7	36.2	7.5 l	22.3 l	4	1
39	VA09W-644	45.5 h	20.5 l	9.6 l	16.2 l	31.5 l	5.8 l	35.2 hl	7	1
40	VA09W-654	49.8	19.0 l	10.8 l	14.0 l	30.9 l	4.4 l	40.8 hl	6	1
100	AVERAGE	49.2	25.7	14.7	21.1	35.6	7.9	26.1		
101	MINUMUM	35.6	12.1	5.8	8.6	22.6	2.4	3.1		
102	MAXIMUM	64.4	44.0	29.3	38.7	47.6	19.5	66.5		
103	LSD(0.05)	10.4	10.6	8.4	11.0	9.7	8.6	38.5		

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

Table 6. Summary of results of the 2010-11 NUWWSN.

NAME	INC	SEV	IND	FDK	ISK	DON	GHSEV	#l	#h
ERNIE	54.3	22.3 l	13.9	16.4	30.9	4.7 l	35.9 l	3	0
TRUMAN	36.6 l	16.5 l	6.7 l	8.7 l	22.5 l	3.6 l	6.4 l	7	0
FREEDOM	55.7	24.4	16.8	28.9	38.9 h	4.7 l	18.1 l	2	1
PIONEER2545	60.9 h	38.9 h	27.0 h	39.1 h	46.8 h	11.2 h	46.1 h	0	7
NY99066-3025	46.9	38.4 h	18.5	22.6	38.4	8.1 h	40.8 h	0	3
OH751	54.1	22.2 l	13.3	18.7	33.7	3.1 l	52.4 h	2	1
NY99068-383	47.3	16.1 l	7.5 l	15.3 l	28.3 l	4.7 l	14.5 l	6	0
NY93246SP-6093	54.5	28.7	16.5	22.5	38.1	6.9	19.9 l	1	0
E6012	58.5 h	30.6	19.4	21.4	38.5	6.2	30.6 l	1	1
E6032	57.7 h	31.1 h	20.3	25.9	41.4 h	9.6 h	26.3 l	1	4
E9022R	66.8 h	37.2 h	25.1 h	25.2	40.6 h	6.3	63.1 h	0	5
E9024R	56.4	29.0	17.3	24.6	38.5	6.6	32.0 l	1	0
OH05-200-74	47.8	19.3 l	11.5 l	26.0	36.6	5.4	8.5 l	3	0
OH06-150-57	51.0	29.8	18.4	26.5	38.8 h	6.0	68.9 h	0	2
OH06-180-57	49.3	31.1 h	16.6	27.1	38.1	5.5	71.6 h	0	2
OH07-98-21	45.3 l	30.0	14.4	22.3	35.5	4.2 l	51.3 h	2	1
OH07-166-49	53.7	34.6 h	19.7	23.7	38.8 h	6.8	69.7 h	0	3
03633A1--5	47.9	16.0 l	9.8 l	14.9 l	27.7 l	5.4	15.1 l	5	0
04704A1--1	63.8 h	39.9 h	29.2 h	26.4	43.7 h	6.3	30.1 l	1	4
04606A1--7	43.5 l	16.6 l	9.9 l	13.0 l	25.0 l	7.0	4.6 l	6	0
05247A1--3	48.0	18.4 l	10.3 l	21.3	31.8	4.8 l	19.8 l	4	0
05264A1--2	58.9 h	25.9	17.2	22.1	37.8	5.1	56.1 h	0	2
M05-1526	53.9	20.5 l	12.5 l	17.4	31.4	4.3 l	27.2 l	4	0
M08*8005#	43.7 l	20.0 l	10.4 l	18.3	29.3 l	3.1 l	65.3 h	5	1
M08-8036#	44.0 l	17.8 l	8.7 l	13.5 l	26.5 l	1.6 l	15.1 l	7	0
M08-8214	45.3 l	16.3 l	9.3 l	13.3 l	27.0 l	3.7 l	12.3 l	7	0
M08-8349	47.6	17.8 l	10.7 l	20.4	31.8	4.1 l	19.6 l	4	0
RCUOG1	45.5 l	27.4	14.3	26.2	36.2	3.6 l	54.7 h	2	1
RCUOG2	49.6	24.0	13.3	20.3	33.1	5.6	35.7 l	1	0
RCUOG3	39.7 l	23.2	10.0 l	17.8	27.9 l	5.6	18.3 l	4	0
RCUOG4	43.4 l	29.1	12.3 l	21.3	32.2	6.1	60.9 h	2	1
RCUOG5	43.7 l	24.5	10.3 l	24.6	33.9	5.1	37.2 l	3	0
IL06-14262	44.7 l	21.1 l	12.8 l	13.4 l	29.5 l	2.7 l	8.8 l	7	0
IL06-14325	53.0	28.8	15.5	17.3	33.7	3.4 l	31.5 l	2	0
IL06-13721	40.5 l	21.7 l	9.3 l	6.2 l	23.2 l	2.1 l	37.2 l	7	0
IL06-13708	48.3	18.6 l	9.5 l	12.5 l	25.8 l	2.1 l	36.5 l	6	0
IL04-24668	47.7	23.6	12.1 l	12.6 l	28.6 l	3.3 l	29.4 l	5	0
KY02C-1002-06	51.6	24.1	14.8	24.8	37.4	3.6 l	15.6 l	2	0
KY03C-1237-32	50.6	25.9	14.9	19.1	33.1	3.9 l	26.0 l	2	0
KY02C-2216-05	54.5	29.4	17.4	18.3	36.5	2.9 l	65.0 h	1	1
KY03C-1075-04	43.8 l	22.7	10.4 l	25.2	34.8	6.2	69.0 h	2	1
KY03C-2047-06	49.8	21.3 l	13.5	11.0 l	31.3	3.1 l	13.5 l	4	0
MD03W485-10-9	52.2	26.6	15.7	20.5	35.6	4.0 l	74.5 h	1	1
MD03W61-10-2	53.5	15.3 l	10.5 l	12.1 l	29.4 l	2.7 l	4.3 l	6	0
MD03W69-15	44.7 l	15.5 l	10.1 l	16.4	30.1 l	2.3 l	3.1 l	6	0
MD03W61-09-7	55.9	20.3 l	14.8	24.8	39.1 h	3.6 l	19.5 l	3	1
MO080104	43.0 l	15.3 l	7.5 l	13.2 l	24.6 l	2.2 l	13.9 l	7	0
MO081652	40.0 l	13.8 l	6.8 l	11.9 l	27.0 l	1.7 l	3.8 l	7	0
MO080589	36.4 l	14.3 l	7.8 l	12.5 l	23.8 l	3.7 l	15.7 l	7	0
MO081777	45.0 l	15.2 l	7.7 l	13.3 l	25.7 l	2.0 l	5.7 l	7	0
MO080789	37.6 l	18.4 l	6.8 l	10.7 l	25.8 l	2.7 l	11.3 l	7	0
NE01481	43.5 l	38.5 h	15.1	30.7 h	35.9	7.6	76.0 h	1	3
NE02558	51.1	29.9	15.4	29.5	36.6	6.1	56.4 h	0	1
NE05548	55.7	37.4 h	19.9	27.4	38.2	7.8 h	49.0 h	0	3
NE06469	49.0	28.6	16.7	32.3 h	38.7 h	7.2	52.6 h	0	3
NE07444	51.5	28.9	14.2	30.9 h	35.6	5.2	62.2 h	0	2
VA08W-176	48.1	27.2	13.4	21.1	35.4	3.7 l	64.4 h	1	1
VA08W-294	47.7	23.7	12.8 l	17.4	32.3	3.9 l	14.1 l	3	0
VA09W-657	49.7	23.3	13.0 l	15.1 l	31.5	3.4 l	17.0 l	4	0
VA09W-659	45.6 l	16.7 l	9.9 l	14.0 l	30.8	3.6 l	10.9 l	6	0
AVERAGE	49.2	24.4	13.7	20.0	33.2	4.7	33.6		
MINUMUM	36.4	13.8	6.7	6.2	22.5	1.6	3.1		
MAXIMUM	66.8	39.9	29.2	39.1	46.8	11.2	76.0		
LSD(0.05)	9.7	8.8	6.3	9.2	8.1	3.5	35.6		

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

VARIATION FOR RESISTANCE TO KERNEL INFECTION AND TOXIN ACCUMULATION IN WINTER WHEAT INFECTED WITH *FUSARIUM GRAMINEARUM*

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ABSTRACT

Host resistance is the main way to control Fusarium head blight (FHB) in wheat. Despite improved levels of resistance to infection and spread in vegetative tissue, the toxin deoxynivalenol (DON) can still accumulate to unacceptable concentration levels. In this study, our objectives were to assess the genetic variation for resistance to kernel infection (RKI) and toxin accumulation (RTA) and their role in controlling DON. We collected spikes with different levels of visual symptoms from each of 32 wheat genotypes and at four environments and determined DON and fungal biomass (FB) from each sample. We assessed RKI by regressing FB on the level of visual symptoms, and RTA by regressing DON on FB for each genotype. Significant genetic effects were found for RKI and RTA. Some genotypes consistently had low FB in their grain despite increasing visual symptoms suggesting RKI. Additionally, some genotypes consistently had low DON in their grain despite increasing FB levels suggesting a higher RTA in these genotypes. The variation for RKI and RTA explained a significant fraction of the variation for DON among genotypes with moderate visual symptoms using independent grain samples. Although RKI and RTA were significantly correlated ($r=0.58$, $P = 0.05$), RTA was more predictive of DON accumulation since it modeled 32-44% of the genotype sum of squares for DON, while only 9-10% were predicted using RKI. Thus, variation for RTA was important in explaining variation for DON among genotypes with acceptable levels of resistance to fungal infection and spread. This work indicates that there is a need to develop a better understanding of RTA and rapid screening methods for this trait.

MAP TYPE I AND COMBINE TYPE I AND TYPE II FHB RESISTANCE

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ABSTRACT

Single genes identified to-date in wheat for resistance to Fusarium head blight (FHB) provide only partial resistance, requiring multiple genes for effective resistance, and disease severity is highly influenced by environment. Our hypothesis is that combining Type I (reduced initial infection) and Type II (inhibition of spread of the disease after infection) FHB resistance can provide more effective resistance. Identifying DNA markers for Type I resistance will be very beneficial for selection in wheat improvement for FHB resistance. Our objectives are: 1) characterize a RIL population from the cross INW0412 (Type I resistance)/992060 (susceptible) for frequency of initial infection and map QTLs for Type I resistance; and 2) combine Type I resistance from cvs. Goldfield, INW0412 and Truman; and Type II resistance of *Fhb1* and *Qfhs.pur-7EL* backcrossed into adapted soft winter wheat lines, and quantify augmentation of FHB resistance. A population of 198 $F_{6:7}$ RILs were characterized for FHB incidence in a field test in 2011 at Lafayette, Indiana, and will again be characterized for Type I resistance in field tests in 2012 at Lafayette, Vincennes and Evansville. Bulked segregate analysis will be utilized to identify DNA markers that co-segregate with Type I resistance of INW0412. BC $F_{1:2}$ lines have been genotyped with respective associated DNA markers for Type I resistance of Goldfield and *Fhb1* and *Qfhs.pur-7EL*. $F_{2:3}$ lines will be characterized in replicated field tests at Lafayette and Vincennes in 2012 for Type I and Type II resistance and genotyped with associated markers. The goal is to identify lines that have augmented FHB resistance by combining effective Type I and Type II resistance.

PRELIMINARY HAPLOTYPING OF FIVE FUSARIUM HEAD BLIGHT RESISTANT WHEAT SOURCES USING MOLECULAR MARKERS

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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 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 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. The most environmentally friendly and efficient FHB control method is genetic 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 moderate-highly FHB resistant wheat cultivars available in South Africa. For a number of years, the well documented FHB resistance QTL (*3B-Fhb1*, *5A, 6B-Fhb2* & *Fhb7AC*) in Sumai 3 have been used throughout the world in the development of FHB resistant varieties. Sumai 3 resistance QTL offer different combinations of the three resistance types. Another well used resistant source is the Brazilian wheat cultivar Frontana for its Type I QTL on 3A. However, there is a critical need for new novel, FHB resistant sources to be identified and characterised to prevent total dependence on the Sumai 3 and Frontana derived sources. This will be an important step in improving FHB resistance levels available in wheat. In this study, five resistant lines identified during a two year phenotypic screening process are being characterised with a number of FHB specific simple-sequence repeat (SSR) markers. 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. Pedigree analysis of selected lines showed no related kinship to Sumai 3 or Frontana. Fusarium head blight specific SSR markers linked to resistance QTL from Sumai 3 and Frontana have been chosen to haplotype these five sources. Once these five lines have been fully haplotyped and confirmed as novel FHB resistant sources, the resistance QTL/genes contained within the lines will be mapped.

Keywords: Scab, SSRs, QTL, FHB, *Fusarium graminearium*, Sumai 3, Frontana, *Gibberealla zeae*

FAMILY BASED MAPPING OF FUSARIUM HEAD BLIGHT RESISTANCE IN SOFT WHEAT CULTIVARS ROANE AND JAMESTOWN

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ABSTRACT

Fusarium Head Blight (FHB), caused by *Fusarium graminearum* Schwabe, is a serious disease of wheat (*Triticum aestivum* L.) worldwide and results in reduced yields, poor quality grain, and accumulation of the mycotoxin deoxynivalenol (DON), in the grain. The objective of this study is to identify QTL (Quantitative Trait Loci) for FHB resistance in two soft red winter (SRW) wheat cultivars Roane and Jamestown. In the first year (2011) study, northern populations including 33 Roane/'Allegiance', 18 Roane/KY93C-1238-17-1 and 23 Roane/KY94C-0094-11-2 recombinant inbred lines (RILs) were evaluated for FHB in five environments (Kentucky, Missouri, Maryland, North Carolina, and Virginia), and 186 $F_{5:7}$ RILs from Pioneer brand '25R47'/ Jamestown were evaluated in three environments (Maryland, North Carolina, and Virginia). Similarly, southern populations including 170 FG95195/Jamestown $F_{5:7}$ RILs and 77 Jamestown/LA97113UC-124 $F_{4:6}$ RILs were evaluated in four environments (Arkansas, Georgia, Louisiana, and Virginia). Over environments, the Roane derived RILs had means that varied from 0% to 100% for FHB incidence , 0% to 60% for severity, and 0% to 55% for index, while the Pioneer brand 25R47/Jamestown RILs had means that varied from 0% to 100% for all three FHB assessment parameters. Analysis of variance indicated that there was significant interaction between lines and locations for FHB severity in the northern populations. Over environments, RILs in the southern populations, FG95195/Jamestown and Jamestown/LA97113UC-124, had means that varied from 0% to 100% for FHB incidence, 0% to 80% for severity, and 0% to 36% for index. Analysis of variance indicated that there was significant interaction between lines and locations for FHB severity in the FG95195 / Jamestown population but not in the Jamestown / LA97113UC-124 population. In the southern populations, DON concentration ranged from 0.22 to 10.76 mg/kg (mean = 1.89 mg/kg) and was correlated with FHB severity ($r = 0.24$, $P < 0.001$) in the Arkansas test. In the Louisiana test, nivalenol (NIV) was more predominant (range = 0.06 to 16.82 mg/kg and mean = 2.95) than DON (range = 0.0 to 4.56 mg/kg and mean = 0.16). A significant correlation was observed between NIV and FHB index ($r = 0.29$, $P < 0.001$). Genotyping with SSR and SNP markers has been initiated in the populations. The presentation will include initial results and putative QTL for resistance to FHB and mycotoxins. Significance of interaction between lines and locations in these mapping populations confirms the complexity of FHB phenotyping, effect of environmental factors on disease expression, and the need for multi-environment testing. The results also indicated that phenotypic selection for low FHB index would indirectly select for low DON or NIV and vice versa. Also, the results indicated that NIV producing isolates likely are predominant in some regions of the U.S.

COMBINING GENES FROM RELATED GRASS SPECIES FOR RESISTANCE TO WHEAT DISEASES

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ABSTRACT

The highly effective disease resistance genes/*QTLs, Lr19*, *Sr25, Bdv3* and *Qfhs.pur-7EL*, each on a segment of E genome chromatin, from wheat-related grasses have been introgressed into the long arm of wheat chromosome 7D, but in different wheat lines. The objectives of this research are to 1) develop combinations of these four resistance factors, including presence of all four resistance factors, in coupling on 7DL, along with gene *Fhb1* on chromosome 3BS and widely deployed in wheat cultivars, in adapted soft winter wheat lines; and 2) determine possible negative effects on plant performance of the various combinations. Augmentation of Type II Fusarium head blight (FHB) resistance has been documented in agronomically unimproved wheat genetic lines; and a 3rd objective of this research is to document augmentation of resistance by this combination of resistance factors in adapted wheat lines. We have identified, based on genotyping with respective co-segregating diagnostic DNA markers, of plant lineages from backcrosses to adapted soft winter wheat lines of plants representing combinations of the four resistance factors. Selected lineages will be phenotyped in greenhouse and field tests for resistance to the four globally important diseases of wheat. Lines will also be observed for possible detrimental effects of combinations of these resistance factors on pollen fertility, seed set, and other observable plant traits.

EVALUATING AND TRACING FUSARIUM HEAD BLIGHT RESISTANCE OF BARLEY VARIETIES

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ABSTRACT

Wheat Fusarium head blight (FHB) is one of the worldwide destructive diseases of barley in the warm, semi-humid and humid regions. FHB not only causes significant losses in yield and reduction of grain quality, but also induces toxin to contaminated seeds, which is harmful to the health of human and livestocks. Barley grain contaminated with deoxynivalenol (DON) is associated with beer gushing and may be rejected by the malting and brewing industry. Genetically inherited resistance is the most effective option for the control of the disease. To identify barley sources of FHB resistance containing new FHB resistance genes in Jiangsu Province, 13 barley varieties in the 2008 Jiangsu provincial trial test, 3 varieties with identified QTLs, and other 3 varieties were evaluated for FHB resistance in 2010 and 2011. Plants were inoculated with *F. graminearum* isolate HG-1 under field conditions by injecting conidia into a single spikelet of each spike and by spraying conidia to the whole spike, respectively. Proportion of scabbed spikelets, proportion of scabbed spikes and infection sites were scored to evaluate FHB resistance to spread and infection, respectively. Markers linked to six known FHB resistance quantitative trait loci (QTLs) were screened in genotypes of the present study to explain variation for resistance and to find new FHB resistance genes. The results indicated that barley varieties in the 2008 Jiangsu provincial trial test possess good FHB resistance, three of which were resistant to infection as well as to spread. Variety Frederickson, a cultivar from Japan that is reported to be moderately resistant to FHB, was susceptible to Chinese *Fusarium* isolates. The dendrogram constructed after SSR data revealed that barley varieties could be classified in to 2 groups at 0.51 similarity coefficient, suggesting high degree of genetic diversity between domestic and overseas barley varieties. Eleven varieties possess at least one known QTL but their FHB resistance behaviors were not associated with numbers of QTLs they had. Barley varieties of Supi 3, 5E003, and Yan 99175 might possess new FHB resistance genes, which could be used as new sources in barley breeding.

EVALUATION OF FUSARIUM HEAD BLIGHT RESISTANCE OF WHEAT VARIETIES CORRESPONDING TO CHEMOTYPE-SPECIFIC *FUSARIUM* ISOLATES

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ABSTRACT

Fusarium head blight (FHB), also called scab, is a devastating and insidious disease of cereals including wheat (*Triticum* spp.) and barley (*Hordeum vulgare* L.) worldwide. Apart from direct yield losses, the most serious concern about FHB is the contamination of the crop with mycotoxins, which poses a health risk to human and livestock[1]. Members of *Fusarium* produce B trichothecenes including nivalenol (NIV), deoxynivalenol (DON) and its acetyl derivatives. Recent research reported that phylogenetic species *F. asiaticum* (Fa) and *F. graminearum* (Fg) were the major causal agents of FHB from infected wheat heads in China[2]. Based on the profile of trichothecenes produced, *Fusarium* isolates can be grouped into one of three chemotypes, which are 3ADON chemotype producing DON and primarily 3ADON, 15ADON chemotype generating DON and primarily 15ADON, or a NIV chemotype producing NIV and its acetylated derivatives. The objective of the present study was to identify the aggressiveness of chemotype-specific *Fusarium* isolates and to investigate the corresponding resistance to FHB of different wheat varieties by detecting the proportion of diseased spikelets and the amount of mycotoxin in the infected heads.

Eight wheat varieties with different resistance levels to FHB were inoculated with spores of randomly selected isolates from above three chemotypes by single-floret injection, respectively. Amount of DON, 3ADON, 15ADON and NIV from harvest grains was quantified using the HPLC method. The results of the FHB evaluation tests showed significant differences of aggressiveness of chemotype-specific *Fusarium* isolates. 3ADON chemotype isolates showed to be more aggressive and produce higher levels of DON than other chemotype isolates did. Variety Sumai 3 is still the best source of resistance to FHB. It has the lowest proportion of diseased spikelets and the lowest amount of NIV or DON and its derivatives after inoculation with the corresponding chemotype isolates. Commercial variety Ningmai 9 also possesses the advantage of lower disease index and toxin amount which could be directly used in wheat breeding programs. The information obtained in this study could have an impact on development of FHB resistant wheat cultivars and disease management.

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IDENTIFICATION AND MAPPING OF QTLS FOR FHB RESISTANCE IN A SYNTHETIC HEXAPLOID WHEAT LINE

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ABSTRACT

The synthetic hexaploid wheat (SHW) lines derived from crosses between tetraploid wheat (AABB genome) and *Aegilops tauschii* (D genome) possess resistance to various diseases including Fusarium head blight (FHB). However, the genetics of FHB resistance in these synthetic lines is poorly understood. Based on two seasons of evaluation in the greenhouse, the SHW line TA4152-60 (Scoop1/*Ae.tauschii* [358]) developed by CYMMIT was found to exhibit a moderate level of resistance to FHB. To understand the genetics and QTL governing the FHB resistance in TA4152-60, a mapping population of 120 double haploid (DH) lines derived from the cross between TA4152-60 FHB and the hard red spring wheat line ND 495 (highly susceptible to FHB) was evaluated for FHB reaction in field and greenhouse. Based on the whole genome linkage maps developed using 643 DNA markers and the phenotype data from two seasons of greenhouse and one season of field experiments, two major QTLs were identified on chromosome 5A and 5B. The 5A QTL peaked at the interval between *Xgdm132.1* and *Xgwm410.4*, and explained up to 11% of the phenotypic variation whereas the 5B QTL explained up to 20% of the trait variation and peaked at the interval between markers *Xbarc100.5* and *Xwmc75*. Based on the chromosomal regions, the QTLs identified in our study appeared to be different from those that have been mapped in other sources of FHB resistance. Therefore, these QTLs may be useful for the improvement of FHB resistance in wheat breeding programs.

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