

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 1,766 field plots incorporating 679 entries were evaluated for Cephalosporium stripe reaction in the 2007-08 season. A mapping population of 268 progeny derived from a cross of Coda x Brundage was evaluated in replicated plots in Pendleton. We found patterns of variation expected of a quantitative trait, and progeny with resistance greater than both parents were identified. Both clubbed heads and presence of awns appeared to be simply inherited and to segregate independently from Cephalosporium stripe reaction, suggesting that it may be possible to move resistance genes between these classes. We also evaluated 167 progeny of the Einstein x Tubbs mapping population. All progeny were more resistant than the more susceptible parent (Tubbs), and one-third to one-half of the progeny showed less disease than the more resistant parent (Einstein). We also evaluated 90 wheat and barley entries for PNW small grain breeders, where white head percentages among the entries ranged from 0.1 to 51%. 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 represents the range of germplasm currently being used in the OSU Wheat Breeding Program. As phenotypic data for the mapping populations become available from the field, associations are being made of disease resistance with molecular markers. In a yield loss study of 12 wheat entries, only the susceptible checks showed sufficient disease to measure yield loss, but these data corresponded well with results of a 2006-07 experiment in which disease levels were higher. A total of 1,594 plots were sown in fall 2008, incorporating 679 entries. This planting includes 300 progeny from each of two populations derived from crosses between resistant Nickerson Seeds lines and Tubbs.

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

Table 1. Entries evaluated for *Cephalosporium* stripe, 2007-08 season. Numbers include checks.

Trial	Pendleton		
	#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

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. Also, 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 (evaluated in both Moro and Pendleton in 2006-2007), begin to evaluate progeny of Oregon x NSA crosses along with the Brundage x Coda population in the second year (Pendleton only, 2007-2008), and focus on the Oregon x NSA lines in the third year (2008-2009).

As in the previous season, disease expression resulting from artificial inoculation and early seeding (September 10-11, 2007) provided very useful separation of entries in the Coda x Brundage population, as indicated by the range of whitehead percentages observed in the checks and progeny (Fig. 1); square-root transformation was used to normalize the data. We found patterns of variation expected of a quantitative trait. 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 segregated in approximately a 1:1 ratio (Table 2). The percentage of whiteheads appeared to segregate independently of both head type (club versus common) and the presence of awns. These results suggest that it may be possible to move resistance genes between these classes, thus providing a rich source of resistance for common soft white winter wheats from club germplasm and also from highly resistant European material, which tends to be awnless.

Table 2. Percent whiteheads (%WH) and head morphology for progeny of the Coda x Brundage mapping population. N = number of progeny.

	Club head		Common head		Total	
	N	%WH	N	%WH	N	%WH
Awned	57	6.8	69	7.3	126	7.3
Awnless	57	6.8	70	5.8	127	6.3
Total	114	6.8	139	6.6	253	6.8

The 167 progeny of the Einstein x Tubbs population showed a population biased toward resistance (Fig. 2). In fact, all progeny were more resistant than the more susceptible parent (Tubbs) and between one-third to one-half of the progeny had lower whitehead percentages than the more resistant parent (Einstein). This transgressive segregation suggests that alleles for resistance were combined from both parents in some of the progeny, which greatly increases the probability of obtaining highly resistant lines with favorable agronomic traits.

We also evaluated 90 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 51% 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 *Cephalosporium stripe*, as well as Coda and Brundage. Candidate regions are being mapped and analyzed for markers. Subsequently, the rest of the genome will be scanned. Preliminary maps have now been developed, and an example for the "A" genome of wheat is shown in Fig. 3. The Diversity Set was evaluated for % whiteheads caused by *Cephalosporium stripe* in 2008 (Fig. 4). Results indicate the presence of substantial diversity and that most of the germplasm currently being utilized in the OSU Wheat Breeding Program is more resistant than Stephens, and some lines are more resistant than Madsen. As phenotypic data for the populations become available from the field, marker trait associations are being 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 *Cephalosporium stripe*: A wheat yield loss study was conducted in the 2007-08 season. The experiment consisted of a factorial arrangement of 12 wheat genotypes x two inoculation treatments (inoculated or non-inoculated). In all cases, plots were 5 x 20 ft. Previous experiments had indicated a close correspondence between % whiteheads and yield loss. Unfortunately, disease levels in the 2008 experiment were too low to determine yield loss relationships in all but the susceptible entries Stephens and Tubbs, which showed nearly a 1:1 correspondence between % whiteheads and % yields loss.

Fall 2008 Planting: A total of 1,594 plots were sown in Pendleton on September 13-14, 2008 (Table 3). This planting includes 300 progeny from each of two populations derived from crosses between resistant Nickerson Seeds lines and Tubbs.

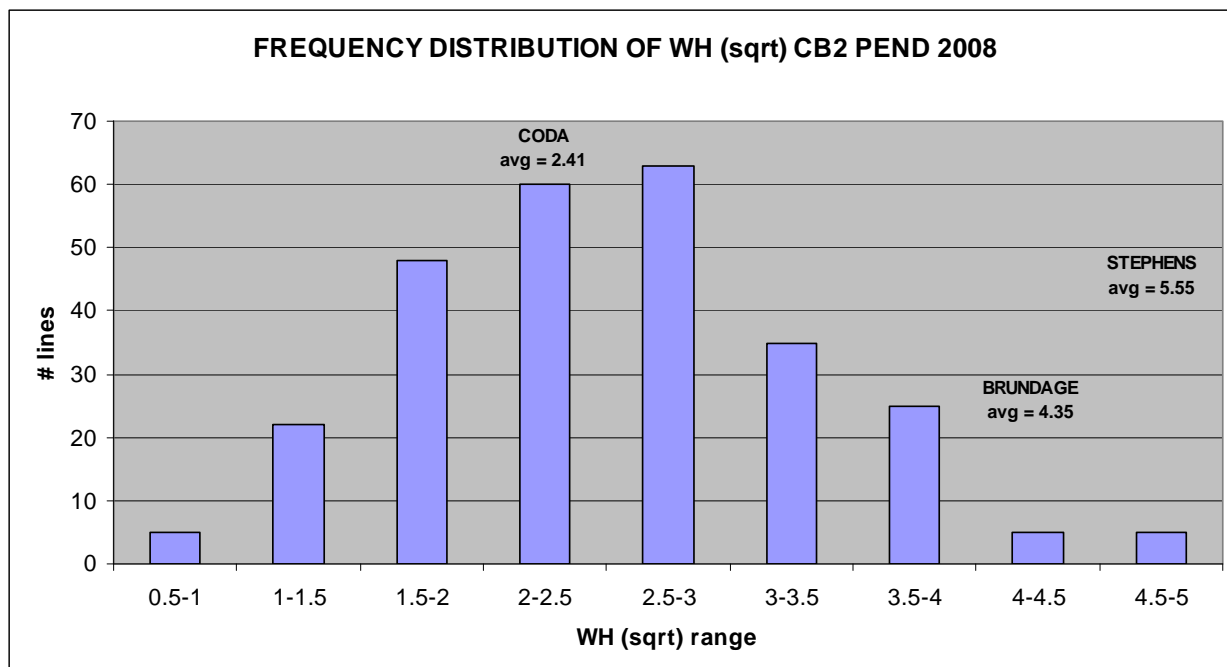


Fig. 1. Frequency distribution for square root(% whiteheads) of progeny in Coda x Brundage mapping population evaluated in Pendleton, 2008.

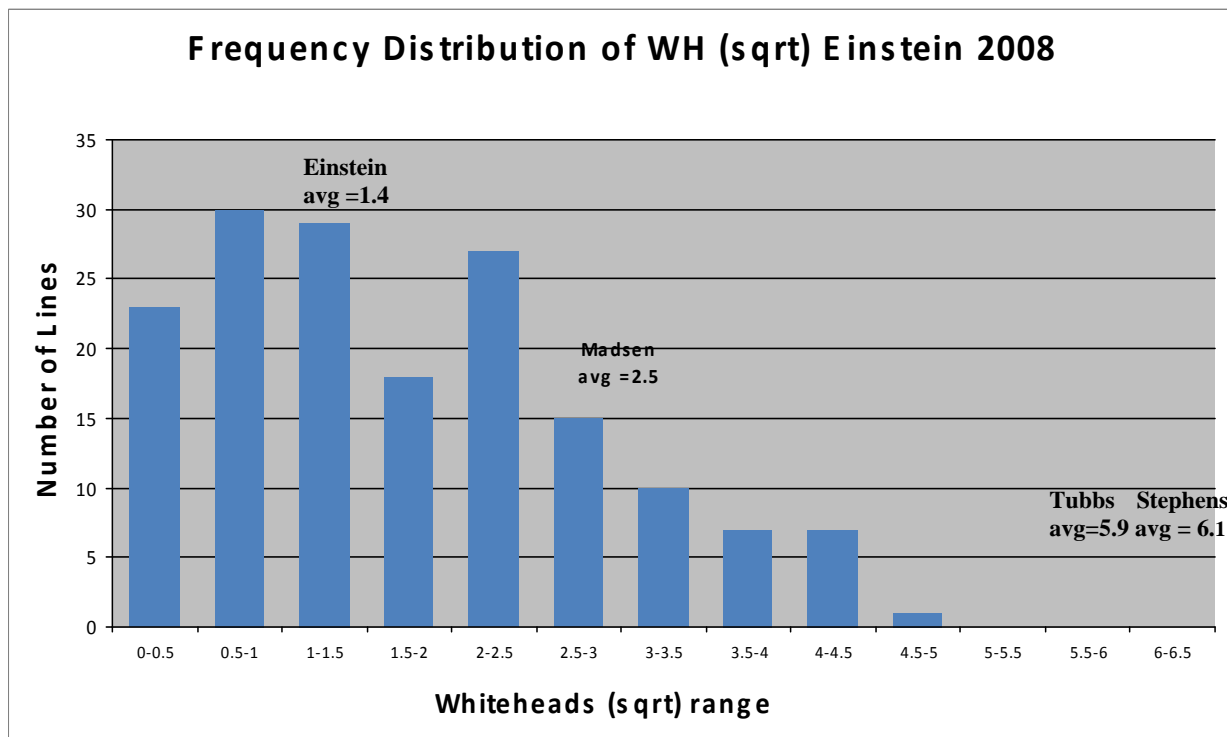


Fig. 2. Frequency distribution for square root(% whiteheads) of progeny in Einstein x Tubbs mapping population evaluated in Pendleton, 2008.

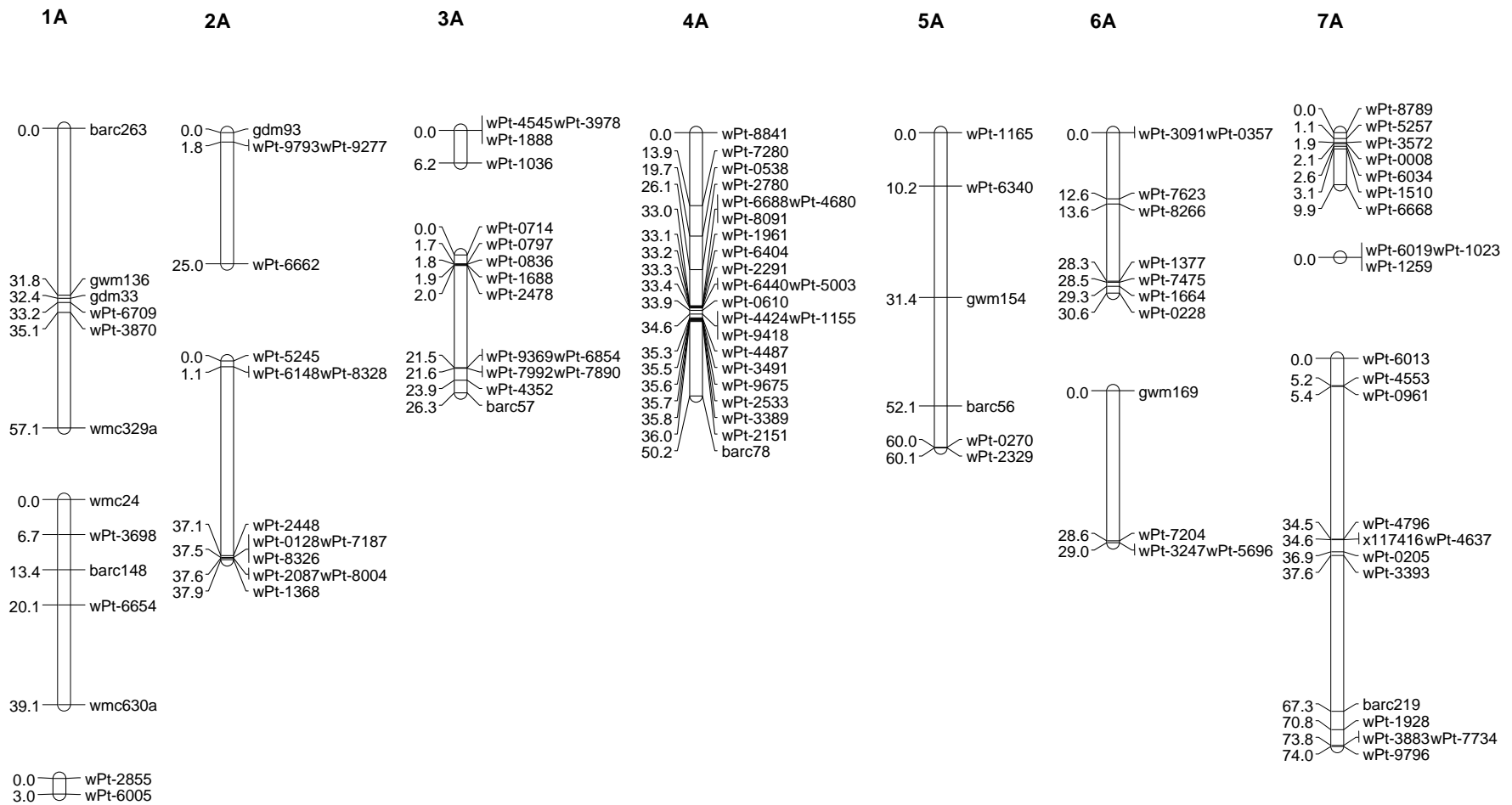


Fig. 3. Preliminary map of the wheat A genome showing currently mapped, informative markers.

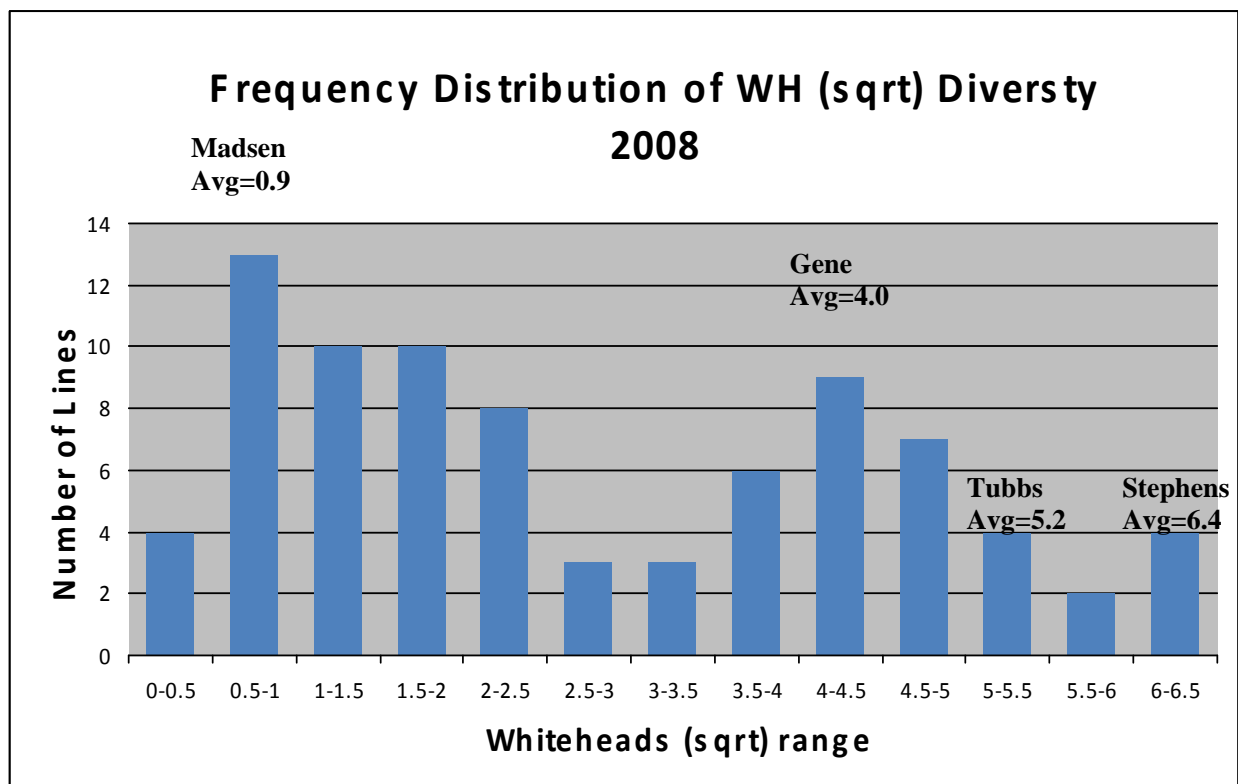


Fig. 4. Frequency distribution for square root(% whiteheads) of entries in a set of 90 wheat genotypes representing the diversity of germplasm currently available in the OSU Wheat Breeding Program.

Table 3. Entries planted in Pendleton for Cephalosporium evaluation, 2007-08 season. Numbers include checks.

Trial	Pendleton		
	#Reps	# Entries	# Plots
Einstein x Tubbs Pop.	2	300	600
0995 x Tubbs Pop.	2	300	600
OSU SW Elite Nursery	3	40	120
OSU HW Elite Nursery	3	30	90
USDA/WSU Nursery	3	40	120
OSU Barley Nursery	4	16	64
Total		726	1,594

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. This work has already contributed to the evaluation and release of three soft white winter wheat varieties (Goetze, Skiles, and ORFC-103).

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:

Zemetra RS, Hansen JL, Koehler T, Chen J, Riera-Lizarazu O, Leonard J, Quincke M, Peterson CJ, Mundt CC, Campbell KG, and Chen X. 2008. Creation of a multiple-use recombinant inbred line population for the development of molecular markers in soft white winter wheat. In: R Appels, R Eastwood, E Lagudah, P Langridge, M Mackay Lynne, eds. The 11th International Wheat Genetics Symposium proceedings. Sydney University Press.