VARIETY DEVELOPMENT AND HOST PLANT RESISTANCE

SCREENING FOR FHB SUSCEPTIBILITY IN BARLEY CULTIVARS IN THE WESTERN U.S.

Arcibal, S.S.[1], Baldwin, T.T.[2], Jackson, C.A.[2], Shelman, T.L.[2] and Marshall, J.M.[3*]

[1]Department of Plant, Soil, and Entomological Sciences, University of Idaho, Aberdeen R&E Center, Aberdeen, ID; [2]Small Grains and Potato Germplasm Research, USDA-ARS, Aberdeen, ID; and [3]Department of Plant, Soil, and Entomological Sciences, University of Idaho, Idaho Falls, ID
[*]Corresponding Author: PH: (208) 529-8376; Email: jmarshall@uidaho.edu

ABSTRACT

Fusarium head blight (FHB) has become a regularly occurring problem with economically significant impacts in Idaho. Until 2015, detectable DON levels in commercial barley production had remained below 0.5 ppm. Levels of DON are now occurring in malt barley that exceed acceptable levels. Identification of highly susceptible advanced lines and widely grown varieties will enable growers to manage risk of FHB and DON with best practices that reduce risk. An inoculated screening trial was conducted at Aberdeen, ID in 2015 to evaluate FHB resistance levels in barley varieties selected and released with or without prior screening. Fifty barley varieties were planted on May 8 with two replications. Nine local isolates of *F. graminearum* were collected, grown on potato dextrose agar and confirmed by PCR. Corn inoculum was prepared by placing corn kernels in spawn bags and autoclaving twice prior to inoculation of the *F. graminearum* isolates. Conidial inoculum was prepared by increasing macroconidial production in mung bean agar and storing spore suspension in one-liter bottles. Corn inoculum was applied at a rate of 30 g/m^2 approximately 2 to 3 weeks before heading while conidial inoculum at 100,000 spores/L was sprayed at heading. FHB incidence and severity were assessed 3 weeks after application of conidial inoculum. Significant differences in FHB index (P=<.0001), yield (P=0.0013) and FDK (P>.0001) among varieties were recorded. FHB indexes range from 0.2 to 19.9% The 6-row malt 'Quest', 2-row feed 'RWA 1758' and 2-row feed 'Conrad' were the most resistant lines. 'Transit', a hulless 2-row feed with high ß-glucan, and 'Goldeneye', a high-yielding 6-row feed, were the most susceptible lines. Yield ranged from 84.0 (2Ab09-X06F084-31) to 693.5 (Conrad) g/plot. FDK of hulless varieties were significantly higher than hulled varieties. DON levels will also be determined.

OBJECTIVE

The objective of this study was to determine FHB host resistance levels in barley varieties released for the arid irrigated production areas of the PNW.

INTRODUCTION

Ten years ago, the incidence of FHB in the irrigated west was regarded as a minor and relatively rare occurrence. With the substantial increase in corn acreage directly due to the increase in the dairy industry and with substantial changes in irrigation practices, FHB has become a regularly occurring problem with economically significant impacts for small grain producers. In barley, DON levels mostly have remained below detectable levels or below 0.5 ppm. However, in 2015 in Idaho, for the first time DON levels exceeded acceptable levels ranging from 0.3 to 4 ppm. Unacceptable levels of DON toxin have been found consistently in irrigated wheat and barley in areas of the PNW and

intermountain West in the past five years. Corn debris, where high levels of *Fusarium graminearum* reside, takes up to three or four years to degrade in arid west environments. Changes in crop rotation have shifted from the predominant *Fusarium spp.* to *F. graminearum*, which produce airborne ascospores that can disperse many miles in the wind. Disease management approaches must change and will depend on the degree of susceptibility of the varieties being grown. Control strategies must incorporate varieties that are less susceptible to FHB.

MATERIALS AND METHODS

Isolate collection. *Fusarium* species were isolated from infected hard white spring wheat WB-Pristea collected in 2014 from a local commercial field near Sugar City, ID. *F. graminearum* was confirmed using conventional polymerase chain reaction (PCR). Cultures were grown in potato dextrose agar (PDA) with streptomycin sulfate (50 mg l^{-1}). DNA was extracted using sodium phosphate buffer. Small amount of mycelia was scraped with a toothpick and mixed in 1000 µl of sodium phosphate in microcentrifuge tube. The extraction was incubated for 30 minutes and centrifuged at 8000 to 10,000 *g* for 1 min. Tubes were incubated at 85°C for 30 minutes and stored at -20°C until used for PCR analysis. Avoiding mycelia, 0.5 µl extraction was taken from top of the tube. PCR was performed using primer pairs (Fg16F and Fg16R).

Corn inoculum preparation. The amount of corn inoculum needed was calculated based on a rate of 30 g/m^2. Spawn bags were prepared by filling with 1500 g of once-autoclaved corn kernels and adding tap water to approximately an inch above the corn level. Corn kernels were allowed to imbibe water for 16 hours prior to draining and sealing the bags the following morning. Five bags were placed in an 11-gallon tub and autoclaved for 90 minutes at 30 psi. Using aseptic techniques, one PDA plate colonized with *F. graminearum* was used to inoculate each spawn bag. An additional 25-30 ml of sterile water amended with streptomycin sulfate (0.2 g per 150 ml water) was added to each spawn bag, sealed and mixed. Inoculum was incubated for 2 to 3 weeks at room temperature, dried for 5-8 days in the a laminar flow hood, and stored at 4°C until needed for field inoculation.

Conidial inoculum preparation. Inoculum was prepared following the protocol provided by Dr. Ruth Dill-Macky (*personal communication*). To increase macroconidial production, spore suspensions obtained from PDA plates were transferred to mung bean agar (MBA) plates and incubated for 10-14 days at room temperature. Inoculum was stored at a standard concentration (800,000 macroconidia per ml) in 1 L Nalgene bottles. Bottles were stored at 4°C and -20°C for short-term and long-term storage, respectively. A diluted concentration (100,000 macroconidia/L) was prepared for field application.

Field nursery establishment. An irrigated field nursery was established at the University of Idaho Aberdeen Research and Extension Center in the 2015 growing season. Fifty barley lines and varieties were tested for level of FHB susceptibility. Eight-foot plots consisting of two rows were planted on May 8 in a complete block design with two replications per variety. Approximately 60 g of corn inoculum was applied per plot on June 22. In addition, each plot was flagged with color-coded flags based on heading date and were sprayed with spore suspension (Table 1). A CO_2 backpack sprayer with 8003 VS nozzle tips calibrated at 40 psi was used to apply inoculum at a rate of 1 sec/ft. A second inoculum spray was repeated one week after the first. From the time of the earliest conidial inoculation and two weeks following, plots were irrigated once a day for 2 hours. Symptomatic heads were picked from Idagold II and Goldeneye plots for reconfirmation of infection by *F. graminearum*

using a PCR assay on infected kernels. DNA was extracted by mashing a single infected kernel in 100-200 µl sodium phosphate buffer with a wooden applicator stick. The extraction was incubated for 30 minutes at 85°C and centrifuged at 14,000 rpm for 5 minutes. Avoiding debris, 0.5 µl was taken from the top extraction for PCR using the same primer pairs detailed above.

Data collection and analyses. Plots were assessed for FHB incidence and severity 20-22 days after conidial inoculation (Table 1). Twenty heads were arbitrarily selected from each plot. Disease severity was determined by visually estimating percent area blighted for each head. Disease incidence was calculated by dividing the number of infected heads by the total number of sampled heads. The FHB index was calculated based on the formula: (% severity x incidence)/100. Percent stand per plot was also noted (data not shown). Plots were harvested on September 23 using a small plot combine. Harvested grains were cleaned using steel mesh sieves and weight recorded. Ten heads per plot were randomly harvested by hand and threshed. *Fusarium*-damaged kernels (FDK) was recorded by counting diseased kernels from a 100 seed sample. Data were analyzed using the generalized linear mixed model procedure (PROC GLIMMIX) in SAS (version 9.2).

RESULTS AND DISCUSSION

FHB indexes significantly differed (P>.0001) from 0.2 to 19.9% (Table 2) among barley varieties. The 6-row malt 'Quest', 2-row feed 'RWA 1758' and 2-row malt Conrad', were the three most resistant varieties. Quest was released for resistance to FHB and resistance to DON accumulation in the grain. The 2-row malt 'Goldeneye" and 2-row feed 'Transit' were two of the most susceptible varieties.

Yield significantly differed (P=0.0013) from 84.0 g/plot in 2Ab09-X06F084-31 to 693.5 g/plot in Conrad (Table 2). Low yields of 2-row lines 'Julie', 'Clearwater', 2Ab09-X06F084-31 (low ß glucan lines) and 'Sawtooth' (low phytate lines) were also affected by low stands. The highest-yielding varieties were the 2-row malt 'Conrad', 2-row feed 'Vespa', 6-row malt 'Celebration' and 6-row feed 'Goldeneye'. Accurate yields for production purposes should be obtained from the Small Grains Research Report published at http://www.uidaho.edu/extension/cereals/scseidaho.

FDK significantly differed between varieties (P>.0001) and ranged from 98.0 % in 'Transit' to 2.0 % in 'CDC Copeland' (Table 2). Hulless, 2-row feed varieties had significantly higher FDK than hulled varieties. Levels of DON will also be tested at a later date.

The planting date was moved later in the season to increase the chances that heading occurred when warm temperatures were favorable for disease development. The barley plots also were inoculated using corn spawn and by spraying a conidial suspension twice to increase chances of infection. In 2014, very little FHB was seen in barley, although a direct comparison with 2014 results is difficult due to inoculum in 2014 being derived from cultures of *F. culmorum*. In addition, temperatures at anthesis were much more favorable for disease development in 2015.

Corn inoculum was spread in the field about three weeks prior to heading of earliest maturing varieties. However, the barley varieties used in this trial have different heading dates and estimating head emergence based on growing-degree days can be difficult to predict. An additional inoculation using a spore suspension helped to even out the effect of differential maturities. However, there still may be bias resulting from heavier disease pressure on later maturing varieties.

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Table 1. Conidial inoculation and disease assessment schedule of spring barley varieties in Aberdeen, ID in 2015.

Heading date	Flag color	Number of plots	Rating date	Days after inoculation
2-Jul	white	8	23-Jul	21
6-Jul	red	18	26-Jul	20
8-Jul	blue	3	29-Jul	21
10-Jul	green	21	1-Aug	22
13-Jul	yellow	25	4-Aug	22
15-Jul	pink	24	6-Aug	22

Table 2. FHB Index, yield and FDK results of spring barley varieties in Aberdeen, ID in 2015.

Variety	Class	Index		Yield (g)		FDK (%)	
Goldeneye	6-row feed	19.9	a	586.8	a-d	20	d-g
Transit *	2-row feed	17.8	ab	170.3	hij	98	a
UT10901-66	6-row feed	17.5	ab	412.1	b-h	17	e-h
2Ab09-X06F084-51	2-row feed	14.8	ab	315.5	e-i	13.5	e-i
Julie *	2-row feed	11.8	bc	145.3	hij	90	ab
Tetonia	2-row feed	11.7	bc	316.4	e-i	16.5	e-h
2Ab09-X06F084-31*	2-row feed	11.5	bc	84	j	84.5	ab
UT2183-85	6-row feed	10.8	bcd	460.9	b-f	21	def
Harriman (08ID2661)	2-row feed	8.3	cde	352.6	e-i	10.5	f-i
Lenetah	2-row feed	8	c-f	456.3	b-f	13.5	e-i
CDC Meredith	2-row malt	8	c-f	433	b-g	7.5	f-i
Herald	6-row feed	7.5	c-g	406.9	b-h	20.5	def
Idagold II	2-row feed	7.1	c-h	263.1	f-j	38.5	c
Oreana (BZ509-448)	2-row feed	6.6	c-i	365.1	d-i	14.5	e-i
LCS Odyssey	2-row malt	5.8	c-j	509.4	a-e	14.5	e-i
2Ab08-X05M010-82	2-row malt	5.8	c-j	374.3	c-i	16.5	e-h
08ARS206-17	2-row feed	5.7	c-j	519	a-e	11	f-i
Sawtooth (081D1549) *	2-row feed	4.8	d-j	103	ij	77	b
Millennium	6-row feed	4.7	d-j	411.1	b-h	11.5	e-i
ABI Balster (B0811)	2-row malt	4.6	e-j	406.8	b-h	12	e-i
LCS Overture	2-row malt	4.5	e-j	538	a-e	9.5	f-i
CDC Fibar *	2-row feed	4.1	e-j	211.9	g-j	85	ab
ACC Synergy	2-row malt	4.1	e-j	313.4	e-i	8.5	f-i
Merit 57	2-row malt	3.7	e-j	392.8	b-h	9.5	f-i
Merem (02Ab17271)	2-row malt	3.4	e-j	470.2	a-f	6.5	ghi
LCS Genie	2-row malt	3.3	e-j	432.8	b-g	13	e-i
Moravian 69	2-row malt	3.2	e-j	330.2	e-i	8	f-i
ABI Voyager	2-row malt	3.2	e-j	398.8	b-h	11	f-i
CDC Copeland	2-row malt	2.9	e-j	480.1	a-f	2	i
ABI Growler (2B09-3425)	2-row malt	2.8	e-j	355.6	e-i	14.5	e-i
Claymore (BZ509-216)	2-row feed	2.8	e-j	523.2	a-e	14.5	e-i
Celebration	6-row malt	2.8	e-j	600.6	abc	25	cde
Baronesse	2-row feed	2.7	e-j	413.1	b-h	12.5	e-i
Tradition	6-row malt	2.5	e-j	436.1	b-g	19.5	d-g
Clearwater *	2-row feed	2.4	e-j	95.8	ij	89.5	ab
AC Metcalfe	2-row malt	2.3	e-j	340.1	e-i	5.5	hi
Xena	2-row feed	2.3	e-j	430.4	b-g	20	d-g
03ARS391-34	2-row feed	2.1	f-j	347.4	e-i	7.5	f-i
Champion	2-row feed	1.8	f-j	540.7	a-e	31.5	cd
Menan (01Ab9663)	6-row malt	1.8	f-j	393.5	b-h	17.5	e-h
Vespa	2-row feed	1.7	hij	610.6	ab	13.5	e-i

Table 2 cont.

Variety	Class	Index	Yield (g)	FDK (%)
ND Genesis	2-row malt	1.6 hij	344.1 e-i	8 f-i
Lacey	6-row malt	1.5 hij	454.6 b-f	17 e-h
2Ab04-X01084-27	2-row malt	1.5 hij	497 a-e	12 e-i
Hockett	2-row malt	1.4 hij	495.5 a-e	11.5 e-i
Harrington	2-row malt	1 hij	533.7 a-e	11 f-i
2Ab07-X031098-31	2-row malt	1 hij	453.4 b-f	15 e-i
Conrad	2-row malt	0.6 ij	693.5 a	5.5 hi
RWA 1758	2-row feed	0.6 ij	363.8 d-i	16.5 e-h
Quest	6-row malt	0.2 j	408 b-h	9 f-i
Pr > F		<.0001	0.0013	<.0001

* hulless

SCREENING SPRING WHEAT FOR SUSCEPTIBILITY TO FUSARIUM HEAD BLIGHT IN THE PACIFIC NORTHWEST

Arcibal, S.S.[1], Baldwin, T.T.[2], Jackson, C.A.[2], Shelman, T.L.[2] and Marshall, J.M.[3*]

[1]Department of Plant, Soil, and Entomological Sciences, University of Idaho, Aberdeen R&E Center, Aberdeen, ID; [2]Small Grains and Potato Germplasm Research, USDA-ARS, Aberdeen, ID; and [3]Department of Plant, Soil, and Entomological Sciences, University of Idaho, Idaho Falls, ID
[*]Corresponding Author: PH: (208) 529-8376; Email: jmarshall@uidaho.edu

ABSTRACT

Fusarium head blight (FHB), caused by *Fusarium graminearum*, has become a recurring problem for wheat producers in Idaho. The occurrence of FHB is directly related to the increase of corn acreage under irrigation. FHB is of particular concern not only due to yield losses, but because of *Fusarium*-damaged kernels (FDK) and deoxynivalenol (DON) accumulation. Determining FHB susceptibility in widely grown wheat varieties is crucial to providing the best management recommendations in irrigated systems in the Pacific Northwest (PNW). A field trial was conducted at Aberdeen, ID in 2015 to evaluate FHB susceptibility of wheat varieties. Forty-four wheat varieties were planted on May 8 with two replications. Nine local isolates of *F. graminearum* were collected, confirmed by using species-specific PCR primers, and used to develop corn spawn. Corn kernels were placed in spawn bags and autoclaved twice prior to inoculation of the *F. graminearum* isolates. Plots were inoculated at a rate of 30 g/m2 approximately 2 to 3 weeks before heading (Feekes 10.1). FHB incidence and severity were assessed 3 weeks after flowering (Feekes 10.5.1) of the earliest maturing variety. Significant differences in FHB index (P=<.0001) and yield (P=<.0001) among varieties were found. FHB indices range from 3.2 to 44.4. Hard white cultivars Klasic and WB-Paloma were highly susceptible while soft white wheat elite lines M12001 and IDO 851 were least susceptible. Yield and FDK ranged from 61.5 (Alpowa) to 318.1 g/plot (Dayn) and 63.5 (UI Stone) to 98.5 % (HRS3530), respectively. Varieties will also be tested for DON levels.

OBJECTIVE

The objective of this study was to determine the level of FHB resistance in wheat varieties released for irrigated production systems in the PNW.

INTRODUCTION

Ten years ago, the incidence of FHB in the irrigated wheat in the Pacific Northwest (PNW) was regarded as a minor and relatively rare occurrence. With the substantial increase in corn acreage directly due to the increase in the dairy industry, and with substantial changes in irrigation practices, FHB has become a regularly occurring problem with economically significant impacts on spring wheat producers. Unacceptable levels of deoxynivalenol (DON) toxin have been found consistently in irrigated wheat in areas of the PNW and intermountain West in the past five years. Corn debris, where high levels of *Fusarium graminearum* reside, takes up to three or four years to degrade in arid western environments. Changes in crop rotation have shifted the predominant species of *Fusarium* to *F. graminearum*, which produce airborne ascospores that can disperse many miles in the wind. Disease management approaches are

changing depending on level of susceptibility of the varieties being grown. Control strategies must also incorporate varieties that are less susceptible to FHB.

MATERIALS AND METHODS

Isolate collection. *Fusarium* species were isolated from infected hard white spring wheat WB-Pristea collected in 2014 from a local commercial field near Sugar City, ID. *F. graminearum* was confirmed using conventional polymerase chain reaction (PCR). Cultures were grown in potato dextrose agar (PDA) amended with streptomycin sulfate (50 mg 1^{-1}). DNA was extracted using a sodium phosphate buffer protocol modified by Zhang et al (2010). A small amount of mycelia was scraped with a toothpick and mixed in 1000 µl of sodium phosphate in a microcentrifuge tube. The extraction was incubated for 30 minutes and centrifuged at 8000 to 10,000 *g* for 1 min. Tubes were incubated at 85°C for 30 minutes and stored at -20°C until used in PCR analysis. Avoiding mycelia, 0.5 µl extraction was removed from top of the tube. PCR was performed using primer pairs (Fg16F and Fg16R) and optimization protocol developed by Nicholson et al (1998).

Inoculum preparation. Inoculum preparation was modified from a protocol used by Gilbert and Woods (2006). The amount of corn inoculum needed was calculated based on a rate of 30 g/m^2.

Spawn bags were prepared by filling with 1500 g of once-autoclaved corn kernels and adding tap water to approximately an inch above the corn level. Corn kernels were allowed to imbibe water for 16 hours prior to draining and sealing the bags the following morning. Five bags were placed in an 11-gallon tub and autoclaved for 90 minutes at 30 psi. Using aseptic techniques, one PDA plate colonized with *F. graminearum* was used to inoculate each spawn bag. An additional 25-30 ml of sterile water amended with streptomycin sulfate (0.2 g per 150 ml water) was added to each spawn bag, sealed and mixed. Inoculum was incubated for 2 to 3 weeks at room temperature, dried for 5-8 days in the a laminar flow hood, and stored at 4°C until needed for field inoculation.

Field nursery establishment. An irrigated field nursery was established at the University of Idaho Aberdeen Research and Extension Center in the 2015 growing season. Forty-four wheat lines and varieties were tested for level of FHB susceptibility. Eight-foot plots consisting of two rows were planted on May 8 in a complete block design with two replications per variety. Approximately 60 g of corn inoculum was applied per plot on June 22. The field nursery was irrigated 2 hours every day after 5 PM for 2 weeks. Symptomatic heads were picked from Klasic fill plots for reconfirmation of infection by *F. graminearum* using a PCR assay on whole infected kernels. DNA was extracted by mashing a single infected kernel in 100-200 µl sodium phosphate buffer with a wooden applicator stick. The extraction was incubated for 30 minutes at 85°C and centrifuged at 14,000 rpm for 5 minutes. Avoiding debris, 0.5 µl was taken from the top extraction for PCR using the same primer pairs detailed above.

Data collection and analyses. Plots were assessed for FHB incidence and severity three weeks after flowering (Feekes 10.5.1) of the earliest maturing variety (Klasic). The first and second replicates were rated 21 and 22 days after flowering, respectively. Twenty heads were arbitrarily selected from each plot. Disease severity was determined by visually estimating percent area blighted for each head. Disease incidence was calculated by dividing the number of infected heads by the total number of sampled heads. The FHB index was calculated based on the formula: (% severity x incidence)/100. Percent stand per plot was also noted. Ten heads per plot were randomly

harvested by hand and threshed. FDK was recorded by counting diseased kernels from a 100 seed count. Plots were harvested on September 23 using a small plot combine. Harvested grains were cleaned using steel mesh sieves and the weight recorded. Data were analyzed using the generalized linear mixed model procedure (PROC GLIMMIX) in SAS (version 9.2).

RESULTS AND DISCUSSION

FHB indices significantly differed from 3.2 in the advanced line IDO851 to 44.4 in the hard white Klasic (Table 1). Hard white wheat varieties WB-Paloma, Snow Crest, LCS-Atomo and WB7328 were highly susceptible. Jefferson and IDO862E were two of the most susceptible lines among the hard red wheat and HRS 3419, HRS3504, HRS3530, WB9411 and WB9229 were the least susceptible. UI Pettit was the most susceptible among soft white varieties and the highest level of resistance in the soft whites were Seahawk, Alpowa, M12001 and IDO 851.

Yield significantly differed from 61.5 g/plot in soft white Alpowa to 318.1 g/plot in hard white Dayn (Table 1). The low yield of Alpowa was influenced by a low stand. HRS 3504 and 3419 were two of the highest yielding hard red wheat varieties. Although highly susceptible, Snow Crest and LCS Atomo had the highest yields among the hard whites next to Dayn and LCS Star. UI Stone, Alum and M12001 were the three highest-yielding soft white wheat varieties. Lines WB9411, HRS3504, HRS 3419, IDO1202S were some of the least susceptible varieties that also produced high yields. Accurate yields for production purposes should be obtained from the SmallGrains Research Report published at http://www.uidaho.edu/extension/cereals/scseidaho.

FDK significantly differed from 63.5 % in soft white UI Stone to 98.5 % in hard red HRS3530 (Table 1). UI Stone was selected for FHB resistance prior to release. Higher yielding lines 'Dayn' and IDO1202S also had the lowest FDK for hard white and hard red varieties, respectively. Other varieties with high yields and low FDK were hard reds WB9411, HRS3504, IDO862E, UI Winchester and HRS3419. DON levels will also be tested at a later date.

The planting date was moved later in the season to increase the chances of anthesis occurring when warm temperatures were favorable for disease development. Interestingly, the susceptible varieties hard white UI Platinum, soft white Alturas and durum wheat Alzada had lower FHB indices than was recorded in 2014, although direct comparison with 2014 results is difficult due to inoculum in 2014 being derived from cultures of *F. culmorum*. In addition, temperatures at anthesis were much more favorable for disease development in 2015.

Corn inoculum should have been spread in the field three weeks prior to heading. However, the wheat varieties used in this trial have different heading dates and estimating head emergence based on growing-degree days is more difficult to predict when based on the heading date of the earliest varieties. This may introduce bias resulting in heavier disease pressure on later maturing varieties.

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Table 1. Yield and FHB Index results of spring wheat varieties in Aberdeen, ID in 2015.

Variety	Class	FHB Index		Yield (g)		FDK (%)	
Klasic	hard white	44.4	a	197	b-k	90	a-g
WB-Paloma	hard white	42.3	ab	133.9	j-m	91.5	a-f
Snow Crest (W)	hard white	39.2	abc	261	a-f	93	a-e
UI Pettit	soft white	37	abc	119.5	j-m	90.5	a-g
WB7589 (W)	hard white	34.1	a-d	182.6	c-l	93	a-e
Jefferson	hard red	33.6	a-d	159.9	h-m	90.5	a-g
IDO862E	hard red	32.2	a-e	217.5	b-j	81.5	d-i
LCS Atomo (W)	hard white	31.5	a-f	255.4	a-h	93.5	a-e
SY3001-2	hard red	29.4	a-g	168.7	e-l	90.5	a-g
WB7328 (W)	hard white	27.6	b-h	160.7	g-m	97.5	ab
WB9668	hard red	27.1	b-h	161.4	f-m	91.5	a-f
WA 8214	soft white	26.9	b-i	83.3	lm	93	a-e
WB6430	soft white	25.8	c-i	178.4	d-l	89.5	a-g
Babe	soft white	25.5	c-j	98.7	klm	89	a-g
LCS Star (W)	hard white	23.9	c-k	278.6	abc	97	ab
UI Winchester	hard red	22.6	c-k	236.3	a-i	83	c-h
Diva	soft white	22	c-l	160.1	g-m	93	a-e
Bullseye	hard red	21.2	c-m	146.7	i-m	96	abc
Alum	soft white	20.7	c-n	184.8	c-k	95	abc
Kelse	hard red	20.4	c-n	104.3	j-m	98.5	a
SY Basalt	hard red	20	d-n	207.7	b-j	94	a-e
IDO1203 (W)	hard white	19.9	d-n	251.2	a-h	88.5	a-g
Dayn (W)	hard white	19.9	d-n	318.1	a	77.5	ghi
SY-10136 (W)	hard red	19.4	d-n	259.9	a-g	92	a-e
Alzada (D)	durum	17.7	e-o	105.8	j-m	96	abc
SY-40292R	hard red	16.3	f-o	268.1	a-e	98.5	a
UI Platinum (W)	hard white	15.8	g-o	189	c-k	96.5	ab
WA 8189	soft white	14.9	g-o	135.9	j-m	95	abc
10SB0087-B	hard white	14.5	g-o	187.5	c-k	91.5	a-f
UI Stone	soft white	14.3	g-o	188.5	c-k	63.5	j
IDO1202S (W)	hard red	13.9	g-o	261.9	a-e	72.5	hij
Alturas	soft white	12.5	h-o	148	i-m	87	a-g
WB9229	hard white	11.6	i-o	97.6	klm	87	a-g
WB9411	hard red	10	j-o	224.1	a-j	78.5	f-i
HRS3530	hard red	9.5	k-o	115.5	j-m	98.5	a
Cabernet	hard red	9.3	k-o	112.3	j-m	94.5	a-d
11SB0096	soft white	8.9	k-o	215.2	b-j	87.5	a-g
HRS3504	hard red	8.7	k-o	289.7	ab	81	e-i
HRS3419	hard red	7.1	l-o	271.9	a-d	85.5	a-h
Seahawk	soft white	6.6	l-o	101.5	klm	69	ij
Alpowa	soft white	6.2	mno	61.5	m	86	a-g
M12001	soft white	5.2	mo	181.2	c-l	88	a-g
IDO 851	soft white	3.2	o	114.2	j-m	85	b-h
Pr < F		<.0001		<.0001		0.0004	

*LCS Kiko not analyzed

MOLECULAR MAPPING OF QTL FOR FUSARIUM HEAD BLIGHT RESISTANCE IN SPRING WHEAT

S. Berraies[1], R.E. Knox[1*], R.D. Cuthbert[1], M.A. Henriquez[2], Y. Ruan[1], R.M. DePauw[3], A. Singh[4], C. Pozniak[5], B.K. Meyer[1], F.R. Clarke[1] and F. Bokore[1]

[1]Agriculture and Agri-Food Canada, Swift Current Research and Development Centre, Swift Current, SK, Canada; [2]Agriculture and Agri-Food Canada, Morden Research and Development Centre, Morden, MB, Canada; [3]870 Field Drive, Swift Current, SK; [4]Iowa State University, Department of Agronomy, Ames IA, USA; and [5]University of Saskatchewan, Crop Development Centre and Department of Plant Sciences, Saskatoon, SK, Canada
[*]Corresponding Author: PH: (306) 770-4499; Email: Ron.Knox@AGR.GC.CA

ABSTRACT

Genetic resistance to Fusarium head blight (FHB), caused by *Fusarium graminearum*, is essential to reduce losses of grain yield and quality. This study was conducted to identify DNA markers linked to important genes controlling FHB resistance in adapted germplasm of spring wheat. A doubled haploid population of 773 lines was developed from the cross between moderately resistant Carberry and moderately susceptible AC Cadillac commercial cultivars. The population was evaluated along with parental controls for response to FHB infection in a corn spawn inoculated FHB nursery located near Morden MB. Continuous distributions of disease incidence (related to Type I resistance) and severity (related to Type II resistance) in the population indicated quantitative inheritance of both types of FHB resistance. Based on a linkage map that consisted of 2408 SNPs (Infinium iSelect 90k SNP wheat array) and four microsatellite markers, analysis revealed four significant FHB resistance QTL. Type I and II resistance mapped to the same chromosome regions. The level of phenotypic variation explained by Type I FHB resistance was 2.5% for a QTL on chromosome 3A, 5.7% for 5A, 1.4% for 2B, and 2.3% for 3B. The level of phenotypic variation explained by Type II FHB resistance was 2.3% for a QTL on chromosome 3A, 4.1% for 5A, 1.8% for 2B and 7.8% for 3B. The QTL on chromosome 5A appeared to be associated mainly with resistance to initial infection, while the QTL on 3B was more associated with resistance to fungal spread. The favourable alleles on chromosomes 5A and 3B derived from Carberry and on chromosomes 3A and 2B from AC Cadillac. These results indicate that the two types of FHB resistance were generally controlled by the same genomic regions in this population. The markers associated with the QTL could be used for marker-assisted selection to accelerate the development of resistant adapted wheat cultivars.

IMPACT OF WHEAT CULTIVAR EVEREST ON YIELD LOSS IN KANSAS FROM FUSARIUM HEAD BLIGHT DURING 2015

W.W. Bockus[1*], J.A. Appel[2], E.D. De Wolf[1], T.C. Todd[1], M.A. Davis[1] and A.K. Fritz[3]

Departments of [1]Plant Pathology and [3]Agronomy, Kansas State University, Manhattan, KS; and [2]Kansas Department of Agriculture, 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. One of the best ways to manage FHB is by planting resistant cultivars. As a result of funding from the U.S. Wheat and Barley Scab Initiative, significant effort has been placed on developing cultivars adapted to Kansas with improved levels of FHB resistance. Because of this effort, the moderately-resistant cultivar Everest was released in 2009 and has gained popularity such that it is now the most-planted cultivar in Kansas and especially dominant in the eastern third of the state where FHB tends to occur. A significant Fusarium head blight epidemic occurred in Kansas during 2015. The goal of this project was to quantify the impact that the adoption of Everest had on the losses due to FHB during the 2014-15 wheat production season. Throughout the 2015 season, commercial wheat fields were visited and the average severity of FHB determined for each of the 9 crop-reporting districts in Kansas. Data on the percentage acres planted to various wheat cultivars for each district, cultivar FHB susceptibility ratings, and the actual bushels produced for each district were also collected. The above data were used to calculate losses due to FHB for each district. For the calculations, the loss for a susceptible cultivar in each district was estimated based upon the disease survey data. Then, it was assumed that losses for cultivars with intermediate susceptibility would be half of those for susceptible cultivars, and the losses for moderately-resistant cultivars would be half those of intermediate cultivars. Because the percentage acres planted to Everest in each district was known, loss estimates with and without Everest were calculated. In calculations without Everest, it was assumed that a susceptible cultivar took the place of Everest. Significant FHB occurred in all three eastern districts of Kansas. It was estimated that susceptible cultivars in those districts sustained 27.2% loss during 2015. Significant losses also occurred in the northcentral district where losses on susceptible cultivars were estimated to be 13.6%. FHB was a minor problem in the other five districts. Statewide losses of 11.69 million bushes were estimated for 2015. This represented a 3.4% loss when compared with the 334.4 million bushel production for the entire state. When Everest was replaced with a susceptible cultivar in the calculations, it was estimated that there would have been a loss of 16.58 million bushels or 4.8% loss. The cash grain price at harvest time in Kansas was about $5.25 per bushel. Therefore, the resistance level in Everest saved $25.7 million during 2015.

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This material is based upon work supported by the U.S. Department of Agriculture, under Agreement No. 59-0206-1-110. 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 authors and do not necessarily reflect the view of the U.S. Department of Agriculture.

QUANTITATIVE TRAIT LOCI ASSOCIATED WITH RESISTANCE TO FUSARIUM HEAD BLIGHT IN A CARBERRY X VESPER DERIVED WHEAT POPULATION

Bokore[1], F.E., R.D. Cuthbert[1*], R.E. Knox[1], M.A. Henriquez[2], Y. Ruan[1], R.M. DePauw[3], C.J. Pozniak[4], A. N'Diaye[4], A. Sharpe[5], F.R. Clarke[1] and S. Barraies[1]

[1]Agriculture and Agri-Food Canada, Swift Current Research and Development Centre, Swifth Current, SK; [2]Agriculture and Agri-Food Canada, Morden Research and Development Centre, Morden, MB; [3]870 Field Drive, Swift Current, SK; [4]University of Saskatchewan, Crop Development Centre, Department of Plant Sciences, Saskatoon, SK; and [5]National Research Council Canada, Saskatoon, SK
[*]Corresponding Author: PH: (306) 770-4496; Email: Richard.Cuthbert@AGR.GC.CA

ABSTRACT

Fusarium head blight (FHB) caused by *Fusarium graminearum*, is a serious disease often inflicting losses through reduced grain yield and quality in wheat. Deployment of FHB resistant cultivars is an economical and environmentally friendly method of controlling the disease. This study was conducted to identify loci associated with FHB resistance in adapted Canada Western Red Spring (CWRS) wheat cultivars. A set of 180 doubled haploid lines developed from the cross of Carberry by Vesper at the Swift Current Research and Development Centre, AAFC, Canada were evaluated for FHB incidence and severity in nurseries near Morden, MB and Bratt's Lake, SK. Genotyping was done using the Infinium iSelect 90K wheat assay, in which 6211 polymorphic SNPs were mapped to 29 linkage groups. A set of 688 non-overlapping markers were used for QTL analysis. Four QTL with significant effects were detected on 1A, 2B, 4B and 6B chromosomes. Resistance alleles for the 1A and 4B QTL were contributed by Carberry and the 2B and 6B QTL were contributed by Vesper. Chromosome 1A and 4B QTL were associated with FHB incidence and severity, the 2B QTL with FHB incidence and the 6B QTL with FHB severity. Among the four QTL, the minimum phenotypic variation explained for FHB incidence was 6.2% and for FHB severity 5.6%. The 1A and 4B QTL seem to be more stable as they were detected in more than one location. This information will be valuable in maker assisted breeding for FHB resistance.

UTILIZING GENOMIC SELECTION TO ACCELERATE THE PACE OF DEVELOPING RESISTANT VARIETIES

A. Cabrera[1*], J. Isidro[4], E. Olson[2], B. Brisco[2], F. Kolb[3], E.A. Brucker[3], A. Krill[3], M.P. Arruda[3], M. Sorrells[4], D. Van Sanford[5], A. Clark[5], A. McKendry[6] and C. Sneller[1]

[1]Department of Horticulture and Crop Science, The Ohio State University, Wooster, OH 44691;
[2]Plant and Soil Sciences Building, Michigan State University, East Lansing, MI 48824;
[3]Department of Crop Sciences, University of Illinois at Urbana-Champaign, IL 61801;
[4]Department of Plant Breeding and Genetics, Cornell University, Ithaca, NY 14853;
[5]Department of Plant and Soil Sciences, University of Kentucky, Lexington, KY 40546;
and [6]Division of Plant Sciences, University of Missouri, Columbia, MO 65211
[*]Corresponding Author: PH: (330) 317-7584; Email: cabreracano.1@osu.edu

ABSTRACT

Fusarium Head Blight (FHB, Fusarium head scab) is a major disease caused by *F. graminearum* that infects wheat (*Triticum aestivum* L.) and other cereals. One major aspect for managing FHB in wheat is breeding for resistant varieties. However, evaluating FHB within a breeding program takes a large amount of resources. Marker assisted selection (MAS) has been effective for a few QTL, but most of the genes controlling resistance are not affected by traditional MAS. Genomic selection (GS) is a new form of MAS and can facilitate breeding for complex traits by estimating all marker effects simultaneously and predicting the genomic estimated breeding values (GEBVs). GS has the potential to increase the genetic gain per year by decreasing the time per cycle. The challenge remains now in implementing GS and identifying the model with the highest prediction accuracy for each trait. We evaluated the prediction accuracy of GS in a population of 640 soft winter wheat lines. The population was evaluated in inoculated FHB nurseries in multiple environments for incidence (INC), severity (SEV), index (IND), *Fusarium*-damaged kernel (FDK), kernel damage index (ISK), and deoxynivalenol concentration (DON). Across all traits we observed high entry-mean heritability (0.88 to 0.93) and trait correlations (0.63 to 0.98). Principal component and Fst analysis support a population stratification of 3 subgroups. Ten-fold cross validation prediction abilities ranged from 0.45 (INC) to 0.57 (SEV). Similar prediction accuracies were obtained within clusters but were much lower when data from one cluster was used to predict another. Eliminating the top 10-15% less predictable individuals increased prediction accuracy by up to 58%. Although accuracy was dependent on population size, accuracies similar to those obtained using elimination approach could be obtained with smaller sample sizes using two optimization approaches (coefficient of determination and predicted error variance). The results from this work will facilitate GS implementation and the identification of the best lines for selection and crossing for FHB resistance within this population.

MAPPING QTL FOR FUSARIUM HEAD BLIGHT RESISTANCE IN CHINESE WHEAT LANDRACE HAIYANZHONG

Jin Cai[1], Shan Wang[1] and Guihua Bai[1,2*]

[1]Dept. 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, gbai@ksu.edu

ABSTRACT

Fusarium head blight (FHB), caused by *Fusarium graminearum* Schwabe, is a devastating disease in wheat (*Triticum aestivum L.*). FHB epidemics reduce not only grain yield, but also grain quality. Use of host resistance is one of the most effective strategies to minimize the disease damage. Haiyanzhong (HYZ) is a Chinese wheat landrace that shows a high level of resistance to FHB type II resistance. To map the quantitative trait loci (QTL) in HYZ and identify markers tightly linked to the QTL for FHB resistance, we genotyped 186 recombinant inbred lines (RILs) derived from a cross between HYZ and Wheaton, a susceptible cultivar, using simple sequence repeat (SSRs) and single-nucleotide polymorphisms (SNPs) derived from genotyping-by-sequencing (GBS). The population was phenotyped for percentage of symptomatic spikelets (PSSs) per spike in three greenhouse experiments using single-floret inoculation in spring and fall 2012 and spring 2013. A GBS library was constructed for 186 RILs and both parents using *PstI* and *MspI*. The library was then sequenced in an Ion Proton Sequencer. GBS data analysis was performed using UNEAK and independent reference pipeline of TASSEL. A total of 21,740 GBS-SNPs were called with 80% missing, but only 6232 showed 20% or less missing data, thus were used together with 132 SSRs to construct a linkage map for QTL mapping. A total of eight QTL were identified, and six of them were from HYZ and two from Wheaton. SNP *GBS3127* and SSR *Xbarc316* on the chromosome 5AS flanked a major QTL for FHB resistance at a 1.9-cM interval. Other SNPs linked to six minor QTL were identified on the chromosomes 6B, 2B (2), 3B, 4B and 4D. Ten GBS-SNPs tightly linked to the QTL on the chromosomes 5A, 6B and 2B-2 were validated using Kbioscience allele-specific polymorphism (KASP) assays in the mapping population. The ten KASP assays were also validated in a set 96 U.S elite winter wheat breeding lines and cultivars. Five of them, *GBS3127*, *GBS5669*, *GBS0158*, *GBS1852* and *GBS4305,* had the alleles different from these of HYZ in most of U.S. elite winter wheat lines, suggesting these SNPs are useful for transferring these QTL from HYZ into U.S. wheat through marker-assisted selection.

ACKNOWLEDGEMENT AND DISCLAIMER

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

ASSESSMENT OF RESISTANCE TO FUSARIUM HEAD BLIGHT IN SPRING WHEAT LINES GROWN IN THE PACIFIC NORTHWEST AND CIMMYT

J. Chen[1*], J. Zhang[2], W. Zhao[1], J. Wheeler[1], N. Klassen[1] and J. Anderson[3]

[1]University of Idaho Aberdeen R & E Center, Aberdeen, ID; [2]University of California, Davis, CA; and [3]University of Minnesota, St. Paul, MN
[*]Corresponding Author: PH: (208) 397-4162; Email: jchen@uidaho.edu

ABSTRACT

Fusarium head blight is one of the destructive diseases of wheat in humid and semi-humid areas of the world. It has emerged in the Pacific Northwest (PNW) in recent years because of changing climate and rotation practice. The objectives of the present study were to characterize FHB resistance in spring wheat lines grown in PNW and CIMMYT and identify QTL associated with FHB resistance using SNPs and markers for two major dwarfing (*Rht1* and *Rht2*) and one for photo responsive (*PPD-D1*) genes. A total of 190 spring wheat cultivars and lines were evaluated in two field experiments in Minnesota, two field and one greenhouse experiments in Aberdeen, ID in 2015. One spring wheat line had disease severity less than 25% in all five data sets, four lines in four out of five data sets, and twenty-four lines in three out of five data sets in 190 lines evaluated. These lines have no Sumai 3 or related backgrounds and can be the starting resource to develop FHB resistant cultivar for the PNW areas. A subset of 134 lines was classified into four groups (*rht1Rht2*PS, *rht1Rht2*PI, *Rht1rht2*PS, *Rht1rht2*PI) based on marker alleles of the two dwarfing (*Rht1* and *Rht2*) and one photo responsive (PS, sensitive; PI, insensitive) genes. Two groups (*rht1rht2*PI, *Rht1Rht2*PS) were excluded in the analysis because of too few lines in each group. The results showed that the mean field incidence of lines in the groups of *rht1Rht2*PS and *Rht1rht2*PS was 10% lower than that of lines in the groups of *rht1Rht2*PI and *Rht1rht2*PI; this difference might be confounded by the differences in heading date of the lines evaluated. The mean field incidence and severity of lines with dwarfing allele at *RhtB1* locus (*rht1Rht2*PI and *rht1Rht2*PS) were 5 to 7% lower than that of lines with dwarfing allele at *RhtD1* locus (*Rht1rht2*PS and *Rht1rht2*PI). This suggests that FHB resistance can be manipulated through selection of the best combination of the three genes in adapted environments. Preliminary QTL associated with the five disease data sets are being identified and will be presented in the final poster.

CHARACTERIZATION OF FHB RESISTANCE IN SIX-ROW, WINTER BARLEY GERMPLASM

Celeste M. Falcon* and Kevin P. Smith

[1]Department of Agronomy and Plant Genetics, University of Minnesota, St. Paul, MN
*Corresponding Author: PH: 612-624-3252; Email: falco058@umn.edu

ABSTRACT

Winter barley would provide a profitable cover crop to use in a double or relay cropping system with soybean in Minnesota. For this cropping system to work, improved winter barley varieties must be developed. In that vein, we have conducted several cycles of genomic selection for an index trait to improve winter barley for winter survival, heading date, plant height, grain yield, and malt extract. Fusarium head blight (FHB) resistance was not a component of this index trait but would be important to ensure that the developed winter barley lines were viable and profitable. The parent lines for the genomic selection breeding program were a combination of facultative and winter lines and a set of spring lines that contributed FHB resistance. The parent lines were genotyped with the Infinium iSelect single nucleotide polymorphism (SNP) assay markers, and the progeny from each cycle of selection were genotyped with a custom assay of 384 SNP markers. For this research, our objectives were to 1) quantify population structure in the genomic selection population using principal components analysis (PCA) of the genotypic marker data; 2) determine the amount of genetic variation present for FHB resistance and two related traits, heading date and plant height; and 3) identify quantitative trait loci (QTL) associated with FHB resistance, heading date, and plant height using association mapping. We evaluated lines from cycle 0 (parents) through cycle 2 of our genomic selection breeding program for FHB severity in three inoculated trials, for heading date in six trials, and for plant height in five trials. Based on a biplot of the first two principal components, we observed that while population structure was not present, the genetic variance of the population decreased over cycles of selection and the population shifted toward more similarity with the winter parent lines. All three traits assessed showed significant genetic variation, allowing us to conduct association mapping for each trait. We detected QTL for FHB resistance on chromosomes 1H and 7H. While the FHB resistance QTL on 7H coincides with a QTL for heading date, the 1H QTL was not associated with other traits. Pending further investigation of this QTL, it could prove useful in developing FHB resistant winter barley lines. Though this population exhibited genetic variation for FHB resistance, just one QTL was found indicating that the trait is quantitative in nature. Accordingly, we would plan to use genomic prediction to breed for this trait.

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MAPPING QUANTITATIVE TRAIT LOCI FOR FUSARIUM HEAD BLIGHT RESISTANCE IN HARD WINTER WHEAT OVERLAND

Nosheen Fatima[1], Guihua Bai[1,2*] and William Bockus[3]

[1]Department of Agronomy, Kansas State University; [2]USDA-ARS-Hard Winter Wheat Genetics Research Unit, Manhattan, KS; and [3]Department of Plant Pathology, Kansas State University Manhattan, KS 66506
[*]Corresponding Author: PH: (785) 532-1124; Email: guihua.bai@ars.usda.gov, gbai@ksu.edu

ABSTRACT

Fusarium head blight (FHB) is a ravaging disease of small grain crops grown in humid and semi-humid areas of the world. FHB epidemics are sporadic in nature, but the affected crops face serious setback once epidemics occur. Among many approaches that are proposed to combat the disease, growing resistant cultivars is the most effective one to minimize disease damage. Overland is a hard winter wheat cultivar released from University of Nebraska, and shows moderate resistance to FHB. To dissect the quantitative trait loci (QTL) that control FHB resistance in Overland, 186 $F_{5:6}$ recombinant inbred lines (RILs) were developed by a cross between Overland and a highly susceptible cultivar Overley from Kansas. The RILs were inoculated by injecting a conidial suspension of *F. graminearum* (field isolate GZ 3639 native to Kansas) into a central spikelet in a spike in the greenhouses at Kansas State University, Manhattan KS. FHB resistance was measured as percentage of symptomatic spikelets (PSS) in an inoculated spike 12d after inoculation. The greenhouse experiments were conducted twice in fall 2014 and spring 2015. The RILs were also evaluated for FHB resistance in the FHB field nursery at Rocky Ford, Manhattan in 2015 using a grain spawn inoculation method. PSS was recorded 3 weeks after flowering. *Fusarium*-damaged kernels (FDK) was also scored for field harvested plants. Mean PSS in this population ranged from 25%-90%, while the mean FDK in the samples harvested from the field plots ranged from 30%-95%. The parents had significant difference in FDK, with 42.5% for Overland and 82.5% for Overley. In the field experiment, the correlation between mean PSS and FDK was 0.68. Both the parents and all the RILs were subjected to analysis of genotyping-by-sequencing (GBS) to discover SNPs tightly linked to QTL for FHB resistance in Overland. GBS was run in a Ion Proton sequencer in USDA Genotyping Lab at Manhattan, KS and SNPs were called using TASSEL pipeline as described by Poland *et al* 2012. A linkage map consisting of 3079 SNPs was constructed using JoinMap 4.1 and QTL analysis was done using ICIMapping software version2.3. Three QTL were detected from the field experiment and one from the greenhouse experiments which explained 15%, 10%, 8.5% and 8.22% of the phenotypic variation, respectively. Two QTL were detected for low FDK explaining 7% and 14% of the phenotypic variation. The QTL on 4D was significant for low PSS in both greenhouse and field experiments and low FDK in the field experiment. The experiments are being repeated in both the greenhouse and field experiments to further confirm these QTL. The results will help us to understand the resistance in Overland and to develop breeder-friendly markers for the QTL.

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RESPONSE OF A COLLECTION OF WAXY (REDUCED AMYLOSE) WHEAT BREEDING LINES TO *FUSARIUM GRAMINEARUM*

Deanna L. Funnell-Harris[1,2*] and Robert A. Graybosch[1,3]

[1]USDA-ARS, Grain, Forage and Bioenergy Research Unit, [2]Department of Plant Pathology, and [3]Department of Agronomy and Horticulture, University of Nebraska, Lincoln, NE 68583-0937
[*]Corresponding Author: PH: 402-472-9099; Email: Deanna.Funnell-Harris@ars.usda.gov

ABSTRACT

Loss of function mutations in the *Waxy* (*Wx*) gene encoding granule bound starch synthase I (GBSSI) that synthesizes amylose, result in starch granules containing mostly amylopectin. Wheat grain with this trait has increased usability for some foods due to the ability to modify starch composition and nutritional value in the end product. However, impaired GBSSI activity may alter grain and starch structure and, consequently, responses to pathogens. There are no published reports on response of *waxy* wheats to Fusarium head scab. A screen of colonization by *Fusarium graminearum* of *waxy* breeding lines and wild-type and *waxy* checks was conducted at Mead, NE, 2014. Grain was either surface disinfested before plating, or directly plated, onto medium semi-selective for *Fusarium* spp., indicating internal or both internal and superficial infections, respectively. Grains with fungal growth were enumerated for each line and grain treatment. Non-disinfested *waxy* grains (69.5%) were significantly less colonized as compared with wild-type (78.9%) ($P < 0.01$). Surface disinfested grains of both phenotypes had similar levels of infection (14.4% for wild-type *versus* 10.0% for *waxy*; $P = 0.07$). Fungal colonies growing onto the medium were transferred and morphologically identified as similar to *Fusarium graminearum*, *Fusarium* spp. or other fungi. Along with *F. graminearum*, *F. verticillioides, F. equiseti* and *F. acuminatum*, were common in wild-type grain, while the most commonly detected species in *waxy* grain was *F. proliferatum.* These preliminary results indicated that *waxy* wheats are not more susceptible to *F. graminearum* than wild-type. Analyses of mycotoxins such as deoxynivalenol will be needed to confirm whether these promising *waxy* lines in development are not more susceptible to *F. graminearum* than non-*waxy* lines.

GENETICS OF FUSARIUM HEAD BLIGHT RESISTANCE IN BARLEY: THE WAY FORWARD

Matthew Haas and Brian J. Steffenson*

Department of Plant Pathology, University of Minnesota, Saint Paul, MN 55108 USA
*Corresponding Author: PH: 612 625-4735; Email: bsteffen@umn.edu

ABSTRACT

Fusarium head blight (FHB) is a perennial problem in many parts of the world, particularly in regions with environmental conditions suitable to disease development. Genetic resistance is considered one of the most cost-effective and environmentally friendly ways to control plant disease, but a global screening of 23,000+ barley accessions has so far yielded very few accessions with adequate levels of resistance and no truly immune accessions. Moreover, quantitative trait locus (QTL) mapping studies spanning two decades of intensive research have so far identified QTL with very small effects ($R^2 < 0.10$). In these previous mapping studies, the most significant QTL are associated with segregating agro-morphological traits, including row type, heading date, and cleistogamy. In an attempt to introduce potentially novel resistance alleles into adapted germplasm, wild barley accessions PI 466423 and W-365 and landrace Kutahya were crossed to Midwest cultivars Rasmusson or Quest. However, every major QTL detected in these three populations was actually contributed by the recurrent parent, which may be attributed to extensive efforts to breed for the distinct, but related, disease of kernel discoloration (KD) using Chevron as source of resistance. The largest effect QTL that we identified is located in chromosome 2H bin 4. This locus is likely novel for FHB resistance, but evidence suggest that we are detecting the photoperiod response gene *Ppd-H1*. Further, the allelic effect (α) varied between environments for this locus as well as other loci, so it may not be suitable for marker assisted selection (MAS). Biotechnological approaches could be used to introduce resistance in the absence of natural variation, but success in this area has also been limited. Techniques such as genomic selection (GS) offer a greater promise for improving upon presently-available FHB resistance. Ultimately, management of FHB will result from incremental improvements in genetic resistance, management of crop residues, and judicious use of fungicides.

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DEVELOPMENT OF ADVANCED CIMMYT WHEAT BREEDING LINES COMBINING *FHB1* AND *SR2*

Xinyao He[1], David Bonnett[1,2], Susanne Dreisigacker[1], Jessica Hyles[3], Wolfgang Spielmeyer[3] and Pawan K. Singh[1*]

[1]International Maize and Wheat Improvement Center (CIMMYT), El Batan, Mexico; [2]Bayer CropScience, Fargo, USA; and [3]CSIRO Agriculture, Canberra, Australia
[*]Corresponding Author: PH: (612) 605-5205 ext. 2217; Email: pk.singh@cgiar.org

ABSTRACT

Fusarium head blight (FHB) and stem rust are two major wheat diseases worldwide and both are breeding targets of the breeding programs at CIMMYT. *Fhb1* confers consistently major effects on FHB resistance and deoxynivalenol (DON) content and played important roles in CIMMYT's early FHB resistance breeding activities. However, due to its tightly repulsive linkage with *Sr2* for adult plant stem rust resistance, *Fhb1* has been gradually lost due to the consistent selection of durable stem rust resistance. In order to get back *Fhb1*, germplasm with *Fhb1* and *Sr2* in coupling linkage needs to be utilized to meet the breeding requirements of both diseases. Using marker-assisted selection, four recombinant lines were developed in the background of the Australian cultivar Hartog (also known as Pavon) at CSIRO, Australia and introduced into the CIMMYT breeding program. The lines were crossed and backcrossed with seven recent CIMMYT bread wheat parents and one durum line. Pseudo-black chaff, a morphological trait tightly linked to *Sr2*, was used to retain *Sr2* during backcrossing. To identify the recombinants, the eight populations were genotyped with linked SNP and SSR markers from the *Fhb1* and *Sr2* region: wMAS000005 (based on csSr2), wMAS000008 (based on snp3BS-8), barc102, umn10, wms533, barc133 and wms493. In 2013, 264 F7 derived lines were screened for FHB resistance and 76 lines with good FHB resistance and *Fhb1- Sr2* haplotypes were selected for field and greenhouse evaluations in 2014. Based on both Type I and Type II FHB resistance and the haplotype data, 30 lines were selected for further testing. The 30 genetically diverse lines were derived from 16 different crosses and were evaluated in 2015 for FHB, yellow rust, Septoria tritici blotch, tan spot, spot blotch, and Stagonospora nodorum botch at CIMMYT, Mexico. They will also be tested for stem rust resistance in Kenya. Lines showing broad spectrum of resistance to tested diseases have been identified. Utilization of these lines in breeding programs has been initiated via marker-assisted backcrossing and will greatly facilitate the development of wheat cultivars with improved resistance to FHB and stem rust simultaneously.

FUSARIUM HEAD BLIGHT RESISTANCE LINES IDENTIFIED IN PRELIMINARY EVALUATION OF USDA-ARS BARLEY BREEDING MATERIALS IN IDAHO

G. Hu[1*], K. Satterfield[1], C. Evans[1], R. Brueggeman[2], P. Schwarz[2] and J. Marshall[3]

[1]USDA-ARS, 1691 S 2700 W. Aberdeen, Idaho; [2]North Dakota State University, Fargo, ND; and [3]Aberdeen R&E Center, University of Idaho, Aberdeen, Idaho
[*]Corresponding Author: PH: (208) 397-4162; Email: Gongshe.Hu@ARS.USDA.GOV

ABSTRACT

Fusarium head blight (FHB) disease is very harmful to barley yield, quality, and commercial value. With the climate change and more corn being planting, FHB infected plants have been sporadically identified in Idaho barley fields in more recent years. That is alarming for future production problems in a high quality barley production state. As the first step to deal with the potential disease, we screened 100 lines of our breeding materials in two screening nurseries of North Dakota State University in 2014. Preliminary results from two North Dakota locations in 2014 identified resistance lines when measuring infection rating and DON levels in seed. Comparing to the 2-row resistance check of Conlon, eight of 100 lines have lower DON content in all of four replications, while 21 lines have low DON than Conlon if the average DON level from four replications is used in the comparison. The 2015 Aberdeen nursery also showed a good level of infection. Early analyses of the results indicate that Aberdeen's elite breeding lines contain useful genetic resistance resources. This will greatly aid the breeding program in rapidly developing FHB-resistant cultivars.

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ENHANCING TOOLS FOR *FUSARIUM* RESISTANCE BREEDING IN CANADIAN WINTER WHEAT

D.G. Humphreys[1*], W. Cao[1], A. Kalikililo[1], L. Langille[1], C. McCartney[2], B. Blackwell[1] and R.J. Graf[3]

[1]Eastern Cereal and Oilseed Research Centre, 960 Carling Avenue, Central Experimental Farm, Ottawa, ON, Canada K1A 0C6; [2]Cereal Research Centre, 101-Route 100, Unit 100, Morden, MB, Canada R6M 1Y5; and [3]Lethbridge Research Centre, 5403-1st Avenue South, Lethbridge, AB, Canada T1J 4B1
[*]Corresponding Author: PH: (613) 759-1636; Email: gavin.humphreys@agr.gc.ca

ABSTRACT

Fusarium head blight (FHB) remains one of the most important diseases affecting wheat production worldwide. FHB damages multiple aspects of the wheat crop including grain yield, grade, and quality for end-use and propagation. The presence of mycotoxins, particularly deoxynivalenol (DON), will result in downgrading and at levels over 1 ppm can render the grain unsuitable for human and livestock consumption. In Canada, FHB associated crop losses in the 1990s exceeded $500 million in eastern Canada and the eastern Prairies where this disease is particularly prevalent. The use of resistant cultivars is central to integrated management approaches for control of FHB. The objective of this research is to enhance three components within the eastern Agriculture & Agri-Food (AAFC) winter wheat breeding program that facilitate the development of FHB resistant cultivars: (i) development and deployment of novel germplasm including wheat species to access untapped FHB resistance; (ii) establishment and maintenance of a robust FHB screening nursery and the highly trained personnel for phenotypic characterization of field symptoms and DON determination; and (iii) high-throughput molecular breeding strategies that enable the genotyping of promising germplasm including breeding lines and parental materials used in marker-assisted backcrossing.

ENHANCING FHB RESISTANCE IN DURUM WHEAT

Shahryar F. Kianian[1*], Farhad Ghavami[2], Seyed M. Pirseyedi[3], Ajay Kumar[3], Jitendra Kumar[4], Ruth Dill-Macky[4], Steven Xu[5] and Elias M. Elias[3]

[1]USDA-ARS Cereal Disease Laboratory, St. Paul, MN; [2]Eurofins BioDiagnostics Inc., River Falls, WI; [3]Department of Plant Sciences, North Dakota State University, Fargo, ND; Department of Plant Pathology, University of Minnesota, St. Paul, MN; and [5]USDA-ARS Cereal Crops Research, Fargo, ND
[*]Corresponding Author: PH: (612) 624-4155; Email: shahryar.kianian@ars.usda.gov

ABSTRACT

Durum wheat (*T. turgidum* L. var. *durum* Desf.), which is grown primarily in North Dakota, has been heavily impacted by Fusarium head blight (FHB). Thus, it is critical to identify means of defeating this disease or reducing its pathogenic effect to enhance durum wheat production. Whole genome association analysis of various Tunisian derived tetraploid sources of resistance revealed a significant region on 5BL (*Qfhs.ndsu-5BL*), which was further confirmed by traditional QTL analysis in a bi-parental population.

Further analysis using two additional Tunisian-derived advanced backcross populations, Tun 108/Lebsock//Lebsock and Tun 108/Ben//Ben, screened for FHB resistance revealed novel regions on 2BL (*Qfhb.ndsu-2BL*) and 5AL (*Qfhb.ndsu-5AL*). The 2BL region provides resistance to multiple FHB components including severity, incidence, mycotoxin production and frequency of damaged kernels while 5AL segment provides resistance to severity of infection. We have been developing KASPar SNP markers, for ease of introgression, and pyramiding these regions into a single cultivar to assist durum breeding programs in their effort to breed for more resistant cultivars.

Additionally, we treated six advanced durum breeding lines with 5-methyl-azacytedine that removes CG methylation. The resulting lines were advanced to the M_4 generation and tested for FHB resistance under greenhouse and field conditions. Twenty four lines were identified that show great promise having less than 20% severity as compared with 80-100% severity for parental lines and susceptible checks. We have further advanced these 24 lines, crossed the most promising to the parental cultivars to test the stability and inheritance of resistance, and are analyzing them further to determine what epigenetic changes are responsible for the enhanced FHB resistance. These could potentially be used as new sources of resistance for the breeding programs.

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INCORPORATION OF GENOMIC SELECTION INTO THE UNIVERSITY OF ILLINOIS' SOFT RED WINTER WHEAT BREEDING PROGRAM

Allison M. Krill[1], Marcio P. Arruda[1], Patrick J. Brown[1], Alexander E. Lipka[1], Gina Brown-Guedira[2] and Frederic L. Kolb[1*]

[1]Dept. of Crop Sciences, University of Illinois at Urbana-Champaign, Urbana, IL 61801; and [2]USDA-ARS Eastern Regional Genotyping Center, Raleigh, NC 27695
[*]Corresponding Author: PH: (217) 333-4256; Email: f-kolb@illinois.edu

ABSTRACT

Breeding for resistance to Fusarium head blight (FHB), a destructive disease of wheat (*Triticum aestivum* L.), is challenging due to its quantitative inheritance and difficulties in obtaining high quality phenotypes. At the University of Illinois soft red winter wheat breeding program, phenotypic selection and early-generation enrichment by marker assisted selection (MAS) have been the main strategies for selecting individuals with higher levels of resistance. More recently, genomic selection (GS) models have been tested for predicting multiple traits associated with FHB resistance. GS is currently being implemented at two stages of the breeding program; for selection of parents and at the preliminary yield trial (PYT) stage.

Genotyping-by-sequencing (GBS) was used to identify a subset of ~ 20,000 informative SNPs across a panel of 273 diverse soft red winter wheat breeding lines. These SNPs were used to compare several MAS and GS model predictions for six FHB related traits (INC, SEV, FHBndx, FDK, ISKndx, and DON). Phenotypic data were obtained in a scab nursery in Urbana, IL in 2011, 2013, 2014, and best linear unbiased predictors (BLUPs) were obtained from a mixed model. SNP effects were estimated using ridge regression-BLUP in the R package PopVar. The analyses were performed using a four-fold cross validation approach. In all cases GS models outperformed the MAS models with prediction accuracies ranging from 0.58 (SEV) to 0.88 *Fusarium*-damaged kernels (FDK).

In a second stage, GS was applied to the PYT lines, consisting of 400 $F_{3:6}$ entries, using 6850 informative SNPs. These PYT lines were grown at four locations throughout Illinois in 2015 and two locations in 2014, including the scab nursery in Urbana. Yield (YLD) and test weight (TW) were obtained for each line. Genomic prediction accuracy for YLD and TW were 0.34 and 0.45 respectively. A combination of genotypic and phenotypic values are used to calculate genomic estimated breeding value (GEBV) predictions for all traits except DON. Typically, DON data from the current year are not available before the following cycle of planting, making GS a valuable tool for selection of resistant lines. GEBVs for DON are calculated from the training population (TP), which consists of those lines previously phenotyped for DON, including lines from the advanced yield trials (AYT) and previous PYTs. About 20% of the lines from PYT are selected to be in the AYT.

Initial results show the implementation of GS into the breeding program can be a useful tool for prediction of several traits and development of high yielding cultivars with FHB resistance. Incorporation of GS into earlier stages of the breeding program will continue as methods are developed to genotype an increasing number of lines while keeping costs low.

CHARACTERIZATION OF FHB RESISTANCE QTL IN SRW WHEAT CULTIVAR TRIBUTE

Malla, S.[1], C. Griffey[1*], J.P. Murphy[2], E. Milus[3], A. Clark[4], D. Van Sanford[4], J. Costa[5], N. McMaster[6], D. Schmale III[6], S. Chao[7] and G. Brown-Guedira[8]

[1]Dept. of Crop and Soil Environmental Sciences, Virginia Tech, Blacksburg, VA 24061; [2]Dept. of Crop Science, North Carolina State University, Raleigh, NC 27695; [3]Dept. of Plant Pathology, University of Arkansas, Fayetteville, AR 72701; [4]Dept. of Plant and Soil Sciences, University of Kentucky, Lexington, KY 40546; [5]USDA-ARS, Grain Crops National Program, Beltsville, MD 20705; [6]Dept. of Plant Pathology, Physiology, and Weed Science, Virginia Tech, Blacksburg, VA 24061; [7]USDA-ARS Cereal Crops Research Unit, Fargo, ND 58102; and [8]USDA-ARS Eastern Regional Genotyping Center, Raleigh, NC 27695
[*]Corresponding Author: PH: 540-231-9789; Email: cgriffey@vt.edu

ABSTRACT

Pyramiding genes from exotic and native sources would be an effective approach to enhance resistance to Fusarium head blight (FHB), caused by *Fusarium graminearum*. The objectives of the study were to identify the FHB resistance QTL in the native soft red winter (SRW) wheat cultivar Tribute and develop diagnostic markers for use in marker-assisted breeding. A total of 114 double haploid (DH) lines, developed at NCSU, were evaluated for FHB incidence and FHB severity by cooperators in AR, KY, MD, NC, and VA during 2013 and 2014 (except MD). Grain samples from each location were visually assessed for *Fusarium*-damaged kernels (FDK) and analyzed for deoxynivalenol (DON) toxin content. The population was also evaluated for type II resistance to disease spread in the greenhouse at Virginia Tech. A set of SSR and 90K SNP markers were used to genotype the mapping population. Genotype-by-location interaction was significant for the population. Composite interval mapping identified five putative QTL on chromosomes 1A, 2A, 2D, 3BS, and 7B for FHB incidence, FHB severity, FDK, and DON content. Putative QTL for FHB resistance were detected on 1A, 2A, and 3BS, whereas putative QTL for FHB susceptibility were detected on 7B. Both FHB resistance and FHB susceptibility were associated with the QTL on 2D. The putative QTL for FHB on 2A and 2D were linked to loci governing heading date and flowering date across locations, whereas the putative QTL for FHB on 1A was linked to 1A.1R translocation. The variation explained by putative QTL on 1A, 2A, 2D, 3BS, and 7B was 8.2% to 27.8% (Additive = -1.9 to -11.3), 4.8% to 24.0% (Additive = -0-0.5 to -13.0), 9.1% to 38.8% (Additive = -10.8 to 14.4), 0.1% to 21.8% (Additive = -3.6 to -10.3), and 7.3% to 17.0% (Additive = 2.5 to 6.5), respectively. The diagnostic markers are IWB49926 (1A), IWB4499 (2A), Xgwm261 (2D), IWB7909 and Xbarc164 (3B), and IWB55522 and IWA1089 (7B). The diagnostic markers could be utilized in marker-assisted breeding in wheat breeding program.

FHB RESISTANCE AND AGRONOMIC PERFORMANCE IN GEORGIA SOFT RED WINTER WHEAT GERMPLASM

Mohamed Mergoum, Jerry Johnson*, James Buck, Zhenbang Chen and Y. Hao

Crop and Soil Sciences, Griffin Campus, University of Georgia, Griffin, GA, 30223
*Corresponding Author: PH: 770-468-5101; Email: jjohnso@uga.edu

ABSTRACT

Development of resistant wheat cultivars is the most efficient approach to control Fusarium head blight (FHB). Local broadly adapted cultivars of soft red winter wheat (SRWW) have been crossed with *Fhb1* derived lines, Truman, Neuse, and Jamestown to introduce FHB resistant QTL into adapted SRWW genetic backgrounds. Elite lines with FHB resistance derived from Truman/Bess, Neuse, MD08-27-E9 and Jamestown, were evaluated under Georgia's field conditions during 2015 for FHB resistance and agronomic performances. Several elite lines have been identified with good FHB resistance derived from Jamestown. GA061050-13ES17 (AGS 2020/Jamestown), GA051207-13ES11 (AGS 2000 / SC996284 // IN981359C1), GA08250-14ES7 (Jamestown/GA991336-6E9), and GA 071171-14ES8 (Jamestown/GA991371-6E12) had similar FHB ratings as Jamestown for incidence, index and ISK. GA061050-13ES17 has the QTL 1A from Neuse, and 2B and 3B QTL from Bess; GA051207-13ES11 has the QTL 1A and 6A from Neuse; GA08250-14ES7 has the QTL 1B and 6A from Jamestown; and GA 071171-14ES8 has the QTL 1B from Jamestown, and 5A from Ernie. Other elite lines with moderate levels of FHB resistance derived from Jamestown, Ernie, or Neuse were identified with high grain yield potential and will be further evaluated. Similarly, double haploid lines, NC 10014 (NC 06-198-96/NC 08-140) and NC 9337 (Jamestown/S8641) showed a high level of FHB resistance and high yield performance.

THE 2014-15 SOUTHERN UNIFORM SOFT RED WINTER WHEAT SCAB NURSERY

J.P. Murphy*, S. Petersen, J.H. Lyerly and B. Poole

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 2014-15 nursery comprised 45 advanced generation breeding lines and four check cultivars, Ernie, Bess, Jamestown (partially resistant) and 'Coker 9835' (susceptible). Five U.S. public programs (Univ. of Arkansas, Univ. of Georgia, Louisiana State University, N.C. State Univ., and VA Tech.), and three private companies (Agripro-Coker, KWS, and Limagrain) submitted entries. The nursery was evaluated at 11 locations in AR, MO, KY, IL, VA, NC, GA, and LA 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.

The mean level of FHB resistance in the nursery was high. Between 87 and 93 percent of entries had significantly better means than the susceptible check for severity and FHB index. DON data are still being reported. Sources of resistance included Chinese and North American germplasms.

Copies of the full report will be available at the 2015 National Fusarium Head Blight Forum and subsequently on line at the USWBSI web site: http://www.scabusa.org/.

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Table 1. Means across locations and genotypic content of regions associated with FHB resistance.

	Cultivar/ Designation	FHB Incidence	RANK	FHB Severity	RANK	FHB Index	RANK	FDK	RANK	ISK	RANK	DON	RANK
1	ERNIE	58	11	36	28	19	16	34	29	36	18	9	23
2	COKER9835	86	49	68	49	55	49	57	49	61	49	13	42
3	BESS	55	8	25	7	15	10	27	15	36	18	6	7
4	JAMESTOWN	54	5	30	12	17	13	23	6	34	13	6	7
5	LA07085CW-P4	62	20	38	35	22	23	43	43	41	32	9	23
6	LANC8170-41-2	69	36	40	38	28	41	30	16	42	35	5	3
7	NC11-22289	50	1	23	5	13	4	26	14	26	2	5	3
8	AR06024-7-2	57	10	21	4	12	3	18	2	27	4	4	2
9	AR06037-17-2	78	47	34	22	26	37	31	18	41	32	10	30
10	AR06045-2-4	54	5	20	2	9	2	25	10	26	2	8	17
11	AR06045-16-4	59	12	24	6	13	4	24	7	31	6	8	17
12	AR06046-10-3	62	18	31	16	20	18	32	20	36	18	13	42
13	AR06061-11-1	61	15	26	8	17	13	20	3	31	6	6	7
14	LW08190C-57-3	64	22	30	12	20	18	33	24	34	13	5	3
15	ARGE08-1398	51	2	14	1	8	1	11	1	22	1	2	1
16	B12*1792	66	29	41	39	28	41	32	20	42	35	13	42
17	B12-2180NC#	78	47	33	20	25	31	25	10	41	32	9	23
18	GA 071171-14ES8	64	22	41	39	25	31	30	16	40	28	9	23
19	GA 071092-14ES11	67	32	36	28	22	23	34	29	34	13	11	38
20	GA071092-14ES13	66	29	39	37	25	31	35	33	37	21	11	38
21	GA 081129-14ES16	64	22	36	35	23	31	36	35	40	28	8	17
22	GA 08250-14ES7	62	18	31	16	20	18	32	20	32	12	9	23
23	GA 08250-14ES5	62	20	36	28	22	23	34	29	38	23	10	30
24	GA 071171-14ES19	67	32	35	26	24	30	31	18	37	21	11	38
25	GA 081562-14ES14	74	43	34	22	26	37	42	41	43	39	14	45
26	KWS 054	66	29	30	12	22	23	45	46	42	35	10	30
27	LA06146E-P4	59	12	32	18	19	16	42	41	44	41	11	38
28	LA08265C-50	71	39	42	42	35	46	33	24	48	45	7	11
29	LA09144C-6	74	43	51	48	36	47	43	43	47	44	16	47
30	LANC8248-1	76	45	49	47	40	48	25	10	48	45	8	17
31	ES13-1591	55	8	29	10	15	10	34	29	31	6	6	7
32	ES13-3423	52	3	36	28	14	7	40	40	34	13	9	23
33	ES12-3030	65	27	36	28	23	29	33	24	39	27	7	11
34	M11-2024#	65	27	37	34	27	39	24	7	40	28	10	30
35	M12-3301	61	15	34	22	16	12	33	24	31	6	8	17
36	M12-2036#	54	5	26	8	14	7	33	24	38	23	10	30
37	NC11-23084	67	32	42	42	22	23	35	33	38	23	10	30
38	NC12-23576	69	36	41	39	27	39	37	36	43	39	14	45
39	NC12-23219	64	22	33	20	25	31	24	7	38	23	7	11
40	NC12-20662	60	14	35	26	14	7	32	20	31	6	7	11
41	NC9305-7	64	22	30	12	20	18	20	3	34	13	7	11
42	VA11W-106	69	36	32	18	22	23	39	38	42	35	16	47
43	VA11W-313	71	39	42	42	29	43	47	47	45	43	10	30
44	VA12W-72	72	41	34	22	25	31	55	48	50	48	16	47
45	VA12W-54	72	41	44	45	30	44	44	45	49	47	9	23
46	VA12FHB-53	61	15	29	10	18	15	38	37	40	28	10	30
47	VA12FHB-4	68	35	36	28	21	22	25	10	31	6	7	11
48	VA13W-177	53	4	20	2	13	4	21	5	27	4	5	3
49	VA08MAS5-39-6-4	76	45	47	46	32	45	39	38	44	41	8	17
	Mean	64		34		22		33		38		9	
	LSD (0.05)	26		26		22		24		18		7	
	CV%	20.7		38.3		50.4		36.8		24.0		37.7	

Table 1 Cont.

	Cultivar/ Designation	Heading Date	RANK	Plant Height	RANK	Flour Yield %	RANK	Softness Equivalent %	RANK	Hessian Fly Biotype L	*Fhb1*	*Fhb Massey 3BL*	*Fhb 5A*	*Fhb 2DL-Wuhan1/W14*	*Bess 2B*	*Bess 3B*	*Jamestown 1B*	*Jamestown 6A*	*NC-Neuse 1A*	*NC-Neuse 6A*
1	ERNIE	129	12	32	16	67	30	55	36	0-15	no	3BL?	het	no	no	no	no	no	yes	yes
2	COKER9835	131	40	31	11	68	18	65	1	0-15	no	no	no	no	no	no	no	no	.	no
3	BESS	130	24	35	42	67	30	61	12	0-15	no	no	no	no	yes	yes	yes	no	.	no
4	JAMESTOWN	128	5	32	18	68	18	59	17	0-14	no	no	no	no	no	no	yes	yes	yes	no
5	LA07085CW-P4	128	5	33	28	69	13	63	7	0-17	no	no	no	no	no	no	no	no	.	no
6	LANC8170-41-2	130	24	31	12	66	41	50	48	11-0	Fhb1	no	no	no	no	no	yes	yes	yes	no
7	NC11-22289	128	5	35	43	66	41	52	45	0-17	no	no	no	no	no	no	yes	no	.	yes
8	AR06024-7-2	130	24	36	49	66	41	56	33	0-15	Fhb1 het	no	no	no	no	no	yes	no	yes	no
9	AR06037-17-2	132	48	30	2	68	18	59	17	0-18	no	no	no	no	no	no	no	no	.	no
10	AR06045-2-4	130	24	36	47	68	18	62	10	0-12	no	no	no	no	yes	yes	yes	no	no	no
11	AR06045-16-4	130	24	35	45	68	18	62	10	0-13	no	no	no	no	.	yes	yes	no	no	no
12	AR06046-10-3	130	24	33	26	68	18	58	23	0-14	no	no	no	no	no	yes	yes	no	no	no
13	AR06061-11-1	131	40	35	44	67	30	63	7	0-14	no	no	no	no	yes	yes	yes	no	yes	no
14	LW08190C-57-3	129	12	32	19	67	30	58	23	0-11	Fhb1	no	no	no	no	no	no	no	yes	no
15	ARGE08-1398	130	24	36	48	67	30	58	23	0-14	Fhb1?	no	no	no	no	no	yes	no	yes	no
16	B12*1792	129	12	33	29	68	18	59	17	16-1	no	no	no	no	no	no	no	no	yes	no
17	B12-2180NC#	130	24	30	3	67	30	60	16	16-0	no	no	no	no	no	no	no	no	no	no
18	GA 071171-14ES8	130	24	35	40	70	5	57	30	9-8	no	no	het	no	no	no	yes	no	.	no
19	GA 071092-14ES11	130	24	32	17	71	1	61	12	0-17	no	no	no	no	no	no	yes	no	no	no
20	GA071092-14ES13	130	24	33	25	71	1	64	2	0-16	no	no	no	no	no	no	yes	no	no	no
21	GA 081129-14ES16	129	12	31	5	70	5	53	41	0-16	no	no	no	no	no	no	yes	no	no	no
22	GA 08250-14ES7	131	40	32	13	70	5	63	7	0-16	no	no	no	no	no	no	yes	yes	no	no
23	GA 08250-14ES5	131	40	34	39	69	13	61	12	0-16	no	no	no	no	no	no	no	no	.	no
24	GA 071171-14ES19	130	24	34	36	70	5	56	33	0-18	no	no	no	no	no	no	yes	no	.	no
25	GA 081562-14ES14	134	49	32	20	71	1	56	33	0-14	no	no	yes	no	no	no	no	no	yes	yes
26	KWS 054	128	5	31	6	69	13	64	2	0-14	no	no	no	no	no	no	no	no	yes	no
27	LA06146E-P4	130	24	34	31	68	18	50	48	0-14	no	no	no	no	no	no	yes	yes	yes	no
28	LA08265C-50	129	12	35	41	68	18	58	23	0-16	no	no	no	no	no	no	yes	no	yes	no
29	LA09144C-6	131	40	34	38	70	5	57	30	0-14	no	no	no	no	no	no	no	yes	no	no
30	LANC8248-1	130	24	29	1	71	1	52	45	0-12	no	no	yes	no	no	no	no	no	yes	no
31	ES13-1591	127	2	34	33	69	13	61	12	0-16	no	no	no	no	no	no	no	no	yes	no
32	ES13-3423	129	12	33	22	65	47	58	23	0-21	no	no	yes	no	no	no	no	no	yes	yes
33	ES12-3030	129	12	34	34	66	41	53	41	0-15	no	no	no	no	no	no	yes	no	yes	no
34	M11-2024#	129	12	31	7	68	18	52	45	0-17	no	3BL	no	no	no	no	no	no	yes	no
35	M12-3301	130	24	34	35	69	13	64	2	0-19	no	no	no	no	no	no	yes	no	no	no
36	M12-2036#	129	12	34	37	70	5	64	2	0-18	no	no	no	no	no	no	no	no	yes	no
37	NC11-23084	131	40	33	23	70	5	55	36	0-18	no	no	yes	no	no	no	yes	no	yes	yes
38	NC12-23576	130	24	33	27	67	30	53	41	0-20	no	no	no	no	no	yes	yes	no	.	no
39	NC12-23219	129	12	33	30	65	47	55	36	0-18	no	no	yes	no	no	no	no	no	.	no
40	NC12-20662	126	1	31	8	66	41	53	41	0-16	no	no	no	no	no	no	no	yes	.	no
41	NC9305-7	131	40	34	32	67	30	58	23	0-17	no	no	no	no	no	yes	no	no	yes	no
42	VA11W-106	131	40	32	15	67	30	64	2	0-20	no	no	no	no	no	no	yes	no	.	no
43	VA11W-313	128	5	31	9	67	30	54	39	0-16	no	no	no	no	no	no	no	no	no	no
44	VA12W-72	128	5	33	24	65	47	57	30	17-1	no	3BL	no	no	no	no	no	no	no	no
45	VA12W-54	128	5	31	4	68	18	58	23	21-0	no	3BL	no	no	no	no	no	no	.	no
46	VA12FHB-53	129	12	32	14	66	41	59	17	0-17	Fhb1 het	no	no	no	no	no	no	no	yes	yes
47	VA12FHB-4	129	12	33	21	67	30	59	17	0-16	Fhb1 het	no	no	no	no	no	no	no	.	no
48	VA13W-177	127	2	35	46	68	18	54	39	0-17	no	no	no	no	no	no	yes	no	.	no
49	VA08MAS5-39-6-4	127	2	31	10	70	5	59	17	0-16	no	no	no	no	no	no	no	no	yes	no
	Mean	129		33		68		58												
	LSD (0.05)	3		2		.		.												
	CV%	1.1		3.6		.		.												

MOISTURE CONTENT OF GRAIN SAMPLES AFFECTS THE PERFORMANCE OF NEAR-INFRARED SPECTROSCOPIC CALIBRATION FOR ESTIMATION OF DON LEVELS 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 Stored Product Insect and Engineering Research Unit, Manhattan, KS

[*]Corresponding Author: PH: (785) 776-2753; Email: Floyd.Dowell@ARS.USDA.GOV

ABSTRACT

We have developed a near infrared (NIR) spectroscopic calibration for the single kernel near infrared spectrometer (SKNIR) for estimation of deoxynivalenol (DON) levels in single wheat kernels. This SKNIR calibration for DON estimation is helpful for nondestructive, rapid estimation of DON levels in small grain samples in that some Fusarium head blight resistance components in wheat germplasm can be evaluated by analyzing the single kernel DON distribution patterns among kernels in grain samples. Further improvement of the robustness and accuracy of DON predictions of the calibration requires the study of the effects of known sources of variation in grain samples on the performance of calibration. Moisture variations in samples of numerous materials have been shown to influence the NIR predictions of composition and quality factors of materials. Moreover, our previous studies, as well as independent studies by other workers with NIR absorption of DON, have shown that the NIR absorption bands of DON are positioned near the NIR absorption bands of water. Since grain samples for DON measurement may have differences in moisture levels at the time of analysis, a study was conducted to investigate the influence of grain sample moisture levels on the accuracy of NIR predictions of DON levels. DON levels of small bulk samples of manually sorted visually sound, scabby, and unsorted grain samples of two wheat cultivars were estimated at four different moisture levels varying from 9.4 -18.2%. NIR predicted single kernel DON levels of individual kernels and average kernel weight of sound and scabby kernels were used to estimate the DON levels of the bulk grain samples. After DON analysis by the SKNIR, DON levels of the grain samples were determined by the standard laboratory method using gas chromatography - mass spectrometry. At higher moisture levels NIR predicted DON levels of scabby kernels were considerably lower while most scabby kernels were predicted as having no DON at moisture contents above 15%. NIR predicted DON levels of scabby kernels increased as moisture contents of the samples decreased. These results showed that moisture content variations of grain samples influence the accuracy of DON predictions of the grain samples. Therefore, appropriate strategies should be followed to mitigate the effect of variation of moisture levels of grain samples to facilitate improvement of the calibration performance.

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QTL ANALYSIS OF FHB AND DON ACCUMULATION RESISTANCE IN THE TURKISH LINE CGN00483

Roshan Sharma Poudel, Jonathan Richards, Patrick Gross and Robert S. Brueggeman*

Department of Plant Pathology, North Dakota State University, Fargo, ND
*Corresponding Author: PH: 701-231-7078; Email: robert.brueggeman@ndsu.edu

ABSTRACT

One of the limiting factors in the development of barley varieties with lower DON accumulation is the availability of resistance sources in the primary barley germplasm pool. The screening of 1550 landraces collected from several countries located in the centers of diversity of *Hordeum* from the Dutch Centre for Genetic Resources, identified a 2-rowed accession collected in Turkey, CGN00483, consistently showing lower DON levels than Conlon. A CGN00483 X Harrington cross was made and advanced to the F_7 generation representing a recombinant inbred line (RIL) population consisting 170 individuals. The RIL population was genotyped using an Ion Torrent 384 SNP PCR genotype-by-sequencing marker panel placing 131 markers on a skeletal genetic map. Utilizing the map and the preliminary DON data collected from two nursery locations on the F_4 generation progeny we identified two putative low DON accumulation QTL at ~ 4 cM on chromosome (ch.) 4H and 17-32 cM on ch. 7H. The major DON QTL on ch. 4H is novel suggesting that CGN00483 contains a new source of DON accumulation resistance that has not been utilized in breeding programs. Further, marker saturation and DON analysis from several FHB nursery site years is being conducted on the RILs to further characterize these QTL. CGN00483 has also been crossed with the cvs Conlon and ND-Genesis and the advanced breeding line 2ND27705 and a backcrossing and MAS scheme will be utilized to introduce the QTL into the elite two-rowed backgrounds. Barley breeders would like to see the levels of DON in released lines lowered and this resistance stacked with other resistance sources already present in 2-rowed lines with lower DON accumulation will be further investigated.

QUANTITATIVE TRAIT LOCI ASSOCIATED WITH FUSARIUM HEAD BLIGHT RESISTANCE IN AN ARGENTINE WHEAT LINE

Staltari, S.[1*], Aulicino, M.B.[1], Astiz Gassó, M.M.[1], Barca, H.[1], Perniola, O.S.[1,] Conway, B.[2], Verges, V.L.[3], Chao, S.[4], Molina, M. del C.[1,5] and Costa, J.M.[4]

[1]Instituto Fitotécnico de Santa Catalina, National University of La Plata, Argentina; [2]University of Maryland, USA; [3]Don Mario S.A., Argentina; [4]USDA-ARS, USA; and [5]CONICET, Argentina
[*]Corresponding Author: PH: 54 11 153257-8566; Email: sstaltari77@gmail.com

OBJECTIVES

To characterize quantitative trait loci (QTL) associated with Fusarium head blight resistance of an experimental spring wheat line (AR5) from Argentina.

INTRODUCTION

Fusarium head blight (FHB), mainly caused by *Fusarium graminearum* Schwabe [telomorph: *Gibberella zeae* Schw. (Petch)], is a destructive disease of wheat (*Triticum aestivum* L.) in Argentina and nearly all temperate wheat-producing regions worldwide. FHB causes both severe yield reductions and decreases grain quality (McMullen et al., 1997). Additionally, infected grains may contain significant levels of mycotoxins such as deoxynivalenol (DON), that can prevent its use for human consumption or feed (Goswami and Kistler, 2004).

The use of host resistance is the most economically and environmentally sound solution to this problem (Zhang et al., 2008). The Argentine spring wheat line AR5 possesses resistance to FHB in field tests and could carry novel genes for FHB resistance (Staltari et al., 2014).

The objective of this study was to characterize QTL associated with different types of resistance, in a wheat recombinant inbred line (RIL) population developed from the cross of AR5 with the highly susceptible Sonalika.

MATERIALS AND METHODS

Plant Material - A RIL wheat population was produced from the cross of AR5 and Sonalika. AR5 (Laj1409/Laj2231//Klat/Pel73001/3/Laj1409/Pel74142//Lr/Pel73001) is a hard red spring experimental wheat line developed by the National Agricultural Technology Institute (INTA Marcos Juarez, Córdoba Province, Argentina). Sonalika is an Indian early maturity spring wheat line highly susceptible to FHB (Zhang et al., 2008).

The initial cross was performed in the greenhouse in the winter of 2008. A 135 RIL population was generated by single-seed descent in the greenhouse through the F6 generation. Further seed increases were also conducted in the greenhouse.

Disease Evaluation and FHB Inoculum - The field trial was sown in November 1 2011 at the Lower Eastern Shore Research and Education Center (LESREC), UMD, Salisbury, MD. The experimental design was a randomized complete block with three replications for 135 RIL and parental lines. Each plot was a 1-m-long row and the sowing date was 300seeds m^{-2}. Inoculum was prepared from a mix of different isolates obtained from symptomatic spikes collected from commercial wheat fields at various Maryland locations in 2011. *Zea mays* L. kernels were

autoclaved and colonized by *F. graminearum* following Zhang et al. (2008). The nursery was inoculated by spreading Fusarium-colonized kernels at a 100 kg ha^{-1} rate 24 d prior mean heading date. To promote production of ascospores, the plots were mist-irrigated daily for 3 min with a 30-min recess between 2000 and 0800 hours. Misting was stopped 27 d post-heading (Fuentes et al., 2005; Zhang et al., 2008). The RIL population and parental lines were evaluated for incidence (Type I resistance) and severity (Type II resistance), 3 weeks after anthesis (Bonin and Kolb, 2009). As plants reached maturity, 15 spikes per plot were hand-harvested and threshed manually with a head thresher. Percentage of *Fusarium*-damaged kernels (FDK) of each plot was determined by counting 200 random seeds from each sample to estimate thousand kernel weight (TKW). A 15-g seed sample from each plot was analyzed for DON concentration at the University of Minnesota (Dr. Yanhong Dong, Department of Plant Pathology) in 2012 (Zhang et al., 2008). In order to improve homogeneity of variance and normal data distribution, incidence, severity, FDK and TKW variables were transformed. DON data was transformed using a log (x + 1) transformation where x represented DON (μg g^{-1}), remainder using arcsine (√x/100) where x represented incidence, severity, FDK and TKW variables in percent.

Molecular Marker Genotyping – The parental lines and the 135 RIL population were screened for single nucleotide polymorphism (SNP) using the 9k SNP chip (Cavanagh et al. 2013) at the USDA-ARS Small Grains Genotyping Lab in Fargo, ND.

Linkage Map Construction and Quantitative Trait Locus Analysis - A linkage map was constructed using GQMol 2007.0.0 (http://www.ufv.br/dbg/gqmol/gqmol.htm) (Cruz and Schuster, 2007). Markers were grouped using a logarithms of odds (LOD) value of 3.0 and distance <30 cM. 316 polymorphic markers distributed regularly throughout the genome were selected and all of them showed expected (1:1) Mendelian segregation. From them, 26 linkage groups were formed. Using the consensus map constructed by Cavanagh et al. (2013), the linkage groups were placed on wheat chromosomes. The QTL analyses were conducted using composite interval mapping (CIM) and permutation test with GQMol 2007.0.0 (Cruz and Schuster, 2007).

RESULTS AND DISCUSSION

Field FHB Evaluation - The RIL population showed a wide and continuous distribution for incidence, severity, FDK, TKW and DON values. Transgressive segregants within the RIL population were observed for all disease traits (Figure 1).

QTL Analysis and Detection - Significant QTL associated with FHB resistance components were detected using CIM (Figure 2). No major QTL associated with Type I and Type II resistance were detected. Two genomic regions on chromosomes 2D and 7A were identified as being associated with FDK resistance and TKW. Three QTL for resistance to DON accumulation were identified on chromosomes 3B, 4D and 7D. Sonalika contributed the resistance alleles for 7A QTL for TKW and AR5 contributed the resistance alleles for remainder of the QTL mentioned above (Table 1).

The major QTL on 3B accounted for 35% of the phenotypic variation in DON accumulation, was flanked by *wsnp_Ku_c12544_20235135* and *wsnp_RFL_Contig2177_1500201*. The QTL peak (82.19 cM) was located away from the region of the well-known QTL from Sumai 3 that is distally located on 3BS (Abate et al 2008).

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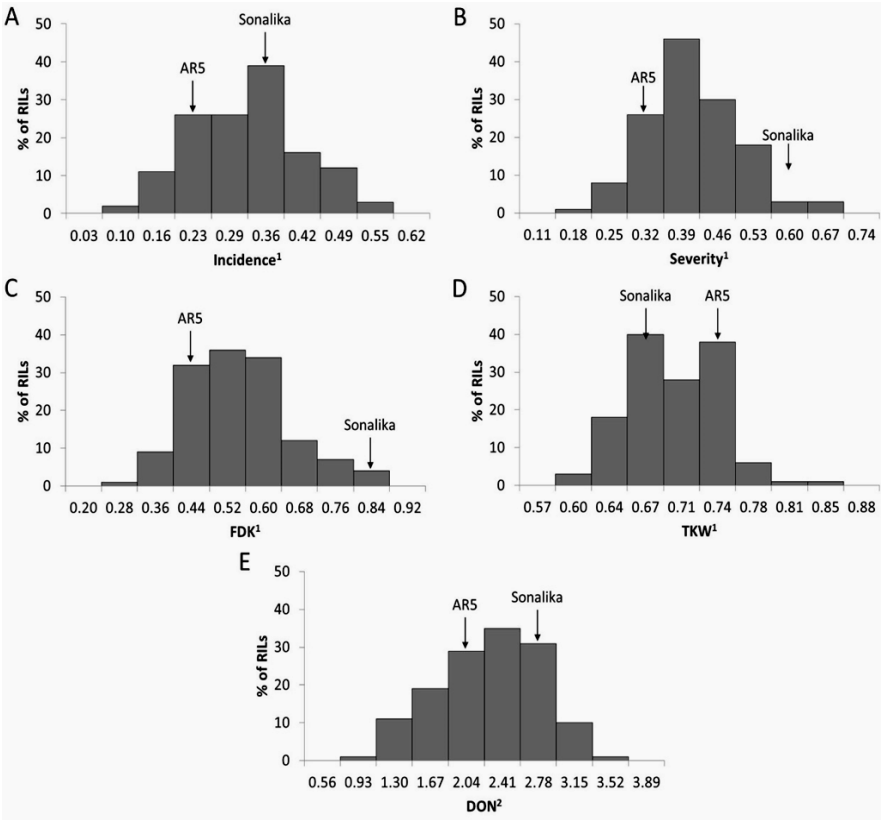

Figure 1. Frequency distributions of 135 wheat RILs developed from a cross between AR5 and Sonalika for (A) incidence, (B) severity, (C) FDK, (D) TKW and (E) DON content. Variables normalized using [1] arcsine ($\sqrt{x}/100$) transformation and [2] log (x + 1) transformation. Average values for the parental lines are indicated with arrows for each trait.

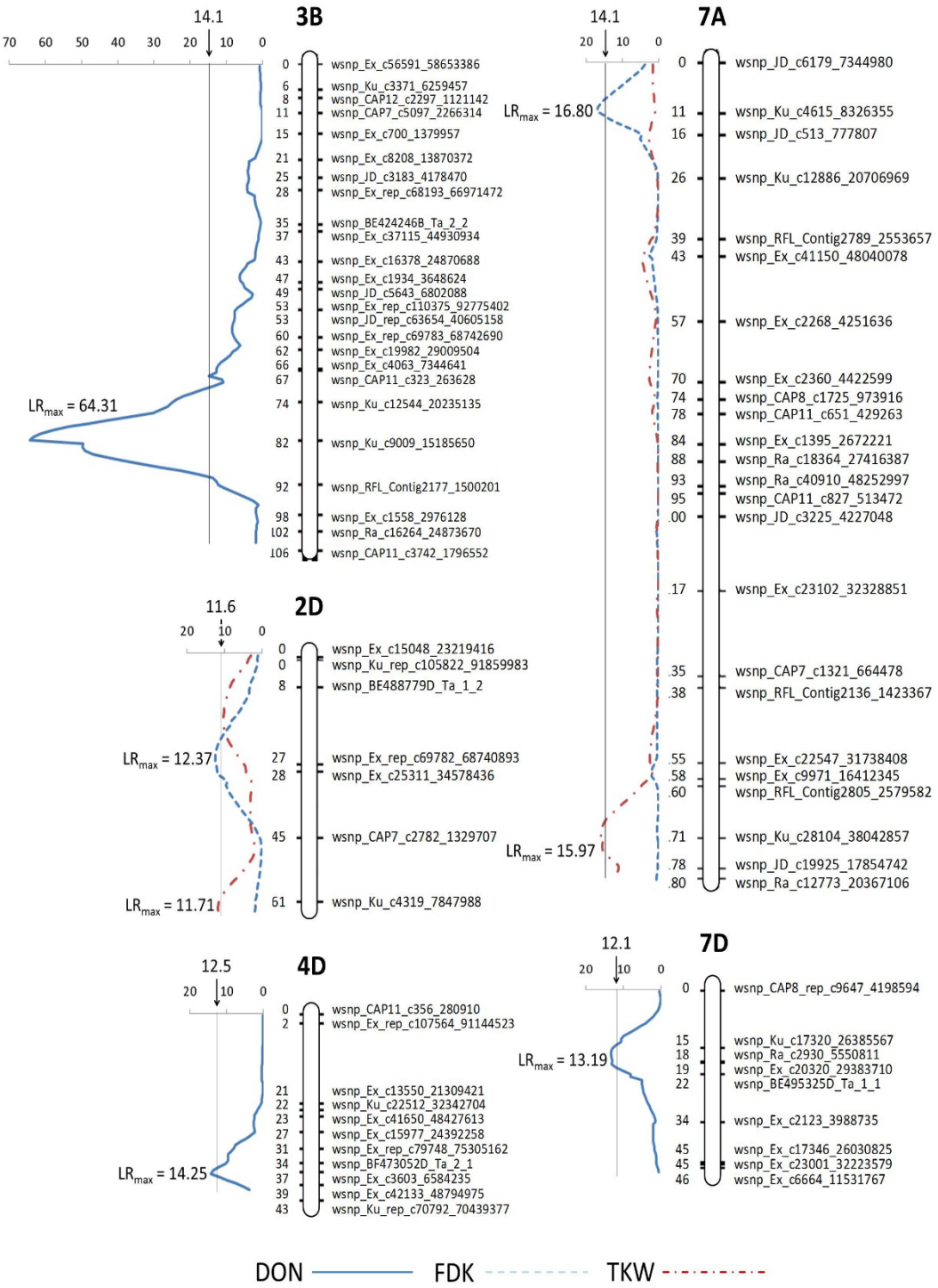

Figure 2. QTL associated with FDK, TWK and DON content in the cross AR5/Sonalika detected by composite interval analysis. The likelihood ratio (LR) scores were plotted against centimorgans on each chromosome. SNP marker locations on chromosomes are based on the Cavanagh et al. (2013) consensus map.

Table 1. Summary of quantitative trait loci (QTL) detected for Fusarium head blight resistance in a wheat RIL population developed from a cross between AR5 and Sonalika.

Trait	Chr[+]	Linked marker	Source	LR value	LOD value	R^2%[¤]
FDK	2D	*wsnp_Ex_c25311_34578436*	AR5	12.4	2.7	8.4
	7A	*wsnp_Ku_c4615_8326355*	AR5	16.8	3.6	10.1
TKW	2D	*wsnp_Ku_c4319_7847988*	AR5	11.7	2.5	10.0
	7A	*wsnp_Ku_c28104_38042857*	Sonalika	16	3.5	9.7
DON	3B	*wsnp_Ex_c700_1379957*	AR5	64.3	14	35.0
	4D	*wsnp_Ex_c42133_48794975*	AR5	14.2	3.1	9.7
	7D	*wsnp_Ex_c20320_29383710*	AR5	13.2	2.9	10.3

[+]Chromosomal location of marker.
[¤]Percent phenotypic variance.

CHARACTERIZATION OF NEW SYNTHETIC WHEAT GERM-PLASM FOR RESISTANCE TO FUSARIUM HEAD BLIGHT

A. Szabo-Hever[1,2], Q. Zhang[2], S. Zhong[3], T.L. Friesen[1], E.M. Elias[2], S.S. Xu[1*] and S. Chao[1]

[1]USDA-ARS, Cereal Crops Research Unit, Fargo, ND; [2]Dept. of Plant Sciences, North Dakota State University, Fargo, ND; and [3]Dept. of Plant Pathology, North Dakota State University, Fargo, ND
[*]Corresponding Author: PH: (701) 239-1327; Email: Steven.Xu@ars.usda.gov

ABSTRACT

The wild and domesticated progenitors and related species of hexaploid bread wheat (*Triticum aestivum*) have been used as a genetic source for improving modern wheat cultivars for resistance to Fusarium head blight (FHB). In order to transfer useful genes from tetraploid wheat (*T. turgidum*) into bread wheat, we developed 153 synthetic hexaploid wheat (SHW) lines using durum wheat (*T.turgidum* subsp. *durum*) and other five tetraploid subspecies (*T turgidum* subsp. *carthlicum*, *dicoccum*, *polonicum*, *turgidum* and *turanicum*) in crosses with *Aegilops tauschii*. The goals of this project are to identify the SHW lines carrying the FHB resistance and to map putative novel FHB-resistant QTL in the FHB-resistant SHW lines. The evaluation experiments were performed using a randomized complete block design (RCBD) with three replications. The common wheat cultivars 'Sumai 3' and 'Grandin' were used in all the experiments as resistant and susceptible checks, respectively. At this stage of the project, 153 of the SHW lines and their 75 tetraploid wheat parents have been evaluated in one greenhouse season and in one field nursery season at two locations (Fargo and Prosper, ND). The statistical analyses of disease severity in the greenhouse and field nurseries showed a significant correlation among the three experiments. A number of SHW lines with high and moderate levels of FHB resistance have been identified. Among these SHW lines, 10, one, and five lines in the greenhouse and in Fargo and Prosper field nurseries, respectively, showed higher level of resistance than the resistant check Sumai 3, with three lines having a high level of resistance both in the greenhouse and in one of the field nurseries. Seventeen SHW lines showed significantly higher resistance than their tetraploid parents, suggesting that the D genome of *Ae. tauschii* may carry the resistance QTL or enhance the FHB resistance through genomic interactions in these lines. Thirteen SHW lines showed high resistance in line with their highly resistant tetraploid parent. The plant materials will be further evaluated in two more greenhouse seasons and in one field nursery season at two locations in order to validate the results. All the SHW lines and their tetraploid wheat parents are currently being genotyped using the Illumina wheat 9K-SNP array. All the phenotypic and genotypic data will be used for mapping of the QTL associated with the FHB resistance. The SHW lines with high levels of FHB resistance will be made available to the U.S. wheat breeding programs for developing adapted wheat germplasm and cultivars.

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CAN MULTIPLE RESISTANCE QTL IN COMBINATION WITH FUNGICIDE APPLICATIONS REDUCE FUSARIUM HEAD BLIGHT SEVERITY IN SPRING WHEAT?

Yaqoob Thurston, Karl D. Glover, Shaukat Ali and Jose L. Gonzalez-Hernandez*

Department of Plant Sciences, South Dakota State University, Brookings, SD 57007
*Corresponding Author: PH: 605-690-3426; Email: jose.gonzale@sdstate.edu

ABSTRACT

Genetic resistance to Fusarium head blight (FHB), caused by *Fusarium graminearum*, is crucial to reduce the wheat grain yield and quality losses caused by this disease. The development of wheat cultivars with resistance to FHB is very difficult to achieve because of the laborious screening methods and the complex mechanisms of resistance, both of which are subject to environmental variability. DNA markers for FHB resistance QTL have been identified and may be used to speed the introgression of resistance genes into adapted germplasm. Previously, screened double haploid (DH) spring wheat lines derived from 4 way crosses showed promise in reducing FHB severity but more evaluation of this material is needed. Selection for resistance QTL and the use of fungicide (Prosaro®) are two different approaches when combined may present a better way of minimizing disease damage as well. Therefore, we conducted a field experiment to evaluate the effect of combining resistance QTL and fungicide application on FHB severity. FHB severity was significantly influenced by both resistant QTL and fungicide application. However, our results showed that the combination of resistant QTL provided reduction in severity without the presence of fungicide as well. Due to a lack of resources in regards to combining resistance QTL and fungicide application approaches, we hope that our finding can provide a better understanding of selection for resistant QTL and the interaction of plant host and pathogen.

VALIDATION OF FUSARIUM HEAD BLIGHT RESISTANCE QTL IN WHEAT USING DOUBLE HAPLOIDS DERIVED FROM FOUR-WAY CROSSES

Yaqoob Thurston[1], Jonathan T. Eckard[1,4], Karl D. Glover[1], James A. Anderson[2], Mohamed Mergoum[3], Melanie Caffe[1], Shaukat Ali[1], Sunish K. Sehgal[1], Francois G. Marais[3] and Jose L. Gonzalez-Hernandez[1*]

[1]Department of Plant Sciences, South Dakota State University. Brookings, SD 57007; [2]Department of Agronomy & Plant Genetics, University of Minnesota. St. Paul, MN 55108; [3]Department of Plant Sciences, North Dakota State University. Fargo, ND 58102; and [4]Current address: Monsanto Vegetable Seeds Division, Monsanto Company, Woodland CA 95695
[*]Corresponding Author: PH: 605-690-3426; Email: jose.gonzalez@sdstate.edu

ABSTRACT

Fusarium head blight (FHB), caused primarily by *Fusarium graminearum*, is one of the most devastating plant diseases in the world. Specifically in wheat, FHB has become responsible for significant economic and health concerns worldwide due to mycotoxin accumulation in infected grain, as well as yield and quality losses. To date, sources of resistance conferring complete resistance to FHB have not been identified in wheat. Thus, extensive research efforts worldwide has focused on development and use of resistant cereal cultivars for the control of FHB. QTL for FHB resistance have been mapped to almost all wheat chromosomes when different mapping populations were investigated. In our research, we are using double haploid (DH) wheat lines derived from selected four-way crosses combining several sources of resistance to validate putative QTL (Xmc758. Gwm33, xbacr176, Xgm120, Xwmc317, Xwmc332, Xwmc522 and Xwmc296) that could minimize the threat of FHB including the reduction of mycotoxins to the producers, processors, and consumers of wheat. We used molecular techniques to validate DH lines and their corresponding parents. In this study, we report on our work on the DH derived lines screened for FHB in multiple Northern Plains location. Our findings will assist ongoing efforts aimed to develop resistant wheat varieties, minimize the impact of the disease, and provide resources that can possibly assist in the advancement of wheat germplasm research.

PREDICTING GENETIC VARIANCE IN BREEDING POPULATIONS: USING HISTORICAL BREEDING RECORDS TO EMPIRICALLY EVALUATE SIX PREDICTION METHODS

Tyler Tiede[1], Leticia Kumar[2], Mohsen Mohammadi[3] and Kevin P. Smith[1*]

[1]University of Minnesota, Department of Agronomy, St. Paul, MN; [2]University of Florida Horticultural Sciences Department, Wimauma, FL; and [3]Purdue University, Department of Agronomy, West Lafayette, IN
[*]Corresponding Author: PH: 612-624-1211; Email: smith376@umn.edu

ABSTRACT

Robust methods to predict genetic variance () of bi-parental breeding populations would facilitate greater gains per breeding cycle. To illustrate its utility, consider a crossing block of 100 elite parents – making all 4,950 pairwise crosses is impractical and evaluating all such crosses at a scale appropriate to quantify is impossible. Previously, metrics such as the phenotypic, genetic (measured as the proportion of non-matching markers), and kinship-based (estimated from genomewide markers) distances between parents have been tested for their ability to predict . In general there is little to no correlation between these metrics and . One explanation for this is the inability of such methods to explicitly model the segregation of associated genetic loci (i.e. QTL). Now, the commonplace use of genomewide markers and genomic selection (GS) in breeding programs, along with recent theoretical work in the area, has enabled the development of three additional methods that, at varying levels, explicitly model the segregation of QTL. The accuracies of six prediction models were evaluated using field-based estimates of from 40 bi-parental barley breeding populations. The accuracies of phenotypic distance, genetic distance, and kinship-based distances between the two parents were all low and non-significant. In contrast, the accuracies of the three methods that explicitly integrate the effects of associated genetic loci were all significant. The method that directly measures variation using the GEBVs of simulated bi-parental populations was the most accurate. The results indicate that predictions based on genome-wide markers may enable plant breeders to target specific parent combinations, or at the least winnow out low- predicted crosses.

A DIVERSE COLLECTION FOR USE IN GENOMIC SELECTION APPROACH TO DEVELOP FHB RESISTANCE AND LOWER DON ACCUMULATION IN TWO-ROW BARLEY

J.R. Tucker[1,2*], A. Badea[1], W.G.D. Fernando[2] and W.G. Legge[1]

[1]Agriculture and Agri-Food Canada, Brandon Research and Development Centre, 2701 Grand Valley Road, P.O. Box 1000A, R.R. 3, Brandon, MB R7A 5Y3, Canada; and [2]Department of Plant Science, 222 Agriculture Building, University of Manitoba, Winnipeg, MB R3T 2N2, Canada
[*]Corresponding Author: PH: (204) 578-6592; Email: james.tucker@agr.gc.ca

ABSTRACT

Fusarium head blight (FHB) primarily incited by *Fusarium graminearum* Schwabe, has remained an economically destructive disease of barley (*Hordeum vulgare* L.) in the Canadian prairies since the mid-90's. As a result of infection, mycotoxins such as deoxynivalenol (DON) render grains unsuitable for use in animal feed or malting and brewing industries. In recent years, this disease has moved westward and become a more common occurrence in contaminated grains within the barley production regions of Saskatchewan and occasionally Alberta. Breeding FHB resistant cultivars has been a long-term goal of all western Canadian barley breeding programs. This objective has been facilitated through use of a large screening nursery at Brandon, MB, however progress has been impeded by numerous factors. Nonetheless, several cultivars have been released to date which demonstrate reduced DON accumulation. Given the significant time and resources that have been invested in developing such cultivars, it may be impractical to assume that reliance on only traditional breeding methods will be adequate to continue advancements. Further DON reductions are predicted to be more difficult to achieve given the low concentration at which the mycotoxin is found in the grain. Genomic selection has been proposed as an alternative method to improve precision of selection and hasten cultivar development. A substantially large (n=400) and diverse set of two-row barley genotypes was phenotyped in three environments in Manitoba (Brandon, Carberry and Carman) over two growing seasons (2014-15). FHB and DON data collected on these genotypes will be used in conjunction with genomic data to develop models for application of selection to breeding populations segregating for FHB resistance. Genomic selection will be evaluated as a method for enhancing FHB resistance in the two-row-malting barley breeding program at Agriculture and Agri-Food Canada's Brandon Research and Development Centre.

IDENTIFICATION OF QUANTITATIVE TRAIT LOCI FOR RESISTANCE TO FUSARIUM HEAD BLIGHT IN WINTER BARLEY CULTIVAR EVE

Ullrich, J.[1], S. Malla[1], C. Griffey[1*], W. Brooks[1], D. Van Sanford[2], A. Clark[2], P. Murphy[3], R. Brueggeman[4], C. Cowger[5], N. McMaster[6], D. Schmale III[6], S. Chao[7] and G. Brown-Guedira[5]

[1]Dept. of Crop and Soil Environmental Sciences, Virginia Tech, Blacksburg, VA 24061; [2]Dept. of Plant and Soil Science, University of Kentucky, Lexington, KY 40546; [3]Dept. of Crop Science, North Carolina State University, Raleigh, NC 27695; [4]Dept. of Plant Pathology, North Dakota State University, Fargo, ND 58108; [5]Plant Science Research Unit, USDA-ARS, Raleigh, NC 27695; [6]Dept. of Plant Pathology, Physiology, and Weed Science, Virginia Tech, Blacksburg, VA 24061; and [7]Biosciences Research Lab, USDA-ARS, Fargo, ND 58105
[*]Corresponding Author: PH: 540-231-9789; Email: cgriffey@vt.edu

ABSTRACT

Interest in winter barley (*Hordeum vulgare*) production for use in livestock rations, health foods, and malt products emphasizes the importance and need for development of elite cultivars having resistances to prevalent diseases. Fusarium head blight (FHB), caused by the pathogen *Fusarium graminearum* Schwabe, can result in severe yield and quality losses for barley producers via kernel damage and production of mycotoxins. The objectives of this study are to identify the FHB resistance QTL in the hulless winter barley cultivar Eve and to develop diagnostic markers for use in marker-assisted selection. Mapping populations, comprised of recombinant inbred lines (RIL), were derived from crosses of Eve to FHB susceptible parents (Eve/'Doyce' and Eve/VA07H-35WS) for use in mapping resistance to FHB. These RIL populations were evaluated for FHB incidence and FHB severity with the assistance from cooperators in KY, NC, VA and China during the 2014-2015 growing season. Genotype by location interaction was significant for FHB incidence, but not for FHB severity. In the Eve/Doyce (E/D) population a significant correlation for FHB incidence was observed between data from Lexington, KY and Mt. Holly, VA (r = 0.13817, $P = 0.045$). Significant correlations among locations in the Eve/VA07H-35WS (E/VA) population were not observed for FHB incidence. Significant correlations for FHB severity in the E/D population were observed between the Lexington and Mt. Holly locations (r = 0.21224, $P = 0.0019$) and between Lexington, KY and Kinston, NC (r = 0.17621, $P = 0.0103$). In the E/VA population, a significant correlation was observed between Lexington and Mt. Holly (r = 0.16072, $P = 0.0139$) for FHB severity. The populations will be genotyped with 9K SNP and second year phenotypic data will be collected in 2015-16 season. The FHB resistant QTL will be validated and diagnostic markers will be identified for use in marker-assisted selection.

DEVELOPMENT OF USER-FRIENDLY DNA MARKERS FOR FUSARIUM HEAD BLIGHT RESISTANCE QTL IN PI 277012

Mingxia Zhao[1], Yan Liu[1], Yueqiang Leng[1], Jianjiang Li[1], Rui Wang[1], Yuming Long[2], Shiaoman Chao[2], Steven S. Xu[2] and Shaobin Zhong[1*]

[1]Department of Plant Pathology, North Dakota State University, Fargo, ND; and [2]USDA-ARS, Cereal Crops Research Unit, Fargo, ND
[*]Corresponding Author: PH: 701-231-7427; Email: Shaobin.Zhong@ndsu.edu

ABSTRACT

The hexaploid wheat line PI 277012 exhibits a high level of Fusarium head blight (FHB) resistance in both greenhouse and field experiments. Previous QTL analysis with SSR markers and a doubled haploid (DH) population consisting of 130 lines from a cross between PI 277012 and 'Grandin' identified two major FHB resistance QTL located on chromosome arms 5AS and 5AL, respectively. The resistance QTL (*Qfhb.rwg-5A.1*) on 5AS peaked at marker *Xbarc40* between markers *Xcfa2104* and *Xgwm617*, while the resistance QTL (*Qfhb.rwg-5A.2*) on 5AL peaked at marker *Xcfd39* between *Xwmc470* and *Xbarc48*. To saturate the two resistance QTL regions with more DNA markers, the DH population was further genotyped using the wheat **9K** SNP iSelect Assay. A total of 2,877 polymorphic SNPs were identified between PI 277012 and 'Grandin', and mapped to the original genetic linkage map developed with SSR markers. To develop additional markers, sequences of the SNP markers flanking the two QTL regions were used to search homologous sequences of the *Brachypodium distachyon* (Bd) genome using blastN and two *B. distachyon* syntenic regions were identified, which contain 248 and 2500 genes, respectively. Then, these Bd genes were used to search for homologous genes in wheat chromosome 5A survey sequences, and 41 and 139 contigs were identified from the 5AS and 5AL sequences, respectively. From these contigs, 250 primer pairs were designed and used to amplify DNA sequences from genomes of PI 277012 and Grandin. Twelve cleaved amplified polymorphic (CAP) markers were developed from those homologous sequences showing polymorphism between PI 277012 and Grandin and further mapped to the resistance QTL regions using the DH population. Three of the CAP markers were located on 5AS while nine were on 5AL. These 12 CAP markers along with seven PCR-based markers converted from SNPs, three SSR markers and a gene specific marker closely linked to the resistance QTL were used to genotype a larger population consisting of 947 recombinant inbred lines (RILs) derived from the cross between PI 277012 and Grandin, which were phenotyped for FHB reaction in greenhouse and field for two seasons using the single floret point inoculation method in 2014 and 2015. The two QTL previously identified using the DH population were also detected using the RIL population. RILs containing the PI 277012 (resistant parental line) alleles at all three marker loci most closely linked to the resistance QTL on 5AS had 19.6% reduction in FHB severity, while RILs with the PI 277012 alleles at all three marker loci most closely linked to the resistance QTL on 5AL showed 46.2% reduction in FHB severity compared to RILs with the Grandin (susceptible parental line) alleles. Average disease severity was reduced by 51.5% when the PI 277012 alleles at all six marker loci in the 5AS and 5AL resistance QTL regions

were combined. These selected markers can be further used for marker-assisted selection of the FHB resistance from PI 277012 in wheat breeding programs.

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CYTOGENETIC DISSECTION OF A, B, AND D GENOME PROVIDES NEW INSIGHTS INTO FUSARIUM HEAD BLIGHT RESISTANCE IN DURUM WHEAT

Xianwen Zhu[1], Shaobin Zhong[2] and Xiwen Cai[1*]

[1]Department of Plant Sciences, and [2]Department of Plant Pathology,
North Dakota State University, Fargo, ND, 58108
[*]Corresponding Author: PH: (701) 231-7404; Email: xiwen.cai@ndsu.edu

ABSTRACT

Durum wheat shares A and B genomes with common wheat, but lacks the D genome that common wheat has. It has been anticipated that the absence of D genome in durum wheat may influence expression of FHB resistance genes in the durum background. In the present study, we used 'Langdon' (LDN) durum-'Chinese Spring' (CS) D-genome disomic substitution lines (LDN-CS DSLs) that dissect CS D genome in LDN durum background by chromosome substitution to characterize the role of individual D-genome chromosomes and their A- and B-genome homoeologs on FHB resistance in durum. In addition, we developed the LDN-*Aegilops tauschii* 'RL5286' amphiploid that combines the entire D genome of RL5286 and LDN A and B genomes to determine whether addition of the entire D genome to durum affects FHB resistance. Also, we dissected the RL5286 D genome in the LDN durum background by producing LDN-RL5286 chromosome addition lines to determine the role of individual D-genome chromosomes on FHB resistance in durum. Both the amphiploid and addition lines had the same LDN durum background, making them ideal for characterizing the effect of D-genome chromosomes on FHB resistance. The reaction of LDN-CS DSLs to FHB indicated that the substitution of chromosome 5A by 5D enhanced resistance to FHB. This might result from absence of the Q gene on chromosome 5A that conditions spike structure. Also, we found that CS chromosome 6D might contain genes for FHB susceptibility and/or suppression of FHB resistance genes. LDN chromosomes 2B and possibly 6A and 6B might contain the genes that enhance FHB resistance. The LDN-RL5286 amphiploid exhibited higher susceptibility to FHB than LDN. However, the RL5286 chromosomes 1D and 5D were found to condition FHB resistance when they were individually or concurrently added to LDN. The FHB resistance genes on these two chromosomes seemed to act additively in LDN. The other RL5286 chromosomes (i.e. 2D, 3D, 4D, 6D, and possibly 7D) appeared to contain suppressors for the FHB resistance genes on chromosome 1D or 5D. Apparently, there are complex interactions among the genes on the RL5286 D-genome chromosomes as well as LDN A- and B-genome chromosomes for FHB resistance in durum background. Proper manipulation of the critical chromosomes may lead to the improvement of durum wheat for FHB resistance.