STEEP PROGRESS REPORT

RESEARCH PROJECT TITLE: Improving genetic resistance to Cephalosporium stripe of wheat through field screening and molecular mapping with novel genetic stocks

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INTERIM REPORT

PROJECT OBJECTIVES:
1. Conduct field evaluation of progeny from single and three-way crosses of PNW wheat cultivars with sources of Cephalosporium resistance from Europe.
2. Evaluate molecular markers for Cephalosporium stripe resistance and the potential for marker-assisted selection.
3. Estimate the level of resistance required to attain minimal yield loss caused by Cephalosporium stripe.

KEY WORDS: Cephalosporium, conservation tillage, disease resistance, wheat

STATEMENT OF PROBLEM: Cephalosporium stripe of wheat is a limiting factor for many Pacific Northwest wheat growers in erosion-prone areas, especially when early planting and/or trashy fallow are practiced. Burning or plowing stubble and delayed seeding can provide substantial control of Cephalosporium stripe. However these cultural control methods conflict strongly with attempts to control soil erosion. Wheat cultivars and common wheat germplasm of the PNW have shown limited resistance to this disease. We have recently identified promising genetic stocks with superior resistance to Cephalosporium stripe. However, incorporating genetic resistance into new wheat cultivars remains difficult due to inconsistencies in expression, environmentally dependent and erratic disease pressures, and the difficulty of screening early generation breeding materials. Though resistance to Cephalosporium stripe has been assumed to be quantitatively inherited, this assumption has not been rigorously tested. Molecular markers for Cephalosporium stripe resistance have been almost non-existent.

ZONE OF INTEREST: Low and intermediate rainfall, winter wheat-fallow

ABSTRACT: A total of 1,888 field plots incorporating 484 entries were evaluated for Cephalosporium stripe reaction in the 2006-07 season. A mapping population of 268 progeny derived from a cross of Coda x Brundage was evaluated in replicated plots in both Pendleton and Moro, OR. We found patterns of variation expected of a quantitative trait. Progeny with resistance greater than both parents were identified at both locations. On average, club progeny were more resistant than progeny with a common head type, and awnless progeny may be slightly more resistant than awnless progeny. However, all possible combinations of resistance level and head traits were found among the progeny, suggesting that it may be possible to move resistance genes between these classes. We also evaluated 144 wheat and barley entries in replicated trials for PNW small grain breeders, where white head percentages among the entries ranged from 0.1 to 62%. A large collection of SSR and other

markers are being used to identify regions of the wheat genome that are associated with Cephalosporium stripe resistance in a Diversity Set of 90 lines that represent the range of germplasm currently being used in the OSU Wheat Breeding Program. As phenotypic data for the populations become available from the field, associations will be made of disease resistance with molecular markers. In a yield loss study of 12 wheat entries, there was nearly a 1:1 correspondence of difference in % whiteheads between uninoculated and inoculated plots and the amount of yield loss between uninoculated and inoculated plots for the majority of entries. A total of 1766 plots were sown in fall 2007, incorporating 679 entries. These entries include the Coda x Brundage population, as well as 167 progeny from a cross of Tubbs x a European resistance source.

RESULTS AND INTERPRETATION: Table 1 shows the trials, entries, and replications established in the field for the first season of the project. Results are then discussed by objective.

Table 1. Entries evaluated for Cephalosporium stripe 2006-07 season. Numbers include checks.

	Pendleton			Moro		
Trial	Reps	# Entries	# Plots	#Reps	#Entries	#Plots
Brundage x Coda Pop.	2	300	600	2	300	600
Wheat Yield Loss	4	24	96	4	48	96
Barley Yield Loss	4	16	64			
Oregon Elite Nursery	3	40	120			
USDA/WSU Elite	3	36	108			
USDA/WSU Screen 1	3	24	72			
USDA/WSU Screen 2	3	24	72			
OSU Barley Nursery	3	20	60			
Total		484	1,192		348	696

Objective 1. Conduct field evaluation of progeny from single and three-way crosses of PNW wheat cultivars with sources of Cephalosporium resistance from Europe: Materials originally targeted for our investigations include populations derived from several single and 3-way crosses of Tubbs and Weatherford with several Nickerson Seeds Advanced (NSA) lines that show very high yield potential and resistance to Cephalosporium stripe. These crosses were made in spring 2002 and were then advanced via single-seed descent in the greenhouse. Several factors caused us to alter the specifics of our studies, though will allow us to better meet our overall objectives. First, a mapping population of 268 recombinant inbred line progeny derived from a cross of Coda x Brundage was provided to us by Bob Zemetra (Univ. of Idaho) for Cephalosporium screening. This is a very desirable population for evaluation as both parents are already adapted to the PNW. Brundage shows an intermediate level of resistance to Cephalosporium stripe and Coda has been among the most resistant PNW varieties we have tested over the years. Also, Brundage is a common head type and awnless, while Coda is an awned club wheat. It is very useful to study the association between these morphology traits and Cephalosporium stripe resistance because club wheats often are more resistant to Cephalosporium than are common

wheats. Further, most of the Cephalosporium-resistant lines we are using from Nickerson Seeds are awnless, whereas many of our susceptible PNW varieties are awned. An additional opportunity arose because of favorable seeding conditions, which allowed us to seed early at the Moro Field Station for the first time in several years. Though not originally proposed, this additional site enabled us to screen the Coda x Brundage population in two environments in the same year. Finally, seed quantities from our Oregon x NSA crosses were not as high as we had hoped in fall 2006 to attain optimum plot size and replication. We thus decided that it would be more fruitful to focus on the Coda x Brundage population in the first year of the study, begin to evaluate progeny of Oregon x NSA crosses along with the Brundage x Coda population in the second year, and focus only on the Oregon x NSA lines in the third year.

Disease expression resulting from artificial inoculation, trashy fallow, and early seeding (September 11-13, 2006) provided very useful separation of entries in the Coda x Brundage population, as indicated by the range of whitehead percentages observed in the checks (Table 2).

Table 2. Percent whiteheads for example check varieties in the Coda x Brundage population study.

	% Whiteheads	
Entry	Pendleton	Moro
Brundage	26.1	14.8
Coda	5.2	13.6
Madsen	12.9	9.9
Rossini	15.6	8.9
Stephens	57.9	34.0
Tubbs	26.1	18.4
WA7437	1.2	6.0

Table 3. Percent whiteheads (%WH) and head morphology for progeny of the Coda x Brundage mapping population. N = number of progeny.

	Pendleton		Moro	
Head Type	N	%WH	N	%WH
Club	124	11.0	124	11.0
Common	141	15.8	141	18.1
Awned	124	15.5	124	16.6
Awnless	132	11.7	132	13.0

We found substantial variation among progeny at both locations (Figs. 1 and 2); square-root transformation was used to normalize the data. We found patterns of variation expected of a quantitative trait. Coda was substantially more resistant than Brundage in Pendleton, but Brundage and Coda showed similar levels of disease in Moro for reasons that are currently unknown. Though Coda was more heavily diseased at Moro, about half of the progeny were more resistant than Coda. Even at Pendleton, there were some progeny with lower whitehead percentages than either parent (Fig. 1), suggesting that progress can be made in stacking resistance genes.

The club/non-clubbed and awned/awnless traits both segregated in approximately a 1:1 ratio (Table 3). On average, club progeny were more resistant than progeny with a common head type,

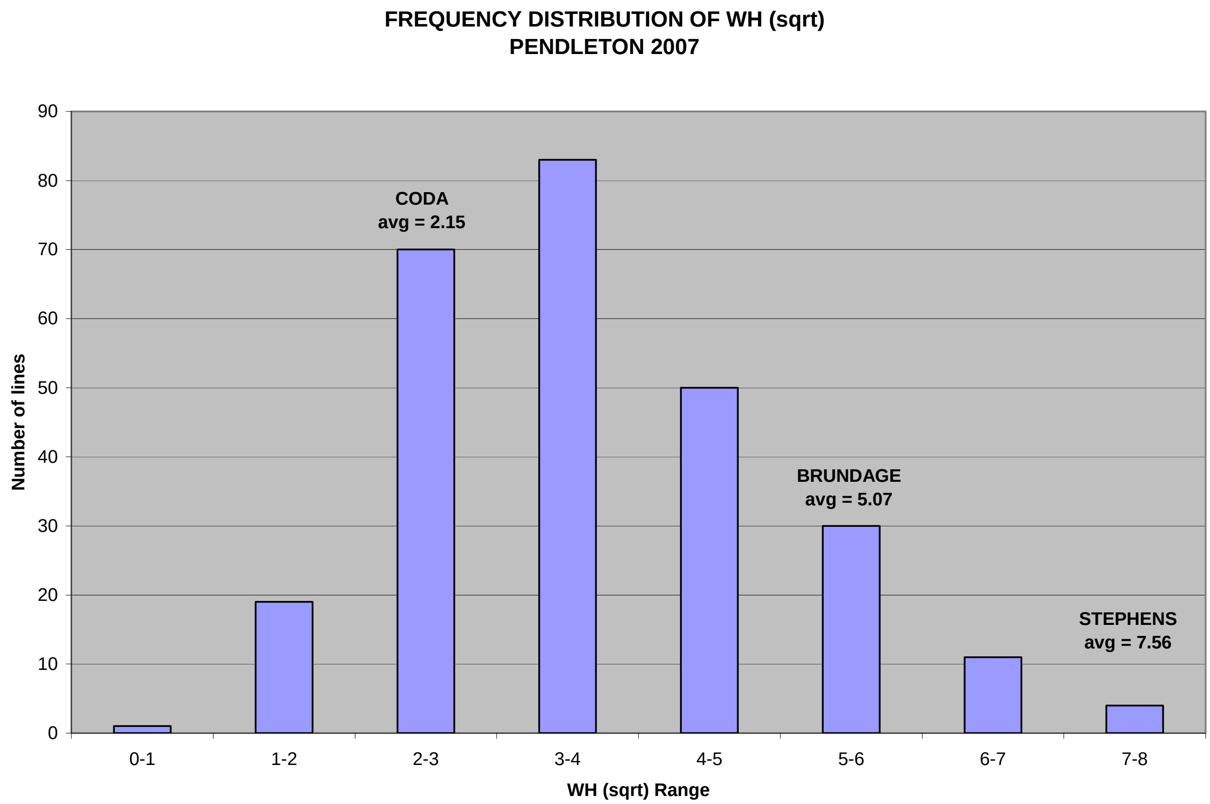

Fig. 1. Frequency distribution for square root(% whiteheads) of progeny in Coda x Brundage mapping population evaluated in Pendleton, 2007.

and awnless progeny may be slightly more resistant than awnless progeny. However, all possible combinations of resistance level and head traits were found among the progeny (data not shown), suggesting that it may be possible to move resistance genes between these classes.

We also evaluated 144 wheat and barley entries in replicated trials for PNW small grain breeders (Table 1). Disease expression was very good, with white head percentages among the entries ranging from 0.1 to 62% and good repeatability among replications.

Objective 2. Evaluate molecular markers for Cephalosporium stripe resistance and the potential for marker- assisted selection: A large (~1000) collection of SSR and other markers are being used to identify regions of the wheat genome that are associated with Cephalosporium stripe resistance in a Diversity Set of 90 lines that represent the range of germplasm currently being used in the OSU Wheat Breeding Program. This of course includes many NSA lines with resistance to Cephalsoporium stripe, as well as Coda and Brundage. Candidate regions will be mapped and analyzed for markers. Subsequently, the rest of the genome will be scanned. The

Diversity Set was planted for phenotypic evaluation in fall 2007 (Table 5); phenotypic data has

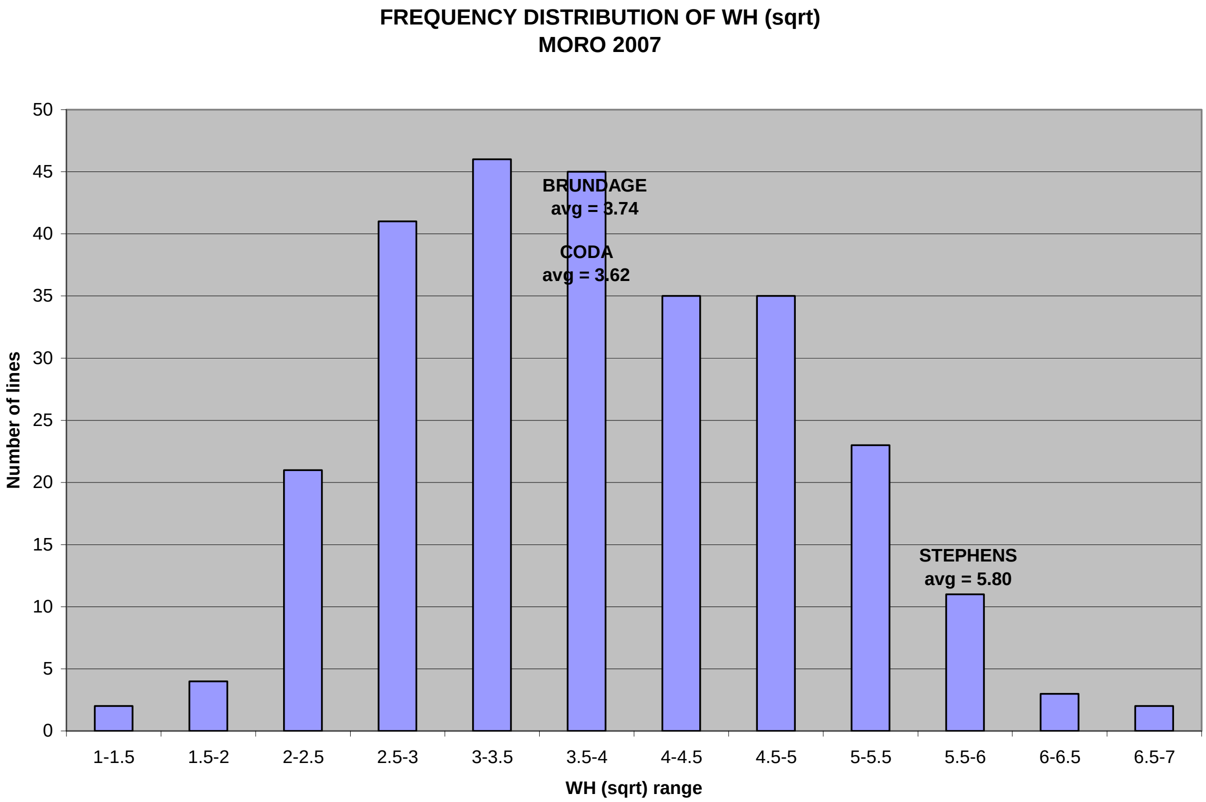

Fig. 1. Frequency distribution for square root(% whiteheads) of progeny in Coda x Brundage mapping population evaluated in Pendleton, 2007.

already been collected for some of the lines in previous STEEP work. As phenotypic data for the populations become available from the field, marker trait associations will be obtained by simple interval regression analysis. This genotypic information will then be used to calculate genotypic distances for all pair-wise comparisons among lines for a given marker. Concurrently, Cephalosporium stripe evaluations and screening will be used to develop a phenotypic distance matrix among lines (resistant vs. resistant, resistant vs.susceptible; susceptible vs. susceptible, etc.). Lastly, a scaled correlation between the genotypic and phenotypic distance matrices will be used to identify markers or regions that are highly correlated with resistance to Cephalosporium stripe.

Objective 3. Estimate the level of resistance required to attain minimal yield loss caused by Cephalopsorium stripe: A wheat yield loss study was conducted in the 2006-07 season in both Pendleton and Moro. The experiment consisted of a factorial arrangement of 12 wheat genotypes x two inoculation treatments (inoculated or non-inoculated). An additional experiment in Pendleton consisted of eight barley genotypes x the two inoculation treatments. In all cases, plots are 5 x 20 ft. Plots were seeded into ground adjacent to our main experiments and was not previously infested. In Pendleton, results were complicated by an unexpectedly high level of natural inoculum. The Pendleton wheat experiment is being repeated in 2007-08 on ground that was plowed to reduce inoculum levels. In Moro, we had a much better distinction between uninoculated and inoculated plots. For the majority of entries, there was nearly a 1:1 correspondence of difference in % whiteheads between the uninoculated and inoculated plots and the amount of yield loss between uninoculated and inoculated plots (Table 4).

Table 4. Effect of Cephalosporium stripe on yield loss of wheat entries in Moro, 2007.

Entry	% Whitehead difference uninoc. – inoc.	% Yield Reduction
Stephens	42.6	41.2
Madsen	11.1	13.1
Tubbs	33.5	24.6
919	28.5	30.0
924	21.6	23.2
Rossinni	12.7	14.8
CephB17	21.6	20.6
CephC75	34.8	36.0
CephD11	20.3	31.6
WA 7437	4.3	12.3
0085	28.0	26.6
1757	32.4	23.7

Fall 2007 Planting: A total of 1,766 plots were sown in Pendleton on September 10-11, 2007 and excellent stands have been obtained. This planting includes 175 progeny from an Einstein x Tubbs mapping population, with Einstein being a resistance source from the Nickerson Seeds Advanced (NSA) lines.

Table 5. Entries planted in Pendleton for Cephalosporium evaluation, 2006-07 season. Numbers include checks.

	Pendleton		
Trial	#Reps	# Entries	# Plots
Brundage x Coda Pop.	3	300	900
Einstein x Tubbs Pop.	2	175	350
Oregon Diversity Set	3	90	270
Wheat Yield Loss	4	24	96
Oregon SW Elite Nursery	2	40	80
Oregon HW Elite Nursery	1	40	40
OSU Barley Nursery	3	10	30
Total		679	1,766

Anticipated outcomes and impacts: The main outcome of the project will be wheat cultivars with superior resistance to Cephalosporium stripe combined with favorable quality, yield, and other important agronomic characteristics. Such cultivars will greatly increase ability of wheat growers to successfully implement conservation tillage practices in erosion-prone areas. Availability of molecular markers linked to Cephalosporium stripe resistance may facilitate rapid pre-screening of breeding materials in absence of the pathogen, saving significant amounts of time, space, and materials. The yield loss studies will help us to determine the level of resistance required to avoid significant economic loss due to Cephalosporium stripe.

INTERACTION (COOPERATION) WITH OTHERS CONDUCTING RELATED ACTIVITIES: Knowledge and germplasm are routinely shared with all other wheat breeding programs in the PNW, as well as with Tim Murray, plant pathologist at Washington State University, and Extension agronomists in the PNW region. Dick Smiley (OSU, Pendleton) evaluates promising germplasm for resistance to Fusarium foot and root rot, a disease complex of high importance in conservation tillage systems, to determine if Cephalosporium stripe resistant lines are also tolerant to the Fusarium complex.

PUBLICATIONS AND PRESENTATIONS:

Presentations

CBARC Moro Station Field Day, Pendleton, OR, June 2006. "Screening wheat for resistance to Cephalosporium stripe".