THE DEVELOPMENT OF SCAB (*FUSARIUM GRAMINEARUM*) RESISTANT VARIETIES OF WHEAT

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OBJECTIVE

The primary objective was to identify and develop elite winter wheat varieties that are tolerant to Fusarium head blight (FHB, scab). The second objective was to field screen the elite hard winter wheat lines including those in the Regional Germplasm Observation Nursery (RGON).

INTRODUCTION

Nebraska is second only to California for irrigated crop production. Hence FHB, though a periodic disease, can be an important disease greatly affecting approximately 35% of Nebraska's wheat acreage. As humans consume virtually all of this wheat and over one half is exported, safe, healthy grain is critical for maintaining the reputation of hard winter wheat in the domestic and export markets. All winter wheat lines to be released by the University of Nebraska shall be screened for FHB resistance. This information will be shared with producers.

The primary objective is to identify and develop elite winter wheat varieties that are tolerant to Fusarium head blight (FHB, scab), using conventional breeding methods. The second objective was to screen elite hard winter wheat lines in the Regional Germplasm Observation Nursery (RGON).

MATERIALS AND METHODS

Sources of FHB resistant germplasm originating from our biotechnology efforts, spring and soft wheat germplasm, and exotic germplasm, were collected for crossing into our elite lines. F2 and F3 seed produced from these crosses was screened for FHB resistance, in the field in 2002.

All solutions of inoculum used in the greenhouse and field, were created by combining 6 isolates of *Giberella zeae* and 5 isolates of *Fusarium graminearum* to create a 70000 conidia/mL solution. We screened the germplasm for FHB tolerance, in the greenhouse to allow for better parent identification. Nine replicates of each line were screened in the greenhouse using a randomized complete block design. One spikelet per head was injected with 0.1 mL of a 70000 conidia/mL solution. The plants were then misted for 72 hrs at 98% humidity. Concerns about induced resistance in response to injury, led us to adjust this method. In later studies, the replication number was increased from nine to twelve and 2 mL of 70000 conidia/mL, was sprayed onto the entire head and sealed it in a 16 x 9.5 cm^2 snack size Ziploc bag for 72 hrs. This procedure avoids false negatives, due to potential induced resistance from awns being cut or injection.

In the field, twenty six transgenics and eight hundred winter wheat breeding lines, which included the RGON nursery were planted and screened, against appropriate controls, for tolerance to FHB, using a system similar to that of Campbell and Lipps (1998). Each variety was planted in a 10 ft^2 plot. Inoculation was carried out in two ways; naturally occurring *F. graminearum* infected corn stalks were spread in the field in fall; and 70000 conidia/mL of inoculum, was sprayed 4 times, at a rate of 50 mL per plot, using a CO^2 powered back pack sprayer, in 2002. This was followed by mist irrigation, using a modified misting system similar to that employed by Zhang *et al*. (1999) to mist the plots for 2 minutes at 30 min intervals. This began 1 week before the plots were inoculated and continued until the first readings were taken. Bordering the scab nursery with forage triticale provided an excellent buffer and greatly reduced wind in the misting nursery.

FHB was rated by counting the number of infected spikelets on 30 individual heads (Shaner and Buechley, 2001). Plot severity or FHB index was calculated by the averaging the 30 FHB ratings. Intensity was calculated by taking a count of the infected heads and dividing it by 30 the total # of heads scored. The grain, from one of our three most advanced nurseries was analyzed for Deoxynivalenol (DON) by the Veterinary Diagnostic Service at North Dakota State University.

RESULTS AND DISCUSSION

Of the eight hundred lines that were screened in 2002, sixty have had extensive FHB screening in at least 3 mutually exclusive trials, including an independent determination using different isolates, by South Dakota State University. Fig 1, shows nineteen lines that have consistently shown significant FHB resistance relative to a FHB susceptible variety “Wahoo”. These lines will be screened again in the field in a replicated trial in 2003. Of the RGON lines, 42% show promise and will be screened in a replicated trail in 2003. The grain, from one of our three most advanced nurseries showed no correlation between levels of DON and the # of FHB infected florets per head (Fig 2).

CONCLUSION

FHB tolerance in winter wheat breeding nurseries was generally high. F2 and F3 seed produced from the FHB crosses was screened in the field in 2002. Additional seed will be produced from the new crosses that have been made for future planting in the field. As soon as we have recovered bulks with the level of agronomic performance required to survive our winters, are resistant to stem rust *(P. graminis* Pers. : Pers. f. sp. *tritici* Eriks & E. Henn), and yield well, head row selection for elite line identification, will begin.

In the 2002-2003 cycle, the most FHB tolerant transgenics will be crossed to varieties having some FHB tolerance, and to Wesley, a very widely grown, but FHB susceptible line. We will screen 420 lines from our elite germplasm (our three most advanced nurseries), 46 lines from the FHB screening nursery, 20 - 50 transgenic spring wheat lines (initially) from our biotechnology efforts, and 277 lines coming from the RGON in the field.

ACKNOWLEDGEMENTS

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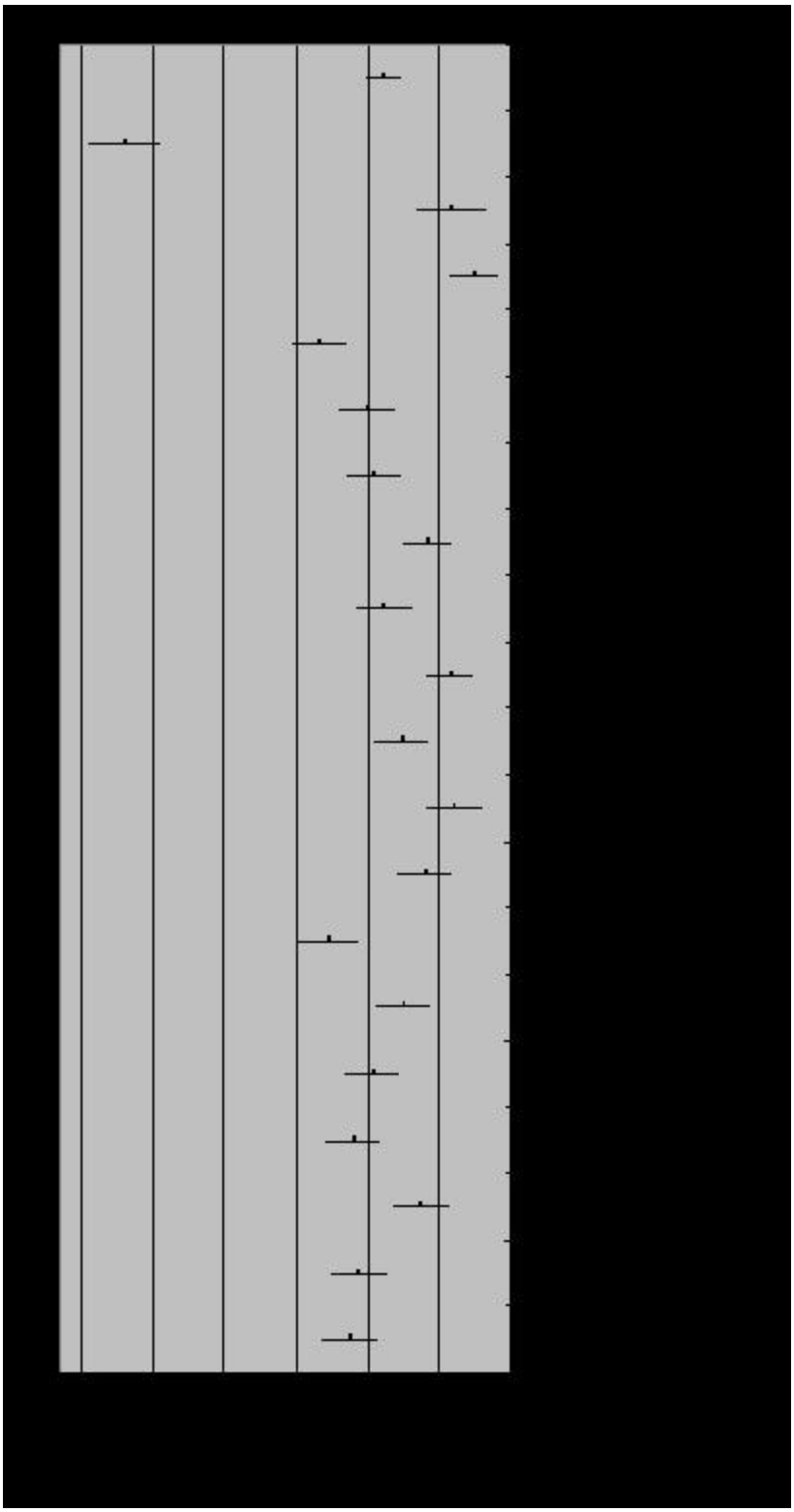

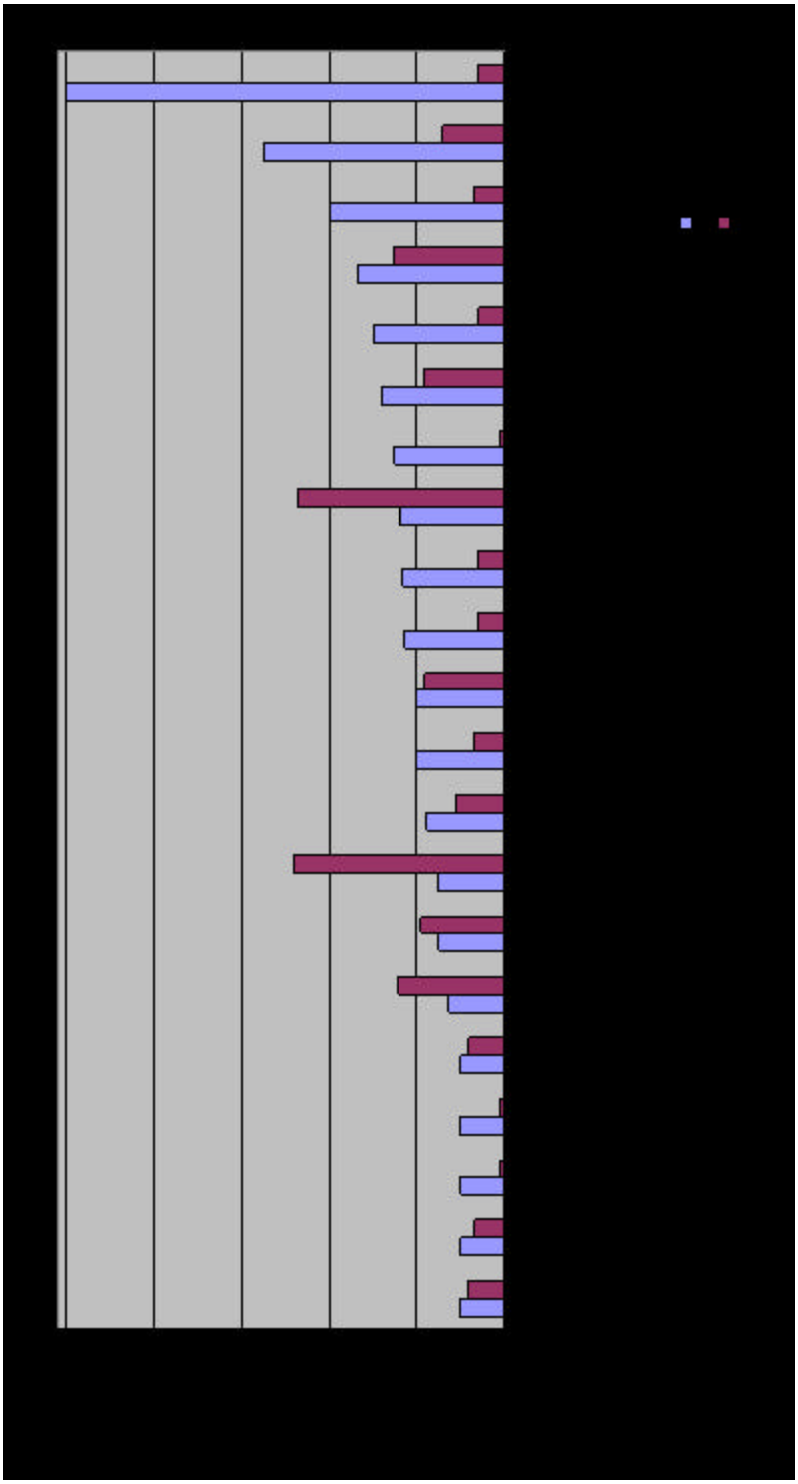

NUMBER OF LOCATION-YEARS NEEDED TO DETERMINE THE REACTION OF WINTER WHEAT CULTIVARS TO FUSARIUM HEAD BLIGHT

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ABSTRACT

Fusarium head blight (FHB) is a serious disease of wheat and barley that is best controlled by host resistance. In KSU Extension publications, the reaction to FHB for winter wheat cultivars is reported to producers using a 1-9 scale where 1-3 = resistant, 4-6 = intermediate, and 7-9 = susceptible. This research sought to determine how many location-years are needed to accurately determine the reaction of a cultivar to FHB. Twenty-nine different winter wheat cultivars were screened 2-12 times in 12 field nurseries over a 3-yr period (n=133). Experimental design for each location-year was a randomized complete block with four replications. Corn grains, colonized by *Fusarium graminearum* and spread on the soil surface, followed by sprinkler irrigation were used to produce the epidemic. FHB index (% diseased spikelets) was determined for each cultivar between four and six times for each experiment and averaged. To compare data across location-years, linear regression was used to fit a 1-to-9-scale model to the data for each location-year. To produce the model, an index value of zero was assigned a scale value of 1 and the highest index value in a location-year was assigned a scale value of 9. The model was then used to calculate scale values for all other cultivars in that location-year. A mean scale value was calculated for each cultivar (n=2-12 location-years) and an overall standard deviation for all cultivar-location-years (n=133) was calculated using the departure from the mean for each scale value for each cultivar-location-year. To estimate the number of location-years needed to determine the reaction of a cultivar to FHB, the formula x-bar +/- t(alpha/2) * s / sqroot(n) was used to calculate 95% confidence intervals. In this formula, x-bar is the observed mean scale value (1-9 scale) of a cultivar, t(alpha/2) is the t-value corresponding to the desired alpha level (0.05) divided by 2, s is the standard deviation among location years, and n is the sample size (number of location years). If an observed mean scale value is within +/- 0.5 units of the correct value, it will be rounded to the correct scale value. Required standard deviations to produce a mean within +/- 0.5 units were calculated for samples of n=2-20 (not shown). If an observed mean scale value is within +/- 1.5 units, it will be rounded to a scale value that is +/- 1 unit from the correct scale value. To achieve a mean scale value within +/- 1.5 units, required standard deviations for samples of n=2, 3, 4, and 5 are 0.167, 0.604, 0.943 and 1.208, respectively. In our data, the overall standard deviation for departure from the mean for all cultivar-location-years (n=133) was 1.05. Based upon the overall standard deviation, 20 location-years would be needed to have a mean scale value that would have a 95% chance of being within +/- 0.5 units of the correct mean and, therefore, rounded to the correct scale value. Based upon the overall standard deviation (1.05), 5 location-years would be needed to have a mean scale value that would have at least a 95% chance of being within +/- 1.5 units and, therefore, rounded to +/- 1 unit of the correct scale value. For most purposes, +/- 1 unit is sufficient accuracy for producers; therefore, we recommend that reactions of winter wheat cultivars that are reported to producers be based upon data from at least five location years.

IDENTIFICATION OF DNA MARKERS FOR FUSARIUM HEAD BLIGHT RESISTANCE OF WHEAT LINE HUAPEI 57-2

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ABSTRACT

Fusarium head blight or scab greatly affects grain yield and quality of wheat (*Triticum aestivum* L.). Because it is a trait of low heritability and costly to evaluate, marker assisted selection is particularly attractive for breeding programs. To identify DNA markers for Fusarium head blight resistance, a population of 163 recombinant inbred lines was developed by single seed descent from the cross between the resistant line 'Huapei 57-2' and the moderately susceptible cultivar 'Patterson'. All lines including parents were evaluated in one field experiment and two greenhouse tests for resistance to spread of disease (Type II resistance). Based on phenotypic data, extreme lines were selected to initiate bulked segregant analysis using microsatellites. Markers suggesting association with a putative quantitative trait locus (QTL) were then tested on the entire population to confirm the linkage. A major QTL was identified on the chromosome 3BS in a region well known from previous studies. Additional QTLs were also found on chromosomes 3A, 3BL and 5B.

COORDINATED FUSARIUM HEAD BLIGHT SCREENING NURSERY FOR WHEAT BREEDING PROGRAMS IN WESTERN CANADA

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ABSTRACT

Fusarium head blight (FHB) continues to be a serious disease of wheat in western Canada and in particular, the eastern prairies. Screening for FHB resistance has been difficult for breeders working outside of the eastern prairie region. As a result, breeders and pathologists entered into a collaborative agreement to establish a common FHB screening nursery at Carman, Manitoba. This region is known to provide an environment that is more conducive to FHB development. The nursery was established in 2001, and lines were evaluated in 2001 and 2002. Advanced lines that are in the final stages of testing for cultivar registration were evaluated in replicated rows, while earlier generation breeding lines were evaluated in non-replicated rows. In 2001 approximately 6000 1 m row plots were grown in the nursery. In 2002 the number of plots was increased to approximately 9900. Five checks were placed every 50 plots within the nursery. In 2001 the checks were AC Morse, AC Vista, CDC Teal, FHB 37 and Glenlea. The same checks were used in 2002 with the exception that CDC Teal was replaced by AC Cora to provide a check with an intermediate FHB reaction. In 2001 FHB infected corn inoculum was applied to plots two to three weeks prior to anthesis. Date of heading and anthesis were recorded for each plot. A macroconidial suspension of *F. graminearum* was applied to plots at 50% anthesis and again three to four days later. After each macroconidial inoculation, plots were irrigated with a mist irrigation system to maintain high humidity. Eighteen to 21 days after inoculation each plot was visually rated for incidence (% of spikes infected) and severity (% area of spike infected) of FHB infection and an FHB index was calculated. In 2002 corn inoculum was not applied to the plots but all other inoculation and evaluation protocols were similar to 2001. In 2001 conditions in the nursery were highly conducive to FHB development. The mean FHB index on susceptible checks ranged from 28 to 41. The resistant check had an FHB index of 5. This provided a good distinction between susceptible and resistant lines. In 2002, weather conditions were drier and cooler than in 2001 and FHB levels were lower in the nursery, overall. The mean FHB index for the susceptible checks ranged from 11 to 21. The intermediate check produced a mean FHB index of 6, while the mean FHB index of the resistant check was 0.3. Therefore, there were still clear distinctions between resistant and susceptible lines. However, disease levels were higher in groups of lines that were inoculated earlier in the season, when conditions were warmer and more humid, than those inoculated later in the season. The variability noted in the nursery indicated that there may be more escapes in the 2002 nursery and that lines with intermediate reactions may be difficult to separate from resistant lines. This emphasizes the need for multi-year testing to fully characterize FHB reaction. In general this nursery is providing useful information to plant breeders and will facilitate development of FHB resistant cultivars.

TIMING OF INOCULATIONS OF DRYLAND WHEAT PLOTS AND THE EFFECT ON FUSARIUM HEAD BLIGHT (FHB) SEVERITY AND MYCOTOXINACCUMULATION DUE TO *FUSARIUM GRAMINEARUM* INFECTION

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ABSTRACT

Eight wheat (*Triticum aestivum*) genotypes were assessed for reaction to FHB in a dryland inoculation study. The test was a randomized complete split-split block design. Main-plots were timings of inoculation (TOI), sprayed at anthesis (SAA), 3 days post-anthesis (DPA), and 6 DPA. Sub-plots consisted of two spray-inoculation treatments, inoculated once or twice, and sub-sub plots were the eight wheat genotypes. Significant differences were found among TOI treatments for FHB severity (7.1 % SAA, 7.7 % sprayed 3 DPA, and 0.6 % sprayed 6 DPA with $l.s.d._{0.05}$ = 2.42) and deoxynivalenol (DON) accumulation (3.0 ppm SAA and 3 DPA, and 0.3 ppm sprayed 6 DPA with $l.s.d._{0.05}$ = 0.60). Average DON ppm accumulations in grain of wheat genotypes were 0.2 for BacUp, 0.2 for ND2710, 0.2 for Ingot, 0.2 for Forge, 0.8 for Oxen, 1.4 for Parshall, 5.3 for Norm, and 8.6 for Wheaton ($l.s.d._{0.05}$ = 1.07). Our data demonstrate that dryland inoculations of wheat can be useful for screening germplasm for reaction to FHB.

VARIETY DEVELOPMENT AND UNIFORM NURSERIES: FHB RESISTANCE IN BARLEY

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ABSTRACT

Acknowledgements: This report is an overview of research progress made on FHB resistance by researchers of cooperating barley improvement programs in the upper Midwest.

Development of barley (*Hordeum vulgare*) cultivars having resistance to Fusarium head blight (FHB), incited primarily by *Fusarium graminearum*, is the main goal of barley improvement programs in the upper Midwest. Unlike many other disease problems, strategies for control of FHB did not exist prior to 1993 when epidemics began to occur annually. Initial goals included: 1) identification of accessions resistant to FHB, 2) establishment of screening procedures, 3) determination of inheritance patterns for FHB resistance, and 4) development of more focused breeding schemes. Nearly ten years later, what have we accomplished? Or more important, have we developed strategies for control of FHB?

FHB screening nurseries were established in North Dakota (ND) and Minnesota using prepared inoculum and mist irrigation systems to enhance disease development. Cooperative nurseries were developed in Eastern China where natural inoculum and favorable weather often cause high levels of FHB. Greenhouse tests using various inoculation procedures were conducted. Laboratory testing of cultivars and breeding lines for deoxynivalenol (DON) content helped determine the effectiveness of genetic and cultural controls of FHB. We have learned that the FHB problem on barley in the upper Midwest has both regional and international aspects. Midwest spring barley cultivars, both two- and six-rowed, have a unique genetic system for control of maturity and plant height. FHB is a problem in barley growing areas where these adaptation genes are used: the Canadian Prairies, Central Mexico, and Uruguay. Thus, the cooperative regional FHB nursery (MinnDak) was expanded in 2002 to include a Canadian cooperator and a test site at Brandon, Manitoba, and renamed the North American Barley Scab Evaluation Nursery (NABSEN). Agreements to have the ICARDA/CIMMYT barley program in Mexico as a full participant in the NABSEN nursery for 2003 season are in place. Contacts have been made regarding a participant in Uruguay. Data from the MinnDak and NABSEN nurseries suggest that progress in development of FHB resistant cultivars has been slow. Differential heading dates or photoperiod responses across sites contribute to the variable data obtained on FHB incidence and DON values. Expanded cooperation on FHB testing should improve our understanding of these problems.

Barley accessions from southern Germany and eastern China were identified as having the high levels of FHB resistance. Some resistance is also present in current Midwest barley cultivars. Cultivars from Brazil (PFC88209) and Mexico (Atahualpa) are being used as sources of FHB resistance. Evaluations of mapping populations have found QTL for FHB resistance on all seven barley chromosomes. The largest ones were consistently located on

chromosome 2H near loci that control spike type (*vrs1*), spike length (*lin1*), plant height (*hcm1*), and heading date (*Eam6*) in Midwest barley cultivars. Most FHB resistant accessions differ from Midwest cultivars in the alleles present at these four loci. Since at least three QTL for FHB resistance on chromosome 2H may be involved, a major breeding problem exists. This linkage group help explain why many FHB resistant selections have two-rowed spikes and are tall and late. A further complication is the lack of recurrent parents having good resistance to leaf spot diseases incited by *Cochliobolus sativus*, *Pyrenophora teres*, and *Septoria passerinii*.

Utilization of the two-rowed cultivar Conlon as a malting barley has provided barley growers in ND with some relief from FHB epidemics. Conlon often has slightly lower FHB readings and significantly lower DON values than other malting barleys recommended in ND. Yet, much higher levels of FHB resistance are needed to keep malting barley as major crop in the upper Midwest. Progress is being made in developing breeding lines with more FHB resistance, accessions as Shenmai 3 with more resistance to FHB are being identified among early-heading two-rowed lines from eastern China, alternative genes for control of plant height and maturity are being investigated, alternative breeding strategies are being evaluated, and results from marker assisted selection experiments are positive. None of these studies, however, offers a quick, easy solution to the FHB problem in barley.

A *FUSARIUM* RESISTANCE GENE AND AN AWN PROMOTOR ARE ASSOCIATED ON CHROMOSOME 5A OF SPRING WHEAT

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ABSTRACT

Fusarium head blight (FHB) has been a serious concern in the spring wheat region of the northern Great Plains for nearly a decade. Most spring wheat cultivar are moderately to highly susceptible to FHB, and no lines are completely immune to infection. Farmers in the region continue to grow susceptible cultivars, in part because most of the lines released as having resistance to FHB have other more severe defects. One North Dakota line, 'ND2710', derived from the Chinese wheat Sumai 3, has shown high resistance to FHB in many environments. Our objective was to determine the chromosome(s) where the FHB resistance gene(s) in ND2710 reside using the set of 21 monosomic lines developed by S.S. Maan in the 1960's and based on the hard red spring wheat cultivar 'Chris'. For the present investigation, the entire set of 21 Chris monosomic plants as female were crossed to ND2710. The monosomic F1's were identified and 20 or more monosomic F1-derived F-2's were grown and advanced to F2:5 by single seed descent. Seed from the F5 lines was planted in a field FHB testing nursery in 1999. Plots of the parents and a non-monosomic Chris X ND2710 check population also were present. In this FHB nursery, disease was produced by inoculation with *Gibberella zeae* and regular mist irrigation. At 3.5 weeks post anthesis, spikes were cut and frozen for later scoring. Individual spikes were scored using a 0 - 100% scale for FHB severity and plot means calculated. On average there were 24 spikes per plot and 45 plots per monosomic cross. In 2000, there were 15 spikes scored per plot and 50 plots per monosomic cross. The control cross Chris (tip awned spikes) X ND2710 (awned spikes) produced F1's with all tip awned spikes, as did 19 of the 21 monosomic F1's. In subsequent generations these displayed segregation for awns. Crosses of monosomic 2A and monosomic 5A produced disomic and monosomic F1's which had awned spikes. Subsequent generations also had awned spikes. In 1999 and 2000, the Chris/ND2710 check population had a mean FHB severity score of 40%, just midway between the scores of the parents Chris (62%) and ND2710 (22%). This is typical of FHB scores in such resistant by susceptible crosses. Several of the monosomic crosses, however, had FHB severity scores significantly lower; in particular, ChrisM5A/ND2710 was nearly as low as the resistant parent ND2710. When the co-occurrence of awn type and FHB score was tested, they were found to be associated and not independent. We suggest that a FHB resistance gene is associated with an awn promotor in chromosome 5A of ND2710. The type of association between these two remains to be determined but we propose that Chris mono 5A has a T 2A 4A translocation chromosome and ND 2710 has an awn promoter on 5A. Chromosome banding is presently being used to verify the translocation. (This poster was presented at the 2001 ASA Annual Meeting, Charlotte NC Nov. 2001)

A HISTORICAL ANALYSIS OF THE UNIFORM REGIONAL SCAB NURSERY FOR SPRING WHEAT PARENTS

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OBJECTIVES

We sought to evaluate progress that has been made by spring wheat breeding programs seeking to enrich their germplasm pool for resistance to Fusarium head blight. Fusarium head blight resistance data of spring wheat germplasm representing several breeding programs in the Upper Midwest and Canada is available through annual reports of the Uniform Regional Scab Nursery for Spring Wheat Parents (URSN). We sought to use the data in these reports to monitor progress in scab resistance enhancement within spring wheat germplasm during the last seven years, during which time breeding programs in the spring wheat region have focused intensively on achieving this goal.

INTRODUCTION

The severe epidemics of Fusarium head blight, or scab, in the 1990's have caused economic losses that measured in the billions of dollars in the spring wheat region encompassing North Dakota, Minnesota, and South Dakota (McMullen, 1997; Nganje, 2001). As a result of these epidemics, concerted efforts to develop scab-resistant wheat varieties were accelerated in several regions of the U.S. and continue today. A component of these efforts was the implementation of regional nurseries specifically devoted to assessing new wheat germplasm emerging from breeding programs for scab resistance at multiple locations. For the northern spring wheat region, Dr. Robert Busch established the Uniform Regional Scab Nursery for Spring Wheat Parents (URSN) in 1995. It has since been conducted annually, with support from the U.S. Wheat and Barley Scab Initiative.

The benefits of the URSN and similar nurseries for other market classes of wheat are two-fold. First, these nurseries provide a vehicle for obtaining multi-site scab resistance data, which is important given the large environmental effect on scab development and severity (Groth *et al*., 1999). Second, these nurseries provide a means of germplasm exchange among wheat breeding programs. An additional benefit of these nurseries is that they provide a record of progress in enhancing scab resistance in wheat germplasm over time. The goal of this paper is to provide a historical review of progress in developing scab-resistant germplasm in the northern spring wheat region, based on several years of URSN data.

MATERIALS AND METHODS

Data on scab resistance were obtained for the years 1996 through 2001. Although 1995 was the first year that of the URSN was run, consistent protocols for rating scab (disease index = incidence x severity) and kernel damage (tombstones or vsk) started in 1996. Thus, the

analysis was restricted to data for the years 1996-2001. Entry lists and complete data for each year of the URSN are available at gopher://greengenes.cit.cornell.edu:70/11/.Performance/.hrswregional/Uniform%20Regional%20Scab%20Nursery/. For purposes of analysis, BacUp and ND 2710 were designated as resistant checks because they were grown in each of these years. For each of these years, the grand mean for disease index across entries (excluding checks, durums, and plant introductions) was calculated. A standardized disease index for each year was obtained by dividing each grand mean by the disease index grand mean for BacUp and ND 2710 in the same year. This same procedure was also completed for tombstone frequency.

RESULTS

Since 1995, the URSN has been grown at six different locations in Minnesota, North Dakota, South Dakota, as well as Canada (attempts to grow the nursery further south in Iowa were attempted for a few years, but were not successful and thus were not continued). The number of entries in each year has increased relatively steadily during this period, and is now averaging over 40 per year. These entries include common wheat, durum wheat and more recently, plant introductions. The entries have come from public breeding programs in the abovementioned states and Canada, as well as from private breeding enterprises. Several resistant and susceptible check varieties were included in each nursery. General information on the URSN from 1996-2001 is summarize in Table 1.

Table 1. Summary statistics for the URSN common wheat entries, 1996-2001.

Year	Number of Locations	Number of Entries[1]	Disease Index	Disease Range	Mean Tombstone	Tombstone Range
1996	6	31	38	12-73	24	7-59
1997	6	31	38	20-65	29	15-45
1998	6	25	40	21-62	25	13-40
1999	7	30	42	24-63	28	16-42
2000	7	26	25	11-39	21	12-32
2001	7	29	32	16-55	27	14-47

[1]Excludes checks, durum entries and unimproved introductions.

URSN entries were categorized by their resistance source(s) by examination of their pedigrees (Table 2). The number of “native” resistance sources (i.e. no identifiable scab resistance source in their pedigree) dropped from 17 of 31 entries in 1996 to only 5 of 25 entries in 1998. This corresponded with an increase in the number of entries with parentage tracing to Sumai 3 and its derivatives. In recent years, entries with South American and European sources of scab resistance were entered in the nursery. Including composite crosses, the number of entries with multiple resistance sources (excluding native sources) in their pedigree have been limited, averaging three per year. The majority of entries in 1995-1997 containing a defined resistance source were 1/4 to 1/2 by pedigree of that resistance source. By comparison, the 2002 nursery contained only one entry that is 1/4 Sumai 3 by pedigree, with all other entries 1/8 or less.

Table 2. Fusarium head blight Scab resistance source of entries in the URSN common wheat entries, 1995-2002.

		Resistance Source[1]				
Year	No. Entries	"Native"	Sumai 3	Nyu Bay	S. Amer.	Europe
1995	28	16	11	1	0	0
1996	31	17	13	1	0	0
1997	31	10	17	0	4	0
1998	25	5	18	2	0	0
1999	30	9	18	3	0	0
2000	26	5	20	1	0	0
2001	29	4	21	2	2	3
2002	27	5	17	2	0	2

[1]"Native" sources include those present in the germplasm prior to 1990 and not containing an identifiable scab resistance source in its pedigree; Sumai 3 includes its derivatives, Ning 8331 and Ning 7840.

Evaluating historical trends in scab resistance and related traits within the URSN over time provides a means of assessing progress by spring wheat breeding programs attempting to enrich for scab resistance in their germplasm. We assessed this progress by calculating standardized disease indices and tombstone frequencies, relative to the resistant checks BacUp and ND 2710. The results of this analysis suggest that the relative scab resistance of the germplasm entries has increased substantially since 1996. In 1996, the disease index of entries was approximately 216% of the mean of BacUp and ND 2710. However, between 1997 and 1999, this decreased significantly, with relative disease levels dropping to 128% of the resistant checks by 1999 (Table 3). This trend reversed somewhat in 2000 and 2001 however, with the relative disease index of entries rising to approximately 153% of the resistant check means in 2001. The standardized tombstone frequencies of entries also exhibited consistently lower values between 1997 and 2001, relative to 1996 (Table 3).

Table 3. Standardized scab disease indices and tombstone frequencies for URSN common wheat entries, 1996-2001.

Year	Standardized Disease Index[1]	Standardized Tombstone[1]
1996	216	228
1997	151	123
1998	129	138
1999	128	144
2000	149	138
2001	153	143

[1]values are the % of the mean of BacUp and ND 2710.

DISCUSSION

The major benefit that the URSN provides to wheat breeders is that it permits germplasm to be evaluated in multiple locations under different environmental conditions. Given the large effect that the environment has on expression of scab resistance, evaluation of a genotype in multiple environments ensures that useful data are obtained. However, the data obtained by the URSN is also useful for assessing overall progress by several different breeding programs each seeking to develop resistance to the same disease. The results of our analysis suggest that the different breeding programs that, as a whole, contribute contributing entries to the URSN for evaluation, as a whole, have made substantial progress in enhancing scab resistance in their germplasm over the last 6 years. The challenge that remains is to determine whether the plateau of resistance that has been obtained to date, principally by deploying Sumai 3-derived resistance, can be reduced further by incorporating new sources of resistance. Entries in the nursery the past few years also have improved agronomic qualities and resistance to rust diseases as the proportion of the pedigree, by resistance source, has dropped to less than 1/8 for the majority of entries. Incorporating additional novel sources of resistance and combining it with the Sumai 3 resistance is necessary to provide higher levels of resistance and genetic diversity.

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GENES WITH MAJOR EFFECTS ON FHB RESISTANCE PROMISE EASY MARKER APPLICATION

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OBJECTIVES

To determine the inheritance of resistance to FHB in three resistant bread wheat lines, and describe the implication of this finding.

INTRODUCTION

Chromosomes and genes with major and minor effects - Many chromosomes have been implied to carry genes conferring resistance to Fusarium head blight (FHB). However, some contribute more to overall resistance than others. Likewise many genes have been reported, but there is evidence that gene effects may vary, with some genes having a stronger effect on phenotype. Molecular analyses also indicate that many different genes are available in genetic stocks (Anonymous, 2001).

The inheritance of FHB resistance in some of the key progenitors, such as Frontana, Sumai 3 and Ning7840, used by wheat breeding programs around the world is likely to be controlled by two or three genes with major effects (Ban and Suenaga, 2000; Singh *et al*., 1995a; van Ginkel *et al*., 1996). The latter study also found evidence that the four genes were distinct, providing promise that pyramiding these genes may result in increased resistance (Singh and van Ginkel, 1997).

In this study we determined the mode of inheritance of FHB resistance in three wheats considered to be genetically distinct based on their pedigrees.

MATERIALS AND METHODS

Genetic materials - We used the following three lines expressing similar FHB resistance but of distinct parentage (see Table 1).

Table 1. Parental lines used in the inheritance study.

GOV/AZ//MUS/3/DODO/4/BOW
CATBIRD
BAU/MILAN

Some of these lines, such as Gov/Az//Mus/3/Dodo/4/Bow and Catbird-derived lines, have been successfully used by participating breeders the U.S. Wheat and Barley Scab Initiative in crosses to locally adapted germplasm (Bacon *et al*., 2000).

Random F2-derived F8 progenies of crosses among the three resistant parents were used in this inheritance study.

Inoculation methodology - Inoculation was carried out at anthesis, using the so-called 'cotton method' to detect Type II resistance (Gilchrist *et al*., 2002, this Proceedings). Evaluation of infection was carried out by counting the total number of spikelets per spike and the number of spikelets infected; an infection percentage was then obtained.

RESULTS

The distributions of the 200 F8 lines per cross displayed discrete classes in each case and X^2 analyses confirmed a relatively simple gene inheritance. The data confirmed a preliminary analysis in 2001 (van Ginkel *et al*., 2001).

1. In the crosses of BAU/MILAN with GOV/AZ//MUS/3/DODO/4/BOW and BAU/MILAN with CATBIRD, two major genes segregated.

2. In the cross of CATBIRD and GOV/AZ//MUS/3/DODO/4/BOW, four genes of major effect segregated.

3. A total of four loci were involved.

DISCUSSION

With some luck and perseverance, FHB may become a textbook example of the application of markers to breeding. Why? Two points in favor need to be considered.

1. It is clear from the literature that while many chromosomes have been implicated and many genes have been described as contributing to FHB resistance, a few key genes often explain most of the variation observed. Their gene action is frequently observed to be additive. This study of just three parents found up to four genes controlling resistance, confirming that genes for scab are not uncommon in wheat. Genes with such major effects should be targeted for use in the application of markers in wheat breeding.

2. The evaluation of germplasm for FHB response is cumbersome, requiring several rounds of inoculation, a minimum of 5-10 inoculated spikes per plot, and replication at each site and across years, to show consistency in resistance response. Frequently, germplasm that is resistant one year may no longer be so the following year. Only after 3-4 years of testing can resistance patterns be confirmed, and confident statements made about resistance/susceptibility. The reason lies in the significant interaction between infection processes and climatic factors. This is not very encouraging for a breeding program hoping to make rapid progress.

Simple genetic resistance (point 1) is confirmed through a time-consuming and extremely laborious process (point 2). Hence, developing and then linking phenotypic data with molecular data is a protracted undertaking requiring great precision. However, unlike the traditional breeding process where progeny from every cross must be screened for the disease, markers promise a quick test for the presence/absence of desired alleles with major effects on resistance.

Environment-neutral marker systems will provide significant savings in time and costs. The liberated funds could be spent more effectively on marker development than on perpetual resistance screening of segregating populations in the field or greenhouse.

Clearly there is no lack of genetic diversity for FHB. It is also clear that some of these genes have major effects, particularly with regards to Type II resistance. It should not be difficult to develop markers for such major genes, and they would have ready application in any wheat-breeding program.

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SOURCES OF COMBINED RESISTANCE TO FUSARIUM HEAD BLIGHT, STRIPE RUST, AND BYD IN TRITICALE

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OBJECTIVES

1) To identify triticale lines that possess high levels of FHB resistance under Mexican conditions and thus could be used as resistance sources in breeding programs, and 2) to find out whether the lines also carry resistance to yellow rust and BYD.

INTRODUCTION

Fusarium head blight (FHB, caused by *Fusarium graminearum*) infects small-grain cereals during flowering and grain filling in temperate and humid weather conditions. It causes considerable yield losses and contaminates grain with mycotoxins, which are harmful to both human and animal health. In general, triticale has been reported to be resistant to many pathogens, but under Mexican conditions, it has shown susceptibility to different *Fusarium* species (*F. nivale, F. graminearum, F. avenaceum, F. culmorum, F. poae*, and *F. equiseti*) that cause fusarium head blight (FHB), as well as to yellow rust (*Puccinia striiformis*) and barley yellow dwarf (BYD), two other serious diseases affecting triticale crops today. In the past few years, changes in the pattern of yellow rust races that attack triticale have been observed in high altitude locations in different parts of the world, including Mexico. Though not a problem every year, BYD has the potential to cause substantial losses when present. For this reason, combined resistance to FHB, stripe rust, and BYD is considered to be highly useful in environments where all three can be present at the same time.

The objectives of this study were 1) to identify triticale lines that possess high levels of FHB resistance under Mexican conditions and thus could be used as resistance sources in breeding programs, and 2) to find out whether these lines also carry resistance to yellow rust and BYD.

MATERIALS AND METHODS

Adequate levels of genetic variation for FHB resistance have been found in primary triticales, which can be used as basic breeding materials through a pre-breeding scheme (Dorman and Oettler, 1993).

The CIMMYT triticale program routinely evaluates advanced hexaploid triticale lines for FHB resistance under natural infection in two hot-spot locations in Mexico: Toluca (state of Mexico) and Patzcuaro (state of Michoacan). Breeders observed signs of FHB resistance in the test triticale lines and pre-selected them for use in this study.

Twenty-six advanced hexaploid triticale lines were planted in small plots under artificial inoculation in Toluca, located in the central highlands of Mexico. During three cycles (2000, 2001, and 2002), the triticale lines were inoculated, evaluated, and characterized for different types of *Fusarium* resistance: penetration (Type I), spread (Type II), toxin content (Type III), and grain filling (Type IV) (Gilchrist *et al*., 1997; Gilchrist, 2001). The methodology and procedures used for inoculating and evaluating the lines have been described by Gilchrist *et al*. (1997). Two triticale varieties, IAPAR 23 and BR 2, reported as FHB resistant by Capan *et al*. (1987), were included as checks.

The test triticale lines and the resistant checks were also planted in Patzcuaro in 2001 and 2002 to confirm the results obtained in Toluca. To that end, two FHB readings under natural infection were conducted at the milk grain stage.

Toxin analysis of triticale grain was carried out in CIMMYT's toxin laboratory following the FluroQuant Romer procedures. Barley yellow dwarf was evaluated using a scale 1 to 9 (Bertschinger, 1994).

RESULTS

Fusarium head blight symptoms are more difficult to observe in triticale than in wheat. Mainly due to the gray-green color of triticale, it is very easy to confuse FHB symptoms with other diseases, and only for a few days is it possible to observe the infected spikelets, which show premature darkening of the straw color. However, if the spikes are carefully evaluated at the correct time and appropriate check cultivars are used for comparison, valuable information can be collected that will allow the identification of triticale lines with superior resistance to FHB.

Sixteen of the twenty-six test lines consistently showed resistant reactions to FHB during the three cycles in Toluca. Results of characterizing the lines for different types of FHB resistance and of evaluating them for resistance to yellow rust and BYD are shown in Table 1. It should be noted that some lines showing FHB resistance were also resistant to stripe rust in the year 2001. A new stripe rust race was detected in 2002, and the damage increased in some of the lines that had shown a resistant reaction the year before. Glume damage was also observed in some lines.

Barley yellow dwarf is not common in Toluca in summer, but a dry period at the beginning of the cycle in 2002 caused a considerable natural increase in the number of aphid vectors of MAV and PAV strains of the BYD virus. This in turn raised the level of BYD infection and provided an ideal testing ground for the disease.

DISCUSSION

In studies by Maier and Oettler (1993), triticale appeared to have higher levels of FHB resistance than the resistant wheat cultivar Frontana. In the evaluations carried out in Toluca and Patzcuaro, a great majority of the lines showed a superior level of FHB resistance. As for the check lines IAPAR 23 and BR2, only the latter proved to have intermediate resistance in both Toluca and Patzcuaro; IAPAR 23 was susceptible in Toluca and the second and third years in

Patzcuaro. This is an indication that FHB resistance expressed in one location is not necessarily effective in all places where FHB is a problem.

CONCLUSION

The combined resistance to FHB, stripe rust, and BYD that we found in triticale has good potential as a source of resistance in improvement programs that apply a plant breeding strategy in which different types of resistance are combined in a single genotype.

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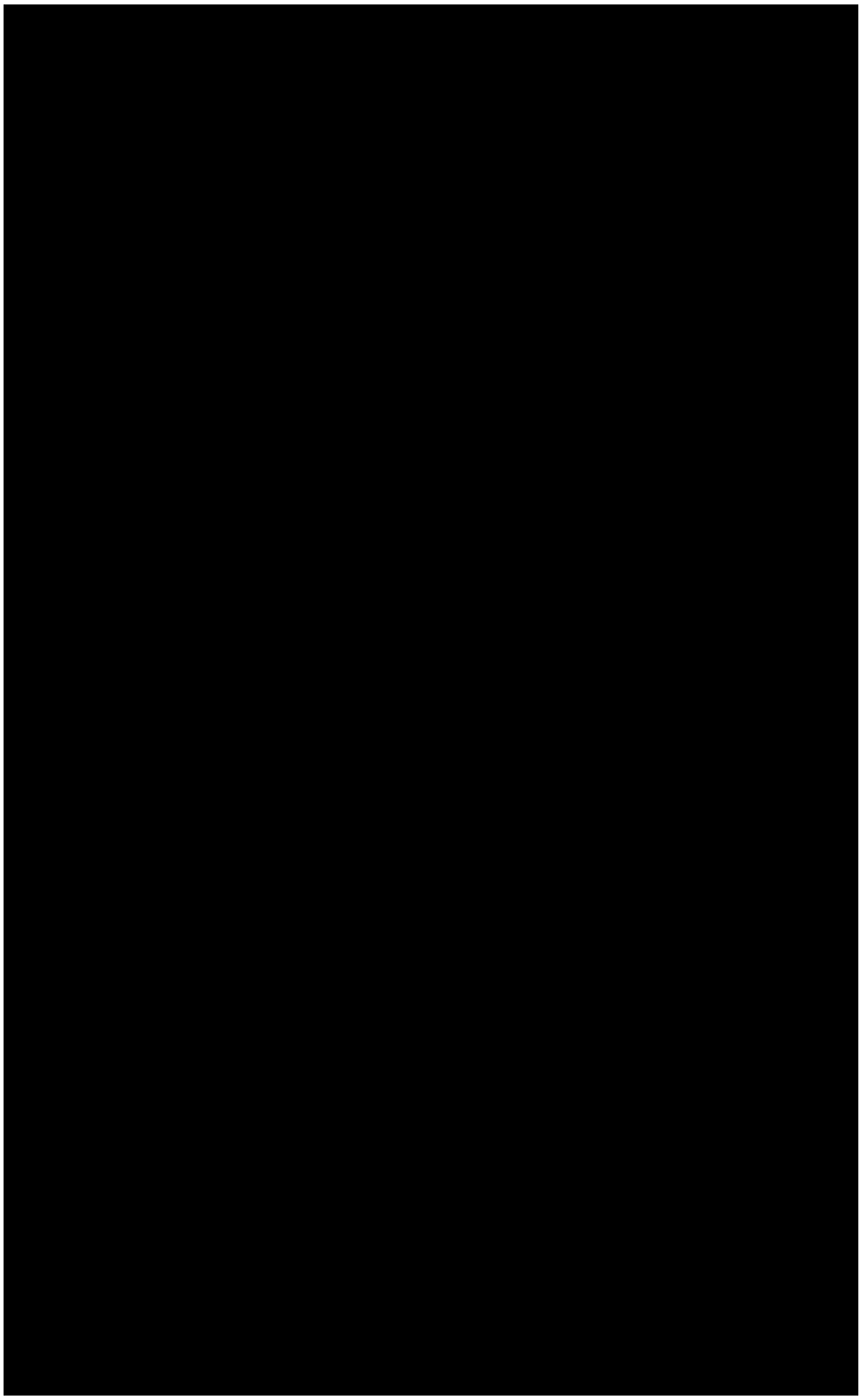

PROGRESS IN BREEDING *FUSARIUM* HEAD BLIGHT RESISTANCE IN SOFT RED WINTER WHEAT

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ABSTRACT

A primary goal of our breeding program is to accelerate the development of adapted and commercially viable Fusarium head blight (FHB) resistant SRW wheat varieties by identifying and incorporating diverse types of resistance into elite genotypes. Breeding methods being used to accomplish this goal include topcrossing, backcrossing, doubled haploid techniques and molecular marker genotyping. In 2002, 229 segregating populations were evaluated in a mist-irrigated FHB nursery, inoculated using colonized maize seed, at Mt. Holly, VA. Seventy-seven of these populations (34%) were advanced on the basis of FHB incidence and severity, agronomic traits, and resistance to other prevalent diseases such as powdery mildew. In field tests, approximately 4500 headrows (F_3-F_8 and various backcross generations) were evaluated for agronomic traits and resistance to diseases other than FHB at Warsaw, VA. In addition, approximately 2800 F_5-F_7 headrows were evaluated for FHB resistance and agronomic traits in an inoculated, mist-irrigated nursery at Blacksburg, VA. From these headrows, 32 backcross-derived lines and 26 topcross-derived lines were selected for further testing in our scab nursery at Blacksburg and in Observation yield tests at two locations in 2003. Twelve lines from the 2001-02 Observation yield test were selected for further testing in Preliminary wheat trials. Four elite lines were selected for testing in our Advance yield trial, and two elite lines will be tested in Virginia's official variety trial. Twelve lines will be tested in the 2002-03 Uniform Winter Wheat FHB Nurseries. Two newly released varieties from the Virginia Tech Small Grains Program, 'McCormick' and 'Tribute', possess a significant level of scab resistance. Progress in transferring type II resistance into SRW wheat genotypes has been accelerated via use of the wheat by maize doubled haploid (DH) system. One DH line, VA01W-476, developed from the cross 'Roane'/W14, was found to have good scab resistance in greenhouse and field tests and also has major genes for scab resistance as determined by DNA analysis this spring. A total of 135 doubled haploid lines derived from nineteen 3-way crosses consisting of diverse scab-resistant parents were selected on the basis of field and greenhouse tests this year and will be evaluated for scab resistance in our inoculated, mist-irrigated nursery at Blacksburg and for agronomic traits at Warsaw. Type II resistance from five different sources (Futai8944, Futai8945, Shaan85, VR95B717 and W14) has been backcrossed into seven adapted SRW wheat backgrounds, and two of the recurrent parents (Roane and Ernie) possess FHB resistance other than Type II. A total of 180 BC_4F_2 and BC_5F_2 individuals were selected on the basis of scab severity in greenhouse tests and will be evaluated for scab resistance in our inoculated, mist-irrigated nursery at Blacksburg and for agronomic traits and similarity to the recurrent parent at Warsaw. Near-isogenic SRW wheat lines with Type II resistance are being developed and will facilitate pyramiding of different types of FHB resistance.

COMPARISON OF FHB DEVELOPMENT ON HARD WINTER WHEAT USING DIFFERENT PLANTING SCHEMES

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ABSTRACT

Fusarium head blight (FHB) is a destructive disease of wheat causing yield loss and poor grain quality. Winter wheat producers in South Dakota have adopted a reduced tillage cropping system and have increased production of winter wheat in traditional corn-soybean rotations. These practices could very well lead to an increase in FHB severity. The winter wheat breeding program at South Dakota State University has established a proactive effort to develop FHB-resistant hard winter wheat varieties. Transplanted hill nurseries have been screened since 1999 utilizing an established mist-irrigated field screening nursery designed to test cultivars, elite lines, and preliminary lines for resistance to FHB. However, transplanting winter wheat is a time consuming process because it involves the vernalization of seedlings in cold chambers, proceeded by hand planting. The root system is far from established in transplanted wheat, often leading to poor plant development. The laborious transplanting process also does not follow the conventional direct seeding method followed by wheat producers. This has led to the investigation of planting schemes to determine if direct seeded row materials are affected differently than transplanted hill plots when they are inoculated with FHB. In October 2000, several multi-location winter wheat trials, including the South Dakota Crop Performance Trials (CPT), were directly seeded into the FHB nursery. The CPT trials were also vernalized and transplanted in May 2001. Significant correlations between the two types of planting techniques were observed for FHB severity and disease indices. However, FHB incidence for the direct seeded rows was low and was not significantly correlated with the incidence levels in the transplanted hills. This was perhaps due to the early flowering of the direct seeded materials. The cooler temperatures at anthesis may have inhibited FHB development. In 2002, we investigated transplanted seedling performance in comparison to delayed seeded CPT lines. The CPT and several other trials were directly seeded on November 26, 2001. This planting scheme helped delay flowering by approximately two to three weeks compared to conventional timely seeding. In May 2002, the CPT trial was transplanted into the mist-irrigated field nursery. Significant correlations ($P < 0.05$) between the two types of planting techniques in 2002 were observed for FHB severity, incidence, and disease indices. Correlations between the different planting types across years were also highly significant. These results suggest that delayed direct seeding could replace transplanting. However, transplanted hills should be used if improper weather conditions prevent a successful direct seeded nursery.

STABILITY OF TYPE II RESISTANCE AND DON LEVELS ACROSS ISOLATE AND SOFT RED WINTER WHEAT GENOTYPE

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ABSTRACT

Fusarium graminearum Schwabe (teleomorph *Gibberella zeae* (Schwein.), also known as scab, is an important disease of wheat world-wide. Although host plant resistance has long been considered the most practical and effective means of control breeding has been hindered by a lack of effective resistance genes and by the complexity of the resistance in identified sources. No source of complete resistance is known, and current sources provide only partial resistance. The identification of new sources of resistance and their incorporation into adapted wheat varieties provides the most economical solution to this problem. Within both germplasm screening programs and breeding programs, the goal is to identify resistance that is stable over genotypes and across geographical areas. Choice of isolate may be an important factor in accomplishing this goal. We evaluated the effect of 5 diverse *Fusarium graminearum* isolates on type II resistance and DON levels in adapted winter wheat germplasm entered into the Northern Uniform Scab Nursery in 1999. Genotypes were planted in the greenhouse in a split-plot arrangement with genotypes as the main plot and isolates as the sub-plot. The experiment was replicated six times. Five plants per isolate per replication were inoculated at first anthesis with 10µL of a macroconidial suspension of *Fusarium graminearum* concentrated to 50,000 macroconidia/mL. Plants were then incubated in a mist chamber for 72 h and rated for type II resistance at weekly intervals post-inoculation. At maturity, inoculated heads were harvested, hand-threshed and seed were bulked for deoxynivalenol (DON) analyses. Results indicated significant differences in the aggressivity of the isolates used with the Missouri isolate being the most aggressive across all genotypes. Mean DON levels varied significantly ranging from 160 ppm to 3 ppm. Significant genotype by isolate effects were evident for DON production.

DEVELOPING FHB-RESISTANT CULTIVARS AND GERMPLASM FOR THE MID SOUTH

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INTRODUCTION

Growing resistant cultivars likely will be the primary component of any management strategy for Fusarium head blight of wheat in the Mid South. None of the currently grown cultivars have a high level of FHB resistance, but a collaborative program has identified promising resistant lines that are agronomically adapted and have resistance to other important diseases.

MATERIALS AND METHODS

A crossing program was initiated in 1991 between adapted genotypes and various sources of resistance. These populations were advanced as bulks for 5 years then lines were developed using pedigree selection. These lines have been evaluated for FHB resistance in an inoculated screening nursery along with a FHB resistant check (Ernie) to allow for FHB evaluation in a natural epidemic. These F_7 derived lines have been selected for FHB resistance, yield and other agronomic traits. Additionally, the most advanced lines from the University's wheat breeding program are being screened to determine the level of resistance (or susceptibility). For future development, many different sources of resistance have been used to develop over 450 populations (F_1- F_4) from which lines will be selected.

Ninety-three F_7, topcross F_6, or topcross F_6 germplasm lines were evaluated for FHB resistance in the greenhouse and in inoculated and misted screening nurseries at Fayetteville and Kibler. The lines also were evaluated for resitance to other diseases that are important in the Mid South and for spring freeze damage, vernalization, lodging, and agronomic phenotype.

RESULTS AND DISCUSSION

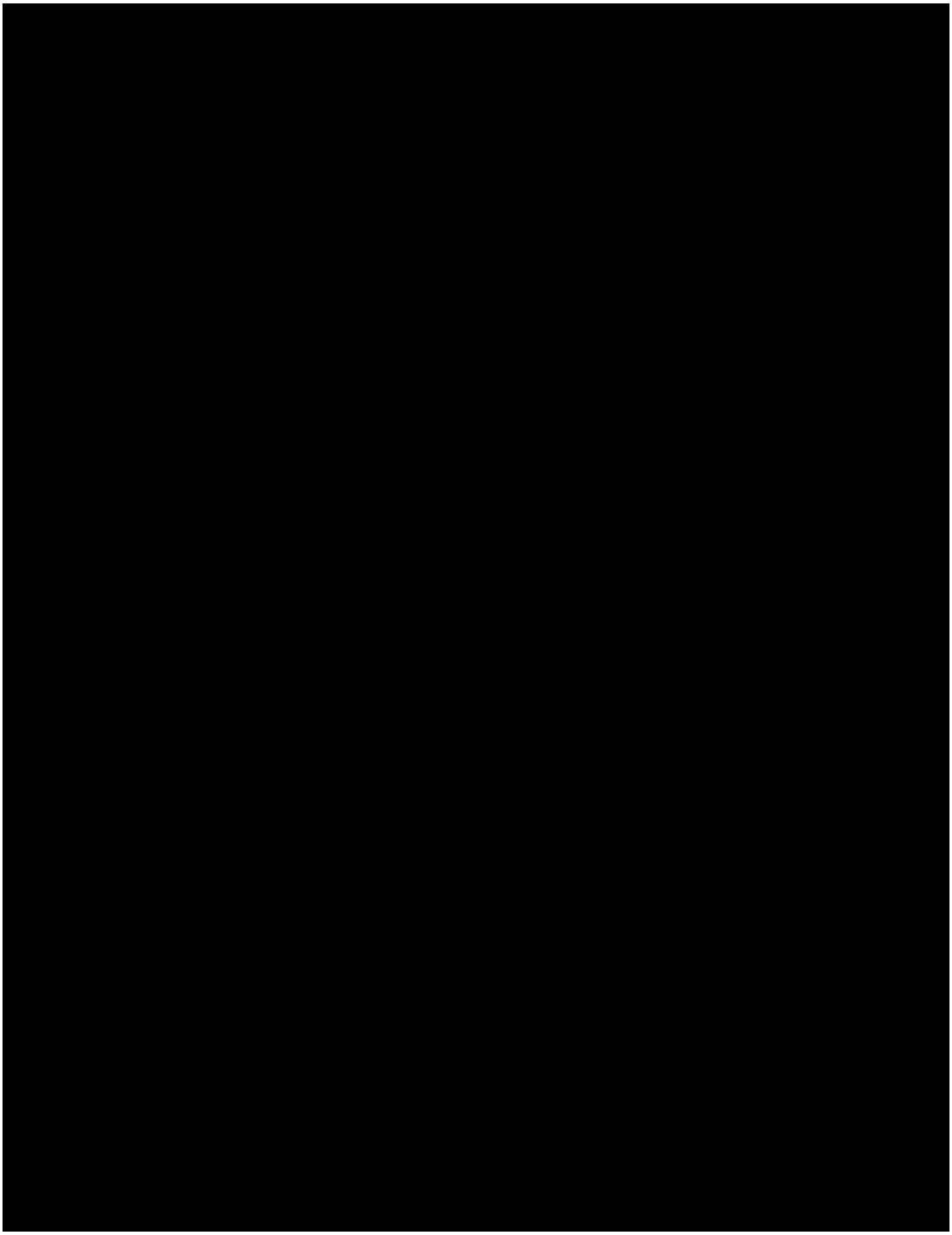
Yield plots harvested in June at Stuttgart and Marianna, AR indicated several high-yielding lines in the scab resistant nursery (Table 1). Of the 34 lines tested at two locations, 17 were not significantly different than Ernie for FHB. Five of these lines actually had lower numerical ratings than Ernie at both locations. Of those five lines, two were not significantly different in yield than the high-yielding check 'Pat.' Four lines were tested in the 2001-02 Southern Winter Wheat Scab Nursery. Field results across eight reporting locations indicated that all four Arkansas lines had ratings for FHB Index that were not significantly different than the resistant check Ernie. Percentage scabby kernels for all the Arkansas lines was also not different than Ernie. The 18 best FHB breeding lines from the 2002 FHB yield test and 8 lines from Milus' germplasm enhancement will be tested in replicated inoculated yield trials at two Arkansas locations in 2003. Four new lines were entered in the 2002-03 Southern Winter Wheat Scab

Nursery. Fifty F_1 populations will be grown in the greenhouse for seed increase. The more advanced populations, which include 100 F_2, 254 F_3, and 49 F_4 populations, were planted at Stuttgart and will be grown in inoculated blocks to help natural selection shift the populations towards resistance.

Thirteen germplasm lines (Table 2) were selected based on level of FHB resistance, parentage, resistance to other diseases, and agronomic characteristics, and these would be useful parents in breeding programs. Five of the selected lines were entered in the 2003 Southern Uniform Winter Wheat FHB Nursery. For evaluation and crossing, seed of all selected lines were provided to Dr. Lucy Gilchrist of CIMMYT and Barton Fogleman of Agripro, and seed of selected lines were provided to Dr. Mohan Kohli of CIMMYT in South America. Seed of lines with Karnal bunt resistance in their parentage were sent via Dr. Art Klatt to CIMMYT for Karnal bunt screening. To determine which lines carry different genes for FHB resistance, lines are being screened by Dr. Guihua Bai for a QTL associated with FHB resistance, and six lines are included in a diallel genetic study.

Table 1. Performance of lines in inoculated scab trials at Marianna and Stuttgart, Arkansas with FHB ratings from Fayetteville and Kibler, Arkansas in 2001-02.

Entry	Yield	Test weight	Heading date	Maturity date	Plant ht	FHB Fayett.	FHB Kibler
	bu/A	lb/bu			in.	%	%
Pat (check)	79.9	56.9	4/20	5/22	39	2.0	1.8
AR93095-4-1	75.8	56.1	4/18	5/21	38	2.5	2.8
AR93035-4-1	75.7	56.6	4/18	5/22	35	1.5	5.5
AR93035-4-3	74.7	57.5	4/17	5/22	36	1.3	5.5
AR93035-4-4	71.5	55.9	4/17	5/21	35	1.3	4.3
Ernie (check)	70.5	55.3	4/15	5/20	34	4.0	4.8
AR93035-4-2	69.1	55.6	4/17	5/22	34	2.0	6.3
AR93188-12-1-1	68.2	55.2	4/18	5/20	34	21.3	33.8
AR93035-7-1	67.8	55.2	4/17	5/22	35	2.3	7.5
AR93108-8-1	66.7	52.8	4/16	5/18	36	30.0	17.5
AR93108-1-3	65.8	54.1	4/18	5/22	34	7.5	6.3
AR93189-3-1	65.6	55.5	4/19	5/20	33	17.5	21.3
AR93188-1-1	65.1	53.9	4/19	5/20	35	11.3	10.0
AR93091-4-2	65.0	56.8	4/19	5/22	39	7.5	2.5
AR93189-4-1	63.7	54.5	4/20	5/21	35	18.8	15.0
AR93108-9-1	63.6	52.9	4/15	5/20	35	12.5	12.5
AR93189-7-1	62.9	55.0	4/18	5/21	34	16.3	37.5
AR93187-6-1	62.6	54.0	4/20	5/21	34	26.3	26.3
AR93108-3-2	62.5	56.3	4/14	5/19	36	8.8	8.0
AR93069-5-1	62.1	58.3	4/18	5/21	37	10.0	11.7
AR93019-2-1	62.1	57.5	4/21	5/21	40	1.6	1.5
AR93048-8-2	61.7	51.9	4/16	5/19	35	16.3	18.8
AR93188-7-1	60.9	53.9	4/20	5/22	34	15.0	17.5
AR93032-6-1	60.4	56.9	4/16	5/20	37	13.8	21.3
AR93108-1-2	60.3	53.1	4/17	5/19	36	23.8	8.8
AR93001-3-2	59.6	56.9	4/17	5/21	36	1.4	5.0
AR878-2-1	59.5	56.1	4/15	5/20	42	2.5	5.5
AR93081-2-1	57.5	53.1	4/18	5/20	40	15.0	7.5
AR93108-8-2	57.2	51.6	4/17	5/19	37	22.5	-
AR857-1-2	57.0	54.2	4/16	5/20	37	0.1	2.0
AR93187-4-2	56.7	54.8	4/19	5/21	34	10.0	12.5
AR93108-4-1	56.3	51.4	4/16	5/20	34	13.8	17.5
AR857-1-1	54.1	55.0	4/16	5/21	35	0.0	0.5
AR880-5-1	53.2	52.9	4/18	5/21	37	2.5	7.5
AR93035-1-1	50.1	56.0	4/18	5/20	37	3.5	5.5
AR922-5-1	46.9	57.3	4/17	5/20	36	3.5	9.3
Mean	63.2	55.1					
CV (%)	11.9	5.4					
LSD_{05}	8.5	3.4				5.1	7.0



UNIFORM SOUTHERN SOFT RED WINTER WHEAT FUSARIUM HEAD BLIGHT SCREENING NURSERY

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ABSTRACT

The Third Uniform Southern Soft Red Winter Wheat Fusarium head blight (FHB) Screening Nursery comprised 28 advanced generation breeding lines and two check cultivars. Five public (Univ. of Arkansas, Univ. of Georgia, Univ. of Maryland, N.C. State Univ., and Virginia Tech) and two private (Syngenta Seeds and AgriPro) cooperators submitted entries. Ten cooperators submitted field, greenhouse, and SSR data for the annual report. Significant genotype and genotype by location variation was observed for FHB incidence, head severity, index, and percent scabby seed in combined analyses of field data and for head severity in greenhouse evaluations. No significant correlations were observed between plant height or head emergence and any of the FHB variables. Matrices containing the means of the 30 genotypes at each location for each FHB variable were subjected to GGE biplot analyses to provide insight into the underlying causes of the genotype by location interaction and to identify consistently superior genotypes across test locations. A single megaenvironment encompassing eight locations was observed for FHB incidence. Two megaenvironments (LA and Bay-AR versus OH, IL, KY, VA, NC, MD, Fayetteville-AR, and Kibler-AR) were observed for head severity. Nevertheless, there was a high degree over overlap among the most resistant genotypes in both megaenvironments. Two megaenvironments were observed for percent scabby seed (NC versus Fayetteville-AR, Bay-AR, IL, KY, and VA) and two megaenvironments were observed for greenhouse estimates of head severity (NC versus Bay-AR, MO, IL, and KY). Again, there was a high degree of overlap amongst the most resistant genotypes in both sets of megaenvironments. VA01W476, a doubled haploid line from the cross between the moderately resistant ‘Roane’ and the resistant Chinese line W14, was the most resistant genotype overall. It rated most resistant for FHB incidence, severity, index in field tests, and head severity in greenhouse evaluations overall.

DEVELOPED EVALUATION METHOD OF FUSARIUM HEAD BLIGHT (FHB) RESISTANCE IN WHEAT BY CONTINUOUS SIMULATED RAINFALL AND DIVERSITY OF FHB RESISTANCE IN DOMESTIC WHEAT

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ABSTRACT

In the Fusarium head blight (FHB) resistance evaluation test of wheat, variances and errors of FHB severities in every test are still big issues for resistance breeding. For this problem, we developed a method by continuous simulated rainfall system with injection inoculation to reduce environmental error factors of each inoculation. Sprinkler system has equipped to cover all the test plots and simulated rainfall were operated every 5 minutes for 60 seconds to keep spikes wet at all time of disease developing. Suspension of *Fusarium graminearum* spore in distilled water ($1x10^5$/ml) was injected into a single sipikelet of middle spike on the each material's flowering day and FHB disease severities were investigated after 21 days of inoculation. The correlation coefficient between field test and greenhouse test were r=0.84(n=70, P<0.01, 2001), r=0.71(n=185, P<0.01, 2002) respectively, they showed high values for 2 years. The correlation coefficient between every year's average FHB severities in the field test and the greenhouse test was r=0.71(n=30, P<0.01, 2001-2002), it also showed high value. While FHB inoculation, leaf disease by *F.graminearum* was observed, so the relationship between FHB and leaf disease was investigated. The correlation coefficient between FHB severities and leaf disease severities was significant, r=0.38(n=70, P<0.01), but it seemed to be difficult to presume FHB resistance from leaf disease severities. The highest resistance cultivar of FHB was Sumai 3 Austria line, a derivative of Sumai 3. Sumai 3 (Kyusyu) and Sumai 3 (CIMMYT) showed a little different plant height, but there observed not so much differences in FHB resistance. The relationship of FHB resistance of domestic cultivars has been investigated. 4 major cultivars of Hokkaido (Takunekomugi, Horoshirikomugi, Chihokukomugi, Hokushin) showed stable FHB severities for 2 years, so they were employed as standard cultivars. Takunekomugi showed highest resistance among of them, as the same resistance as Saikai 165 in Kyusyu. Saikai 165 was bred from a cross of Sumai 3/ Asakazekomugi for the purpose of improved FHB resistant line, but the resistance was a little inferior to Sumai 3. Hokushin has a good quality for white salt noodle (Udon), and it is a leading cultivar of Hokkaido at the present time, but it was most susceptible among Hokkaido's materials. We found Kachikei 28, showed more FHB resistance than Takunekomugi, but both of their parents were susceptible to FHB. We developed a high reliability evaluation method for FHB resistance, and elucidated the relationship of FHB resistance in domestic wheat and Sumai 3.

PHENOTYPIC EFFECTS OF *QFHS.NDSU-3BS* ON FUSARIUM HEAD BLIGHT RESISTANCE IN NEAR-ISOGENIC WHEAT LINES

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OBJECTIVE

To use QTL near-isogenic lines to evaluate phenotypic effects of *Qfhs.ndsu-3BS* in multiple genetic backgrounds

INTRODUCTION

Despite high levels of FHB resistance identified in some wheat cultivars, progress in breeding for FHB resistance has been relatively slow due to complex inheritance, large environmental influences on disease development, and the resources required to conduct successful breeding nurseries. Recent QTL studies have identified chromosomal regions carrying putative genes for FHB resistance by exploiting statistical associations between molecular markers and resistance phenotypes. A major QTL, *Qfhs.ndsu-3BS*, associated with reduced pathogen spread (Schroeder and Christensen, 1963) has been identified from Chinese wheat cultivar 'Sumai 3', or its derivatives, in several studies (Waldron *et al*. 1999; Anderson *et al*. 2001; Buerstmayr *et al*. 2002; Zhou *et al*. 2002).

The consistent ability to detect *Qfhs.ndsu-3BS* and the magnitude of effect in each mapping population imply that it should be useful for marker-assisted selection (MAS). However, to justify MAS for the QTL region, increased levels of resistance due to this QTL should be observed in multiple genetic backgrounds. To test the robustness of *Qfhs.ndsu-3BS,* near-isogenic lines (NILs) contrasting for the QTL region were tested in greenhouse point-inoculation experiments and field FHB screening nurseries. NILs are particularly effective genetic stocks to study FHB resistance that is attributable to a QTL because NILs standardize the genetic background, morphology, and agronomic characters that may influence disease assessment.

MATERIALS AND METHODS

Plant materials. Co-dominant microsatellite markers gwm493, barc133, and gwm533 (Roder *et al*., 1998; Cregan and Song, 2002) were selected to develop NILs with alternate marker alleles for Qfhs.ndsu-3BS. Homozygous near-isolines were identified by genotyping the progeny of self-pollinated, heterozygous, $F_{3:4}$ lines from 17 unique cross combinations that were grown in summer breeding nurseries in 2000 and 2001. Each of the 17 selected populations had a FHB resistant parent with Sumai 3 in its pedigree and correct marker alleles that are unique to this region (Liu and Anderson, in press). In total, 33 QTL-NIL pairs were produced.

Field Screening. In the summer of 2002, all entries were tested at St. Paul and Crookston misted and inoculated nurseries. Check cultivars and NIL parents, including: 'Sumai 3' (resistant), 'Roblin' (susceptible), 'Wheaton' (susceptible), 'Alsen' (moderately resistant), 'ND 2710' (resistant), 'ND 2603' (resistant), and 'Bacup' (resistant) were included to represent a range of maturity, height, and disease resistance phenotypes. NIL pairs were randomized with check cultivars in a complete block design with 4 replications.

At St. Paul, macroconidia [$1x10^5$/ml] of *Fusarium graminearum* were applied at anthesis at a rate 30 ml m^{-1} row, followed by a second application 3 days later. At Crookston, infested corn-kernel inoculum was spread evenly throughout the field at a rate of 112 kg ha^{-1} at the 5 leaf stage. For both nurseries, the number of infected spikelets were counted on 20 spikes per row approximately 20 days post-inoculation. Rows were harvested by hand using a sickle and then 30 spikes per row were threshed from two replications in a manner that retained diseased kernels. The weight of seed from 30 threshed spikes was measured. Percent visually scabby kernels (VSK) was estimated based on the scale of Jones and Mirocha (1999). Data analyses were performed using SAS PROC GLM. QTL alleles were considered as fixed effects. Replications, NIL pair, and NIL pair by QTL interaction were considered random effects.

Greenhouse Screening. Approximately 15 plants per genotype were tested in two experiments by inoculation of 10µl macroconidia [$1x10^5$/ml] into a central spikelet at anthesis. Plants were incubated in a dew chamber (100% RH, 20°C) for 72 hours after inoculation. The number of symptomatic spikelets and total spikelet number were counted at 21 days post-inoculation. The difference in number of symptomatic spikelets between near-isolines was analyzed using t-tests.

RESULTS AND DISCUSSION

Field. Statistical analysis of individual field experiments revealed that error variances were not homogeneous; therefore, locations were not combined for ANOVA. Significantly lower disease pressure at the Crookston nursery and different inoculation methods between the two locations are the most probable causes (Table 1). The effect of *Qfhs.ndsu-3BS* was highly significant ($P<0.01$) for 5 of 6 trait by location combinations (Tables 2 & 3). The marginal significance ($P=0.046$) of *Qfhs.ndsu-3BS* in increasing 30-spike seed weight at Crookston is likely due to low disease pressure. As expected when sampling lines from diverse populations, the effect of NIL pairs was highly significant ($P<0.001$) for all traits in each location. The interaction between *Qfhs.ndsu-3BS* and genetic background (NIL pair) was only highly significant for disease severity at St. Paul and was marginally significant for 30-spike seed weight at Crookston. The average reduction in disease severity with *Qfhs.ndsu-3BS* present was 22% at St. Paul and 14% at Crookston. The average reduction in VSK was 19% at St. Paul and 24% at Crookston (data not shown).

Greenhouse. Sixteen of twenty-nine pairs had significantly reduced spread within the spike in isolines with *Qfhs.ndsu-3BS* across two point-inoculation experiments (Figure 1). Pairs with no statistically significant difference generally had lower disease levels, but the trend was towards more resistant genotypes with *Qfhs.ndsu-3BS*. The average reduction in symptom-

atic spikelets with *Qfhs.ndsu-3BS* present was 27% in the first experiment and 36% in the second.

These results confirm that selecting for *Qfhs.ndsu-3BS* with molecular markers should enhance FHB resistance in breeding populations. The absence of consistent QTL by NIL pair interaction across 17 different cross combinations indicates that *Qfhs.ndsu-3BS* should increase FHB resistance independent of genetic background. We are producing fine mapping populations developed from the most promising NIL pairs to further define this QTL region.

Table 1. Trait means for check cultivars and *Qfhs.ndsu-3BS* NIL pairs at two nursery locations.

	St. Paul			Crookston		
Entry	Disease Severity (%)	VSK (%)	30-Spike Seed Weight (g)	Disease Severity (%)	VSK (%)	30-Spike Seed Weight (g)
Alsen	33	20	9.5	16	7	17.9
BacUp	24	20	14.2	12	9	20.6
HJ98	55	19	12.5	19	19	19.9
Ivan	34	38	9.0	9	25	18.5
ND2603	18	12	17.2	8	6	22.3
ND2710	10	14	22.4	4	3	28.1
Reeder	58	40	7.6	18	15	18.9
Parshall	39	30	9.9	17	13	20.9
Roblin	74	40	9.4	54	12	18.8
Sumai3	5	2	21.5	3	2	19.2
Verde	42	24	11.1	19	18	17.9
Wheaton	75	45	13.7	53	40	18.9
NIL pairs	28	20	14.5	15	11	23.1

Table 2. ANOVA of *Qfhs.ndsu-3BS* NILs for three FHB traits at St. Paul field nursery.

Source	Disease Severity		VSK's		Spike Seed Wt	
	df	MS	df	MS	df	MS
Replication	3	0.07***	1	172*	1	0.1
NIL-Pair	39	0.12***	39	238***	39	54.6***
Qfhs.ndsu-3BS	1	0.41***	1	677***	1	32.6**
NIL-Pair*QTL	39	0.01***	39	14	39	4.1
Error	241	0.005	81	28	81	4.4

*, **, *** Effect significant at $P<0.05$, 0.01, and 0.001, respectively

Table 3. ANOVA of *Qfhs.ndsu-3BS* NILs for three FHB traits at Crookston field nursery.

Source	Disease Severity		VSK's		30-Spike Seed Wt	
	df	MS	df	MS	df	MS
Replication	3	0.01**	1	2	1	12.7
NIL-Pair	39	0.03***	39	132***	39	60.4***
Qfhs.ndsu-3BS	1	0.03***	1	359***	1	19.1*
NIL-Pair*QTL	39	0.003	39	19	39	7.2*
Error	239	0.003	81	18	81	4.7

*, **, *** Effect significant at $P<0.05$, 0.01, and 0.001, respectively

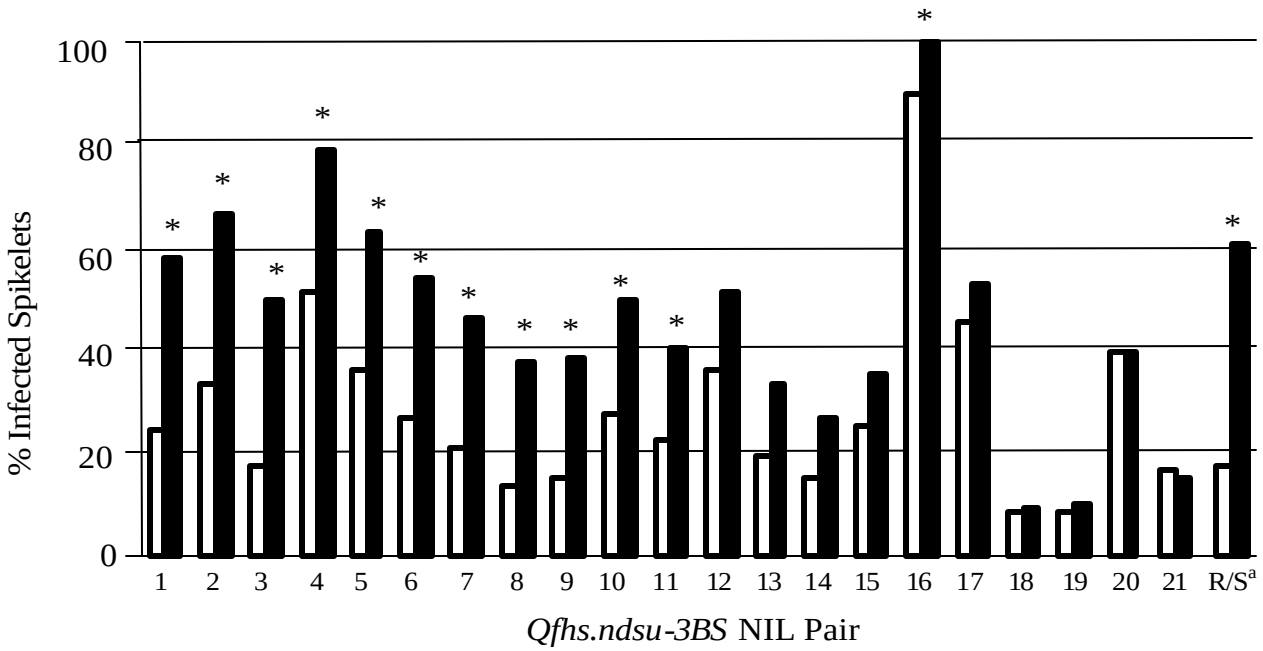

Figure 1. Results from one greenhouse point-inoculation disease screening of QTL-NIL pairs. Fifteen of the twenty-one pairs are from unique cross combinations. Open bars indicate lines with *Qfhs.ndsu-3BS* alleles; black bars indicate sib lines without *Qfhs.ndsu-3BS*. [a]Mean of resistant (R) parents with *Qfhs.ndsu-3BS* and susceptible (S) parents. *Significant at $P<0.05$

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SSR MAPPING OF FUSARIUM HEAD BLIGHT RESISTANCE IN WHEAT

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ABSTRACT

Fusarium head blight (FHB) of wheat, caused mainly by *Fusarium graminearum* Schwabe (telemorph *Gibberella zeae*), causes reduced yield and lowered grain quality. Identification of resistance sources and understanding the genetic basis of the resistance is beneficial to wheat breeding for FHB resistance. Two recombinant inbred wheat populations were developed by single-seed descent from the crosses 'Ning 894037 × Alondra' and 'Patterson × F201R', respectively. The phenotypic evaluation of the RI population Ning 894037 × Alondra displayed a continuous distribution with two peaks, suggesting a gene with large effect controlling the resistance coupled with some genes with relatively small effects. SSR marker analysis revealed three chromosomal regions associated with FHB resistance in this population, located on chromosomes 3B, 2D and 6B. The QTL on 3B accounted for 42.5% of the phenotypic variation. The three QTLs collectively explained 51.6% of the phenotypic variation. SSR marker analysis also provides evidence that the 3BS QTL in Sumai 3 was derived from Taiwan Wheat instead of the Italian line 'Funo', which was thought to be the donor of FHB resistance from previous pedigree analysis. In the RI population of Patterson × F201R, the phenotypic distribution is bell-shaped, suggesting quantitative inheritance of FHB resistance. Four chromosomal regions associated with resistance to FHB were identified in this population with SSR markers. The QTLs on chromosomes 1B and 3A have relatively large effects and accounted for 18.7% and 13.0% of the phenotypic variation, respectively. The four QTLs jointly accounted for 32.7% of phenotypic variation. The mapping results showed the genetic diversity of resistance genes in Ning 894037 and F201R, which represent the Chinese and European resistant sources, respectively. SSR markers closely linked to FHB resistance QTLs in these two parent lines may be helpful in breeding programs using marker assisted selection.

SUMMARY REPORT ON THE 2002 NORTHERN UNIFORM WINTER WHEAT SCAB NURSERY (NUWWSN)

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OBJECTIVE AND INTRODUCTION

This report is a compilation and analysis of data from the cooperative assessment of resistance to **Fusarium head blight (scab) (causal agent** *Fusarium graminearum* (teleomorph: *Gibberella zeae* Schwabe.)) in winter wheat germplasm adapted to the northern regions of North America. The report can be accessed in its entirety on the USWBSI web site.

METHODS

There were 46 lines and four checks in the 2002 trial (Table 1). The entries were successfully evaluated in 13 field tests and five greenhouse tests. Data was collected on heading date (HD), height (HGT), disease severity (SEV), disease incidence (INC), disease index (IND), kernel rating (KR), percent scabby seed (%SS), and DON.

Entry means were analyzed and least square estimate of means over tests were obtained. The entry x test interaction (ETI) appeared quite large for disease index, incidence, and severity from the field and greenhouse, so multivariate statistics were used to analyze the interaction and group those tests that produced similar results for each trait. Entry means were then calculated over the tests that produced similar rankings. Sets of test that produced similar rankings of entries were called megaenvironments (ME).

RESULTS

Entry was a significant source of variance for all traits. There was little ETI for heading date, height, kernel rating, % scabby seed, or DON. Thus, entry means over all tests are appropriate estimators of genetic value (Table 1). ETI seemed to be an important source of variation of disease severity from field and greenhouse trials, disease incidence, and disease index.

The ETI for incidence accounted for 30% of the treatment sum of squares. Seven of the nine tests were place into two ME. One ME consisted of IL+VA and the other consisted of IN+KY+MO+NY+OH. The correlation of entry means within an ME was generally greater than 0.50. The NE and ONT tests did not fit in any ME. The correlation between the two MEs was 0.12, suggesting that entry ranking varied between the two MEs. If we were to select the five entries with lowest incidence in each ME, only one of the selections (IL97-6755) would be the same in both MEs. Only three (IL97-6755, IL97-1828, and MO981020) of the best 10 selections would be the same in both MEs. None of five selections for highest incidence would be the same in both MEs. IL97-6755 had the lowest incidence in both MEs, but would be ranked 10th in NE and 28th in ONT. Better selection concordance would be expected between ONT and NE, or between either outlier test and either ME. None of the 10 entries selected for low incidence in either ME would be among the five worst in the other ME. The entry means for incidence in the IL+VA ME were positively correlated with heading date suggesting the earlier lines may have escaped some affect of the disease. The

opposite trend was present in the other ME (IN+KY+MO+NY+OH) and this may explain why these MEs gave different entry rankings.

The ETI for field severity accounted for 25% of the treatment sum of squares. Six of nine tests were places into two MEs (IL+KY+MO+VA and IN+OH). The remaining four tests (NE, NY, ONT, and SD) were outliers. The correlation of entry means between the two MEs was 0.43, though entry ranking was different in each ME. Only one (MO980829) of five selections for low severity would be the same in both ME. There is better concordance if selection pressure is relaxed as six of 10 selections for low severity would be the same in both MEs. None of the five entries selected for high severity were the same in both MEs. One entry (KY92C-0158-63) among the 10 entries with lowest severity in the IN+OH ME would be among the five worst in the IL+KY+MO+VA ME.

The ETI interaction for index accounted for 24% of the treatment sum of squares. The ETI pattern for index was similar to that found for severity as tests that grouped in the same ME for severity were also grouped together for index. Nine of the 13 tests were placed into two MEs: IL+KY+MO+VA and AR(2)+IN+KS+OH. The remaining tests (NE, NY, ONT and SD) appeared to be outliers. The existence of two MEs and four outlier tests show the complex ETI pattern for disease index. The correlation of entry means between the two MEs was 0.10. Assuming selection of five entries for low index in each ME, only two entries (IL97-1828 and MO980829) would be selected in both MEs. Only only four (IL97-1828, MO980829, IL97-6755, and MO981020) would be selected in both MEs if the ten entries with the lowest index were selected in both MEs. No entry would be select among the five worst entries in both MEs. None of the 10 entries selected for low index in either ME would be among the five worst in the other ME. The entry means for index for the AR(2)+IN+KS+OH ME were negatively correlated to heading date, while entry means for index from the other ME were positively correlated with heading date. Thus the interaction of heading date with index may explain why these ME provided different entry rankings.

The ETI for severity in greenhouse assays accounted for 27% of the treatment sum of squares and three of five tests were placed in a ME (AR+IL+MO). Correlation among these three tests all exceeded 0.55. The IN and KY tests were outliers, though both were more correlated to the ME ($r = 0.42$) than to each other ($r = 0.22$). Assuming selection of the best six entries in each AR+IL+MO, IN, and KY, only about 25% of the selections would be the same between any two tests. Only 20% of the entries selected for high severity would be the same between two tests.

Using entry means over all tests, heading date and height were not correlated to any disease trait (exceptions within certain ME are discussed above). There was a high correlation between the three head disease traits (incidence, severity, and index), and between the head disease traits and kernel rating and percent scabby seed. Field severity and index were correlated to greenhouse severity, and this relationship held even when severity and index were averaged within MEs.

Each entry was compared using LSD to the entries with the highest and lowest value for each of the seven disease traits. Three entries from Missouri and three from Illinois had low values for all seven traits (Tables 1 and 2). One entry from New York had low scores for six of seven traits while the two resistant checks (Ernie and Freedom) were low for five of seven traits. All nine of the resistant entries had low scores for percent scabby seed, DON, and severity in the greenhouse. Twelve entries had high scores for at least five of seven disease traits. All 12 had high scores for incidence, field severity, disease index, and kernel rating. Two entries had high scores for all seven traits, including the susceptible check (Pioneer 2545).

Table 1. Entry means for 2002 NUWWSN. Each entry was compared to the lowest (l) and highest (h) means in each column using LSD(0.05). "# low scores" is the number of disease traits for which an entry received a low score, "# high scores" is the times it received a high score.

	Trait:	HD	HGT	INC	SEV	IND	KR	%SS	DON	SEV-GH		
	# of tests:	9	7	9	10	13	4	4	2	5	# low	# high
	Units	Days	in	%	%	%	0-100	%	PPM	%	scores	scores
1	KY90C-054-6	139	37.3	55 h	34.1 h	23.2	21.4 h	22	16.6 l	54.2 h	1	4
2	KY93C-0876-66	140	35.3	64.9 h	40 h	30.1 h	30.9 h	21.5	21 h	44.8	0	5
3	KY92C-0010-17	140	37	67.2 h	38.5 h	29.5 h	31.1 h	26.7 h	26.3 h	31.2 l	1	6
4	KY92C-0158-63	142	36.3	68.3 h	31.8	27 h	21.6 h	23.6 h	19.8 l	42.8	1	4
5	VA01W447	135	35.6	61.4 h	41.8 h	31.9 h	27.3 h	27.3 h	12 l	48.8 h	1	6
6	VA01W461	137	36.6	53.8 h	28.8 l	18.8	24.9 h	14.3 l	15.8 l	40.2	3	2
7	VA01W462	135	34.6	61.8 h	38.4 h	29.4 h	27.5 h	17.5 l	13 l	34.9	2	4
8	VA01W465	139	32.6 l	66.9 h	36 h	28.4 h	20.1 h	22.5 h	28.8 h	40.6	0	6
9	VA01W469	137	35.1	62.9 h	36.8 h	30.2 h	29.2 h	24.1 h	14.3 l	55.5 h	1	6
10	P97397J1-4-1-4	135	34 l†	52.9 h	37 h	24.2	25.3 h	17.1 l	20.3	36.5	1	3
11	P97395B1-4-5-9	133 l	34.1 l	48	41.4 h	31.3 h	18 lh	22.2 h	18 l	46.7	2	4
12	P97395B1-4-2-7	134 l	34.6	46.9	33	22.3	13.3 l	14.2 l	14 l	32.7 l	4	0
13	P981128A1-23-1	137	36.3	52.9 h	37.7 h	25.3 h	22.4 h	20.5	15 l	48.9 h	1	5
14	P981238A1-1-11	137	33.6 l	44.3	28.2 l	17.2	21.8 h	19 l	18.3 l	15 l	4	1
15	OH708	140	38.1	54.9 h	41 h	28 h	16.5 l	15.2 l	15 l	48.8 h	3	4
16	OH712	141	41 h	56.4 h	38.7 h	25.3 h	23 h	22.5 h	15.3 l	56.4 h	1	6
17	OH719	142	38.9 h	53.4 h	28.8 l	19.7	21.9 h	16.9 l	14.5 l	31.5 l	4	2
18	OH720	141	39.9 h	53.2 h	41.2 h	25.6 h	24.7 h	23.5 h	11 l	44.8	1	5
19	OH685	136	37	54.6 h	45.9 h	28.2 h	26 h	23.3 h	24.8 h	63.7 h	0	7
20	IL96-6472	135	36.1	41.9 l	30.9	19	12.5 l	7.8 l	8 l	34.1	4	0
21	IL97-1828	137	36.3	29.5 l	24.6 l	13.6 l	7.7 l	11 l	11.4 l	32.8 l	7	0
22	IL97-6755	138	40.6 h	26 l	26.4 l	14.6 l	8.6 l	8.7 l	3 l	19.6 l	7	0
23	IL97-7010	136	39.1 h	38.6 l	29 l	15.7 l	14.4 l	12.7 l	16.3 l	18.6 l	7	0
24	IL98-6718	135	37.7	43.6	35.2 h	22.3	10.2 l	14 l	9.5 l	44.9	3	1
25	MILLENNIUM	142	39 h	38.6 l	30.2	15.1 l	15.6 l	25.6 h	7.5 l	43.4	4	1
26	NE98632	141	39 h	48.2	31.7	18.8	23.3 h	29.2 h	17.3 l	42.4	1	2
27	NE99543	139	38.3	40.7 l	38.1 h	21.6	23.9 h	30.7 h	14.3 l	64.3 h	2	4
28	NY89052SP-9	143 h	38.6	42.6	38.3 h	19.2	11.6 l	17.6 l	22.3 h	53.6 h	2	3
29	NY89086-7120	142	38.9 h	48.9	39.6 h	23.6	19.8 h	20.4	37.5 h	40.5	0	3
30	NY89082-7159	144 h	35.9	48.9	35.5 h	19.7	15.1 l	19.3 l	12.3 l	50.3 h	3	2
31	NY89064SP-7139	143 h	37.6	41.6 l	36.1 h	15.6 l	11.7 l	14.5 l	9.5 l	31.9 l	6	1
32	NY89088-7401	143 h	38.9 h	48.4	32.8	18	18.4 h	20.5	21.5 h	39.8	0	2
33	MDV11-52	136	32.4 l	59.1 h	41.5 h	32.9 h	30.2 h	24.8 h	28 h	46.6	0	6
34	M94*1549-1	137	34.3 l	56.7 h	35 h	26.9 h	22 h	24.6 h	14.5 l	38.6	1	5
35	M95-2994-1	140	35	46	31.3	20.2	20.9 h	23.1 h	20.3	25.5 l	1	2
36	MO980829	141	39.3 h	25.9 l	17.1 l	8.4 l	5.7 l	12.8 l	6.9 l	16.3 l	7	0
37	MO981020	137	36.7	37.2 l	23.5 l	15.9 l	8.6 l	11 l	18.3 l	19.8 l	7	0
38	MO000925	138	36.1	43.6	28.6 l	20.3	21.8 h	15.2 l	16.8 l	34	3	1
39	MO000926	136	34.4 l	40.3 l	26 l	16.9 l	13.8 l	14.3 l	17.8 l	24.7 l	7	0
40	MO000969	137	36.1	46.9	42.8 h	23.1	24.8 h	27 h	23.8 h	30.3 l	1	4
41	PATTERSON	136	37.1	50.8	40.1 h	29.6 h	18.1 lh	21.4	11.5 l	60.3 h	2	4
42	FREEDOM	140	37.6	44.6	22.4 l	15.7 l	20.4 h	17.9 l	13.3 l	16 l	5	1
43	PIONEER 2545	140	36.6	59.1 h	38.3 h	28.4 h	28.4 h	34.2 h	33.3 h	52.1 h	0	7
44	ERNIE	134 l	34.1 l	42.6	23.6 l	20	17 l	16.9 l	13.8 l	24.9 l	5	0
45	D9046-1	136	35.7	41.3 l	31.5	22.9	26.7 h	18.2 l	25.8 h	67.3 h	2	3
46	D9070-1	141	37.7	52	36.7 h	19.7	18.3 lh	13.3 l	17.5 l	33.5 l	4	2
	Average	138	37	49.3	34	22.5	19.7	19.5	17.1	38.9		
	LSD (0.05)	1.8	2.2	16.1	12.7	8.7	13.2	12.2	15	19		

† Indicates a mean that is not different from the lowest (l) or highest (h) mean in the column based on $LSD_{(0.05)}$

Table 2. Entry means for the most tolerant (top) and susceptible (bottom) entries in the 2002 NUWWSN

	Trait:	HD	HGT	INC	SEV	IND	KR	%SS	DON	SEV-GH		
	# of tests:	9	7	9	10	13	4	4	2	5	# low	# high
	Units	Days	in	%	%	%	0-100	%	PPM	%	scores	scores
21	IL97-1828	137	36.3	29.5 l	24.6 l	13.6 l	7.7 l	11 l	11.4 l	32.8 l	7	0
22	IL97-6755	138	40.6 h†	26 l	26.4 l	14.6 l	8.6 l	8.7 l	3 l	19.6 l	7	0
23	IL97-7010	136	39.1 h	38.6 l	29 l	15.7 l	14.4 l	12.7 l	16.3 l	18.6 l	7	0
36	MO980829	141	39.3 h	25.9 l	17.1 l	8.4 l	5.7 l	12.8 l	6.9 l	16.3 l	7	0
37	MO981020	137	36.7	37.2 l	23.5 l	15.9 l	8.6 l	11 l	18.3 l	19.8 l	7	0
39	MO000926	136	34.4 l	40.3 l	26 l	16.9 l	13.8 l	14.3 l	17.8 l	24.7 l	7	0
31	NY89064SP-7139	143 h	37.6	41.6 l	36.1 h	15.6 l	11.7 l	14.5 l	9.5 l	31.9 l	6	1
42	FREEDOM	140	37.6	44.6	22.4 l	15.7 l	20.4 h	17.9 l	13.3 l	16 l	5	1
44	ERNIE	134 l	34.1 l	42.6	23.6 l	20	17 l	16.9 l	13.8 l	24.9 l	5	0
1	KY90C-054-6	139	37.3	55 h	34.1 h	23.2	21.4 h	22	16.6 l	54.2 h	1	4
4	KY92C-0158-63	142	36.3	68.3 h	31.8	27 h	21.6 h	23.6 h	19.8 l	42.8	1	4
40	MO000969	137	36.1	46.9	42.8 h	23.1	24.8 h	27 h	23.8 h	30.3 l	1	4
27	NE99543	139	38.3	40.7 l	38.1 h	21.6	23.9 h	30.7 h	14.3 l	64.3 h	2	4
15	OH708	140	38.1	54.9 h	41 h	28 h	16.5 l	15.2 l	15 l	48.8 h	3	4
11	P97395B1-4-5-9	133 l	34.1 l	48	41.4 h	31.3 h	18 lh	22.2 h	18 l	46.7	2	4
41	PATTERSON	136	37.1	50.8	40.1 h	29.6 h	18.1 lh	21.4	11.5 l	60.3 h	2	4
7	VA01W462	135	34.6	61.8 h	38.4 h	29.4 h	27.5 h	17.5 l	13 l	34.9	2	4
2	KY93C-0876-66	140	35.3	64.9 h	40 h	30.1 h	30.9 h	21.5	21 h	44.8	0	5
34	M94*1549-1	137	34.3 l	56.7 h	35 h	26.9 h	22 h	24.6 h	14.5 l	38.6	1	5
18	OH720	141	39.9 h	53.2 h	41.2 h	25.6 h	24.7 h	23.5 h	11 l	44.8	1	5
13	P981128A1-23-1	137	36.3	52.9 h	37.7 h	25.3 h	22.4 h	20.5	15 l	48.9 h	1	5
3	KY92C-0010-17	140	37	67.2 h	38.5 h	29.5 h	31.1 h	26.7 h	26.3 h	31.2 l	1	6
33	MDV11-52	136	32.4 l	59.1 h	41.5 h	32.9 h	30.2 h	24.8 h	28 h	46.6	0	6
16	OH712	141	41 h	56.4 h	38.7 h	25.3 h	23 h	22.5 h	15.3 l	56.4 h	1	6
5	VA01W447	135	35.6	61.4 h	41.8 h	31.9 h	27.3 h	27.3 h	12 l	48.8 h	1	6
8	VA01W465	139	32.6 l	66.9 h	36 h	28.4 h	20.1 h	22.5 h	28.8 h	40.6	0	6
9	VA01W469	137	35.1	62.9 h	36.8 h	30.2 h	29.2 h	24.1 h	14.3 l	55.5 h	1	6
19	OH685	136	37	54.6 h	45.9 h	28.2 h	26 h	23.3 h	24.8 h	63.7 h	0	7
43	PIONEER 2545	140	36.6	59.1 h	38.3 h	28.4 h	28.4 h	34.2 h	33.3 h	52.1 h	0	7
	Average	138	37	49.3	34	22.5	19.7	19.5	17.1	38.9		
	LSD (0.05)	1.8	2.2	16.1	12.7	8.7	13.2	12.2	15	19		

† Indicates a mean that is not different from the lowest (l) or highest (h) mean in the corresponding column in Table 1 based on $LSD_{(0.05)}$

Table 3. Possible sources of resistance for the most resistant entries in Table 2.

Entry	Pedigree	Possible source of resistance
IL97-1828	P818311-16-2-1-2-3-3/IL90-4813	
IL97-6755	IL90-4813//IL85-3132-1/NING7840	Ning 7840
IL97-7010	IL90-6363//IL90-9464/NING7840	Ning 7840
MO980829	MO11769/MADISON	MO11769 which is not a descendent of Ernie, Sumai 3, or Ning 7840
MO981020	MO11769/MADISON	MO11769 which is not a descendent of Ernie, Sumai 3, or Ning 7840
MO000926	ERNIE/AP HICKORY	Ernie
NY89064SP-7139	88029(84061(6120-15/F29-76)/AUGUSTA)/HARUS	Harus and 6120-15 (Geneva) are moderately resistant

FUSARIUM HEAD BLIGHT IN HEXAPLOID WHEAT POPULATIONS DERIVED FROM LINES WITH TYPE I RESISTANCE

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ABSTRACT

Fusarium head blight (FHB) of wheat, caused mainly by *Fusarium graminearum* Schwabe, is a serious problem in North Dakota spring wheat.

An adapted, FHB resistant spring wheat, ND2710, was selected from some Sumai 3 derived lines in 1993 and been used in many crosses in the North Dakota breeding program since that time. It was a parent of the ND cultivar 'Alsen', released in 2000, and planted on over 2 million acres in 2002. The FHB resistance of ND2710 has proven durable over several years and in a wide range of environments. One flaw of the resistance pattern of ND2710 is its acceptance of individual primary infections, even though these infections do not spread to adjacent spikelets. To find a parent which will better resist primary infection we tested two populations derived from three-way crosses between adapted ND spring wheat and two lines thought to possess resistance to primary infection (= "Type 1" resistance). One parent was 'Frontana', the line in which type 1 resistance was first described; the other was 'W9207', a line derived from intercrossing of 6 of the best Chinese resistance sources. The two populations were advanced to F-5 by single seed descent and the lines were tested for FHB in an inoculated, mist-irrigated field nursery in 2001. At 3.5 weeks post-inoculation, approx. 50-60 spikes in each of two reps were individually scored for FHB on a 0-100% scale. Grain was harvested from mature spikes and proportion of visually scabby kernels and level of deoxynivalenol (DON) in the harvested grain determined. The two populations were similar in mean and distribution for all FHB measures. Overall about 5% of lines had FHB disease measures similar to or better than ND2710, but 22% and 27% of lines from these populations had FHB incidence values lower than this standard. The best lines from these populations had incidence values indicating less than half as many primary infections as ND2710.

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SCAB SCREENING USING FROZEN SPIKES

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ABSTRACT

Evaluation of Fusarium head blight (FHB) in the field environment is difficult. The amount of material in the scab nursery is large and reading the symptoms before the heads begin to mature can be problematic. To extend the days of reading symptoms a method was suggested in which spikes are harvested 21 days after flowering and frozen (Personal communication, R. Stack via D. Hershman). Spikes from two elite tests, Magnum and Mondo, along with the checks in the Kentucky variety trial were frozen and data collected from the spikes in 2002. A sample of approximately 100 spikes per row was harvested with a hand sickle at two locations, Lexington and Princeton, KY. The spikes were placed into resealable bags then placed into an ice chest. The samples were transferred into a freezer and were kept there until needed. The frozen spikes were read at various times. The samples remained green and symptoms were still visible. Disease incidence was calculated by counting the number of infected spikes per bag divided by the total number of spikes. Average head severity was assessed by evaluating 15 infected heads per bag. The preliminary data indicates that freezing infected heads is an effective tool for reading scab symptoms. The data was analyzed by comparing severity rankings of entries that were frozen in 2002 to field samples in 2001. Severity values were also compared to greenhouse severity values. Harvesting wheat at 21 days after flowering does not give peak severity of FHB on the entry row; however, the severity of the checks were similar between field rankings and frozen spike rankings in 2002 (r^2=0.88, P=0.01). The correlation from the elite test field spikes in 2001 and frozen spikes in 2002 was less encouraging (r^2=0.18 P=0.07, both locations). Further testing will occur during the upcoming year on improving the method into a efficient tool for screening and selection of resistant FHB genotypes.

FUSARIUM GRAMINEARUM AND DON IN SINGLE SEEDS FOLLOWING GREENHOUSE POINT INOCULATION

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ABSTRACT

The single floret inoculation system is commonly used to screen wheat cultivars and germplasm for FHB Type II resistance in the greenhouse by a visual rating of the spread of fungal hyphae in the spike and spikelets. Evaluation of this system in our laboratory across a wide range of germplasm has shown that the visual ratings of spikelet infection are poorly associated with the *Fusarium graminearum* (Schwabe) infection occurring in the seed, rachis and other floral components the same spikelets. The objective of this research was to use the single floret inoculation system to relate ratings of visual spikelet infection in the greenhouse to *F. graminearum* infection and deoxynivalenol levels in seeds of adjoining florets in all individual spikelets on each infected spike. The movement of fungal hyphae and DON into the various components of the spike was evaluated following point inoculation (PI) of a floret at a middle location of the spike for two susceptible (P 2555 and VA 96W-326) and three resistant (P 25R18, Roane, Coker 9474) cultivars. Although high levels of spikelet infection occurred in the susceptible cultivars in the greenhouse, the fungal movement in the spike occurred primarily in two ways; localization around the PI and movement down the spike from the PI. Thus, severity of greenhouse infection overestimated *F. graminearum* seed infection and DON presence in susceptible cultivars and underestimated fungal infection and DON in resistant cultivars. A close relationship was shown between the presence of *F. graminearum* in seed from the right floret with the presence of DON in seed from the left floret in both susceptible and resistant cultivars. Although DON was present in seed of resistant cultivars the levels were much lower than susceptible cultivars and often did not exceed 1 PPM. This investigation should allow us to evaluate the current methods for screening for Type II resistance to FHB infection in an attempt to develop more accurate methods. (This research will be presented as a poster at the annual meeting of the US Barley and Wheat Scab Initiative in Covington, KY on December 7-9, 2002.)

HOW TO MAKE INTELLIGENT CROSSES TO ACCUMULATE FUSARIUM HEAD BLIGHT RESISTANCE GENES BASED ON KNOWLEDGE OF THE UNDERLYING RESISTANCE MECHANISMS

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OBJECTIVES

To describe crossing strategies to accumulate mechanisms of resistance to FHB.

INTRODUCTION

A number of mechanisms or Types of resistance, likely coded for by specific genes, underpin wheat's final response to Fusarium head blight (FHB). Accumulating additively inherited resistance genes to enhance genetic control of FHB has been proposed (Anonymous, 2001; Singh and van Ginkel, 1997). But in the absence of specific information on these genes gene-based breeding is not yet feasible. Until the specific genes that cause these phenotypic response mechanisms are identified, disease evaluation for each mechanism has to be conducted independently.

However, in the case of FHB, intelligent crosses can be made by applying our knowledge of the various resistance mechanisms responsible for its genetic control.

Characterizing FHB Resistance

Before applying the mechanisms of resistance present in genetic stocks to a crossing scheme, they must be carefully characterized, which can be an arduous process.

A description of how the different mechanisms of resistance to FHB are determined at CIMMYT follows. We base our approach on published literature and local experience. The *Fusarium* sp. used mainly in our work is *F. graminearum*.

Specific inoculation, screening, and evaluation techniques are used for each type of resistance to avoid confounding the disease response observations of the various resistance mechanisms. Because genotype x environment interactions may affect the ranking of genotypes for any one of the resistance mechanisms, an appropriate number of replications across and within years is needed. The level of interaction appears to be linked to the level of resistance: if a genotype's resistance level is already pretty high and based on the presence of several mechanisms, it will be less affected by the environment and will express more stable resistance. Resistance based on just one mechanism is more susceptible to environmental effects.

The targeted germplasm and check cultivars are always inoculated on the same day. Later upon harvest the response of the tested lines is compared with that of the checks inoculated on the same day. If this is not done, erroneous and spurious response readings may result. A broad spectrum of checks is used, ranging from the highest level of susceptibility to the highest level of resistance, with at least two representatives at each level.

Type I (penetration by the fungus) and II (spread of mycelium throughout the spike) resistances were identified as distinct mechanisms by Schroeder and Christensen in 1963. Two other mechanisms or types were proposed by Miller and Arnison (1986), Wang and Miller (1988), and Mezterhazy (1995).

Type I resistance - To avoid interaction with height and maturity, inoculation for Type I resistance is done by spraying a fusarium spore suspension (50,000 spores per ml) on a horizontal plane onto labeled spikes at the onset of anthesis. Spikes are evaluated for resistance a fixed number of days post inoculation, depending on the prevailing conditions and the disease reaction of the resistant and susceptible checks. The interval (25 to 35 days) between inoculation and evaluation may vary from year to year. However, within the same year a fixed number of days is used. Thirty days is generally appropriate under Mexican conditions.

Type II resistance - A tuft of cotton gently soaked in inoculum (50,000 spores per ml) is inserted into a floret in the center of the spike at the onset of anthesis with a pair of tweezers; each spike is then covered with a glassine pollination bag. The lightweight, narrow bag prevents additional FHB inoculum from entering the spike through allo-infection and helps maintain a high level of humidity, which favors disease development. Spikes are evaluated for resistance 25-35 days post-inoculation.

Type III resistance - *Fusarium graminearum* produces mycotoxins, especially trichothecenes, during the infection process. Type III resistance is associated with degradation of toxins in the grain, as described by Miller and Arnison (1986). In preparation for toxin evaluation and quantification, genotypes are sprayed with an inoculum suspension when 50% of the spikes in a plot have reached anthesis. A 20-g seed sample from the inoculated spikes is collected at harvest, and resistance is evaluated by quantifying the accumulated toxin in the laboratory using the FluoroQuant Rommer method.

Resistance types IV and V - Wang and Miller (1988) described Type IV resistance as tolerance to high DON concentrations. They reported that some cultivars can tolerate high mycotoxin concentrations with no negative effects on growth. A six-year study led to the conclusion that this tolerance should be evaluated as a relative parameter of infection, and that yield response may help describe the disease reaction of the genotypes (Mezterhazy, 1995).

To identify Type IV resistance, a paired plot of each genotype is planted. One plot is treated as described for Type I, and the other is sprayed with a functional fungicide (e.g., Folicur Plus) three times during the cycle. The test weight of grain harvested from the fungicide-treated plot is compared with that of grain from the inoculated plot to calculate the percentage loss.

To evaluate for Type V resistance, grain from the two plots described above is visually scored (1=very healthy and plump; 5=diseased and shriveled) at the same time to determine relative

grain filling. This parameter has not been described in the literature as a FHB resistance mechanism, but is used at CIMMYT to complement and aid in identifying Type IV resistance.

EVALUATING PARENTAL STOCKS

All germplasm being considered for crossing is first characterized for FHB resistance, as described above and as depicted in the Table 1. Commonly these materials include established sources of resistance, promising introductions contributed by colleagues, good combiners for the desired agronomic traits, and major varieties in the target region. This information is later used as the basis for making appropriate crosses.

Table 1. Parental characterization for FHB resistance mechanisms. Codings using bold/ Italics/underline/non-underline indicate the relative levels of resistance, with bold and underlined lettering representing the highest level.

		RESISTANCE MECHANISM or TYPE				
		I	II	III	IV	V
Entry	Cross	Damage (%)	Damage (%)	Toxin (ppm)	Grain losses (%)	Grain (1-5)
1	GOV/AZ//MUS/3/DODO/4/BOW	**2.51**	**2.66**	**0**	*21.16*	*2*
2	MILAN/SHA7	**0.00**	**6.07**	**0.14**	*13.29*	*2*
3	ALUCAN/DUCULA	*13.73*	*21.12*	**0.52**	*13.18*	*2*
4	CBRD/KAUZ	**3.21**	**6.43**	*2.3*	**2.36**	**1***
5	R37/GHL121//KAL/BB/3/JUP/MUS/4/2*YMI #6/5/CBRD	**1.49**	*10.53*	**0.026**	**7.68**	**1**
6	GUAM92//PSN/BOW	**4.90**	*13.16*	**0.21**	**6.62**	**1**
7	NG8675/CBRD	**0.26**	**8.20**	**0.48**	**7.67**	**1**
8	ALTAR 84/AE.SQUARROSA (224)//ESDA	**4.42**	*16.89*	**0.49**	**1.75**	**1**
9	BCN*2//CROC_1/AE.SQUARROSA (886)	*11.56*	**4.82**	**0.38**	**1.68**	**1***
10	MAYOOR//TK SN1081/AE.SQUARROSA (222)	**0.86**	**7.26**	**0.49**	**1.3**	**1***
11	SABUF/5/BCN/4/RABI//GS/CRA/3/AE.SQUARROSA (190)	**1.98**	**8.46**	**0.069**	*8.07*	*2*
12	SHA3/CBRD	**3.87**	**5.99**	**0**	**6.94**	**1**

Coding	*FHB score*
123	very good
123	good
123	moderate
123	poor

CROSSING STRATEGIES

If crossing is to be effective, the mechanisms of resistance should be complementary among parental stocks, as is evident in Table 1.

Using the information in Table 1, cross combinations can be designed to cross parents that fully complement one another in the sense that one or the other contributes high levels of resistance (scored as ‘very good’) for each of the five mechanisms. With luck and properly executed selection, transgressive segregants will subsequently be identified that express high levels for all five resistance types.

Following parental stock characterization and crossing, the segregating F2 generations are grown and selected. But also additional crosses can be made on the F1s. We usually opt for a

top cross or, in some cases, a limited backcross, to a line with desirable agronomic type, high yield potential and yield stability, durable resistance (to other relevant diseases), good combining ability, and excellent quality. In the case of FHB, we also make doubled haploids (DH) on a limited number of simple crosses, to enhance our ability to identify homozygous transgressive progeny in replicated experiments that combine multiple resistance mechanisms.

CONCLUSION

Our approach uses data gathered on the various mechanisms of resistance on relevant parental stocks to allow more intelligent crossing. Such an approach increases, at least in theory; the chance of identifying superior progeny carrying accumulated resistance mechanisms against FHB.

EPILOGUE

An improved understanding of the FHB infection process and related resistance mechanisms reveals the potential relationship between FHB and Karnal bunt (KB) resistance. The infection processes of the two diseases are similar: in both cases, florets are infected during anthesis, and resistance is very much influenced by environmental fluctuations. Consequently, the same lines may seem resistant in some years but susceptible in others. Alleles with large effects on resistance have been noted in both diseases (Fuentes-Davila *et al*., 1995; Singh *et al*., 1995), with some lines expressing high levels of resistance following the introgression of just 2-3 desired alleles. Significant genetic variation for both diseases is available, and anecdotal evidence suggests that some genetic sources (especially among the Chinese materials) are resistant to both diseases. If the same genes confer resistance to the two diseases, this would explain why many Chinese wheats are resistant to KB, though the disease has not been reported in China. Should this be proven, then these two threats to wheat production in the USA could be addressed, at least in part, through a concerted research effort involving groups now independently engaged in research on these two diseases.

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APPARENT AND ACTUAL SEED QUALITY IN SOFT RED WINTER WHEAT INFECTED WITH *FUSARIUM GRAMINEARUM*

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ABSTRACT

Head scab caused by *Fusarium graminearum* (Schwabe) has caused significant losses in the soft red winter wheat crop in Kentucky and in small grain crops in many regions of North America. Head scab epidemics not only result in significant yield losses, but also can cause serious reductions in seed quality. To investigate associations between apparent infection based on spike symptoms, apparent damage to the kernel and the actual seed infection, we evaluated fifteen (15) lines of the 2002 Southern Scab Nursery. Seeds of each line were separated into three categories, depending on the visual aspect of the seed, so as to define "good quality" seed (without any symptom of infection), "shriveled" seed and "poor" seed (tombstones).Then, to determine the presence of *Fusarium graminearum* in these three classes of seed, seeds were plated, five (5) plates of each class, with ten seeds per plate. Plates were incubated at 20°C and at seven and fourteen days the presence of *F. graminearum* was recorded. Also a DON test was run to test the concentration of DON in these three categories of seeds. Seeds showed high levels of infection, above 90 % in seeds of poor quality, between 70-80% in shriveled seed and 40-50 % in seed of good quality. The good quality seed showed more variation, depending on the line, and conditions in the field. To evaluate the relation between this actual infection in the seed and field data, percentage of visually scabby kernels was measured for each line, and then correlated with the actual presence of *F. graminearum* in the seed. A better correspondence between apparent infection and actual seed infection could be useful in assessing varieties in the field, and predicting the real infection in the seed, depending on its quality. Correlations of seed quality and the presence of *F. graminearum* with DON will be presented.

EFFECT OF SUMAI 3 CHROMOSOMES ON TYPE II AND TYPE V SCAB RESISTANCE IN WHEAT

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ABSTRACT

Two sets of substitution lines were developed by crossing individual monosomic lines of Chinese Spring (recipient) with scab resistant cultivar Sumai 3 (donor) and then using the monosomics as the recurrent male parent for four backcrosses (without selfing after each backcross). The disomic substitution lines were separated from selfed BC_4F_2 plants. Chromosome specific SSR markers were analyzed for polymorphism between Sumai 3 and Chinese Spring. Polymorphic markers were used to identify substitution lines for specific chromosomes. Based on the specific SSR markers, chromosome substitutions occurred in thirty-six lines, and six lines segregated alleles from the two parents or were homozygous for the allele from Chinese Spring. These substitution lines were used to evaluate Type II (spread within the head) and Type V (deoxynivalenol accumulation within kernels) scab resistance. The objective was to use the substitution lines to evaluate the effect of individual chromosomes of Sumai 3 on Type II and Type V scab resistance in the greenhouse. Significant differences in Type II scab resistance and deoxynivalenol (DON) levels among different Chinese Spring (Sumai 3) substitution lines were detected. Positive chromosome substitution effects on Type II scab resistance were found on chromosomes 2B, 3B, 6B, and 7A from Sumai 3. Chromosomes 3B and 7A also reduced DON accumulation within the kernels, while chromosomes 1B, 2D, and 4D from Sumai 3 increased DON concentration. Chromosome 7A from Sumai 3 had the largest effect on resistance to scab spread and DON accumulation. Additional research is in progress on the scab resistance conferred by chromosome 7A.

Key words: Type II scab resistance, Type V scab resistance, substitution lines, SSR, *Triticum aestivum*.