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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

James A. Anderson[1*], Karl Glover[2] and Mohamed Mergoum[3]

[1]Dept. of Agronomy and Plant Genetics, University of Minnesota, St. Paul, MN; [2]Dept. of Plant Sciences, South Dakota State University, Brookings, SD; and [3]Dept. of Plant Sciences, North Dakota State University, Fargo, ND
[*]Corresponding Author: PH: (612) 625-9763, Email: ander319@umn.edu

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

P. Stephen Baenziger[1*], Stephen N. Wegulo[2], William Berzonsky[3],
Guihua Bai[4] and Ali Bakhsh[1]

[1]Dept. of Agronomy and Horticulture, University of Nebraska, Lincoln, NE 68583-0915; [2]Dept. of Plant Pathology, University of Nebraska, Lincoln, NE 68583-0722; [3]Dept. of Plant Science, South Dakota State University, Brookings, SD 57007; and [4]USDA-ARS and Dept. of Plant Pathology, Kansas State University, Manhattan, KS 66506
[*]Corresponding Author: PH: 402-472-1538, Email: pbaenziger1@unl.edu

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

Guihua Bai[1*], P. Stephen Baenaiger[2], William Berzonsky[3], Amy Bernardo[4], Paul St Amand[1], Dadong Zhang[5], Jin Cai[5], Feng Jin[5], Tao Li[4], Jianbin Yu[5], William Bockus[4] and Fred Kolb[6]

[1]USDA-ARS-HWWGRU, Manhattan, KS 66506; [2]Dept. of Agronomy and Horticulture, University of Nebraska, Lincoln, NE; [3]Dept. of Plant Science, South Dakota State University, Brookings, SD, [4]Dept. of Plant Pathology, and [5]Dept. of Agronomy, Kansas State University, Manhattan, KS; and [6]Dept. of Crop Sciences, University of Illinois, Urbana, IL 61801
[*]Corresponding Author: PH: 785-532-1124, Email: guihua.bai@ars.usda.gov

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

Ana Balut[1], Anthony Clark[1], Gina Brown-Guedira[2], Yanhong Dong[3], Edward Souza[4] and David Van Sanford[1*]

[1]University of Kentucky, Dept. of Plant and Soil Sciences, Lexington, KY 40546; [2]USDA-ARS, Plant Science Research Unit, Raleigh, NC 27695; [3]University of Minnesota, Plant Pathology Dept., St. Paul, MN 55108; and [4]USDA-ARS, Soft Wheat Quality Lab, Wooster, OH 44691
[*]Corresponding Author: PH: 859-338-2409, Email: dvs@uky.edu

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

Gregory Berger[1*], Piyum Khatibi[2], Wynse Brooks[1], Shuyu Liu[3], Marla Hall[4], Andrew Green[1], Carl Griffey[1] and David Schmale III[2]

[1]Dept. of Crop and Soil Environmental Sciences, Virginia Tech, Blacksburg, VA 24061; [2]Dept. of Plant Pathology, Physiology, and Weed Science, Virginia Tech, Blacksburg, VA 24061; [3]Texas AgriLife Research, Texas A&M University, Amarillo, TX 79106; and [4]Limagrain Cereal Seeds, Wichita, KS 67204
[*]Corresponding Author: PH: 979-224-7698, Email: gberg06@vt.edu

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 ($P = 0.008$) 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

A.N. Bernardo[1], J-B Yu[2], H-X. Ma[2], F. Kolb[3] and G-H. Bai[4*]

[1]Dept. of Plant Pathology, [2]Dept. of Agronomy, Kansas State University, Manhattan, KS;
[3]Dept. of Crop Sciences, University of Illinois, Urbana, IL; and [4]USDA-ARS
Hard Winter Wheat Genetics Research Unit, Manhattan, KS
[*]Corresponding Author: PH: (785) 532-1124, Email: guihua.bai@ars.usda.gov

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)

Jin Cai[1] and Guihua Bai[2*]

[1]Department of Agronomy, Kansas State University, Manhattan, KS 66506; and [2]USDA-ARS
Hard Winter Wheat Genetics Research Unit, Manhattan, KS 66506,
[*]Corresponding Author: PH: (785) 532-1124, Email: guihua.bai@ars.usda.gov

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

X. Cai[1*], E. Elias[1], S. Xu[3], S. Kianian[1], S. Zhong[2] and S. Chao[3]

[1]Department of Plant Sciences, [2]Department of Plant Pathology, North Dakota State University,
Fargo, ND, 58108; and [3]USDA-ARS, Northern Crop Science Lab, Fargo, ND 58105
[*]Corresponding Author: PH: 701-231-7404, Email: xiwen.cai@ndsu.edu

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

W. Cao[1], G. Fedak[1*], D. Somers[2], H. Voldeng[1],
A. Xue[1], J. Gilbert[2] and X. Wang[1]

[1]Eastern Cereals and Oilseeds Research Centre, AAFC, Central Experimental Farm 960 Carling Ave,
Ottawa, ON, K1A 0C6; and [2]Cereal Research Centre, 195 Dafoe Road, Winnipeg, MN, R3T 2M9
[*]Corresponding Author: PH: (613) 759-1393, Email: george.fedak@agr.gc.ca

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

Anthony Clark[1*], Cindy Finneseth[2,3] and David Van Sanford[1]

[1]Dept. of Plant and Soil Sciences, [2]Division of Regulatory Services, University of Kentucky,
Lexington, KY 40546; and [3]Current address: Improcrop, Nicholasville, KY 40356
[*]Corresponding Author: PH: (859) 218-0809, Email: anthony.clark@uky.edu

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.

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

Benjamin, Conway[1], Jinfeng Gao[2], Yajuan Wang[2], J. Paul Murphy[3], Gina Brown-Guedira[4], Carl Griffey[5], Yanhong Dong[6] and Jose Costa[1*]

[1]University of Maryland, PSLA Dept. 2102 Plant Sciences Bldg., College Park, MD 20742-4452; [2]College of Agronomy, Northwest A&F University, Yangling, Shaanxi Province, 712100, China; [3]Dept. of Crop Science, North Carolina State University, Raleigh, NC, 27695-7620; [4]USDA-ARS, Plant Science Research Unit, Raleigh, NC 27695; [5]Virginia Polytechnic Institute and State University, Blacksburg, Department of Crop and Soil Environmental Sciences, VA 24061; and [6]Plant Pathology Dept., University of Minnesota, St. Paul, MN 55108
[*]Corresponding Author: PH: (301) 405-1317, Email: costaj@umd.edu

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

C. De Villiers

ARC-Small Grain Institute, Private Bag X 29, Bethlehem, 9700, South Africa
Corresponding Author: PH: 27 58 3073452, Email: devilliersc@arc.agric.za

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

J.T. Eckard, J.L. Gonzalez-Hernandez*, K.D. Glover and W.A. Berzonsky

South Dakota State University, Department of Plant Science, Brookings, SD
*Corresponding Author: PH: (605) 688-6907, Email: jose.gonzalez@sdstate.edu

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

E. Falconí[1,3], E. Duveiller[2], J. Crossa[2], R. Singh[2], J. Huerta[2], S. Herrera-Fossel[2], J. Ochoa[3], J. Garofalo[3], L. Ponce[3] and J. Lewis[1,4*]

[1]Department of Crop and Soil Sciences, Michigan State University, East Lansing, MI, USA; [2]Global Wheat Program of CIMMYT, Mexico; [3]Instituto Nacional Autónomo de Investigaciones Agropecuarias (INIAP)-Ecuador, and [4]Current address: Bayer CropScience, 206 Biochemistry Hall, UNL East Campus, Lincoln NE, 68583-074
[*]Corresponding Author: PH: (517) 648-7139, Email: lew.janet@gmail.com

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

G. Fedak[1*], W. Cao[1], D. Chi[1], D. Somers[2], S. Miller[1], T. Ouellet[1], A. Xue[1], J. Gilbert[3], M. Savard[1] and H. Voldeng[1]

[1]Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, 960 Carling Ave. Building 50, Ottawa, ON Canada K1A 0C6; [2]Vineland Research and Innovation Center, 4890 Victoria Ave. N. Po Box 4000, Vineland Station ON Canada L0R 2E0; and [3]Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Rd, Winnipeg MB, R3T 2M9 Canada
[*]Corresponding Author: PH: 613-759-1393, Email: George.Fedak@agr.gc.ca

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 upregulated 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

Steve Haber* and Jeannie Gilbert

AAFC, Cereal Research Centre, 195 Dafoe Rd., Winnipeg, MB, Canada R3T 2M9
*Corresponding Author: PH: (204) 983-1467, Email: steve.haber@agr.gc.ca

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

Steve Haber[1*], Jeannie Gilbert[1], Asheesh Singh[2] and John Clarke[2,3]

[1]AAFC, Cereal Research Centre, 195 Dafoe Rd., Winnipeg, MB, Canada R3T 2M9; [2]AAFC, Semi-Arid Prairie Agricultural Research Centre, PO Box 1030, Swift Current, SK, Canada S9H 3X2. [3]Present address: Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK., Canada S7N 5A8
[*]Corresponding Author: PH: (204) 983-1467, Email: steve.haber@agr.gc.ca

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

A. Hoffstetter, C. Sneller* and A. Cabrera

Department of Horticulture and Crop Science, The Ohio State University and the Ohio
Agriculture Research and Development Center, 1680 Madison Ave, Wooster, Ohio 44691
*Corresponding Author: PH: (330) 263-3944, Email: sneller.5@osu.edu

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

P. Horevaj[1], G. Brown-Guedira[2], D.E. Moon[1] and E.A. Milus[1*]

[1]Department of Plant Pathology, University of Arkansas, Fayetteville, AR and
[2]USDSA-ARS Eastern Regional Small Grains Genotyping Lab, Raleigh, NC
[*]Corresponding Author: PH: (479) 575-2676, Email: gmilus@uark.edu

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

Md. Sariful Islam[1], Gina Brown-Guedira[2], Herb Ohm[3],
David Van Sanford[4] and Anne L. McKendry[1*]

[1]Division of Plant Sciences, 106 Curtis Hall, University of Missouri, Columbia, MO, 65211; [2]Eastern Regional Small Grains Genotyping Lab, USDA-ARS, NCSU, Raleigh, NC 27695; [3]Department of Agronomy, Purdue University, West Lafayette, IN 47907; and [4]Department of Plant and Soil Science, University of Kentucky, Lexington, KY40546
[*]Corresponding Author: PH: (573) 882-7708, Email: mckendrya@missouri.edu

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

Md. Sariful Islam[1], Gina Brown-Guedira[2], Herb Ohm[3], David Van Sanford[4], Yanhong Dong[5] and Anne L. McKendry[1*]

[1]Division of Plant Sciences, 106 Curtis Hall, University of Missouri, Columbia, MO, 65211; [2]Eastern Regional Small Grains Genotyping Lab, USDA-ARS, NCSU, Raleigh, NC 27695; [3]Department of Agronomy, Purdue University, West Lafayette, IN 47907; [4]Department of Plant and Soil Science, University of Kentucky, Lexington, KY40546; and [5]Department of Plant Pathology, University of Minnesota, St. Paul, MN 55108
[*]Corresponding Author: PH: (573) 882-7708, Email: mckendrya@missouri.edu

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

Md. Sariful Islam[1], Gina Brown-Guedira[2] and Anne L. McKendry[1*]

[1]Division of Plant Sciences, 106 Curtis Hall, University of Missouri, Columbia, MO, 65211; and
[2]Eastern Regional Small Grains Genotyping Lab, USDA-ARS, NCSU, Raleigh, NC 27695
[*]Corresponding Author: PH: (573) 882-7708, Email: mckendrya@missouri.edu

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

Feng Jin[1], Dadong Zhang[1], William Bockus[2],
P. Stephen Baenziger[3] and Guihua Bai[4*]

[1]Dept. of Agronomy, [2]Dept.of Plant Pathology, Kansas State University, Manhattan, KS;
[3]Dept. of Agronomy and Horticulture, University of Nebraska, Lincoln, NE; and
[4]USDA-ARS-HWWGRU, Kansas State University, Manhattan, KS
[*]Corresponding Author: PH: (785) 532-1124, Email: guihua.bai@ars.usda.gov

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

J. Johnson*, D. Bland, Y.F. Hao and Z.B. Chen

Crop and Soil Sciences, Griffin Campus, The University of Georgia, Griffin, GA
*Corresponding Author: PH: (770) 228-7345, Email: jjohnso@uga.edu

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

Shuyu Liu[1,2], Mark D. Christopher[1], Carl A. Griffey[1*], Marla D. Hall[1,3], Patty G. Gundrum[1] and Wynse S. Brooks[1]

[1]Department of Crop and Soil Environmental Sciences, Virginia Tech, Blacksburg, VA, 24061; [2]Texas AgriLife Research, Texas A&M University, Amarillo, TX 79106; and [3]Limagrain Cereal Seeds, 6414 N. Sheridan, Wichita, KS 67204, USA
[*]Corresponding Author: PH: 540-231-9789, Email: CGriffey@vt.edu.

ABSTRACT

Many quantitative trait loci (QTL) in wheat (*Triticum aestivum*) conferring resistance to Fusarium head blight (FHB), caused by the pathogen *Fusarium graminearum* 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

Shuyu Liu[1a], Carl A. Griffey[1*], Marla D. Hall[1b], Anne L. McKendry[2], Jianli Chen[1c], Gina Brown-Guedira[3], David Van Sanford[4] and David G. Schmale[5]

[1]Dept. of Crop and Soil Environmental Sciences, Virginia Tech, Blacksburg, VA 24060; [2] Dept of Plant Science, University of Missouri, Columbia, MO 65201; [3] Eastern Regional Small Grains Genotyping Lab, USDA-ARS, Raleigh, NC 27695; [4]Dept. of Plant and Soil Sciences, University of Kentucky, Lexington, KY 40546; [5]Dept. of Plant Pathology, Physiology and Weed Science, Virginia Tech, Blacksburg, VA 24060; [a]Current Address: Texas AgriLife Research and Extension Center, Texas A&M University System, 6500 Amarillo Blvd W., Amarillo, TX, USA 79106; [b]Current Address: Limagrain Cereal Seeds, 6414 N. Sheridan, Wichita, KS 67204, USA; and [c]Current Address: Dept of Agronomy, University of Idaho Aberdeen Research & Extension Center, Aberdeen, ID, 83210, USA
[*]Corresponding Author: PH: 540-231-9789, Email: CGriffey@vt.edu.

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

P.V. Maloney[1], J.H. Lyerly[1], R.A. Navarro[1], C. Cowger[2], J.B. Holland[2],
G. Brown-Guedira[2], D. Marshall[2] and J.P. Murphy[1*]

[1]Department of Crop Science, Box 7629, North Carolina State University, Raleigh,
NC 27695; and [2]USDA-ARS, Plant Science Research Unit, Raleigh, NC 27695;
[*]Corresponding Author: PH: (919) 513-0000, Email: paul_murphy@ncsu.edu

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

Curt McCartney[1*], Daryl Somers[2], Anita Brûlé-Babel[3], George Fedak[4], Jeannie Gilbert[1] and Wenguang Cao[3]

[1]Agriculture and Agri-Food Canada – Cereal Research Centre, 195 Dafoe Road, Winnipeg, MB, Canada R3T 2M9; [2]Vineland Research and Innovation Centre, 4890 Victoria Ave. N., PO Box 4000, Vineland Station, ON, Canada L0R 2E0; [3]Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada R3T 2N2; and [4]Agriculture and Agri-Food Canada - Eastern Cereals and Oilseeds Research Centre, 960 Carling Ave. Building 50, Ottawa, ON, Canada K1A 0C6

[*]Corresponding Author: PH: 204-984-4503, Email: curt.mccartney@agr.gc.ca

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

J.P. Murphy* and R.A. Navarro

Department of Crop Science, Box 7629, North Carolina State University, Raleigh, NC 27695
*Corresponding Author: PH: (919) 513-0000, Email: paul_murphy@ncsu.edu

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/.

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

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

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

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

S. Navara and K.P. Smith*

Department of Agronomy and Plant Genetics, 1991 Upper Buford Circle, University of Minnesota, St. Paul MN
*Corresponding Author: PH: (612) 624-1211, Email: smith376@umn.edu

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

K.H.S. Peiris[1], Y. Dong[2], W.W. Bockus[3]and F.E. Dowell[4*]

[1]Department of Biological and Agricultural Engineering, Kansas State University, Manhattan, KS; [2]Department of Plant Pathology, University of Minnesota, St. Paul, MN; [3]Department of Plant Pathology, Kansas State University, Manhattan, KS; and [4]USDA-ARS, CGAHR Engineering and Wind Erosion Research Unit, Manhattan, KS
*Corresponding Author: PH: (785) 776-2753, Email: Floyd.Dowell@ARS.USDA.GOV

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.

ACKNOWLEDGEMENT AND DISCLAIMER

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

K.H.S. Peiris[1] and F.E. Dowell[2*]

[1]Department of Biological and Agricultural Engineering, Kansas State University, Manhattan, KS;
and [2]USDA-ARS, CGAHR Engineering and Wind Erosion Research Unit, Manhattan, KS
[*]Corresponding Author: PH: (785) 776-2753, Email: Floyd.Dowell@ARS.USDA.GOV

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

Seyed Mostafa Pirseyedi, Farhad Ghavami, Ajay Kumar Gupta,
Elias Elias, Shaukat Ali and Shahryar F. Kianian*

Department of Plant Sciences, North Dakota State University, Fargo, ND 58105
*Corresponding Author: PH: 701-231-7574, Email: s.kianian@ndsu.edu

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

Jessica Rutkoski[1], Jared Benson[2], Gina Brown-Guedira[3],
Jean-Luc Jannink[4] and Mark Sorrells[1*]

[1]Department of Plant Breeding and Genetics, 240 Emerson Hall, Cornell University, Ithaca, NY 14853;
[2]Dept. of Crop Science, North Carolina State University, Raleigh, NC 27695; [3]USDA-ARS, Plant
Science Research Unit, Raleigh, NC 27695 USA; and [4]USDA-ARS, R.W. Holley Center
for Agriculture and Health, Cornell University, Ithaca, New York, 14853
[*]Corresponding Author: PH: 607-255-2180, Email: mes12@cornell.edu

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

Daniela Sarti[1], Anthony Clark[1], Gina Brown-Guedira[2],
Yanhong Dong[3] and David Van Sanford[1*]

[1]University of Kentucky, Plant & Soil Science Dept., Lexington, KY 40546; [2]USDA-ARS, Plant Science Research Unit, Raleigh, NC 27695; and [3]University of Minnesota, Plant Pathology Dept., St Paul, MN 55108
[*]Corresponding Author: PH: 859-338-2409, Email: dvs@uky.edu

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

Brian Seda[1], Ruth Dill-Macky[2], Shiaoman Chao[3] and James Anderson[1*]

[1]University of Minnesota, Department of Agronomy & Plant Genetics, St. Paul, MN; [2]University of Minnesota, Department of Plant Pathology, St. Paul, MN; and [3]USDA-ARS, Biosciences Research Lab, Fargo, ND
[*]Corresponding Author: PH: (612) 625-9763, Email: ander319@umn.edu

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

Kevin P. Smith[1*], Aaron Lorenz[2], Jean-Luc Jannink[3],
Shiaoman Chao[4], Vikas Vikram[1] and Richard Horsley[5]

[1]Dept. of Agronomy and Plant Genetics, University of Minnesota, St. Paul, MN 55108; [2]Dept. of Agronomy and Horticulture, University of Nebraska, Lincoln, NE 68583; [3]USDA-ARS, Robert W. Holley Center for Agriculture and Health, Ithaca, NY 14853; [4]USDA-ARS, Northern Crop Science Lab, Fargo, ND 58105; and [5]Dept. of Plant Sciences, North Dakota State University, Fargo, ND 58108
*Corresponding Author: PH: 612-624-1211, Email: smith376@umn.edu

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

C. Sneller[1*], J-L. Jannink[2], A. Hoffstetter[1] and A. Cabrera[1]

[1]Department of Horticulture and Crop Science, The Ohio State University and the Ohio
Agriculture Research and Development Center, 1680 Madison Ave, Wooster,
Ohio 44691; and [2]USDA-ARS, Cornell University, Ithaca, NY
[*]Corresponding Author: PH: (330) 263-3944, Email: sneller.5@osu.edu

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)

C. Sneller[1*], P. Paul[2], M. Guttieri[1], L. Herald[1] and B. Sugerman[1]

[1]Dept. of Horticulture and Crop Science, and [2]Dept. of Plant Pathology, The Ohio State University, Wooster, OH, 44691
[*]Corresponding Author: PH: (330) 263-3944, Email: sneller.5@osu.edu

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*

C. Sneller[1*], M. Guttieri[1], P. Paul[2], J. Costa[3] and R. Jackwood[1]

[1]Department of Horticulture and Crop Science, The Ohio State University and the Ohio Agriculture Research and Development Center, 1680 Madison Ave, Wooster, Ohio 44691; [2]Department of Plant Pathology, The Ohio State University and the Ohio Agriculture Research and Development Center, 1680 Madison Ave, Wooster, Ohio 44691; and [3]Department of Plant Science and Landscape Architecture, University of Maryland, 2102 Plant Sciences Bldg., College Park, MD 20742-4452
[*]Corresponding Author: PH: (330) 263-3944, Email: sneller.5@osu.edu

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

Jin Sun, Yanyan Liu and Herbert Ohm*

Department of Agronomy, Purdue University, 915 W. State Street, West Lafayette, IN 47907
*Corresponding Author: PH: (765) 494-8072, Email: hohm@purdue.edu

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

S.L. Sydenham*, C. de Villiers, J.A.N. Asiwe and T.J. Tsilo

ARC-Small Grain Institute, Private Bag X 29, Bethlehem, 9700, South Africa
*Corresponding Author: PH: 27 58 3073408, Email: sydenhams@arc.agric.za

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

E. Wright[1], C. Griffey[1*], S. Malla[1], D. Van Sanford[2], S. Harrison[3],
J.P. Murphy[4], J. Costa[5], G. Milus[6], J. Johnson[7], A. McKendry[8],
D. Schmale III[9] and N. McMaster[9]

[1]Dept. of Crop and Soil Environmental Sciences, Virginia Tech, Blacksburg, VA 24061; [2]Dept. of Plant Sciences, University of Kentucky, Lexington, KY 40546; [3]Dept. of Plant, Environmental and Soil Sciences, Louisiana State University, Baton Rouge, LA 70803; [4]Dept. of Crop Science, North Carolina State University, Raleigh, NC 27695; [5]Dept. of Plant Science and Landscape Architecture, University of Maryland, College Park, MD 20742; [6]Dept. of Plant Pathology, University of Arkansas, Fayetteville, AR 72701; [7]Dept. of Crop and Soil Science, University of Georgia, Griffin, GA 30223; [8]Department of Plant Sciences, University of Missouri, Columbia, MO 65201; and [9]Dept. of Plant Pathology, Physiology, and Weed Science, Virginia Tech, Blacksburg, VA 24061
[*]Corresponding Author: PH: 540-231-9789, Email: CGriffey@vt.edu

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

Xiangye Xiao, Yanyan Liu and Herbert Ohm*

Department of Agronomy, Purdue University, 915 W. State Street, West Lafayette, IN, 47907
*Corresponding Author: PH: (765) 494-8072, Email: hohm@purdue.edu

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

Zhang, X.[1], Qiao, S.L.[1], Ma, H.X.[1*], Chen, H.[2],
Yu, G.H.[1], Sun, X.B.[1], and Shen H.Q.[2]

[1]Provincial Key Laborator of Agrobiology, Jiangsu Academy of Agricultural Sciences,
Nanjing 210014, China; and [2]Institute of Agricultural Sciences in the Coastal Area
in Jiangsu, Jiangsu Academy of Agricultural Sciences, Yancheng, 224002, China
[*]Corresponding Author: PH: (86) 25-84390300, Email: hxma@jaas.ac.cn

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

X. Zhang, Y.J. Zhou, D. Yang and H.X. Ma*

Provincial Key Laboratory of Agrobiology, Jiangsu Academy of Agricultural Sciences, Nanjing, P.R.China
*Corresponding Author: PH: (86) 25-84390300, Email: hxma@jaas.ac.cn

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.

ACKNOWLEDGEMENT

This work was financed by Chinese ISTCP (grant No.2009DFA32020), Modern Agro-industry Technology Research System (MATRS, grant No.nycytx-03), and by Provincial Key Technology R&D Program (grant No. BE2009343). We thank J.H. Chen, J.C. Xing, C.C. Wu, and L. Wang for sampling of *Fusarium* isolates and technical contribution.

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

S. Zhong[1*], C.G. Chu[1], S.S. Xu[2], S. Ali[1], K.D. Puri[1],
M. Mergoum[3] and S. Chao[2]

[1]Departments of Plant Pathology, North Dakota State University; [2]USDA-ARS, Northern Crop Science Lab, Fargo, ND 58105; and [3]Departments of Plant Sciences, North Dakota State University, Fargo, ND 58108
[*]Corresponding Author: PH: 701-231-7427, Email: shaobin.zhong@ndsu.edu

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.

ACKNOWLEDGEMENT AND DISCLAIMER

This material is based upon work supported by the U.S. Department of Agriculture, under Agreement No. 59-0790-8-067. This is a cooperative project with the U.S. Wheat & Barley Scab Initiative. Any opinions, findings, conclusions, or recommendations expressed in this publication are those of the author(s) and do not necessarily reflect the view of the U.S. Department of Agriculture.

SESSION 2:

PATHOGEN BIOLOGY AND GENETICS

Chairperson: Ivan Rayment

INTERACTIONS BETWEEN *FUSARIUM GRAMINEARUM* AND THE HOST PLANT

Drew Afton[1] and Frances Trail[1,2*]

[1]Department of Plant Biology, and [2]Department of Plant Pathology, Michigan State University, MI 48824
[*]Corresponding Author: PH: (517) 432-2939, Email: trail@msu.edu

ABSTRACT

Fusarium graminearum infects and produces disease on 3 major crops in the US: barley, wheat and corn. In barley and wheat, the disease affects the development and quality of grain. In corn, the disease may affect kernels, but can also cause rot of the lower stalks. *F. graminearum* grows in each host uniquely, and each host responds differently to the fungus. Our research attempts understand the fungal relationship to each of these three hosts. All three hosts support the generation of perithecia in the crop residue. However, in wheat and barley, these structures are associated with specific cell types, whereas in corn, the specificity is not as clear. The three hosts have been shown by other researchers to have differential sensitivity to DON. This may dictate the way infection is initiated and colonization progresses. We will present our findings on perithecium production, colonization, and mycotoxin accumulation. Differences in fungal-host dynamics clearly affect disease manifestation and carryover from one year to the next.

CHEMOTYPES OF *FUSARIUM GRAMINEARUM* FROM WHEAT IN 2009 AND 2010 IN NORTH DAKOTA

S. Ali, K.D. Puri, M. McMullen and S. Zhong*

Department of Plant Pathology, North Dakota State University, Fargo, ND
*Corresponding Author: PH: 701-231-7427, Email: Shaobin.zhong@ndsu.edu

ABSTRACT

Fusarium graminearum, the major causal agent of Fusarium head blight on cereals in the USA northern Great Plains, consists of three chemotypes, 3ADON, 15ADON, and NIV. Of these three chemotypes, 3ADON and 15ADON are commonly observed in North Dakota, and increase of 3ADON isolates in the *F. graminearum* population has been reported in recent years. Also, the 3ADON population has been shown to produce higher DON and disease severity in spring wheat cultivars. To monitor the prevalence of the two chemotype isolates in North Dakota, we collected FHB infected wheat samples from 12 and 28 counties across ND during 2009 and 2010, respectively. A total of 436 isolates (90 isolates from 2009 and 346 isolates from 2010) were obtained from these samples and DNA was extracted from the 2-3 days old mycelia of each isolate for PCR-based chemotyping using the trichothecene specific multiplex primers (3CON, 3NA, 3D15A, and 3D3A). Among those isolates collected in 2009, 91% (n= 82) and 9% (= 8) were of 15ADON and 3ADON chemotypes, respectively, and the eight 3ADON isolates were all from samples collected in Ransom County in northeast ND. Among the 346 isolates collected in 2010, 55.8% (n=193) and 44.2% (n=153) belonged to the 15ADON and 3ADON chemotypes, respectively. No 3ADON isolates were recovered from the samples collected from the three counties (Dickey, Richland, Sargent) located in the southeast corner of North Dakota in both years. However, more 3ADON isolates were recovered from the samples collected from most of the northern counties of the state. This study indicated that the 15ADON isolates were still predominant in general in North Dakota although 3ADON isolates were more common than the 15ADON isolates recovered from the samples collected in the northern counties of the state. The occurrence of more 3ADON isolates in the northern counties of North Dakota might be due to the cooler weather conditions during the growing season. Population genetics and aggressiveness of the isolates are still under investigation.

ACKNOWLEDGEMENT AND DISCLAIMER

This material is based upon work supported by U.S. Department of Agriculture, under Agreement No. 59-0790-8-067. This is a cooperative project with the U.S. Wheat and Barley Scab Initiative. Any opinions, findings, conclusions, or recommendations expressed in this publication are those of authors and do not necessarily reflect the view of the U.S. Department of Agriculture.

FUSARIUM HEAD BLIGHT INTENSITY, MYCOTOXIN LEVELS AND CHEMOTYPES OF *FUSARIUM GRAMINEARUM* SPECIES COMPLEX IN INDIVIDUAL FIELDS FROM PARANÁ STATE, BRAZIL

H.R. Feksa[1], J.L. de Almeida[1*], C.N. da Silva[2], D.A. de Lima[2],
E.M. Del Ponte[3] and D.J. Tessmann[2]

[1]Fundação Agrária de Pesquisa Agropecuária – FAPA, Guarapuava, PR, Brazil; Universidade Estadual
de Maringá, Departamento de Agronomia,Maringá, PR, Brazil; and [3]Universidade Federal do
Rio Grande do Sul, Departamento de Fitossanidade, Porto Alegre, RS, Brazil
[*]Corresponding Author: PH: 55 (42) 3625-8048, Email: juliano@agraria.com.br

ABSTRACT

Fusarium head blight (FHB) in Brazil is caused by members of the *Fusarium graminearum* species complex (Fg complex) that posses either a deoxynivalenol (DON) or nivalenol (NIV) chemotype. The relationship between disease intensity, mycotoxin levels and fungal chemotypes has not been determined at the field level, especially in Paraná State. The objective of this study was to determine the within-field distribution of Fg complex chemotypes, FHB intensity and trichotecenes (DON and NIV) and zearalenone (ZON) contamination in three commercial fields across the central and central-southern regions of Parana State, Brazil, during the 2011 growing season. At each field, during the soft dough grain state, twenty sampling points were randomly defined and three symptomatic spikes were taken to the laboratory. Strains were isolated (one per spike), purified and its DNA extracted with a cetyltrimethylammonium bromide (2% CTAB) method from mycelia of pure cultures growing in potato-dextrose broth. All isolates were identified to species level using a Fg16F/R primer sets. The Fg chemotypes were determined by a multiplex PCR assay that amplifies portions of Tri3 and Tri12 genes. For FHB ratings, four sampling points were defined in a single field and 100 spikes were randomly harvested. FHB incidence and severity and percentage of *Fusarium*-damaged kernels (FDK) of symptomatic spikes were estimated visually. In a subsample of kernels, DON, NIV and ZON were determined using a liquid chromatography–mass spectrometry method. Results showed that both 15-ADON and NIV co-occurred in the field with a slightly higher prevalence of 15-ADON (55 to 57%) over NIV (40.8 to 42.5%). Identification to species using TEF-based sequencing confirmed previous studies by showing that NIV-producers are *F. meriodionale* and 15-ADON are *F. graminearum sensu stricto*. FHB incidence and severity ranged from 12.8 to 29.0% and from 1.8 to 15.9%, respectively, across the three fields; FDK incidence ranged from 6.6 to 18.9%. The mean DON and ZON content in grains ranged from 33.3 to 1,427.2 µg/kg, and from 0 to 49.7 µg/kg, respectively. NIV was not detected in the samples. A higher correlation among the variables was found between FHB severity and DON levels. This study adds to the current knowledge by showing that mixed populations that produced either DON or NIV co-occur in wheat fields of Paraná State, although only DON has been determined by the current methods. Further investigations need to focus on the toxigenic potential of the populations and factors driving toxin production in the field.

GENOME SEQUENCING OF *FUSARIUM PSEUDOGRAMINEARUM* REVEALS A HORIZONTALLY ACQUIRED AMIDOHYDROLASE INVOLVED IN VIRULENCE

D.M. Gardiner[1*], P. Solomon[2], M. McDonald[3], M. Marshall[4], K. Kazan[1], S. Chakraborty[1], B. McDonald[3] and J.M. Manners[1]

[1]CSIRO Plant Industry, Queensland Biosciences Precinct, Brisbane, Queensland 4067, Australia. [2]Research School of Biology, College of Medicine, Biology and Environment, The Australian National University, Canberra ACT 0200, Australia. [3]Plant Pathology, Institute of Integrative Biology, ETH Zurich, LFW, Universitaetstrasse 2, CH-8092 Zürich, Switzerland. [4]Queensland Facility for Advanced Bioinformatics, The University of Queensland, Brisbane, Queensland 4072, Australia
[*]Corresponding Author: PH: 61 7 3214 2370, Email: Donald.Gardiner@csiro.au

ABSTRACT

Fusarium crown rot disease is a chronic problem in wheat and barley in arid environments such as Australia and there are currently no fully resistant wheat cultivars. In Australia, *F. pseudograminearum* is the pathogen predominantly associated with crown rot although related *Fusarium* species such as *F. graminearum* and *F. culmorum* have the ability to cause crown rot in some regions. These three *Fusarium* species can also cause globally important head blight disease of wheat. To increase our understanding of factors affecting pathogen virulence, we have sequenced the genome of an *F. pseudograminearum* isolate and compared it to the publically available genome sequence of *F. graminearum*. Despite overall sequence conservations, striking differences have also been observed between the genomes of these two *Fusaria*, including the presence of completely novel secondary metabolite gene clusters. Most strikingly we also identified a gene encoding an amidohydrolase that appears to have been acquired by horizontal gene transfer. This gene has a clear orthologue in the genome of the wheat pathogen *Phaeosphaeria nodorum* but not in any other fungal genome and the next closest sequence matches are from bacteria. Deletion of this gene from *F. pseudograminearum* resulted in a reduction in virulence on barley but not wheat. Population surveys suggest the gene has been present in both *F. pseudograminearum* and *Phaeosphaeria* lineages for a long time and could have been independently acquired by both species, possibly from bacteria. Its presence in these two unrelated pathogens but not in any other fungal species suggests a role for this gene in a common pathogenesis mechanism that targets an important defence pathway in cereals.

VEGETATIVE COMPATIBILITY – A NATIVE FUNGAL MECHANISM FOR INDUCING DEATH IN *G. ZEAE*

John F. Leslie* and Christopher Toomajian

Department of Plant Pathology, Throckmorton Plant Sciences Center,
Kansas State University, Manhattan, Kansas 66506-5502
*Corresponding Author: PH: 785-532-6176, Email: jfl@ksu.edu

ABSTRACT

Vegetative compatibility/incompatibility (vic) is a fungal version of self/nonself recognition and interaction that is known in many ascomycete fungi that results from two different alleles at a single locus being combined in the same cell, usually a heterokaryon, and collectively triggering apoptotic cell death. Genes responsible for the *vic* interaction are neither similar to one another nor necessarily evolutionarily conserved. Thus, individual *vic* loci may have this function in only a relatively few species. New anti-fungal control measures that rely on the ability to trigger apoptotic cell death on demand could result from an understanding of the mechanism used to trigger apoptotic cell death in response to the presence of *vic* heteroalleles in a common cytoplasm. At present we are mapping functional *vic* loci of *F. graminearum* onto an existing genetic map so that they can be localized in the physical genomic sequence and cloned. *vic* loci cannot be placed directly on a physical map since they are not evolutionarily conserved and easily identified by searching the published genome sequence, so they must first be mapped by their function. We have made a cross in which multiple *vic* loci are segregating and will select progeny that all have the same set of alleles at the *vic* loci. ORFs in the identified regions of the physical sequence will be screened for their ability to confer a vegetative incompatibility phenotype, with ORFs near or containing HET or WD0 domains in these regions tested first. Hypotheses regarding the mode of action for triggering cell death can be formulated once at least two alleles have been sequenced for several loci. Cloned *vic* alleles could be transformed into wheat with the goal of inducing apoptosis in *G. zeae* cells that penetrated beyond the surface of the wheat seed or seed head.

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This material is based upon work supported by the U.S. Department of Agriculture, under agreement no. 59-0206-1-113. This is a cooperative project with the U.S. Wheat and Barley Scab Initiative. Any opinions, findings, conclusions or recommendations expressed in this publication are those of the authors and do not necessarily reflect the view of the U.S. Department of Agriculture.

EFFECT OF FUSARIUM GRAMINEARUM CHEMOTYPES ISOLATED FROM CANADA ON SYMPTOMS, DAMAGED KERNELS AND MYCOTOXINS IN WINTER WHEAT GRAIN

A. Muckle, A. Schaafsma, V. Limay-Rios and L. Tamburic-Illincic*

Department of Plant Agriculture, University of Guelph Ridgetown Campus, Ridgetown, ON
*Corresponding Author: PH: (519) 674-1500 x63557, Email: ltamburi@ridgetownc.uoguelph.ca

ABSTRACT

Fusarium head blight (FHB) caused by *Fusarium graminearum* (Schwabe) is a serious wheat disease in North America and most cereal growing areas of the world. FHB results in economic loss due to decreased yield and quality, and the accumulation of mycotoxins such as deoxynivalenol (DON) in grain. The objective of this study was to investigate if there were differences in aggressiveness and mycotoxin production between Canadian *F. graminearum* strains (15-acetyl-DON (15DON) and 3-acetyl-DON (3DON)) in the moderately susceptible winter wheat 'Emmit'. In the fall of 2010, 'Emmit' was planted at Ridgetown Ontario in a randomized complete block design with four replications. One 15DON and one 3DON producing isolate was chosen from each of Nova Scotia, Quebec, Ontario and Manitoba for a total of eight isolates. At 50% anthesis, plots were inoculated with a backpack sprayer using each single isolate or a mixture of both isolates from each region for a total of twelve treatments, plus a control plot inoculated with water alone. To ensure spores were not transferred between experimental plots, guard plots were placed around each inoculated plot. We measured FHB symptoms by incidence (I), severity (S) combined into an FHB index (I X S/100), percentage of *Fusarium* damaged kernels (FDKs) using a monochromator near infrared reflectance spectrometer and DON, 15DON, 3DON content using a GC-MS system. Inoculated treatments resulted in significantly (P=0.05) higher field symptoms and FDKs compared to control. FHB indices 21 days after inoculation were highest after inoculation with 3DON *F. graminearum* isolates, followed by the mixture of isolates, 15DON isolates and control. In this moderately susceptible winter wheat cultivar 3-ADON *F. graminearum* isolates appear more aggressive in terms of field symptoms and when analyses are complete we expect to find higher levels of DON and its corresponding acetylated compound compared to mixture of both chemotypes and 15DONchemotypes.

DISCOVERY OF GENOME-WIDE VARIANTS IN THE *FUSARIUM GRAMINEARUM* CLADE FOR MAPPING AND EVOLUTIONARY ANALYSIS

Christopher Toomajian

Department of Plant Pathology, 4024 Throckmorton Plant Sciences Center,
Kansas State University, Manhattan, KS 66506-5502
Corresponding Author: PH: 785-532-0879, Email: toomajia@ksu.edu

ABSTRACT

Next-generation sequencing technologies provide a rapid entry into the characterization of DNA variation within many species. Variable DNA markers, such as AFLP, are abundant in *F. graminearum* and have been used to characterize the relationship between distinct pathogen populations, but since the genome sequence of *F. graminearum* has been determined, sequencing-based markers provide an added layer of information that can reveal what parts of the genome and thus what genes even diverged populations still share in common. This information can lead to a more rapid identification of the functional genetic differences between populations that can affect pathogen management and strategies for developing host plant resistance. Here we present results from a next-generation sequencing strategy for the efficient discovery of thousands of sequence variants across a sample of 24 isolates from the *F. graminearum* clade. We describe how these variants are being used to highlight genome regions that are highly differentiated between members of this clade as well as describe population structure within *F. graminearum sensu stricto* samples and genetic recombination patterns among these samples. We also describe similar next-generation sequencing strategies that are expected to lead to development of markers efficiently targeted in larger samples for mapping and evolutionary studies of the *F. graminearum* clade species. Finally, we highlight a methodology to use such high-density, sequence-based markers to identify novel pathogen variants that rapidly spread in populations. These rapidly spreading variants represent pathogen adaptations such as overcoming host plant resistance, and mapping these variants to the gene level will provide candidates for pathogen control targets and a better understanding of the pathogen adaptation process.

ACKNOWLEDGEMENT

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TIMING AND EVENTS OF *F. PSEUDOGRAMINEARUM* INFECTION OF WHEAT LEADING TO CROWN ROT

R.A. Westecott[1*], F. Obanor[2], D.M. Gardiner[2],
E.A. Aitkin[1] and S. Chakraborty[2]

[1]School of Agriculture & Food Sciences, The University of Queensland, 4067
Brisbane, Australia; and [2]Plant Industry, CSIRO, 4067 Brisbane, Australia
[*]Corresponding Author: PH: 61 7 3214 2256, Email: Rhyannyn.westecott@csiro.au

ABSTRACT

Crown rot (CR) is an economically important disease of wheat in several countries around the world. One of the most common causal agents of CR around the world is *F. pseudograminearum*, however, little has been done to study the process by which *F. pseudograminearum* infects wheat stems leading to CR development. To characterise the infection process of *F. pseudograminearum*, histological and real-time quantitative polymerase chain reaction analyses were used to assess fungal colonisation following a time course from infection to plant maturity.

Seven distinct phases were identified: i) attachment of spores to leaf sheath surface, ii) detachment or break down of non-germinating spores, iii) colonisation of external leaf sheath surface by hyphae, iv) penetration of host tissues, possibly through stomatal openings, followed by a reduction of superficial hyphae, v) migration of fungi to basal stem tissue, vi) colonisation of stem tissue from the base, and vii) a large increase of fungal biomass in all colonised stem tissue towards maturity of host. Fungal DNA was detected from plant tissues well in advance of those tissue showing visible CR symptoms of stem discoloration at all-time points assessed during the experiment, however, fungal colonisation never exceeded 50% of the stem length.

These results indicate that CR disease development involves multiple phases of colonisation possibly leading to the pathogen to prepare for a saprophytic phase following pathogenic colonisation of tissue. They also indicate that CR infection is unlikely to lead to the development of Fusarium head blight leading to a contamination of mycotoxins in the grain.

MICROBIAL DETOXIFICATIONS OF DEOXYNIVALENOL (DON) AND THEIR POTENTIAL APPLICATIONS IN MITIGATING MYCOTOXIN CONTAMINATIONS

Ting Zhou

Agriculture and Agri-Food Canada, Guelph Food Research Center, Guelph, Ontario, Canada
Corresponding Author: PH: (519) 780-8036, Email: ting.zhou@agr.gc.ca

ABSTRACT

It has been found that microbial communities of different ecological niches such as soils, plants and animal digesta are able to transform mycotoxins into their less or non-toxic forms. Bacterial strains capable of transforming DON under aerobic conditions into its isomer, 3-*epi*-DON, have been isolated from enhanced agricultural soil mixtures. Both in vitro and in vivo evaluations have indicated that this transformation results in significant toxicity reduction. In addition, several bacterial isolates, identified from different sources, are able to transform DON into its de-epoxy derivative DOM-1, a compound much less toxic than DON, under both aerobic and anaerobic conditions. These bacterial isolates are also capable of transforming certain other trichothecene mycotoxins into their less toxic forms. An animal trial has confirmed that pre-feeding treatment of DON contaminated feed with a DON transforming bacterial isolate can eliminate the adverse effects of DON on pig performance. Also, the identification of genes responsible for mycotoxin detoxification may result in applications for reducing mycotoxins in *Fusarium* infested cereals.

SESSION 3:

GENE DISCOVERY AND ENGINEERING RESISTANCE

Chairperson: Nilgun Tumer

TRICHOTHECENE MYCOTOXINS INHIBIT MITOCHONDRIAL TRANSLATION- IMPLICATIONS FOR FHB RESISTANCE

Anwar Bin-Umer[1], John McLaughlin[1], Debaleena Basu[1],
Susan McCormick[2] and Nilgun E. Tumer[1*]

[1]Department of Plant Biology and Pathology, School of Environmental and Biological Sciences,
Rutgers University, New Brunswick, NJ, 08901-8520; and [2]Bacterial Foodborne Pathogens
and Mycology Unit, National Center for Agricultural Utilization Research,
USDA, Agricultural Research Service, Peoria, IL, 61604
[*]Corresponding Author: PH: 732-932-8165 ext. 213, Email: tumer@aesop.rutgers.edu

ABSTRACT

Trichothecenes are foodborne toxins produced by various fungi including the plant pathogen *Fusarium graminearum*, which causes head blight (FHB) or scab of wheat and barley, resulting in yield reduction and contamination of grains with trichothecene mycotoxins. Conventional approaches have not yet yielded effective resistance in the field. Identifying molecular mechanisms underlying trichothecene toxicity will therefore aid in understanding *Fusarium* pathology and engineering effective resistance against FHB. Trichothecenes first identified as inhibitors of translation are known to have multiple effects on eukaryotes, including inhibition of DNA, RNA synthesis, cell division, membrane structure and integrity and mitochondrial function. It is not clear if these are primary or secondary effects of inhibition of cytosolic translation. We previously showed that mitochondria play a critical role in the toxicity of a type B trichothecene, trichothecin (Tcin). In this study, we investigated the direct effects of type A and type B trichothecenes on mitochondrial translation and membrane integrity in *Saccharomyces cerevisiae*. Sensitivity to trichothecenes increased when yeast cells required functional mitochondria for growth, while cells devoid of mitochondria (ρ^0) showed increased tolerance. T-2, DAS and Tcin inhibited translation in isolated yeast mitochondria by 67% (T-2), 54% (DAS) and 70% (Tcin). Trichothecenes caused fragmentation of mitochondrial membrane when yeast cells were treated for 6 h with high doses at which total translation was inhibited by 44% (T-2), 33% (DAS) and 91% (Tcin). A corresponding drop in mitochondrial membrane fragmentation (ψ_{mito}) and ROS levels was also observed. Trichothecenes, at low doses, did not promote severe membrane fragmentation or affect mitochondrial membrane integrity. Mitochondrial translation was significantly inhibited by 48% (T-2), 42% (DAS), and 34% (Tcin) at the low doses, but not total translation. These results indicate that trichothecenes directly target mitochondrial translation. Inhibition of mitochondrial translation is a primary target of trichothecenes and is not secondary to the disruption of mitochondrial membranes or cytosolic translation inhibition.

FIELD TESTS OF TRANSGENIC BARLEY LINES IN NORTH DAKOTA

Lynn S. Dahleen[1*], Robert Brueggeman[2], Tilahun Abebe[3] and Ron Skadsen[4]

[1]USDA-ARS, Fargo, ND; [2]Dept. of Plant Pathology, North Dakota State University, Fargo, ND;
[3]Dept.of Biology, University of Northern Iowa, Cedar Falls, IA; and [4]USDA-ARS, Madison, WI
Corresponding Author: PH: 701-239-1384, Email: lynn.dahleen@ars.usda.gov

ABSTRACT

Testing transgenic barley lines for FHB in the greenhouse does not necessarily give the same results as field tests. The objective of this project was to test 18 transgenic lines in replicated trials in an inoculated FHB nursery. Several programs have developed barley lines expressing anti-fungal and/or anti-toxin genes through partial funding from the USWBSI (Abebe, Dahleen, Skadsen). The Skadsen and Abebe labs inserted transgenes into the cultivar Golden Promise. These lines were backcrossed to Conlon for transgene expression in a cultivar that can be tested in North Dakota and Minnesota. In 2010, BC_1F_2 pooled seed of each line were tested. After another cross in 2010, the BC_2F_2 pooled seed were tested in 2011. In addition, 14 Conlon transgenic lines previously tested that showed reduced FHB and DON were evaluated again in 2011 along with wild type Conlon as the susceptible check and CI4196 as the resistant check. The mean FHB severity across all lines and replicates was 3.6%, mean FHB incidence was 48.5% and mean DON was 5.6 μg/g. Conlon and most of the transgenic lines showed significantly less DON than CI4196, but few other differences were detected in this single year trial. Comparison of seven lines tested in multiple years reveals that two transgenic lines (321-Tri12 and 823-tlp) consistently showed a 40% reduction in DON. Efforts to transfer these transgenes into resistant 6-rowed lines (Quest, ND20448) are underway to determine whether the transgene effect is additive to resistance being incorporated by the breeding programs.

ACKNOWLEDGEMENT

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IDENTIFICATION OF CANDIDATE GENES FOR HEAD BLIGHT AND DEOXYNIVALENOL RESISTANCE

F.M. Doohan[*]

Molecular Plant-Microbe Interactions Laboratory, University College Dublin, Belfield, Dublin 4, Ireland
[*]Corresponding Author: PH: (003531) 7162248, Email: Fiona.doohan@ucd.ie

ABSTRACT

We are investigating the mechanisms underpinning host resistance to deoxynivalenol (DON) and Fusarium head blight disease of wheat and barley. We use a three-pronged approach to identify genes and pathways that enhance DON resistance – genes of interest have been identified based on studies of host resistance, biocontrol and hormonal signaling pathways. Using a double haploid wheat population segregating for QTL *Fhb1*, we identified several genes associated with DON resistance. These genes were up-regulated in response to DON and segregated at the RNA accumulation level with *Fhb1*. Ongoing characterisation of these genes includes analysis of the effect of gene knockout on disease and toxin resistance and cellular studies on protein -protein interactions. *Pseudomonas flourescens* strain MKB158 was indentified as a bacterium that reduces FHB levels, associated toxin accumulation and yield losses. Using a microarray, we identified wheat genes potentiated by this bacterium to respond to *Fusarium culmorum*. Serpins and lipoxygenase genes were highly potentiated to respond to the pathogen. Future studies will focus on the role of serpins in induced resistance to FHB. Studies on brassinsteroid signaling identified the receptor *Bri1* as a key regulator of FHB resistance and toxin build-up in grain. On the basis of microarray analysis, we identified genes and pathways differentially regulated in a *Bri1* mutant as compared to wild type barley. These pathways are currently being investigated. On the basis of all our studies, we can conclude that there is a biochemically diverse array of genes that can be targeted to control FHB, thus offering great scope for breeding genotypes with effective long-term resistance to FHB. However, in the context of a practical breeding programme, the effect of some such genes on other biotic and abiotic interactions must now be investigated.

ACKNOWLEDGEMENTS

This research was funded by the Irish Department of Agriculture and Science Foundation Ireland.

UTILIZING ALIEN SOURCES OF RESISTANCE TO FUSARIUM HEAD BLIGHT FOR WHEAT IMPROVEMENT

Bernd Friebe[1*], Joey Cainong[1], Peidu Chen[2],
William W. Bockus[1] and Bikram S. Gill[1]

[1]Wheat Genetic and Genomic Resources Center, Department of Plant Pathology, Throckmorton Plant Sciences Center, Kansas State University, Manhattan, KS 66506-5502; and [2]The National Key Laboratory of Crop Genetics and Germplasm Enhancement, Nanjing Agricultural University, Nanjing, Jiangsu, PR China
[*]Corresponding Author: PH: (785) 532-2364, Email: friebe@ksu.edu

ABSTRACT

We are currently working with *Fhb3* for resistance to Fusarium head blight (FHB) transferred from *Leymus racemosus* and a second source of resistance derived from *Elymus tsukushiensis*. *Fhb3* is located in the short arm of the *L. racemosus* chromosome 7Lr#1 and was transferred to wheat in the form of a compensating T7AL·7Lr#1S Robertsonian translocation (RobT). Chromosome engineering was used to produce two distal (T7AL·7AS-7Lr#1S, rec 679 and rec 989) and one proximal (T7AL·7Lr#1S-7AS, rec124) recombinants in an Overley background. Our second source of FHB resistance is derived from a group-1 *E. tsukushiensis* chromosome $1E^{st}$#1. Chromosome engineering was used to produce distal (TWL·WS-$1E^{st}$#1S) and interstitial (Ti1WL·1WS-$1E^{st}$#1S-1WS) recombinants that are being evaluated for their resistance to FHB and DON accumulation. In addition, as one of our long-term objectives of conserving and utilizing wild germ plasm in wheat improvement, we are constructing chromosome introgression libraries of various alien species in Chinese Spring wheat. We are evaluating the following 23 RobTs for their resistance to FHB in the greenhouse using single-point inoculation. Promising lines will be crossed with Everest.

A PUTATIVE FUNGAL MIRNA THAT MIGHT PLAY A ROLE IN FUSARIUM HEAD BLIGHT PATHOGENESIS IN WHEAT

Aravind Galla, Yongbin Zhunag and Yang Yen*

Department of Biology and Microbiology, South Dakota State University, Brookings, South Dakota
*Corresponding Author: PH: (605) 688-4567, Email: yang.yen@sdstate.edu

ABSTRACT

miRNAs are endogenous, non-coding 21-23 nt RNA molecules that play important regulatory roles in eukaryotic gene expression by targeting mRNAs for cleavage or translational repression. Direct cloning has enabled the identification of many miRNAs; however, significant variation in their expression levels has made it difficult to clone low abundance miRNAs. No miRNAs has been reported so far by the traditional cloning method in Fungi. In our study of the role of miRNAs in the pathogenesis of Fusarium head blight in wheat, we identified a potential fungal miRNA which was specific to Fusarium inoculated wheat spikelets. Searching the genome of *Fusarium graminerum PH1* for its coding sequences revealed one where the putative transcript has the potential to form a hair pin loop secondary structure. Hence, the present study is taken up to prove it is indeed a fungal miRNA. The presence of this sequence will be verified in the genome of *Fusarium graminerum* isolate 4 by RT-PCR cloning of putative transcript. 5' and 3' RACE will be done to find the sequence of full length pre miRNA transcribed. A search against Rfam database that lists all the non-coding mRNAs will be useful to know if there is any protein being translated from this sequence. A target mRNA for the putative miRNA will be searched for in both *Fusarium* and wheat genomes which would be later verified by Northern or/and RT-PCR. RNAi studies will be conducted to better understand its function and relate its role in pathogenesis of Fusarium head blight in wheat.

ETHYLENE-SIGNALING IN WHEAT IS ESSENTIAL FOR TYPE I AND II RESISTANCE TO F*USARIUM GRAMINEARUM* AND TOLERANCE TO DEOXYNIVALENOL

Gillespie, Megan[1] and Scofield, Steve[2*]

[1]Agronomy Department, Purdue University, West Lafayette, IN 47907, USA; and [2]USDA-ARS,
Crop Production and Pest Control Research Unit, West Lafayette, IN 47907, USA
[*]Corresponding Author: PH: (765) 496-2926, Email: scofield@purdue.edu

ABSTRACT

Ethylene (ET) has been shown to be important for resistance to necrotrophic pathogens in *Arabidopsis*. While it remains unclear as to whether *Fusarium graminearum* is a hemibiotroph or a necrotroph, its necrotrophic mode of growth is most damaging. Thus, ET is a potential candidate for disease resistance signaling. We have used a Virus- Induced Gene Silencing (VIGS) system to silence genes in both the ethylene biosynthesis pathway and the ethylene signaling pathway. The genes were silenced in the resistant variety 'Ning' 7840. Upon application of the virus containing a portion of a wheat gene, the plants were screened for conversion from resistance to susceptibility. S-adenosylmethionine synthetase (SAMs) and an Ethylene Response Factor (ERF) in particular demonstrated remarkable conversion to susceptibility upon silencing. The importance of ethylene signaling was also observed using the gaseous inhibitor of ethylene signaling 1-Methylcyclopropene (1-MCP). Ning plants exposed to this inhibitor became significantly more susceptible to *F. graminearum* than control plants. These plants also become substantially more sensitive to the toxin deoxynivalenol. Additionally, the susceptible variety 'Bobwhite' becomes significantly more susceptible when exposed to 1-MCP and challenged with *F. graminearum*. 1-aminocyclopropane-1-carboxylic-acid (ACC) is a precursor of ethylene and is converted by the enzyme ACC-oxidase into ethylene. Both varieties become significantly more resistant to spray (Type I resistance assay) and point (Type II resistance assay) inoculations when treated with ACC. Our findings contradict recently published work proposing that *F. graminearum* exploits ethylene signaling to create susceptibility in wheat.

IDENTIFYING FHB RESISTANCE GENES IN WHEAT USING A NEXT-GENERATION SEQUENCING APPROACH

Anna Hofstad, Haiyan Jia, Benjamin P. Millett and Gary J. Muehlbauer*

Department of Agronomy and Plant Genetics, University of Minnesota, St. Paul, MN 55108
*Corresponding Author: PH: 612-625-6228, Email: muehl003@umn.edu

ABSTRACT

The *Fhb1* QTL on wheat chromosome 3BS confers type II resistance to Fusarium Head Blight (FHB). To gain a better genetic understanding of the *Fhb1* QTL locus, a near-isogenic line (NIL) pair carrying the resistant and susceptible alleles for *Fhb1* was subjected to SNP genotyping and gene expression analysis. We genotyped the NIL pair with 9,000 SNPs and defined the extent of the introgression and background variation. We established three experiments to examine gene expression in the NIL pair and to identify candidates for the *Fhb1* gene. These three experiments include: (1) point inoculation of spikelets with *Fusarium graminearum* and sampling the inoculated spikelets at 96 hours after inoculation; (2) deoxynivalenol (DON) inoculation and sampling at 12 hours after inoculation; and (3) point inoculation of *F. graminearum* and sampling the rachis at 48 and 96 hours after inoculation. We used next-generation sequencing of RNA to obtain the gene expression data. For experiment #1, approximately 250 million sequencing reads were obtained from each genotype. Overall, we identified approximately 425 genes that exhibited differential expression between the two genotypes. The expression of these genes provided the opportunity to better understand the resistant and susceptible interaction. In addition, we identified 31 candidate genes that showed high expression in the genotype containing the *Fhb1* resistant allele and no expression in the genotype with the *Fhb1* susceptible allele. Results of the differentially expressed genes will be presented.

SEQUENCE DIVERSITY AND HAPLOTYPE ANALYSIS OF FUSARIUM HEAD BLIGHT-RESPONSIVE GENES IN DIVERSE WILD AND CULTIVATED BARLEY

Yadong Huang[1], Benjamin P. Millett[1], Karen A. Beaubian[1], Stephanie K. Dahl[2], Brian J. Steffenson[2], Kevin P. Smith[1] and Gary J. Muehlbauer[1*]

[1]Department of Agronomy and Plant Genetics, and [2]Department
of Plant Pathology, University of Minnesota, St Paul, MN 55108
[*]Corresponding Author: PH: 612-625-6228, Email: muehl003@umn.edu

ABSTRACT

Wild (*Hordeum vulgare* subsp. *spontaneum*) and cultivated barley (*Hordeum vulgare*) accessions possess various degrees of resistance to Fusarium head blight (FHB). Integration of resistance from diverse sources into elite lines has the potential to enhance resistance, ultimately helping barley producers manage FHB. To identify potential alleles for FHB resistance, a candidate gene-based approach was used to associate nucleotide polymorphisms with variation in disease resistance. Previous GeneChip experiments have identified hundreds of barley genes exhibiting significantly up-regulated transcript levels in response to treatment with *Fusarium graminearum* or deoxynivalenol (DON). Thirty-five of these genes, including those implicated in defense responses such as cytochrome P450s, ABC transporters, glutathione-S-transferases, and UDP-glucosyltransferases, and those with regulatory and signal transduction roles such as zinc finger proteins, transcription factors and protein kinases, have been successfully re-sequenced from 16-30 diverse barley genotypes and analyzed using an association-based approach. Ectopic expression of one of the candidate genes, *HvUGT13248*, conferred DON resistance in yeast and *Arabidopsis*. A 2.5 kb genomic region of the *HvUGT13248* gene was re-sequenced from 30 genotypes. *HvUGT13248* maps to chromosome 5H bin4, which does not correspond with any previously mapped FHB resistance QTL. Interestingly, a SNP was identified only in the two most susceptible genotypes, ICB111809 (two-rowed) and PI383933 (six-rowed) and caused an amino acid change from glycine to arginine, suggesting that it may have functional significance. Significant associations between SNP sites and disease resistance within a mitogen-activated protein kinase (MAPK) gene were also detected. The map location of the MAPK gene is on chromosome 1H bin12 which is coincident with an FHB resistance QTL identified from populations carrying Chevron or Zhedar2 alleles, indicating that this gene is a promising candidate for further analysis. Haplotype and diversity analysis of the other 33 genes will also be reported.

SUBCELLULAR TARGETING OF A PLANT DEFENSIN MTDEF4.1 PLAYS A MAJOR ROLE IN CONFERRING RESISTANCE TO HEMIBIOTROPHIC AND BIOTROPHIC PATHOGENS IN TRANSGENIC *ARABIDOPSIS*

Jagdeep Kaur[1], Mercy Thokala[1], Alexandre Robert-Selianiantz[2],
Anita Snyder[1], Lauren Pitt[1], Patrick Zhao[3], Howard Berg[1],
Sona Pandey[1], Jonathan Jones[2] and Dilip Shah[1*]

[1]Donald Danforth Plant Science Center, Saint Louis, MO, USA; [2]Sainsbury Laboratory, John Innes Center, Norwich, UK; and [3]Plant Biology Division, The Samuel Roberts Noble Foundation, Ardmore, OK, USA
[*]Corresponding Author: PH: 314-587-1481, Email: dshah@danforthcenter.org

ABSTRACT

Plant defensin MtDef4.1 isolated from *Medicago truncatula* was shown to inhibit the hyphal growth of several *Fusarium* spp. *in vitro* at micromolar concentrations, including hemibiotroph *F. graminearum* which produces harmful mycotoxins. Transgenic *Arabidopsis* lines were generated in which MtDef4.1 was targeted to the extracellular space or to vacuoles or retained in the endoplasmic reticulum (ER), and tested for resistance to *F. graminearum* and to an obligate oomycete biotroph *Hyaloperonospora arabidopsidis* (*Hpa*). Using silique inoculations, we determined that transgenic *Arabidopsis* lines expressing MtDef4.1 targeted either extra- or intracellularly provided low level of resistance to this fungus. Interestingly, a couple of transgenic *Arabidopsis* lines expressing ER-retained and extracellular MtDef4.1 produced significantly reduced levels of mycotoxin deoxynivalenol. When evaluated for resistance to *Hpa*, transgenic lines expressing only extracellular MtDef4.1 displayed strong resistance to this pathogen, but the lines expressing intracellularly targeted MtDef4.1 did not. This is consistent with the lifestyle of this biotroph which grows intercellularly in the leaf. In contrast, since the lifecycle of *F. graminearum* consists of a brief biotrophic phase and a long necrotrophic phase, we postulate that co-expression of MtDef4.1 both extra- and intracellularly is required for effective control of this pathogen and mycotoxin accumulation in transgenic crop plants.

AN ACTIVATION TAGGING SCREEN TO IDENTIFY NOVEL GENES FOR FUSARIUM HEAD BLIGHT (FHB) RESISTANCE

John McLaughlin[1], Anwar Bin Umer[1], Debaleena Basu[1],
Susan McCormick[2] and Nilgun E. Tumer[1*]

[1]Biotechnology Center, School of Environmental and Biological Sciences, Rutgers University, New Brunswick,NJ 08901; and [2]Mycotoxin Research Unit, USDA-ARS-NCAUR, Peoria, Illinois 61604
[*]Corresponding Author: PH: (732) 932-8165 ext. 215, Email: tumer@aesop.rutgers.edu

ABSTRACT

The goal of this project is to identify plant genes that confer resistance against FHB and reduced DON accumulation. The identification of such genes offers the possibility to more fully understand the mechanisms of *Fusarium* susceptibility and to design transgenic strategies to increase FHB resistance in barley and wheat. We are using activation tagging to identify genes which confer resistance to trichothecenes. Activation tagging uses a modified T-DNA vector which contains multiple copies of the cauliflower mosaic virus (CaMV) 35S gene enhancer arranged in tandem. In addition to knocking out genes, the modified T-DNA vector can also function as an enhancer when inserted either upstream or downstream of a gene to produce gain-of-function phenotypes. The genomic location of the tag is readily identifiable by thermal asymmetric interlaced (TAIL) PCR. Using this approach, we have screened ~250,000 activation tagged *Arabidopsis* seeds for resistance to trichothecin and identified 30 lines that showed resistance. These plants were able to form roots on 4 µM Tcin, a concentration which severely inhibits germination and prevents root formation of the Col-0 wild type. Characterization of two of these lines using RT-qPCR identified an activation genotype in one line, termed *Arabidopsis thaliana resistant root formation1* or *At*RRF1 and a knockout genotype in the other, termed *At*RRF5. In *AtTRRF1*, two novel lipid transfer protein (LTP) genes, designated as LTP4 and LTP5, were overexpressed compared to the wild-type control. LTPs are small cysteine-rich proteins that transfer lipids between membranes *in vitro*. To verify resistance, both *LTP4* and *5* have been cloned into Gateway expression vectors and transformed into *Arabidopsis*. In *At*RRF5, the activation tag was found in the second exon of TBR (Trichome Birefringence-Like), a gene that controls synthesis and deposition of secondary wall cellulose. Expression of *At*RRF5 was not detected in the activation tagged line while the wild-type control showed a detectable level of expression, confirming that the insertion created a knockout genotype. Resistance in *At*RRF5 was confirmed by testing two independent knockout lines which were obtained from the Arabidopsis Information Resource (TAIR) collection. This research has shown that activation tagging is a useful method to identify plant genes which play a role in trichothecene resistance. The next step will be to determine if the novel genes identified from the screen in *Arabidopsis* will confer resistance to DON and FHB in transgenic wheat and barley plants. In addition, we are exploring the use of activation tagging in both wheat and barley to directly identify genes for trichothecene resistance in these crop species.

ENGINEERING DEFENSE REGULATORY GENES AND HOST SUSCEPTIBILITY FACTORS FOR ENHANCING FHB RESISTANCE IN WHEAT

Vamsi Nalam[1], Guy Klossner[1], Sujon Sarowar[1],
Hyeonju Lee[2], Harold Trick[2] and Jyoti Shah[1*]

[1]Department of Biological Sciences, University of North Texas, Denton, TX 76201; and
[2]Department of Plant Pathology, Kansas State University, Manhattan, KS 66506
[*]Corresponding Author: PH: (940) 565-3535, Email: shah@unt.edu

ABSTRACT

Fusarium head blight (FHB)/scab is a destructive disease of wheat and barley. *Fusarium graminearum* is one of the major causative agents of FHB in the US. The interaction between *Arabidopsis thaliana* and *F. graminearum* has provided an excellent system to identify and characterize genes and mechanisms that are critical to host defense as well as genes that predispose plants to *F. graminearum* infection. These studies in *Arabidopsis*, and more recently in wheat have demonstrated that a complex interaction between salicylic acid (SA) and jasmonic acid (JA) signaling contribute to the overall basal resistance against *F. graminearum*. Previously, we showed that constitutive expression of the *Arabidopsis NPR1* gene, which is a key regulator of SA signaling, enhanced basal resistance against *F. graminearum* in *Arabidopsis* and wheat (Makandar et al. 2006, 2010). The *PAD4* and *WRKY18* genes are two other *Arabidopsis* genes that promote FHB resistance when constitutively expressed in wheat. *PAD4* encodes a putative lipase/hydrolase that regulates multiple defense mechanisms, including SA and phytoalexin accumulation, and *WRKY18* encodes a transcription factor involved in the activation of defense genes. In contrast to *NPR1*, *PAD4*, and *WRKY18*, which promotes defense against *F. graminearum*, a lipoxygenase (LOX) activity contributes to host susceptibility to this fungus. This LOX activity has been targeted for silencing in wheat to promote FHB resistance. In addition, the non-host resistance mechanism is also being targeted for enhancing FHB resistance in wheat.

ACKNOWLEDGEMENT AND DISCLAIMER

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DEVELOPING A TRANSPOSON BASED GENOMIC APPROACH TO EXPLORE STRESS RESPONSIVE GENES IN WILD BARLEY

Prabhjot S. Nandha, Surinder Singh, Neil Dylan Lamb-Palmer,
Ravneet Kaur, Manjit Singh and Jaswinder Singh*

Plant Science Department, McGill University, Ste Anne De Bellevue, QC, Canada H9X3V9
*Corresponding Author: PH: (514) 398-7906, Email: Jaswinder.Singh@mcgill.ca

ABSTRACT

Biotic and abiotic stresses pose major threats to crop species and result in heavy yield losses worldwide. The wild barley subspecies, *Hordeum spontaneum*, has shown high genetic variation in biotic and abiotic stress responses and represents an excellent candidate for improvement of cultivated barley. Although *H. spontaneum* and cultivated barley are inter-fertile, introgressions of complex traits from wild material are often unsuccessful due to linkage drag. Modern genetic and genomic tools, however, have the potential to provide new avenues for identification of unique genes from wild species and their introgression into cultivated barley and beyond to meet the challenges posed by biotic stresses such as tolerance to FHB. The transposon-based gene tagging system is an effective technique for identifying and determining gene functions in large genome crops. Maize Activator (*Ac*) and Dissociation (*Ds*) elements have been utilized for insertional mutagenesis in heterologous plant species by introducing *Ds* elements in one plant and then crossing with a transposase (*Ac*TPase) expressing plant. This transposon system is now well established in cultivated barley (*Hordeum vulgare* L.). The main objective of this study is to develop a transposon tagging system in wild barley (*H. spontaneum*) to explore genes related to biotic and abiotic stress. In the present study, two approaches are being applied to develop *Ds* insertion lines (TNPs) in wild barley population. Two wild barley accessions, Damon and Shechem of *H. spontaneum* were independently hybridized and back crossed with *Ds* containing lines from cultivated barley. In addition, a tissue culture system for this species has been explored for introduction of *Ac* and *Ds* elements through particle gun bombardment. After establishing *Ac*/*Ds* system in wild barley, we aim to perform functional genomics studies for identification of stress response genes for later improvement of small grain cereals.

CAN *BRACHYPODIUM* PROVIDE INSIGHT INTO FHB?

P. Nicholson*, A. Peraldi, A. Steed and X. Chen

John Innes Centre, Norwich Research Park, Norwich NR4 7UH, UK
*Corresponding Author: PH: 44 1603 450616, Email: paul.nicholson@jic.ac.uk

ABSTRACT

Model species have the potential to provide significant insight into mechanisms involved in interactions between pathogens and crop hosts. We, along with others have used *Arabidopsis* as a model species to unravel aspects of the interactions between *Fusarium* and plant hosts. Our work revealed that *F. graminearum* exploits ethylene signalling to aid colonisation of *Arabidopsis* and wheat[1]. Although useful in many respects it is often difficult to undertake meaningful translation from a dicot model to crop species to identify candidate genes involved in FHB resistance. For this reason we turned to *Brachypodium distachyon* as an alternative. *Brachypodium* is a fully sequenced monocot species that has a small stature, rapid life cycle and non-demanding growth requirements. The high degree of genome conservation and synteny between *Brachypodium* and wheat makes this species even more attractive for providing information of direct relevance to cereal crop species. Furthermore, *Brachypodium* is being widely used in relation to bio-fuels and this is being accompanied by large-scale programmes to develop functional genomics resources in *Brachypodium*.

The ability of *F. graminearum* and *F. culmorum* to infect a range of *Brachypodium* tissues was examined in various bioassays. Histological studies were undertaken to investigate details of infection, colonisation and host response. Susceptibility to *Fusarium* and DON was assessed in two Brachypodium ecotypes.

Both *Fusarium* species infected all *Brachypodium* tissues examined and DON was produced in infected spike tissues. Hair cells were observed to be important sites of infection, supporting findings from other species. We also observed variation between ecotypes in resistance to both *F. graminearum* and DON.

Brachypodium exhibits characteristics of susceptibility highly similar to those of wheat, including susceptibility to spread of disease in the spikelets. This contrasts markedly with barley which exhibits almost complete resistance to spread between spikelets. We also found that DON appears to function as a virulence factor for infection of *Brachypodium* by *F. graminearum* as it does in wheat[2]. We concluded that *Brachypodium* potentially provides an excellent model for FHB in wheat.

More recently, we have been using T-DNA tagged lines (Brachy-TAG) to study the influence of a number of *Brachypodium* genes on resistance to *F. graminearum*. We will present some of our findings and discuss how they might influence attempts to improve FHB resistance in wheat and barley.

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IDENTIFICATION AND CHARACTERIZATION OF WHEAT GENES THAT ENHANCE PLANT RESISTANCE TO DON

Alexandre Perochon, Stephanie Walter, Guillaume Erard, Khairul Ansari,
Josephine Brennan, Chan Arunachalam and Fiona Doohan*

Molecular Plant Microbe Interactions Group, School of Biology and Environmental Science,
College of Life Sciences, University College Dublin, Belfield, Dublin 4, Ireland
*Corresponding Author: PH: 353-1-7162248, Email: fiona.doohan@ucd.ie

ABSTRACT

We focus on identifying biochemical pathways involved in the wheat response to the *Fusarium* virulence factor deoxynivalenol (DON). Using functional genomics techniques, DON-responsive transcripts were identified: these included transcripts encoding a basic leucine zipper transcription factor, a multidrug resistance protein ABC transporter, cytochrome P450s and novel proteins [1, 2]. Based on the results, we propose a model whereby the early oxidative stress response and a detoxification pathway contribute to DON tolerance. These studies have also highlighted that there are genes involved in the wheat response to DON that are not represented on the Affymetrix chip. For example, one DON-responsive wheat gene was identified via differential display analysis. It encodes a novel, evolutionary divergent protein. We are currently characterizing this gene at the molecular level.

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THE UDP-GLYCOSYLTRANSFERASE (UGT) GENE FAMILY OF *BRACHYPODIUM DISTACHYON*: FUNCTIONAL CHARACTERIZATION OF A CLUSTER OF CANDIDATE UGTS INVOLVED IN DETOXIFICATION OF DON TO DON-3-O-GLUCOSIDE

W. Schweiger[1], M.P. Kovalsky[1], F. Berthiller[2], M. Lemmens[3],
T. Nussbaumer[4], K. Mayer[4] and G. Adam[1*]

[1]Department of Applied Genetics and Cell Biology, University of Natural Resources and Life Sciences (BOKU),
Konrad Lorenz Str. 24, A-3430 Tulln, Austria; [2]Department IFA Tulln (BOKU), Center for Analytical
Chemistry and Christian Doppler Laboratory for Mycotoxin Metabolism, Konrad Lorenz Str. 20,
A-3430 Tulln, Austria; [3]Department IFA Tulln (BOKU), Biotechnology in Plant Production,
Konrad Lorenz Str. 20, A-3430 Tulln, Austria; and [4]Institute of Bioinformatics and
Systems Biology, Helmholtz Zentrum München, Neuherberg, Germany
[*]Corresponding Author: PH: 0043-1-47654-6380, Email: Gerhard.adam@boku.ac.at

ABSTRACT

Deoxynivalenol production is a virulence factor supporting fungal spread in infected wheat ears. Resistance to *Fusarium* in wheat is at least partly determined by the ability to convert DON into the non-toxic conjugate DON-3-O-glucoside (Poppenberger *et al.* 2003, Lemmens et al. 2005). Also during infection of the model grass *Brachypodium distachyon* with *F. graminearum* the detoxification product DON-3-O-glucoside (D3G) is formed. The gene family of *Brachypodium* UDP-glycosyltransferases consists of 177 predicted genes. Frequently theses genes occur in clusters. We functionally characterized a cluster of six BdUGT genes displaying the highest sequence similarity with the DON resistance conferring barley *HvUGT13248* (Schweiger *et al.* 2010). The six BdUGT genes were cloned with an N-terminal cMYC-tag to monitor protein levels in yeast. Only two out of the six homologs conferred DON resistance in yeast.

UGT genes highly similar to *HvUGT13248* are also present in the genomes of *Sorghum bicolor* and rice. The cluster of the Bd genes on chromosome 5 consists of 4 genes in a row and another 2 separated by 6 and 52 unrelated ORFs. The two separated genes were identified as functional DON detoxification genes, while the gene with the highest blast score (Bradi5g03390, 1.3e-190) was inactive. In *Sorghum* the gene with the highest similarity to *HvUGT13248* is a single copy gene on chromosome 6 (BlastP score 6.5e-185). Yet, two complex clusters of also highly similar genes (5 genes in mixed orientation from Sb02g030020 to Sb02g030060 with scores from 2.6e-126 to 8.5e-74) are present on chromosomes 2, and on chromosome 1 (two genes Sb01g031560 and Sb01g031540, scores 5.9e-168 and 7.4e-161), respectively. Also in rice the situation is complex, with a cluster of 3 homologous genes on chromosome 4 (Os04g0206500 to Os04g0206700 with scores of 1.4e-180 and 1.8e-166). UGT gene clusters seem to evolve rapidly and with changes in copy number. We therefore expect that it will be difficult to identify the true orthologs of UGT genes in different crop plants. Validation of the presumed function of candidate genes by heterologous expression and functional testing in yeast seems therefore warranted.

ACKNOWLEDGEMENT

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IDENTIFYING AND CHARACTERIZING BARLEY GENES THAT PROTECT AGAINST TRICHOTHECENES

S. Shin[1], A. Torres-Acosta [2], M. Lemmens[2], P. Paris[2], F. Berthiller[2], G. Adam[2], S. McCormick[3] and G.J. Muehlbauer[1*]

[1]Department of Agronomy and Plant Genetics, 411 Borlaug Hall, 1991 Upper Buford Circle, University of Minnesota, St. Paul, MN 55108; [2]Center of Applied Genetics, BOKU-University of Natural Resources and Applied Life Sciences, Muthgasse 18, A-1190 Vienna, Austria; and [3]USDA-ARS Mycotoxin Research Unit, Peoria, Illinois 61604, USA
[*]Corresponding Author: PH: 612-625-6228, Email: muehl003@umn.edu

ABSTRACT

Our overall goal is to identify genes that play a role in resistance to Fusarium Head Blight (FHB) and to develop and test transgenic wheat carrying these genes. In particular, we are interested in identifying genes that protect barley and wheat from the effects of trichothecenes. Previously, we conducted a large set of RNA profiling experiments during *Fusarium graminearum* infection of barley and inoculation with the trichothecene deoxynivalenol (DON). We identified a set of potential resistance genes that respond to trichothecene accumulation that encode a cysteine synthase, ABC transporters, UDP-glucosyltransferases (UGTs), cytochrome P450s, and glutathione-S-transferases (GST). In parallel, we developed an *Arabidopsis* assay to functionally test genes for their efficacy against trichothecenes. We then generated transgenic *Arabidopsis* over expressing one of the barley UGTs and five GSTs and tested these plants for their ability to grow on media containing trichothecenes. Transgenic *Arabidopsis* overexpressing the barley UGT and the GST genes exhibited high and moderate levels of tolerance to DON, respectively. Resistance to DON via UGT activity is considered an important component of resistance against FHB and is related to the ability to detoxify DON into DON-3-O-glucoside (D3G). DON feeding studies on the transgenic *Arabidopsis* carrying the barley UGT showed that DON was converted to D3G. More recently, we developed 18 events of transgenic wheat overexpressing the barley UGT and tested the transgenic lines for resistance to FHB. We identified five transgenic lines that expressed the UGT transgene and exhibited high type II FHB resistance.

TESTING TRANSGENIC SPRING WHEAT AND BARLEY LINES FOR REACTION TO FUSARIUM HEAD BLIGHT: 2011 FIELD NURSERY REPORT

Syverson, R.L.[1], Elakkad, A.M.[1], Dahleen L.S,[2] Nalam, V.J.[3], Klossner, G.[3], Shah, J.[3], and Dill-Macky, R.[1*]

[1]Department of Plant Pathology, University of Minnesota, St. Paul, MN; [2]USDA-ARS, RRVARC, Fargo, ND; and [3]Department of Biological Sciences, University of North Texas, Denton, TX
[*]Corresponding Author: PH: (612) 625-2227, Email: ruthdm@umn.edu

ABSTRACT

The 2011 field screening nursery, with 56 wheat and 88 barley plots was located at UMore Park, Rosemount MN. Trial entries and untransformed controls were submitted by the University of North Texas (9+1 wheat), and USDA (17+2 barley). Lines with known reactions to Fusarium head blight (FHB) were also included as checks. The wheat checks used were the moderately resistant Alsen, the susceptible cultivars Wheaton and Roblin, and a non-inoculated Wheaton check. The barley checks were the moderately resistant Quest and the susceptible cultivars Conlon (2-rowed), Robust and Stander. The experimental design was a randomized block with four replicates. Plots were 2.4 m long single rows. The trial was planted on May 18, 2011. All plots, except a non-inoculated Wheaton check, were inoculated twice. The first inoculation was applied at anthesis for wheat and at head emergence for barley. The second inoculation was applied three days after the initial inoculation (dai) for each plot. The inoculum was a composite of 50 *F. graminearum* isolates at a concentration of 100,000 (barley) or 200,000 (wheat) macroconidia.ml^{-1} with Tween 20 (polysorbate) added at 2.5 ml.L^{-1} as a wetting agent. The inoculum was applied using a CO_2-powered backpack sprayer fitted with a SS8003 TeeJet spray nozzle with an output of 10ml.sec^{-1} at a working pressure of 275 kPa. Mist-irrigation was applied from the first inoculation on July 7 till July 25 to facilitate FHB development. FHB incidence and severity were assessed visually 17 d.a.i. for wheat and 13 d.a.i. for barley on 20 arbitrarily selected heads per plot. FHB incidence was determined by the percentage of spikes with visually symptomatic spikelets of the 20 heads observed. FHB severity was determined as the percentage symptomatic spikelets of the total of all spikelets observed. Plots were harvested at maturity on August 5 (barley) and 11 (wheat). Fifty (barley) and 30 (wheat) heads where harvested from each plot, threshed and the seed cleaned manually. The wheat sub-samples were used to determine the percentage of *Fusarium* damaged kernels (FDK) and then all samples (wheat and barley) were ground and submitted for deoxynivalenol (DON) analysis. The data indicated that resistance was expressed in some of the transformed lines.

ACKNOWLEDGEMENTS AND DISCLAIMER

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AN OVERVIEW OF WHEAT TRANSFORMATION AT K-STATE

Harold N. Trick

Department of Plant Pathology, Kansas State University, Manhattan, KS 66506, USA
Corresponding Author: PH: (785) 532-1426, Email: hnt@ksu.edu

ABSTRACT

Genetic engineering of wheat holds great potential for trait development and plays a critical role in gene validation. Many wheat breeders see this technology as a valuable component of their wheat breeding toolbox. The U.S. wheat industry has also recognized the benefits and value of biotech wheat and is willing support the commercialization of transgenic wheat. More than half of the research projects at Kansas State University's Plant Transformation Facility are now focused on transgenic wheat. Over the past decade, the facility has collaborated on a number of projects both applied and basic, including projects funded through USWBSI. This presentation will give an overview of wheat transformation at K-State: the overall transformation process; past and present transformation capacities of the facility and; examples of the collaborative projects using transgenic wheat.

ACKNOWLEDGEMENT AND DISCLAIMER

This material is based upon work supported by Kansas Wheat Commission and the U.S. Department of Agriculture, under Agreements No. 59-0790-8-060 and 58-3602-9-775. These are cooperative projects with the U.S. Wheat & Barley Scab Initiative. Any opinions, findings, conclusions, or recommendations expressed in this publication are those of the author(s) and do not necessarily reflect the view of the U.S. Department of Agriculture.

A NEW SOURCE OF RESISTANCE TO FUSARIUM HEAD BLIGHT FROM WHEAT- *ELYMUS REPENS* INTROGRESSIONS

J. Zeng[2], W. Cao[1], G. Fedak[1*], P. Hucl[3], Y. Yang[2], A. Xue[1] and D. Chi[1]

[1]Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, 960 Carling Ave., Ottawa, ON, K1A 0C6; [2]Triticeae Research Institute of Chengdu Science Academy, Sichuan Agricultural University, Wenjiang District 611130, Sichuan, China; and [3]Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK, S7N 5A8 Canada
[*]Corresponding Author: PH: (613) 759-1393, Email: george.fedak@agr.gc.ca

ABSTRACT

Elymus repens (L.) Gould (2n = 6x = 42, **StStStStHH**) is a hexaploid wild grass species, distantly related to bread wheat (*Triticum aestivum* L. em Thell; 2n = 6x =42, **AABBDD**). It has a high level of resistance to Fusarium head blight (FHB). The objective of this study was to transfer genes for resistance to FHB from *E. repens* to common bread wheat. The cross Crocus/*E. repens* was made in Crop Development Center experimental field, Department of Plant Sciences, University of Saskatchewan. The F_1 plants were backcrossed to Crocus, then seeds from the BC_1F_1 plants were bulked and advanced to the BC_1F_7 generation. Sixteen lines were selected and evaluated for FHB reaction in the nursery in Ottawa in 2007 and 2008. Two lines, P1142 and P1131 (F8), were re-selected based on agronomic traits and FHB resistance performance. The results showed that the line P1142 was still segregating, with chromosome numbers ranging from 42 to 56, while the line P1131 with 56 chromosomes was stable morphologically. Cytological study and *in situ* hybridization analyses indicated that we obtained several wheat-*E. repens* addition and translocation lines, and two partial amphiploids. The results of greenhouse FHB evaluation by point inoculation showed that all the lines had a high level of resistance to FHB with only one spikelet infected (6%), compared to the check Roblin (100%) and the parent Crocus (85%). This new resistance source will be useful for the improvement of FHB resistance in wheat.

IDENTIFYING AND CHARACTERIZING CANDIDATE GENES ASSOCIATED WITH FHB RESISTANT QTL *QFHB1*

Yongbin Zhuang, Aravind Galla and Yang Yen*

Department of Biology and Microbiology, South Dakota State University, Brookings, SD 57007, USA
*Corresponding Author: PH: (605) 688-4567, Email:Yen.Yang@sdstate.edu

ABSTRACT

The goal of this research is to identify and characterize genes associated with *Qfhb1*, a major FHB resistance QTL that has been mapped on wheat chromosome 3BS. Our previous study of FHB molecular mechanism has identified 281 resistance-related and 79 susceptibility-related genes. We screened these 360 genes for their differential expression with qPCR between a pair of near-isogenic lines 260-2 (R) and 260-4 (S) developed by Anderson's group at University of Minnesota and potential candidates were confirmed by screening their differential expression between a resistant and a susceptible pools, which consist 10 most resistant or susceptible lines from a $F_{2:8}$ recombinant inbred population between Sumai 3 and Y1193-6. Plants were grown in green house under a light cycle of 16 h light and 8 h dark. The first flowering floret of randomly chosen plants was either challenged with *Fusarium graminearum* macroconidia diluted in water (70,000~ (100,000 conidia /mL) or with water as the control. The inoculated spikes were immediately covered with plastic bags to maintain the humidity. RNA samples were isolated from spikelets collected from 10 plants in 24, 48 or 72 h after inoculation, respectively, for each treatment, and used for qPCR assay. Each qPCR assay was composed of three biologic and three technic repeats. Statistic analysis was done to identify significant differential expressions at $p \leq 0.05$. Of the genes screened, 16 potential candidates have been identified. Further validation and gene-disease association are in progress.

SESSION 4:

FOOD SAFETY, TOXICOLOGY AND UTILIZATION OF MYCOTOXIN-CONTAMINATED GRAIN

Chairperson: David Kendra

INVESTIGATING THE IMPACT OF HISTOLOGICAL AND / OR CHEMICAL DIFFERENCES IN THE BRAN OF WHITE AND RED WHEAT NEAR-ISOGENIC LINES ON FUSARIUM MYCOTOXIN ACCUMULATION

H.D.P. Damecharla[1], W.A. Berzonsky[1*] and P.G. Krishnan[2]

[1]Department of Plant Science, Seed Technology Laboratory, and [2]Department of Health and Nutritional Sciences, Crop Quality Lab, South Dakota State University, Brookins, SD
[*]Corresponding Author: PH: 605-688-5334, Email: william.berzonsky@sdstate.edu

ABSTRACT

Hard white wheat (*Triticum aestivum* L.) is the newest U.S. class of wheat, and demand for this class has increased since milling it can provide higher flour yields and end-product appearance and taste are improved. However, many white wheat varieties are highly susceptible to Fusarium head blight (FHB), caused by *Fusarium graminearum* (teleomorph *Gibberella zeae*). Furthermore, the FHB mycotoxin, deoxynivalenol (DON) accumulates primarily in the bran layer of kernels. Since significant levels of DON can accumulate in infected wheat kernels, the bran may be a significant source of DON, particularly in whole white wheat products. Moreover, differences in bran thickness between white and red wheat kernels may impact the DON in such products, presenting a potential food contamination risk. Near-isogenic lines (NILs) of red and white winter wheat were developed for use in this study to examine potential bran differences and identify the impact of any genetic differences on the accumulation of DON in bran. Parents, NILs, and control varieties were artificially infected with FHB, and samples were collected from both infected and uninfected plants. For DON content analyses, samples from infected plants were visually sorted into kernels without damage and into *Fusarium* damaged kernels (FDK). To compare accumulation of DON in the bran layer, the same samples were pearl-milled to produce bran and non-bran fractions. DON accumulation in bran fractions was significantly higher than in non-bran fractions. The mean DON content in the bran fraction from the white parent was higher than for the red parent, but the mean DON content in the bran fraction from the red NILs was higher than for the white NILs. Continuing research is designed to determine if differences in DON accumulation are due to differences in the morphological or chemical properties of the white compared with the red bran layer.

NOVEL FEEDING BIOASSAY FOR CHARACTERIZATION OF DEOXYNIVALENOL-INDUCED FEED REFUSAL IN THE MOUSE

Brenna Flannery[1,2] and James J. Pestka[1,2,3*]

[1]Department of Food Science and Human Nutrition, [2]Center for Integrative Toxicology, and [3]Department of Microbiology and Molecular Genetics, Michigan State University, East Lansing, MI 48824
[*]Corresponding Author: PH: (517) 353-1709, Email: pestka@msu.edu

ABSTRACT

Deoxynivalenol (DON) is a trichothecene mycotoxin that is resistant to heat processing, and as a result, contaminates grain products worldwide. DON causes feed refusal and growth retardation, the latter of which has been used to establish a Tolerable Daily Intake (TDI) in Europe. Despite being a primary adverse effect, the mechanisms of DON-induced feed refusal are not well understood. In order to relate feed refusal to other DON-induced physiological changes, the dose and timing at which feed refusal occurs needs to be elucidated. Using a novel mouse feeding bioassay, we determined DON's short-term effects on feed refusal following intraperitoneal injection. DON caused a significant, dose-dependent reduction in food intake that could be measured with-in two hours of exposure. In naïve mice, the lowest dose that caused feed refusal was 1 mg/kg bw. At 1 mg/kg bw DON, the duration of feed refusal was 3 hr; while at 5 mg/kg bw feed refusal lasted 6 hr. Mice appeared to become resistant to DON-induced feed refusal upon subsequent 24 hr exposures; yet, mice re- exposed to DON (5 mg/kg bw) 14 days after the last exposure exhibited a feed refusal response comparable to that of naïve mice. Taken together, these data suggest DON induced transient feed refusal. Furthermore, these data suggest that feed refusal and possibly other DON-induced physiological changes can be affected by the number of DON exposures and time since the last exposure. This information is important because risk assessments of DON have been based on chronic feeding studies.

CONVERSION OF DEOXYNIVALENOL TO 3-ACETYLDEOXYNIVALENOL IN BARLEY-DERIVED FUEL ETHANOL CO-PRODUCTS WITH YEAST EXPRESSING TRICHOTHECENE 3-*O*-ACETYLTRANSFERASES

Piyum A. Khatibi[1], Justin Montanti[2], Nhuan P. Nghiem[2], Kevin B. Hicks[2], Greg Berger[3], Wynse S. Brooks[3], Carl A. Griffey[3] and David G. Schmale III[1*]

[1]Department of Plant Pathology, Physiology, & Weed Science, Virginia Polytechnic Institute & State University, Blacksburg, VA; [2]Eastern Regional Research Center, Agricultural Research Service, Department of Agriculture, Wyndmoor, PA; and [3]Department of Crop and Soil Sciences, Virginia Polytechnic Institute and State University, Blacksburg, VA, USA
[*]Corresponding Author: PH: (540) 231-6943, Email: dschmale@vt.edu

ABSTRACT

The trichothecene mycotoxin deoxynivalenol (DON) is a common contaminant of distillers dried grains with solubles (DDGS; a co-product of fuel ethanol fermentation). Even low levels of DON (≤ 5 ppm) in DDGS pose a significant threat to the health of monogastric animals. Enzymes known as trichothecene 3-O-acetyltransferases convert DON to 3-acetyldeoxynivalenol (3ADON), and may reduce its toxicity. Two *Fusarium* trichothecene 3-*O*-acetyltransferases (FgTRI101 and FfTRI201) were cloned and expressed in yeast during a series of small-scale ethanol fermentations using barley. During the fermentation process, FgTRI101 converted 9.2% to 55.3% of the DON to 3ADON, resulting in DDGS with reductions in DON and increases in 3ADON in the Virginia winter barley cultivars Eve, Thoroughbred and Price, and experimental line VA06H-25. Analysis of barley mashes prepared from the barley line VA04B-125 showed that yeast expressing FfTRI201 were more effective at acetylating DON than those expressing FgTRI101; DON conversion for FfTRI201 ranged from 26.1% to 28.3%, whereas DON conversion for FgTRI101 ranged from 18.3% to 21.8% in VA04B-125 mashes. Ethanol yields were highest with the industrial yeast strain Ethanol Red, which also consumed galactose when present in the mash. This work demonstrates the potential of using transgenic yeast to modify DON during commercial fuel ethanol fermentation and has been published in the journal *Biotechnology for Biofuels*.

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COMPARISON OF DON ACCUMULATION IN BRAN AND FLOUR FRACTIONS OF FHB INFECTED WINTER WHEAT

Swasti Mishra[1*], Lee Siler[1], Sue Hammar[1], Yanhong Dong[2] and Janet Lewis[1,3]

[1]Dept. of Crop and Soil Science, Michigan State University, E. Lansing MI, 48824; [2]Dept. of Plant Pathology, University of Minnesota, St. Paul, MN 55108; and [3]Current Address: Bayer CropScience, 206 Biochemistry Hall, UNL East Campus, Lincoln NE, 68583-074
[*]Corresponding Author: PH: (517) 488-9885, Email: mishrasw@msu.edu

ABSTRACT

Fusarium head blight (FHB) in wheat is caused by the fungus *Fusarium graminearum*, which infects wheat heads at anthesis. One of the biggest causes of loss due to infection by *F. graminearum* is the production of mycotoxins in the infected grains, which are mainly type B trichothecenes. Studies have reported that a higher fraction of the total DON in the kernel accumulates in the bran. The aim of this study is to determine if genetic variation for resistance to toxin accumulation in the bran exists in locally adapted soft wheat varieties. Thirty-nine locally adapted cultivars and breeding lines (20 soft red, 19 soft white) having varying levels of visual FHB resistance and whole grain DON ppm were selected. The genotypes were planted in a multi-year (2009, 2010 and 2011) and multi-location study (2 locations per year) with artificial inoculation using two different methods. The two inoculation methods were 1) grain spawn followed by misting and 2) spray inoculation followed by bagging to maintain humidity. Visual symptoms were measured at 21dpi as % Incidence and % Severity. *Fusarium* damaged kernel scoring was carried out on harvested and cleaned subsamples by comparing to a set of standards. Accumulation of toxin was quantified by the GC-MS at the University of Minnesota, on a whole grain sample, and milled bran and flour fractions. Toxin (DON) data is presented for samples from 2009 and 2010.

A NEW UNDERSTANDING OF DON'S MECHANISMS OF ACTION

James J. Pestka*

Department of Food Science and Human Nutrition, Michigan State University, East Lansing, MI 48823
*Corresponding Author: PH: 517-353-1709, Email: pestka@msu.edu

ABSTRACT

Deoxynivalenol (DON, vomitoxin), a trichothecene mycotoxin produced by the field fungus *Fusarium*, is a very frequent contaminant of cereal-based foods throughout the world. A joint committee of the WHO-FAO designated DON as a global public health concern based on its capacity to cause growth suppression and emesis in experimental animals as well as its etiologic association with non-infectious human gastroenteritis. Biomarker studies have recently confirmed that human exposure to this toxin is relatively common and closely correlated with grain consumption. This problem has been exacerbated by recent changes in global climate and agricultural practices that have greatly increased fusarial blight. The inherent challenge of balancing risks (human growth stunting and acute illness) and benefits (availability of essential dietary staples) associated with consuming DON-containing grains has created a public health dilemma. DON's anorexic and emetic effects are highly consistent with aberrant hormonal and neuronal signaling within the "gut-brain axis" that is responsible for appetite control, however, the underlying mechanisms for such dysregulation remain undetermined. We propose that DON induces anorexia and emesis by aberrantly inducing secretion of gut satiety hormones by enteroendocrine cells. This hypothesis is based on our studies demonstrating that: 1) in the mouse, a emesis-resistant species, DON-induced anorexia corresponds with rapid, robust elevation in plasma levels of the gut satiety hormones cholecystokinin (CCK) and peptide YY (PYY), 2) in the mink, an emesis-susceptible species, DON causes both anorexia and emesis, and 3) DON induces CCK secretion in the murine STC-1 enteroendocrine cell, an established model for bitter taste receptor activation. Our hypothesis is further supported by studies of other researchers demonstrating that CCK and PYY dose-dependently induce anorexia and emesis in animals as well as humans. The rationale for conducting this research is that once it is known how DON disrupts regulation of the gut-brain axis, it will enable the rational design of targeted cell, animal and epidemiological studies to better understand the potential for adverse chronic and acute effects in individuals who consume this and related trichothecene mycotoxins.The expected outcomes of these studies will be an increased understanding of trichothecene-induced anorexia and emesis relative to critical initiating events, hormonal mediators, neuronal targets, and longevity of these effects. These findings will have a positive impact, because it will be an initial step in the path to predicting the specific thresholds of DON and other foodborne toxins for eliciting adverse human effects as well as the persistence and reversibility of these effects. Such knowledge can facilitate more precise science-based safety assessment and result in improved management strategies that reduce the risk of foodborne illness from DON and other trichothecenes while at the same time assuring food security through the availability of low cost, nutritionally important wheat- and barley-based foods.

THE ECONOMICS OF MYCOTOXIN CONTAMINATION TO THE MILLING INDUSTRY AND CONSUMERS

R. Don Sullins, PH.D.

Vice-President, Technical Services, ADM Milling Company
*Corresponding Author: PH: (913) 491-7563, Email: Don.Sullins@adm.com

ABSTRACT

Since there appears to be limited natural genetic disease resistance in our grains, Mother Nature holds the upper-hand in the manifestation of the diseases and the toxins many of them produce. It is imperative to fund and provide research for identification and implementation of disease resistance into our grain supply. Mycotoxin outbreaks occur from year to year and we as processors, ingredient manufacturers and food companies have to be extremely careful not to permit these compounds into our food products and ultimately reaching the consumer. The European Union has specific regulations for deoxynivalenol (DON) and Ochratoxin A in food systems. Canada only has standards for deoxynivalenol in Soft Wheat with no standards for Hard Red Winter or Spring wheats. The United States has standards for Aflatoxin in Corn, Guidelines for DON in wheat products only (bran, germ, flour) and none for Ochratoxin in Food Products. With the recent food recalls, the Food Safety Modernization Act and consumer demands for safer foods, the pressure is on us – the Processing Industry – to remove all concerns regarding potential contaminants and food safety for the consumer. To the processor, this responsibility becomes a very expensive exercise of determining initially whether to Accept or Reject in-bound commodities solely based on mycotoxin levels. The Canadian Food Inspection Agency (CFIA) and the United States Food Inspection Agency (FDA) have stepped up and/or staffed up to increase surveillance by on-site inspections and collecting of samples for mycotoxin analysis. In-house testing is necessary to assure the grain is acceptable for food use and this directly impacts food prices. The cost of mycotoxin test kits, time and labor to sample and conduct the analysis could cost the processor from .5M to $1M annually. If the local crop is unacceptable and one must reach out beyond the local grain draw area for origination, freight costs could be an additional $9M for a given geographic location. Therefore, as a processor, we would encourage even greater research efforts to develop resistant varieties that provide the producer a better quality crop, the processor a raw material that is more consistent year-to-year for quality and the consumer a quality retail product mitigating rising food prices.

RELATION OF 8-KETOTRICHOTHECENE STRUCTURE TO ANOREXIGENIC RESPONSE IN THE MOUSE

Wenda Wu[1], Brenna Flannery[1,2], Watanabe Maiko[4],
Sugita-Konishi Yoshiko[4] and James J. Pestka[1,2,3]

[1]Department of Food Science and Human Nutrition, [2]Center for Integrative Toxicology,
[3]Department of Microbiology and Molecular Genetics, Michigan State University,
East Lansing, MI, USA; and [4]National Institute of Health Sciences, Tokyo, Japan
[*]Corresponding Author: PH: (517) 353-1709, Email: pestka@msu.edu

ABSTRACT

The trichothecene mycotoxin deoxynivalenol (DON) is well known to cause food refusal in experimental animals. However, the relative anorexic potencies of structurally related 8-keto-trichothecene are not known. A simple food refusal bioassay employing the mouse was used to compare the effects of 8-keto-trichothecene following by oral and intraperitoneal (ip) exposure. The results suggested that, similar to DON, the anorexic effects of 3-acetyldeoxynivalenol (3-ADON) and 15-acetyldeoxynivalenol (15-ADON) were transient (lasting only a few hours) and food intake recovered within 16 h. In contrast, the food refusal responses to nivalenol (NIV) and fusarenon X (FX) were markedly different, persisting from 36 to 96 h depending on administration route. For both ADONs, the no observed adverse effect levels (NOAEL) and lowest observed adverse effect levels (LOAEL) were 0.5 and 1 mg/kg bw for ip, respectively, and 1 and 2.5 mg/kg bw for oral, respectively. The NOAEL and LOAEL for FX were 0.025 and 0.25 mg/kg bw, respectively, for both ip and oral exposure. The NOAEL and LOAEL for NIV were 0.01 and 0.1 mg/kg bw, respectively, for ip and 0.1 and 1, respectively, for oral exposure. To summarize, the anorexic effects of 8-ketotrichothecene followed the rank order NIV>FX>DON=15-ADON=3-ADON, based on the NOAEL and LOAEL, with effects being greater when administered ip as compared to oral exposure. 3-ADON and 15-ADON caused acute anorexia, similar to DON, whereas, the anorexic effects of NIV and FX were more persistent.

SESSION 5:

FHB MANAGEMENT

Co-Chairpersons: Larry Madden and
Stephen Wegulo

NON-CHEMICAL APPROACH FOR CONTROL OF FUSARIUM HEAD BLIGHT OF WHEAT

N. Aitkhozhina

Plant Pathology Laboratory, Institute of Microbiology and Virology,
Ministry of Education and Science, Almaty, Kazakhstan
Corresponding Author: PH: (727) 2921852, Email: nag_aitkhozhina@yahoo.com

ABSTRACT

Fusarium head blight (FHB) is a serious disease worldwide, of economic importance. FHB of wheat and other cereals in Kazakhstan is mainly caused by *Fusarium graminearum* and/or *F.culmorum*. Both pathogens are of moderate virulence. Nevertheless, they can cause yield decrease and grain quality. Traditionally applied synthetic fungicides are of high cost and not ecologically safe. Thus, effective, low cost and environmentally friendly control agents are of significant importance. Several species of *Brassicaceae* are known as suppressive agent of plant pathogenic fungi, especially of soil-borne ones. This study provides a novel approach to manage FHB based on alternative non-chemical strategy of biofungicide search. A laboratory bioassays and a field experiment were conducted over 3 years to evaluate efficacy of ground horseradish (*Armoraceae lapathifolia*) tuber tissue atmosphere and squeezed juice as a biocontrol agent. Three variants in vitro bioassays were made with *F. graminearum*, *F. culmorum* and *Bipolaris sorokiniana* strains: i) on PDA medium amended with ground horseradish tuber mass; ii) on PDA plates with two 0,5 cm diameter wells filled with squeezed juice mixed with water 1:1 (v/v); iii) PDA plates with fungal cultures exposed to horseradish tuber tissue atmosphere. Control constitutes plates with fungal strains only. Radial growth of cultures incubated at 23ºC after 7 d was 3 (i), 2,5 (ii), and 1,5 (iii) cm, respectively. Surface of control plates by 7th d was fully covered with mycelium mat. Light microscope observation revealed deformed hyphae, swollen tips and weakly germinating conidial aggregates compared to profuse sporulating culture and actively germinating conidia in control plates. Results made in collaboration with wheat growers have shown that seeds treated with squeezed juice mixed with water and seed lot placed for 7 hrs under the atmosphere of ground horseradish tuber tissue germinated in field condition up to 100%, plants were healthy. Seed treatment reduced FHB (up to 75%), and yield increased over 60-65%, grain were high in weight. Together our results suggest the potential for *Brassicaceae* species to use as ecologically safe and effective antifungal agents.

EFFECT OF *FUSARIUM GRAMINEARUM* CHEMOTYPES 3ADON AND 15ADON AND FUNGICIDE APPLICATION ON FUSARIUM HEAD BLIGHT (FHB) DEVELOPMENT AND DON PRODUCTION IN SPRING WHEAT UNDER NORTH DAKOTA FIELD CONDITIONS IN 2011

Ali, S., K.D. Puri, M. McMullen, and S. Zhong*

Department of Plant Pathology, North Dakota State University, Fargo, ND 58108
*Corresponding Author: PH: (701) 231-7427, Email: Shaobin.zhong@ndsu.edu

ABSTRACT

Two wheat cultivars, Alsen (with the *Fhb1* gene for FHB resistance) and Briggs (FHB susceptible), were planted in randomly complete block design with a split plot arrangement and three replications at the NDSU Research Station at Fargo on May 18. The plot size was 10×10 feet and each plot was separated with a 20 feet strip of Alsen to minimize the chances of inoculum interferences among the treatments. Three plots of each cultivar treated with or without fungicide were spray inoculated with a spore suspension of 100K spores/ml containing a mixture of 10 isolates of 3ADON chemotype or 15ADON chemotype or a mixture of both chemotypes at the mid-flowering stage (Feekes GS 10.52). For the fungicide treated plots, Prosaro™ (prothioconazole + tebuconazole, 6.5fl oz/acre) was sprayed four hours prior to inoculations at 8:30 pm. FHB disease parameters were recorded at late milk to early dough stage (Feekes GS 11.1-11.2). One hundred heads within each plot were randomly rated for disease. Fifty diseased heads in each plot of all treatments were tagged at the time of disease rating, and then harvested at the crop maturity. These samples were thrashed, ground and submitted to the Veterinary Diagnostic Lab at NDSU for DON analysis. In plots not treated with fungicide, the FHB severity of Alsen and Briggs were significantly higher in the treatments inoculated with the mixture of 3ADON isolates (mean disease severity = 12.8% and 42.5%, respectively) and with the mixture of the two chemotypes isolates (mean disease severity = 9.6% and 36.3%, respectively) than those with the mixture of the 15ADON isolates (mean disease severity = 8.6% and 30.4%, respectively). For untreated, inoculated plots, the DON levels were higher in inoculation with the 3ADON isolates (29.7 ppm in Alsen, 39.7 ppm in Briggs), as compared to inoculations with the 15ADON isolates (9.0 ppm in Alsen, 15.9 ppm in Briggs). In the plots treated with the fungicide, the disease incidence, severity, and DON were significantly lower as compared to non-fungicide treated plots, regardless of which chemotype was used as the source of inoculum. Our study indicates that the 3ADON population is more aggressive than 15ADON population in FHB development and should be considered in screening for resistance, and that fungicides are effective against both chemotypes.

ACKNOWLEDGEMENT AND DISCLAIMER

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INFLUENCE OF VARIABLE MISTING PATTERNS ON FUSARIUM HEAD BLIGHT AND DON IN SOFT RED WINTER WHEAT

Kelsey Andersen, Katelyn Willyerd, Laurence Madden and Pierce Paul*

Department of Plant Pathology, The Ohio State University, OARDC, Wooster, OH. 44691
*Corresponding Author: PH: (330) 263-3842, Email: paul.661@osu.edu

ABSTRACT

FHB intensity and DON contamination of wheat are dependent on environmental conditions, most notably moisture. Pre-anthesis moisture drives inoculum production, while moisture during anthesis promotes spore germination and infection of wheat spikes. Post-anthesis moisture affects DON accumulation and may also contribute to secondary infections. The majority of research to date, including research on FHB risk prediction, has focused on the effects of continuous moisture on FHB and DON. There is circumstantial evidence suggesting that discontinuous moisture also affects the development of FHB and accumulation of DON. However, there is very little quantitative, research-based information on the effects of different intermittent moisture patterns on FHB and DON. A field trial was established during the 2010/11 wheat-growing season to examine the effects of intermittent moisture before, during, and after anthesis on FHB and DON in soft red winter wheat (SRWW). A moderately susceptible SRWW variety (Hopewell) was planted on three different dates to stagger anthesis (PD1, PD2 and PD3) and four 7-day supplemental misting treatments were employed in the spring (Mist_1: mist every day; Mist_2: 2 days of mist, 3 days off, 2 days of mist; Mist_3: 2 days off, 3 days of mist, 2 days off; Mist_4: mist every other day). Misting treatments occurred before, during, and after anthesis for PD3, PD2 and PD1, respectively. In addition to a control (ambient inoculum), colonized corn kernels or corn stalks were spread in plots as an inoculum source. Head washes were used to estimate inoculum levels as a result of each PD x Mist x Inoculum combination at the end of the 7-day mist treatment period. FHB incidence and index were estimated approximately 3 weeks post-anthesis for PD3 and DON was quantified post-harvest. Anthesis occurred on May 28, 30 and June 2 for PD1, PD2 and PD3, respectively; while misting treatments were assigned from May 26 to June 1. Ambient rainfall totaled approximately 80 mm from May 23 to 26. In addition to ambient rainfall, Mist_1-4 delivered approximately 286, 145, 83 and 144 mm of total precipitation during the 7 days. In general, spike inoculum density, incidence, index and DON decreased with planting date, suggesting precipitation immediately following anthesis also has a positive effect on FHB development and DON contamination, in addition to pre-anthesis moisture. Considering PD1, in which treatments primarily occurred post-anthesis, incidence, index and DON were all greatest as a result of Mist_1 and similar for the other mist treatments. Regardless of treatment and inoculum source, DON was > 2 ppm in all plots of PD1. Considering PD2, in which anthesis occurred during intermittent misting treatments, MIST_1 also had the highest mean levels of incidence, index and DON. For both PD1 and PD2, FHB incidence and index as a result of Mist_2, 3 and 4 were not considerably different from that observed under ambient conditions. For PD3, in which intermittent misting treatments concluded immediately prior to anthesis, plots receiving corn stalk inoculum generally had the highest levels of incidence, index and DON, within each misting treatment. Of those corn stalk plots, Mist_1 and 4 consistently had the highest levels of incidence (> 30%), index (> 8%) and DON (> 5 ppm). Although Mist_2 and 3 had relatively low FHB symptoms (< 3% index), these treatments resulted in > 5 and > 2 ppm DON, respectively. This work suggests that the pattern of intermittent moisture before and after anthesis may differentially affect FHB development and DON accumulation, and as a result should be considered when developing FHB/DON risk prediction models.

ACKNOWLEDGEMENT

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EFFECTS OF LOCAL CORN DEBRIS MANAGEMENT ON FHB AND DON LEVELS IN SEVEN U.S. WHEAT ENVIRONMENTS IN 2011

G.C. Bergstrom[1*], K.D. Waxman[1], C.A. Bradley[2], A.L. Hazelrigg[3], D.E. Hershman[4], M. Nagelkirk[5], L.E. Sweets[6] and S.N. Wegulo[7]

[1]Dept. of Plant Pathology and Plant-Microbe Biology, Cornell University, Ithaca, NY 14853; [2]Crop Sciences Dept., University of Illinois, Urbana, IL 61801; [3]Plant and Soil Science Dept., University of Vermont, Burlington, VT 05405; [4]Dept. of Plant Pathology, University of Kentucky, Princeton, KY 42445; [5]Michigan State University Extension, Sanilac County, Sandusky, MI 48471; [6]University of Missouri, Columbia, MO 65211; and [7]Plant Pathology Dept., University of Nebraska, Lincoln, NE 68583
[*]Corresponding Author: PH: (607) 255-7849, Email: gcb3@cornell.edu

ABSTRACT

Reduction or elimination of within-field sources of inoculum of *Gibberella zeae* is the basis for cultural control measures such as crop rotation sequences in which cereals follow non-cereal crops. In USWBSI-supported microplot experiments conducted in twenty-one winter wheat fields over five states in 2009 and 2010, DON level differed significantly between corn debris and no debris microplots in only one location, strongly suggesting that regional atmospheric inoculum is the strongest contributor to infection even when corn debris is present in a wheat field. Small area sources of debris, however, may result in an underestimation of the contribution of spores from a larger field of corn debris to FHB and DON. The goal of the current USWBSI research project is to provide realistic estimates of 'DON reduction' that can be expected from cultural controls that reduce within-field inoculum sources. We utilized moldboard plowing of corn debris as a proxy for planting after a non-cereal crop to compare directly with wheat planted no-till into corn debris in commercial-scale wheat fields planted following grain corn harvest in Illinois, Kentucky, Michigan, Missouri, Nebraska, New York, and Vermont. Following corn harvest in 2010, replicated wide (60 ft) strips were moldboard plowed or left non-plowed prior to sowing wheat over the entire field with a no-till drill. Wheat in each strip was monitored for FHB and sampled for laboratory quantification of head infection by *Gibberella zeae* and contamination of grain by DON in 2011. Results from year one of this research project with winter wheat in six states (IL, KY, MI, MO, NE, and NY) and spring wheat in one state (VT) are shown in Fig. 1. FHB symptoms at soft dough stage were low to moderate at every location except Missouri. Yet, at crop maturity, a high percentage of wheat heads was found to be infected by *G. zeae* in all locations except Nebraska and Vermont. Measurable DON was found in grain from every environment and the levels were lowest in Vermont and highest in Kentucky and Nebraska. It is interesting that the Nebraska site showed the lowest disease index and lowest incidence of head infection, but the highest average toxin level. Moldboard plowing resulted in a significant decrease in FHB index in four environments (IL, MO, NY, MI), though the magnitude of the difference was large only in Missouri. In Nebraska, FHB index was significantly higher in the moldboard-plowed treatment in which the wheat crop matured earlier than in the no-till corn debris treatment. Moldboard plowing was associated with a small but significant decrease in recovery of *G. zeae* from mature heads in three environments (IL, MI, NY). There was no significant effect of plowing on DON level in five environments (IL, KY, MO, NY, VT) and there were small, but significant decreases in toxin in moldboard-plowed compared to no-till strips in two environments (MI and NE). An additional treatment of minimum tillage (chisel plow) was added in the Michigan experiment; DON levels in the minimum-till plots were intermediate between moldboard and no-till but not significantly different from no-till. There is a strong trend in year one data suggesting that inoculum from area atmospheric sources exerts a far greater effect than inoculum from in-field corn

residue on the level of DON contamination. A second year of experimentation in seven additional wheat environments in 2012 will provide increased evidence of the magnitude of the effect of corn residue management on DON reduction.

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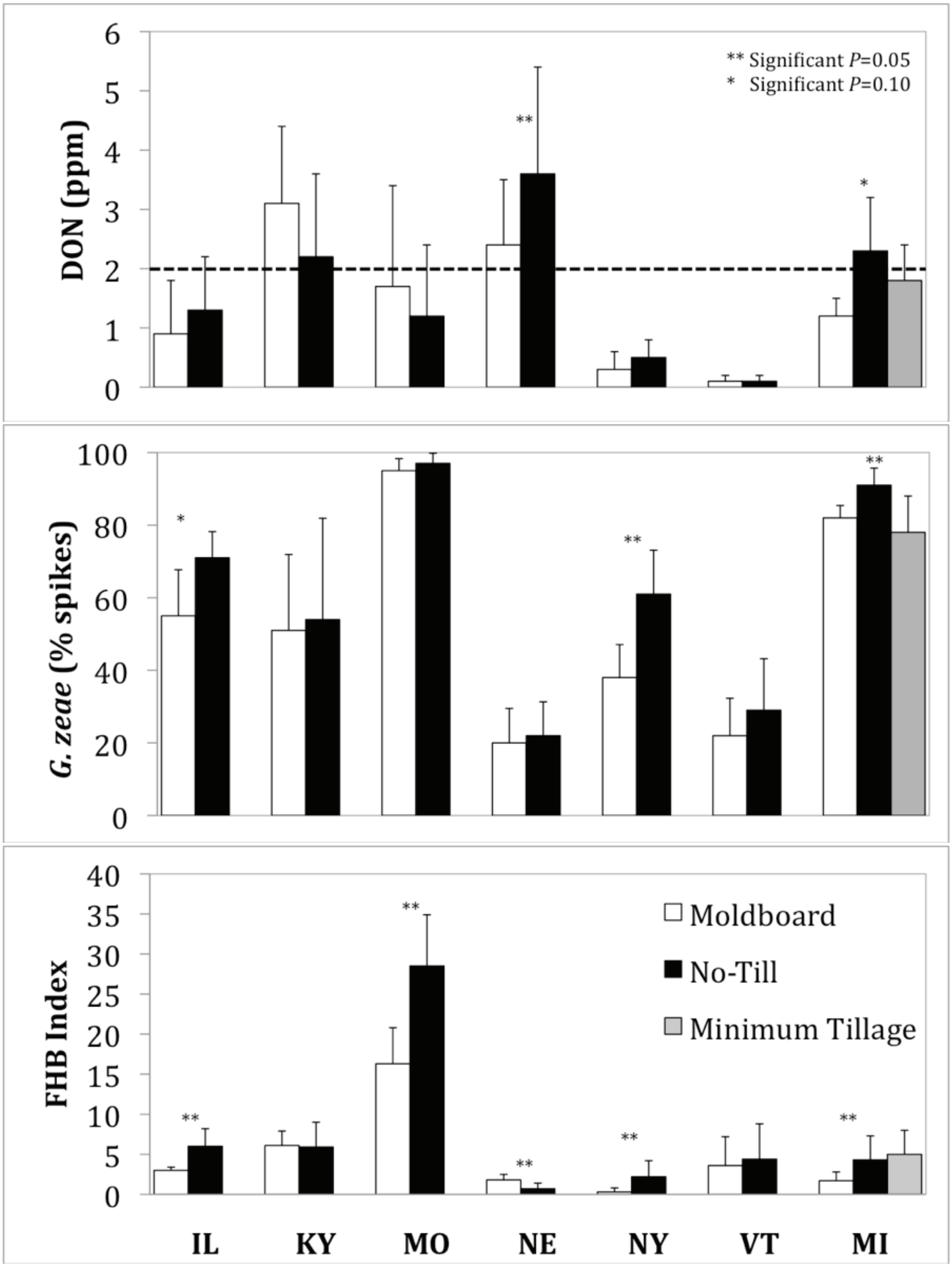

Figure 1. Effects of corn debris management by plowing on FHB parameters in wheat (FHB index at soft dough stage; incidence of infection by *G. zeae* in mature heads; and deoxynivalenol contamination in harvested grain) in experiments in seven states in 2011.

2011 TRIAL OF THE PERFORMANCE OF SELECTED BIOLOGICAL CONTROL AGENTS FOR THE SUPPRESSION OF FUSARIUM HEAD BLIGHT IN SOUTH DAKOTA AND NORTH DAKOTA

B.H. Bleakley[1,2*], K.R. Ruden[1], N. Srinivasa Murthy[2] and S. Halley[3]

[1]Plant Science Department, [2]Biology/Microbiology Department, South Dakota State University,
Brookings, SD 57007; and [3]North Dakota State University, NDSU Langdon
Research Extension Center, Langdon, ND 58249
[*]Corresponding Author: PH: (605) 688-5498, Email: bruce.bleakley@sdstate.edu

ABSTRACT

Fusarium Head Blight (FHB, or scab) remains a potential problem for wheat and barley producers in South Dakota and North Dakota. The objective of this study was to continue evaluating the efficacy of selected biological control agents (BCAs), alone or in combination with fungicide, that can suppress different measures of FHB under field conditions in the Dakotas. Briggs hard red spring wheat was planted at Brookings, SD. Trial treatments included an untreated check; the fungicide premix Prosaro®; *Bacillus* strain 1BA; *Bacillus* strain 1D3; a combination of *Bacillus* strain 1BA and *Bacillus* strain 1D3; and combinations of Prosaro with one or more of the *Bacillus* BCAs. Chelated manganese was added to the spray mix for some treatments. All treatments were applied at anthesis. Plots were treated with pathogen by spreading *Fusarium graminearum* (isolate Fg4) inoculated corn (*Zea mays*) grain throughout the field, and applying overhead mist irrigation each day for 10 days following anthesis. Following the treatments, plots were evaluated for FHB incidence, FHB head severity, and FHB field severity. Plots were harvested for yield and test weight and samples were collected for *Fusarium* damaged kernels (FDK) and deoxynivalenol (DON). Similar treatments and analyses were conducted in Langdon, ND.

In Brookings, SD, grain yield was about 20 bushel/acre or less, much less than for average years, probably due in large part to high moisture, as well as other diseases than FHB being present. Damage due to Bacterial Blight and Black Chaff was widespread, and may have caused excessive damage to the vascular and photosynthetic apparatus of the wheat. Readings of FHB effects in the wheat were difficult to make due to the excessive bacterial disease. No DON was detected in the grain. Grain yield and measures of FHB from our BCA treatments at Langdon, ND were more normal and/or evident, and will be reported.

EFFECT OF SEED TREATMENT OF SCABBY SEED ON PLANT STANDS AND GRAIN YIELDS OF WINTER WHEAT

W.W. Bockus*, M.A. Davis and E.D. De Wolf

Department of Plant Pathology, Kansas State University, Manhattan, KS
*Corresponding Author: PH: (785) 532-1378, Email: Bockus@ksu.edu

ABSTRACT

Fusarium head blight (FHB) is a serious disease of small grains such as wheat. Significant losses can occur due to the blighting of many heads in the field. Besides limiting production in the head, harvested grain can contain *Fusarium*-damaged ("scabby") kernels that can display white or pink discoloration. Kernels from a field that has been affected by FHB may be alive and healthy, dead, or infected by the fungal pathogen although alive. If a seed lot is sown that has viable, infected kernels, the fungus can become active in the moist soil and rot the seed or kill the young seedling resulting in reduced or weak stands. The goal of this research was to determine if fungicide seed treatment of scabby wheat seed could increase plant stands and grain yields. Seven winter wheat field experiments were established near Manhattan, Kansas during 2008-2011; two experiments each year except 2011 which had only one experiment. Scabby seed was obtained from inoculated FHB phenotyping nurseries established by the authors. The amounts of *Fusarium*-damaged kernels in the seed were relatively high (10-40%). Besides the non-treated check, each experiment had three to nine seed treatments, most with currently-labeled chemicals. Experimental design was a randomized complete block with plots 5' by 15' and five replications. Plots were sown around the first week of October which is the optimum planting date for Riley County in Kansas. Plant stands were determined after full emergence by counting all emerged plants in the center row of each plot. Upon maturity, grain yields were determined with a small-plot combine. In five of the seven experiments, there were significant ($P<0.10$) increases in plant stands with seed treatment. In two experiments, increases averaged over 50%. The average stand increase over all experiments was about 26%. Despite significant increases in stand, there were no significant increases in yield for any experiment. However, the average (non-significant) yield increase was 1.0 bu/A which, if real, would more than offset the cost of the treatment. In conclusion, fungicide seed treatments can significantly increase stands with scabby seed but do not consistently result in a grain yield increase.

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ASSESSING THE BEST FUNGICIDE APPLICATION TIMING FOR FUSARIUM HEAD BLIGHT AND MYCOTOXIN MANAGEMENT

Carl A. Bradley

University of Illinois, Department of Crop Sciences Urbana, IL 61801
Corresponding Author: PH: (217) 244-7415, Email: carlbrad@illinois.edu

ABSTRACT

Previously conducted research has identified the demethylation inhibitor (DMI) fungicide products Caramba® (metconazole; BASF Corp.) and Prosaro® (prothioconazole + tebuconazole; Bayer CropScience) as being the most efficacious products for management of Fusarium head blight (FHB) and the associated mycotoxin deoxynivalenol (DON) of all the fungicide products currently registered for use on wheat in the United States. Current recommendations for use of these fungicide products for FHB and DON management are that they be applied at the beginning of anthesis (Feekes growth stage – FGS – 10.5.1). In a “real-world” setting, wheat producers may not be able to time a fungicide application according to the “perfect” growth stage due to several constraints that include unfavorable weather, lack of flexibility in reserving a professional applicator, and variability in wheat growth and development within a field. Multi-state research funded by the USWBSI evaluated Caramba and Prosaro fungicides for their effect on FHB and DON when applied at three different growth stages (FGS 10.5, 10.5.1, and 5 days following 10.5.1) in 2010. Across all locations combined, the mean control of FHB with Caramba was 43%, 54%, and 41% for FGS 10.5, 10.5.1, and 5 days following 10.5.1, respectively. Across all locations combined, the mean control of DON with Caramba was 15%, 45%, and 41% for FGS 10.5, 10.5.1, and 5 days following 10.5.1, respectively. For Prosaro, the mean control of FHB was 28%, 53%, and 42% for FGS 10.5, 10.5.1, and 5 days following 10.5.1, respectively. The mean control of DON with Prosaro was 34%, 25%, and 45% for FGS 10.5, 10.5.1, and 5 days following 10.5.1, respectively. An additional study was conducted at the University of Illinois in 2011, where Prosaro or Caramba was applied to wheat at FGS 10.5.1, 3 days following 10.5.1, or 6 days following 10.5.1. In this study, wheat heads in all plots were inoculated with a *Fusarium graminearum* conidial suspension at FGS 10.5.1 (approximately 6 hours after FGS 10.5.1 fungicide applications were made). Results from this research indicated that FHB was significantly reduced ($P \leq 0.05$) by all fungicide treatments when compared to the non-treated control; however Caramba and Prosaro applied at FGS 10.5.1 provided the greatest control of FHB (93.7% and 93.4%, respectively). None of the treatments significantly reduced DON compared to the non-treated control in this study. In general, FGS 10.5.1 appears to be the most effective timing for control of FHB and DON, but applications made a few days after FGS 10.5.1 may also provide a benefit in reducing FHB and DON levels.

ACKNOWLEDGEMENT AND DISCLAIMER

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EFFECTS OF TRIAZOLE, STROBILURIN, AND TRIAZOLE + STROBILURIN FUNGICIDES ON FUSARIUM HEAD BLIGHT AND ASSOCIATED MYCOTOXINS

C.A. Bradley[1*], E.A. Adee[1], S.A. Ebelhar[1], G.C. Bergstrom[2], R. Dill-Macky[3], J.J. Wiersma[3], A.P. Grybauskas[4], W.W. Kirk[5], M.P. McMullen[6], S. Halley[6], E.A. Milus[7], L.E. Osborne[8], K.R. Ruden[8] and K.A. Wise[9]

[1]University of Illinois, Urbana, IL; [2]Cornell University, Ithaca, NY; [3]University of Minnesota, St. Paul, MN; [4]University of Maryland, College Park, MD; [5]Michigan State University, East Lansing, MI; [6]North Dakota State University, Fargo, ND; [7]University of Arkansas, Fayetteville, AR; [8]South Dakota State University, Brookings, SD; and [9]Purdue University, West Lafayette, IN
[*]Corresponding Author: PH: (217) 244-7415, Email: carlbrad@illinois.edu

ABSTRACT

A multi-state research project was conducted across nine states (Arkansas, Illinois, Indiana, Maryland, Michigan, Minnesota, North Dakota, South Dakota, and New York) encompassing five wheat market classes (durum, hard red spring, hard red winter, soft red winter, and soft white winter) to evaluate the effects of triazole, strobilurin, and triazole + strobilurin fungicides on Fusarium head blight (FHB) and associated mycotoxins. Previously conducted research has indicated that the strobilurin fungicide pyraclostrobin (Headline) can increase FHB-associated mycotoxins such as deoxynivalenol (DON) and nivalenol (NIV). Because of this, strobilurin fungicides are not recommended for FHB control, but they still are valuable tools for controlling leaf diseases. One component of our research was to evaluate other strobilurin fungicides, such as azoxystrobin (Quadris) and fluoxastrobin (Evito), to determine if they also can increase FHB-associated mycotoxins. In addition, strobilurin + triazole mixtures (trifloxystrobin + prothioconazole, Stratego YLD; azoxystrobin + propiconazole, Quilt Xcel; and pyraclostrobin + metconazole, Twinline) as well as a sequential treatment of pyraclostrobin followed by the triazole fungicide metconazole (Caramba®) were evaluated to determine if triazole fungicides would negate any increases in mycotoxin levels due to the strobilurin fungicides. Headline applied at Feekes' growth stage (FGS) 9 or 10.5 significantly ($P \leq 0.05$) increased DON levels when compared to the non-treated control in 2 out of 12 locations and 2 out of 9 locations tested, respectively. When Caramba was applied (FGS 10.5.1) following a FGS 9 application of Headline, neither DON or NIV (NIV was evaluated only in Arkansas) levels were significantly greater than the non-treated control at any of the locations, but DON levels were significantly less than the non-treated control with this combination treatment at 5 out of 12 locations. Quadris and Evito (FGS 10.5) significantly increased DON levels over the non-treated control at 1 out of 9 and 2 out of 9 locations, respectively. When the strobilurin + triazole fungicide products, Stratego YLD, Quilt Xcel, and Twinline, were evaluated (FGS 10.5), they increased DON levels over the non-treated control at 1 out of 12, 2 out of 12, and 2 out of 11 locations, respectively. In light of our results, there is a risk of increasing DON levels when solo strobilurin products or strobilurin + triazole products are applied to wheat. However, it does appear that if a strobilurin fungicide was applied at FGS 9 and followed with an effective triazole application at FGS 10.5.1, that the strobilurin effect on DON was negated.

Previously conducted research has shown that Caramba and Prosaro® fungicides are the most effective in reducing FHB and associated mycotoxins. Another objective of our research was to evaluate the experimental fungicide A9232D (Syngenta Crop Protection) for control of FHB and mycotoxins and compare

its performance with the industry standards, Caramba and Prosaro (all applied at FGS 10.5.1). A9232D significantly decreased DON levels compared to the non-treated control at 4 out of 13 locations, whereas Caramba and Prosaro both significantly decreased DON at 6 out of 13 locations. A9232D, Caramba, and Prosaro significantly reduced FHB index compared to the non-treated control at 9 out of 21 locations; however, the level of control achieved with A9232D was equal to the level of control with either Caramba or Prosaro at only 7 of these locations. In general, our research indicates that A9232D at the rate used in these trials does have efficacy for control of FHB and DON, but it may not be quite at the same level as the industry standards, Caramba and Prosaro.

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INFLUENCE OF FUSARIUM HEAD BLIGHT MANAGEMENT PRACTICES ON MYCOTOXINS IN WHEAT STRAW

C.A. Bradley[1*], K.A. Ames[1], Y. Dong[2], E.A. Brucker[1] and F.L. Kolb[1]

[1]University of Illinois, Urbana, IL; and [2]University of Minnesota, St. Paul, MN
[*]Corresponding Author: PH: (217) 244-7415, Email: carlbrad@illinois.edu

ABSTRACT

The effect of crop rotation, foliar fungicides, and resistant cultivars have been evaluated for their effects on mycotoxins in grain associated with Fusarium head blight (FHB) of wheat; however, little is known about how these FHB management practices affect mycotoxins in wheat straw. The occurrence of high mycotoxin levels in grain is considered a major problem for wheat producers and millers, but high mycotoxin levels in wheat straw also could be a serious problem for livestock producers who use wheat straw for bedding in their livestock facilities. This could be most detrimental to non-ruminant animals such as swine sows, which can eat 2 to 4 kg of wheat straw bedding per day. Research trials were conducted in Illinois to determine mycotoxin levels present in wheat straw (stems only) and if typical FHB management practices had an effect on mycotoxin levels. To determine the mycotoxin levels, stem samples were collected immediately after harvest, were ground into small particles, and then sent to the University of Minnesota mycotoxin testing lab.

Fungicide trials were conducted at four locations in Illinois (Brownstown, Dixon Springs, Monmouth, and Urbana) to determine the effects of Headline® (pyraclostrobin; BASF Corp.), Caramba® (metconazole; BASF Corp.), Prosaro® (prothioconazole + tebuconazole; Bayer CropSciences), and Folicur® (tebuconazole; Bayer CropSciences) on mycotoxins in wheat straw. All locations were planted into corn stubble and were mist-irrigated. Headline was applied at Feekes growth stage (FGS) 9, while all other fungicides were applied at FGS 10.5.1. Ranges of DON, 3ADON, 15ADON, NIV, and ZEA at these locations were 0.6-104.6 ppm, 0.01-5.7 ppm, 0.1-17.8 ppm, 0-1.6 ppm, and 0-1.3 ppm, respectively. When averaged over all locations, none of the fungicides decreased mycotoxin levels compared to the non-treated control, but Headline fungicide significantly ($P \leq 0.10$) increased 3ADON and 15ADON compared to the non-treated control.

Non-irrigated FHB integrated management trials designed to evaluate cultivar (susceptible vs. moderately-resistant) × fungicide (Prosaro vs. non-treated) effects (Dixon Springs and Monmouth) and cultivar × fungicide × previous crop (corn vs. soybean) effects (Urbana) were conducted. Ranges of DON, 3ADON, 15ADON, NIV, and ZEA at these locations were 0.1-5.1 ppm, 0-0.19 ppm, 0-0.82 ppm, 0-0.5 ppm, and 0-1.5 ppm, respectively. Foliar fungicides did not affect mycotoxin levels, but the susceptible cultivar (Pioneer 25R47) generally had higher DON levels compared to the moderately resistant cultivar (BW5228). At the Urbana trial, the susceptible cultivar planted into corn stubble had a significantly greater DON level than when planted into soybean stubble.

A mist-irrigated fungicide (non-treated, Prosaro, Caramba) × cultivar (susceptible vs. moderately resistant) trial was conducted at Urbana. Ranges of DON, 3ADON, 15ADON, NIV, and ZEA in this trial were 6.8-33.5 ppm, 0.3-1.3 ppm, 0.9-10.1 ppm, 0-0.3 ppm, and 0-0.06 ppm, respectively. The moderately resistant cultivar (BW5228) had significantly lower levels of DON and 15ADON than the susceptible cultivar

(Pioneer 25R47). Foliar fungicides significantly reduced DON levels compared to the non-treated controls for both cultivars, but fungicides significantly reduced 15ADON levels only in the susceptible cultivar.

A mist-irrigated cultivar evaluation trial was conducted at Urbana. Ranges of DON, 3ADON, 15ADON, and ZEA at these locations were 8.9-54.1 ppm, 0.6-3.1 ppm, 4.9-16.6 ppm, and 0-0.5 ppm, respectively. No NIV was detected in this trial. Significant differences in levels of DON, 3ADON, and 15ADON were observed among the cultivars. A significant, positive Spearman correlation ($P = 0.0001$; $R = 0.50$) was detected between DON levels observed in straw and DON levels observed in grain, indicating that a cultivar's FHB resistance level may play a role in the level of DON observed in the straw.

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

E.A. Brucker, N.H. Karplus, C.A. Bradley and F.L. Kolb*

Department of Crop Sciences, University of Illinois, Urbana, IL 61801, USA
*Corresponding Author: PH: (217) 333-9485, Email: f-kolb@illinois.edu

ABSTRACT

Researchers and breeders have been challenged by the U.S. Wheat and Barley Scab Initiative to find a solution for managing Fusarium head blight (FHB; caused by *F. graminearum*) in the United States. Especially important is keeping the mycotoxin, deoxynivalenol (DON), level below the threshold of 2 ppm in the grain, so that it may be used for human consumption. Fungicide technology is improving and fungicides in the demethylation inhibitor (DMI) class have proven to be the most effective in managing FHB, although results are variable. Caramba® (metconazole; BASF) and Prosaro® (tebuconazole + prothioconazole; Bayer CropScience) are currently the most effective fungicides available for reducing FHB and deoxynivalenol (DON) in the U.S. Planting a FHB-resistant cultivar is another management tool for producers; however, neither fungicide nor resistant cultivar can provide complete control. Our objective was to evaluate the effectiveness of two foliar applied fungicides and host plant resistance on suppression of FHB, DON accumulation, yield, and test weight. The experiment was a split-plot design with fungicide treatment as the main plot and cultivar as the sub-plot, blocked into four replications and repeated in two years. An inoculated, mist-irrigated disease nursery was used to evaluate Caramba and Prosaro fungicides, and twelve wheat cultivars ranging from susceptible to resistant to FHB. Data were collected on FHB incidence, severity, *Fusarium* damaged kernels (FDK), DON, yield, and test weight. FHB index and incidence/severity/kernel quality index (ISK index) were also calculated. In individual non-treated plots, FHB incidence ranged from 23% to 100% thereby confirming high disease pressure and varying cultivar FHB resistance levels. Averaged over all cultivars, both Caramba and Prosaro resulted in significantly ($P < 0.001$) greater yield and test weight, and significantly lower FHB incidence, severity, FHB index, FDK, ISK index, and DON compared to the non-treated control. No significant difference was found between Caramba and Prosaro for any variable measured. When the cultivars were split into a resistant and a susceptible group, FHB-resistant cultivars significantly ($P < 0.0001$) outperformed the FHB-susceptible cultivars, regardless of the fungicide treatment, for all parameters. In the non-treated plots, FHB–resistant cultivars had higher yield (15.4 bu/A) and test weight (5.6 lbs/bu.), and FHB index was reduced by 51%, FDK by 78%, and DON by 59% when compared to the FHB-susceptible cultivars. Notably, IL06-13708 and IL01-11934 yielded significantly ($P < 0.05$) more in the non-treated plots than Sisson when treated with either fungicide. Also, the most FHB-resistant cultivar, IL02-18228, was the only cultivar to not realize a significant yield increase from the addition of fungicides. No single cultivar or fungicide individually reduced DON below 1ppm; however, the combination of the most FHB-resistant cultivars, IL01-16170 and IL02-18228, and the fungicide Caramba reduced DON, on average, below 1 ppm. Based on our results from this test and a similar, previous test, we can conclude that under severe FHB pressure, wheat producers can produce high yields of sound grain by using cultivars with high FHB resistance levels in combination with either Caramba or Prosaro fungicide.

A TIME COURSE OF SCAB IN DEVELOPING FIELD-GROWN WHEAT SPIKES

C. Cowger[1*] and C. Arellano[2]

[1]USDA-ARS, Department of Plant Pathology, NCSU, Raleigh, NC; and
[2]Department of Statistics, North Carolina State University, Raleigh, NC
[*]Corresponding Author: PH: (919) 513-7388, Email: Christina.Cowger@ars.usda.gov

ABSTRACT

Although the relationship of visual FHB symptoms (e.g., index) to levels of deoxynivalenol (DON) and *Fusarium*-damaged kernels (FDK) in mature grain has been well studied, little is known about the time course of DON levels in wheat spikes over the period from infection to harvest. This is of interest because whole small-grain plants may be harvested at the milk, soft-dough, or medium-dough stages for silage production. Also, wheat and barley straw is used as litter for turkey and swine production, and swine may consume their bedding. In addition, cereal straw and chaff is used as a source of roughage in dairy and beef cattle rations. A field experiment was conducted in Kinston, North Carolina, in 2006 and 2007 to investigate the progress of FHB in wheat spikes following infection. In the first year, eight soft red winter wheat cultivars with varying degrees of FHB resistance were grown in 3.1-m plots. At mid-anthesis for each cultivar, plots were sprayed with a suspension of 10^5 macroconidia/ml of *Fusarium graminearum*. Plots received daily misting for either 0, 10, 20, or 30 days after anthesis (daa). *Fusarium* index (incidence x severity / 100) was determined in each plot at soft-dough. From each plot, 30 spikes were blindly chosen at 10-day intervals from medium-milk (10 daa) to kernel-loosening (64 daa), and bulked by plot. The samples were separated into three fractions: grain, glumes, and rachises. Weight and DON were assayed in all fractions, and FDK and percent *Fusarium*-infected kernels (PIK) were also determined in the grain. In the second year, the experiment was repeated with four of the eight cultivars.

The first year was naturally wetter and more scab-conducive than the second year. In both years, when averaging across mist durations, PIK increased during the sampling period; FDK increased between early kernel-hard and harvest-ripe; and grain DON dropped following the first or second sample. Increasing durations of mist were generally associated with increasing levels of PIK, FDK, and grain DON in the first year, but mist made less difference in the second year. As has been previously reported, peak DON in glumes and rachises, and also those at harvest-ripe, was significantly higher than DON in grain of the same samples. DON in glumes and rachises varied greatly over time. Maximum DON concentrations were attained in rachises at kernel-hard, and in glumes at kernel-hard (2006) or early kernel-hard (2007) stage. The results suggest that in a scab epidemic, total spike DON may increase between infection and the later timepoints for silage harvest. Combining the data from both years, DON in grain was significantly correlated with DON in both glumes and rachises ($P \leq 0.003$), but DON in glumes was only marginally correlated with DON in rachises ($P = 0.089$). Correlation of index to grain, glume, and rachis DON at silage harvest and harvest-ripeness will be reported. The question whether cultivar grain resistance level is a good predictor of relative DON levels in other spike fractions will also be addressed.

ECOLOGY OF *BACILLUS AMYLOLIQUEFACIENS* ON WHEAT FLORETS IN RELATION TO BIOLOGICAL CONTROL OF FHB/DON

J.M. Crane[1], D.M. Gibson[1, 2] and G.C. Bergstrom[1*]

[1]Dept. of Plant Pathology and Plant-Microbe Biology, Cornell University, Ithaca, NY 14853;
and [2]USDA-ARS Robert Holley Center for Agriculture and Health, Ithaca, NY 14853
[*]Corresponding Author: PH: (607) 255-7849, Email: gcb3@cornell.edu

ABSTRACT

The TrigoCor strain of *Bacillus amyloliquefaciens* is one of a handful of biological control agents (BCAs) that shows potential in the integrated management of FHB/DON. We are using TrigoCor as a model to understand why it, like many promising BCAs tested through the USWBSI, provides excellent and consistent FHB control in the greenhouse but not in the field. Using dilution plating, we quantified *Bacillus* populations on wheat heads at 0h, 24h, 72h, 7d, and 14d post- *Bacillus* application in the greenhouse and in two field locations in 2009. Although *Bacillus* populations were fairly stable on heads in both the greenhouse and the field, the population level in the greenhouse (10^8CFUs/head) was significantly higher than in the field (10^6-10^7CFUs/head). In addition to these hand-sprayed field trials, we also quantified population levels from field plots sprayed with *Bacillus* using a commercial sprayer (20 gal/A, paired Twinjet nozzles facing front and back and aimed 30° from horizontal), and found that *Bacillus* population levels on heads in these fields were even lower (10^4-10^6 CFUs/head at 0h and 24h after *Bacillus* application from fields in New York, North Dakota, and Missouri in 2008, as well as throughout a 14d sampling period from a field trial in New York in 2009). Treatment with TrigoCor did not provide significant reductions in FHB in any of the hand-sprayed or commercially sprayed trials. In 2010 field trials, we increased the amount of *Bacillus* applied per head, resulting in levels initially comparable to those recovered from the greenhouse (10^8 CFUs/mL at 0 and 1d post-application). Despite these high *Bacillus* levels, there was still insufficient FHB control, suggesting that population levels alone do not explain biocontrol.

We used high performance liquid chromatography to monitor the persistence of a key *Bacillus*-produced antifungal compound on wheat heads from the greenhouse and from a spring wheat field in 2010. Although levels of the compound on heads decreased rapidly by 3d post-application in both environments, the quantity per head was significantly higher in the greenhouse than in the field over critical infection periods. Greenhouse experiments with diluted TrigoCor inoculum indicate that the difference in metabolite levels observed between the greenhouse and the field is significant for FHB disease control. It is likely that the inadequate persistence of antifungal metabolites on wheat heads in the field is an important factor limiting disease control.

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EFFECT OF POST-ANTHESIS FUNGICIDE APPLICATION ON FUSARIUM HEAD BLIGHT AND DON IN SOFT RED WHEAT

Daisy D'Angelo, Katelyn Willyerd, Jorge David Salgado,
Laurence Madden and Pierce Paul*

Department of Plant Pathology, The Ohio State University, OARDC, Wooster, OH, 44691
*Corresponding Author: PH: (330) 263-3842, Email: paul.661@osu.edu

ABSTRACT

High relative humidity and frequent rainfall during anthesis (Feekes 10.5.1) and early grain fill are considered environmental risk factors for FHB development and DON accumulation in small grain crops. For best efficacy and FHB control it is recommended that fungicides be applied at early anthesis (Feekes 10.5.1), as this is when small grain crops are most susceptible to *F. graminearum*, especially when anthesis coincides with wet weather. Despite these recommendations, producers often find it difficult to adhere to these best management guidelines due to the physical limitations of spraying fungicides in the rain and driving equipment in soggy fields. Field studies in Wooster and South Charleston, OH were established to evaluate the effectiveness of fungicide applications made post-anthesis. At Wooster, one moderately resistant and one susceptible SRWW cultivar were planted as whole plots in a randomized complete block design, with three replicate blocks. Fungicide treatment served as the sub-plot: untreated check, Prosaro® (6.5 fl oz/acre + NIS) at anthesis, 2, 4 and 6 days post-anthesis (dpa) and inoculum density as the sub-sub plot: 1, 3, 5 and 7 x 10^4 macroconidia/mL applied at anthesis. At South Charleston a susceptible cultivar was used, and seven fungicide treatments were assigned to plots in a randomized complete block design, with 4 blocks. The treatments were: untreated check, Prosaro (6.5 fl oz/acre + NIS) at anthesis, 2 and 5 dpa and Caramba® (13.5 fl oz/acre + NIS) at anthesis, 2 and 5 dpa. Plots were naturally infected at South Charleston. FHB incidence and index were estimated approximately 3 weeks post-anthesis; while percent *Fusarium* damaged kernels (FDK) and DON concentration were assessed post-harvest. Proc GLIMMIX in SAS was used to evaluate the effects of variety, inoculum density, treatment and their interactions on FHB, DON, FDK, and yield. In Wooster, variety had a marginal effect on index ($P = 0.087$) and a significant effect ($P < 0.05$) on FDK, DON and yield. Inoculum density did not have a significant effect on any of the measured responses. At both locations, fungicide treatment had significant effects on FHB incidence, index, FDK, DON and yield. All fungicide treatments, regardless of timing, resulted in significantly higher yield and significantly lower index, incidence, FDK and DON than the untreated check. In Wooster, the levels of index, incidence, FDK and DON as a result of Prosaro treatment at anthesis were not significantly different from the values resulting from applications made 2, 4 or 6 dpa. However, Prosaro at anthesis resulted in significantly higher grain yield than later applications. Results from South Charleston, where it rained on the day treatments were applied (at 50% anthesis) and the day after, suggested that post-anthesis applications of fungicide provided better disease and DON control than applications made at anthesis itself. Under the conditions of this study, these results suggest that relative to applications made at anthesis, the efficacy of Prosaro and Caramba, in terms of FHB and DON control, is not greatly reduced when these products are applied at label-recommended rates within a week of anthesis. While producers should continue to identify anthesis timing and actively monitor risk prediction tools, this preliminary research suggests that applications of foliar fungicide may still provide effective FHB and DON control when applied up to 5-6 days post-anthesis. These "delayed" applications may provide adequate protection of upper- and lower-most wheat spikelets and secondary tillers which may continue to flower for a period beyond the main spike.

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EVALUATING THE IMPACT OF THE FHB PREDICTION MODELS AND FHB ALERTS, 2009-2011

E. De Wolf[1*], P. Paul[2], D. Hane[3], S. Canty[4], D. Van Sanford[5], P. Knight[6] and D. Miller[7]

[1]Kansas State University, Department of Plant Pathology, Manhattan, KS; [2]The Ohio State University, Department of Plant Pathology, Wooster, OH; [3]USDA-ARS-WRRC, 800 Buchanan Street, Albany, CA; [4]USWBSI-NFO, Michigan State University, East Lansing, MI; [5]University of Kentucky, Dept. of Plant and Soil Sciences, Lexington, KY; [6]The Pennsylvania State University, Pennsylvania State Climate Office, University Park, PA; and [7]The Pennsylvania State University, Earth and Environmental Systems Institute, University Park, PA
[*]Corresponding Author: PH: (785) 532-3968, Email: dewolf1@ksu.edu

ABSTRACT

The cooperative effort to deploy the prediction models for FHB and DON currently affects 30 states. This effort includes the support of commentary tools for each state, and partnerships with the USWBSI-NFO to implement the FHB Alert System. The FHB Alert System sends the commentary developed by the state specialists via email to subscribers and automatically posts the information on the USWBSI blog (http://scabusa.org/modules/wordpress/). Subscribers can also request that the FHB Alert System send text messages to their mobile devices each time a new commentary is submitted for their region. Users of the prediction models and the FHB Alert System were surveyed in 2009-2010. The survey results included input from 1016 respondents, and indicated that 66% of these users were either farm advisors or farmers. Other users of the system included university extension personnel (16%), university educators (4%) and members of the grain marketing (2.5%) and milling industries (4%). The results also indicated that 73% of the users applied the information provided by the prediction system directly on their farm, or to make recommendations about disease management to others. In the two years covered by this survey, 94% of the users considered the information to be of high or moderate value for their farm operations or organization. The 2010 survey included a subset of questions that further documented the impact of the information. The responses to these questions indicated that 86% of the users experienced a moderate or great improvement in their awareness of the disease risk in their area. The results also showed that the information influenced the decision about the need for management action directly for 37% of the respondents, and motivated another 24% to seek advice from others. In 2011, the prediction tools received over 13,000 visits during the growing season in the U.S. (April – August), representing 6,579 visitors. Nearly all of the wheat disease specialists in the 30 states covered by the disease prediction system contributed commentary to the disease prediction effort. A total of 132 commentaries were submitted in 2011 (similar levels to 2010), with specialists in AR, IN, KS, KY, MD, MN, NC, ND, OH, OK, PA and WI each contributing more than 5 commentary updates to the prediction system. The FHB Alerts sent commentary to over 800 subscribers in 2011, nearly doubling the number of participants from 2010. A survey evaluating the impact of the disease prediction system and the FHB Alerts during the 2011-growing season is currently underway.

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THE RISK OF FHB EPIDEMICS BASED ON WEATHER, HOST RESISTANCE AND CORN RESIDUE

E. De Wolf[1*], D. Shah[1], P. Paul[2], L. Madden[2] and K. Willyerd[2]

[1]Kansas State University, Department of Plant Pathology, Manhattan, KS; and [2]The Ohio State University / OARDC, Department of Plant Pathology, Wooster, OH
[*]Corresponding Author: PH: (785) 532-3968, Email: dewolf1@ksu.edu

ABSTRACT

Severe epidemics of Fusarium head blight (FHB) are often associated with environmental and cultural practices. Many historical accounts of FHB epidemics suggest that above normal rainfall during anthesis, when the crop is most vulnerable to infection by *Fusarium*, is often associated with epidemics. Some practitioners have also observed that planting wheat into fields containing large amounts of corn or other host crop residues also increases the risk of severe FHB. When such observations are cited repeatedly in the literature, they begin to transition from a generalized theory, based on limited observation, to scientifically accepted common knowledge. The objective of this study was to evaluate the influence of weather factors, host resistance, and the presence of corn residue on the risk of FHB epidemics. The data available for modeling included 527 location-years, from 15 states collected between 1982 and 2009, and consisted of observations from the hard red spring, hard red winter, and soft red winter wheat market classes. All data sets were subjected to extensive quality control, checking for missing data, out-of-range values, or other errors. Missing weather observations were estimated by multiple imputation. The disease intensity was coded as a binary variable where a given location-year was considered an epidemic if the FHB index was >10%. Logistic regression was used to model the probability of a location experiencing an FHB epidemic, given input predictors such as the genetic resistance to FHB of a variety, the presence of residue from a previous corn crop, and different representations of hourly temperature, relative humidity and rainfall. Variable selection procedures identified that relative humidity and temperature variables were frequently associated FHB epidemics. Variables summarizing either the total rainfall or the duration of rainfall were identified far less frequently. These results suggest that precipitation may be indirectly related to FHB epidemics and that other measures of atmospheric moisture are more strongly associated with epidemics of FHB. The analysis supports evidence that planting cultivars with moderate levels of genetic resistance reduces the risk of severe FHB; however, planting wheat in fields containing large amounts of corn residue increases the risk of disease. This analysis verifies the role of risk factors associated with FHB and establishes a framework for the development of prediction models that can be used in disease management. The accuracy of prediction models developed in this analysis is similar to the benchmarks established in previous modeling efforts, and we are now positioned to explore more advanced approaches to modeling FHB epidemics.

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BARLEY SCAB: FORECASTING TO MANAGEMENT

Pravin Gautam[1], Krishna D. Bondalapati[1*] and Jeffrey M. Stein[2]

[1]Plant Science Department, South Dakota State University, Brookings, SD 57007; and
[2]Corn Pathology, Waterman Research Facility, Monsanto, Waterman, IL 60556
[*]Corresponding Author: PH: 605-688-5158, Email: Krishna.Bondalapati@sdstate.edu

ABSTRACT

Fusarium head blight (FHB), caused by the fungus *Gibberella zeae* (Schwein) Petch (anamorph: *Fusarium graminearum* Schwabe), continues to be a serious problem for barley producers in the U.S. Northern Great Plains and elsewhere. Economic losses associated with FHB occur due to contamination of grain with trichothecene mycotoxins, primarily deoxynivalenol (DON). Predictive models were developed to predict economic level of DON (DON≥ 0.5 mg/kg) using the weather conditions prior to full head emergence. Three commonly grown cultivars were planted throughout the region over six growing seasons (2005-10) and FHB disease and DON concentration were recorded. Nine predictor variables were calculated using hourly temperature and relative humidity during the 10-days preceding the full head emergence day and nine simple logistic regression models were developed using these predictor variables. Four of the nine models had sensitivity greater than 80% (n=150). The results of this study confirm that weather conditions prior to full head emergence could be used to accurately predict the risk of economically significant DON accumulation for spring malting barley.

An experiment, split-split plot with five replications, was established at SDSU research station, Brookings, SD, during summer 2011 to study the relationship between Fusarium head blight (FHB) symptoms and DON concentration by examining the contribution of main stem and secondary tillers as it relates to the final DON concentration. Main plots were resistance levels of cultivars [Quest, a moderately resistant (MR) and Robust, a moderately susceptible (MS) cultivar], inoculation timing (at Feekes 10.5 and 11.2) as sub-plots, and sub-sub plots included *Fusarium graminearum* or mock inoculation.

FHB severity was not statistically different between main heads and tillers. Robust had significantly higher FHB severity than Quest only in main heads. Levels of DON were statistically higher in main heads in each cultivar compared to its tillers. Robust had significantly higher DON levels at each inoculation compared to that of Quest. Our results suggest that main heads has larger contribution towards total DON levels at harvest than tillers. However, it should be noted that this year, environmental condition was not suitable for optimum growth of barley. During the growing season, especially at pre-booting to anthesis there was a strong heat wave in the mid west region, resulting into stunted plants and very small heads, especially tillers, with abrupt anthesis. This might have resulted in anthesis of main heads and tillers at around same time leading to the similar duration of time frame available for infection from inoculation. Thus we suggest further study on wheat and barley with normal growth, which might provide us more accurate information.

CONTRIBUTION OF SECONDARY TILLERS TO TOTAL DEOXYNIVALENOL CONCENTRATION IN HARVEST GRAIN

Pravin Gautam

Plant Science Department, South Dakota State University, Brookings, SD 57007
Corresponding Author: PH: 605-688-5158, Email: pravin.gautam@sdstate.edu

ABSTRACT

Studies in the past have reported that late infection of wheat and barley results in low disease development but high deoxynivalenol (DON) concentration. Formation of higher number of tillers is desirable as it has positive impact on final grain yield. Lateral tillers of wheat and barley, however, have delayed physiological development, which might correlate with the late infection findings. The objective of this study was to improve our understanding of the relationship between Fusarium head blight (FHB) symptoms and DON concentration by examining the contribution of main stem and secondary tillers as it relates to the final DON concentration.

Experiments, split-split plot with five replications, were established at SDSU research station, Brookings, SD, during summer 2011. Main plots were resistance levels of cultivars [moderately resistant (MR) and moderately susceptible (MS)], inoculation timing (at Feekes 10.5 and 11.2) as sub-plots, and sub-sub plots included *Fusarium graminearum* or mock inoculation. Two cultivars each of barley; 'Robust' (MS to FHB) and 'Quest' (MR); hard red spring wheat (HRSW); SD3851 (cv 'Brick' MR, possesses *Fhb1* QTL) and SD3854 (MS, lacks *Fhb1* QTL) and hard red winter wheat (HRWW); WesleyBC6 (MR, possesses *Fhb1* QTL) and WesleyBC70 (MS, lacks *Fhb1* QTL) were planted in mid-May. Individual plot was of 5 x 15 square ft. in size. Twenty-five main heads and secondary tillers were tagged in plot that was inoculated at Feekes 10.5 (at anthesis of main heads) and Feekes 11.2 (~ at anthesis of secondary tillers), respectively. Plots were inoculated using backpack sprayer with a mixture of 15 isolates of *F. graminearum* inoculum at the concentration at 80,000 spores ml^{-1}. Mist-irrigation system was run for 10 min immediately following inoculation to avoid drying of inoculum. Mist-irrigation was run until 14 days after inoculation (DAI) for 10 minutes per hour from 5 p.m. to 7 a.m. to create conducive environment for FHB development. FHB severity was assessed on 18 DAI by counting total and symptomatic spikelets in tagged 25 heads. At maturity, tagged heads were hand harvested, and threshed. Heads from individual plot were bulked and analyzed for *Fusarium* damaged kernel (FDK) by counting scabby kernels in 100 seeds (3 reps), ground and analyzed for DON at mycotoxin laboratory at North Dakota State University. The rest of the plots were harvested mechanically, threshed, analyzed for FDK following Jones and Mirocha (1999), and analyzed for DON. Arcsine transformed data of barley severity and HRWW FDK, log transformed barley DON data, and square root transformed HRSW FDK and DON data were used for analyses. Data on HRSW severity, and HRWW severity and DON were analyzed without transformation. Data were analyzed using proc mixed procedure in SAS.

Though FHB severity in mock inoculated was high up to 50%, it was significantly low compared to the *F. graminearum* inoculated plots. In barley, FHB severity was not statistically different between main heads and tillers. Robust had significantly higher FHB severity than Quest only in main heads. In HRSW, there was no statistical difference between FHB severity in main heads and tillers. SD3854 had significantly higher

FHB severity than Brick in both inoculations. In HRWW, while WesleyBC6 had significantly higher main head FHB severity than tillers, there was no difference in Wesley BC70.

Percentage of FDK was significantly high in main heads of SD3854 compared to its tillers and main heads and tillers of Brick. In Brick there was no statistical difference between FDK observed in main heads and tillers. In HRWW, none of the variables were significant.

Levels of DON were statistically higher in main heads of barley in each cultivar compared to its tillers. Robust had significantly higher DON levels at each inoculation of compared to that of Quest. In HRSW, DON levels were significantly higher in main heads than tillers in each cultivar. SD3854 had statistically higher DON than Brick for main tillers or early inoculation but Brick had higher DON than SD3854 in tillers or late inoculation. In HRWW, though there was higher DON level in tillers than main heads in each cultivar, it was not statistically different.

Our results suggest that main heads has larger contribution towards total DON levels at harvest than tillers. However, it should be noted that this year, environmental condition was not suitable for optimum growth of wheat. During the growing season, especially at pre-booting to anthesis there was a strong heat wave in the mid west region, resulting into stunted plants and very small heads, especially tillers, with abrupt anthesis. This might have resulted in anthesis of main heads and tillers at around same time leading to the similar duration of time frame available for infection from inoculation. Thus we suggest further study on wheat and barley with normal growth, which might provide us more accurate information.

MANAGING FUSARIUM HEAD BLIGHT IN BARLEY WITH CULTIVAR RESISTANCE, FUNGICIDE CHEMISTRY AND SEQUENTIAL APPLICATIONS

S. Halley[1*], R. Horsley[2,] K. Misek[1] and S. Neate[3]

[1]Langdon Research Extension Center, North Dakota State University, Langdon, ND, 58249, USA;
[2]Department of Plant Science, North Dakota State University, Fargo, ND, 58105, USA;
and [3]Department of Primary Industries and Fisheries Leslie Research
Centre, Toowoomba, Queensland 4350 Australia
[*]Corresponding Author: PH: 701-256-2582, Email: Scott.Halley@ndsu.edu

ABSTRACT

Fungicide application to control Fusarium head blight (FHB) can affect wheat and barley yield and substantially reduce deoxynivalenol accumulation (DON) in both barley and wheat seed. Studies conducted in 2007-2009 at Langdon and Osnabrock North Dakota on 6-row spring barley showed that sequential fungicide applications at Feekes growth stage (GS) 10.51 and 10.53 reduced DON on the main stem and boot GS tillers and subsequently the whole plot compared to the untreated. Sequential fungicide treatments were applied to improve on the approximately 60% DON reduction previously reported from single fungicide applications at GS 10.51. In some locations single treatment with prothioconazole was more effective in reducing DON than tebuconazole. Tebuconazole applied as the first sequential treatment was usually but not always as effective in reducing DON as prothioconazole as at the first sequential timing. The studies show that the boot growth stage tillers can contribute large concentrations of DON to the overall plot and will warrant treatment in some environments. Sequential treatments of prothioconazole increased yield. Both sequential treatments increased 1000 seed weight. Untreated North Dakota State University experimental barley line 'ND20448' had less DON accumulation than untreated 'Tradition'. 'ND20448' had greater plump than 'Tradition'. Tebuconazole is desired by growers because it costs significantly less to apply than prothioconazole.

UNIFORM BIOLOGICAL FUNGICIDE EVALUATIONS FOR CONTROL OF FUSARIUM HEAD BLIGHT AND DEOXYNIVALENOL IN WHEAT

S. Halley[1*], G. Yuen[2], C. Jochum[2], B.H. Bleakley[3], N.K.S. Murthy[3], K.R. Ruden[3], K.D. Waxman[4], G.C. Bergstrom[4] and L.E. Sweets[5]

[1]North Dakota State University, Langdon, ND; [2]University of Nebraska, Lincoln, NE; [3]South Dakota State University, Brookings, SD; [4]Cornell University, Ithaca NY; and [5]University of Missouri, Columbia, MO
[*]Corresponding Author: PH: (701) 256-2582, Email: Scott.Halley@ndsu.edu

ABSTRACT

A multi-location research project was conducted on various wheat market classes at six locations; North Dakota (hard red spring-HRSW), Nebraska (2 locations hard red winter), South Dakota (HRSW), New York (soft red winter-SRWW) and Missouri [2 cultivars-SRWW with different susceptibility to Fusarium head blight (FHB)]. Treatments applied as a single application at Feeke's Growth Stage (FGS) 10.51 included i) Taegro™; ii)Taegro + Prosaro™ iii) Taegro + Prosaro + chelated manganese (Mn) (Pro-manganese 5 chelated manganese solution; Tetra Micronutrients; Woodlands, TX); and iv) Prosaro. Treatments applied sequentially at FGS 10.51 and 5 to 7 days later included v) Taegro and Taegro; vi) Taegro + Prosaro and Taegro; and viii) Taegro + Prosaro + Mn and Taegro. A vii) nontreated was included as a control. All fungicides and biological fungicides were tank mixed with the adjuvant Induce (Helena Chemical Co.) at 0.125% v/v. Taegro (Novozymes Biologicals, Inc.) is a *Bacillus subtilis var. amyloliquefacians* Strain FZB24 containing 5.0 x 10^{10} colony forming units per gram and was include at 3.5 oz. / acre. Prosaro (Bayer CropScience) is a 50:50 blend of tebuconazole and prothioconazole and was applied at 6.5 fl. oz. /acre. Manganese is known to stimulate antibiotic production by some *Bacillus* species. The Mn was added at a rate of 0.01% v/v. Out of seven trials, significant ($P \leq 0.05$) F-tests for FHB incidence were reported at NY (five of seven treatments less than the nontreated) and MO-Roane (five of seven treatments less than the nontreated), severity at ND (four of seven treatments less than the nontreated), and index at NY (five of seven treatments less than the nontreated), at Mead, NE (three of seven treatments less than the nontreated), and at ND (four of seven treatments less than the nontreated). Significant differences for yield were reported from three of seven reporting locations at NY, ND and MO-Roane (one of seven treatments increased yield over the nontreated). Significant differences for test weight were reported at MO-Elkhart (five of seven treatments different from the untreated). Of four reporting trials significant differences in deoxynivalenol accumulation in the seed (DON) were reported at NY (seven of seven treatments less than the nontreated), Mead, NE (three of seven treatments less than the nontreated) and MO-Elkhart (six of seven treatments less than the nontreated). Significant differences for % *Fusarium* damaged kernels were reported at Mead, NE (two of seven treatments less than the nontreated) and MO-Elkhart (four of seven treatments less than the untreated) from two of four reported trials. Significant differences for foliar disease levels were reported from three of three reporting trials, NY (six of seven treatments less than the nontreated), MO-Elkhart (five of seven treatments less than the nontreated) and MO-Roane (five of seven treatments less than the untreated).

In summary, treatments with significant improvement over the nontreated included ii, iii, iv, vi, and viii for visual symptoms of FHB. Treatments with reduction in DON compared to the nontreated included ii, iii, and vi and in two studies iv, vi and viii. Deoxynivalenol accumulations were low in the reported trials. Treatments that increased yield over the nontreated included iii, vii, and viii. Prosaro was effective in

reducing the visual symptoms of FHB at NY and Mead, NE but not ND. However, there were examples where the addition of a biological in a tank mix or as a sequential treatment reduced FHB symptoms or yield over Prosaro including treatments vi, and viii for severity, iii, vi and viii for index and iii for yield in ND, viii for yield in NY and MO-Roane, and ii, vi and viii for DON in MO-Elkhart. This year's results lend further evidence for combining a biological with a fungicide to maximize control of FHB and DON.

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INTEGRATED MANAGEMENT OF FHB IN HARD RED SPRING WHEAT, FARGO, ND 2011

M. McMullen*, S. Meyer and J. Jordahl

Dept. of Plant Pathology, North Dakota State University, Fargo, ND 58108
*Corresponding Author: PH: (701) 231-7627, Email: marcia.mcmullen@ndsu.edu

ABSTRACT

Integrated management trials for FHB have been supported by the USWBSI in ND for multiple locations and grain classes. In 2011, a hard red spring wheat study was conducted at Fargo in which previous crop and fungicide treatment effects on FHB, DON, and yield and quality were examined on four hard red spring wheat cultivars. Cultivars of varying FHB resistance levels were seeded on May 16 in ground previously planted to either spring wheat or dry beans in 2010. Individual plots were 5 feet by 20 feet, with four replications of each fungicide treatment x cultivar treatment. The previous crop components were in side by side fields. Because of the previous crop component, plots were not inoculated with *Fusarium graminearum*; all infections were from natural inoculum. Spring wheat cultivars tested and their FHB resistance level included: Glenn (MR), Samson (S), Steele ND (MS) and Briggs (MS). Plots were either not fungicide treated or treated at the flowering stage with 6.5 fl oz of Prosaro® (prothioconazole + tebuconazole) fungicide. Dates of fungicide application for each cultivar varied because of stage of maturity: July 6 for Briggs, July 8 for Briggs and July 11 for Samson and Steele ND. Fungicide applications were made with a CO_2 backpack sprayer delivering 18 gpa with 40 psi. The average July temperature was 75^0 F, four degrees above the 30 year normal, and night-time temperatures in July averaged five degrees above normal, with some nighttime temperatures not dropping below 73^0 F. June rainfall totaled 4 inches, which was 0.5 inches above the 30 year normal. July rainfall total was 4.1 inches, which was 1.2 inches above the 30 year normal. FHB ratings were taken at soft dough stage of kernel development. Harvest was on August 22. DON levels were determined by the NDSU Veterinary Toxicology Lab using gas chromatography and electron capture techniques. Disease and yield and quality parameters were analyzed using ANOVA at $P = 0.05$. FHB field severities ranged from 0.6 to 9.4 % across varieties and treatments. DON levels ranged from 0.3 to 2.13 ppm across all treatments and cultivars. These levels of disease were relatively low considering moisture levels during June and July. The highest level of DON (2.13 ppm) was observed in untreated Samson (Susceptible to FHB) grown on wheat ground. Untreated Samson on dry bean ground had 1.43 ppm DON. Significant reductions of DON were achieved with fungicide treatment in Samson on wheat ground, and in Samson, Briggs and Steele ND on bean ground. The FHB field severity values and the DON levels in Glenn (Mod. Resistant to FHB) were consistently low and not significantly impacted by previous crop or fungicide treatment. The highest average yield across all cultivars was with fungicide treatment on dry bean ground.

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IMPACT OF INFORMATION SOURCES ON FHB CONTROL STRATEGIES ADOPTED BY SPRING WHEAT GROWERS

Joel Ransom[1*], Gregory McKee[2] and Marcia McMullen[3]

[1]Department of Plant Sciences, [2]Department of Agribusiness and Applied Economics, and
[3]Department of Plant Pathology, North Dakota State University, Fargo, ND 58108
[*]Corresponding Author: PH: (701) 231-7405, Email: joel.ransom@ndsu.edu

ABSTRACT

A survey of the adoption of Fusarium Head Blight (FHB) control practices in the FHB-prone spring wheat region of North Dakota and Minnesota was conducted in 2010. Data on current use of five management practices known to be beneficial in controlling FHB as well as socio-economic factors were obtained from more than 1000 wheat growers, using questionnaires mailed by the USDA-NASS office in Fargo. The rate of adoption of the three practices considered to be the most effective in controlling FHB was very high, with 81% of the growers using a resistant variety, 76% rotating crops so that wheat does not follow another small grain or corn crop, and 68% applying a fungicide at flowering. Just over half of the growers used all three of these methods. The two practices that have potential in reducing the risk of FHB infection at the whole farm level, growing varieties with differing flowering dates and staggering the planting date so that not all fields flower on the same date, were each used by only 22% of the respondents. More farmers ranked extension information sources as being most valuable (72%), than professional sources (20%) and media sources (7%). Farmers using resistant varieties that valued extension sources highest were most likely to use fungicides only when the weather seemed conducive to FHB development, while farmers using resistant varieties that valued professional sources highest were more likely to apply fungicides on all varieties every year. Use of resistant varieties tended to be greatest by farmers that valued extension sources the highest. Education level did not seem to impact level of adoption, although younger farmers using fungicides tended to be better educated than older farmers in the sample. A significant correlation existed between the number of FHB control practices used and having a computer. Other factors found to be correlated with the number of FHB control practices used were: computers used for searches for information about farming practices, visiting extension and product websites for information on varieties and pesticide, visiting extension sites to obtain copies of extension bulletins, and viewing the FHB forecasting website during the critical period of the growing season. These data suggest a general relationship between computer use and higher levels of FHB management. Extension meeting attendance, including field days, was considered low (about half attended meetings once in three years or less frequently) even by those that valued extension information sources highly, suggesting that extension publications and web-based information is a preferred way of obtaining extension information. Most farmers (86%) have a computer with internet access but only 18% used their computer for viewing the FHB forecasting website. Furthermore, less than 50% indicated an interest in obtaining information on the risk and management of FHB through any new electronic technology (Internet blogs, Twitter, Facebook, YouTube, message sent to a cell phone). This survey suggests a very high level of adoption of currently available FHB control practices. The availability of multiple sources of information has been vital in promoting the high level of adoption of the multiple control practices that are currently available.

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2011 UNIFORM FUNGICIDE PERFORMANCE TRIALS FOR THE SUPPRESSION OF FUSARIUM HEAD BLIGHT IN SOUTH DAKOTA

K.R. Ruden[1*], G.S. Redenius[1], K.D. Glover[1], J.L. Kleinjan[1] and L.E. Osborne[2]

[1]Plant Science Department, South Dakota State University, Brookings, SD 57007;
and [2]Pioneer Hi-Bred Int'l - Northern Business Unit, Brookings, SD 57007
[*]Corresponding Author: PH: (605) 688-6246, Email: kay.ruden@sdstate.edu

ABSTRACT

Fusarium head blight (FHB – scab) has been a serious concern for wheat and barley producers in South Dakota for over fifteen years. The objective of this study was to continue to evaluate the effects of various fungicides and fungicide combinations along with different application timings for the suppression of Fusarium head blight and other wheat diseases. Two hard red spring wheat cultivars, 'Select' and 'Reeder', were planted at three South Dakota locations (Brookings, Groton, and South Shore/Watertown). 'Wesley' winter wheat study sites were also established at South Shore/Watertown and Brookings. Studies at both of these sites were conducted under ambient conditions. Due to the overwhelming presence and damage from bacterial diseases at Brookings, only the spring wheat data from the Groton and South Shore/Watertown trials are presented in this report. Trial treatments from the Uniform Fungicide Trial treatments list for the suppression of FHB included an untreated check and the following fungicides: Applied at Feekes growth stage 10.51: A9232D (7.0 fl oz/A), Caramba® (14 fl oz/A), Prosaro® (6.5 fl oz/A); Applied at Feekes growth stage 9: Headline SC (6 fl oz/A); Applied at Feekes growth stage 9: Headline SC (6 fl oz/A) followed by Caramba (14 fl oz/A) at Feekes growth stage 10.51; Applied at Feekes growth stage 10.5: Headline SC (6 fl oz/A), Quadris (6.2 fl oz/A), Evito (4 fl oz/A), Stratego YLD (4 fl oz/A), Quilt (10.5 fl oz/A) and TwinLine (9 fl oz/A). All treatments except the A9232D treatment included Induce, a non-ionic surfactant, applied at 0.125% v/v. Spring wheat trials were planted in a factorial randomized complete block design with six replications. Winter wheat locations had four replications. Plots at the Brookings location were inoculated by spreading *Fusarium graminearum* (isolate Fg4) inoculated corn (*Zea mays*) grain throughout the field and providing overhead mist irrigation applied from 5:00 pm until 10:00 pm each day for two weeks following anthesis. Other sites had natural inoculum from corn stalk residue and natural moisture conditions. Twenty-one days following treatment, plots were evaluated for leaf diseases, FHB incidence, FHB head severity, and FHB field severity. Samples were collected for *Fusarium* damaged kernels (FDK), deoxynivalenol (DON), grain yield and test weight. Even though the Groton location had low levels of Fusarium head blight this year, there were some significant results seen. On the resistant variety 'Select' at Groton, the following products significantly reduced FDK: Prosaro, Headline SC applied at Feekes 9 followed by Caramba at Feekes 10.51, Headline SC applied at Feekes 10.5, Evito and TwinLine. On the susceptible variety 'Reeder' at Groton, the following fungicides significantly reduced FHB Incidence: Caramba, Prosaro and Headline SC applied at Feekes 9 followed by Caramba at Feekes 10.51 while only Caramba reduced the FHB Disease Index. At the South Shore/Watertown location for spring wheat, the following products significantly reduced DON on the resistant variety, 'Select': Caramba, Prosaro, Headline SC, Stratego YLD and TwinLine. On the susceptible variety, 'Reeder', the following fungicides: A9232D, Caramba, Prosaro, Stratego YLD and TwinLine significantly reduced DON. In 'Reeder', Stratego YLD and TwinLine reduced FHB Disease Index. In the more resistant variety 'Select': A9232D, Caramba, Headline SC applied at Feekes 10.5, Quadris, Evito, Stratego YLD, Quilt and TwinLine all significantly reduced FHB Disease Index. At this location and this growing season, it appears that an early application of fungicide, prior to flowering, had a positive impact on *Fusarium* control. The improvement in control

seen with early applications vs. "standard" at-flowering applications is unique to this location this season, and was not seen at other locations in SD. A possible explanation is related to the rapid loss of leaf tissue around wheat flowering from severe bacterial disease infection, reducing leaf and head uptake of the later fungicide applications. It also appears that, at this location, effective triazole fungicides on *Fusarium*, such as prothioconazole and metconazole, can partially mask the known negative impact of a strobilurin fungicide on components of *Fusarium* epidemics, such as DON level, when applied in a combination triazole/strobilurin fungicide. These effects from some of the strobilurins and the strobilurins + triazole fungicides which were only seen in the spring wheat trial at the South Shore/Watertown location may be unique to the environmental conditions and hastened plant development at this location in 2011. No change in current recommendations for Fusarium head blight management can be construed from this data set.

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COMBINED EFFECTS OF STAGONOSPORA LEAF BLOTCH AND FUSARIUM HEAD BLIGHT ON GRAIN YIELD AND QUALITY OF SOFT RED WINTER WHEAT

J.D. Salgado, L.V. Madden and P.A. Paul*

Department of Plant Pathology, The Ohio State University, OARDC, Wooster, OH, 44691
*Corresponding Author: PH: (330) 263-3842 ext 2850, Email: paul.661@osu.edu

ABSTRCT

Stagonospora nodorum Berk [teleomorph: *Phaeosphaeria nodorum* (Müll.) Hedjar] and *Fusarium graminearum* Schwabe (teleomorph: *Gibberella zeae*) are major necrotrophic pathogens of wheat (*Triticum aestivum* L.) and related cereals. *S. nodorum* affects wheat leaves and spikes, causing Stagonospora leaf and glume blotch (SLB and SGB, respectively), while *F. graminearum* is the primary causal agent of Fusarium head blight (FHB). Both pathogens are favored by wet, humid conditions, thus, it is quite common for SLB, SGB, and FHB to occur simultaneously in naturally infected fields, with similar effects on grain yield and quality. A previous model of the relationship between FHB and grain yield reported that wheat class affected the intercept but not the slope of this relationship. However, this relationship may also vary among cultivars with different levels of resistance to FHB and could be influenced by the presence and severity of foliar diseases. Field experiments were conducted at the Ohio Agricultural Research and Development Center, near Wooster, OH to characterize the relationships between FHB and grain yield and quality as influenced by cultivar FHB resistance and SLB severity. The experimental design was a split-split-plot with cultivar (Cooper, Hopewell and Truman) as whole plot, *S. nodorum* inoculum density (0 to 1 x 10^6 spore/ml) as sub-plot, and *F. graminearum* inoculum density (0 to 1.5 x 10^4 spores/ml) as sub-sub-plot. *S. nodorum* and *F. graminearum* inoculations were done at full flag leaf emergence (Feekes 9.0) and early anthesis (Feekes 10.5.1), respectively. SLB severity was rated on the flag leaf at the milky ripe stage (Feekes 11.1), and FHB index was rated at soft dough (Feekes 11.2). Results from the 2010 growing season showed that there were significant differences in SLB and FHB intensity among inoculation treatments, with the severity of both diseases increasing as the inoculum density of their respective causal agent increased. The effect of cultivar on both SLB severity and FHB index was also significant ($P \leq 0.001$). Hopewell had the highest level of mean SLB (34.6%) and FHB (23.2%), followed by Cooper (SLB, 19.5% and FHB, 18.3%), and Truman (SLB, 12.2%, and FHB 7.83%). The interaction between cultivar and inoculum density was significant for FHB, but not for SLB. Grain yield and test weight were also evaluated at different levels of FHB index and SLB severity and among cultivars. Both responses were affected by FHB index, with mean yield and test weight decreasing with increasing index. However, the interaction between cultivar and FHB index was not significant ($P = 0.711$ for yield and 0.218 for TW), suggesting that the rates of yield and test weight reduction with increasing FHB index were similar among the cultivars. The effect of SLB severity on yield and test weight was no statistically significant. However, when both SLB severity and FHB index were used as predictors in a mixed model multiple regression analysis, both were significant predictors ($P= 0.031$ and <0.0001, respectively) of yield response. Our results also indicated that the interaction effect of cultivar and FHB index on DON accumulation was statistically significant ($P = 0.018$), thus the rate of toxin accumulation as index increased varied among cultivars. A more comprehensive analysis of the effects of SLB, FHB, and wheat cultivars on grain yield and quality will be conducted using results from the 2011 and 2012 seasons. Models will be developed for the combined effects of SLB and FHB on wheat yield and test weight.

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MANAGEMENT OF MYCOTOXINS IN GRAIN: THE ONTARIO EXPERIENCE

Art Schaafsma[1*], Victor Limay-Rios[1], Rishi R. Burlakoti[2], Aman Thakral[2],
Sandy Vervaet[2], Lily Tamburic-Illincic[1] and David Hooker[1]

[1]University of Guelph, Ridgetown Campus, Ridgetown, Ontario, Canada;
and [2]Weather INnovations Incorporated, Chatham, Ontario, Canada
[*]Corresponding Author: PH: 519-674-1500 x6350, Email: aschaafsma@ridgetownc.uoguelph.ca

ABSTRACT

The severe Fusarium head blight epidemic of wheat in the great lakes region of 1996 stimulated an incredible response by stakeholders along the value chain in a very unusual display of solidarity in a normally competitive environment, resulting in several significant and integrated steps forward in how mycotoxins are managed. Similar to many groups around North America and Europe our group developed and adapted an integrated strategy to manage the occurrence of deoxynivalenol in wheat based products, tailored to the market, regulatory, economic, and production environments of the region. Early on, it was clear to most that weather played the most significant role in epidemics, with genetics placing a close second, and agronomic practices other than variety selection placing an important but more distant third. Over the ensuing years a management strategy emerged combining a significant effort in plant breeding, with best agronomic practices, with a weather-based mycotoxin forecast (DONcast), and prescriptive fungicide applications. With these tools available, if the weather of 1996 was duplicated today an estimated 50-75% reduction in mycotoxin can be expected. The tools as currently used for wheat in Ontario will be described. By comparison, the same great lakes region also happens to be the most frequently infected corn growing region by the same pathogen manifested as Gibberella ear rot. In contrast against the success achieved in wheat in only 10 years after 1996, no progress was apparent in corn in 2006, 20 years after a severe epidemic in corn in 1986, of similar magnitude to the one in wheat in 1996. Some explanations for this marked contrast will be proffered, as well as some recent progress in managing mycotoxins in corn discussed.

REDUCTION OF FUSARIUM HEAD SCAB INCIDENCE AND SEVERITY, AND DON LEVELS, AND YIELD INCREASES USING PROSARO™ FUNGICIDE

M.R. Schwarz*, B.E. Ruden and R.A. Myers

Bayer CropScience, Research Triangle Park, NC
*Corresponding Author: PH (919) 549-2741, Email: Mike.schwarz@bayer.com

ABSTRACT

Prosaro™ is a broad spectrum head and leaf disease foliar fungicide that was introduced in 2009 by Bayer CropScience. Prosaro is registered for use in spring wheat, durum wheat, winter wheat, and barley. Prosaro is a mixture of prothioconazole and tebuconazole; these two active ingredients provide control of Fusarium head blight (FHB) as well as several important cereal leaf diseases. Prosaro is formulated as a soluble concentrate for ease of handling. It is applied at 6.5 to 8.2 fl oz/ac with a non-ionic surfactant to wheat or barley up to 30 days prior to harvest.

Replicated trials were completed in 2008, 2009, 2010, and 2011 at multiple locations in the soft red winter wheat growing region of Illinois, Indiana, Kentucky, Michigan, Ohio, and Tennessee. Prosaro was applied once at 6.5 fl oz/ac with a non-ionic surfactant when the winter wheat initiated flag leaf emergence (Feekes 8) to flowering (Feekes 10.51). The objective of these trials was to evaluate the effect of Prosaro on grain yield (bushels/acre) and test weight (lbs/bushel) in winter wheat. FHB incidence and severity were recorded where applicable. DON levels (ppm) were evaluated at some sites where FHB was present.

Test results from 2008 to 2010 (237 trials) showed Prosaro applied at Feekes 8.0 to 10.51 increased the grain yield of soft red winter wheat by an average of 10.4 bu/ac, independent of FHB, over non-treated plots. Test weight was also increased by an average of more than 1.5 lb/bu by using Prosaro. DON levels were reduced from an average of 3.57 ppm in non-treated plots to 1.18 ppm in Prosaro-treated plots (40 sites). In a trial conducted on two varieties in 2011 in Illinois, FHB incidence and severity were controlled by Prosaro an average of 82% and 81%, respectively, using Prosaro applied at Feekes 10.51 and compared to the non-treated check.

LIPASE ACTIVITY OF BACILLUS STRAINS USED FOR BIOLOGICAL CONTROL OF FUSARIUM HEAD BLIGHT

N. Srinivasa Murthy[2] and B.H. Bleakley[1,2*]

[1]Plant Science Department, and [2]Biology/Microbiology Department,
South Dakota State University, Brookings, SD
[*]Corresponding Author: PH: (605) 688-5498, Email: bruce.bleakley@sdstate.edu

ABSTRACT

The growth medium used for producing microorganisms used as biological control agents can be critical to optimizing their effectiveness in controlling plant disease. Including vegetable oil in the broth medium might promote biosurfactant production in some bacterial strains. If oil has a positive effect on biosurfactant production, then the microorganism should have mechanisms to utilize the oil present in the broth medium. Most organisms utilize the oil or lipid sources through the production of extracellular lipases. We hypothesize that including plant oil in the broth medium used to grow several *Bacillus* strains promotes biosurfactant production via production of extracellular lipase(s). The *Bacillus* biological control agents (*Bacillus amyloliquefaciens* strains 1-BA, 1-BC, 1-BE and 1-D3) were inoculated into a broth medium containing Tryptic soy broth + yeast extract + manganese with or without plant oil. Later, the broth culture medium was subjected to biosurfactant analysis through three assays (droplet collapse, oil spreading, and turbidometric analysis). Also, assays were done to examine the strains for extracellular lipase production. Oil amendment and shaking of broth cultures had a significant impact on biosurfactant production. All the strains experienced increased biosurfactant production, with differences observed among the strains. Strain 1D3 showed the best biosurfactant production, in comparison to all other strains. Lipase production was observed for all the strains. Further work will examine the effect of different oils on the production of extracellular lipase and its influence on biosurfactant production.

INTEGRATED MANAGEMENT STRATEGIES FOR FUSARIUM HEAD BLIGHT OF SOFT RED WINTER WHEAT IN MISSOURI: SUMMARIZATION OF TRIAL DATA FROM FIVE YEARS

Laura E. Sweets

Division of Plant Sciences, University of Missouri, Columbia, MO
Corre4sponding Author: PH: (573) 884-7307, Email: SweetsL@missouri.edu

OBJECTIVE

To evaluate the importance of crop sequence, variety selection and fungicide application as components of an integrated management program for Fusarium head blight (FHB) of soft red winter wheat in Missouri.

INTRODUCTION:

The severity of FHB or scab epidemics in the United States has caused enormous yield and quality losses in both wheat and barley over the last decade. The development of this disease is dependent on the genetics of the host, favorable environmental conditions, the prevalence of the causal fungus and the survival and spread of the causal fungus. Control of this disease has been difficult because of the complex nature of the host/pathogen interaction. Management of FHB and the associated mycotoxin DON have not been achieved by any single control measure. An integrated approach is critical to attaining the best possible management of FHB and DON in any given environment.

As a result of a workshop sponsored by the Chemical, Biological and Cultural Control Research Area of the U.S. Wheat & Barley Scab Initiative in 2006, a protocol for a multi-state project focusing on integrated management strategies for FHB was developed. The research portion of the project has been multi-state trials evaluating crop sequence, variety selection and fungicide application as an integrated management program for FHB.

The University of Missouri has participated in the multi-state integrated management project for the past five growing seasons. Results from the five years are summarized in this poster abstract.

MATERIALS AND METHODS

During the fall of 2006 two adjacent fields at the University of Missouri Bradford Research and Extension Center just east of Columbia, MO, were identified for this study. The fields had been in a corn/soybean rotation for at least five years prior to the initiation of the study and were separated by a small drainage ditch. The wheat trials were planted into standing corn residue or soybean residue on the same day. The remainder of each field was planted into the normal rotational crop of corn or soybeans. In subsequent years, the wheat trials were shifted to other areas of the same fields with the remainder of the fields planted to the normal rotational crop.

Five soft red winter wheat varieties with similar heading times and varying reactions to FHB were selected for the trial. The five varieties included the public varieties Bess and Roane which are widely grown in Missouri, the Agri-Pro variety Elkhart and the Pioneer varieties 25R47 and 25R54. The FHB resistance reactions for the five varieties are as follows: Bess is considered as tolerant, Elkhart as susceptible, Pioneer variety 25R37 as moderately susceptible, Pioneer variety 25R54 as moderately tolerant and Roane as moderately tolerant.

In the fall of 2006 the trials were planted no-tillage into either soybean residue or standing corn residue on the same day. Individual plots were 7 rows (~7.5" row spacings) by 30' in length. Each trial was set up as a split plot trial with fungicide application as the main plot and variety as the sub-plot. There were

6 replicates in each trial. Sub-plots were separated by buffer plots. The foliar fungicide treatment Prosaro® (6.5 fl oz/A) was applied at Feekes Growth Stage 10.51. A non-ionic surfactant was added to the fungicide at a rate of 0.125% v/v, and application was made using a CO2 pressurized backpack sprayer with TwinJet XR8002 nozzles mounted at an angle (30 and 60 degrees) forward and backward.

Plots were evaluated for incidence and severity of FHB, yield was taken, grain samples were submitted to North Dakota State University for DON analysis and grain samples were rated for percent of *Fusarium* damaged kernels (FDK). Data has been submitted annually to the regional coordinator for inclusion in the multi-state project report. Analysis of variance was used to determine the effects of variety, fungicide and their interactions on yield, DON levels, FHB index (average of 100 wheat heads per plot) and percent FDK for each residue type.

The trial was repeated following the same protocol during the next four growing seasons.

RESULTS

Weather conditions during the 2006-2007 season were not conducive for the development of FHB at the Columbia, MO location. Conditions as the wheat crop was flowering were too dry for infection to occur and disease to develop. However, the following four seasons were quite conducive for the development of FHB. In 2008, 2009 and 2010 weather conditions were unusually wet and cool as the wheat crop flowered and after flowering so both scab and DON levels were high. The 2011 season was wet during flowering so scab developed but was hot and dry during grain fill so DON levels were lower than in the previous three years.

The results from the five years of this trial demonstrate the importance of crop sequence, variety selection and fungicide application in reducing FHB and DON levels in soft red winter wheat in Missouri. Planting winter wheat after soybean rather than corn showed a reduction in both FHB and DON even in years which were not particularly favorable for the development of FHB. Crop sequence and variety selection appear to valuable preventative measures for reducing FHB and DON levels. The application of the fungicide Prosaro at FGS 10.51 tended to reduce FHB levels and increase yields for most of the varieties on both crop sequences with effects being more pronounced on susceptible and moderately tolerant varieties. The data from the five years of this trial indicate that an integrated management approach employing crop sequence and variety selection as pre-plant preventative management measures and fungicide application during the growing season if weather conditions at flowering warrant application may be beneficial in reducing FHB, reducing DON levels and increasing yield for soft red winter wheat grown in Missouri.

ACKNOWLEDGEMENT AND DISCLAIMER

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EVALUATION OF INTEGRATED METHODS FOR MANAGING FHB AND DON IN WINTER WHEAT IN NEW YORK IN 2011

K.D. Waxman and G.C. Bergstrom*

Dept. of Plant Pathology and Plant-Microbe Biology, Cornell University, Ithaca, NY 14853
*Corresponding Author: PH: (607) 255-7849, Email: gcb3@cornell.edu

OBJECTIVE

To evaluate the individual and interactive effects of moderately resistant cultivars and the foliar fungicide Prosaro® on wheat yield and the integrated management of Fusarium head blight (FHB) and deoxynivalenol (DON) under two environments in New York.

INTRODUCTION

In response to the USWBSI goal to validate integrated management strategies for FHB and DON, the Disease Management RAC of USWBSI initiated a multi-state, multi-year, coordinated field study. In New York during 2011, we observed the disease and yield impact of cultivar susceptibility, inoculation with *Fusarium graminearum*, and treatment with Prosaro in two experimental environments.

MATERIALS AND METHODS

All experiments were performed at the Musgrave Research Farm in Aurora, NY following cultural practices recommended for soft red winter wheat in the region. The four cultivars included were 'Pioneer 25R47' (susceptible to FHB), 'SW 80' (susceptible to FHB), 'Otsego' (classified initially as moderately resistant to FHB), and 'Truman' (established as moderately resistant to FHB). The two experimental environments, both planted on October 13, 2010, were characterized by the planting of winter wheat no-till into 1) soybean residue and 2) corn residue in immediately adjacent parcels of land. Each experimental design was a split-split plot with four wheat cultivars as whole plots, inoculation treatment as subplot, and fungicide treatment as sub-subplot, in four replicate blocks. Main plots were planted with a 10 ft wide commercial grain drill. Spray treatments applied at Feekes GS10.5.1 on 6/3/11 were 1) non-sprayed, non-inoculated 2) Prosaro 6.5 fl oz/A & Induce 0.125%, non-inoculated 3) non-sprayed and inoculated with *F. graminearum*; and 4) Prosaro 6.5 fl oz/A & Induce 0.125% and inoculated with *F. graminearum*. Treatments 3 and 4 were inoculated with a conidial suspension of *F. graminearum* (40,000 conidia/ml) on the same day as the Prosaro application after the fungicide had dried and in early evening to provide a better environment for infection. Prosaro and *F. graminearum* applications were applied with a tractor-mounted sprayer with paired Twinjet nozzles mounted at an angle (30° from horizontal) forward and backward and calibrated to deliver at 20 gallons per A. FHB and foliar diseases were assessed at soft dough stages. Grain was harvested from a 4 ft wide x 20 ft long area in each subplot using a Hege plot combine. Grain moistures, plot yields, and test weights were recorded and the latter two were adjusted for moisture. Means were calculated and subjected to a split plot Analysis of Variance. Fisher's protected LSD was calculated at *P*=0.05. Analysis of DON content in grain was conducted in the USWBSI-supported mycotoxin laboratory of Dr. Dong.

RESULTS AND DISCUSSION

Both experimental environments were located in the same field that in the previous year was split, growing corn in one half and soybean in the other. Flowering occurred simultaneously in both environments during a relatively dry period, considered low risk for FHB infection. The average incidence of FHB in the experiment following corn was 7% in non-inoculated plots, 15% in inoculated plots, and 11% overall. The average incidence of FHB in the experiment following soybean was 3% in non-inoculated plots, 11% in inoculated plots, and 7% overall. This suggests that the corn residue provided a slightly more favorable environment and/or higher background inoculum for FHB development. This pattern was observed also for FHB index and DON contamination. The average FHB index and DON contamination in the experiment following corn were 2% and 0.6 ppm in non-inoculated plots, 5% and 1.2 ppm in inoculated plots, and 3% and 0.9 ppm overall. The average incidence of FHB and DON levels in the experiment following soybean were 1% and 0.1 ppm in non-inoculated treatments, 4% and 0.7 ppm in inoculated plots, and 2% and 0.4 ppm overall. The DON contamination exceeded the 2 ppm threshold for sale at flour mills more frequently in the experiment following corn but only in the non-sprayed, inoculated plots. DON concentrations exceeding the threshold occurred in Otsego, Pioneer 25R47, and SW 80 in the environment following corn and in SW 80 in the environment following soybean. Interestingly, while the disease pressure was greater in the experiment following corn, average yields were lower in the experiment following soybean. This is likely to due to greater weed pressure and deer feeding observed in the wheat plots following soybean.

The impact of *F. graminearum* inoculation was determined by comparing the non-inoculated and inoculated treatments (combining non-sprayed and Prosaro treatments). Inoculation did not significantly decrease yield except for Truman in the no-till corn debris environment (but the differences disappeared once fungicide treatment was considered). Inoculation did significantly impact FHB ratings but not for all cultivars in both environments. Inoculation resulted in significantly higher FHB index and DON contamination for Otsego and SW 80 in both environments, and DON contamination for Pioneer 25R47 in the soybean debris environment. FHB index of Truman following soybean was significantly increased due to inoculation, but again, differences were not significant when all four treatments were considered. In general, there were no differences in cultivar response to inoculation between the two environments with the exception of a significantly higher FHB index for Pioneer 25R47 in the corn debris environment.

Significant differences in FHB index between the treatments were observed in two, SW 80 and Otsego, of the four cultivars in both environments. FHB index was significantly greater than all other plots in the non-sprayed, inoculated plots of SW 80 following corn and both cultivars following soybean. For Otsego following corn, FHB index in the two non-sprayed plots were significantly higher than in the two Prosaro plots. When compared to the non-sprayed, inoculated plots, either Prosaro application (with and without inoculation) significantly decreased the FHB index. Due to low levels of natural disease, the Prosaro applications did not always significantly decrease the FHB index compared to the non-sprayed, non-inoculated plots. For Pioneer 25R47 and Truman in both environments and Otsego following corn, there was no significant increase in FHB index due to inoculation.

Significant differences in DON contamination between the treatments were observed with Pioneer 25R47, SW 80 and Otsego. DON contamination was significantly greater than all other plots in the non-sprayed, inoculated plots of SW 80 and Otsego following corn and all three cultivars following soybean. When compared to the non-sprayed, inoculated plots, either Prosaro application (with and without inoculation) significantly decreased DON contamination. In the corn debris environment, there was significantly less DON contamination in the non-inoculated Prosaro plots than the non-sprayed, non-inoculated plots. In contrast, in the soybean debris environment, there were no significant differences observed between the two non-inoculated and the inoculated Prosaro plots, again indicating lower natural disease pressure following soybean. There were no statistically significant differences in DON between any treatments observed for Truman in either environment.

In general, *F. graminearum* inoculation and/or application of Prosaro did not cause significant differences in yield for any of the cultivars in either environment. The one exception was observed in Otsego following soybean where plots with the non-inoculated

Prosaro treatment had a significantly greater average yield than plots with the two non-sprayed treatments.

When results of all the cultivars were combined, the overall impact of the Prosaro applications varied between the two environments and mirrored the patterns observed when considering the cultivars separately. In the corn debris environment, both Prosaro applications (with and without inoculation) resulted in significantly lower FHB indices and DON concentrations compared to the either non-sprayed plots. In the soybean debris environment, both Prosaro applications resulted in significantly lower FHB indexes and DON concentrations only when compared to the inoculated non-sprayed plots. While not statistically significant, plots treated with Prosaro were generally higher yielding.

When results of all the treatments were combined, the four cultivars demonstrated some differences in both disease responses and yield capabilities. Significantly greater FHB indices were observed in the susceptible cultivars (Pioneer 25R47 and SW 80) compared to the moderately resistant cultivars (Otsego and Truman) in the corn debris environment. Only Truman had statistically significantly lower levels of DON contamination in the corn debris environment. In the soybean debris environment, SW 80 was the only cultivar that had significantly higher FHB indices and DON concentrations. In summary, SW 80 demonstrated susceptibility in both environments, Pioneer 25R47 demonstrated susceptibility and Otsego demonstrated moderate resistance in the higher disease pressure environment (following corn), and Truman demonstrated moderate resistance in both environments. Although not always statistically significant, the FHB susceptible cultivars had higher yields than the moderately resistant varieties in both environments.

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Table 1. Main effect of treatment on grain yield, Fusarium head blight index, and deoxynivalenol contamination at Aurora, NY.

	Adjusted grain yield (bu/A)		
Treatment:	After corn	After soybean	Average
Non-sprayed	71	55	63
Prosaro	73	60	66
Non-sprayed, inoculated	68	53	61
Prosaro, inoculated	72	57	65
LSD (*P*=0.05)	NS	NS	
	Fusarium head blight index (%)		
Treatment:	After corn	After soybean	Average
Non-sprayed	3	1	2
Prosaro	1	0	1
Non-sprayed, inoculated	7	6	7
Prosaro, inoculated	2	2	2
LSD (*P*=0.05)	3	2	
	Contamination of grain by DON (ppm)		
Treatment:	After corn	After soybean	Average
Non-sprayed	1.0	0.1	0.6
Prosaro	0.2	0.1	0.2
Non-sprayed, inoculated	1.9	1.2	1.6
Prosaro, inoculated	0.4	0.2	0.3
LSD (*P*=0.05)	0.6	0.4	

Table 2. Main effect of cultivar on grain yield, Fusarium head blight index, and deoxynivalenol contamination at Aurora, NY.

	Adjusted grain yield (bu/A)		
Treatment:	After corn	After soybean	Average
Otsego	69	52	61
Pioneer 25R47	76	62	69
SW 80	73	57	65
Truman	65	54	60
LSD (*P*=0.05)	6	6	
	Fusarium head blight index (%)		
Treatment:	After corn	After soybean	Average
Otsego	2	2	2
Pioneer 25R47	6	2	4
SW 80	5	5	5
Truman	0	0	0
LSD (*P*=0.05)	3	3	
	Contamination of grain by DON (ppm)		
Treatment:	After corn	After soybean	Average
Otsego	0.9	0.3	0.6
Pioneer 25R47	1.2	0.3	0.8
SW 80	1.3	0.8	1.1
Truman	0.2	0.1	0.4
LSD (*P*=0.05)	0.7	0.5	

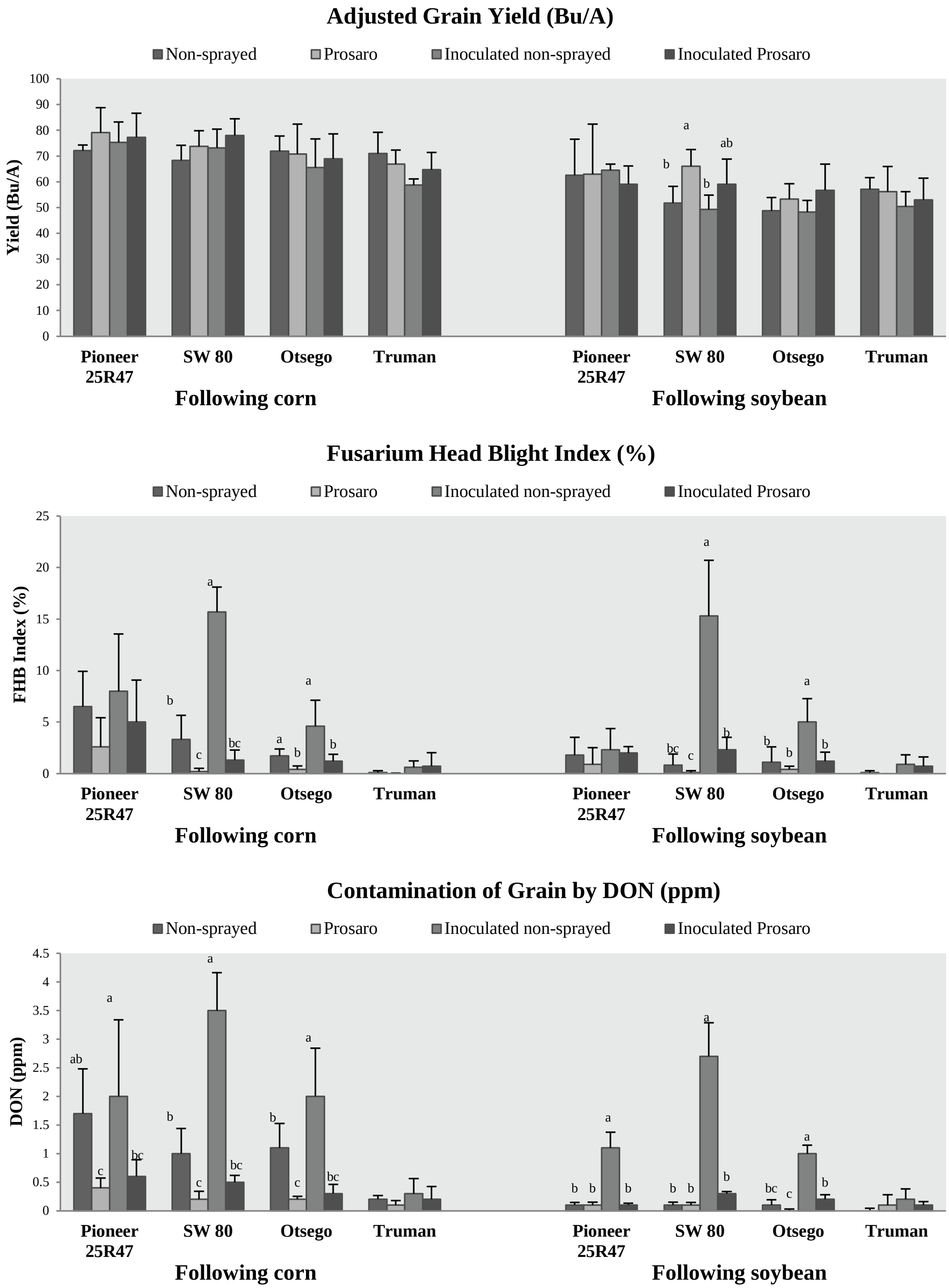

Figure 1. Effect of flowering stage application of Prosaro fungicide and *F. graminearum* inoculation on yield, FHB index and DON contamination of four winter wheat cultivars in Aurora, NY. Letters denote treatment means that differ significantly at *P*=0.05.

EFFECTS OF WINTER WHEAT CULTIVARS AND PROSARO™ FUNGICIDE ON FHB AND DON

Stephen N. Wegulo[1*], Julie A. Stevens[1], Emmanuel Z. Byamukama[1], P. Stephen Baenziger[2] and William W. Bockus[3]

[1]Department of Plant Pathology, University of Nebraska, Lincoln, NE; [2]Department of Agronomy and Horticulture, University of Nebraska, Lincoln, NE; and [3]Department of Plant Pathology, Kansas State University, Manhattan, KS
[*]Corresponding Author: PH: (402) 472-8735, Email: swegulo2@unl.edu

ABSTRACT

Fusarium head blight (FHB), caused by *Fusarium graminearum*, is a destructive disease of wheat. The disease causes premature bleaching of spikelets on the wheat head. Bleached spikelets are sterile or contain discolored and/or shriveled kernels commonly known as *Fusarium*-damaged kernels (FDK). In addition to lowering yield and grain quality, *F. graminearum* also produces the mycotoxin deoxynivalenol (DON) which can be harmful to humans and animals. A management approach for FHB that integrates cultivar resistance and fungicide application is more effective than either strategy. The objective of this study was to determine the effects of cultivar resistance and fungicide application on FHB, DON, FDK, and yield in winter wheat. Four cultivars differing in levels of resistance to FHB were planted following soybean in the fall of 2010 at the University of Nebraska Agricultural Research and Development Center near Mead, NE. The cultivars were 2137 (susceptible), Jagalene (susceptible), Harry (moderately resistant), and Overland (moderately resistant). In the fall of 2010, chopped corn stalks were spread on the soil surface in the wheat plots to serve as a source of inoculum during the following spring. In addition, corn kernels colonized by *F. graminearum* were applied to the soil surface in the wheat plots three weeks before flowering at a rate of 50 g/m^2. At early flowering, plots were spray-inoculated with spores of *F. graminearum* (1 x 10^5 spores/ml). Plots were not irrigated. The experimental design was a split plot in randomized complete blocks with six replications. Cultivars were the main plots and fungicide treatments (check or treated with Prosaro at 6.5 fl. oz/acre + Induce non-ionic surfactant at 0.125% v/v) were the subplots. Plot size was 5 ft x 44 ft. A CO$_2$-powered backpack sprayer and four Teejet 800-1 VS nozzles spaced 12 in. apart on a boom were used to apply fungicide to heads at early flowering. Disease severity and incidence were assessed on 25 randomly selected heads in each plot on June 21 and used to calculate FHB index. Plots were harvested with a small plot combine. The percentage of *Fusarium*-damaged kernels was visually estimated. A grain sample from each plot was ground and sent to the North Dakota Veterinary Diagnostic Laboratory at North Dakota State University, Fargo, ND for DON analysis. FHB index was generally low; it was significantly higher in Jagalene than in the other three cultivars (Table 1). Prosaro reduced index in three of the four cultivars, but this reduction was not significant at $P = 0.05$. DON was similarly low; it was highest in the check treatments in Jagalene and Harry and lowest in the Prosaro treatment in Overland. Prosaro reduced DON in all four cultivars, but the reduction was not significant at $P = 0.05$ in any of the cultivars. FDK was significantly lower in Overland than in the other three cultivars. Prosaro reduced FDK the greatest in Jagalene; however, this reduction was not significant at $P = 0.05$. Prosaro did not reduce FDK in Overland. Yield in Harry and Overland was significantly higher than yield in Jagalene and 2137. Prosaro significantly increased yield only in Harry.

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This material is based upon work supported by the U.S. Department of Agriculture, under Agreement No. 59-0790-7-080. This is a cooperative project with the U.S. Wheat & Barley Scab Initiative. Any opinions, findings, conclusions, or recommendations expressed in this publication are those of the author(s) and do not necessarily reflect the view of the U.S. Department of Agriculture.

Table 1. FHB index, DON, FDK, and yield in four winter wheat cultivars not treated or treated with Prosaro fungicide in a field experiment conducted in Nebraska, USA in 2011.

Cultivar	Fungicide treatment	Index (%)	DON[a] (ppm)	FDK (%)	Yield (bu/A)
Jagalene	Check	3.15 a[b]	1.90 a	28.8 a	44.5 c
Jagalene	Prosaro	2.33 a	1.25 ab	20.8 ab	48.0 c
Harry	Check	0.20 b	1.83 a	30.5 a	57.3 b
Harry	Prosaro	0.05 b	1.03 a-c	28.0 a	62.8 a
2137	Check	0.88 b	1.25 ab	27.3 a	45.5 c
2137	Prosaro	1.03 b	0.68 bc	25.3 a	46.5 c
Overland	Check	0.35 b	0.83 bc	13.0 b	62.3 ab
Overland	Prosaro	0.08 b	0.13 c	14.3 b	62.0 ab

[a] Abbreviations: DON, deoxynivalenol; FDK, *Fusarium*-damaged kernels.

[b] Means within a column followed by the same letter are not significantly different according to the least significant difference test at $P = 0.05$.

UNIFORM FUSARIUM HEAD BLIGHT INTEGRATED MANAGEMENT TRIALS: A 2011 UPDATE

K. Willyerd[1], G. Bergstrom[2], C. Bradley[3], R. Dill-Macky[4], P. Gross[5],
A. Grybauskas[6], S. Halley[5], D. Hershman[7], L. Madden[1], M. McMullen[5],
G. Milus[8], L. Osborne[9], K. Ruden[9], J.D. Salgado[1], L. Sweets[10],
S. Wegulo[11], K. Waxman[2], K. Wise[12] and P. Paul[1*]

[1]The Ohio State University/OARDC, Dept. of Plant Path., Wooster, OH 44691; [2]Cornell University, Dept. of Plant Path., Ithaca, NY 14853; [3]University of Illinois, Dept. of Crop Sci., Urbana, IL 61801; [4]University of Minnesota, Dept. of Pant Path., St. Paul, MN 55108; [5]North Dakota State University, Dept. of Plant Pathology, Fargo, ND 58102; [6]University of Maryland, Dept. of Plant Sci. and Landscape Architecture, College Park, MD 20742; [7]University of Kentucky, Dept. of Plant Path., Princeton, KY 42445; [8]University of Arkansas, Dept of Plant Path., Fayetteville, AR 72701; South Dakota State University, Plant Sci. Dept., Brookings, SD 57007; [10]University of Missouri, Dept. of Plant Microbiology and Pathology, Columbia, MO 65211; [11]University of Nebraska, Dept. of Plant Path., Lincoln, NE 68583; and [12]Purdue University, Department of Botany and Plant Path., West Lafayette, IN 47907

[*]Corresponding Author: PH: 330-263-3842, Email: paul.661@osu.edu

OBJECTIVE

To evaluate the integrated effects of fungicide and genetic resistance on FHB and DON in all major grain classes in different cropping systems.

INTRODUCTION

FHB and DON management options include genetic resistance, cultural practices, and chemical and biological control. However, when used individually, these control measures are not fully effective under environmental conditions favorable to disease development. Moderately-resistant wheat and barley cultivars may accumulate DON levels above critical thresholds for human and livestock consumption (2). Triazole fungicide efficacy varies among studies, with mean percent control between 40 and 60% for FHB index and 30 to 50% for DON accumulation (3). In general, more effective control is achieved when moderate resistance is combined with appropriate fungicide applications (1, 4). However, this control is variable among grain classes and cropping systems. From 2009 to 2011, coordinated, uniform trials were conducted in multiple states to evaluate the effects of grain class, crop rotation, cultivar resistance, and fungicide application on the reduction of FHB and DON. This report summarizes results from trials conducted during the 2011 season.

MATERIALS AND METHODS

Trials were established in fields following a host or non-host crop of *F. graminearum*. At least two commercial small grain cultivars, classified as susceptible (S), moderately susceptible (MS) or moderately resistant (MR), were planted in four to six replicate blocks in each trial. The standard experimental design was a randomized complete block, with a split-split-plot arrangement of cultivar (whole-plot), inoculation (sub-plot) and fungicide treatment (sub-sub-plot). Some trials used fungicide as whole-plot and cultivar as sub-sub-plot; while others did not include inoculation as a factor. Fungicide (Prosaro®, 6.5 fl. oz/A + NIS) was applied at anthesis, using CO_2 powered sprayers, equipped with Twinjet XR8002 or paired XR8001 nozzles, mounted at a 30 or 60^o angle, forward or backward. For trials with artificial inoculations, either *F. graminearum*-colonized corn kernel were spread on the soil surface of plots prior to anthesis or plots were spray-inoculated with a spore suspension of the fungus approximately 24 hours following fungicide treatments. FHB index (plot severity) was assessed during the dough stages of grain development. Milled grain samples were sent to a USWBSI-supported laboratory for toxin analysis. Analysis of variance (linear mixed model) was used to evaluate the effects of fungicide, cultivar, (and inoculation, when appropriate) and their interactions on index, DON and yield (assuming a significance level $\alpha = 0.05$). Percent control was calculated to compare the effect of control measures to the susceptible, untreated check.

RESULTS AND DISCUSSION

At the time of this summary, data were collected from 29 trials, conducted in 12 states (AR, IL, IN, KY, MD, MN, MO, ND, NE, NY, OH and SD) (Table 1). These included 15 soft red winter wheat (SRWW), 2 hard red winter wheat (HRWW), 4 hard red spring wheat (HRSW), 2 two-row barley, 4 six-row barley and 2 durum wheat trials. FHB intensity and DON accumulation varied among locations and grain classes (Table 1). Trials with < 5% mean index and/or < 1 ppm mean DON in the susceptible, untreated check were not included in this analysis. Means for cultivar resistance class x fungicide treatment combinations and percent control of index and DON, relative to the untreated susceptible check (S_UT), are found in Table 2.

Arkansas. Four SRWW cultivars were planted near Kibler. Index values ranged from 4 to 76%; however, DON values were relatively low and mean DON in the susceptible untreated check was < 1 ppm (Table 1). Yield data were unavailable for this trial. Cultivar, fungicide and their interaction all had significant effects ($P < 0.05$) on index. Inoculation had a marginal effect ($P = 0.0541$) on index. Approximately 38% control of index was achieved by using a fungicide on the S cultivar and nearly 60% control of index was achieved by using an MR cultivar in combination with fungicide treatment (Table 2).

Illinois. Six SRWW cultivars were planted into host residue near Dixon Springs, Monmouth and Urbana. At Urbana, plots were also planted into non-host residue. Trials at Dixon Springs and Monmouth were inoculated while the trial at Urbana was naturally infected. *Dixon Springs.* Index and yield ranged from 0 to 55.5% and 48.2 and 81.2 bu/A, respectively. Despite substantial index values, mean DON levels in the susceptible untreated check were < 2 ppm (Table 1). Cultivar, fungicide and their 2-way interaction had significant effects on index, while only cultivar had a significant effect on yield. Over 90% control of index was achieved by combining a MS or MR cultivar with fungicide treatment (Table 2). *Monmouth.* Index, DON and yield ranged from 0 to 19.5%, 0.2 to 6 ppm and 78.4 to 106.6 bu/A, respectively. Cultivar, fungicide and inoculation all had significant effects on index, DON and yield. Two-way interactions between cultivar and fungicide and inoculation and fungicide also had significant effects on index. Two-way interactions between cultivar and inoculation and inoculation and fungicide also had significant effects on yield. Combining a MS or MR cultivar with fungicide resulted in > 80% control of index (Table 2). MR combined with fungicide resulted in the greatest reduction (65%) of DON (Table 2) *Urbana.* Index ranged from 0 to 26 and 0 to 32.5% and DON from 0.1 to 3 and 0.1 to 2.1 ppm in the host and non host residue trials, respectively. Cultivar effect was significant for index and DON in both host and non-host residue trials. The effects of fungicide and the cultivar x fungicide interaction were only significant for DON accumulation. Yield data were unavailable for this location. MR and fungicide combination resulted in the greatest reductions in both index (76 and 89%) and DON (82 and 78%) in the host and non-host residue trials, respectively.

Indiana. Four SRWW cultivars were planted into host residue near Tippecanoe. Index and yield values ranged from 4.3 to 35% and 41.7 to 95.5 bu/A, respectively. Cultivar, fungicide and the cultivar x fungicide interaction all had significant ($P < 0.05$) effects on both index and yield. Inoculation did not have a significant effect on index or yield. DON data were not available at publication time. The greatest reduction in index (67.5%), relative to the susceptible, untreated check, was observed as a result of an MR cultivar combined with fungicide treatment. This was followed closely by MR cultivar without fungicide treatment (62%)

Kentucky. Three SRWW cultivars were planted into host residue near Princeton, KY. Cultivar, fungicide and the cultivar x fungicide interaction all had significant effects on index, DON and yield. Inoculation did not have significant effect on index or yield; however, inoculation and the inoculation x fungicide interaction significantly affected DON accumulation. The greatest reductions in index and DON resulted from the use of an MR cultivar in combination with a fungicide treatment, nearly 94 and 88%, respectively (Table 2).

Maryland. Six SRWW cultivars were planted near Wye into both host and non-host residues, and into host residue only near Keedysville. *Wye.* When planted into host residue, index and yield ranged from 1.3 to 48.6% and 56.4 and 92.8 bu/A, respectively. DON data were not available at publication time. Cultivar and fungicide had significant effects on index and yield. Inoculation and the inoculation x cultivar interaction had significant effects on yield. Following non-host residue, index and yield ranged from 0.9 to 61.1% and 51.6 to 96.0 bu/A. Cultivar, fungicide and inoculation all had significant effects on index, while only inoculation had a significant effect on yield. Regardless of the previous crop, the MR and fungicide combination resulted in the greatest reduction of index; however, percent control was higher in the trial planted into host crop residue than in the trial planted into non-host residue (83 and 57%, respectively) (Table 2) *Keedysville.* This location did not receive artificial inoculations. Index, DON and yield ranged from 6.4 to 75.3%, 0.3 to 13.1 ppm and 50.3 to 98.4, respectively. Fungicide had significant effects on index, DON and yield. Cultivar only had a significant effect on index. The greatest control of index and DON was achieved by combining an MS cultivar with fungicide (58 and 79%, respectively) (Table 2).

Minnesota. Four HRSW and four 6-row barley cultivars were used in two separate trials near St. Paul. In the barley trial, mean index and DON in the susceptible untreated check were below 5% and 1 ppm, respectively (Table1). Higher levels of FHB were observed in the HRSW trial, with index and DON ranging from 0 to 23.4% and 0 to 9.4 ppm, respectively. Yield data were not available at publication time. Cultivar, inoculation, fungicide and the cultivar x fungicide and inoculation x fungicide interactions all had significant effects on index. Inoculation, fungicide and their 2-way interaction had significant effects on DON accumulation. Fungicide application reduced index by > 70% and DON by > 55%, regardless of host resistance; however, the highest percent reduction occurring when the MR cultivar was treated (82% for index and 69% for DON) (Table 2).

Missouri. Five SRWW cultivars were planted into host and non-host residue near Columbia. These trials were not inoculated. In the host residue trial, index, DON and yield ranged from 9.9 to 43.1%, 0.5 to 14.7 ppm and 26.6 to 84.8 bu/A, respectively. In the non-host residue trial, index, DON and yield ranged from 6.6 to 35.4%, 0 to 2 ppm and 41.7 to 91.3 bu/A, respectively. Cultivar had significant effects on index, DON and yield in both trials. Fungicide had significant effects on index and yield in the host crop residue trial and on index and DON in the non-host residue trial. The cultivar x fungicide interaction had significant effects on index in the host residue trial and on DON in the non-host residue trial. The greatest reductions in index were observed as a result of combining MR with fungicide in the host and non-host trials (66 and 50%) (Table 2). In the trial planted into non-host crop residue, as DON levels were relatively low, all management combinations resulted in < 1 ppm DON. In the trial planted into host residue, combining MR with fungicide resulted in the highest percent control (80%).

Nebraska. Four hard red winter wheat cultivars were planted into host residue near Mead. Index, DON and yield ranged from 0 to 19.2%, 0 to 2.8 ppm and 41.2 to 68.6, respectively. Cultivar and fungicide were not statistically significant for index in this trial. However, both cultivar and fungicide had significant effects on DON and yield. Additionally, the cultivar x fungicide interaction also had a significant effect on DON. The S cultivar combined with fungicide resulted in the greatest reduction in index (48%), while greatest reduction in DON was observed as a result of the MR and fungicide combination (64%) (Table 2).

New York. Four SRWW cultivars were planted into both host and non-host residue near Aurora. Despite artificial inoculations, mean index and DON levels were relatively low in this trial and mean levels in the susceptible, untreated check were below 5% and 2 ppm, respectively (Table 1).

North Dakota. Fargo. Four cultivars each of HRSW, two-row barley and six-row barley were planted into both host and non-host residue near Fargo. Index values were > 5% only in the HRSW and two-row barley trials planted into host residue (Table 1), with means ranging from 1.1 to 16.8 and 1.1 to 8.8%, respectively. Cultivar was the only factor to have a significant effect on index in these trials. DON levels in the susceptible, untreated check were > 1 ppm only in the HRSW trials (Table 1). DON ranged from 0.3 to 1.6 and 0.2 to 5.7 ppm in non-host and host crop residue HRSW trials, respectively. In HRSW, cultivar, fungicide and their two-way interaction had significant effects on DON in non-host residue only. In HRSW, the combination of MR and fungicide resulted in the highest control of DON, followed by the use of fungicide alone, regardless of residue type. Cultivar had a significant effect on yield in the 2 two-row barley trials only. *Langdon.* Five durum cultivars were also planted into both host and non-host residue near Langdon; however, index and DON data were not available for these trials at publication time. Cultivar had significant effects on yield in both durum trials. In durum planted into host residue, fungicide and cultivar x fungicide interaction also had significant effects on yield.

Ohio. Four SRWW cultivars were planted into non-host residue near Wooster. Index, DON and yield observations ranged from 0.1 to 15.7%, 0.7 to 3.7 ppm and 34.1 to 93.5 bu/A, respectively. The effects of cultivar, fungicide and their interaction had significant effects on index and DON, while only cultivar and fungicide had significant effects on yield. Inoculation did not have a significant effect on FHB, DON or yield in this trial. Fungicide reduced index and DON, regardless of cultivar resistance. Over 90% control of index and DON was observed as a result of the MR and fungicide combination (Table 2).

South Dakota. Three HRWW, three HRSW and three six-row barley cultivars were planted in separate trials. Index data were not available for these trials and DON data were not available for the HRSW trial at the time of publication. DON values for HRWW and barley ranged from 0 to 3 and 0 to 1.6 ppm, respectively. In HRWW, cultivar had a significant effect on DON; however, the effect of fungicide on DON was not significant. In barley, cultivar, fungicide and the cultivar x fungicide interaction all had significant effects on DON. In both HRWW and barley, the use of MS or MR cultivars resulted in DON levels < 1 ppm (Table 2). Yield ranged from 29.8 to 59.1, 9.7 to 24.5 and 31 to 73.7 bu/A for HRWW, HRSW and barley, respectively. Cultivar had significant effects on yield in all three grain classes. Additionally, fungicide and the cultivar x fungicide interaction had significant effects on yield for HRWW only.

CONCLUSIONS

In most trials, the use of a MS or MR cultivar reduced both index and DON, relative to the untreated, susceptible check. The effect of fungicide was slightly more variable across trials, potentially due to interactions between fungicide efficacy and environmental conditions. In general, fungicide application increased percent control of index and DON, within each resistance category. Most frequently the combination of moderate resistance to FHB and an appropriately timed fungicide application resulted in the greatest level of control, across trials. The goal of including artificial inoculum as factor was to increase the number of "useable" trials. It is difficult to assess the efficacy of integrated management strategies in trials with very low FHB intensity, this is index < 5% and DON < 1 ppm. In 2011, 17 out of 24 trials with index data and 14 out of 23 trials with DON data had mean index and DON in the untreated susceptible check above 5% and 1 ppm, respectively.

AKNOWLEDGEMENT AND DISCLAIMER

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Table 1. Study descriptions and trial-wide mean FHB index, DON and yield (averages across all treatments and reps) from twenty-nine coordinated integrated management trials, conducted in twelve states in 2011.

					Trial-wide mean			Susceptible-untreated check	
State	Location	Grain Class	Previous Crop	Trial No.	Index %	DON (ppm)	yield	Index %	DON (ppm)
AR	Kibler	SRWW	.	1	32.78	0.16	.	41.50	0.29
IL	Dixon Springs	SRWW	host	2	12.67	0.25	62.26	34.34	0.52
	Monmouth	SRWW	host	3	4.44	2.16	97.27	9.88	3.26
	Urbana	SRWW	host	4	7.99	0.89	.	12.63	1.82
	Urbana	SRWW	non-host	5	5.99	0.62	.	17.38	1.28
IN	Tippecanoe	SRWW	host	6	11.01	.	87.99	11.98	.
KY	Princeton	SRWW	host	7	13.30	0.74	92.11	31.77	1.56
MD	Keedysville	SRWW	host	8	31.40	4.32	77.41	44.24	6.88
	Wye	SRWW	host	9	15.62	.	75.72	24.96	.
	Wye	SRWW	non-host	10	28.75	.	77.87	38.55	.
MN	StPaul	HRSW	.	28	5.03	1.04	.	9.15	1.70
	StPaul	6ROWB	.	29	1.82	1.13	.	1.02	0.17
MO	Columbia	SRWW	host	15	21.00	2.71	46.33	33.08	5.21
	Columbia	SRWW	non-host	16	17.78	0.37	64.99	24.57	1.14
ND	Fargo	HRSW	non-host	19	2.24	0.76	58.91	3.65	1.04
	Fargo	HRSW	host	20	4.69	0.82	59.39	7.10	1.43
	Fargo	2ROWB	host	21	5.14	0.46	46.18	5.24	0.56
	Fargo	2ROWB	non-host	22	3.47	0.25	46.20	4.85	0.31
	Fargo	6ROWB	host	23	4.20	0.50	43.12	4.28	0.27
	Fargo	6ROWB	non-host	24	4.26	0.84	50.69	3.71	0.47
	Langdon	durum	non-host	25	.	.	46.29	.	.
	Langdon	durum	host	26	.	.	42.70	.	.
NE	Mead	HRWW	host	27	5.51	1.11	45.19	6.98	1.58
NY	Aurora	SRWW	host	17	3.25	0.89	77.06	2.26	0.44
	Aurora	SRWW	non-host	18	2.18	0.38	61.72	1.32	0.12
OH	Wooster	SRWW	host	11	5.78	1.06	53.75	11.71	2.33
SD	Brookings	HRWW	host	12	.	0.95	39.39	.	1.87
	Brookings	HRSW	host	13	.	.	15.29	.	.
	Brookings	6ROWB	host	14	.	0.52	51.98	.	1.05

Table 2. Trial-wide means for index and DON and percent control for each management combination, relative to the untreated, susceptible check.

		Cultivar Resistance Class x Fungicide Means[2]						% Control				
	Trial No.[1]	S_UT	S_FUN	MS_UT	MS_FUN	MR_UT	MR_FUN	S_FUN	MS_UT	MS_FUN	MR_UT	MR_FUN
INDEX (%)	**1**	41.50	25.75	45.25	35.75	30.00	16.75	37.95	-9.04	13.86	27.71	59.64
	2	34.34	14.72	15.31	3.13	9.56	2.27	57.14	55.41	90.90	72.15	93.39
	3	9.88	4.34	5.19	1.69	4.29	1.71	56.10	47.49	82.92	56.56	82.71
	4	12.63	12.44	5.88	10.25	6.83	3.04	1.52	53.48	18.84	45.90	75.92
	5	17.38	7.00	4.63	3.25	3.21	1.88	59.72	73.39	81.30	81.54	89.21
	6	20.79	11.98	13.92	11.67	7.94	6.75	42.38	33.06	43.88	61.82	67.53
	7	31.77	12.69	18.37	7.88	7.08	2.00	60.06	42.18	75.21	77.71	93.70
	8	44.24	34.63	25.37	18.43	31.00	21.57	21.73	42.66	58.33	29.93	51.25
	9	24.96	12.60	21.30	9.21	16.56	4.27	49.54	14.65	63.11	33.66	82.91
	10	38.55	31.03	34.52	18.47	30.32	16.50	19.50	10.45	52.10	21.36	57.20
	11	11.71	5.46	11.39	3.27	4.13	1.02	53.34	2.75	72.11	64.77	91.25
	15	33.08	21.76	21.18	14.10	18.52	11.20	34.23	35.99	57.38	44.02	66.14
	16	24.57	16.99	17.04	14.62	19.17	12.23	30.84	30.64	40.51	21.99	50.21
	20	7.10	4.59	5.03	3.43	1.63	4.10	35.39	29.23	51.76	77.11	42.25
	21	5.24	5.43	6.09	4.00	.	.	-3.60	-16.13	23.65	.	.
	27	6.98	3.60	.	.	5.91	5.55	48.42	.	.	15.29	20.49
	28	9.15	2.25	8.84	2.71	4.31	1.63	75.45	3.41	70.43	52.94	82.18
DON (ppm)	**3**	3.26	2.94	2.85	2.25	1.67	1.14	9.70	12.58	30.98	48.80	65.16
	4	1.82	1.20	0.87	0.60	0.65	0.40	34.07	52.34	67.03	64.19	78.16
	5	1.28	0.88	0.62	0.51	0.38	0.24	31.05	51.76	60.55	70.51	81.53
	7	1.56	0.44	1.25	0.44	0.54	0.19	71.63	19.63	72.04	65.63	87.58
	8	6.88	3.40	3.36	1.45	7.97	3.38	50.65	51.14	78.88	-15.79	50.92
	11	2.33	0.72	2.23	0.80	0.62	0.20	69.05	4.22	65.72	73.25	91.31
	12	1.87	1.30	0.82	0.52	0.32	0.90	30.48	56.33	72.37	83.07	51.87
	14	1.05	0.45	.	.	0.13	0.00	57.14	.	.	88.10	100.00
	15	5.21	3.63	2.28	1.29	1.27	1.03	30.42	56.33	75.21	75.69	80.17
	16	1.14	0.59	0.09	0.04	0.00	0.00	48.10	91.96	96.35	100.00	100.00
	19	1.04	0.70	0.93	0.63	0.55	0.45	32.69	11.06	39.90	47.12	56.73
	20	1.43	0.50	0.95	0.70	0.65	0.43	65.03	33.57	51.05	54.55	70.28
	27	1.58	0.96	.	.	1.33	0.58	39.08	.	.	16.14	63.61
	28	1.70	0.68	1.39	0.75	0.93	0.54	60.00	18.46	55.66	45.29	68.53

[1] Only trials with > 5% index and >1 ppm DON were included in this analysis.

[2] S_UT = susceptible, untreated check; S_FUN = susceptible, fungicide-treated; MS_UT = moderately susceptible, untreated; MS_FUN = moderately susceptible, fungicide-treated; MR_UT = moderately resistant, untreated; MR_FUN = moderately resistant, fungicide-treated.

OTHER PAPERS

OVERVIEW OF THE USWBSI WEB SITE

D. Hane[1*], S. Canty[2], D. Van Sanford[3] and O. Anderson[1]

[1]USDA-ARS-WRRC, 800 Buchanan Street, Albany, CA; [2]USWBSI-NFO, Michigan State University, East Lansing, MI; and [3]University of Kentucky, Dept. of Plant and Soil Sciences, Lexington, KY
[*]Corresponding Author: PH: (510) 559-6194, Email: davidhane@gmail.com

ABSTRACT

The US Wheat and Barley Scab Initiative (USWBSI) web site (http://www.scabusa.org) is the central location for information and services related to the USWBSI. An important goal of the site is the rapid communication of information to the community using various technologies. The site offers several subscription services such as the FHB Alert System, various mailing lists, and RSS/ATOM news feeds.

These subscription services can send important information and updates directly to users' mobile devices and computers. The USWBSI website also hosts the USWBSI Database which is a web-accessible database that provides information relating to Projects, Institutions, Grants, Documents, and Contacts. Additionally a wide array of information is available through standard web pages and links. The site also offers many tools that allow users to store and share information with the community. Examples of user content applications include a photo library, document repository, blogs, and calendars, just to name a few. Another goal of the site is to host the various web forms used for the National Fusarium Head Blight Forum registration, purchasing Forum Proceedings, and submitting Forum abstracts. Lastly the site hosts the Electronic Pre-Proposal Submission System. This is a suite of applications that provide an easy to use interface for Pre-Proposal submitters and reviewers. This poster provides an overview of the USWBSI web site and some of the features and applications listed here.

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