

AN ABSTRACT OF THE THESIS OF

Miles Andrew Barrett for the degree of Master of Science in Horticulture presented on August 17, 2009.

Title: Pyramiding quantitative trait loci conditioning partial resistance to *Sclerotinia sclerotiorum* in bush blue lake green beans (*Phaseolus vulgaris*)

Abstract Approved:

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James R. Myers

*Sclerotinia sclerotiorum* (Lib.) de Bary is a necrotrophic pathogen capable of causing white mold, a severe disease in common bean. White mold is of particular concern to the Oregon snap bean processing industry, where processors allow less than 3% incidence in harvested shipments. Breeding for white mold resistance in beans has been difficult due to quantitative inheritance and low heritability. We combined two quantitative trait loci (QTL) for physiological resistance to white mold: a QTL located on linkage group 7 from G122 and a B8 QTL from NY6020. The B7 QTL is linked to phaseolin for which a sequence characterized amplified region (SCAR) marker phaseolin has been used successfully to transfer the QTL in dry bean. The transfer in snap bean is more challenging because this QTL is also linked to the *p* locus which conditions the white-seeded trait. While most snap beans have T phaseolin seed protein, the OSU bush blue lake (BBL) materials have the S form of phaseolin, facilitating the use of T phaseolin as a selectable marker in breeding for white mold resistance. Thus, transfer of this QTL has to be coupled with breaking the linkage between colored seed and the resistance QTL. The B8 QTL is linked to the SS18<sub>1650</sub> SCAR and AW19<sub>1200</sub> random amplified polymorphic DNA (RAPD) markers. Oregon State University BBL bean germplasm originally developed with single QTL were crossed to pyramid the two

resistance QTL. The assumptions made in combining these two sources of resistance are that the QTL are non-allelic and are additive. OSU 6229, OSU 6230, and OSU 6241 are advanced breeding lines that have the SS18<sub>1650</sub> allele from NY6020 and show statistically significant higher levels of resistance in the field and greenhouse (straw) test compared to susceptible cultivars. White-seeded, T phaseolin types were selected from a OR 91G x G122 BC<sub>2</sub>F<sub>3</sub> population. The selected lines showed levels of resistance significantly better than the susceptible check cultivars in the straw test. The two sources were crossed and the progeny were subjected to three or more generations of phenotypic selection in the straw test. One hundred and forty eight families were planted in a randomized complete block design (RCBD). All families had been previously genotyped using the PHAS and SS18<sub>1650</sub> SCAR molecular markers. Plants were inoculated using actively growing mycelium of *S. sclerotiorum* and scored using a modified straw test to test for genetic additivity among marker classes. None of the lines were statistically more resistant than G122, a QTL donor and standard resistant check. In a separate study, data collected in NY6020-5 x OR 91G and NY6020-5 x OSU 5613 populations suggest that NY6020-5 has a B7 QTL equivalent to G122. Other researchers have presented evidence that G122 has a B8 QTL equivalent to NY6020. Finally in a mixed linear model study we identified two markers, B18<sub>1500</sub> and C8<sub>1200</sub>, which should prove useful in breeding for white mold resistance. While the material that we developed does not show significantly higher levels of resistance than the resistant parents, we have transferred the resistance QTL into a bush blue lake background, and the lines derived from this work should have significantly higher levels of resistance than existing commercial cultivars. We also present evidence of a QTL not previously identified in NY6020-5.

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Pyramiding quantitative trait loci conditioning partial resistance to *Sclerotinia sclerotiorum* in bush blue lake green beans (*Phaseolus vulgaris*)

by  
Miles Andrew Barrett

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I understand that my thesis will become part of the permanent collection of Oregon State University libraries. My signature below authorizes release of my thesis to any reader upon request

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Miles Andrew Barrett, Author

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## DEDICATION

To my father, Mike Barrett, for being a constant role model of the man I aspire to be

Pyramiding quantitative trait loci conditioning partial phenotypic resistance to *Sclerotinia sclerotiorum* into a bush blue lake green bean (*Phaseolus vulgaris*) background

## **CHAPTER 1**

### **Literature Review**

## Literature Review

The common bean, *Phaseolus vulgaris*, is the most widely cultivated member of the genus *Phaseolus*. Other domesticated species of this genus include *P. lunatus* (Lima bean), *P. coccineus* (Scarlet runner bean), *P. dumosus* (Year-long bean), and *P. acutifolius* (Tepary bean). The earliest records of the domestication of *P. vulgaris* are dated approximately 7,000 BP (before present). There is evidence for two regions of domestication for *P. vulgaris* (Evans, 1980, Gepts *et al.*, 1986).

*P. vulgaris* is a diploid species ( $2n=22$ ) that has a very low rate of outcrossing due to the anthers being enclosed in a complete sheath of keel petals. This trait makes the flowers effectively cleistogamous; the flowers do open, but the stigma has already been pollinated by this point (Watts, 1980).

Phaseolin is a seed storage protein that has been used as a selectable marker for white mold resistance in crosses to G122 (Miklas, 2007; Chung *et al.*, 2008). Gepts *et al.* (1986) characterized the Phaseolin protein in a collection of wild and domesticated beans. Multiple forms were described in the wild populations. The Mesoamerican wild populations had predominantly the “S” and “M” alleles, while the Andean wild populations had “T”, “C”, “S”, “H” and “A” alleles. Among the domesticated beans, the S allele was most common among Mesoamerican lines, while the T allele was most common among Andean lines. Additionally there was significant morphological variation among the S and T types, with the S phaseolin types being smaller seeded and the T phaseolin types being larger seeded. These data were used to suggest two independent domestication centers for bean in Mesoamerica and in Andean South America.

The major producers of *P. vulgaris* include Brazil, China, the United States, and Mexico. *P. vulgaris* is one of the most widely cultivated legume crops, and it is the most commonly consumed legume in the Americas. The common bean is a good source of protein, calcium, iron, and thiamine. These properties make it an important food crop, especially in developing nations where inhabitants lack access to animal protein. Common beans are typically 20-30% protein by weight and 60-65% carbohydrate. The protein component is primarily phaseolin, while the carbohydrate component is primarily starch (Nwokolo, 1996).

White mold, caused by *Sclerotinia sclerotiorum* (Lib.) de Bary has a worldwide distribution (Purdy, 1979). *S. sclerotiorum* is pathogenic on more than 400 species of plants, primarily dicots (Boland & Hall, 1994). In the United States, *S. sclerotiorum* is the pathogen that causes the highest yield loss in bean (Schwartz *et al.*, 1987). Yield losses under irrigation can range from 13 to 80% (Kerr *et al.*, 1978). Breeders are attempting to incorporate genetic sources of resistance along with architectural avoidance mechanisms: upright plant structure, low canopy density, branching patterns and resistance to lodging (Kolkman & Kelly, 2002). *S. sclerotiorum* is of particular concern to the snap bean industry where processors strictly enforce a maximum infection tolerance of 3%.

*S. sclerotiorum* overwinters as hard black structures called sclerotia. Upon germination, the sclerotia produce apothecia, which bear ascospores capable of initiating infection (Agrios 1997). Signs of *S. sclerotiorum* include white cottony mycelium and production of sclerotia on colonized tissues while symptoms of white mold include browning and necrosis of the main stem, and total plant collapse. Biological control can

be achieved using the parasitic fungus *Coniothyrium minitans*. However, the resulting reduction in viable sclerotia does not necessarily result in lower disease pressures in the field (McQuilken *et al.*, 1995).

Previously, the fungicides Ronilan and Benomyl were useful in the control of *S. sclerotiorum*. However, both of these chemicals were removed from the market due to environmental and human health concerns. Currently chemicals such as Topsin M and Endura are available to control *S. sclerotiorum*. However, these chemicals require multiple applications, are costly to use, and require precise timing to maximize effectiveness (Bolton *et al.*, 2006).

Germination of *S. sclerotiorum* is favored by temperatures of 10 to 25°C and moist conditions (Weiss *et al.*, 1980). It requires dead tissues for ascospore colonization, and wounded stems and senescing flower petals provide the initial entry point. Senescing petals often lodge on lower leaves and stems, where the mycelium may spread to living tissues, resulting in colonization of stems, leaves and pods. Cultural practices such as reduced irrigation, wide row spacing, lower plant density (Steadman, 1983), and canopy management (Fuller *et al.*, 1984) have the potential to reduce disease severity.

*S. sclerotiorum* is capable of producing millimolar amounts of oxalate in infected plant tissues (Ferrar & Walker, 1993). Oxalate serves as an important virulence factor for *S. sclerotiorum*, because mutant lines of the fungus which are unable to produce oxalate are less virulent than wild types (Godoy *et al.*, 1990). The excretion of oxalic acid leads to the acidification of infected tissue (Dutton & Evans, 1996). Oxalic acid suppresses the oxidative burst, which is important in plant defense, and inhibits the production of H<sub>2</sub>O<sub>2</sub> (Cessna *et al.*, 2000). Oxalate causes foliar wilting by deregulating the guard cells and

interfering with normal stomate function. This is accomplished by ion accumulation and interference with abscisic acid-induced stomatal closure (Guimaraes & Stotz, 2004). In addition to the production of oxalic acid, *S. sclerotiorum* alters host-plant pH and excretes pathogenic enzymes capable of causing and exacerbating infection (Callahan & Rowe, 1991). Chipps *et al.*, (2005) demonstrated that sensitivity to *S. sclerotiorum* may be partially dependent on oxalate sensitivity, and that the highly resistant *P. coccineus* accession PI255956 has a high degree of oxalate tolerance.

There are a number of methods available to evaluate *P. vulgaris* germplasm for resistance to *S. sclerotiorum*. The oxalate test directly measures a plant's tolerance to oxalate, an important virulence factor for *S. sclerotiorum*. In the oxalate test, 20 day old plants are cut and placed in an oxalate solution for 12 hours, and then evaluated based on the degree of wilting observed (Kolkman & Kelly, 2000). The straw test (Petzoldt & Dickson, 1996) involves using cut lengths of soda straw to transfer mycelium of *S. sclerotiorum* growing on PDA directly to a decapitated stem. At 8 days after infection, plants are scored from 1-9 on the basis of stem necrosis (Petzoldt & Dickson, 1996). In field screening, plants are planted in rows spaced 46 cm apart in order to favor disease development. The plants are then evaluated near physiological maturity and ranked on a 1-9 scale on the basis of the percentage of plants infected per plot (Hauf & Grafton, 2001).

At present, there is no source for complete resistance to *S. sclerotiorum*. Rather, resistance seems to be quantitative. All beans are susceptible to the pathogen, but to varying degrees. Lines with partial physiological resistance have a lower degree of incidence and symptom severity. Breeding for resistance has proven difficult, because

the trait is inherited quantitatively with a low heritability (Miklas & Grafton, 1992). Also, it is difficult to fully evaluate physiological resistance mechanisms, because of the additional influence of physical avoidance traits and architecture (Schwartz *et al.*, 1987). The identification of a number of white mold resistance quantitative trait loci (QTL) allows breeders to effectively transfer physiological resistance through the use of marker-assisted breeding. A QTL refers to a region of a linkage map that cosegregates with the observed phenotype, and is potentially causative of the phenotype. An individual QTL may be the result of single major genes of large effect, or several genes of small effect mapping to a small region of a chromosome or linkage group.

To date, there have been a number of independently described QTL for physiological resistance to *S. sclerotiorum* in *P. vulgaris* germplasm. Linkage group locations and  $R^2$  values for the percent of phenotypic variation explained by QTL are reported in Table 1.1.

Table 1.1. List of published white mold QTL mapping studies with linkage group location and associated  $R^2$  value.

Cross	Linkage group	$R^2$	
		Percent	Citation
Wolven Pole x <b>PI255956</b> <sup>z</sup>	B1	9	Gilmore, 2007
<b>G122</b> x CO75248	B1	20	Maxwell, <i>et al.</i> , 2007
<b>Bunsi</b> x Raven	B2	10	Ender & Kelly, 2005
<b>Bunsi</b> x Newport	B2	12	Kolkman & Kelly, 2003
<b>G122</b> x CO75248	B2	15	Maxwell, <i>et al.</i> , 2007
Aztec x <b>ND88-106-04</b>	B2	24	Miklas <i>et al.</i> , 2007
Aztec x <b>ND88-106-04</b>	B3	16	Miklas <i>et al.</i> , 2007
<b>PC50</b> x XAN-159	B4	5	Park <i>et al.</i> , 2001
<b>Bunsi</b> x Raven	B5	11	Ender & Kelly, 2005
<b>Benton</b> x NY6020-4	B6	13	Miklas & Delorme, 2003
<b>Bunsi</b> x Raven	B7	14	Ender & Kelly, 2005
<b>Bunsi</b> x Newport	B7	17	Kolkman & Kelly, 2003
A55 x <b>G122</b>	B7	26	Miklas <i>et al.</i> , 2001
<b>PC50</b> x XAN-159	B7	16	Park <i>et al.</i> , 2001



Table 1.1 (Continued). List of published white mold QTL mapping studies with linkage group location and associated R<sup>2</sup> value.

Cross	Linkage group	R <sup>2</sup>	
		Percent	Citation
<b>G122</b> x CO75248	B8	11	Maxwell, <i>et al.</i> , 2007
Benton x <b>NY6020-4</b>	B8	26	Miklas & Delorme, 2003
<b>PC50</b> x XAN-159	B8	9	Park <i>et al.</i> , 2001
OR 91G x <b>PI255956</b>	B9	6	Haggard, 2007
<b>G122</b> x CO75248	B9	13	Maxwell, <i>et al.</i> , 2007
<b>Tacana</b> x PI318695	B9	17	Terpstra & Kelly, 2006
<b>PC50</b> x XAN-159	B11	3	Park <i>et al.</i> , 2001
Wolven Pole x <b>PI255956</b>	C	72	Gilmore, 2007

<sup>z</sup> resistance donor is bold

Recent work in the Miklas laboratory has revealed seven QTL identified in more than one population (Soule & Miklas, 2008). Of those seven, four QTL have been verified in marker-assisted selection projects: a B2, B8, and two B7 QTL. These include the B7 and B8 QTL of interest in the present study. The B7 QTL was described from the A55 x G122 recombinant inbred population (Miklas *et al.*, 2001) while the B8 QTL was observed in the Benton x NY6020-4 population (Miklas & Delorme, 2003). G122 is a dry bean from India, and the source of two resistance QTL located on linkage groups B1 and B7 (Miklas *et al.*, 2001). The B7 QTL accounted for 38% of the phenotypic variation in straw tests and 26% of the variation in the field tests. The B7 QTL is located near the genes for phaseolin seed storage protein (*Phs*) and white vs. pigmented seed coat color conditioned by the *p* locus (Figure 1.1). In this study the T allele of the phaseolin locus was associated with physiological resistance to white mold, while the S allele was associated with susceptibility. The B1 QTL was located near *fin*, which conditions determinate vs. indeterminate growth habit. The B1 QTL appears to be associated with the architectural trait of canopy porosity. Having an open canopy probably enhances

disease avoidance by modifying the plant microenvironment so leaf surfaces dry quicker (Miklas *et al.*, 2001).

G122 was also used as a resistant parent in a G122 x CO72548 mapping population (Maxwell *et al.*, 2007). Five QTL were identified on linkage groups B1, B2, B8 and B9. The previously described B7 QTL was found to be significant under single-factor analysis of variance, but was not significant when composite interval mapping was employed. The B1, B2, and B9 markers in the G122 allele state conditioned a reduction in white mold severity, while the B8 marker in the CO72548 state was associated with higher white mold susceptibility.

NY6020-4 and its sister line NY6020-5 are snap bean germplasm lines with two resistance QTL located on B6 and B8. The B6 QTL explained 12% of the phenotypic variation in the straw test and 13% of the variation in the field test. The B6 QTL is located near the *Ur-4* rust resistance gene and was also associated with canopy height and lodging traits. The B8 QTL explained 38% of variation in the straw test and 26% of variation in the field test in the original Benton x NY6020-4 mapping population. The B8 QTL was also associated with an increase in internode length (Miklas & Delorme, 2003), which is an undesirable growth habit trait in snap beans.

The primary goal of this project is the successful transfer of the B7 QTL from G122 and the B8 QTL from NY6020-5 into a single germplasm base, a strategy called pyramiding. R.R. Nelson (1978) was among the first to advocate pyramiding horizontal resistance genes. The basic principle is to incorporate multiple resistance genes into germplasm with the working assumption that possessing multiple resistance genes gives a definitive advantage over a single resistance gene.

These QTL are suitable for transfer because they have stable expression across environments, explain greater than 10% of the phenotypic variation, and are present in Type I growth habit lines. Also, the partial resistance conferred by these two QTL is likely conditioned by physiological mechanisms rather than disease avoidance traits because they exhibit greater expression in the greenhouse straw tests than in the field trials (Miklas, 2007).

The presence of the B7 QTL is associated with a codominant, sequence characterized amplified region (SCAR) marker for phaseolin (Kami *et al.*, 1995; Miklas, 2007). The primer pair amplifies three bands for T phaseolin, which is linked in coupling with the QTL and amplifies two bands for the susceptible S-phaseolin. The B8 QTL can be tracked using the SS18<sub>1650</sub> SCAR and the OP AW9<sub>1200</sub> random amplified polymorphic DNA (RAPD) marker, which are 1.9 cM apart (Miklas & Delorme, 2003). In the case of SS18<sub>1650</sub> the presence of a band of 1650bp is associated with resistance, while the absence of a band at this molecular weight is associated with susceptibility. The final conclusion of Miklas (2007) was that marker-assisted selection (MAS) was an effective strategy for introgressing the B7 and B8 QTL, but would also require additional selection for agronomic traits to yield commercially viable germplasm.

Chung *et al.*, (2008) stated that in G122 x Astrel and (G122 x PLS8088)x PLS8088 populations the phaseolin (*Phs*) SCAR marker and OP J09<sub>950</sub> and OP OC07<sub>850</sub> RAPD markers were associated with physiological resistance in both field tests and the straw test. OP J09<sub>950</sub> was mapped as a significant marker for white mold resistance in the PC-50xXAN-159 mapping population (Park *et al.*, 2001). The authors suggested that the B7 QTL derived from PC-50 may be the same as the QTL derived from G122.

Additionally, the significance of the B8 marker OP OC07<sub>850</sub> derived from NY6020-5 being significant suggests that G122 may also have the same B8 QTL as NY6020-5.

Association mapping (AM) seeks to exploit historical and evolutionary recombination events in establishing marker-trait associations (Nordborg & Tavaré, 2002). There are two primary approaches for AM. The first approach uses candidate genes, often of known function, to test for significant marker-trait associations. The second approach is similar to conventional QTL mapping, where a large set of randomly located markers is used to screen the genome for statistically significant associations (Risch & Merikangas, 1996). A combination of the two techniques, termed Nested Association Mapping, has been implemented in maize (Yu *et al.*, 2008). Single nucleotide polymorphisms, or SNPs, are recommended for association mapping due to their low cost in high-throughput settings and relative abundance within the genome (Syvanen, 2005; Clark *et al.*, 2007). SNPs are also useful as markers in candidate gene studies.

In AM, it is important to account for underlying population structure, as the technique tends to give false positives. Correction factors such as Structured Analysis (SA) and Genomic Control (GC) are useful in accounting for structure and reducing Type 1 errors (Yu *et al.*, 2006; Zhao *et al.*, 2007). AM is dependent upon the extent of linkage disequilibrium (LD). Where LD extends for long distances, fewer markers are needed, but the precision to detect the gene controlling polymorphisms is lower. Inversely, if LD decays rapidly, the power of resolution is high, but a larger number of markers must be screened.

Association Mapping has the potential to circumvent some of the limitations of

QTL mapping. First, association mapping uses a large set of cultivars or elite breeding lines rather than a set of progeny from one or few limited crosses. This allows for a greater chance to capture and analyze genetic variation. Second, because of the structure of an association mapping population, presumably any significant marker trait association is immediately transferable to a much wider collection of germplasm.

This is not so say, however, that AM is without its own drawbacks. Association mapping is dependent upon the extent of linkage disequilibrium. Therefore, good marker coverage is needed to identify significant markers. Additionally, the technique is prone to giving false positives. Properly accounting for population structure reduces the potential for false positives (Pritchard *et al.*, 2001).

Wang *et al.*, (2008) reported significant marker-trait associations in soybean for iron deficiency chlorosis. The study used 139 soybean lines from maturity groups 00, 0, and 1, and tested these lines with 84 SSR markers. Researchers reported two SSR markers significantly associated with the resistant phenotype. Presumably, it would be possible to replicate this success in *P. vulgaris* using a similar number of lines and markers. Such a study could be used to confirm marker utility with known QTL and possibly identify other, previously undiscovered, QTL. Rossi *et al.*, (2009) have suggested that genome-wide LD extends up to 10-15 cM in domesticated bean, which is significantly larger than in wild bean. This large extent of LD suggests that association mapping may be possible with a relatively small number of markers.

## CHAPTER 2

**Population development and germplasm performance in a B7 and B8 quantitative trait loci pyramiding strategy for resistance to *Sclerotinia sclerotiorum* in bush blue lake common bean, *Phaseolus vulgaris***

### Abstract

*Sclerotinia sclerotiorum*, the causal organism of white mold, is a cosmopolitan pathogen capable of infecting many species including the common bean, *Phaseolus vulgaris*. In *P. vulgaris*, there is no complete source of resistance to white mold. There have been multiple mapping strategies to identify quantitative trait loci (QTL), areas of the genome associated with white mold resistance. We attempted to combine, or pyramid, two sources of resistance to white mold: a B7 QTL from G122 and a B8 QTL from NY6020-5. We hypothesized that pyramiding these two QTL would have an additive effect and produce germplasm more resistant than the original QTL donors. We selected OSU 6229, OSU 6230, and OSU 6241 as B8 donor parents on the basis of previously described resistance and presence of the QTL marker. We selected white seeded, white mold resistant T Phaseolin types out of an OR 91G x G122 backcross population as B7 donor parents. We made crosses between lines carrying the B7 and B8 resistance alleles and evaluated the progeny of these crosses for white mold resistance using the straw test in the greenhouse. The progeny of these crosses, while showing partial phenotypic resistance, were not statistically more resistant than either G122 or NY6020-5. This observation suggests that the two QTL may not be additive.

## Introduction

Breeding for partial physiological resistance to *S. sclerotiorum*, the causal organism of white mold, has proven difficult because the trait is inherited quantitatively with a low heritability (Miklas & Grafton, 1992). Additionally, physiological resistance mechanisms are difficult to fully evaluate because of possible interactions with physical avoidance traits and architecture (Schwartz *et al.*, 1987). Prostrate growth habit and closed canopies promote conditions favorable for infection, while upright growth and open canopies allow for better air circulation, and lower rates of infection.

Two partial physiological resistance QTL were selected as candidate QTL for a pyramiding study: a QTL on linkage group B7 QTL derived from G122 (Miklas & Delorme, 2003; Miklas, 2007) and a QTL on linkage group B8 derived from NY6020-4 and its sister line NY6020-5 (Miklas *et al.*, 2001; Miklas 2007). We selected these QTL because both condition partial physiological resistance to white mold and not architectural avoidance. Each QTL accounts for a relatively high percentage of phenotypic variation when compared with QTL identified in other mapping studies. Both of the QTL are effective in field and greenhouse tests, the latter serving as a basis for screening plants and making selections based on straw test scores. Miklas (2007) described both QTL as contributing a 15-20% reduction in disease severity, or a reduction of 1.0 in the straw test mean.

Each QTL is closely linked to one or more molecular markers. The B8 QTL is tightly linked to the SS18<sub>1650</sub> SCAR and OP AW9<sub>1200</sub> RAPD markers (Miklas *et al.*, 2001; Miklas 2007). The B7 QTL is tightly linked to the Phaseolin (*Phs*) SCAR marker (Miklas *et al.*, 2001; Miklas 2007).



G122 and NY6020-5 have type 1 (determinate) growth habit, which makes them readily adaptable to breeding with bush blue lake processing snap beans, as they have the same determinate growth habit. NY6020-5 has the added benefit of being a snap bean, which makes it more immediately adaptable than G122, a dry bean.

Partial physiological resistance from NY6020-5 has been integrated into the bush blue lake breeding program successfully. Three OSU advanced selections (OSU 6229, OSU 6230, and OSU 6241) were selected as donors of the B8 QTL based on the presence of the SS18<sub>1650</sub> marker (the resistant allele for B8), multiple years of white mold resistance data, and suitable horticultural characteristics.

The transfer of resistance QTL from G122 into bush blue lake germplasm required additional selection because G122 is a colored seeded dry bean. Colored seed is unacceptable in processing green beans, so white seeded types were produced by crossing G122 to OR 91G, an OSU bush blue lake snap bean and standard variety of the Willamette Valley processing industry, followed by backcrossing twice to OR 91G. The locus for colored seed vs. white seed (*p*) is about 10 cM from *Phs* and the B7 QTL is located between the two loci. We therefore had to break the linkage between the QTL and *p* while selecting for the T phaseolin allele associated with the QTL. White seeded T phaseolin types were selected from the backcross and evaluated in the straw test. The most resistant types were used as donor parents of the B7 QTL (Appendix Table A1 and A2).

It was our hypothesis that crossing B7 QTL donor parents from the G122 x OR 91G backcross population to the B8 QTL donor parents OSU 6229, OSU 6230, and OSU 6241 would successfully pyramid the two white mold partial physiological resistance

QTL. The parents and identities of all crosses made are summarized in Appendix Table A3. It was our assumption that once combined, these two QTL would have an additive effect resulting in progeny superior to G122, NY6020-5, and the QTL donor parents. On the basis of results from Miklas (2007), germplasm possessing both partial physiological resistance QTL should have a mean that is approximately 1.0 less than G122 or NY6020-5 on a straw test scale (Petzoldt & Dickson, 1996; Teran *et al.*, 2006).

## Materials and Methods

### Straw Test

Plants were inoculated in the greenhouse using the straw test described by Petzoldt and Dickson (1996). All plants were inoculated using actively growing mycelia of the *S. sclerotiorum* isolate T001.1, obtained from the Navy bean cultivar ‘Newport’ and provided to OSU by Phil Miklas (USDA-ARS, Prosser, WA). Experimental lines were planted five seeds per 15 cm pot in Sunshine® SB40 professional growing mix. Each pot was given a top-dressing of Osmocote® 14-14-14 slow release fertilizer at planting. Following seedling emergence, each pot was thinned to three plants. Plants were grown under high-pressure sodium and metal halide lights that provided a 16-hour photoperiod. Plants were inoculated 3-5 weeks after planting as described by Petzoldt and Dickson (1996). The main stem was cut 4 cm above the third node, and an agar plug containing actively growing mycelia was placed over the cut stem. After inoculation, pots were arranged in complete blocks, each of which contained all experimental selections and standard checks, and were placed in a misting chamber for the duration of the experiment. Disease severity was quantified by the length of stem necrosis following eight days of incubation. Plants were rated using a 1-9 scale (Petzoldt & Dickson, 1996; Teran *et al.* 2006), where 1=no symptoms and 9=infection has progressed to or beyond the 3<sup>rd</sup> node leading to total plant collapse. For the fall 2006, spring 2007, and summer 2007 growing seasons, the Petzoldt and Dickson scale was used for phenotyping. The modified Petzoldt and Dickson scale described by Teran *et al.* (2006) was adopted thereafter. Under the Petzoldt and Dickson scale, necrosis to the first node is scored as a 3 and necrosis to the second node is scored as a 6, while under the modified Teran scale, these are scored as 4 and 7, respectively.

### Parental Materials and Standard Check Varieties

Check varieties included susceptible OR 91G and OSU 5630, resistance QTL donor parents G122 and NY6020-5, and moderately resistant Ex Rico (Bunsi) and M0162 (PI 527856) as well as the B8 QTL advanced breeding lines OSU 6229, OSU 6230, and OSU 6241. All parental materials had determinate growth habit.

OR 91G is a bush blue lake snap bean released by Drs. W.A. Frazier and J.R. Baggett in 1980 and remains the most widely used processing green bean in Oregon. OR 91G is a snap bean of Mesoamerican descent as inferred by the presence of the S phaseolin allele (Davis & Myers, 2002). While possessing excellent quality and high yield, it is highly susceptible to *S. sclerotiorum*.

OSU 5630 is an advanced selection from the OSU breeding program that has been released informally to the Oregon processing industry. It was derived from a cross of OR 91G x OSU5402 (OR54). It is a bush blue lake green bean, S phaseolin type, of Mesoamerican decent. It has processing characteristics similar to OR 91G, but has better quality and higher yields. Unfortunately, it is similar to OR 91G in its susceptibility to white mold.

Ex Rico, also called Bunsi, is a dry bean that has type 2 (upright short vine indeterminate) growth habit, a porous canopy, and moderate physiological resistance to white mold (Kolkman & Kelly, 2003). QTL mapping studies with Ex Rico have identified QTL on linkage groups B2, B5, and B7 (Kolkman & Kelly, 2003; Ender & Kelly, 2005). While possessing physiological resistance, it is more susceptible than G122 and NY6020-5 in the straw test but equivalent under field conditions.

M0162 is a yellow seeded line with type 1 determinate growth habit. It is a possible hybrid of *P. vulgaris* and *P. coccineus* developed by H. Lamprecht which has partial physiological resistance to white mold (Steadman et al., 2006). M0162 has resistance similar to G122 and NY6020-5, and it has the SS18<sub>1650</sub> allele, suggesting that it may have the same B8 resistance as NY6020-5. It also has the T phaseolin allele and the OP J09<sub>950</sub> RAPD marker, which suggests it may have the same B7 resistance as G122.

NY6020-5 and NY6020-4 are sister snap bean lines developed by Dr. Mike Dickson at the Geneva Agricultural Experiment Station, NY, with physiological resistance to white mold expressed in both the field and the straw test (Steadman *et al.*, 2001). We crossed NY6020-5 to OR 91G and OSU 5630 and advanced the population using single seed decent to produce the breeding lines OSU 6229, OSU 6230, and OSU 6241 with resistance to white mold and the SS18<sub>1650</sub> SCAR marker for the B8 QTL. OSU 6229 and OSU 6230 were derived from a NY6020-5 x OR 91G cross. Both possess the T phaseolin allele and have large-leaves, and a long internode, more prostrate growth habit. OSU 6241 is from an OSU 5630 x NY6020-5 cross and was selected because of its more desirable plant architecture (smaller leaves, shorter internodes, more upright growth habit). It possesses the S phaseolin allele from the OSU 5630 parent and the SS18<sub>1650</sub> SCAR from NY6020-5, but expression of resistance is more variable than OSU 6229 and OSU 6230.

G122 is a dry bean Indian land race also known as “Jatu Rong.” It is available from the plant introduction collection in Pullman, WA, as PI 163120. It was used as a resistant check and as a parent in crosses to transfer resistance into a bush blue lake background.

## Population Development

The development of this pyramiding population took place in multiple stages. First, G122 was crossed to OR 91G and F<sub>2</sub> with white seed, the T phaseolin allele and resistance to white mold in the straw test were selected. F<sub>2</sub>s were backcrossed twice to OR 91G with selection for T phaseolin and resistance to white mold in the BC<sub>1</sub>F<sub>2</sub> and BC<sub>2</sub>F<sub>2</sub> generations. Their BC<sub>2</sub>F<sub>3</sub> progeny were evaluated in two straw tests during the winter of 2006 and spring of 2007 in preparation to use in crosses to combine B7 and B8 QTL (Tables 2.1,2.2). Pedigrees of all crosses made are summarized in Table 2.3.

G122-derived, T phaseolin, BC<sub>2</sub>F<sub>3</sub> individuals with high levels of white mold resistance were crossed to OSU elite breeding lines during the fall 2006 and spring 2007. Individual F<sub>2</sub>, F<sub>3</sub>, F<sub>4</sub>, and F<sub>5</sub> plants were selected based on straw test scores over four generations (summer 2007, winter 2007, spring 2008, and summer 2008). During generations one and two, individual identities were retained, whereas in generations three and four, lines were selected on the basis of family straw test performance being equal to or better than G122. Within families, individual resistant plants were selected for a generation advance. In all generations, plants with scores of four or lower in the straw test were retained. During all rounds of selection, a small proportion of susceptible lines were saved. These selections include A115, E40, G44 and their derived families among others. Details for each season are given below.

### *Winter 2006*

Eighteen experimental lines from a OR 91G x G122 BC<sub>2</sub>F<sub>2</sub> population were replicated three times in pots of three plants each in straw tests with OSU 5630, OSU 6229, OSU 6230, OSU 6241, OR 91G, G122, and NY6020-5 as checks (Table 2.1)

during the winter of 2006. Lines were tested for white mold resistance using a Petzoldt and Dickson (1996) scale. Three experimental lines (5.3.8, 5.3.10, and 5.3.24) were selected as B7 donor parents on the basis of having the T phaseolin allele and straw test means not statistically different from G122. Two additional lines were selected (5.3.4 and 5.3.18) on the basis of having the T phaseolin allele, but a higher straw test mean to test additional genetic variability. These B7 QTL donor lines were crossed to B8 QTL donor parents OSU 6229, OSU 6230, and OSU 6241. Cross identities are summarized in Table 2.3.

Table 2.1. Straw test least squared (LS) means for winter 2006 G122 BC<sub>2</sub>F<sub>3</sub> *Phaseolus vulgaris* screening for resistance to white mold. (Petzoldt & Dickson scale<sup>z</sup>)

Line	Straw Test LS Mean	Check <sup>x</sup>		
		G122	NY6020- 5	OR 91G
<b>5.3.8</b>	<b>2.75</b>	<b>0.3266<sup>y</sup></b>	<b>0.9392</b>	<b>0.0002</b>
<b>5.3.10</b>	<b>4.00</b>	<b>0.4486</b>	<b>0.1030</b>	<b>0.0150</b>
<b>5.3.24</b>	<b>5.00</b>	<b>0.2915</b>	<b>0.0566</b>	<b>0.0297</b>
5.3.29	5.00	0.2915	0.0566	0.0297
5.3.9	5.17	0.2297	0.0412	0.0412
5.3.27	5.33	0.1783	0.0297	0.0566
<b>5.3.4</b>	<b>5.40</b>	<b>0.1188</b>	<b>0.0179</b>	<b>0.0891</b>
<b>5.3.18</b>	<b>5.75</b>	<b>0.0412</b>	<b>0.0051</b>	<b>0.2297</b>
5.3.14	5.80	0.0660	0.0088	1.1562
5.3.17	5.83	0.0768	0.0106	0.1365
5.3.22	6.00	0.0891	0.0126	0.1188
5.3.30	6.00	0.0566	0.0074	0.1783
5.3.31	6.25	0.0351	0.0042	0.2592
5.3.19	6.50	0.0212	0.0024	0.3645
5.3.20	6.50	0.0212	0.0024	0.3645
5.3.11	6.60	0.0297	0.0035	0.2915
5.3.26	7.00	0.0088	0.0009	0.5947
5.3.23	8.33	0.0011	0.0002	0.3517
OSU 5630	7.80	0.0011	0.0001	0.7606
OSU 6229	3.00	0.4486	0.8788	0.0040
OSU 6230	4.00	0.6481	0.1783	0.0074

Table 2.1. (Continued) Straw test least squared (LS) means for winter 2006 G122 BC<sub>2</sub>F<sub>3</sub> *Phaseolus vulgaris* screening for resistance to white mold. (Petzoldt & Dickson scale<sup>z</sup>)

Line	Straw Test LS Mean	Check <sup>x</sup>		
		G122	NY6020- 5	OR 91G
OSU 6241	3.00	0.4486	0.8788	0.0040
OR 91G	7.50	0.0024	0.0002	
G122	3.83		0.3645	0.0024
NY6020-5	2.83	0.3645		0.0002

<sup>z</sup> Scale of 1-9 where 1=no infection and 9=total plant collapse (Petzoldt & Dickson, 1996 scale).

<sup>y</sup> Probability of LS mean of experimental line equal to LS mean of the check

<sup>x</sup> G122 and NY6020-5 are partially resistant, OR 91G is susceptible

### *Spring 2007*

Sixteen additional lines from a the BC<sub>2</sub>F<sub>2</sub> population of OR 91G x G122 were replicated three times in individual pots of three plants each in a trial that included the checks OSU 5630, OSU 6229, OSU 6230, OSU 6241, OR 91G, and G122 (Table 2.2). Lines were tested using the straw test and the Petzoldt and Dickson (1996) scale. Three experimental lines (4.1.3, 9.12.4, and 9.12.8) were selected as B7 donor parents on the basis of having the T phaseolin allele and a straw test mean that was not statistically different from G122. Two additional lines were selected (8.6.1 and 8.6.16) on the basis of having the T phaseolin allele, but a higher straw test mean to test additional genetic variability. These B7 QTL donor lines were crossed to B8 donor parents OSU 6229, OSU 6230, and OSU 6241. Cross identities are summarized in Table 2.3. Concurrently, seed from winter 2006 crosses were advanced a generation in the greenhouse.



Table 2.2. Straw test least squared (LS) means for spring 2007 G122 BC<sub>2</sub>F<sub>3</sub> *Phaseolus vulgaris* screening for resistance to white mold. (Petzoldt & Dickson scale<sup>z</sup>)

Line	Straw Test LS Mean	Check <sup>x</sup>	
		G122	OR 91G
<b>9.12.8</b>	<b>3.33</b>	<b>0.9439<sup>y</sup></b>	<b>0.0018</b>
<b>4.1.3</b>	<b>3.50</b>	<b>0.8329</b>	<b>0.0025</b>
<b>9.12.4</b>	<b>4.40</b>	<b>0.4420</b>	<b>0.0094</b>
8.6.17	4.67	0.1017	0.0677
9.12.9	5.00	0.1492	0.0441
8.6.14	5.17	0.1158	0.0588
<b>8.6.1</b>	<b>5.25</b>	<b>0.1017</b>	<b>0.0677</b>
9.12.6	5.33	0.0890	0.0777
9.12.1	5.40	0.0777	0.0890
8.6.13	5.83	0.0381	0.1686
8.6.9	6.00	0.0381	0.1686
9.12.10	6.00	0.0282	0.2135
8.6.8	6.75	0.0068	0.5284
8.6.3	6.80	0.0057	0.5748
<b>8.6.16</b>	<b>6.83</b>	<b>0.0057</b>	<b>0.5748</b>
9.12.7	6.83	0.0057	0.5748
8.6.15	7.00	0.0041	0.6735
OSU 5630	6.50	0.0110	0.4022
OSU 6229	3.00	0.8329	0.0009
OSU 6230	5.00	0.1492	0.0441
OSU 6241	3.67	0.7253	0.0035
OR 91G	7.50	0.0015	
G122	3.25		0.0015

<sup>z</sup> Scale of 1-9 where 1=no infection and 9=total plant collapse (Petzoldt & Dickson, 1996 scale).

<sup>y</sup> Probability of LS mean of experimental line equal to LS mean of the check

<sup>x</sup> G122 is partially resistant, OR 91G is susceptible

Table 2.3. Crossing records for pyramiding partial physiological resistance QTL to white mold from B7<sup>z</sup> and B8<sup>y</sup> linkage groups into *Phaseolus vulgaris*.

Cross No.	Female Parent	Female QTL Contribution	Male Parent	Male QTL Contribution
Q001-1	5.3.4	B7	OSU 6229	B8
Q002-1	OSU 6241	B8	5.3.10	B7
Q002-2	OSU 6241	B8	5.3.10	B7
Q003-1	OSU 6241	B8	5.3.8	B7
Q004-1	OSU 6230	B8	5.3.10	B7
Q005-1	5.3.10	B7	OSU 6241	B8
Q006-1	5.3.10	B7	OSU 6230	B8
Q007-1	5.3.24	B7	OSU 6241	B8
Q007-2	5.3.24	B7	OSU 6241	B8
Q008-1	5.3.24	B7	OSU 6229	B8
Q008-2	5.3.24	B7	OSU 6229	B8
Q009-1	5.3.18	B7	OSU 6229	B8
Q010-1	OSU 6229	B8	5.3.10	B7
Q011-1	OSU 6230	B8	5.3.10	B7
Q012-1	OSU 6230	B8	5.3.8	B7
Q013-1	5.3.8	B7	OSU 6241	B8
Q014-1	5.3.8	B7	OSU 6230	B8
Q015-1	9.12.8	B7	OSU 6229	B8
Q016-1	9.12.8	B7	OSU 6230	B8
Q016-2	9.12.8	B7	OSU 6230	B8
Q017-1	9.12.8	B7	OSU 6241	B8
Q017-2	9.12.8	B7	OSU 6241	B8
Q017-3	9.12.8	B7	OSU 6241	B8
Q017-4	9.12.8	B7	OSU 6241	B8
Q017-5	9.12.8	B7	OSU 6241	B8
Q018-1	9.12.4	B7	OSU 6241	B8
Q018-2	9.12.4	B7	OSU 6241	B8
Q019-1	9.12.4	B7	OSU 6229	B8
Q020-1	8.6.1	B7	OSU 6230	B8
Q020-2	8.6.1	B7	OSU 6230	B8
Q021-1	8.6.1	B7	OSU 6229	B8
Q022-1	8.6.1	B7	OSU 6241	B8
Q023-1	OSU 6241	B8	9.12.4	B7
Q023-2	OSU 6241	B8	9.12.4	B7
Q024-1	OSU 6241	B8	4.1.3	B7

Table 2.3. (Continued) Crossing records for pyramiding partial physiological resistance QTL to white mold from B7<sup>z</sup> and B8<sup>y</sup> linkage groups into *Phaseolus vulgaris*.

Cross No.	Female Parent	Female QTL Contribution	Male Parent	Male QTL Contribution
Q025-1	OSU 6241	B8	9.12.8	B7
Q026-1	OSU 6241	B8	8.6.16	B7
Q026-2	OSU 6241	B8	8.6.16	B7
Q027-1	OSU 6241	B8	8.6.1	B7
Q027-2	OSU 6241	B8	8.6.1	B7
Q028-1	OSU 6230	B8	4.1.3	B7
Q029-1	OSU 6230	B8	9.12.4	B7
Q030-1	OSU 6230	B8	8.6.16	B7
Q031-1	OSU 6229	B8	9.12.8	B7
Q031-2	OSU 6229	B8	9.12.8	B7
Q032-1	OSU 6229	B8	8.6.1	B7
Q033-1	OSU 6229	B8	9.12.9	B7
Q033-2	OSU 6229	B8	9.12.9	B7
Q034-1	4.1.3	B7	OSU 6241	B8
Q035-1	4.1.3	B7	OSU 6230	B8
Q035-2	4.1.3	B7	OSU 6230	B8
Q035-3	4.1.3	B7	OSU 6230	B8
Q035-4	4.1.3	B7	OSU 6230	B8
Q036-1	8.6.1	B7	OSU 6229	B8

<sup>z</sup> B7 QTL originally described in A55 x G122 mapping population (Miklas et al., 2001)

<sup>y</sup> B8 QTL originally described in a Benton x NY6020 mapping population (Miklas & Delorme, 2003)

### Summer 2007

F<sub>2</sub> seed from crosses between B7 donor parents and B8 donor parents made winter of 2006 were planted in the greenhouse during the summer of 2007. Individual plants were assigned a letter, A, B, or C based on the bench it was placed on, and a number based on its position within the bench. Plants were phenotyped in a straw test using a Petzoldt and Dickson (1996) scale. One-hundred-fifty-six plants were selected and advanced based on straw test performance. Plants with low (resistant) straw test

scores were selected, as well as a few plants with (susceptible) straw test scores to preserve physiological susceptibility. There was no replication in this test, as only individual plants were selected during this testing season. Plants potentially escaping infection were retained for further testing. Performance of selected plants is presented in Appendix Table A1. Check variety straw test means are summarized in Appendix Table A2.

#### *Winter 2007*

F<sub>3</sub> seed from winter 2006 crosses and F<sub>2</sub> seed from spring 2007 crosses were planted in the greenhouse during the summer of 2007. Plants already assigned an A, B, or C identity maintained this identity. F<sub>2</sub> seed was assigned a D or E identity based on the bench, and additional F<sub>3</sub> seed was assigned an F, G, or H identity based on bench. Plants were inoculated and phenotyped using the straw test modified scale (Teran *et al.*, 2006). The scores and identities of all 175 selected plants are summarized in Appendix Table A3. There was no replication in this test, as only individual plants were selected during this testing season. A summary of check variety straw test means is available in Appendix Table A4.

#### *Spring 2008*

Selections from winter 2007 were advanced to produce 68 F<sub>2:3</sub> families and 106 F<sub>3:4</sub> families. With individual identities preserved, plants were inoculated and phenotyped using the straw test and modified Teran *et al.* (2006) scale. One hundred sixty four plants were selected based on individual plant and family phenotypes (Appendix Table A5). The Least Squares (LS) Mean for the straw test of each family was compared to the LS Mean of three checks (OR 91G, G122, and NY6020-5)

(Appendix Table A6). Each family was replicated three times, with a single pot of three plants as the experimental unit.

#### *Summer 2008*

The 164 plants selected during spring 2008 were advanced to produce 75  $F_{3:4}$  families and 96  $F_{4:5}$  families. Plants were phenotyped using the straw test and modified Teran *et al.* (2006) scale. In a final round of selection, 141 plants were selected (Appendix Table A7) comprised of 69  $F_4$  plants and 72  $F_5$  plants. The LS means of selected families is summarized in Appendix Table A8. Nineteen selections were subjected to four generations of selection (A,B) and 122 selections had been subjected to three generations of selection on the basis of straw test scores (D, E, G, H). This was the final round of phenotypic selection based on straw test performance. Each family was replicated three times, with a single pot of three plants as the experimental unit.

#### *Winter 2008*

Following a final round of selection and advancement, a set of 69  $F_{4:5}$  and 71  $F_{5:6}$  families were phenotyped using the straw test mean and a Teran *et al.* (2006) scale. The LS mean of each family was compared to the LS means of three checks (OR 91G, G122, and NY6020-5)(Appendix Table A9). No selection was made on the basis of straw test performance during winter 2008. Each family was replicated three times, with a single pot of three plants as the experimental unit.

#### *Spring 2009*

Families tested during the winter of 2008 were advanced to produce 67  $F_{4:6}$  and 71  $F_{5:7}$  families. These families were tested for white mold resistance using the straw test and Teran *et al.*, (2006) scale. The LS mean of each family was compared to the LS

means of three checks (OR 91G, G122, and NY6020-5)(Appendix Table A10). No selection was made on the basis of straw test performance during spring 2009. Each family was replicated three times, with a single pot of three plants as the experimental unit.

### Data Analysis

Data analysis was performed using SAS for Windows 9.1 (SAS Institute, Cary NC) using ANOVA, GLM, and MIXED procedures. For individual growing seasons, the SAS model was SCORE = LINE BLOCK. The winter 2008 and spring 2009 results were combined into a cross-season analysis, because the final selections were made in the summer of 2008, and so winter 2008 and spring 2009 represent all advanced selections replicated over two growing seasons. The goal of the cross-site analysis was to compare all data collected after the final round of single plant selection. For the cross-site analysis of the winter 2008 and spring 2009 growing seasons, a model SCORE = LINE SEASON BLOCK(SEASON) was used.

## Results and Discussion

Figures 2.1-2.5 show the frequency distributions and normality curves associated with the straw test LS means from the F<sub>3</sub> through F<sub>7</sub> progeny evaluations. In all frequency distributions, few lines had LS means  $\leq 3$  or  $> 8$ . All families were evaluated with the modified Petzoldt and Dickson scale (Teran *et al.* 2006). Like the original Petzoldt and Dickson scale, the modified scale ranges from 1 to 9. These data suggest that we are only able to capture a moderate level of resistance that is equivalent to G122 and NY6020-5.

Table 2.1. Frequency distribution and normality plot for straw test least squared (LS) means of F<sub>3</sub> experimental families with OR 91G and G122 used as standard check varieties.

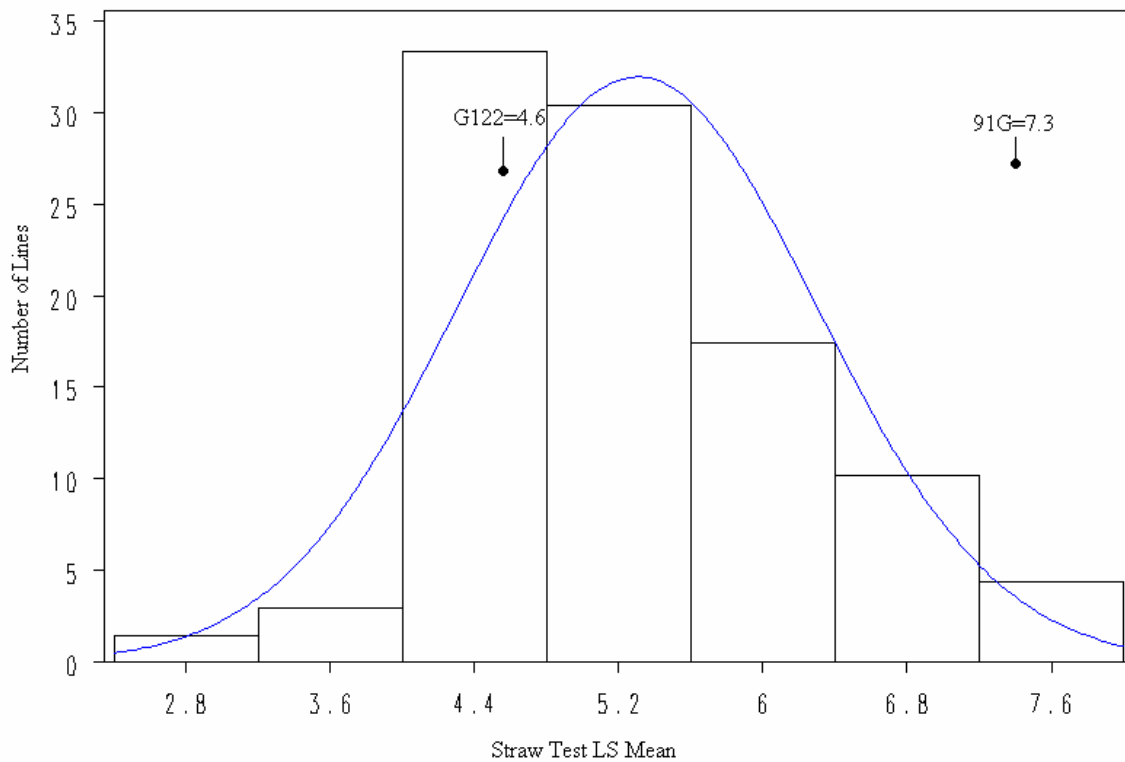


Table 2.2. Frequency distribution and normality plot for straw test least squared (LS) means of  $F_4$  experimental families with OR 91G and G122 used as standard check varieties.

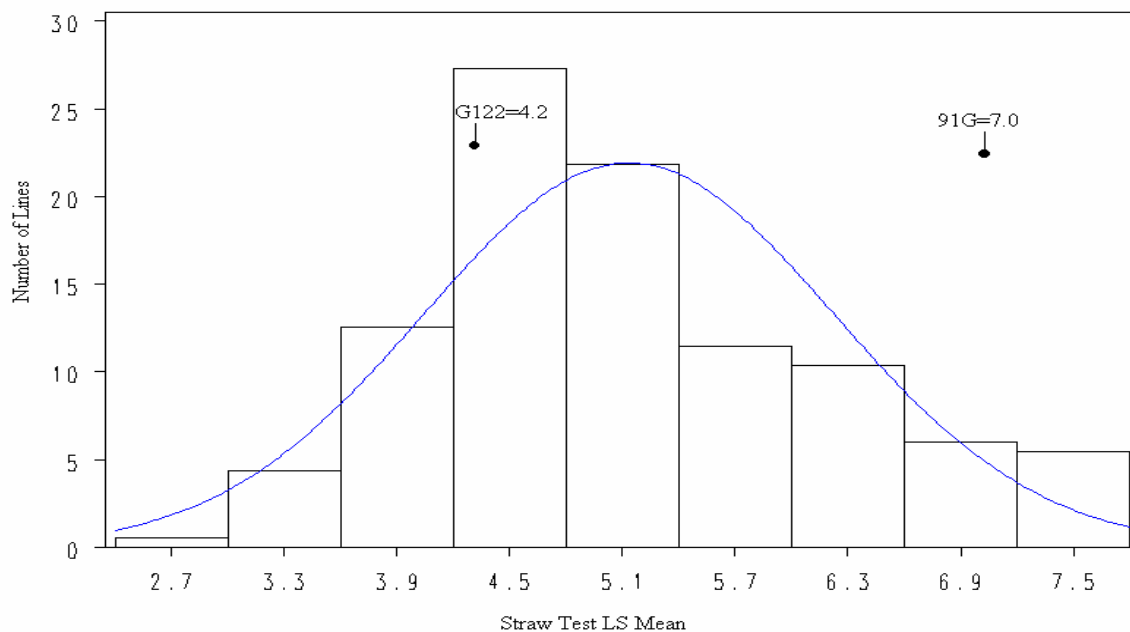


Table 2.3. Frequency distribution and normality plot for straw test least squared (LS) means of  $F_5$  experimental families with OR 91G and G122 used as standard check varieties.

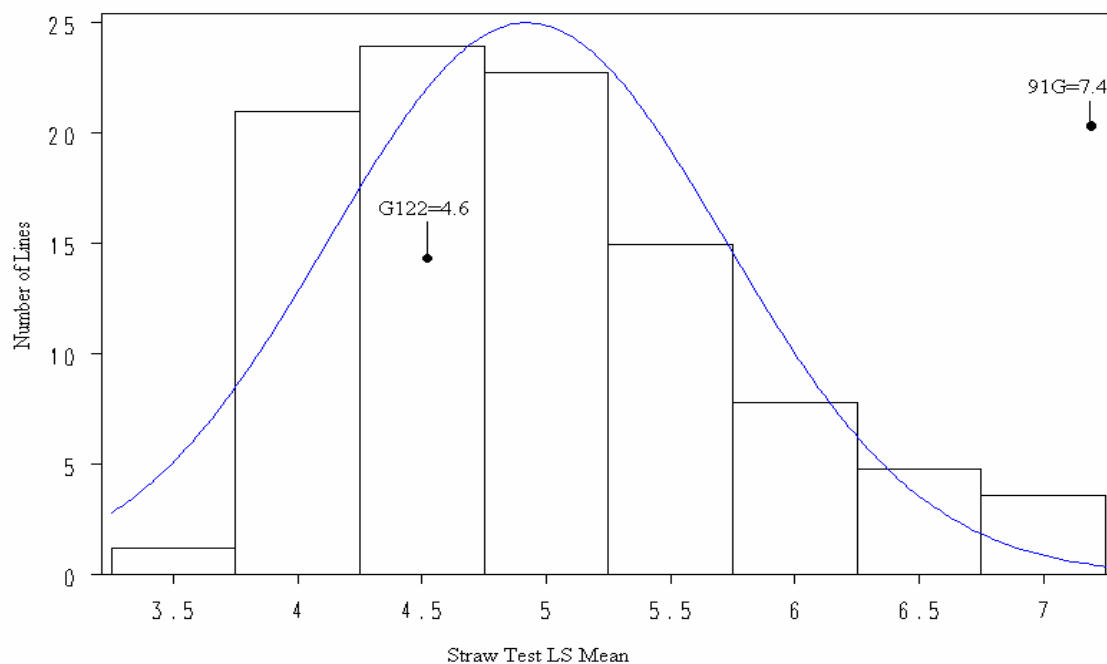




Table 2.4. Frequency distribution and normality plot for straw test least squared (LS) means of  $F_6$  experimental families with OR 91G and G122 used as standard check varieties.

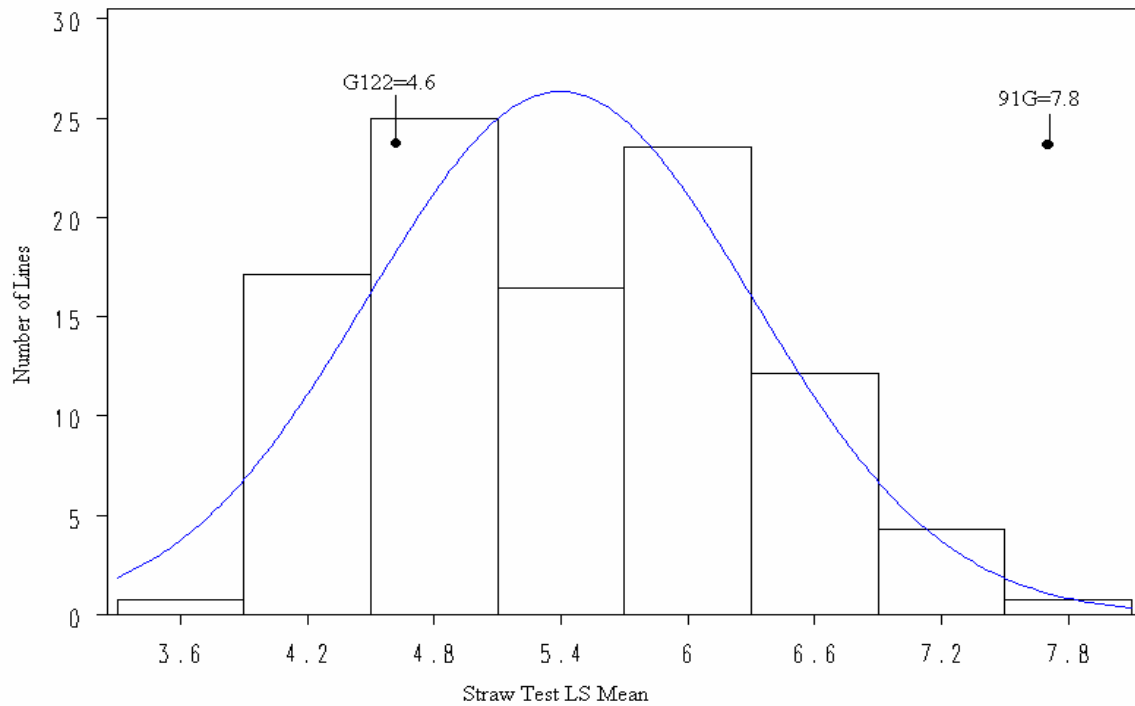
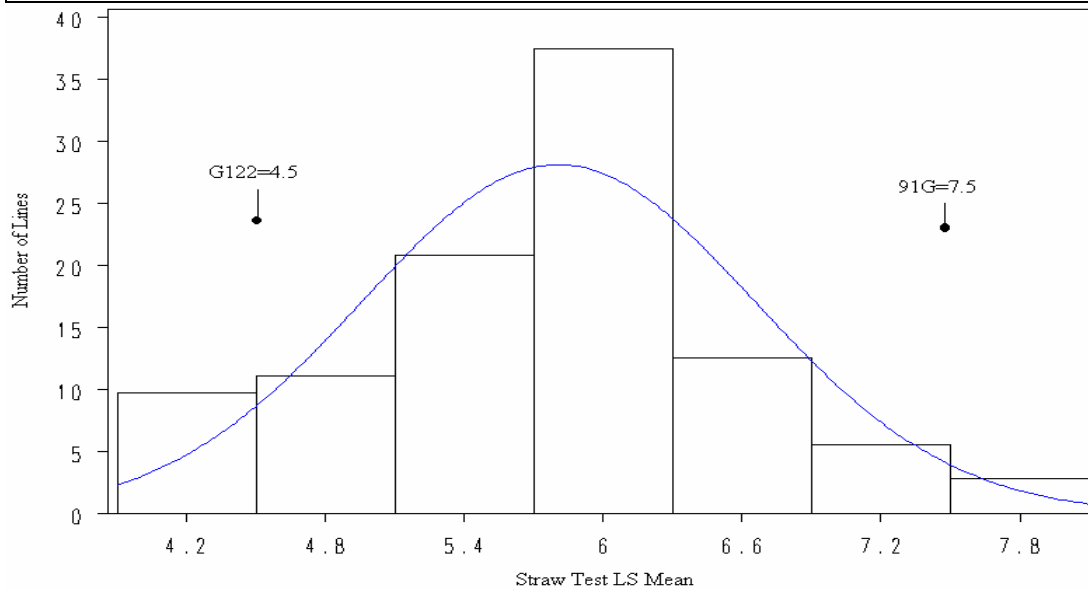


Table 2.5. Frequency distribution and normality plot for straw test least squared (LS) means of  $F_7$  experimental families with OR 91G and G122 used as standard check varieties.



There does not appear to be a genetic change in the population due to phenotypic selection. Figures 2.1 and 2.2 show similar trends, while figure 2.3 seems skewed towards resistant types. However, Figures 2.4 and 2.5 seem to be skewed more towards susceptible types. This is likely due to the spring 2009 straw test, in which many F<sub>6</sub> and F<sub>7</sub> families were evaluated, being particularly extreme in disease progression.

There were 9 families from spring 2008 that were significantly more resistant than G122. During summer 2008 and winter 2008, only single and different families, respectively were significantly more resistant than G122: D138.2 in summer 2008, and G174.1.1 in winter 2008. The straw tests from spring 2009 did not reveal any families as having significantly greater white mold resistance than G122 (Table 2.1). In looking across growing seasons, the line G174 and the subfamily G174.1.1 were significantly more resistant than G122 during spring 2008 and winter 2008 (Table 2.2).

Table 2.4. Number of experimental families of *Phaseolus vulgaris* with LS means significantly less than, greater than, or not significantly different from G122 (partially resistant check) in six environments as determined by the straw test for white mold resistance.

LS Mean relative to G122	Environment				Composite (Winter 2009, Spring 2009)
	Spring 2008	Summer 2008	Winter 2008	Spring 2009	
	Number of Families				
Lower (res.)	9	1	1	0	0
Equivalent	115	131	113	86	70
Higher (suscep.)	51	40	27	53	69
Total	175	172	141	139	139

In general, however, this pyramiding population is characterized by a lack of lines which are statistically more resistant than G122 (Tables 2.1, & 2.2) This may be due to a

lack of transgressive segregants lines which outperform either of the parent lines. Other possible reasons for this observation include the two QTL not being additive, one or both of the QTL being absent in the progeny, or an interference due to environmental factors and variations. There were lines that had significantly lower LS means than G122 in individual straw tests (Tables 2.1 & 2.2). However, the number of lines having greater levels of resistance decreased over time (dropping from nine in spring 2008 to zero by spring 2009). From examination both within and across straw test generations, it is unlikely that any of the experimental lines selected are truly more resistant to *S. sclerotiorum* than G122.

Table 2.5. List of experimental families of *Phaseolus vulgaris* and straw test least squared (LS) means for lines more resistant to white mold resistance than G122 from the spring 2008, summer 2008, winter 2008, and spring 2009 growing seasons and cross-site analysis of winter 2009 and spring 2009 seasons.

Line	Cross No.	Generation	Straw Test LS Mean <sup>z</sup>
Spring 2008			
E106	Q033-1	F <sub>2:3</sub>	2.57
A11	Q012-1	F <sub>3:4</sub>	3.32
E159	Q017-3	F <sub>2:3</sub>	3.32
G117	Q001-1	F <sub>3:4</sub>	3.32
G174	Q008-2	F <sub>3:4</sub>	3.32
G205	Q012-1	F <sub>3:4</sub>	3.32
G207	Q012-1	F <sub>3:4</sub>	3.32
G2	Q002-1	F <sub>3:4</sub>	3.51
H5	Q012-1	F <sub>3:4</sub>	3.51
Summer 2008			
D138.2	Q017-2	F <sub>3:4</sub>	2.54
Winter 2008			
G174.1.1	Q008-2	F <sub>5:6</sub>	3.65

<sup>z</sup> Scale of 1-9 where 1=no infection and 9=total plant collapse (Teran *et al.*, 2006).

By looking at the twenty most resistant families across multiple seasons of testing (Table 2.3), certain individuals and their derived families consistently ranked as the most resistant. This suggests that these lines are relatively fixed at resistance loci, and should be considered for future evaluation to determine their utility as potential varieties. Thirteen lines ranked in the top twenty in multiple seasons. Subfamilies of A6, A182, D224, E55, E97, E106, and G1 were present in the top twenty in two growing seasons. Subfamilies of A11,

D138, E52, and G174 occurred in the top twenty most resistant lines in three growing seasons. The line G207 and its subfamilies was the only line to occur in the top twenty in all four growing seasons.

Table 2.6. Least squared family means of the twenty lowest straw test scores (Teran scale<sup>2</sup>) from spring 2008, summer 2008, winter 2008, and spring 2009 of experimental lines of *Phaseolus vulgaris* screening for resistance to white mold.

Straw Test			Straw Test		
Line	LS Mean	Season	Line	LS Mean	Season
A6	3.65	Spring 2008	E106	2.57	Spring 2009
A6.2	3.88	Summer 2008	E106.4.1	4.58	Spring 2009
A11	3.32	Spring 2009	E159	3.32	Spring 2008
A11.1.1	4.05	Winter 2008	E168.10	3.96	Summer 2008
A11.3.1	4.01	Winter 2008	E185.6.2	4.08	Spring 2009
A11.4.1	4.66	Spring 2009	G1	3.84	Spring 2008
A115.4	3.71	Summer 2008	G1.3.6	3.97	Spring 2009
A126.10.5	4.01	Winter 2008	G2	3.51	Spring 2009
A182.2	3.83	Summer 2008	G6.7.2	4.41	Spring 2009
A182.6	3.96	Summer 2008	G66	4.01	Spring 2008
A182.6.3	4.05	Winter 2008	G79	3.79	Spring 2008
B78.1.2	4.47	Spring 2009	G106.2.2	3.91	Spring 2009
D70.2.4	4.05	Winter 2008	G110	3.79	Spring 2009
D138.1	3.54	Summer 2008	G113	3.98	Spring 2008
D138.2	2.54	Summer 2008	G117	3.32	Spring 2008
D138.2.6	4.72	Spring 2009	G174	3.32	Spring 2009
D138.2.6	3.76	Winter 2008	G174.1	3.77	Summer 2008
D169.3.1	3.76	Winter 2008	G174.1.1	3.65	Winter 2008
D169.7.7	3.89	Winter 2008	G174.2	3.77	Summer 2008
D224.6.4.	4.63	Spring 2009	G205	3.32	Spring 2009
D224.7.1	4.58	Spring 2009	G207	3.32	Spring 2008
D224.7.1	4.01	Winter 2008	G207.1	3.93	Summer 2008
D224.7.3	3.93	Winter 2008	G207.1.1	4.08	Winter 2008
E19.6.1	3.80	Winter 2008	G207.4.4	4.58	Spring 2009
E46.4	3.98	Summer 2008	G210	3.79	Spring 2008
E47.2	3.82	Summer 2008	G44.P3.2	3.96	Spring 2009
E52.1.5	4.13	Winter 2008	H2.2	3.93	Summer 2008
E52.2.7	4.47	Spring 2009	H2.2.3	4.14	Spring 2009
E52.3	3.82	Summer 2008	H5	3.51	Spring 2008
E52.3.6	3.92	Spring 2009	H5.5	3.77	Summer 2008
E52.3.6	3.80	Winter 2008	H9	4.01	Spring 2009

Table 2.6. (continued) Least squared family means of the twenty lowest straw test scores (Teran scale<sup>z</sup>) from spring 2008, summer 2008, winter 2008, and spring 2009 of experimental lines of *Phaseolus vulgaris* screening for resistance to white mold.

Line	Straw Test		Line	Straw Test	
	LS Mean	Season		LS Mean	Season
E55.1.6	4.64	Spring 2009	H9.1.3	4.47	Spring 2009
E55.1.6	4.13	Winter 2008	H9.2	3.93	Summer 2008
E65.1.5	4.25	Spring 2009	H12	3.79	Spring 2008
E66.4	3.97	Summer 2008	H13	3.79	Spring 2008
E84	3.89	Spring 2008	H15.1.4	4.01	Winter 2008
E84.6	3.77	Summer 2008	H15.4	3.77	Summer 2008
E97.4.2	4.30	Spring 2009	H15.5	3.48	Summer 2008
E97.5.3	4.31	Spring 2009	H15.5.2	4.01	Winter 2008
E97.7.6	3.99	Winter 2008	H15.5.4	4.01	Winter 2008

<sup>z</sup> Scale of 1-9 where 1=no infection and 9=total plant collapse (Teran *et al.*, 2006 scale).

Single plant selection stopped after the summer 2008 growing season. By looking at the least squared (LS) means of the straw test from the winter 2008 and spring 2009 growing season, and a cross site analysis of the winter 2008 and spring 2009 growing seasons, a number of lines have resistance levels equivalent to G122 across all three analyses. This consistency of statistical significance suggests that the resistance in these lines is both fixed and stable. Out of the 139 lines evaluated in common between both growing seasons, 54 lines were the statistical equivalent of G122 across all three analyses. The LS means and phenotypic characteristics of those lines are presented in Table 2.4.

Table 2.7. Straw test LS means (Teran scale<sup>2</sup>) of experimental families of *Phaseolus vulgaris* evaluated during winter 2009, spring 2008 and cross-site analysis of winter 2008 and spring 2009 growing seasons screening for resistance to white mold and phenotypes for pod shape and plant growth habit.

Line	Cross No.	Pod Shape <sup>y</sup>	Internode Length <sup>x</sup>	SS18	Phas	Straw Test LS Mean		
						Winter 2009	Spring 2009	Combined
A11.3.1	Q012-1	Rd	3	-	T	4.01	5.75	5.1
A126.8.7	Q006-1	Rd	2	+	T	4.80	5.42	4.92
A126.10.5	Q006-1	Rd	3	+	S	4.01	5.25	4.65
A182.1.2	Q012-1	Rd	2	+	T	4.17	5.47	4.62
A182.3.3	Q012-1	Rd	2	+	T	4.55	5.58	4.90
A182.5.3	Q012-1	Rd	2	+	T	4.55	5.36	4.88
A182.6.3	Q012-1	Rd	2	+	T	4.05	5.75	4.73
B78.1.2	Q008-2	Rd	3	+	T	5.22	4.47	4.68
B78.5.3	Q008-2	Rd	3	+	T	4.65	5.31	4.83
D70.2.4	Q020-1	Rd	2	+	T	4.05	5.92	4.92
D70.3.4	Q020-1	Rd	2	+	S	4.34	5.58	4.97
D138.2.6	Q017-2	Flat	3	+	T	3.76	4.72	4.47
D169.3.1	Q017-1	Rd	1	-	S	3.76	5.92	5.21
D169.7.7	Q017-1	Rd	2	+	S	3.89	5.75	5.08
D224.6.4	Q017-4	Rd	2	+	T	4.43	4.63	4.31
D224.7.1	Q017-4	Rd	2	+	S	4.01	4.58	4.61
D224.7.3	Q017-4	Rd	1	+	S	3.93	5.25	4.84
E19.6.1	Q027-1	Rd	3	+	T	3.80	5.25	4.54
E47.2.1	Q028-1	Oval	2	+	S	5.30	4.75	4.74
E52.1.5	Q028-1	Rd	2	+	T	4.13	4.75	4.21
E52.2.7	Q028-1	Rd	3	+	T	4.40	4.47	4.24
E52.3.6	Q028-1	Rd	3	+	T	3.80	3.92	3.78
E55.1.6	Q028-1	Flat	3	+	T	4.13	4.64	4.26
E64.1.2	Q028-1	Flat	3	+	T	5.30	4.81	4.81
E65.1.5	Q028-1	Rd	2	+	T	5.51	4.25	4.81
E66.5.2	Q028-1	Flat	2	+	S	4.14	5.53	4.67
E97.4.2	Q018-2	Flat	3	+	T	5.10	4.30	5.26
E97.7.6	Q018-2	Flat	3	+	S	3.99	5.19	4.86
E106.4.1	Q033-1	Rd	2	+	T	4.51	4.58	4.56
E115.2.4	Q035-4	Rd	3	+	T	4.51	5.25	4.94
E120.1.2	Q035-4	Rd	3	+	T	4.14	5.92	4.65
E120.2.5	Q035-4	Rd	3	+	T	4.81	5.36	5.00
E120.3.1	Q035-4	Rd	3	+	T	4.61	5.75	5.06

Table 2.7. (continued) Straw test LS means (Teran scale<sup>z</sup>) of experimental families of *Phaseolus vulgaris* evaluated during winter 2009, spring 2008 and cross site analysis of winter 2008 and spring 2009 growing seasons screening for resistance to white mold and phenotypes for pod shape and plant growth habit.

Line	Cross No.	Pod Shape <sup>y</sup>	Internode Length <sup>x</sup>	SS18	Phas	Straw Test LS Mean		
						Winter 2009	Spring 2009	Combined
E185.4.2	Q023-1	Rd	1	-	S	4.21	4.75	4.9
E185.6.2	Q023-1	Rd	1	-	S	4.43	4.08	4.58
E217.1.3	Q030-1	Rd	2	+	T	4.51	4.92	4.66
E229.7.7	Q030-1	Rd	1	+	S	4.61	5.86	5.15
E229.9.5	Q030-1	Rd	1	+	T	4.34	5.47	4.8
E249.1.4	Q020-2	Rd	3	+	T	4.81	4.92	4.83
E256.2.4	Q035-4	Flat	2	+	T	5.01	5.25	4.99
G1.3.6	Q002-1	Rd	2	+	T	4.76	3.97	4.64
G106.1.4	Q004-1	Rd	3	+	T	4.83	5.47	5.03
G106.2.2	Q004-1	Rd	3	+	T	4.93	3.91	4.94
G108.9.6	Q004-1	Rd	2	+	T	4.83	5.47	5.07
G110.1.3	Q004-1	Rd	2	+	T	4.72	5.70	4.9
G110.3.2	Q004-1	Rd	2	+	T	4.43	5.70	4.95
G161.4.8	Q008-2	Rd	2	+	T	5.43	5.03	4.93
G161.5.6	Q008-2	Rd	2	+	T	4.68	5.81	5.23
G174.1.1	Q008-2	Rd	3	+	T	3.65	5.08	4.25
G174.2.4	Q008-2	Rd	2	+	T	4.3	5.08	4.46
G207.1.1	Q012-1	Rd	2	+	S	4.08	4.92	4.29
G207.4.4	Q012-1	Rd	2	+	T	5.22	4.58	4.73
H9.1.3	Q012-1	Rd	2	+	T	4.41	4.47	4.23
H15.1.4	Q012-1	No Data	No Data	+	T	4.01	5.64	4.24
H15.5.4	Q012-1	No Data	No Data	+	T	4.01	5.50	4.9
OR 91G		Rd	2	-	S	7.43	7.84	7.64
G122		Flat	3	+	T	4.66	4.64	4.65
NY6020-5		Rd	3	+	T	4.71	5.59	5.15

<sup>z</sup> Scale of 1-9 where 1=no infection and 9=total plant collapse (Teran *et al.*, 2006).  
<sup>y</sup> Flat, Oval, or Rd (Round)  
<sup>x</sup> Scale of 1-3 where 1=short and 3=long

Based on these data there are several families that have partial white mold resistance as well as acceptable horticultural characteristics. Subfamilies of A11, A182, D224, E52, E106, G1, G174, and G207 were present in the top twenty most resistant lines in multiple seasons, had LS means equivalent to G122, and had round pods acceptable for processing. Subfamilies of D138, E55, and E97 had similar levels of resistance, but had flat pods which would make them unsuitable for processing. Lines of greatest interest include subfamilies of G174, which was statistically more resistant than G122 during two growing seasons, G207, which was in the top twenty most resistant lines during all growing seasons, and A182 which was observed to produce vigorous growth and substantial seed yields in the greenhouse.



## Conclusions

The trends in these data show a decrease in the number of lines found to be more resistant than G122 over time, decreasing from 9 families in the earliest generation of evaluation to 0 in the most recent generation of evaluation. While it is possible that these results may be due to inbreeding depression or a loss of a resistance factor due to segregation, I attribute this trend to two other factors. First, I believe that there was a lack of technical consistency in the earlier generations of evaluation that was corrected in later generations. In later generations, I began treating seed to improve germination, and exercising greater caution during planting to minimize variation. Second, during the earlier generations of development, seed was a limiting factor. Therefore, fewer plants were used to estimate a mean during early generations of selection. As a result of this, the means would have been estimated with less precision.

By looking at the twenty most resistant lines in each test, certain lines consistently ranked well for white mold resistance. Multiple occurrences in the top twenty across growing seasons suggest that there is some consistency among evaluations, and that the resistance attributed to these lines is fixed and durable.

Although some lines showed moderate levels of physiological resistance to *S. sclerotiorum*, none of the experimental lines are consistently and significantly more resistant than G122. It should be noted that this observation is based solely on greenhouse phenotyping using the straw test. It is possible that further field testing may reveal lines statistically more resistant than G122, though this is unlikely. In general, snap bean varieties show greater susceptibility to white mold than dry beans (Myers, unpublished data). This difference may be related to the reduced lignin content of snap beans and is supported by data that show a correlation between pod fiber and white mold

resistance. As such, obtaining snap bean lines that are as resistant as G122 is a significant achievement.

The absence of transgressive segregants in the pyramiding population suggests that the original hypothesis that the B7 and B8 QTL would show linear additivity may not be true, or that one or both of the QTL of interest may be missing from the germplasm. However, a recent publication by Chung *et al.* (2008) states that “QTL for field resistance based on disease incidence and disease severity and derived from PC-50 and NY6020-4 may be the same as those derived from G122. This observation would suggest that the initial assumption behind pyramiding, that NY6020 and G122 would contribute different QTLs, may not be true. In the next chapter, marker data are considered for the purpose of studying QTL additivity.

### CHAPTER 3

**Marker assisted confirmation of presence of B7 and B8 quantitative trait loci (QTL) for resistance to *Sclerotinia sclerotiorum* in *Phaseolus vulgaris* and evaluation of QTL additivity on the basis of phenotype and marker scores.**

### Abstract

We used molecular markers to confirm the presence of the B7 and B8 QTL in the pyramiding population described in Chapter 2. The *Phs* SCAR marker was used to confirm presence of the B7 QTL, while the SS18<sub>1650</sub> was used to confirm presence of the B8 QTL. Additionally, we investigated two crosses to NY6020-5: NY6020-5 x OSU 5613 and NY6020-5 x OR 91G. In these populations we tested the hypothesis that NY6020-5 has a QTL associated with phaseolin that is similar to that in G122. We compared four marker classes, S,- (no resistance), T,- (B7 QTL only), S,+ (B8 QTL only) and T,+ (B7 and B8 QTL combined) in a one-way analysis of variance to test for marker class significance. Results from the NY6020-5 crosses, particularly the NY6020-5 x OSU 5613 cross suggest that NY6020-5 has a B7 QTL, and that the B7 and B8 QTL have a linear effect. We observed, however, that in the pyramiding population the markers did not have a linear additive effect. We believe that the two QTL are likely additive, but that linear additivity may only be functioning in particular genetic backgrounds. Selecting for the SS18<sub>1650</sub> and T phaseolin alleles in crosses with NY6020-5 is likely to yield more resistant lines than selecting for SS18<sub>1650</sub> alone, and these lines are likely to have resistance levels equivalent to resistant donors NY6020-5 and G122.

## Introduction

In this chapter we consider marker data from the pyramiding population described in Chapter 2 to evaluate the assumptions of QTL additivity. We will similarly evaluate assumptions of QTL additivity in NY6020-5 x OR 91G and NY6020-5 x OSU 5613 populations.

In a G122 mapping population, the B7 QTL accounted for 38% of the phenotypic variation in the straw tests and 26% of the variation in the field tests (Miklas *et al.*, 2001). Miklas (2007), reported successful transfer of the B7 QTL into pinto market class breeding lines using the *Phs* SCAR marker.

In the NY6020 mapping population, the B8 QTL explained 38% of variation in the straw test and 26% of variation in the field test (Miklas & Delorme, 2003). However, this QTL was also associated with an increase in internode length, which is an undesirable growth habit trait in snap beans. Miklas (2007) employed a strategy of selecting for the B8 QTL using both the SS18<sub>1650</sub> SCAR and AW9<sub>1200</sub> RAPD markers. In this study, however, we used only the SS18<sub>1650</sub> SCAR marker for its ease of use in routine scoring.

By looking at the percent phenotypic variation described in each study, the two QTL appear to be similar in terms of explanatory power. Similarly, Miklas (2007) described both QTL as contributing a 15-20% reduction in disease severity, or, similarly, a reduction of 1.0 in the straw test mean. This logic supports the conclusion that the two QTL of interest, B7 and B8, are essentially equal in magnitude.

The lack of transgressive segregants for straw test score in the pyramiding project was noted as early as spring 2008, and as a result, we sought marker data for the QTL of

interest in this population. One possible reason for the lack of transgressive segregants was due to a lack of QTL additivity in contradiction of our original hypothesis concerning the combination of the B7 and B8 QTL. In the present study we evaluate a second hypothesis that both parents had both QTL already present.

The fact that OSU 6229 and OSU 6230 are more resistant than OSU 6241 formed the basis of this hypothesis. These lines all have the SS18<sub>1650</sub> allele, and the B8 QTL as verified by disease testing. OSU 6229 and OSU 6230 have the T phaseolin allele and a higher level of disease resistance than OSU 6241, which has the S phaseolin allele. Given the pedigrees of these elite lines, both the SS18<sub>1650</sub> and T phaseolin alleles could only have come from the NY6020-5 parent. The previous description of *Phs* having been associated with resistance (Miklas *et al.*, 2001; Miklas, 2007) was considered to be a possible explanation for the observed difference. In the NY6020-4 x Benton population used to map the B8 QTL, the phaseolin locus was not polymorphic (Miklas *et al.*, 2001). Using remnant seed from NY6020-5 x OR 91G and NY6020-5 x OSU 5613 we set up segregating populations to evaluate the significance of a T phaseolin allele donated from NY6020-5. It was our hypothesis that NY6020 may have the same B7 QTL as G122. If this were true, it would explain the lack of superior germplasm found in the initial pyramiding population, and would provide new context in which to interpret QTL additivity.

## Materials and Methods

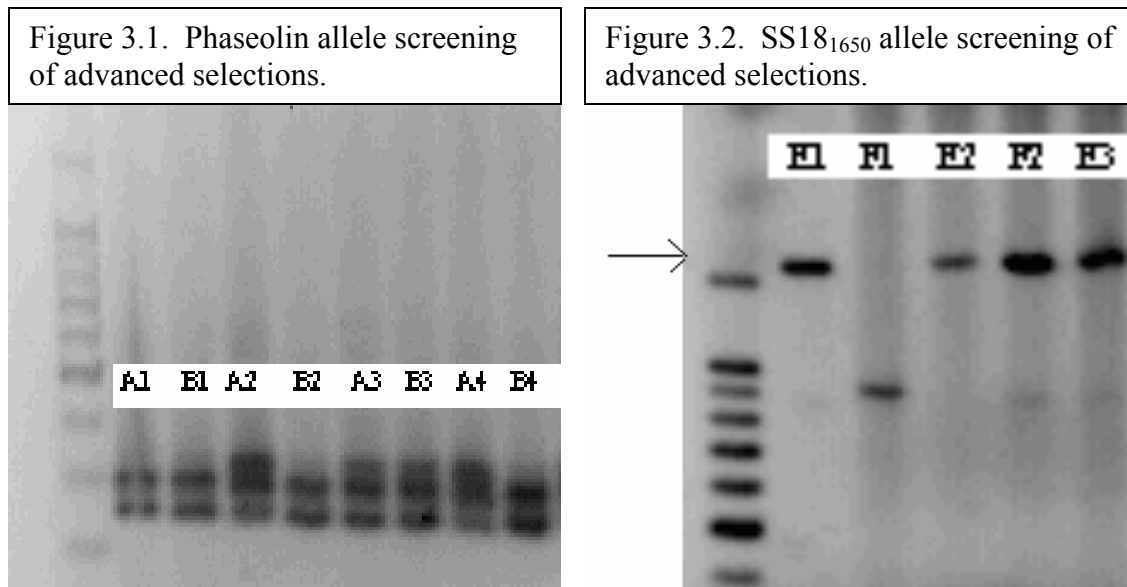
### DNA extraction and molecular marker analysis

DNA was extracted from young, actively growing leaves of single plants in the greenhouse using a procedure described by Fulton *et al.* (1995). DNA quantity and quality of samples was checked using a NanoDrop ND-1000 UV-vis spectrophotometer. Samples were diluted at 10x and 100x to form working stock concentrations for the polymerase chain reaction (PCR).

Reactions were amplified in GeneAmp® PCR 9700 (Applied Biosystems), MJ Mini™ Personal Thermocycler (BioRad), DNA Engine® Peltier Thermal Cycler (BioRad), and PTC-100™ Programmable Thermal Controller (MJ Research, Inc.) thermocyclers. Gels were run in Sub-Cell® GT (BioRad), B1A (Owl Separation Systems, Inc.), and Recirculating Midi-Horizontal System (Fisher Biotech) gel casting rigs and electrophoresis buffer tanks using EC 105 (EC Apparatus Corporation) and Power Pac 300 (Biorad) power supplies.

The phaseolin SCAR marker, and the SS18 SCAR marker were amplified (Figures 3.1 and 3.2) using 2.2µl of template DNA, 11.06µl nanopure water, 1.5µl 10x reaction buffer, 0.9µl 2.5 mM dNTPs, 0.12µl 10mM forward primer, 0.12µl mM reverse primer, and 0.1µl AmpliTaq® polymerase (Applied Biosystems). The PCR protocol for the phaseolin SCAR was 40 cycles of 10 sec at 94°C, 40 sec at 50°C, 1.5 min at 72°C followed by a 5 min hold at 72°C and a final hold at 4°C, and the 2% agarose 0.5x TBE gels were run for 80 min at 100 volts. The SS18 SCAR marker was amplified using 40 cycles of 10 sec at 94°C, 40 sec at 63°C, 2 min at 72°C followed by a 5 min hold at 72°C

and a hold at 4°C and was run on 1.5% agarose 0.5x TBE gels for 60 minutes at 100 volts.



Gels were stained using a 0.5 µg/ml solution of ethidium bromide and were imaged using a Mini Darkroom UV Transilluminator (UVP).

#### Straw Test

Plants were evaluated for white mold resistance using the Petzoldt and Dickson straw test as modified by Teran et al. (2006) and as described in chapter 2 of this thesis.

#### Experimental Populations and Tissue Sampling

Following the final generation of selection, a single leaf of each plant was sampled during winter 2008 from the pyramiding project described in chapter 2 for the purpose of marker screening. The progeny of crosses with OSU 6229 and OSU 6230 were combined into a single data set that consisted of all four possible marker combinations; S,- “no resistance”, S,+ “B8 QTL only”, T,- “B7 QTL only”, and T,+ “B7 and B8 QTL combined.” Single leaf tissue for each family was taken during both winter 2008 and spring 2009 for the purpose of genotyping families.



Additional straw test and marker data were collected on two populations derived from crosses to NY6020. Remnant seed of OSU experimental lines B7708 and B7714 originally advanced to F<sub>4</sub> using single seed descent was grown in the field during the summer of 2008. All plants were harvested individually, and were used to create a set of experimental F<sub>4:5</sub> families for the purpose of testing the significance of the T phaseolin allele contributed by NY6020. B7708 came from the cross of NY6020-5 x OR 91G, and B7714 was derived from NY6020-5 x OSU 5613. OR 91G was described in chapter 2. OSU 5613 is a small sieve advanced selection from a cross Rapier x OSU 5163. The original screening populations consisted of 99 families from B7708 and 85 families from B7714. From the initial screen we selected 48 families from each of the lines: 12 highly resistant, 24 moderately resistant, and 12 highly susceptible. However, not all of the selected families germinated reliably, and this reduced the number of families to 48 for B7708 (Appendix Table A11) and 47 for B7714 (Appendix Table A12). These selected families were screened using the straw test in a randomized complete block design (RCBD) with 3 blocks. Leaf tissue was collected from a single plant for each family in each block for the purpose of genotyping.

#### Data Analysis

Data analysis was performed using SAS for Windows 9.1 (SAS Institute, Cary NC) using Proc GLM and MIXED procedures. The genotypes for the *Phs* and SS18<sub>1650</sub> markers were composited into a single variable, class; 0=(S,-), 1=(S,+), 2=(T,-), 3=(T,+) where S and T represent the alleles at the phaseolin locus and + or - is the state of the SS18 marker. The SAS Model was MEAN SCORE= BLOCK CLASS LINE(CLASS). The analysis was conducted as a One-way ANOVA with selected contrast statements.

The model was run twice to accommodate two sets of three contrasts. The first set (Breeding contrasts) tested the null hypothesis that there were no differences among lines for resistance to white mold with the alternate hypothesis being that significant differences exist. The second set (Genetic contrasts) tested the hypothesis that there was an additive effect on disease score associated with the addition of resistance alleles.

For the pyramiding project described in Chapter 2, lines were fixed, because lines had been intentionally selected for white mold resistance and did not represent a random sample from common bean. For the B7708 and B7714 populations, lines were random, because no selection pressure had previously been imposed.

Broad-sense heritability was calculated in accordance with procedures outlined in Holland et al. (2002).

## Results and Discussion

### Pyramiding Population

In the pyramiding population, 140 lines were genotyped: 16 were (S,-), 9 were (T,-), 28 were (S,+), and 87 were (T,+). First, considering the significance of marker class in the pyramiding population described in Chapter 2, the results from the winter 2008 population (Table 3.1, Figure 3.3) showed the contrasts resistance vs. susceptible and one vs. two QTL as being significant, but not B7 vs. B8 QTL. The statistical significance of the resistant vs. susceptible contrast suggests that presence of one or more markers associated with resistance is significantly better than having only susceptible alleles. The contrast of B7 vs. B8 was not significant, suggesting that the individual “single positive” marker classes are indistinguishable with regards to white mold resistance. Considering the genetic contrasts, SS18 + and – states were significantly different, but the contrast of *Phs* T and S states was not. The phaseolin alleles ranked as expected with the T class being more resistant than the S class; however the difference was too small to obtain statistical significance. The fact that the interaction contrast (B7 x B8) was not significant suggests linear additivity for these two QTL.

Results from the spring 2009 differed (Table 3.2, Figure 3.4) in that the contrast of resistant vs. susceptible marker classes was not significant. This suggests that the observed variation may be due more to environment than to genetics. Presence of two QTL was significantly better than having a single QTL. Unlike the first test, the contrast of “single positive” marker classes showed that the B8 QTL associated with the SS18 marker was statistically more resistant than the B7 QTL. The contrast of QTL interaction

was significant in this data set, suggesting that the QTL are not additive, and that another genetic phenomenon such as epistasis may be conditioning the observed variation. When comparing the two growing seasons, the spring 2009 straw test was more severe (Figures 3.3 and 3.4). Additionally, in the winter 2009, the T,- marker class had an abnormally high score, which influenced contrasts involving marker class.

When the two repetitions were combined (Table 3.3, Figure 3.5) the statistical significance of contrasts from the cross site analysis was identical to that in the spring 2009 growing season.

Across all three analyses, the contrast of the T vs. S phaseolin was not significant. This suggests that the effects of the B7 QTL may not have been preserved when the linkage between *Phs* and *p* was intentionally broken. However mean straw test scores for the white seeded G122 derived lines were not significantly different from the resistant parent (Appendix Table A1 and A2).

One observation that was consistent across all growing seasons was that the differences between the most susceptible and most resistant marker classes did not exceed one unit on the straw test scale. For spring 2009, the difference was 1.00, for winter 2008 the difference was 0.40, and averaged over the two tests it was 0.74. These small differences combined with relatively large variances make obtaining statistical significance difficult. This calls into question how much of the observed straw test variance is due to environment rather than genetics.

Table 3.1. One-way analysis of variance and contrasts of marker class significance for white mold resistance in the straw test of B7 x B8 QTL pyramiding population of *Phaseolus vulgaris* for the winter 2008 growing season.

Source	DF	SS	MSE	F-Value	P-value
<i>Fixed Effects</i>					
Class	3	7.59	2.53	7.97	<.0001
Line(Class)	138	222.18	1.61	5.08	<.0001
<i>Random Effects</i>					
Block	2	49.74	24.87	78.24	<.0001
Residual	269	85.52	0.32		
<i>Breeding Contrasts</i>					
Res. vs Sus. <sup>z</sup>	1	3.38	3.38	7.29	0.0074
1 vs 2 QTL <sup>y</sup>	1	3.52	3.52	7.60	0.0062
B7 vs B8 <sup>x</sup>	1	0.69	0.69	1.48	0.2248
<i>Genetic Contrasts</i>					
S vs T <sup>w</sup>	1	1.07	1.07	1.95	0.1636
SS18+ vs SS18- <sup>v</sup>	1	6.50	6.50	11.85	0.0007
B7*B8 Interaction <sup>u</sup>	1	0.02	0.02	0.04	0.8492

<sup>z</sup> Class (S,-) vs (S,+), (T,-), (T,+)

<sup>y</sup> Class (S,+), (T,-) vs (T,+)

<sup>x</sup> Class (S,+), (T,-) vs (T,+)

<sup>w</sup> Class (S,-), (S,+) vs (T,-), (T,+)

<sup>v</sup> Class (S,-), (T,-) vs (S,+), (T,+)

<sup>u</sup> Class (S,-), (T,+) vs (S,+), (T,-)

Figure 3.3. LS means and 95% confidence intervals for marker classes in straw tests of B7 x B8 QTL pyramiding population of *Phaseolus vulgaris* for the winter 2008 growing season.

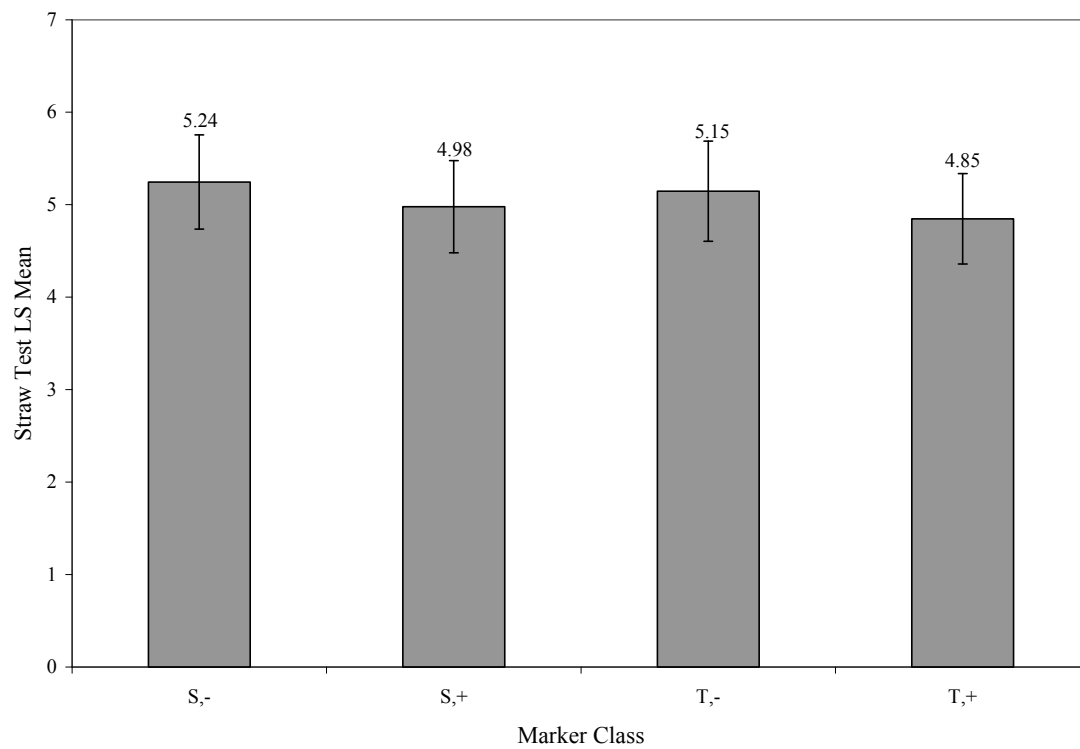


Table 3.2. One-way analysis of variance and contrasts of marker class significance for white mold resistance in the straw test of B7 x B8 QTL pyramiding population of *Phaseolus vulgaris* for the spring 2009 growing season.

Source	DF	SS	MSE	F-Value	P-value
<i>Fixed Effects</i>					
Class	3	21.33	7.11	6.76	0.0002
Line(Class)	139	284.95	2.05	1.95	<.0001
<i>Random Effects</i>					
Block	2	2.60	1.30	1.24	0.2926
Residual	248	260.89	1.05		
<i>Breeding Contrasts</i>					
Res. vs Sus. <sup>z</sup>	1	0.09	0.09	0.10	0.7581
1 vs 2 QTL <sup>y</sup>	1	12.71	12.71	14.88	0.0001
B7 vs B8 <sup>x</sup>	1	8.53	8.53	9.99	0.0018
<i>Genetic Contrasts</i>					
S vs T <sup>w</sup>	1	1.47	1.47	1.58	0.2101
SS18+ vs SS18- <sup>v</sup>	1	15.16	15.16	16.34	<.0001
B7*B8 Interaction <sup>u</sup>	1	4.70	4.70	5.07	0.0252

<sup>z</sup> Class (S,-) vs (S,+), (T,-), (T,+)

<sup>y</sup> Class (S,+), (T,-) vs (T,+)

<sup>x</sup> Class (S,+), (T,-) vs (T,+)

<sup>w</sup> Class (S,-), (S,+), vs (T,-), (T,+)

<sup>v</sup> Class (S,-), (T,-) vs (S,+), (T,+)

<sup>u</sup> Class (S,-), (T,+), vs (S,+), (T,-)

Figure 3.4. LS means and 95% confidence intervals for marker classes in straw tests of B7 x B8 QTL pyramiding population of *Phaseolus vulgaris* for the spring 2009 growing season.

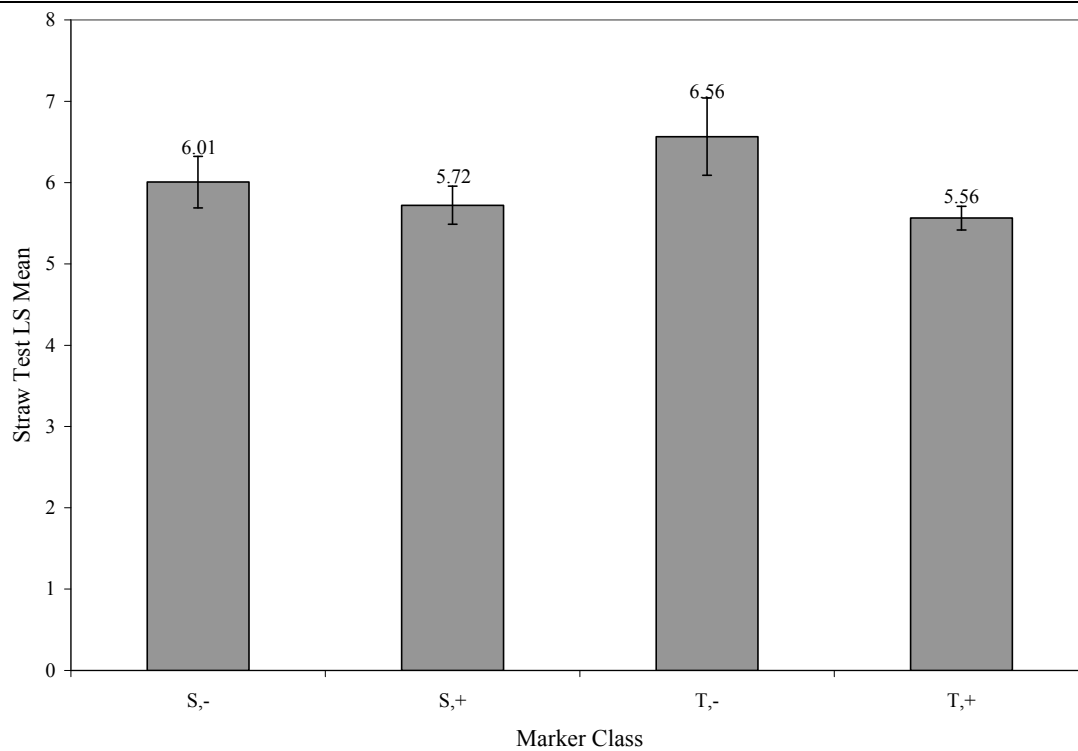




Table 3.3. One-way analysis of variance and marker class contrasts for white mold resistance in the straw test of the *Phaseolus vulgaris* B7 x B8 QTL pyramiding population. Combined analysis of winter 2008 and spring 2009 growing seasons.

Source	DF	SS	MSE	F-Value	P-value
<i>Fixed Effects</i>					
Class	3	33.30	11.10	13.07	<.0001
Line(Class)	142	305.30	2.15	2.53	<.0001
Season	1	133.80	133.80	157.55	<.0001
Block(Season)	4	48.44	12.11	14.26	<.0001
Residual	655	556.28	0.85		
<i>Breeding Contrasts</i>					
Res. vs Sus. <sup>z</sup>	1	1.91	1.91	2.21	0.1374
1 vs 2 QTL <sup>y</sup>	1	21.43	21.43	24.80	<.0001
B7 vs B8 <sup>x</sup>	1	9.96	9.96	11.53	0.0007
<i>Genetic Contrasts</i>					
S vs T <sup>w</sup>	1	0.17	0.17	0.17	0.6836
SS18+ vs SS18- <sup>v</sup>	1	27.77	27.77	27.95	<.0001
B7*B8 Interaction <sup>u</sup>	1	5.36	5.36	5.40	0.0204

<sup>z</sup> Class (S,-) vs (S,+), (T,-), (T,+)

<sup>y</sup> Class (S,+), (T,-) vs (T,+)

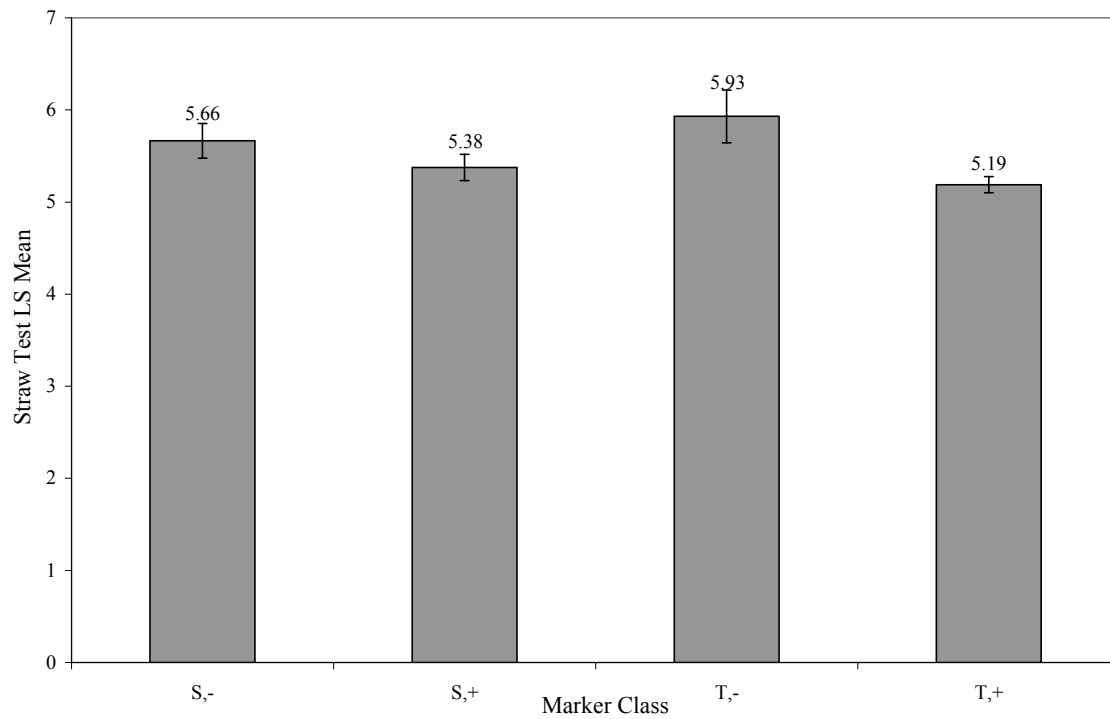
<sup>x</sup> Class (S,+), (T,-) vs (T,+)

<sup>w</sup> Class (S,-), (S,+), (T,-), (T,+)

<sup>v</sup> Class (S,-), (T,-) vs (S,+), (T,+)

<sup>u</sup> Class (S,-), (T,+), (S,+), (T,-)

Figure 3.5. LS means and 95% confidence intervals for marker classes in straw tests of B7 x B8 QTL pyramiding population of *Phaseolus vulgaris* for the cross site analysis of winter 2008 and spring 2009 growing seasons.



### B7704 and B7714 Experimental Populations

The B7704 and B7714 populations were originally analyzed as a single data set (Table 3.4, Figure 3.6) with 95 families: 16 (S,-), 14 (T,-), 38 (S,+), and 27 (T,+). The contrast of resistant and susceptible marker classes showed that the resistant marker classes are statistically better than the susceptible class. The contrast comparing the “single positive” and “double positive” marker classes was not statistically significant. The contrast of the B7 and B8 QTL was also not significant. The contrast of SS18 + and – alleles was significant, as was the contrast of *Phs* T and S alleles. In the composite populations of B7704 and B7714, both the B7 and B8 QTL were significant. The contrast for a B7 x B8 interaction was not significant, which suggests that these QTL have linear additivity.

The variable parent was used as a model term for male parent, either OR 91G or OSU 5613. The progeny of the NY6020-5 x OSU 5613 (B7714) population have a higher overall straw test LS mean than the progeny of the NY6020-5 x OR 91G (B7704) population. Additionally, the interaction term of class x parent was significant. The significant interaction term suggests that the two populations performed differently and should be analyzed separately.

For B7714, where the highly susceptible OSU 5613 was the male parent, the contrast patterns of significance were identical to the composite data set (Table 3.5, Figure 3.7). There were 47 lines in total with 10 (S,-), 7 (T,-), 14 (S,+), and 16 (T,+). The susceptible marker class (S,-) was statistically worse than the resistant marker classes. Additionally, the T,+ marker class was significantly better than the S,+ and T,- classes. Differences between the two “single positive” marker classes were not statistically

significant. Both of the markers were statistically significant, and the two QTL appeared to have linear additivity. The significance of blocking in Tables 3.4 and 3.6 is likely due to the first replication being performed one month prior to the second and third replications.

The B7708 population, with OR 91G as the male parent, revealed very different trends (Table 3.6, Figure 3.8). There were 48 lines in total with 6 (S,-), 7 (T,-), 24 were (S,+), and 11 (T,+). In this data set, none of the contrasts were significant. Both block and line(class) variables were significant.

Similar to the pyramiding materials, the difference between the most susceptible and resistant marker class was often quite small. The difference was smallest in the NY6020-5 x OR 91G, where it was only 0.75. In the combined dataset, the difference was 0.99, whereas in the NY6020-5 x OSU 5613 population the difference was 1.65. I would attribute my ability to get statistical significance in this population to the fact that the differences between the means are most pronounced in this population. The difference in response to white mold in these two populations may be related to differences in genetic background. At one time, OSU 5613 was considered for release, but was dropped when it became apparent that it was significantly more susceptible to white mold in the field than OR 91G (Myers, unpublished data). OSU 5613 apparently lacks one or more uncharacterized resistance factors that OR 91G and many other bush blue lake beans have.

Table 3.4. One-way analysis of variance and marker class contrasts for white mold resistance in the straw test of F<sub>4</sub> populations NY6020-5 x OR 91G and NY6020-5 x OSU 5613 of *Phaseolus vulgaris*

Source	DF	SS	MSE	F-Value	P-value
<i>Fixed Effects</i>					
Class	3	29.79	9.93	5.12	0.0026
Parent	1	20.96	20.96	10.80	0.0015
Parent*Class	3	22.62	7.54	3.89	0.0117
<i>Random Effects</i>					
Block	2	8.98	4.49	4.17	0.017
Line(Class*Parent)	86	166.84	1.94	1.80	0.0005
Residual	184	198.09	1.08		
<i>Breeding Contrasts</i>					
Res. vs Sus. <sup>z</sup>	1	25.35	25.35	12.06	0.0008
1 vs 2 QTL <sup>y</sup>	1	3.78	3.78	1.80	0.1827
B7 vs B8 <sup>x</sup>	1	0.65	0.65	0.31	0.5793
<i>Genetic Contrasts</i>					
S vs T <sup>w</sup>	1	9.68	9.68	5.23	0.0246
SS18+ vs SS18- <sup>v</sup>	1	17.49	17.49	9.44	0.0028
B7*B8 Interaction <sup>u</sup>	1	2.61	2.61	1.41	0.238

<sup>z</sup> Class (S,-) vs (S,+), (T,-), (T,+)

<sup>y</sup> Class (S,+), (T,-) vs (T,+)

<sup>x</sup> Class (S,+), (T,-) vs (T,+)

<sup>w</sup> Class (S,-), (S,+) vs (T,-), (T,+)

<sup>v</sup> Class (S,-), (T,-) vs (S,+), (T,+)

<sup>u</sup> Class (S,-), (T,+) vs (S,+), (T,-)

Figure 3.6. LS means and 95% confidence intervals for marker classes in straw tests of *Phaseolus vulgaris* populations NY6020-5 x OR 91G and NY6020-5 x OSU 5613.

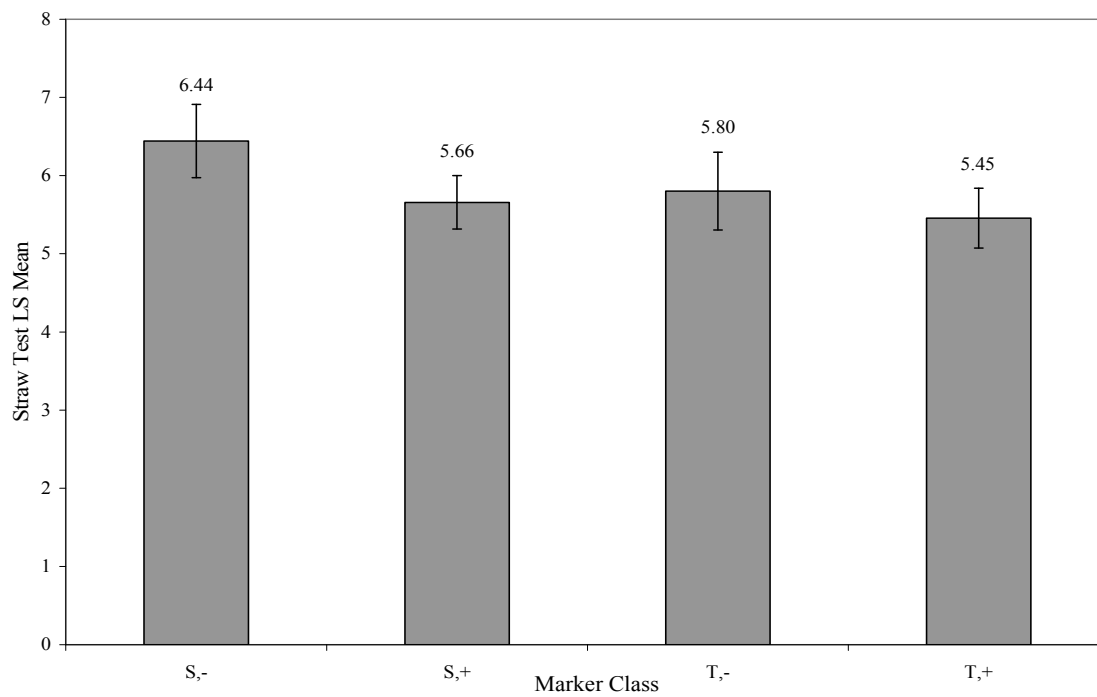


Table 3.5. One-way analysis of variance and marker class contrasts for white mold resistance in the straw test of F4 population NY6020-5 x OSU 5613 of *Phaseolus vulgaris*.

Source	DF	SS	MSE	F-Value	P-value
<i>Fixed Effects</i>					
Class	3	46.98	15.66	8.24	0.0002
<i>Random Effects</i>					
Block	2	8.14	4.07	4.55	0.0131
Line(Class)	42	79.80	1.90	2.12	0.0016
Residual	88	78.65	0.89		
<i>Breeding Contrasts</i>					
Res. vs Sus. <sup>z</sup>	1	23.06	23.06	10.68	0.0022
1 vs 2 QTL <sup>y</sup>	1	23.47	23.47	10.87	0.0020
B7 vs B8 <sup>x</sup>	1	0.45	0.45	0.21	0.6463
<i>Genetic Contrasts</i>					
S vs T <sup>w</sup>	1	18.38	18.38	8.09	0.0069
SS18+ vs SS18- <sup>v</sup>	1	28.31	28.31	12.46	0.001
B7*B8 Interaction <sup>u</sup>	1	0.29	0.29	0.13	0.7235

<sup>z</sup> Class (S,-) vs (S,+), (T,-), (T,+)

<sup>y</sup> Class (S,+), (T,-) vs (T,+)

<sup>x</sup> Class (S,+), (T,-) vs (T,+)

<sup>w</sup> Class (S,-), (S,+), vs (T,-), (T,+)

<sup>v</sup> Class (S,-), (T,-) vs (S,+), (T,+)

<sup>u</sup> Class (S,-), (T,+), vs (S,+), (T,-)

Figure 3.7. LS means and 95% confidence intervals for marker classes in straw tests of *Phaseolus vulgaris* population NY6020-5 x OSU 5613.

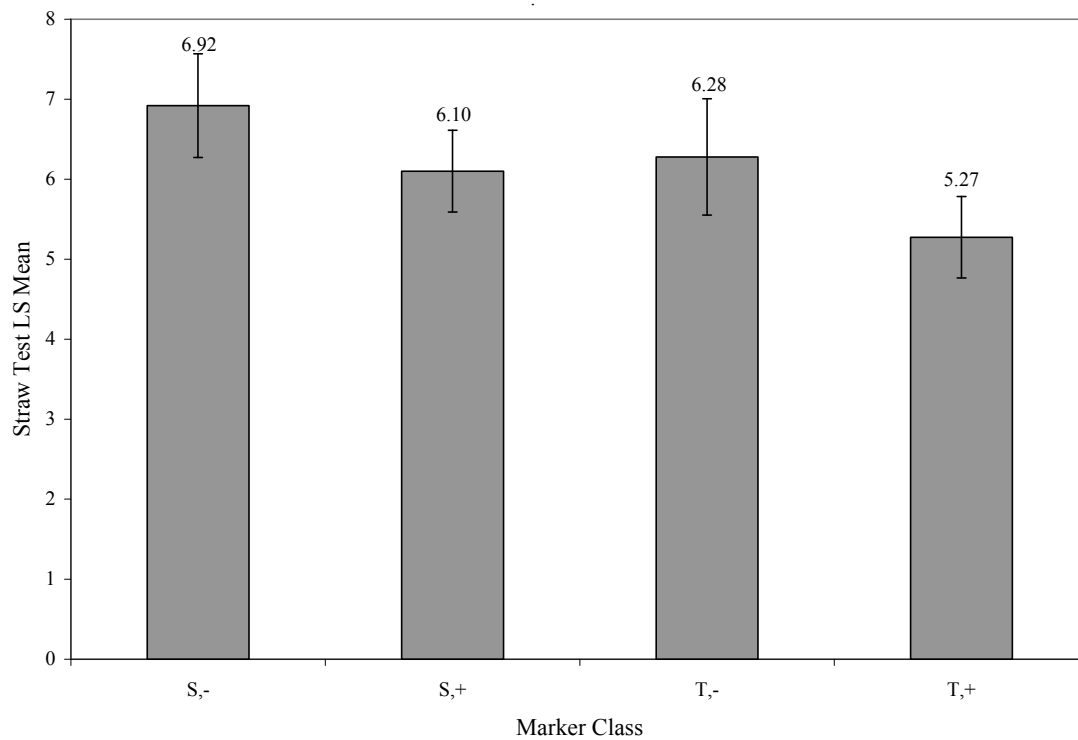




Table 3.6. One-way analysis of variance and marker class contrasts for white mold resistance in the straw test of F4 population NY6020-5 x OR 91G of *Phaseolus vulgaris*

Source	DF	SS	MSE	F-Value	P-value
<i>Fixed Effects</i>					
Class	3	10.68	3.56	1.80	0.1617
<i>Random Effects</i>					
Block	2	11.88	5.94	5.15	0.0076
Line(Class)	44	87.12	1.98	1.72	0.0148
Residual	94	108.40	1.15		
<i>Breeding Contrasts</i>					
Res. vs Sus. <sup>z</sup>	1	6.93	6.93	2.85	0.0985
1 vs 2 QTL <sup>y</sup>	1	3.53	3.53	1.45	0.2355
B7 vs B8 <sup>x</sup>	1	0.22	0.22	0.09	0.7622
<i>Genetic Contrasts</i>					
S vs T <sup>w</sup>	1	0.39	0.39	0.18	0.6738
SS18+ vs SS18- <sup>v</sup>	1	1.51	1.51	0.69	0.4114
B7*B8 Interaction <sup>u</sup>	1	8.78	8.78	4.01	0.0514

<sup>z</sup> Class (S,-) vs (S,+), (T,-), (T,+)

<sup>y</sup> Class (S,+), (T,-) vs (T,+)

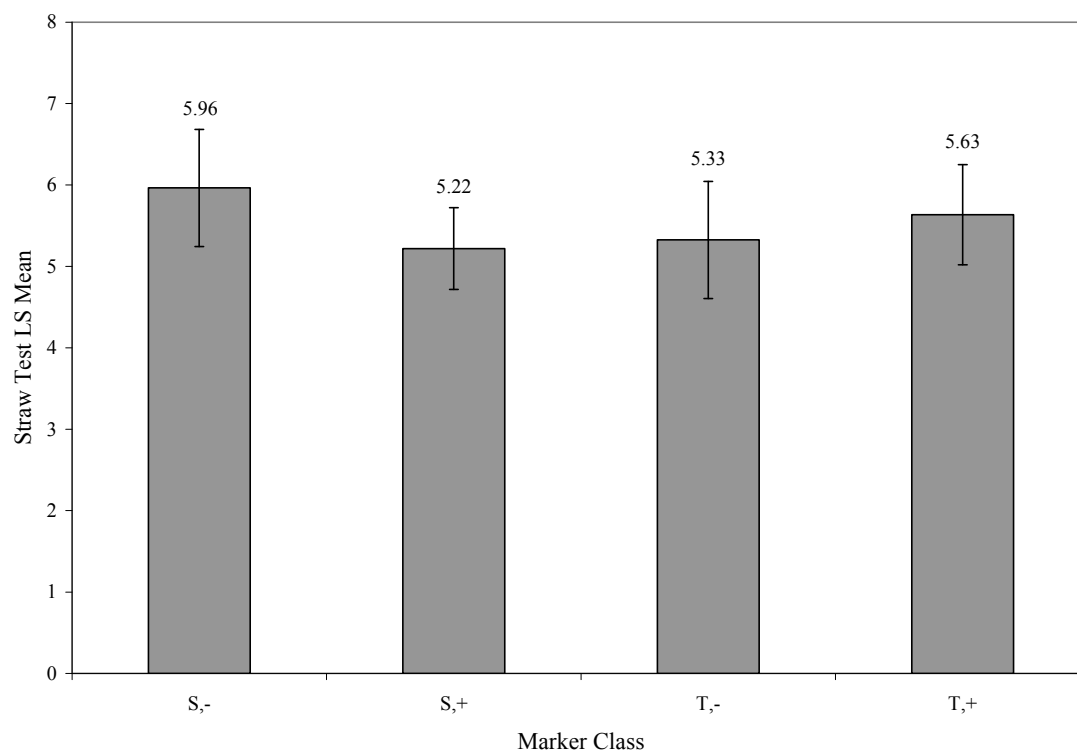
<sup>x</sup> Class (S,+), (T,-) vs (T,+)

<sup>w</sup> Class (S,-), (S,+) vs (T,-), (T,+)

<sup>v</sup> Class (S,-), (T,-) vs (S,+), (T,+)

<sup>u</sup> Class (S,-), (T,+) vs (S,+), (T,-)

Figure 3.8. LS means and 95% confidence intervals for marker classes in straw tests of *Phaseolus vulgaris* population NY6020-5 x OR 91G.



## Conclusions

The pyramiding project revealed different results. Across the winter 2008, spring 2009, and cross site analysis, the SS18<sub>1650</sub> marker associated with B8 resistance was statistically significant, confirming that the QTL is associated with white mold resistance in the pyramiding population. However, the *Phs* marker associated with the B7 QTL was not significant, suggesting it was of smaller magnitude or that the QTL had been lost when the linkage between phaseolin and *p* was broken. The statistical significance of linear additivity varies among the analyses. The winter 2008 analysis shows linear additivity for the two markers, but the spring 2009 and cross site analyses do not show linear additivity, due to the significant B7 x B8 interaction.

These results are most likely attributed to the poor performance of the T,- marker class during the spring 2009 growing season, which resulted in a lack of significance of the B7 marker and a lack of linear additivity in both the spring 2009 and cross site analyses. During the winter 2008 growing season, this marker class had a much better performance. The spring 2009 straw test was much more destructive than previous straw tests (Figure 3.4). The other classes (S,-, S,+, and T,+) all had mean increases of 0.77, 0.74, and 0.71, respectively when compared with the winter 2009 analysis. The T,- class saw a mean increase that was twice as large, with a difference of 1.41. This may suggest the marker class as being more sensitive to environmental variation. It should be noted that this marker class also had the fewest representative families. With only 9 lines having this marker profile, this class is the least robust. Presumably with a larger number of representative lines, and with more replication, it would be possible to capture a more accurate estimate of the mean for this marker class.

I believe the spring 2009 test to be a particularly variable test. This observation is corroborated by the fact that the estimates for heritability on the basis of family decreased 25% from what was predicted in the winter 2008 test. Combining the two analyses into a single cross-site analysis decreased the heritability on a per pot basis, but increased heritability on a per family basis, suggesting that pooling the spring 2009 data with the winter 2008 data may be a better approach than evaluating the spring 2009 data by itself (Table 3.7).

With respect to marker additivity, the pyramiding project seems to offer two different conclusions. The winter 2008 analysis suggests linear marker additivity, while the spring 2009 and cross site analyses deviate from this hypothesis.

Table 3.7. Broad-sense heritabilities calculated for B7 x B8 QTL pyramiding population and NY6020-5 x OSU5613 and NY6020-5 x OR 91 G populations.

B7 x B8 QTL Pyramiding Population	Pot Basis		Family Basis	
	H <sup>2</sup>	SE	H <sup>2</sup>	SE
Winter 2008	60.80%	4.31%	81.84%	2.69%
Spring 2009	30.60%	5.73%	56.11%	6.65%
Winter 2008 and Spring 2009	15.77%	5.18%	62.99%	10.00%
<u>NY6020-5 Progeny</u>				
NY6020-5 x OSU 5613 and NY6020-5 x OR 91G	32.65%	6.68%	58.44%	7.37%
NY6020-5 x OSU 5613	41.95%	9.24%	67.69%	8.30%
NY6020-5 x OR 91G	21.15%	9.44%	43.75%	13.94%

Data from the B7714 (NY6020-5 x OSU 5613) and combined analysis of the B7714 and B7708 populations suggest that there may be a resistance factor associated with *Phs* contributed by NY6020-5. This is supported by the S vs. T and 1 vs. 2 QTL contrasts being significant and the B7 x B8 interaction being not significant in both the NY6020-5 x OSU 5613 and combined data sets. As shown in Figures 3.6 and 3.7, the T

allele is associated with resistance and the S allele with susceptibility. The significance of the 1 vs 2 QTL contrast suggests that selecting for both the SS18<sub>1650</sub> and T phaseolin alleles is likely to produce more resistant germplasm than selecting for only the SS18<sub>1650</sub> allele. Finally the lack of significance of the B7 x B8 contrast suggests that these two QTL have linear additivity.

The heritability values on a per pot and per family basis were highest in the NY6020-5 x OSU 5613 population, lowest in the NY6020-5 x OR 91G population, and intermediate in the analysis combining both populations. These results suggest that more of the observed variation is genetic in the NY6020-5 x OSU 5613 population than was observed for the NY6020-5 x OR 91G population.

The results in the B7708 population are contradictory but are at odds with what is currently known about the B8 QTL, which has been validated more than once (Miklas & Delorme, 2003, Miklas, 2007). Therefore, data sets where the SS18 marker is not associated with significant differences in disease resistance are immediately suspect. Possible reasons for the lack of significance are a strong environmental effect, additional unidentified genetic factors may have been contributed by OR 91G or linkage between the SCAR and the QTL had been broken in early generations.

One trend that holds constant across multiple data sets is that the difference between the most susceptible and most resistant marker class rarely exceeds 1.00 in the straw test. The population of NY6020-5 x OSU 5613 is the only population that is an exception. This has obvious implications for this project; the small differences between the means coupled with relatively large variances it difficult to detect statistical significance. The 1-9 ranking scale does not currently employ ½ point scoring, so

variations within pots and families are often large due to minor differences accounting for full point differences in scoring. Additionally, tests typically have assigned plant scores that are between four and eight. The main reason why the observed range is narrower than the potential range is probably a lack of genetic variability, (especially for the resistant side of the range). In the NY6020-5 x OSU 5613 population, more scores of 8 and 9 were recorded, and it was easier to resolve differences between marker classes. A critique of the straw test is that plants go from a score of 1-5 in only 3-4 inches of tissue while the scores of 6-9 cover a much larger proportion of the plant (Figure 3.9).



Figure 3.9. Plant of common bean, *Phaseolus vulgaris*, with straw test scoring criteria shown in yellow (Teran et al., 2006). 1 = no infection, 4 = infection to the first node, 7 = infection to the second node, 9 = total plant collapse.

We attempted to develop a more accurate test by quantifying necrosis length, taking proportion of stem necrosis to internode length, and using non-parametric rank-based tests. None of these methods provided any additional information beyond the standard protocol (Petzoldt & Dickson, 1996; Teran *et al.*, 2006).

While differences in marker class within a test rarely exceed one, our results have been very consistent. This led me to evaluate coancestry in these populations.

Practically all materials have at least some heritage with OR 91G. In the case of the pyramiding population, all of the potential B7 donor parents have a high coefficient of parentage (predicted 7/8ths of the genome from OR 91G) due to being derived from a G122 x OR 91G population that was backcrossed twice to OR 91G. The B8 donor parents OSU 6229 and OSU 6230 were derived from NY6020-5 x OR 91G and OR 91G x NY6020-5 respectively. Even OSU 6241, which was derived from OSU 5630 x NY6020-5 is highly related to OR 91G due to OSU 5630 itself having been selected from a cross of OR 91G x OSU 5402. It is likely that ideotype selection for blue lake processing traits has led to the selection of OR 91G and related blue lake alleles at higher frequency than would be predicted by chance. In this regard the NY6020-5 x OSU 5613 population is unique in its lower proportion of heritage from OR 91G.

In the case of materials derived from OR 91G, it is worth considering the possibility that there is a factor missing from the statistical model. It is possible that there is a resistance or susceptibility factor in the OR 91G background that I have been unable to account for. Such a factor could possibly contribute to the lack of differences between marker class means and lack of statistical significance of individual markers and marker classes.

There is another possible explanation. OR 91G and OSU 5630 are S phaseolin, Mesoamerican type beans. OSU 5613 is of hybrid ancestry, being derived from a Mesoamerican x Andean cross. It has S phaseolin, but in other regards is more similar to Andean types. There may be a potential background effect, where the Andean

background allows for full expression of the QTL, but moving it into a Mesoamerican background reduces the effect. This would be possible if the genes underlying the QTL were part of a pathway, and the Andean alleles at other loci were more conducive to expression patterns.

Looking across data sets and drawing on the scientific literature, we are able to draw a number of conclusions. Chung *et al.* (2008) presented data to suggest that G122 has a B8 QTL analogous to NY6020. The data collected in the NY6020-5 x OSU 5613 populations provide a reciprocal conclusion, that NY6020 has a B7 QTL analogous to G122. These results would explain the differences in white mold resistance between OSU 6229, OSU 6230, and OSU 6241 given the polymorphism at the *Phs* locus. These two separate observations point towards a single conclusion: that NY6020 and G122 are identical in their resistance alleles. This conclusion has a profound impact on the original pyramiding strategy. We had assumed the original QTL donor parents were contributing different QTL, because in both cases a second homologous QTL was not detected (Miklas *et al.*, 2001.; Miklas & Delorme, 2003) The possibility that they may be contributing identical QTL would explain the absence of transgressive segregants. Any lines having markers for both QTL of interest are expected to be roughly equal to G122 and NY6020 in terms of white mold resistance. G122 and NY6020-5 are not statistically different in straw tests, though G122 typically ranks as more resistant than NY6020-5. This is likely due to G122 being a dry bean and accumulating higher lignin content than NY6020-5, which is a snap bean.

Ascertaining QTL additivity is more difficult due to conflicting results. Results from NY6020-5 x OSU 5613, combined populations of B7708 and B7714, and results



from the winter 2008 pyramiding population suggest an additive model, while results from the spring 2009, cross site analysis, and NY6020-5 x OR 91G populations suggest that the QTL may not have an additive effect. I would favor the conclusion that the markers do have an additive effect, based on the lines having both resistance markers being the most resistant across a wider range of tests. However, due to small differences among the means and possible background effects it has been difficult to consistently detect the difference.

Lastly, it should be stated that these results were described using only greenhouse phenotyping with the straw test. Further field testing would be useful to further investigate QTL additivity.

## **CHAPTER 4**

**Mixed linear model analysis of marker-trait associations for white mold resistance and general discussion of QTL and pyramiding efficacy.**

### Abstract

Mixed linear model analysis was performed in a subset of lines originally used in a phylogeny study, for which the marker data was already available. Replicated straw tests were performed to measure susceptibility to white mold caused by *S. sclerotiorum* on a collection of 31 snap beans of *Phaseolus vulgaris*. Marker data were analyzed using the program STRUCTURE to estimate the number of subpopulations. Output components of the K-matrix were used as a covariate in statistical analysis. All markers were tested for statistical significance. Only markers B18<sub>1500</sub> and C8<sub>1200</sub> were highly significant. These markers were combined in a second analysis that included markers and an interaction term as model effects. Both markers retained statistical significance in the second round of analysis. The interaction term was not significant ( $p=0.07$ ), but was near the cutoff value of  $p=0.05$ , so additional analysis may be necessary to determine if there is a linear additive effect of these two markers. While the statistical significance of B18<sub>1500</sub> and C8<sub>1200</sub> is interesting and seems to have implications for breeding white mold resistant bush blue lake snap bean germplasm, the markers must first be validated through additional screening and evaluation in controlled populations.

## Introduction

In this final chapter we consider the results of a mixed linear model study as well as attempt to make general conclusions regarding QTL additivity and pyramiding.

Data presented by Chung *et al.* (2008) suggest the presence of a B8 QTL in G122 that may be homologous to the one described in NY6020. Our data with NY6020-5 x OR 91G and NY6020-5 x OSU 5613 suggest that there may also be a B7 QTL present in NY6020. The implications for pyramiding these QTL have already been discussed in detail. However, there is another underlying trend that is worth considering. In two separate QTL mapping studies, individual major effect QTL were not detected. This is due, in part, to a lack of polymorphism between the parents in these candidate regions. However, this original oversight has significant ramifications for understanding the nature of genetic resistance and how to best utilize resistance in developing new cultivars.

Association mapping and mixed linear model analysis are two relatively new techniques that may prove useful in establishing marker-trait associations. Association mapping populations use collections of cultivars or advanced breeding lines. Since the lines are not the progeny of a single cross, the extent of linkage disequilibrium is expected to be reduced. Through sexual recombination events during evolutionary history, only those markers most closely linked to the trait are likely to be significant, while any markers more distant (but still less than 50cM from the trait) are likely to not be significant due to linkage disequilibrium decay. The rate of linkage disequilibrium decay varies from species to species and may vary among populations within a species.

The primary advantage of association mapping is that markers that are statistically associated with phenotype are almost immediately amenable to marker-assisted selection

because of their characterization in a wide base of germplasm. There are two disadvantages to association mapping. The first disadvantage is that due to the extent of linkage disequilibrium, it may require a greater saturation of markers than QTL mapping in order to detect significant markers. There have been some studies that have been able to achieve success using a relatively small number of lines and markers (Wang *et al.*, 2008). The second disadvantage to association mapping is that failing to properly account for population substructure can lead to false positives (Pritchard *et al.*, 2001).

The description of T phaseolin being associated with white mold resistance made me wonder if this observation would extend to other T phaseolin types. It was my hypothesis that for snap bean (being a relatively recent derivative of domestication), linkage disequilibrium would extend farther than in other collections of *P. vulgaris* germplasm. Data were available from a previously compiled phylogeny study where the *Phs* SCAR marker had been used in genotyping. In the current study, a subset of this population was screened and analyzed using mixed linear model analysis. It was my hypothesis that lines with the T allele would be significantly more resistant than lines possessing the S allele. It was also my goal to screen the SS18<sub>1650</sub> SCAR marker in this population, but due to time constraints this was not possible. While phaseolin was not significant in this study, there were markers that were statistically significant and are worthy of further consideration.

## Materials and Methods

### DNA extraction and molecular marker analysis

Davis & Myers (2002) genotyped 98 bean lines with 53 markers (52 RAPD markers, and a single SCAR marker - *Phs*). The purpose of the original study was to generate a snap bean phylogeny (Davis & Myers, 2002).

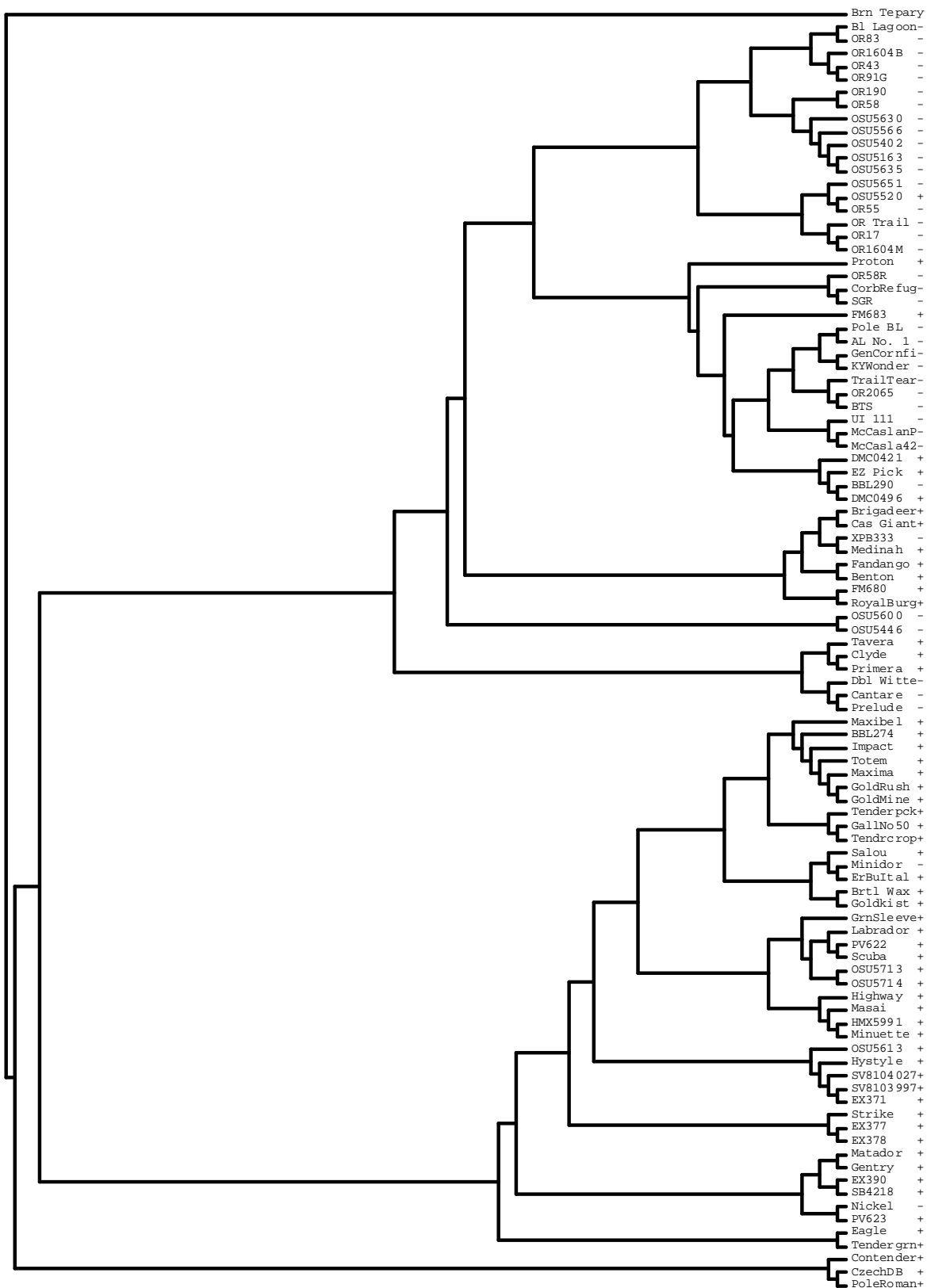
### Straw Test

Plants were characterized for white mold resistance using the straw test and a modified Petzoldt and Dickson scale (Teran *et al.*, 2006) described in chapter 2 of this thesis.

### Experimental Populations

Fifty pure lines were selected from a phylogeny study by Davis & Myers (2002) from a previous total of 98 lines. The phylogeny is summarized as Figure 4.1, reproduced with permission of the authors. Not all of the lines germinated reliably, and this dropped the number of lines tested from 50 to 32. These 32 lines were planted 3 plants to a pot in 3 randomized complete blocks in a greenhouse straw test. Additionally, the line OSU 5613 was dropped from analysis due to marker discrepancies. This brought the grand total of lines for marker:trait association analysis to 31.

Figure 4.1 Snap bean phylogeny of *Phaseolus vulgaris* using 52 RAPD markers and 1 SCAR marker. Brn Tepary is a *P. acutifolius* accession used as an outgroup. UI 111 is a pinto dry bean (race Durango); BTS or Black Turtle Soup is a small black dry bean (race Mesoamerica), and Czech DB is an Andean dry bean. Names followed by (+) or (-) correspond to T (or C) and S phaseolin alleles, respectively.



## Data Analysis

Because the selected lines were of both Mesoamerican and Andean origin, we expected the population to have a genetic structure that might affect the number of markers that were significant. In association mapping, it is important to account for population structure to determine that markers are correlated with phenotype and not with the structure of the population. Failure to properly account for population structure can lead to false positive, Type 1, statistical error.

The genotypic data for 31 lines characterized for 53 markers was entered into the software STRUCTURE 2.2 to analyze population structure. An initial scan of the data was performed to determine the appropriate number of population groups. We used 20,000 Burnin and 20,000 MCM reps after Burnin with 3 iterations for values of population groups,  $K=1-4$  to do a preliminary estimate for the number of groups in this population. The Burnin repetitions parameter performs an initial scan to estimate genetic differences, while the MCM reps analyze the data for population structure. Setting larger values for Burnin and MCM provides more robust estimates of population structure, but requires more processing time to complete the analysis. This initial scan suggested that the population had two major groups on the basis of  $\ln(P/d)$ . The  $\ln(P/d)$  is a value that predicts how well a particular value of  $K$  fits the data set. A smaller negative value of  $\ln(P/d)$  is indicative of a better fit to the data set. We performed a more detailed scan using 100,000 Burnin and 100,000 MCM reps after Burnin for a single iteration for  $K=2$  groups.

Proc mixed models were run on each marker individually using a basic model statement `MEAN= MARKER GROUP`. The term group was a linear covariate estimated



by the K matrix output by STRUCTURE, with values ranging from 0-1. The model was run for each marker individually to identify the most significant markers. Any markers where  $p < 0.05$  were retained for additional analyses.

In the final analysis, any markers that were still significant after two rounds of data analyses were entered into a single model statement with two-way interaction terms: MEAN= MARKER A MARKER B (MARKER A x MARKER B) GROUP.

## Results and Discussion

Straw test least square (LS) means, K matrix data, and marker states for lines tested are summarized in Table 4.1.

Table 4.1. Straw test least squared (LS) means for snap bean phylogeny materials of *Phaseolus vulgaris* screening for resistance to white mold. (Teran scale<sup>z</sup>)

Line	Straw Test LS Mean	K matrix values <sup>y</sup>		B18 <sub>1500</sub>	C8 <sub>1200</sub>
		Group 1 (Andean) K matrix	Group 2 (Mesoamerican) K matrix		
5600	4.00	0.18	0.83	0	0
5630	6.33	0.19	0.81	0	1
5713	4.50	0.91	0.10	0	0
OR 91G	6.50	0.10	0.90	0	1
Black Turtle	4.78	0.04	0.96	1	1
Blue Lake Pole	5.50	0.02	0.98	1	0
Brittle Wax	6.50	0.98	0.02	0	0
Bush Blue Lake 290	6.80	0.10	0.91	0	1
Contender	4.00	0.98	0.02	0	0
Corbette Refuge	6.00	0.27	0.73	0	1
Dubbele Witte	4.33	0.07	0.93	1	0
Eagle	4.50	0.98	0.02	0	0
Fandango	4.80	0.50	0.50	0	0
Gold Mine	4.00	0.99	0.01	0	0
Greensleeves	5.00	0.95	0.05	0	0
Kentucky Wonder 814	5.25	0.07	0.93	1	1
Masai	4.38	0.78	0.22	1	0
Maxibel	4.83	0.72	0.28	0	0
McCaslan No. 42	5.00	0.01	0.99	1	0
McCaslan Pole 543	5.60	0.01	0.99	1	0
Medinah	4.50	0.41	0.59	1	0
Minuette	5.20	0.97	0.03	0	0
Nickel	4.00	0.51	0.49	1	0
Prelude	5.00	0.46	0.54	1	0
PV 623	5.67	0.77	0.23	0	0
Royal Burgundy	4.60	0.59	0.41	0	0
SGR	5.57	0.19	0.81	0	0
Tendercrop	4.00	0.98	0.02	0	0
Totem	5.40	0.97	0.03	0	0
Trail of Tears	5.25	0.03	0.97	1	1
UI 111	4.60	0.02	0.98	1	0
Trail of Tears	5.25	0.03	0.97	1	1

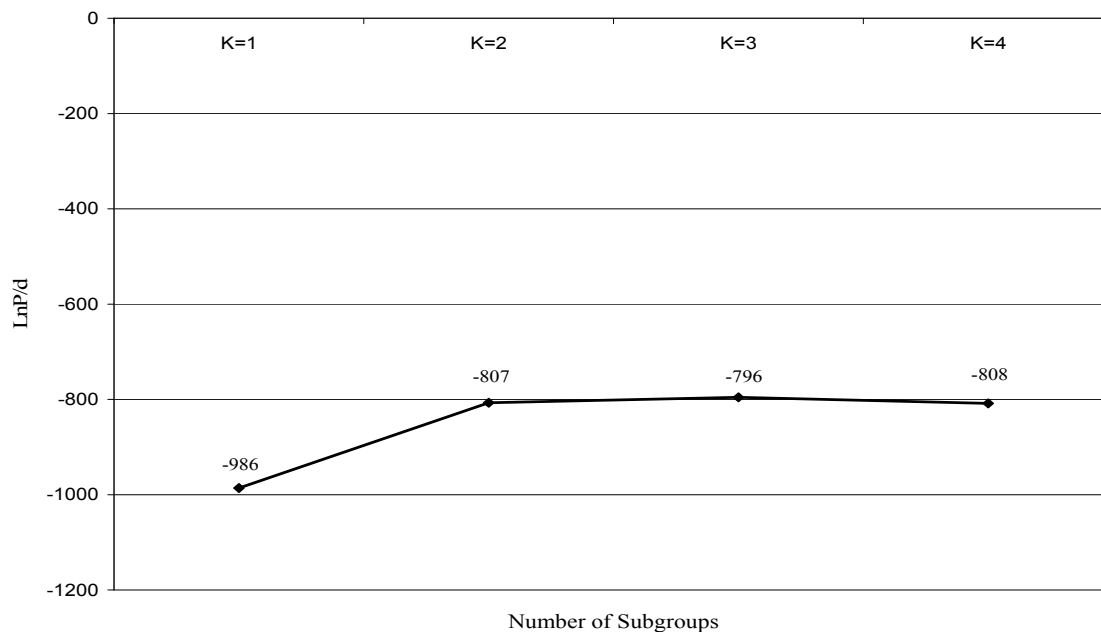
<sup>z</sup> Scale of 1-9 where 1=no infection and 9=total plant collapse (Teran et al., 2006 scale).

<sup>y</sup> Membership in Andean or Mesoamerican group based on K matrix values

The initial phylogeny served as *a priori* knowledge for running the program STRUCTURE, with the number of groups likely to either be two or three. Two groups would be predicted based on historical observations by Gepts *et al.* (1986) with separation of Andean and Mesoamerican lines into different groups. However, the inclusion of a single “C” Phaseolin type, Contender, which appears to be more distantly related to the Andean gene pool suggests that there may be three subpopulations.

Based on the results from STRUCTURE, models with two or three groups appear to give the best explanatory power. Although the LnP/d value is at a minimum value at K=3, a value of K=2 has a smaller standard deviation associated with it, and the graph appears to be asymptotic at K=2 (Figure 4.1). Based on this, a K matrix with two groups, representing Andean and Mesoamerican origins was generated for the data set.

Figure 4.2. LnP/d values versus number of subgroups for snap bean phylogeny of *Phaseolus vulgaris*.



Based on the first analysis of individual markers, two markers were highly significant ( $p < 0.01$ ). These markers were the OP B18<sub>1500</sub> and OP C8<sub>1200</sub> RAPD markers (Table 4.1).

In the analysis of B18<sub>1500</sub>, both the marker and the covariate predicted by the K matrix were significant. However, for the C8<sub>1200</sub> marker, the covariate was not significant in the model. This result suggests that B18<sub>1500</sub> is only significant at certain levels of population substructure, and not at others. This trend suggests that the marker may be gene pool specific; the marker may only be associated with white mold resistance in one of the population groups.

The presence of an amplified band at 1500bp of the B18 primer is associated with resistance, while the absence of the band is associated with susceptibility (Figure 4.3). The marker is primarily present in the Mesoamerican population subgroup.

For the C18 primer, the presence of a band at 1200bp is associated with susceptibility, while the absence is associated with resistance (Figure 4.4). This marker has a more uneven distribution. The marker is only present in a subset of the Mesoamerican group.

Table 4.2. Mixed linear model analysis of single marker significance of B18<sub>1500</sub> and C8<sub>1200</sub> RAPD markers for white mold resistance in the straw test of snap bean phylogeny materials.

Source	DF	SS	MSE	F-Value	P-value
<i>B18<sub>1500</sub> RAPD Marker</i>					
Marker	1	3.88	3.88	8.04	0.0084
Population (Covariate)	1	4.93	4.93	10.23	0.0034
Residual	28	13.50	0.48		
<i>C8<sub>1200</sub> RAPD Marker</i>					
Marker	1	4.00	4.00	8.36	0.0073
Population (Covariate)	1	0.02	0.02	0.04	0.8396
Residual	28	13.38	0.48		

Figure 4.3. LS means and standard errors for B18<sub>1500</sub> RAPD marker in straw test of snap bean phylogeny materials.

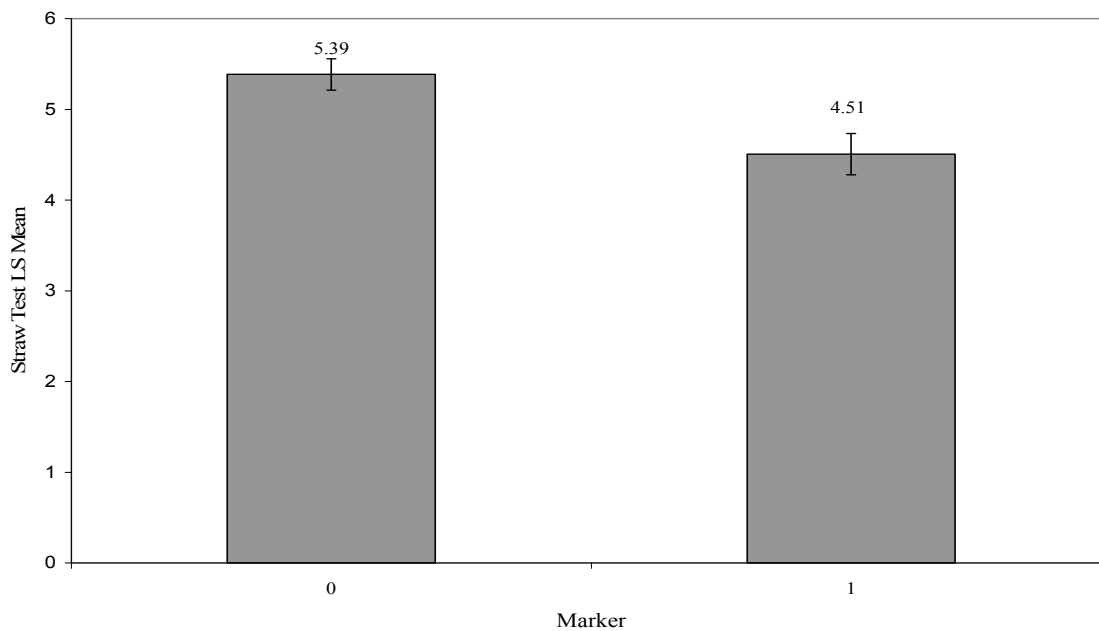
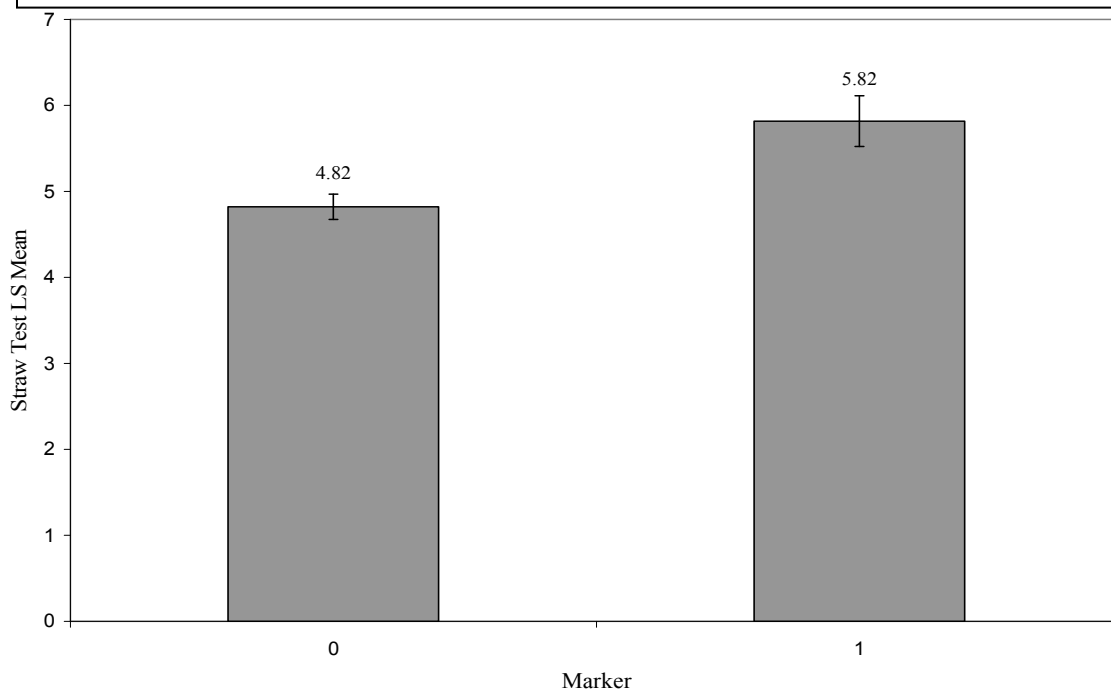


Figure 4.4. LS means and standard errors for C8<sub>1200</sub> RAPD marker in straw test of snap bean phylogeny materials.



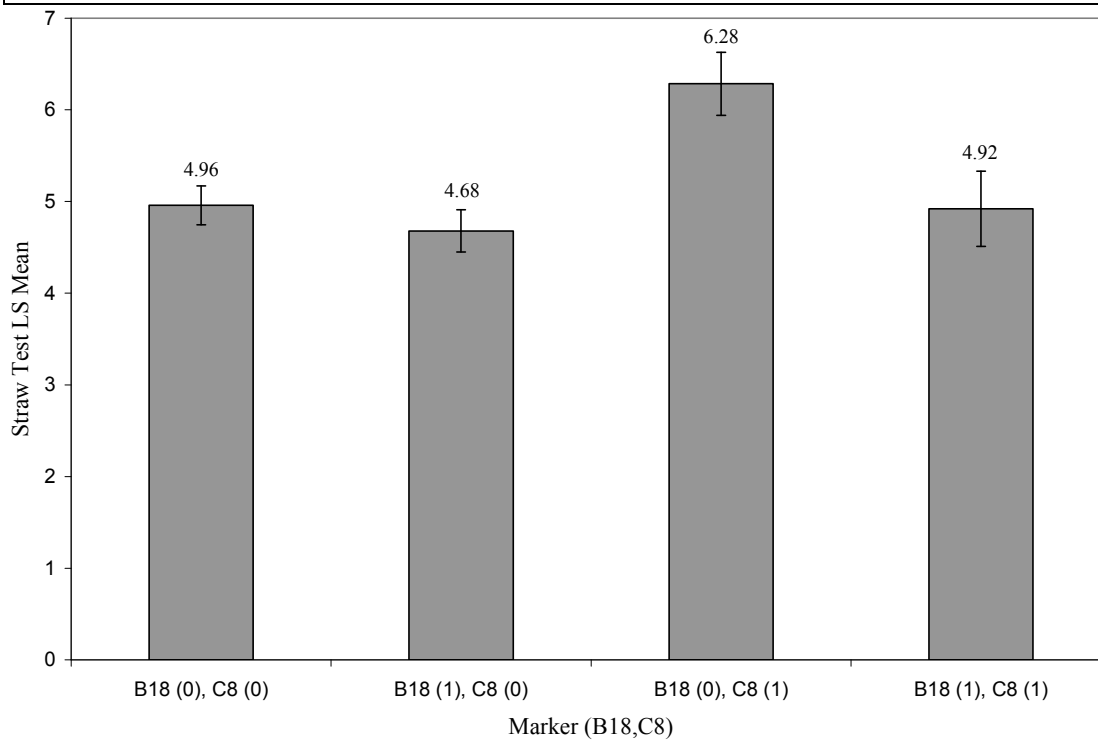
When B18<sub>1500</sub> and C8<sub>1200</sub> were placed in a combined analysis (Table 4.2) both markers retained statistical significance. The R<sup>2</sup> value for the B18<sub>1500</sub> and C8<sub>1200</sub> markers were 0.16 and 0.13, respectively. Additionally, the K-matrix covariate was not significant, suggesting that marker significance is not dependent on gene pool. The interaction of the two marker terms was nearly-significant (P=0.07). Additional replication may be needed to fully determine if these two markers have an additive or non-additive effect.

The combination of absence of the B18<sub>1500</sub> marker and presence of the C8<sub>1200</sub> marker seemed to be a particularly susceptible marker class, with a straw test LS mean of 6.28 (Figure 4.5). All other marker combinations appear to have roughly equal LS means.

Table 4.3. Mixed linear model analysis of multiple marker significance of B18<sub>1500</sub> and C8<sub>1200</sub> RAPD markers for white mold resistance in the straw test of snap bean phylogeny materials.

Source	DF	SS	MSE	F-Value	P-value
B18 <sub>1500</sub>	1	2.74	2.74	7.04	0.0134
C8 <sub>1200</sub>	1	2.18	2.18	5.60	0.0256
B8 <sub>1500</sub> x C8 <sub>1200</sub>	1	1.38	1.38	3.55	0.0707
Population (Covariate)	1	0.29	0.29	0.75	0.3938
Residual	26	10.11	0.39		

Figure 4.5. LS means and standard errors for B18.1500 and C8.1200 RAPD marker combined class in straw test of snap bean phylogeny materials.



## Conclusions

All of the results presented should be considered preliminary data. This was a small study, and additional lines, markers, and replications are needed to determine the utility of the two significant markers.

It was my original hypothesis in undertaking this study that the *Phs* SCAR marker would be significant. I postulated that since the T allele from NY6020 was associated with resistance, this association would hold true for other T phaseolin lines. This was not the case. Although the T phaseolin group had an LS mean that was ~0.50 less than the S phaseolin group, which is consistent with expectation, the marker was not significant. The phaseolin marker conditioned a 0.5 point difference in the straw test, while the B18<sub>1500</sub> and C8<sub>1200</sub> markers each conditioned a 1.0 point difference in the straw test.

Each of the markers predicted as significant deserves to be considered as a possible candidate as a selectable marker for a linked white mold resistance QTL.

The B18<sub>1500</sub> allele appears to be gene pool specific given the covariate significance. This suggests that the marker may only be associated with white mold resistance in the Mesoamerican gene pool, and not in the Andean gene pool. This is unusual since most of the described QTL have been associated with the Andean, and not the Mesoamerican gene pool. Ex Rico and Tacana are two Mesoamerican lines with partial physiological resistance to white mold that are the exception to this rule (Kolkman & Kelly, 2003, Ender & Kelly 2005, Terpstra & Kelly, 2006). No Andean lines had the B18<sub>1500</sub> allele. Two things are needed to further study the effects of this marker. First, it would be helpful to find or breed Andean lines with the B18<sub>1500</sub> presence allele to determine if this marker has utility in the Andean background. Second, additional



Mesoamerican lines should be screened to determine if this marker retains statistical significance. The B18<sub>1500</sub> marker is currently unmapped, and it would be interesting to place it on a linkage map to see if it resides anywhere near known white mold resistance QTL.

The C8<sub>1200</sub> marker may also be gene pool specific. While the covariate is not significant, the marker is only present in a small subset of the Mesoamerican group. The presence state is something of a rare allele, which calls into question how accurately the mean performance of this group has been measured. When the marker is present, it is often associated with extreme susceptibility. Given its rarity and association with extreme phenotypes, it is possible that this marker is only coincidental with phenotype, and not causative. Therefore, additional C8<sub>1200</sub> present lines would need to be scored to determine if this statistical significance is real.

The C8<sub>1200</sub> marker has been mapped in a Minuette x OSU 5630 population to linkage group B6. By cross referencing with Soule & Miklas (2008) the marker may be located near the B6 white mold resistance QTL for canopy height and internode length first described in the Benton x NY6020-4 mapping population (Miklas & Delorme, 2003). Additional work is needed to determine if this marker is associated with the known QTL on B6. The effect of this marker could be verified in the Minuette x OSU 5630 mapping population by testing a selection of polymorphic lines for white mold resistance and canopy height.

The interaction term was near-significant in the analysis. Additional testing is necessary to properly resolve if these two markers act in an additive fashion. For both

markers, it would be useful to convert the original RAPD allele to a SCAR marker for greater ease of phenotyping.

It is interesting that two successful bush blue lake lines, OR 91G and OSU 5630, have the absence of the B18<sub>1500</sub> and the presence of the C8<sub>1200</sub> bands, and are both highly susceptible. I have wondered if the selection for types acceptable to the local processing industry, background selection, has led to the preservation of these alleles within the OSU germplasm. It may be possible to improve white mold resistance within this germplasm by seeking to alter the marker state at these two loci.

One interesting observation to come out of this study was the description of “Contender” as having white mold resistance in the straw test. Contender was originally described as having field resistance (Kuehn & Baggett, 1986). The description of greenhouse resistance adds to the description of Contender’s white mold resistance. Contender has a more upright and compact growth habit when compared to NY6020, so it may prove useful in breeding due to contributing both physiological resistance and architectural resistance. I have wondered if there is physiological resistance associated with phaseolin in Contender, which is the “C” type for the phaseolin allele. Such a finding would potentially add to the knowledge about the B7 QTL, and would suggest additional utility for this distantly related snap bean germplasm.

In closing, I would like to recap some of the major findings of these studies. In Chapter 2, the performance of germplasm from a pyramiding population was evaluated. While these efforts produced resistant germplasm, none of the lines produced had resistance levels that were statistically superior to G122.

I would posit this lack of superior germplasm on observations made by Chung *et al.* (2008) and observations made in Chapter 3 of this thesis. Chung *et al.* (2008) described a B8 marker as having statistical significance for white mold resistance in their G122. In Chapter 3 results from crosses of NY6020 to OSU 5613 and OSU 5630 demonstrated that the T allele from NY6020 is significant for white mold resistance. This suggests that NY6020 has a B7 QTL. These two observations collectively suggest that G122 and NY6020 have the same B7 and B8 QTL for partial white mold resistance. As such, dry bean breeders should utilize G122 as a QTL donor parent, while snap bean breeders should primarily use NY6020 as a QTL donor. My pyramiding population could only reconstitute the marker states of NY6020 and G122, as well as OSU 6229 and OSU 6230. It is also possible that differences in plant architecture between families and genotypes may be an additional confounding factor in the straw test. For selectable markers, no novel combinations were made, and this accounts for the lack of transgressive germplasm.

It has been difficult to determine if the two QTL have an additive effect. It is likely that the two QTL do have an additive effect, but there are some data sets that would suggest otherwise. There are two possible reasons to account for these observations. First, it has been difficult to obtain statistical significance in the straw test. This is due to observed differences between means being small, and variations associated with the means being relatively large. To date, we have not utilized ½ point ratings in the straw test, which could possibly account for the large variations. Additionally, the ratings of 5-9 are dependent on internode length. If the rate of infection is assumed to be constant, shorter plants will progress to more susceptible ratings quicker than taller

plants. I have made efforts to refine the straw test by measuring length of necrosis, expressing necrosis as a proportion of the whole plant, and using non-parametric tests. These methods did not give me any additional explanatory power. Therefore, field testing may be necessary to finally resolve the issue of QTL additivity.

Second, there may be additional factors segregating that have not been accounted for that are interfering with estimates of QTL additivity. There are several possibilities for factors. Chung *et al.* (2008) described the J09<sub>950</sub> RAPD marker on B7 as being significant for white mold resistance/susceptibility. The authors suggest that this may be the same QTL as described in the PC-50 mapping population (Park *et al.*, 2001). At this time the literature is ambiguous if this marker is linked to the same B7 QTL as *Phs*, or if it is linked to a smaller minor effect QTL. If it were the latter, this may be a factor worth considering in my populations.

I had previously indicated in the Conclusion section of Chapter 3 that these QTL may have full expression in an Andean background, but lose some of their expression in a Mesoamerican background. This idea has been corroborated by Dr. Miklas in personal correspondence. While it would be difficult to test this hypothesis in my populations, at this time it is still worth considering.

The description of the B18<sub>1500</sub> and C8<sub>1200</sub> RAPD markers being associated with white mold resistance suggests that they might be candidate factors worth considering. If either of these factors were segregating, it would be possible to test for their significance. The fact that these markers seem to be most polymorphic in the Mesoamerican subgroup may allow them to tie in to the gene pool hypothesis I alluded to earlier.

In conclusion, this pyramiding strategy was unlikely to yield superior germplasm due to lack of QTL polymorphism between parents. This suggests that further research into the genetic nature of white mold resistance is needed before pyramiding strategies are likely to prove effective. I would advocate for additional linkage mapping, candidate-gene studies, and association mapping. Additional linkage mapping is likely to increase our understanding of the breadth and distribution of white mold resistance QTL. Already there have been efforts to consolidate QTL mapping under a consensus map (Soule & Miklas, 2008). Certain QTL have shown up in multiple populations and appear to be the best candidate QTL for selection. Candidate gene studies have the potential to identify the genes underlying the observed phenotype. Having markers located within the gene of interest, as opposed to nearby in the genome, is likely to facilitate marker assisted selection efforts while reducing the effects of linkage drag. Association mapping has the potential to determine if any of the known QTL have a wider distribution within the bean germplasm.

Finally, I would advocate improving the straw test procedures. The observation that no lines have resistance that is statistically better than G122 is not unique to my population. I have noted similar findings in the populations of a colleague, as well as in the national white mold trials. Save for lines of *P. coccineus*, I have not observed any bean lines that consistently have a straw test mean lower than 4. This suggests that nearly 1/3 of the entire scale for ranking is not being properly captured. Additionally, high variations have been observed within families resulting in reduced power to detect statistically significant differences. It is possible that other sites are able to capture the

full range of values. However, I worry that without change, the straw test will be unable to properly detect superior resistant types.

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Table A1. Straw test scores for summer 2007 selected plants of *Phaseolus vulgaris* screening for resistance to white mold; mean performance of checks in this experiment are shown in Table A2. (Petzoldt & Dickson scale<sup>z</sup>)

Line	Cross No.	Generation	Straw Test Score
A6	Q012-1	F <sub>2</sub>	5
A9	Q012-1	F <sub>2</sub>	3
A11	Q012-1	F <sub>2</sub>	E <sup>y</sup>
A106	Q001-1	F <sub>2</sub>	5
A115	Q003-1	F <sub>2</sub>	1
A126	Q006-1	F <sub>2</sub>	E
A144	Q009-1	F <sub>2</sub>	E
A176	Q012-1	F <sub>2</sub>	8
A182	Q012-1	F <sub>2</sub>	2
B109	Q007-1	F <sub>2</sub>	2
B167	Q008-2	F <sub>2</sub>	3
B44	Q004-1	F <sub>2</sub>	2
B73	Q008-2	F <sub>2</sub>	E
B78	Q008-2	F <sub>2</sub>	4
B97	Q012-1	F <sub>2</sub>	E
C66	Q006-1	F <sub>2</sub>	3
C230	Q006-1	F <sub>2</sub>	2
C244	Q004-1	F <sub>2</sub>	3

<sup>z</sup> Scale of 1-9 where 1=no infection and 9=total plant collapse (Petzoldt & Dickson, 1996 scale).

<sup>y</sup> E= plant escaped infection

Table A2. Straw test least squared (LS) means for summer 2007 standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold; LS means from checks used in experiment from Table A1. (Petzoldt & Dickson scale<sup>z</sup>)

Line	Straw Test LS Mean	Check <sup>x</sup>		
		G122	NY6020-5	OR 91G
OSU 6229	3.44	0.4319 <sup>y</sup>	0.6541	0.0007
OSU 6230	3.95	0.9473	0.7773	0.0020
OSU 6241	5.23	0.1073	0.0602	0.0381
OR 91G	6.89	0.0009	0.0005	
G122	4.00		0.6902	0.0009
NY6020-5	3.75	0.6902		0.0005

<sup>z</sup> Scale of 1-9 where 1=no infection and 9=total plant collapse (Petzoldt & Dickson, 1996 scale).

<sup>y</sup> Probability of LS mean of experimental line equal to LS mean of the check

<sup>x</sup> G122 and NY60205-5 are partially resistant, OR 91G is susceptible

Table A3. Straw test scores for winter 2007 selected plants of *Phaseolus vulgaris* screening for resistance to white mold; mean performance of checks in this experiment are shown in Table A4. (Teran scale<sup>z</sup>)

Line	Cross No.	Generation	Straw Test Score	Line	Cross No.	Generation	Straw Test Score
A6	Q012-1	F <sub>3</sub>	4	G4	Q002-1	F <sub>3</sub>	4
A9	Q012-1	F <sub>3</sub>	E <sup>y</sup>	G11	Q002-1	F <sub>3</sub>	4
A11	Q012-1	F <sub>3</sub>	4	G26	Q002-1	F <sub>3</sub>	4(A) <sup>x</sup>
A106	Q001-1	F <sub>3</sub>	6	G44	Q002-1	F <sub>3</sub>	4
A115	Q003-1	F <sub>3</sub>	8	G49	Q004-1	F <sub>3</sub>	4
A126	Q006-1	F <sub>3</sub>	4	G50	Q004-1	F <sub>3</sub>	3
A144	Q009-1	F <sub>3</sub>	4	G51	Q004-1	F <sub>3</sub>	4
A176	Q0012-1	F <sub>3</sub>	7	G57	Q004-1	F <sub>3</sub>	7
A182	Q0012-1	F <sub>3</sub>	4(A)	G66	Q004-1	F <sub>3</sub>	4
B44	Q004-1	F <sub>3</sub>	3	G67	Q004-1	F <sub>3</sub>	2
B73	Q008-2	F <sub>3</sub>	4	G68	Q004-1	F <sub>3</sub>	6
B78	Q008-2	F <sub>3</sub>	8	G69	Q004-1	F <sub>3</sub>	4
B97	Q012-1	F <sub>3</sub>	E	G72	Q004-1	F <sub>3</sub>	4
B109	Q007-1	F <sub>3</sub>	4	G76	Q004-1	F <sub>3</sub>	5
B167	Q008-2	F <sub>3</sub>	4	G79	Q004-1	F <sub>3</sub>	3
C66	Q006-1	F <sub>3</sub>	4	G80	Q004-1	F <sub>3</sub>	4
C230	Q006-1	F <sub>3</sub>	4	G81	Q004-1	F <sub>3</sub>	4
C244	Q004-1	F <sub>3</sub>	6	G84	Q004-1	F <sub>3</sub>	E
D28	Q018-1	F <sub>2</sub>	2	G85	Q004-1	F <sub>3</sub>	E
D29	Q018-1	F <sub>2</sub>	2	G92	Q004-1	F <sub>3</sub>	4
D31	Q018-1	F <sub>2</sub>	8	G94	Q004-1	F <sub>3</sub>	4
D36	Q018-1	F <sub>2</sub>	2	G97	Q004-1	F <sub>3</sub>	4
D58	Q018-2	F <sub>2</sub>	2	G99	Q004-1	F <sub>3</sub>	4
D70	Q020-1	F <sub>2</sub>	1	G100	Q004-1	F <sub>3</sub>	4(A)
D84	Q023-2	F <sub>2</sub>	2	G104	Q004-1	F <sub>3</sub>	4
D91	Q024-2	F <sub>2</sub>	2	G106	Q004-1	F <sub>3</sub>	E
D95	Q024-2	F <sub>2</sub>	2	G108	Q004-1	F <sub>3</sub>	4(A)
D96	Q024-2	F <sub>2</sub>	2	G110	Q004-1	F <sub>3</sub>	4
D123	Q026-1	F <sub>2</sub>	2	G111	Q004-1	F <sub>3</sub>	4
D138	Q017-2	F <sub>2</sub>	2	G112	Q004-1	F <sub>3</sub>	4
D148	Q017-2	F <sub>2</sub>	2	G113	Q001-1	F <sub>3</sub>	4
D149	Q017-2	F <sub>2</sub>	2	G114	Q001-1	F <sub>3</sub>	4(A)
D150	Q017-2	F <sub>2</sub>	2	G115	Q001-1	F <sub>3</sub>	4
D157	Q017-2	F <sub>2</sub>	2	G116	Q001-1	F <sub>3</sub>	4(A)

Table A3. (Continued) Straw test scores for winter 2007 selected plants of *Phaseolus vulgaris* screening for resistance to white mold; mean performance of checks in this experiment are shown in Table A4. (Teran scale<sup>2</sup>)

Line	Cross No.	Generation	Straw Test Score	Line	Cross No.	Generation	Straw Test Score
D169	Q017-1	F <sub>2</sub>	7	G117	Q001-1	F <sub>3</sub>	4(A)
D211	Q017-3	F <sub>2</sub>	2	G120	Q001-1	F <sub>3</sub>	4
D224	Q017-4	F <sub>2</sub>	2	G121	Q001-1	F <sub>3</sub>	3
E16	Q027-1	F <sub>2</sub>	2	G122	Q001-1	F <sub>3</sub>	7
E19	Q027-1	F <sub>2</sub>	7	G130	Q006-1	F <sub>3</sub>	4
E37	Q027-2	F <sub>2</sub>	8	G131	Q006-1	F <sub>3</sub>	4
E40	Q027-1	F <sub>2</sub>	7	G133	Q006-1	F <sub>3</sub>	4
E41	Q028-1	F <sub>2</sub>	4	G134	Q006-1	F <sub>3</sub>	4
E44	Q028-1	F <sub>2</sub>	4	G136	Q006-1	F <sub>3</sub>	4
E46	Q028-1	F <sub>2</sub>	4	G138	Q006-1	F <sub>3</sub>	4
E47	Q028-1	F <sub>2</sub>	4	G140	Q006-1	F <sub>3</sub>	4(A)
E51	Q028-1	F <sub>2</sub>	4	G141	Q006-1	F <sub>3</sub>	4(A)
E52	Q028-1	F <sub>2</sub>	4	G142	Q006-1	F <sub>3</sub>	4(A)
E55	Q028-1	F <sub>2</sub>	2	G144	Q006-1	F <sub>3</sub>	4
E56	Q028-1	F <sub>2</sub>	3	G145	Q006-1	F <sub>3</sub>	4
E60	Q028-1	F <sub>2</sub>	1	G146	Q006-1	F <sub>3</sub>	4
E61	Q028-1	F <sub>2</sub>	4	G147	Q006-1	F <sub>3</sub>	5
E64	Q028-1	F <sub>2</sub>	3	G148	Q006-1	F <sub>3</sub>	4
E65	Q028-1	F <sub>2</sub>	3	G154	Q008-2	F <sub>3</sub>	4(A)
E66	Q028-1	F <sub>2</sub>	3	G161	Q008-2	F <sub>3</sub>	4(A)
E67	Q028-1	F <sub>2</sub>	3	G163	Q008-2	F <sub>3</sub>	4
E72	Q028-1	F <sub>2</sub>	4	G164	Q008-2	F <sub>3</sub>	4
E73	Q028-1	F <sub>2</sub>	2	G165	Q008-2	F <sub>3</sub>	4
E79	Q029-1	F <sub>2</sub>	4	G168	Q008-2	F <sub>3</sub>	4
E84	Q029-1	F <sub>2</sub>	7	G169	Q008-2	F <sub>3</sub>	7
E85	Q029-1	F <sub>2</sub>	4	G170	Q008-2	F <sub>3</sub>	4
E90	Q029-1	F <sub>2</sub>	4	G174	Q008-2	F <sub>3</sub>	4
E97	Q018-2	F <sub>2</sub>	2	G175	Q008-2	F <sub>3</sub>	4
E106	Q033-1	F <sub>2</sub>	7	G178	Q008-2	F <sub>3</sub>	4
E108	Q035-4	F <sub>2</sub>	4	G186	Q008-2	F <sub>3</sub>	4
E112	Q035-4	F <sub>2</sub>	4	G191	Q012-1	F <sub>3</sub>	4
E113	Q035-4	F <sub>2</sub>	4	G199	Q012-1	F <sub>3</sub>	4(A)
E115	Q035-4	F <sub>2</sub>	4	G203	Q012-1	F <sub>3</sub>	4
E116	Q035-4	F <sub>2</sub>	3	G204	Q012-1	F <sub>3</sub>	E
E118	Q035-4	F <sub>2</sub>	4(A)	G205	Q012-1	F <sub>3</sub>	4(A)

Table A3. (Continued) Straw test scores for winter 2007 selected plants of *Phaseolus vulgaris* screening for resistance to white mold; mean performance of checks in this experiment are shown in Table A4. (Teran scale<sup>z</sup>)

Line	Cross No.	Generation	Straw Test Score	Line	Cross No.	Generation	Straw Test Score
E120	Q035-4	F <sub>2</sub>	4	G206	Q012-1	F <sub>3</sub>	4(A)
E134	Q017-3	F <sub>2</sub>	8	G207	Q012-1	F <sub>3</sub>	4(A)
E159	Q017-3	F <sub>2</sub>	9	G210	Q012-1	F <sub>3</sub>	4
E168	Q017-3	F <sub>2</sub>	8	H1	Q012-1	F <sub>3</sub>	3
E185	Q023-1	F <sub>2</sub>	8	H2	Q012-1	F <sub>3</sub>	4(A)
E211	Q030-1	F <sub>2</sub>	2	H3	Q012-1	F <sub>3</sub>	4
E214	Q030-1	F <sub>2</sub>	2	H4	Q012-1	F <sub>3</sub>	4(A)
E217	Q030-1	F <sub>2</sub>	4	H5	Q012-1	F <sub>3</sub>	E
E226	Q030-1	F <sub>2</sub>	4	H9	Q012-1	F <sub>3</sub>	4(A)
E229	Q030-1	F <sub>2</sub>	2	H11	Q003-1	F <sub>3</sub>	4(A)
E233	Q030-1	F <sub>2</sub>	3	H12	Q003-1	F <sub>3</sub>	E
E234	Q030-1	F <sub>2</sub>	3	H13	Q003-1	F <sub>3</sub>	E
E235	Q030-1	F <sub>2</sub>	2	H15	Q012-1	F <sub>3</sub>	4
E241	Q016-1	F <sub>2</sub>	4	H16	Q012-1	F <sub>3</sub>	4(A)
E245	Q035-4	F <sub>2</sub>	4	H17	Q012-1	F <sub>3</sub>	4(A)
E249	Q020-2	F <sub>2</sub>	4	H57	Q007-1	F <sub>3</sub>	9
E256	Q035-4	F <sub>2</sub>	4	H112	Q003-1	F <sub>3</sub>	8
E258	Q035-4	F <sub>2</sub>	4	H201	Q003-1	F <sub>3</sub>	4
G1	Q002-1	F <sub>3</sub>	4	H202	Q003-1	F <sub>3</sub>	6
G2	Q002-1	F <sub>3</sub>	4(A)				

<sup>z</sup> Scale of 1-9 where 1=no infection and 9=total plant collapse (Teran *et al.*, 2006 scale).

<sup>y</sup> E= plant escaped infection.

<sup>x</sup> 4(A)= abscission layer formed at the first node preventing further white mold infection.



Table A4. Straw test least squared (LS) means for winter 2007 standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold; LS means from checks used in experiment from Table A3. (Teran scale<sup>z</sup>)

Line	Straw Test LS Mean	Check <sup>x</sup>		
		G122	NY6020-5	OR 91G
OSU 5630	7.54	<0.0001 <sup>y</sup>	<0.0001	0.6655
OSU 6229	4.85	0.9471	0.9171	<0.0001
OSU 6230	4.93	0.9352	0.9707	<0.0001
OSU 6241	6.10	0.0099	0.0137	0.0190
OR 91G	7.30	<0.0001	<0.0001	
G122	4.78		0.9664	<0.0001
NY6020-5	4.63	0.9664		<0.0001

<sup>z</sup> Scale of 1-9 where 1=no infection and 9=total plant collapse (Teran *et al.*, 2006 scale).

<sup>y</sup> Probability of LS mean of experimental line equal to LS mean of the check

<sup>x</sup> G122 and NY60205-5 are partially resistant, OR 91G is susceptible

Table A5. Straw test scores for spring 2008 selected plants of *Phaseolus vulgaris* screening for resistance to white mold; mean performance of checks in this experiment are shown in Table A6. (Teran scale<sup>2</sup>)

Line	Cross No.	Generation	Straw Test		Line	Cross No.	Generation	Straw Test
			Score	Score				Score
A6.2	Q012-1	F <sub>4</sub>	4		E217.1	Q030-1	F <sub>3</sub>	4
A11.1	Q012-1	F <sub>4</sub>	4		E229.2	Q030-1	F <sub>3</sub>	4
A11.3	Q012-1	F <sub>4</sub>	4		E229.7	Q030-1	F <sub>3</sub>	2
A11.4	Q012-1	F <sub>4</sub>	4		E245.1	Q035-4	F <sub>3</sub>	4
A115.1	Q003-1	F <sub>4</sub>	4		E245.4	Q035-4	F <sub>3</sub>	4
A115.2	Q003-1	F <sub>4</sub>	7		E245.7	Q035-4	F <sub>3</sub>	4
A115.4	Q003-1	F <sub>4</sub>	4		E245.10	Q035-4	F <sub>3</sub>	3
A126.8	Q006-1	F <sub>4</sub>	4		E256.1	Q035-4	F <sub>3</sub>	E <sup>y</sup>
A126.10	Q006-1	F <sub>4</sub>	4		E256.2	Q035-4	F <sub>3</sub>	E
A182.1	Q012-1	F <sub>4</sub>	4(A) <sup>x</sup>		E256.3	Q035-4	F <sub>3</sub>	4
A182.2	Q012-1	F <sub>4</sub>	4		E258.3	Q035-4	F <sub>3</sub>	4
A182.3	Q012-1	F <sub>4</sub>	4		E258.6	Q035-4	F <sub>3</sub>	4
A182.4	Q012-1	F <sub>4</sub>	6		E258.8	Q035-4	F <sub>3</sub>	4
A182.5	Q012-1	F <sub>4</sub>	E		G1.2	Q002-1	F <sub>4</sub>	5
A182.6	Q012-1	F <sub>4</sub>	6		G1.3	Q002-1	F <sub>4</sub>	4
B78.1	Q008-2	F <sub>4</sub>	4		G4.10	Q002-1	F <sub>4</sub>	8
B78.5	Q008-2	F <sub>4</sub>	4		G6.7	Q002-1	F <sub>4</sub>	4
B78.9	Q008-2	F <sub>4</sub>	4		G26.4	Q002-1	F <sub>4</sub>	8
B109.6	Q007-1	F <sub>4</sub>	4		G49.7	Q004-1	F <sub>4</sub>	4
B167.3	Q008-2	F <sub>4</sub>	7		G49.12	Q004-1	F <sub>4</sub>	4(A)
B167.4	Q008-2	F <sub>4</sub>	4		G66.1	Q004-1	F <sub>4</sub>	4
D31.1	Q018-1	F <sub>3</sub>	6		G69.1	Q004-1	F <sub>4</sub>	4
D31.3	Q018-1	F <sub>3</sub>	4		G69.3	Q004-1	F <sub>4</sub>	6
D31.4	Q018-1	F <sub>3</sub>	4		G69.4	Q004-1	F <sub>4</sub>	4
D70.1	Q020-1	F <sub>3</sub>	4		G79.4	Q004-1	F <sub>4</sub>	4
D70.2	Q020-1	F <sub>3</sub>	4		G84.5	Q004-1	F <sub>4</sub>	8
D131.2	Q017-2	F <sub>3</sub>	E		G99.7	Q004-1	F <sub>4</sub>	6
D138.1	Q017-2	F <sub>3</sub>	5		G106.1	Q004-1	F <sub>4</sub>	6
D138.2	Q017-2	F <sub>3</sub>	6		G106.2	Q004-1	F <sub>4</sub>	4
D169.3	Q017-1	F <sub>3</sub>	4		G108.6	Q004-1	F <sub>4</sub>	5
D169.4	Q017-1	F <sub>3</sub>	4		G108.9	Q004-1	F <sub>4</sub>	5
D169.7	Q017-1	F <sub>3</sub>	4		G110.1	Q004-1	F <sub>4</sub>	4
D224.6	Q017-4	F <sub>3</sub>	7		G110.2	Q004-1	F <sub>4</sub>	4
D224.7	Q017-4	F <sub>3</sub>	7		G110.3	Q004-1	F <sub>4</sub>	4

Table A5. (Continued) Straw test scores for spring 2008 selected plants of *Phaseolus vulgaris* screening for resistance to white mold; mean performance of checks in this experiment are shown in Table A6. (Teran scale<sup>2</sup>)

Line	Cross No.	Generation	Straw Test		Line	Cross No.	Generation	Straw Test
			Score	Score				Score
E19.6	Q027-1	F <sub>3</sub>	6		G112.1	Q004-1	F <sub>4</sub>	6
E40.1	Q027-1	F <sub>3</sub>	4		G112.3	Q004-1	F <sub>4</sub>	4
E40.7	Q027-1	F <sub>3</sub>	4		G113.1	Q001-1	F <sub>4</sub>	4
E41.1	Q028-1	F <sub>3</sub>	3		G113.2	Q001-1	F <sub>4</sub>	4
E41.9	Q028-1	F <sub>3</sub>	4		G140.2	Q006-1	F <sub>4</sub>	5
E46.1	Q028-1	F <sub>3</sub>	4		G141.1	Q006-1	F <sub>4</sub>	4
E46.2	Q028-1	F <sub>3</sub>	4		G141.3	Q006-1	F <sub>4</sub>	4
E46.4	Q028-1	F <sub>3</sub>	4		G141.4	Q006-1	F <sub>4</sub>	7
E51.1	Q028-1	F <sub>3</sub>	4		G141.5	Q006-1	F <sub>4</sub>	7
E51.2	Q028-1	F <sub>3</sub>	4		G141.6	Q006-1	F <sub>4</sub>	4
E51.5	Q028-1	F <sub>3</sub>	E		G145.1	Q006-1	F <sub>4</sub>	4
E52.1	Q028-1	F <sub>3</sub>	4		G145.2	Q006-1	F <sub>4</sub>	4
E52.2	Q028-1	F <sub>3</sub>	4		G161.1	Q008-2	F <sub>4</sub>	7
E52.3	Q028-1	F <sub>3</sub>	4		G161.2	Q008-2	F <sub>4</sub>	6
E55.1	Q028-1	F <sub>3</sub>	4		G161.3	Q008-2	F <sub>4</sub>	4
E55.2	Q028-1	F <sub>3</sub>	4		G161.4	Q008-2	F <sub>4</sub>	4(A)
E55.3	Q028-1	F <sub>3</sub>	4		G161.5	Q008-2	F <sub>4</sub>	3
E64.1	Q028-1	F <sub>3</sub>	4		G165.1	Q008-2	F <sub>4</sub>	4
E64.4	Q028-1	F <sub>3</sub>	4		G165.3	Q008-2	F <sub>4</sub>	6
E65.1	Q028-1	F <sub>3</sub>	4		G170.1	Q008-2	F <sub>4</sub>	4
E66.1	Q028-1	F <sub>3</sub>	2		G170.2	Q008-2	F <sub>4</sub>	5
E66.3	Q028-1	F <sub>3</sub>	4(A)		G170.3	Q008-2	F <sub>4</sub>	6
E66.4	Q028-1	F <sub>3</sub>	4		G174.1	Q008-2	F <sub>4</sub>	4
E66.5	Q028-1	F <sub>3</sub>	2		G174.2	Q008-2	F <sub>4</sub>	4
E84.2	Q029-1	F <sub>3</sub>	E		G191.1	Q012-1	F <sub>4</sub>	6
E84.4	Q029-1	F <sub>3</sub>	4		G191.3	Q012-1	F <sub>4</sub>	4
E84.6	Q029-1	F <sub>3</sub>	4		G191.4	Q012-1	F <sub>4</sub>	4
E97.4	Q018-2	F <sub>3</sub>	4		G205.1	Q012-1	F <sub>4</sub>	4
E97.5	Q018-2	F <sub>3</sub>	4		G205.2	Q012-1	F <sub>4</sub>	4
E97.6	Q018-2	F <sub>3</sub>	4		G207.1	Q012-1	F <sub>4</sub>	4
E97.7	Q018-2	F <sub>3</sub>	4		G207.4	Q012-1	F <sub>4</sub>	4
E97.11	Q018-2	F <sub>3</sub>	6		G207.6	Q012-1	F <sub>4</sub>	4
E106.4	Q033-1	F <sub>3</sub>	1		H1.1	Q012-1	F <sub>4</sub>	4
E112.1	Q035-4	F <sub>3</sub>	2		H1.2	Q012-1	F <sub>4</sub>	4
E112.3	Q035-4	F <sub>3</sub>	4		H2.1	Q012-1	F <sub>4</sub>	4

Table A5. (Continued) Straw test scores for spring 2008 selected plants of *Phaseolus vulgaris* screening for resistance to white mold; mean performance of checks in this experiment are shown in Table A6. (Teran scale<sup>z</sup>)

Line	Cross No.	Generation	Straw Test		Line	Cross No.	Generation	Straw Test
			Score	Line				Score
E115.1	Q035-4	F <sub>3</sub>	4	H2.2	Q012-1	F <sub>4</sub>	4	
E115.2	Q035-4	F <sub>3</sub>	4	H2.4	Q012-1	F <sub>4</sub>	4	
E118.1	Q035-4	F <sub>3</sub>	4	H5.1	Q012-1	F <sub>4</sub>	4	
E118.8	Q035-4	F <sub>3</sub>	4	H5.3	Q012-1	F <sub>4</sub>	4	
E120.1	Q035-4	F <sub>3</sub>	E	H5.5	Q012-1	F <sub>4</sub>	4	
E120.2	Q035-4	F <sub>3</sub>	4	H9.1	Q012-1	F <sub>4</sub>	4	
E120.3	Q035-4	F <sub>3</sub>	4	H9.2	Q012-1	F <sub>4</sub>	4	
E159.3	Q017-3	F <sub>3</sub>	E	H9.4	Q012-1	F <sub>4</sub>	4	
E159.4	Q017-3	F <sub>3</sub>	4	H12.2	Q003-1	F <sub>4</sub>	4	
E159.7	Q017-3	F <sub>3</sub>	E	H15.4	Q012-1	F <sub>4</sub>	4	
E168.10	Q017-3	F <sub>3</sub>	4	H15.5	Q012-1	F <sub>4</sub>	4	
E185.3	Q023-1	F <sub>3</sub>	4	H17.1	Q012-1	F <sub>4</sub>	4	
E185.4	Q023-1	F <sub>3</sub>	4	H112.2	Q003-1	F <sub>4</sub>	4	
E185.6	Q023-1	F <sub>3</sub>	4	H112.8	Q003-1	F <sub>4</sub>	4	

<sup>z</sup> Scale of 1-9 where 1=no infection and 9=total plant collapse (Teran *et al.*, 2006 scale).

<sup>y</sup> E= plant escaped infection.

<sup>x</sup> 4(A)= abscission layer formed at the first node preventing further white mold infection.

Table A6. Straw test least squared (LS) means for spring 2008 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold; LS means from checks used in experiment from Table A5. (Teran scale<sup>z</sup>)

Line	Cross No.	Generation	Straw Test LS Mean	Check <sup>x</sup>		
				G122	NY6020-5	OR 91G
E106	Q033-1	F <sub>2:3</sub>	2.57	0.0005 <sup>y</sup>	0.0008	<0.0001
A11	Q012-1	F <sub>3:4</sub>	3.32	0.0141	0.0213	<0.0001
E159	Q017-3	F <sub>2:3</sub>	3.32	0.0141	0.0213	<0.0001
G117	Q001-1	F <sub>3:4</sub>	3.32	0.0141	0.0213	<0.0001
G174	Q008-2	F <sub>3:4</sub>	3.32	0.0141	0.0213	<0.0001
G205	Q012-1	F <sub>3:4</sub>	3.32	0.0141	0.0213	<0.0001
G207	Q012-1	F <sub>3:4</sub>	3.32	0.0141	0.0213	<0.0001
G2	Q002-1	F <sub>3:4</sub>	3.51	0.0306	0.0461	<0.0001
H5	Q012-1	F <sub>3:4</sub>	3.51	0.0306	0.0461	<0.0001
A6	Q012-1	F <sub>3:4</sub>	3.65	0.0517	0.0763	<0.0001
G110	Q004-1	F <sub>3:4</sub>	3.79	0.0941	0.1252	<0.0001
G210	Q012-1	F <sub>3:4</sub>	3.79	0.0941	0.1252	<0.0001
G79	Q004-1	F <sub>3:4</sub>	3.79	0.0941	0.1252	<0.0001
H12	Q003-1	F <sub>3:4</sub>	3.79	0.0941	0.1252	<0.0001
H13	Q003-1	F <sub>3:4</sub>	3.79	0.0941	0.1252	<0.0001
G1	Q002-1	F <sub>3:4</sub>	3.84	0.1025	0.1485	<0.0001
E84	Q029-1	F <sub>2:3</sub>	3.89	0.1187	0.1701	<0.0001
G113	Q001-1	F <sub>3:4</sub>	3.98	0.1611	0.2274	<0.0001
G66	Q004-1	F <sub>3:4</sub>	4.01	0.1752	0.2469	<0.0001
H9	Q012-1	F <sub>3:4</sub>	4.01	0.1752	0.2469	<0.0001
E185	Q023-1	F <sub>2:3</sub>	4.03	0.1865	0.2610	<0.0001
H15	Q012-1	F <sub>3:4</sub>	4.11	0.2357	0.3257	<0.0001
B78	Q008-3	F <sub>3:4</sub>	4.15	0.2612	0.3583	<0.0001
A9	Q012-1	F <sub>3:4</sub>	4.15	0.2637	0.3607	<0.0001
D169	Q017-1	F <sub>2:3</sub>	4.15	0.2637	0.3607	<0.0001
E112	Q035-4	F <sub>2:3</sub>	4.17	0.2767	0.3779	<0.0001
E168	Q017-3	F <sub>2:3</sub>	4.22	0.3162	0.4266	<0.0001
E66	Q028-1	F <sub>2:3</sub>	4.24	0.3350	0.4505	<0.0001
G44	Q002-1	F <sub>3:4</sub>	4.26	0.3540	0.4738	<0.0001
G120	Q001-1	F <sub>3:4</sub>	4.30	0.2784	0.3979	<0.0001
G145	Q006-1	F <sub>3:4</sub>	4.32	0.4078	0.5383	<0.0001
G69	Q004-1	F <sub>3:4</sub>	4.32	0.4078	0.5353	<0.0001
D70	Q020-1	F <sub>2:3</sub>	4.38	0.4809	0.6248	<0.0001
G140	Q006-1	F <sub>3:4</sub>	4.51	0.6266	0.7908	<0.0001

Table A6. (Continued) Straw test least squared (LS) means for spring 2008 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold; LS means from checks used in experiment from Table A5. (Teran scale<sup>2</sup>)

Line	Cross No.	Generation	Straw Test LS Mean	Check <sup>x</sup>		
				G122	NY6020-5	OR 91G
G170	Q008-2	F <sub>3:4</sub>	4.51	0.6266	0.7908	<0.0001
H17	Q012-1	F <sub>3:4</sub>	4.51	0.6266	0.7908	<0.0001
G191	Q012-1	F <sub>3:4</sub>	4.52	0.6355	0.8006	<0.0001
H112	Q003-1	F <sub>3:4</sub>	4.57	0.7003	0.8714	<0.0001
A182	Q012-1	F <sub>3:4</sub>	4.59	0.7370	0.9033	<0.0001
G161	Q008-2	F <sub>3:4</sub>	4.59	0.7370	0.9033	<0.0001
E37	Q027-2	F <sub>2:3</sub>	4.65	0.8136	0.9927	<0.0001
G112	Q004-1	F <sub>3:4</sub>	4.65	0.8136	0.9927	<0.0001
E120	Q035-4	F <sub>2:3</sub>	4.67	0.8366	0.9836	<0.0001
E226	Q030-1	F <sub>2:3</sub>	4.67	0.8366	0.9836	<0.0001
E245	Q035-4	F <sub>2:3</sub>	4.67	0.8366	0.9836	<0.0001
E249	Q020-2	F <sub>2:3</sub>	4.67	0.8366	0.9836	<0.0001
E46	Q028-1	F <sub>2:3</sub>	4.67	0.8366	0.9836	<0.0001
E52	Q028-1	F <sub>2:3</sub>	4.67	0.8366	0.9836	<0.0001
E73	Q028-1	F <sub>2:3</sub>	4.67	0.8366	0.9836	<0.0001
B44	Q004-1	F <sub>3:4</sub>	4.72	0.9087	0.9107	<0.0001
E115	Q035-4	F <sub>2:3</sub>	4.72	0.9087	0.9107	<0.0001
E217	Q030-1	F <sub>2:3</sub>	4.72	0.9087	0.9107	<0.0001
E256	Q035-4	F <sub>2:3</sub>	4.72	0.9087	0.9107	<0.0001
E51	Q028-1	F <sub>2:3</sub>	4.72	0.9087	0.9107	<0.0001
E55	Q028-1	F <sub>2:3</sub>	4.72	0.9087	0.9107	<0.0001
E79	Q029-1	F <sub>2:3</sub>	4.72	0.9087	0.9107	<0.0001
H1	Q012-1	F <sub>3:4</sub>	4.72	0.9087	0.9107	<0.0001
H2	Q012-1	F <sub>3:4</sub>	4.72	0.9087	0.9107	<0.0001
D29	Q018-1	F <sub>2:3</sub>	4.79	0.9908	0.8092	<0.0001
E97	Q018-2	F <sub>2:3</sub>	4.79	0.9908	0.8092	<0.0001
G106	Q004-1	F <sub>3:4</sub>	4.79	0.9908	0.8092	<0.0001
G141	Q006-1	F <sub>3:4</sub>	4.79	0.9908	0.8092	<0.0001
E229	Q030-1	F <sub>2:3</sub>	4.79	0.9859	0.8042	<0.0001
E64	Q028-1	F <sub>2:3</sub>	4.81	0.9604	0.7793	0.0001
E40	Q027-1	F <sub>2:3</sub>	4.82	0.9497	0.7680	0.0001
G130	Q006-1	F <sub>3:4</sub>	4.82	0.9497	0.7680	0.0001
E234	Q030-1	F <sub>2:3</sub>	4.83	0.9265	0.7463	0.0001
E90	Q029-1	F <sub>2:3</sub>	4.83	0.9265	0.7463	0.0001
G76	Q004-1	F <sub>3:4</sub>	4.84	0.9129	0.7333	0.0001

Table A6. (Continued) Straw test least squared (LS) means for spring 2008 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold; LS means from checks used in experiment from Table A5. (Teran scale<sup>2</sup>)

Line	Cross No.	Generation	Straw Test LS Mean	Check <sup>x</sup>		
				G122	NY6020-5	OR 91G
B109	Q007-1	F <sub>3:4</sub>	4.94	0.7797	0.6079	0.0002
G6	Q004-1	F <sub>3:4</sub>	4.94	0.7797	0.6079	0.0002
G49	Q004-1	F <sub>3:4</sub>	4.95	0.7580	0.5881	0.0002
E19	Q027-1	F <sub>2:3</sub>	4.98	0.7176	0.5503	0.0002
E56	Q028-1	F <sub>2:3</sub>	5.00	0.6964	0.5323	0.0002
A176	Q012-1	F <sub>3:4</sub>	5.01	0.6839	0.5211	0.0003
G115	Q001-1	F <sub>3:4</sub>	5.01	0.6839	0.5211	0.0003
G165	Q008-2	F <sub>3:4</sub>	5.01	0.6839	0.5211	0.0003
D31	Q018-2	F <sub>2:3</sub>	5.04	0.6561	0.4890	0.0003
E118	Q035-4	F <sub>2:3</sub>	5.05	0.6326	0.4773	0.0003
E65	Q028-1	F <sub>2:3</sub>	5.05	0.6326	0.4773	0.0003
G108	Q004-1	F <sub>3:4</sub>	5.08	0.5932	0.4416	0.0004
E258	Q035-4	F <sub>2:3</sub>	5.11	0.5567	0.4104	0.0004
G116	Q001-1	F <sub>3:4</sub>	5.12	0.5491	0.4028	0.0004
G92	Q004-1	F <sub>3:4</sub>	5.12	0.5491	0.4028	0.0004
E241	Q016-1	F <sub>2:3</sub>	5.17	0.4928	0.3566	0.0005
E41	Q028-1	F <sub>2:3</sub>	5.17	0.4928	0.3566	0.0005
E47	Q028-1	F <sub>2:3</sub>	5.17	0.4928	0.3566	0.0005
A126	Q006-1	F <sub>3:4</sub>	5.22	0.4406	0.3151	0.0007
E214	Q030-1	F <sub>2:3</sub>	5.24	0.4171	0.2948	0.0007
G26	Q002-1	F <sub>3:4</sub>	5.26	0.3958	0.2778	0.0008
E85	Q029-1	F <sub>2:3</sub>	5.27	0.3889	0.2723	0.0008
A106	Q001-1	F <sub>3:4</sub>	5.29	0.3823	0.2572	0.0009
A115	Q003-1	F <sub>3:4</sub>	5.29	0.3823	0.2572	0.0009
B167	Q008-2	F <sub>3:4</sub>	5.29	0.3823	0.2572	0.0009
B73	Q008-2	F <sub>3:4</sub>	5.29	0.3823	0.2572	0.0009
D138	Q017-2	F <sub>2:3</sub>	5.29	0.3823	0.2572	0.0009
G121	Q001-1	F <sub>3:4</sub>	5.29	0.3823	0.2572	0.0009
G206	Q012-1	F <sub>3:4</sub>	5.42	0.2640	0.1771	0.0018
H11	Q003-1	F <sub>3:4</sub>	5.42	0.2606	0.1736	0.0017
B97	Q012-1	F <sub>3:4</sub>	5.43	0.2537	0.1695	0.0019
D157	Q017-2	F <sub>2:3</sub>	5.46	0.2486	0.1557	0.0020
D224	Q017-4	F <sub>2:3</sub>	5.46	0.2486	0.1557	0.0020
G104	Q004-1	F <sub>3:4</sub>	5.46	0.2486	0.1557	0.0020
E67	Q028-1	F <sub>2:3</sub>	5.47	0.2273	0.1491	0.0021

Table A6. (Continued) Straw test least squared (LS) means for spring 2008 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold; LS means from checks used in experiment from Table A5. (Teran scale<sup>2</sup>)

Line	Cross No.	Generation	Straw Test LS Mean	Check <sup>x</sup>		
				G122	NY6020-5	OR 91G
G142	Q006-1	F <sub>3:4</sub>	5.51	0.2005	0.1297	0.0024
G94	Q004-1	F <sub>3:4</sub>	5.52	0.1935	0.1253	0.0025
H3	Q012-1	F <sub>3:4</sub>	5.52	0.1982	0.1289	0.0027
E16	Q027-1	F <sub>2:3</sub>	5.56	0.1858	0.1113	0.0032
D149	Q017-2	F <sub>2:3</sub>	5.59	0.1696	0.1002	0.0036
G81	Q004-1	F <sub>3:4</sub>	5.62	0.1533	0.0893	0.0042
G169	Q008-2	F <sub>3:4</sub>	5.65	0.1285	0.0796	0.0047
E44	Q028-1	F <sub>2:3</sub>	5.67	0.1227	0.0756	0.0050
E113	Q035-4	F <sub>2:3</sub>	5.72	0.1054	0.0647	0.0066
A144	Q009-1	F <sub>3:4</sub>	5.79	0.0900	0.0489	0.0086
D150	Q017-2	F <sub>2:3</sub>	5.79	0.0900	0.0489	0.0086
D58	Q018-4	F <sub>2:3</sub>	5.79	0.0900	0.0489	0.0086
G203	Q012-1	F <sub>3:4</sub>	5.79	0.0900	0.0489	0.0086
G97	Q004-1	F <sub>3:4</sub>	5.79	0.0900	0.0489	0.0086
C66	Q006-1	F <sub>3:4</sub>	5.81	0.0773	0.0463	0.0097
G11	Q002-1	F <sub>3:4</sub>	5.81	0.0755	0.0447	0.0093
E108	Q035-4	F <sub>3:4</sub>	5.81	0.0755	0.0477	0.0093
G131	Q006-1	F <sub>3:4</sub>	5.93	0.0551	0.0282	0.0157
G114	Q001-1	F <sub>3:4</sub>	5.94	0.0464	0.0262	0.0158
D148	Q017-2	F <sub>2:3</sub>	5.96	0.0506	0.0257	0.0173
E72	Q028-1	F <sub>2:3</sub>	5.97	0.0436	0.0250	0.0186
G85	Q004-1	F <sub>3:4</sub>	6.04	0.0374	0.0184	0.0242
G80	Q004-1	F <sub>3:4</sub>	6.11	0.0246	0.0135	0.0317
E134	Q017-3	F <sub>2:3</sub>	6.12	0.0274	0.0130	0.0336
G68	Q004-1	F <sub>3:4</sub>	6.18	0.0189	0.0102	0.0410
G72	Q004-1	F <sub>3:4</sub>	6.18	0.0189	0.0102	0.0410
E61	Q028-1	F <sub>2:3</sub>	6.22	0.0165	0.0090	0.0493
G204	Q012-1	F <sub>3:4</sub>	6.24	0.0172	0.0078	0.0533
D28	Q018-1	F <sub>2:3</sub>	6.29	0.0144	0.0064	0.0630
D91	Q024-2	F <sub>2:3</sub>	6.29	0.0144	0.0064	0.0630
G136	Q006-1	F <sub>3:4</sub>	6.29	0.0144	0.0064	0.0630
G164	Q008-2	F <sub>3:4</sub>	6.29	0.0144	0.0064	0.0630
H16	Q012-1	F <sub>3:4</sub>	6.29	0.0144	0.0064	0.0630
G146	Q006-1	F <sub>3:4</sub>	6.32	0.1015	0.0054	0.0682
D96	Q024-2	F <sub>2:3</sub>	6.39	0.0096	0.0042	0.0899



Table A6. (Continued) Straw test least squared (LS) means for spring 2008 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold; LS means from checks used in experiment from Table A5. (Teran scale<sup>2</sup>)

Line	Cross No.	Generation	Straw Test LS Mean	Check <sup>x</sup>		
				G122	NY6020-5	OR 91G
G144	Q006-1	F <sub>3:4</sub>	6.39	0.0096	0.0042	0.0899
G163	Q008-2	F <sub>3:4</sub>	6.41	0.0087	0.0037	0.0980
C230	Q006-1	F <sub>3:4</sub>	6.46	0.0073	0.0031	0.1129
D84	Q023-2	F <sub>2:3</sub>	6.46	0.0073	0.0031	0.1129
G138	Q006-1	F <sub>3:4</sub>	6.46	0.0073	0.0031	0.1129
G100	Q004-1	F <sub>3:4</sub>	6.51	0.0047	0.0024	0.1343
G84	Q004-1	F <sub>3:4</sub>	6.51	0.0047	0.0024	0.1343
G99	Q004-1	F <sub>3:4</sub>	6.51	0.0047	0.0024	0.1343
H57	Q007-1	F <sub>3:4</sub>	6.59	0.0042	0.0017	0.1738
G51	Q004-1	F <sub>3:4</sub>	6.69	0.0028	0.0011	0.2348
G148	Q006-1	F <sub>3:4</sub>	6.71	0.0026	0.0010	0.2464
C244	Q006-1	F <sub>3:4</sub>	6.79	0.0018	0.0007	0.3108
D123	Q026-1	F <sub>2:3</sub>	6.79	0.0018	0.0007	0.3108
D36	Q018-3	F <sub>2:3</sub>	6.79	0.0018	0.0007	0.3108
E116	Q035-4	F <sub>2:3</sub>	6.79	0.0018	0.0007	0.3108
E235	Q030-1	F <sub>2:3</sub>	6.79	0.0018	0.0007	0.3108
G4	Q002-1	F <sub>3:4</sub>	6.81	0.0013	0.0060	0.3276
G199	Q012-1	F <sub>3:4</sub>	6.82	0.0012	0.0006	0.3325
G67	Q004-1	F <sub>3:4</sub>	6.83	0.0012	0.0006	0.3478
G168	Q008-2	F <sub>3:4</sub>	6.97	0.0008	0.0003	0.4893
E233	Q030-1	F <sub>2:3</sub>	7.07	0.0004	0.0002	0.6032
G178	Q008-2	F <sub>3:4</sub>	7.07	0.0050	0.0020	0.6135
G50	Q004-1	F <sub>3:4</sub>	7.12	0.0004	0.0002	0.6751
E211	Q030-1	F <sub>2:3</sub>	7.17	0.0003	0.0001	0.7346
G154	Q008-2	F <sub>3:4</sub>	7.22	0.0002	0.0001	0.8063
D95	Q024-2	F <sub>2:3</sub>	7.29	0.0020	<0.0001	0.9065
G57	Q004-1	F <sub>3:4</sub>	7.29	0.0002	<0.0001	0.9065
H4	Q012-1	F <sub>3:4</sub>	7.29	0.0002	<.0001	0.9065
E60	Q028-1	F <sub>2:3</sub>	7.72	<.0001	<.0001	0.5123
D211	Q017-3	F <sub>2:3</sub>	7.79	<0.0001	<0.0001	0.4325
G111	Q004-1	F <sub>3:4</sub>	7.79	<0.0001	<0.0001	0.4325
G133	Q006-1	F <sub>3:4</sub>	7.79	<0.0001	<0.0001	0.4325
G134	Q006-1	F <sub>3:4</sub>	7.79	<0.0001	<0.0001	0.4325
G175	Q008-2	F <sub>3:4</sub>	7.79	<0.0001	<0.0001	0.4325
G186	Q008-2	F <sub>3:4</sub>	7.79	<0.0001	<0.0001	0.4325

Table A6. (Continued) Straw test least squared (LS) means for spring 2008 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold; LS means from checks used in experiment from Table A5. (Teran scale<sup>z</sup>)

Line	Cross No.	Generation	Straw Test LS Mean	Check <sup>x</sup>		
				G122	NY6020-5	OR 91G
H201	Q003-1	F <sub>3:4</sub>	7.79	<0.0001	<0.0001	0.4325
H202	Q003-1	F <sub>3:4</sub>	7.79	<0.0001	<0.0001	0.4325
OSU 5630			6.84	<0.0001	<0.0001	0.0989
OSU 6229			4.86	0.8099	0.5018	<0.0001
OSU 6230			4.95	0.6368	0.3752	<0.0001
6241 OSU			5.47	0.0435	0.1260	<0.0001
OR 91G			7.35	<0.0001	<0.0001	
G122			4.66	0.6968		<0.0001
NY6020-5			4.78		0.6968	<0.0001

<sup>z</sup> Scale of 1-9 where 1=no infection and 9=total plant collapse (Teran et al., 2006 scale).

<sup>y</sup> Probability of LS mean of experimental line equal to LS mean of the check

<sup>x</sup> G122 and NY60205-5 are partially resistant, OR 91G is susceptible

Table A7. Straw test scores for summer 2008 selected plants of *Phaseolus vulgaris* screening for resistance to white mold; mean performance of checks in this experiment are shown in Table A8. (Teran scale<sup>z</sup>)

Line	Cross No.	Generation	Straw Test		Line	Cross No.	Generation	Straw Test	
			Score	Score				Score	Score
A6.2.2	Q012-1	F <sub>5</sub>	2		E159.7.4	Q017-3	F <sub>4</sub>	4	
A11.1.1	Q012-1	F <sub>5</sub>	4		E168.1.1	Q017-3	F <sub>4</sub>	E <sup>y</sup>	
A11.3.1	Q012-1	F <sub>5</sub>	4		E168.10.4	Q017-3	F <sub>4</sub>	4	
A11.4.1	Q012-1	F <sub>5</sub>	4		E185.3.3	Q023-1	F <sub>4</sub>	4	
A115.1.3	Q003-1	F <sub>5</sub>	4		E185.3.6	Q023-1	F <sub>4</sub>	5	
A115.2.1	Q003-1	F <sub>5</sub>	6		E185.4.2	Q023-1	F <sub>4</sub>	4	
A115.4.4	Q003-1	F <sub>5</sub>	4		E185.6.2	Q023-1	F <sub>4</sub>	5	
A126.8.7	Q006-1	F <sub>5</sub>	4(A) <sup>x</sup>		E185.6.7	Q023-1	F <sub>4</sub>	4	
A126.10.5	Q006-1	F <sub>5</sub>	5		E217.1.3	Q030-1	F <sub>4</sub>	5	
A182.1.2	Q012-1	F <sub>5</sub>	3		E229.7.7	Q030-1	F <sub>4</sub>	4	
A182.2.6	Q012-1	F <sub>5</sub>	4		E229.9.5	Q030-1	F <sub>4</sub>	4	
A182.3.3	Q012-1	F <sub>5</sub>	4		E245.1.6	Q035-4	F <sub>4</sub>	4	
A182.4.1	Q012-1	F <sub>5</sub>	4		E245.7.6	Q035-4	F <sub>4</sub>	6	
A182.5.3	Q012-1	F <sub>5</sub>	4(A)		E245.10.6	Q035-4	F <sub>4</sub>	4	
A182.6.3	Q012-1	F <sub>5</sub>	2		E249.1.4	Q020-2	F <sub>4</sub>	5	
B78.1	Q008-2	F <sub>5</sub>	4		E256.2.4	Q035-4	F <sub>4</sub>	6	
B78.5	Q008-2	F <sub>5</sub>	4		E256.3.2	Q035-4	F <sub>4</sub>	4	
B109.6.5	Q007-1	F <sub>5</sub>	4		E258.6.7	Q035-4	F <sub>4</sub>	4	
B167.3.4	Q008-2	F <sub>5</sub>	4		G1.2.6	Q002-1	F <sub>5</sub>	4	
B167.4.5	Q008-2	F <sub>5</sub>	4		G1.3.6	Q002-1	F <sub>5</sub>	4(A)	
D31.1.1	Q018-1	F <sub>4</sub>	4		G4.10.1	Q002-1	F <sub>5</sub>	4	
D31.1.6	Q018-1	F <sub>4</sub>	4		G6.7.2	Q002-1	F <sub>5</sub>	E	
D31.2.2	Q018-1	F <sub>4</sub>	E		G44.P2.4	Q002-1	F <sub>5</sub>	7	
D31.3.5	Q018-1	F <sub>4</sub>	4		G44.P3.2	Q002-1	F <sub>5</sub>	4	
D31.4.2	Q018-1	F <sub>4</sub>	4(A)		G44.P4.1	Q002-1	F <sub>5</sub>	4	
D70.2.4	Q020-1	F <sub>4</sub>	4		G44.P5.1	Q002-1	F <sub>5</sub>	4	
D70.3.4	Q020-1	F <sub>4</sub>	4		G44.P6.4	Q002-1	F <sub>5</sub>	4	
D138.1.2	Q017-2	F <sub>4</sub>	4		G44.P7.1	Q002-1	F <sub>5</sub>	E	
D138.2.6	Q017-2	F <sub>4</sub>	2		G44.P8.3	Q002-1	F <sub>5</sub>	5	
D169.3.1	Q017-1	F <sub>4</sub>	4		G44.P9.1	Q002-1	F <sub>5</sub>	4	
D169.7.7	Q017-1	F <sub>4</sub>	4		G44.P9.4	Q002-1	F <sub>5</sub>	E	
D224.6.4	Q017-4	F <sub>4</sub>	4		G49.7.4	Q004-1	F <sub>5</sub>	4	
D224.7.1	Q017-4	F <sub>4</sub>	4		G49.12.3	Q004-1	F <sub>5</sub>	5	
D224.7.3	Q017-4	F <sub>4</sub>	5		G84.5.1	Q004-1	F <sub>5</sub>	5	

Table A7. (Continued) Straw test scores for summer 2008 selected plants of *Phaseolus vulgaris* screening for resistance to white mold; mean performance of checks in this experiment are shown in Table A8. (Teran scale<sup>2</sup>)

Line	Straw Test			Line	Straw Test		
	Cross No.	Generation	Score		Cross No.	Generation	Score
E19.6.1	Q027-1	F <sub>4</sub>	4	G106.1.4	Q004-1	F <sub>5</sub>	4
E40.1.3	Q027-1	F <sub>4</sub>	E	G106.2.2	Q004-1	F <sub>5</sub>	3
E40.7.1	Q027-1	F <sub>4</sub>	4	G108.9.6	Q004-1	F <sub>5</sub>	4
E41.9.4	Q028-1	F <sub>4</sub>	4	G110.1.3	Q004-1	F <sub>5</sub>	5
E46.1.4	Q028-1	F <sub>4</sub>	4(A)	G110.2.4	Q004-1	F <sub>5</sub>	4
E46.4.3	Q028-1	F <sub>4</sub>	5	G110.3.2	Q004-1	F <sub>5</sub>	4
E47.2.1	Q028-1	F <sub>4</sub>	4	G112.1.5	Q004-1	F <sub>5</sub>	4
E47.5.7	Q028-1	F <sub>4</sub>	5	G112.1.7	Q004-1	F <sub>5</sub>	5
E52.1.5	Q028-1	F <sub>4</sub>	6	G112.3.5	Q004-1	F <sub>5</sub>	4
E52.2.7	Q028-1	F <sub>4</sub>	5	G113.1.3	Q001-1	F <sub>5</sub>	4
E52.3.6	Q028-1	F <sub>4</sub>	4	G113.2.3	Q001-1	F <sub>5</sub>	E
E55.1.6	Q028-1	F <sub>4</sub>	E	G140.2.4	Q006-1	F <sub>5</sub>	4
E55.2.1	Q028-1	F <sub>4</sub>	6	G141.1.5	Q006-1	F <sub>5</sub>	4
E55.3.7	Q028-1	F <sub>4</sub>	6	G141.3.3	Q006-1	F <sub>5</sub>	5
E64.1.2	Q028-1	F <sub>4</sub>	E	G141.4.5	Q006-1	F <sub>5</sub>	5
E64.4.3	Q028-1	F <sub>4</sub>	4	G141.5.4	Q006-1	F <sub>5</sub>	5
E65.1.5	Q028-1	F <sub>4</sub>	4	G141.6.3	Q006-1	F <sub>5</sub>	4
E66.4.1	Q028-1	F <sub>4</sub>	4	G161.1.5	Q008-2	F <sub>5</sub>	E
E66.5.2	Q028-1	F <sub>4</sub>	4	G161.4.8	Q008-2	F <sub>5</sub>	4
E84.6.1	Q029-1	F <sub>4</sub>	4	G161.5.6	Q008-2	F <sub>5</sub>	4
E97.4.2	Q018-2	F <sub>4</sub>	4(A)	G174.1.1	Q008-2	F <sub>5</sub>	4
E97.5.3	Q018-2	F <sub>4</sub>	4	G174.2.4	Q008-2	F <sub>5</sub>	4
E97.6.1	Q018-2	F <sub>4</sub>	4	G205.1.2	Q012-1	F <sub>5</sub>	E
E97.6.8	Q018-2	F <sub>4</sub>	3	G207.1.1	Q012-1	F <sub>5</sub>	4
E97.7.6	Q018-2	F <sub>4</sub>	4	G207.4.4	Q012-1	F <sub>5</sub>	2
E97.11.2	Q018-2	F <sub>4</sub>	6	G207.6.6	Q012-1	F <sub>5</sub>	4
E106.4.1	Q033-1	F <sub>4</sub>	4	H1.2.1	Q012-1	F <sub>5</sub>	2
E112.2.8	Q035-4	F <sub>4</sub>	E	H2.2.3	Q012-1	F <sub>5</sub>	4
E112.3.7	Q035-4	F <sub>4</sub>	4	H2.4.5	Q012-1	F <sub>5</sub>	E
E115.1.7	Q035-4	F <sub>4</sub>	4	H5.5.2	Q012-1	F <sub>5</sub>	4
E115.2.4	Q035-4	F <sub>4</sub>	5	H9.1.3	Q012-1	F <sub>5</sub>	4
E118.1.3	Q035-4	F <sub>4</sub>	4	H9.2.1	Q012-1	F <sub>5</sub>	4
E120.1.2	Q035-4	F <sub>4</sub>	4	H12.2.2	Q003-1	F <sub>5</sub>	4(A)
E120.2.5	Q035-4	F <sub>4</sub>	5	H15.1.4	Q012-1	F <sub>5</sub>	4
E120.3.1	Q035-4	F <sub>4</sub>	6	H15.5.2	Q012-1	F <sub>5</sub>	2

Table A7. (Continued) Straw test scores for summer 2008 selected plants of *Phaseolus vulgaris* screening for resistance to white mold; mean performance of checks in this experiment are shown in Table A8. (Teran scale<sup>z</sup>)

Line	Cross No.	Generation	Straw Test		Line	Cross No.	Generation	Straw Test
			Score	Line				Score
E159.3.3	Q017-3	F <sub>4</sub>	4		H15.5.4	Q012-1	F <sub>5</sub>	4
E159.4.7	Q017-3	F <sub>4</sub>	5		H17.1.3	Q012-1	F <sub>5</sub>	4
E159.7.3	Q017-3	F <sub>4</sub>	4					

<sup>z</sup> Scale of 1-9 where 1=no infection and 9=total plant collapse (Teran *et al.*, 2006 scale).

<sup>y</sup> E= plant escaped infection.

<sup>x</sup> 4(A)= abscission layer formed at the first node preventing further white mold infection.

Table A8. Straw test least squared (LS) means for summer 2008 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold; LS means from checks used in experiment from Table A7. (Teran scale<sup>z</sup>)

Line	Cross No.	Generation	Straw Test LS Mean	Check <sup>x</sup>		
				G122	NY6020-5	OR 91G
D138.2	Q017-2	F <sub>3:4</sub>	2.54	0.0003 <sup>y</sup>	<0.0001	<0.0001
H15.5	Q012-1	F <sub>4:5</sub>	3.48	0.0928	0.0024	<0.0001
D138.1	Q017-2	F <sub>3:4</sub>	3.54	0.1342	0.0049	<0.0001
A115.4	Q003-1	F <sub>4:5</sub>	3.71	0.4861	0.1290	<0.0001
E84.6	Q029-1	F <sub>3:4</sub>	3.77	0.4015	0.0525	<0.0001
G174.1	Q008-2	F <sub>4:5</sub>	3.77	0.5378	0.1525	<0.0001
G174.2	Q008-2	F <sub>4:5</sub>	3.77	0.2920	0.0155	<0.0001
H15.4	Q012-1	F <sub>4:5</sub>	3.77	0.3569	0.0336	<0.0001
H5.5	Q012-1	F <sub>4:5</sub>	3.77	0.5378	0.1525	<0.0001
E47.2	Q028-1	F <sub>3:4</sub>	3.82	0.3775	0.0292	<0.0001
E52.3	Q028-1	F <sub>3:4</sub>	3.82	0.3775	0.0292	<0.0001
A182.2	Q012-1	F <sub>4:5</sub>	3.83	0.3237	0.0136	<0.0001
A6.2	Q012-1	F <sub>4:5</sub>	3.88	0.5662	0.1166	<0.0001
G207.1	Q012-1	F <sub>4:5</sub>	3.93	0.5174	0.0518	<0.0001
H2.2	Q012-1	F <sub>4:5</sub>	3.93	0.5174	0.0518	<0.0001
H9.2	Q012-1	F <sub>4:5</sub>	3.93	0.5174	0.0518	<0.0001
A182.6	Q012-1	F <sub>4:5</sub>	3.96	0.6092	0.1020	<0.0001
E168.10	Q017-3	F <sub>3:4</sub>	3.96	0.6092	0.1020	<0.0001
E66.4	Q028-1	F <sub>3:4</sub>	3.97	0.5911	0.0808	<0.0001
E46.4	Q028-1	F <sub>3:4</sub>	3.98	0.5904	0.0657	<0.0001
G161.1	Q008-2	F <sub>4:5</sub>	4.02	0.6628	0.0992	<0.0001
E106.4	Q033-1	F <sub>3:4</sub>	4.07	0.7568	0.1564	<0.0001
G205.1	Q012-1	F <sub>4:5</sub>	4.10	0.8213	0.2283	<0.0001
G207.6	Q012-1	F <sub>4:5</sub>	4.10	0.7621	0.1085	<0.0001
E118.8	Q035-4	F <sub>3:4</sub>	4.10	0.7563	0.0902	<0.0001
E249.1	Q035-4	F <sub>3:4</sub>	4.19	0.9042	0.1149	<0.0001
E46.1	Q028-1	F <sub>3:4</sub>	4.19	0.9042	0.1149	<0.0001
A115.1	Q003-1	F <sub>4:5</sub>	4.21	0.9627	0.3826	0.0002
A182.1	Q012-1	F <sub>4:5</sub>	4.21	0.9434	0.1888	<0.0001
A182.4	Q012-1	F <sub>4:5</sub>	4.21	0.9388	0.1563	<0.0001
B78.1	Q008-2	F <sub>4:5</sub>	4.21	0.9434	0.1888	<0.0001
D169.3	Q017-1	F <sub>3:4</sub>	4.21	0.9388	0.1563	<0.0001
D169.7	Q017-1	F <sub>3:4</sub>	4.21	0.9487	0.2324	<0.0001
E159.3	Q017-3	F <sub>3:4</sub>	4.21	0.9550	0.2931	<0.0001

Table A8. (Continued) Straw test least squared (LS) means for summer 2008 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold; LS means from checks used in experiment from Table A7. (Teran scale<sup>2</sup>)

Line	Cross No.	Generation	Straw Test LS Mean	Check <sup>x</sup>		
				G122	NY6020-5	OR 91G
E159.7	Q017-3	F <sub>3:4</sub>	4.21	0.9388	0.1563	<0.0001
E185.3	Q023-1	F <sub>3:4</sub>	4.21	0.9434	0.1888	<0.0001
E97.5	Q018-2	F <sub>3:4</sub>	4.21	0.9950	0.2931	<0.0001
G1.2	Q002-1	F <sub>4:5</sub>	4.21	0.9311	0.1120	<0.0001
G1.3	Q002-1	F <sub>4:5</sub>	4.21	0.9348	0.1315	<0.0001
G44.P4	Q002-1	F <sub>4:5</sub>	4.21	0.9627	0.3826	0.0002
E115.1	Q035-4	F <sub>3:4</sub>	4.32	0.8803	0.2461	<0.0001
E19.6	Q027-1	F <sub>3:4</sub>	4.32	0.8986	0.3251	<0.0001
E245.1	Q035-4	F <sub>3:4</sub>	4.32	0.8664	0.1963	<0.0001
A182.3	Q012-1	F <sub>4:5</sub>	4.33	0.8307	0.1951	<0.0001
G141.6	Q006-1	F <sub>4:5</sub>	4.33	0.8307	0.1951	<0.0001
E245.10	Q035-4	F <sub>3:4</sub>	4.34	0.8403	0.2352	<0.0001
E52.2	Q028-1	F <sub>3:4</sub>	4.34	0.8403	0.2352	<0.0001
A126.8	Q006-1	F <sub>4:5</sub>	4.35	0.8079	0.2341	<0.0001
E115.2	Q035-4	F <sub>3:4</sub>	4.37	0.8172	0.3234	<0.0001
G205.2	Q012-1	F <sub>4:5</sub>	4.37	0.8172	0.3234	<0.0001
E47.5	Q028-1	F <sub>3:4</sub>	4.39	0.7514	0.2822	<0.0001
G161.5	Q008-2	F <sub>4:5</sub>	4.39	0.7514	0.2822	<0.0001
A11.3	Q012-1	F <sub>4:5</sub>	4.41	0.7463	0.3546	<0.0001
D70.2	Q020-1	F <sub>3:4</sub>	4.44	0.6478	0.3136	<0.0001
E118.1	Q035-4	F <sub>3:4</sub>	4.44	0.6478	0.3136	<0.0001
E97.6	Q018-2	F <sub>3:4</sub>	4.46	0.6072	0.3163	<0.0001
G110.2	Q004-1	F <sub>4:5</sub>	4.46	0.6072	0.3163	<0.0001
G49.7	Q004-1	F <sub>4:5</sub>	4.46	0.7020	0.4515	<0.0001
H9.1	Q012-1	F <sub>4:5</sub>	4.48	0.6063	0.3799	<0.0001
E55.1	Q028-1	F <sub>4:5</sub>	4.48	0.6206	0.4127	<0.0001
A11.1	Q012-1	F <sub>4:5</sub>	4.49	0.5700	0.3836	<0.0001
A182.5	Q012-1	F <sub>4:5</sub>	4.49	0.5700	0.3836	<0.0001
G141.5	Q006-1	F <sub>4:5</sub>	4.49	0.5700	0.3836	<0.0001
H5.1	Q012-1	F <sub>4:5</sub>	4.52	0.6363	0.5215	<0.0001
A11.4	Q012-1	F <sub>4:5</sub>	4.54	0.5260	0.4721	<0.0001
D224.7	Q017-4	F <sub>3:4</sub>	4.54	0.6407	0.5939	<0.0001
D31.1	Q018-1	F <sub>3:4</sub>	4.54	0.5260	0.4721	<0.0001
E159.4	Q017-3	F <sub>3:4</sub>	4.54	0.5260	0.4721	<0.0001
E97.7	Q018-2	F <sub>3:4</sub>	4.54	0.5260	0.4721	<0.0001

Table A8. (Continued) Straw test least squared (LS) means for summer 2008 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold; LS means from checks used in experiment from Table A7. (Teran scale<sup>2</sup>)

Line	Cross No.	Generation	Straw Test LS Mean	Check <sup>x</sup>		
				G122	NY6020-5	OR 91G
G113.2	Q001-1	F <sub>4:5</sub>	4.54	0.5260	0.4721	<0.0001
D70.3	Q020-1	F <sub>3:4</sub>	4.57	0.5725	0.5819	<0.0001
E112.3	Q035-4	F <sub>3:4</sub>	4.57	0.5725	0.5819	<0.0001
E229.9	Q030-1	F <sub>3:4</sub>	4.57	0.5725	0.5819	<0.0001
G112.3	Q004-1	F <sub>4:5</sub>	4.58	0.4155	0.4788	<0.0001
G141.3	Q006-1	F <sub>4:5</sub>	4.58	0.4155	0.4788	<0.0001
D131.2	Q017-2	F <sub>3:4</sub>	4.64	0.3719	0.5805	<0.0001
G106.2	Q004-1	F <sub>4:5</sub>	4.64	0.3719	0.5805	<0.0001
G110.3	Q004-1	F <sub>4:5</sub>	4.64	0.3719	0.5805	<0.0001
G141.1	Q006-1	F <sub>4:5</sub>	4.64	0.3719	0.5805	<0.0001
E229.7	Q030-1	F <sub>3:4</sub>	4.67	0.3453	0.6485	<0.0001
G161.4	Q008-2	F <sub>4:5</sub>	4.67	0.3453	0.6485	<0.0001
E52.1	Q028-1	F <sub>3:4</sub>	4.69	0.3013	0.6612	<0.0001
B167.4	Q008-2	F <sub>4:5</sub>	4.71	0.3225	0.7117	<0.0001
E185.4	Q023-1	F <sub>3:4</sub>	4.71	0.3225	0.7117	<0.0001
G141.4	Q006-1	F <sub>4:5</sub>	4.71	0.3225	0.7117	<0.0001
E245.7	Q035-4	F <sub>3:4</sub>	4.77	0.2820	0.8066	<0.0001
E55.2	Q028-1	F <sub>3:4</sub>	4.77	0.2531	0.7592	<0.0001
E55.3	Q028-1	F <sub>3:4</sub>	4.77	0.2293	0.7851	<0.0001
E64.4	Q028-1	F <sub>3:4</sub>	4.77	0.4220	0.8542	0.0005
G191.4	Q012-1	F <sub>4:5</sub>	4.77	0.3176	0.8198	<0.0001
G207.4	Q012-1	F <sub>4:5</sub>	4.77	0.3628	0.8354	<0.0001
H1.2	Q012-1	F <sub>4:5</sub>	4.77	0.2531	0.7952	<0.0001
H17.1	Q012-1	F <sub>4:5</sub>	4.77	0.4220	0.8542	0.0005
H2.4	Q012-1	F <sub>4:5</sub>	4.77	0.3176	0.8198	<0.0001
D224.6	Q017-4	F <sub>3:4</sub>	4.78	0.2234	0.8151	<0.0001
B109.6	Q007-1	F <sub>4:5</sub>	4.81	0.2661	0.8822	<0.0001
H112.2	Q003-1	F <sub>4:5</sub>	4.81	0.2661	0.8822	<0.0001
E217.1	Q030-1	F <sub>3:4</sub>	4.82	0.1092	0.8534	<0.0001
E256.3	Q035-4	F <sub>3:4</sub>	4.82	0.3167	0.9070	0.0001
E41.9	Q028-1	F <sub>3:4</sub>	4.82	0.3167	0.9070	0.0001
G108.9	Q004-1	F <sub>4:5</sub>	4.83	0.1573	0.9042	<0.0001
B167.3	Q008-2	F <sub>4:5</sub>	4.88	0.1788	0.9840	<0.0001
G112.1	Q004-1	F <sub>4:5</sub>	4.88	0.0554	0.9776	<0.0001
G113.1	Q001-1	F <sub>4:5</sub>	4.90	0.0580	0.9640	<0.0001



Table A8. (Continued) Straw test least squared (LS) means for summer 2008 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold; LS means from checks used in experiment from Table A7. (Teran scale<sup>2</sup>)

Line	Cross No.	Generation	Straw Test LS Mean	Check <sup>x</sup>		
				G122	NY6020-5	OR 91G
D31.3	Q018-1	F <sub>3:4</sub>	4.92	0.1231	0.9323	<0.0001
G84.5	Q004-1	F <sub>4:5</sub>	4.92	0.1231	0.9323	<0.0001
G106.1	Q004-1	F <sub>4:5</sub>	4.96	0.2020	0.8963	0.0002
G49.12	Q004-1	F <sub>4:5</sub>	4.96	0.2020	0.8963	0.0002
E120.1	Q035-4	F <sub>3:4</sub>	4.96	0.1164	0.8699	<0.0001
E120.2	Q035-4	F <sub>3:4</sub>	4.96	0.1164	0.8699	<0.0001
E258.6	Q035-4	F <sub>3:4</sub>	4.96	0.1164	0.8699	<0.0001
E65.1	Q028-1	F <sub>3:4</sub>	4.96	0.1164	0.8699	<0.0001
E120.3	Q035-4	F <sub>3:4</sub>	4.98	0.1266	0.8391	<0.0001
E256.2	Q035-4	F <sub>3:4</sub>	5.02	0.1381	0.8008	0.0001
G110.1	Q004-1	F <sub>4:5</sub>	5.04	0.0892	0.7417	<0.0001
A126.10	Q006-1	F <sub>4:5</sub>	5.07	0.0620	0.6863	<0.0001
E64.1	Q028-1	F <sub>3:4</sub>	5.07	0.1505	0.7513	0.0006
E66.5	Q028-1	F <sub>3:4</sub>	5.07	0.0577	0.6773	<0.0001
E185.6	Q023-1	F <sub>3:4</sub>	5.08	0.0441	0.6402	<0.0001
E97.11	Q018-2	F <sub>3:4</sub>	5.08	0.0441	0.6402	<0.0001
G140.2	Q006-1	F <sub>4:5</sub>	5.08	0.0441	0.6402	<0.0001
E66.3	Q028-1	F <sub>3:4</sub>	5.10	0.0777	0.6631	<0.0001
H5.3	Q012-1	F <sub>4:5</sub>	5.10	0.1879	0.7437	0.0028
E51.2	Q028-1	F <sub>3:4</sub>	5.10	0.0597	0.6358	<0.0001
E112.1	Q035-4	F <sub>3:4</sub>	5.15	0.0097	0.4564	<0.0001
E51.1	Q028-1	F <sub>3:4</sub>	5.19	0.0288	0.4834	<0.0001
E66.1	Q028-1	F <sub>3:4</sub>	5.19	0.0373	0.5040	<0.0001
B78.5	Q008-2	F <sub>4:5</sub>	5.21	0.1305	0.6146	0.0041
G44.P1	Q002-1	F <sub>4:5</sub>	5.21	0.2104	0.6758	0.0171
G44.P6	Q002-1	F <sub>4:5</sub>	5.21	0.0850	0.5673	0.0011
E84.2	Q029-1	F <sub>3:4</sub>	5.27	0.1901	0.6271	0.0224
G165.3	Q008-2	F <sub>4:5</sub>	5.27	0.1901	0.6271	0.0224
E258.8	Q035-4	F <sub>3:4</sub>	5.32	0.0268	0.3764	0.0004
E97.4	Q018-2	F <sub>3:4</sub>	5.33	0.0009	0.2914	<0.0001
G191.3	Q012-1	F <sub>4:5</sub>	5.37	0.0316	0.3619	0.0013
G66.1	Q004-1	F <sub>4:5</sub>	5.38	0.0160	0.3038	0.0004
G161.2	Q008-2	F <sub>4:5</sub>	5.44	0.0058	0.2041	0.0002
G161.3	Q008-2	F <sub>4:5</sub>	5.44	0.0058	0.2041	0.0002
G145.2	Q006-1	F <sub>4:5</sub>	5.46	0.0036	0.1774	0.0002

Table A8. (Continued) Straw test least squared (LS) means for summer 2008 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold; LS means from checks used in experiment from Table A7. (Teran scale<sup>2</sup>)

Line	Cross No.	Generation	Straw Test LS Mean	Check <sup>x</sup>		
				G122	NY6020-5	OR 91G
G79.4	Q004-1	F <sub>4:5</sub>	5.46	0.0036	0.1774	0.0002
E41.1	Q028-1	F <sub>3:4</sub>	5.48	0.0105	0.2206	0.0013
H1.1	Q012-1	F <sub>4:5</sub>	5.52	0.0034	0.1521	0.0005
G145.1	Q006-1	F <sub>4:5</sub>	5.64	0.0016	0.0933	0.0015
H2.1	Q012-1	F <sub>4:5</sub>	5.64	0.0013	0.0862	0.0013
E51.5	Q028-1	F <sub>3:4</sub>	5.65	0.0037	0.1175	0.0041
G165.1	Q008-2	F <sub>4:5</sub>	5.65	0.0037	0.1175	0.0041
D169.4	Q017-1	F <sub>3:4</sub>	5.71	0.0090	0.1458	0.0172
G108.6	Q004-1	F <sub>4:5</sub>	5.71	0.0018	0.0842	0.0046
G26.4	Q002-1	F <sub>4:5</sub>	5.71	0.0090	0.1458	0.0172
G69.1	Q004-1	F <sub>4:5</sub>	5.71	0.0090	0.1458	0.0172
E256.1	Q035-4	F <sub>4:5</sub>	5.77	0.0079	0.1274	0.0255
G170.1	Q008-2	F <sub>4:5</sub>	5.77	0.0510	0.2608	0.0999
G170.2	Q008-2	F <sub>4:5</sub>	5.77	0.0017	0.0726	0.0084
H112.8	Q003-1	F <sub>4:5</sub>	5.81	0.0021	0.0727	0.0151
A115.2	Q003-1	F <sub>4:5</sub>	5.88	0.0106	0.1237	0.0665
G99.7	Q004-1	F <sub>4:5</sub>	5.96	0.0022	0.0580	0.0525
E245.4	Q035-4	F <sub>3:4</sub>	5.96	0.0002	0.0198	0.0175
E57.3	Q028-1	F <sub>3:4</sub>	6.10	0.0001	0.0134	0.0509
G44.P2	Q002-1	F <sub>4:5</sub>	6.21	0.0021	0.0397	0.1885
G44.P8	Q002-1	F <sub>4:5</sub>	6.21	0.0021	0.0397	0.1885
G191.1	Q012-1	F <sub>4:5</sub>	6.34	<0.0001	0.0017	0.1201
E84.4	Q029-1	F <sub>3:4</sub>	6.39	<0.0001	0.0011	0.1490
G44.P3	Q002-1	F <sub>4:5</sub>	6.41	<0.0001	0.0031	0.2088
G69.4	Q004-1	F <sub>4:5</sub>	6.41	<0.0001	0.0031	0.2088
G170.3	Q008-2	F <sub>4:5</sub>	6.43	0.0008	0.0179	0.3417
G4.10	Q002-1	F <sub>4:5</sub>	6.46	<0.0001	0.0055	0.2929
G69.3	Q004-1	F <sub>4:5</sub>	6.58	<0.0001	<0.0001	0.2671
H9.4	Q012-1	F <sub>4:5</sub>	6.77	0.0197	0.0824	0.7916
B78.9	Q008-2	F <sub>4:5</sub>	6.78	<0.0001	<0.0001	0.5422
E46.2	Q028-1	F <sub>3:4</sub>	6.82	<0.0001	<0.0001	0.6112
G44.P9	Q002-1	F <sub>4:5</sub>	6.88	<0.0001	0.0020	0.7843
D31.4	Q018-1	F <sub>3:4</sub>	6.96	<0.0001	<0.0001	0.8271
G44.P5	Q002-1	F <sub>4:5</sub>	7.01	<0.0001	<0.0001	0.9346
OSU 5630			6.57	<0.0001	<0.0001	0.0421

Table A8. (Continued) Straw test least squared (LS) means for summer 2008 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold; LS means from checks used in experiment from Table A7. (Teran scale<sup>z</sup>)

Line	Cross No.	Generation	Straw Test LS Mean	Check <sup>x</sup>		
				G122	NY6020-5	OR 91G
OSU 6229			4.38	0.5849	0.0439	<0.0001
OSU 6230			4.74	0.0354	0.5506	<0.0001
OSU 6241			6.30	<0.0001	<0.0001	0.0015
OR 91G			7.05	<0.0001	<0.0001	
G122			4.24		0.0084	<0.0001
NY6020-5			4.88	0.0084		<0.0001

<sup>z</sup> Scale of 1-9 where 1=no infection and 9=total plant collapse (Teran et al., 2006 scale).

<sup>y</sup> Probability of LS mean of experimental line equal to LS mean of the check

<sup>x</sup> G122 and NY60205-5 are partially resistant, OR 91G is susceptible

Table A9. Straw test least squared (LS) means for winter 2008 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold. (Teran scale<sup>2</sup>)

Line	Cross No.	Generation	SS18	PHAS	Straw Test LS Mean	Check <sup>x</sup>		
						G122	NY6020-5	OR 91G
G174.1.1	Q008-2	F <sub>5:6</sub>	+	T	3.65	0.0518 <sup>y</sup>	0.0420	<0.0001
D138.2.6	Q017-2	F <sub>4:5</sub>	+	T	3.76	0.0812	0.0666	<0.0001
D169.3.1	Q017-1	F <sub>4:5</sub>	-	S	3.76	0.0812	0.0666	<0.0001
E19.6.1	Q027-1	F <sub>4:5</sub>	-	S	3.80	0.0918	0.0755	<0.0001
E52.3.6	Q028-1	F <sub>4:5</sub>	+	T	3.80	0.0918	0.0755	<0.0001
D169.7.7	Q017-1	F <sub>4:5</sub>	+	S	3.89	0.1305	0.1084	<0.0001
D224.7.3	Q017-4	F <sub>4:5</sub>	+	S	3.93	0.1516	0.1266	<0.0001
E97.7.6	Q018-2	F <sub>4:5</sub>	+	S	3.99	0.1840	0.1547	<0.0001
A11.3.1	Q012-1	F <sub>5:6</sub>	-	T	4.01	0.1997	0.1683	<0.0001
A126.10.5	Q006-1	F <sub>5:6</sub>	+	S	4.01	0.1997	0.1683	<0.0001
H15.1.4	Q012-1	F <sub>5:6</sub>	+	T	4.01	0.1997	0.1683	<0.0001
H15.5.2	Q012-1	F <sub>5:6</sub>	+	T	4.01	0.1997	0.1683	<0.0001
H15.5.4	Q012-1	F <sub>5:6</sub>	+	T	4.01	0.1997	0.1683	<0.0001
D224.7.1	Q017-4	F <sub>4:5</sub>	+	S	4.01	0.2021	0.1705	<0.0001
A11.1.1	Q012-1	F <sub>5:6</sub>	-	T	4.05	0.2243	0.1899	<0.0001
A182.6.3	Q012-1	F <sub>5:6</sub>	+	T	4.05	0.2243	0.1899	<0.0001
D70.2.4	Q020-1	F <sub>4:5</sub>	+	T	4.05	0.2243	0.1899	<0.0001
G207.1.1	Q012-1	F <sub>5:6</sub>	+	S	4.08	0.2517	0.2140	<0.0001
E52.1.5	Q028-1	F <sub>4:5</sub>	+	T	4.13	0.2919	0.2498	<0.0001
E55.1.6	Q028-1	F <sub>4:5</sub>	+	T	4.13	0.2919	0.2498	<0.0001
E120.1.2	Q035-4	F <sub>4:5</sub>	+	T	4.14	0.2977	0.2550	<0.0001
E66.5.2	Q028-1	F <sub>4:5</sub>	+	S	4.14	0.2977	0.2550	<0.0001
A182.1.2	Q012-1	F <sub>5:6</sub>	+	T	4.17	0.3306	0.2845	<0.0001
D138.1.2	Q017-2	F <sub>4:5</sub>	+	T	4.21	0.3689	0.3191	<0.0001
E185.4.2	Q023-1	F <sub>4:5</sub>	-	S	4.21	0.3689	0.3191	<0.0001
E256.3.2	Q035-4	F <sub>4:5</sub>	+	T	4.26	0.4258	0.3709	<0.0001
D31.1.6	Q018-1	F <sub>4:5</sub>	-	T	4.26	0.4301	0.3748	<0.0001
G174.2.4	Q008-2	F <sub>5:6</sub>	+	T	4.30	0.4673	0.4090	<0.0001
D31.1.1	Q018-1	F <sub>4:5</sub>	-	S	4.32	0.4971	0.4365	<0.0001
E168.10.4	Q017-3	F <sub>4:5</sub>	+	T	4.32	0.4971	0.4365	<0.0001
D70.3.4	Q020-1	F <sub>4:5</sub>	+	S	4.34	0.5278	0.4651	<0.0001
E229.9.5	Q030-1	F <sub>4:5</sub>	+	T	4.34	0.5278	0.4651	<0.0001
B109.6.5	Q007-1	F <sub>5:6</sub>	+	T	4.36	0.5547	0.4901	<0.0001
A182.4.1	Q012-1	F <sub>5:6</sub>	+	T	4.40	0.5975	0.5303	<0.0001

Table A9. (Continued) Straw test least squared (LS) means for winter 2008 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold. (Teran scale<sup>z</sup>)

Line	Cross No.	Generation	SS18	PHAS	Straw Test LS Mean	Check <sup>x</sup>		
						G122	NY6020-5	OR 91G
E52.2.7	Q028-1	F <sub>4:5</sub>	+	T	4.40	0.5975	0.5303	<0.0001
H9.1.3	Q012-1	F <sub>5:6</sub>	+	T	4.41	0.6182	0.5498	<0.0001
E245.10.6	Q035-4	F <sub>4:5</sub>	+	S	4.43	0.6472	0.5772	<0.0001
G110.3.2	Q004-1	F <sub>5:6</sub>	+	T	4.43	0.6472	0.5772	<0.0001
G140.2.4	Q006-1	F <sub>5:6</sub>	+	S	4.43	0.6472	0.5772	<0.0001
G141.6.3	Q006-1	F <sub>5:6</sub>	+	S	4.43	0.6472	0.5772	<0.0001
G84.5.1	Q004-1	F <sub>5:6</sub>	-	T	4.43	0.6472	0.5772	<0.0001
A115.1.3	Q003-1	F <sub>5:6</sub>	+	T	4.43	0.6472	0.5772	<0.0001
D224.6.4	Q017-4	F <sub>4:5</sub>	+	T	4.43	0.6472	0.5772	<0.0001
E185.6.2	Q023-1	F <sub>4:5</sub>	-	S	4.43	0.6472	0.5772	<0.0001
E185.6.7	Q023-1	F <sub>4:5</sub>	-	S	4.43	0.6472	0.5772	<0.0001
E106.4.1	Q033-1	F <sub>4:5</sub>	+	T	4.51	0.7657	0.6904	<0.0001
E217.1.3	Q030-1	F <sub>4:5</sub>	+	T	4.51	0.7657	0.6904	<0.0001
A182.3.3	Q012-1	F <sub>5:6</sub>	+	T	4.55	0.8201	0.7431	<0.0001
B167.3.4	Q008-2	F <sub>5:6</sub>	+	S	4.55	0.8201	0.7431	<0.0001
H2.4.5	Q012-1	F <sub>5:6</sub>	+	T	4.57	0.8521	0.7742	<0.0001
E258.6.7	Q035-4	F <sub>4:5</sub>	+	T	4.60	0.9021	0.8230	<0.0001
E120.3.1	Q035-4	F <sub>4:5</sub>	+	T	4.61	0.9228	0.8434	<0.0001
E229.7.7	Q030-1	F <sub>4:5</sub>	+	S	4.61	0.9228	0.8434	<0.0001
G141.1.5	Q006-1	F <sub>5:6</sub>	+	T	4.63	0.9554	0.8756	<0.0001
G141.5.4	Q006-1	F <sub>5:6</sub>	+	T	4.63	0.9554	0.8756	<0.0001
E159.3.3	Q017-3	F <sub>4:5</sub>	+	T	4.64	0.9688	0.8888	<0.0001
B78.5.3	Q008-2	F <sub>5:6</sub>	+	T	4.65	0.9906	0.9105	<0.0001
G141.3.3	Q006-1	F <sub>5:6</sub>	+	S	4.68	0.9643	0.9554	<0.0001
G161.5.6	Q008-2	F <sub>5:6</sub>	+	T	4.68	0.9643	0.9554	<0.0001
G110.1.3	Q004-1	F <sub>5:6</sub>	+	T	4.72	0.9071	0.9873	<0.0001
G113.2.3	Q001-1	F <sub>5:6</sub>	+	T	4.72	0.9071	0.9873	<0.0001
G49.12.3	Q004-1	F <sub>5:6</sub>	+	T	4.76	0.8318	0.9109	<0.0001
G1.3.6	Q002-1	F <sub>5:6</sub>	+	T	4.76	0.8317	0.9109	<0.0001
A126.8.7	Q006-1	F <sub>5:6</sub>	+	T	4.80	0.7828	0.8609	<0.0001
A182.5.3	Q012-1	F <sub>5:6</sub>	+	T	4.80	0.7828	0.8609	<0.0001
E245.7.6	Q035-4	F <sub>4:5</sub>	+	S	4.81	0.7671	0.8448	<0.0001
E249.1.4	Q020-2	F <sub>4:5</sub>	+	T	4.81	0.7671	0.8448	<0.0001
E120.2.5	Q035-4	F <sub>4:5</sub>	+	T	4.81	0.7600	0.8376	<0.0001
G106.1.4	Q004-1	F <sub>5:6</sub>	+	T	4.83	0.7291	0.8057	<0.0001

Table A9. (Continued) Straw test least squared (LS) means for winter 2008 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold. (Teran scale<sup>2</sup>)

Line	Cross No.	Generation	SS18	PHAS	Straw Test LS Mean	Check <sup>x</sup>		
						G122	NY6020-5	OR 91G
G108.9.6	Q004-1	F <sub>5:6</sub>	+	T	4.83	0.7291	0.8057	<0.0001
E115.2.4	Q035-4	F <sub>4:5</sub>	+	T	4.84	0.7069	0.7855	<0.0001
D31.4.2	Q018-1	F <sub>4:5</sub>	-	T	4.87	0.6632	0.7375	<0.0001
E168.1.1	Q017-3	F <sub>4:5</sub>	+	T	4.89	0.6432	0.7165	<0.0001
E97.11.2	Q018-2	F <sub>4:5</sub>	+	T	4.89	0.6432	0.7165	<0.0001
H9.2.1	Q012-1	F <sub>5:6</sub>	+	T	4.90	0.6287	0.7013	<0.0001
E245.1.6	Q035-4	F <sub>4:5</sub>	+	S	4.93	0.5848	0.6552	<0.0001
G106.2.2	Q004-1	F <sub>5:6</sub>	+	T	4.93	0.5848	0.6552	<0.0001
G110.2.4	Q004-1	F <sub>5:6</sub>	+	T	4.93	0.5848	0.6552	<0.0001
G112.3.5	Q004-1	F <sub>5:6</sub>	+	T	5.00	0.4911	0.5557	<0.0001
E256.2.4	Q035-4	F <sub>4:5</sub>	+	T	5.01	0.4809	0.5448	<0.0001
E159.7.3	Q017-3	F <sub>4:5</sub>	+	T	5.01	0.4764	0.5400	<0.0001
G161.1.5	Q008-2	F <sub>5:6</sub>	+	T	5.03	0.4562	0.5183	<0.0001
A6.2.2	Q012-1	F <sub>5:6</sub>	+	T	5.05	0.4378	0.4994	<0.0001
A115.4.4	Q003-1	F <sub>5:6</sub>	+	T	5.10	0.3807	0.4365	<0.0001
E97.4.2	Q018-2	F <sub>4:5</sub>	+	T	5.10	0.3807	0.4365	<0.0001
E97.6.8	Q018-2	F <sub>4:5</sub>	+	T	5.10	0.3807	0.4365	<0.0001
G113.1.3	Q001-1	F <sub>5:6</sub>	+	T	5.10	0.3807	0.4365	<0.0001
E112.2.8	Q035-4	F <sub>4:5</sub>	+	S	5.12	0.3556	0.4090	<0.0001
H1.2.1	Q012-1	F <sub>5:6</sub>	+	T	5.13	0.3480	0.4008	<0.0001
E159.4.7	Q017-3	F <sub>4:5</sub>	+	T	5.14	0.3379	0.3897	<0.0001
E185.3.3	Q023-1	F <sub>4:5</sub>	+	T	5.14	0.3379	0.3897	<0.0001
G1.2.6	Q002-1	F <sub>5:6</sub>	+	T	5.14	0.3379	0.3897	<0.0001
G112.1.7	Q004-1	F <sub>5:6</sub>	+	T	5.14	0.3321	0.3832	<0.0001
H5.5.2	Q012-1	F <sub>5:6</sub>	+	T	5.15	0.3241	0.3745	0.0001
E97.5.3	Q018-2	F <sub>4:5</sub>	+	T	5.16	0.3139	0.3632	0.0001
B167.4.5	Q008-2	F <sub>5:6</sub>	+	T	5.20	0.2853	0.3316	0.0001
E185.3.6	Q023-1	F <sub>4:5</sub>	+	T	5.21	0.2742	0.3191	0.0001
A182.2.6	Q012-1	F <sub>5:6</sub>	+	T	5.22	0.2611	0.3045	0.0001
B78.1.2	Q008-2	F <sub>5:6</sub>	+	T	5.22	0.2611	0.3045	0.0001
G207.4.4	Q012-1	F <sub>5:6</sub>	+	T	5.22	0.2611	0.3045	0.0001
E115.1.7	Q035-4	F <sub>4:5</sub>	+	T	5.26	0.2326	0.2726	0.0002
E47.2.1	Q028-1	F <sub>4:5</sub>	+	S	5.30	0.2072	0.2439	0.0002
E64.1.2	Q028-1	F <sub>4:5</sub>	+	T	5.30	0.2072	0.2439	0.0002
G112.1.5	Q004-1	F <sub>5:6</sub>	+	T	5.31	0.2003	0.2361	0.0002

Table A9. (Continued) Straw test least squared (LS) means for winter 2008 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold. (Teran scale<sup>z</sup>)

Line	Cross No.	Generation	SS18	PHAS	Straw Test LS Mean	Check <sup>x</sup>		
						G122	NY6020-5	OR 91G
E97.6.1	Q018-2	F <sub>4:5</sub>	+	T	5.36	0.1640	0.1947	0.0003
G141.4.5	Q006-1	F <sub>5:6</sub>	+	S	5.43	0.1292	0.1547	0.0004
G161.4.8	Q008-2	F <sub>5:6</sub>	+	T	5.43	0.1292	0.1547	0.0004
E118.1.3	Q035-4	F <sub>4:5</sub>	+	T	5.51	0.0959	0.1158	0.0007
E65.1.5	Q028-1	F <sub>4:5</sub>	+	T	5.51	0.0959	0.1158	0.0007
E66.4.1	Q028-1	F <sub>4:5</sub>	+	S	5.51	0.0959	0.1158	0.0007
D31.3.5	Q018-1	F <sub>4:5</sub>	-	S	5.51	0.0945	0.1142	0.0007
G4.10.1	Q002-1	F <sub>4:5</sub>	+	S	5.51	0.0945	0.1142	0.0007
E159.7.4	Q017-3	F <sub>4:5</sub>	+	T	5.60	0.0681	0.0830	0.0010
D31.2.2	Q018-1	F <sub>4:5</sub>	-	S	5.62	0.0618	0.0756	0.0012
E84.6.1	Q029-1	F <sub>4:5</sub>	+	T	5.72	0.0402	0.0496	0.0019
E41.9.4	Q028-1	F <sub>4:5</sub>	+	T	5.76	0.0345	0.0427	0.0023
E40.1.3	Q027-1	F <sub>4:5</sub>	+	S	5.76	0.0339	0.0420	0.0024
E47.5.7	Q028-1	F <sub>4:5</sub>	+	S	5.80	0.0296	0.0367	0.0028
E40.7.1	Q027-1	F <sub>4:5</sub>	+	S	5.87	0.0207	0.0259	0.0041
A11.4.1	Q012-1	F <sub>5:6</sub>	-	T	5.92	0.0169	0.0212	0.0051
G44.P9.4	Q002-1	F <sub>5:6</sub>	-	S	5.93	0.0161	0.0202	0.0054
G49.7.4	Q004-1	F <sub>5:6</sub>	+	T	5.93	0.0161	0.0202	0.0054
G6.7.2	Q002-1	F <sub>5:6</sub>	+	S	5.93	0.0161	0.0202	0.0054
E55.3.7	Q028-1	F <sub>4:5</sub>	+	T	5.96	0.0139	0.0175	0.0063
G205.1.2	Q012-1	F <sub>5:6</sub>	-	T	6.01	0.0111	0.0141	0.0079
G44.P2.4	Q002-1	F <sub>5:6</sub>	-	S	6.10	0.0074	0.0093	0.0120
G44.P3.2	Q002-1	F <sub>5:6</sub>	-	S	6.10	0.0074	0.0093	0.0120
G44.P4.1	Q002-1	F <sub>5:6</sub>	-	S	6.10	0.0074	0.0093	0.0120
G44.P8.3	Q002-1	F <sub>5:6</sub>	-	T	6.10	0.0074	0.0093	0.0120
E64.4.3	Q028-1	F <sub>4:5</sub>	+	T	6.17	0.0052	0.0066	0.0168
A115.2.1	Q003-1	F <sub>5:6</sub>	-	T	6.19	0.0046	0.0059	0.0186
G207.6.6	Q012-1	F <sub>5:6</sub>	+	S	6.20	0.0046	0.0058	0.0188
G44.P5.1	Q002-1	F <sub>5:6</sub>	-	S	6.21	0.0043	0.0055	0.0200
E112.3.7	Q035-4	F <sub>4:5</sub>	+	S	6.26	0.0033	0.0043	0.0252
G44.P6.4	Q002-1	F <sub>5:6</sub>	-	S	6.43	0.0014	0.0018	0.0524
H2.2.3	Q012-1	F <sub>5:6</sub>	+	T	6.43	0.0014	0.0018	0.0524
E55.2.1	Q028-1	F <sub>4:5</sub>	+	T	6.51	0.0009	0.0012	0.0752
G44.P7.1	Q002-1	F <sub>5:6</sub>	-	S	6.56	0.0007	0.0010	0.0867
H17.1.3	Q012-1	F <sub>5:6</sub>	+	S	6.58	0.0007	0.0008	0.0959

Table A9. (Continued) Straw test least squared (LS) means for winter 2008 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold. (Teran scale<sup>z</sup>)

Line	Cross No.	Generation	SS18	PHAS	Straw Test LS Mean	Check <sup>x</sup>		
						G122	NY6020-5	OR 91G
G44.P9.1	Q002-1	F <sub>5:6</sub>	-	S	6.68	0.0004	0.0005	0.1387
E46.1.4	Q028-1	F <sub>4:5</sub>	+	S	6.80	0.0002	0.0003	0.2066
E46.4.3	Q028-1	F <sub>4:5</sub>	+	T	6.80	0.0002	0.0003	0.2066
4.1.3					4.41	0.6182	0.5498	<0.0001
5.3.10					5.01	0.4809	0.5448	<0.0001
5.3.18					5.01	0.4809	0.5448	<0.0001
5.3.24					4.81	0.7600	0.8376	<0.0001
5.3.4					5.68	0.0491	0.0604	0.0015
5.3.8					5.51	0.0959	0.1158	0.0007
8.6.1					5.84	0.0239	0.0298	0.0035
8.6.16					5.41	0.1391	0.1661	0.0004
9.12.4					6.34	0.0022	0.0028	0.0363
9.12.8					5.61	0.0646	0.0789	0.0011
OSU 5630					6.47	<0.0001	<0.0001	0.0037
OSU 6229					4.87	0.4954	0.6036	<0.0001
OSU 6230					5.00	0.2732	0.3489	<0.0001
OSU 6241					5.40	0.0213	0.0306	<0.0001
Ex Rico					6.63	<0.0001	<0.0001	0.0129
M0162					5.42	0.0182	0.0263	<0.0001
OR 91G					7.43	<0.0001	<0.0001	
G122					4.66		0.8694	<0.0001
NY6020-5					4.71	0.8694		<0.0001

<sup>z</sup> Scale of 1-9 where 1=no infection and 9=total plant collapse (Teran *et al.*, 2006 scale).

<sup>y</sup> Probability of LS mean of experimental line equal to LS mean of the check

<sup>x</sup> G122 and NY6020-5 are partially resistant, OR 91G is susceptible



Table A10. Straw test least squared (LS) means for spring 2009 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold. (Teran scale<sup>2</sup>)

Line	Cross No.	Generation	SS18	PHAS	Straw Test LS Mean	Check <sup>x</sup>		
						G122	NY6020-5	OR 91G
G106.2.2	Q004-1	F <sub>5:7</sub>	+	T	3.91	0.4751 <sup>y</sup>	0.0098	0.0001
E52.3.6	Q028-1	F <sub>4:6</sub>	+	T	3.92	0.2824	0.0131	<0.0001
G44.P3.2	Q002-1	F <sub>5:7</sub>	-	S	3.96	0.5082	0.0116	0.0002
G1.3.6	Q002-1	F <sub>5:7</sub>	+	T	3.97	0.3193	0.0163	<0.0001
E185.6.2	Q023-1	F <sub>4:6</sub>	-	S	4.08	0.4063	0.0251	<0.0001
H2.2.3	Q012-1	F <sub>5:7</sub>	+	T	4.14	0.5160	0.0606	<0.0001
E65.1.5	Q028-1	F <sub>4:6</sub>	+	T	4.25	0.5630	0.0466	<0.0001
E97.4.2	Q018-2	F <sub>4:6</sub>	+	T	4.30	0.7374	0.2055	0.0006
E97.5.3	Q018-2	F <sub>4:6</sub>	+	T	4.31	0.6682	0.0979	<0.0001
G6.7.2	Q002-1	F <sub>5:7</sub>	+	S	4.41	0.8241	0.2476	0.0008
B78.1.2	Q008-2	F <sub>5:7</sub>	+	T	4.47	0.805	0.0967	<0.0001
E52.2.7	Q028-1	F <sub>4:6</sub>	+	T	4.47	0.805	0.0967	<0.0001
H9.1.3	Q012-1	F <sub>5:7</sub>	+	T	4.47	0.805	0.0967	<0.0001
D224.7.1	Q017-4	F <sub>4:6</sub>	+	S	4.58	0.9325	0.1337	<0.0001
E106.4.1	Q033-1	F <sub>4:6</sub>	+	T	4.58	0.9354	0.1346	<0.0001
G207.4.4	Q012-1	F <sub>5:7</sub>	+	T	4.58	0.9354	0.1346	<0.0001
D224.6.4.	Q017-4	F <sub>4:6</sub>	+	T	4.63	0.9939	0.3479	0.0018
E55.1.6	Q028-1	F <sub>4:6</sub>	+	T	4.64	0.9985	0.1575	<0.0001
A11.4.1	Q012-1	F <sub>5:7</sub>	-	T	4.66	0.981	0.3625	0.0019
D138.2.6	Q017-2	F <sub>4:6</sub>	+	T	4.72	0.9025	0.1958	<0.0001
E185.4.2	Q023-1	F <sub>4:6</sub>	-	S	4.75	0.8698	0.2105	<0.0001
E47.2.1	Q028-1	F <sub>4:6</sub>	+	S	4.75	0.8669	0.2118	<0.0001
E52.1.5	Q028-1	F <sub>4:6</sub>	+	T	4.75	0.8669	0.2118	<0.0001
E64.1.2	Q028-1	F <sub>4:6</sub>	+	T	4.81	0.8022	0.2437	<0.0001
H17.1.3	Q012-1	F <sub>5:7</sub>	+	S	4.81	0.8022	0.2437	<0.0001
E249.1.4	Q020-2	F <sub>4:6</sub>	+	T	4.92	0.6772	0.317	<0.0001
G207.1.1	Q012-1	F <sub>5:7</sub>	+	S	4.92	0.6772	0.317	<0.0001
E217.1.3	Q030-1	F <sub>4:6</sub>	+	T	4.92	0.7152	0.3863	0.0002
G161.4.8	Q008-2	F <sub>5:7</sub>	+	T	5.03	0.5605	0.4037	<0.0001
G1.2.6	Q002-1	F <sub>5:7</sub>	+	T	5.08	0.5085	0.4497	<0.0001
G174.1.1	Q008-2	F <sub>5:7</sub>	+	T	5.08	0.5061	0.4519	<0.0001
G174.2.4	Q008-2	F <sub>5:7</sub>	+	T	5.08	0.5061	0.4519	<0.0001
E97.7.6	Q018-2	F <sub>4:6</sub>	+	S	5.19	0.4083	0.555	<0.0001
D224.7.3	Q017-4	F <sub>4:6</sub>	+	S	5.25	0.3631	0.6118	0.0001

Table A10. (Continued) Straw test least squared (LS) means for spring 2009 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold. (Teran scale<sup>z</sup>)

Line	Cross No.	Generation	SS18	PHAS	Straw Test LS Mean	Check <sup>x</sup>		
						G122	NY6020-5	OR 91G
E115.2.4	Q035-4	F <sub>4:6</sub>	+	T	5.25	0.3611	0.6144	0.0001
E19.6.1	Q027-1	F <sub>4:6</sub>	-	S	5.25	0.3611	0.6144	0.0001
E256.2.4	Q035-4	F <sub>4:6</sub>	+	T	5.25	0.3611	0.6144	0.0001
A126.10.5	Q006-1	F <sub>5:7</sub>	+	S	5.25	0.3611	0.6144	0.0001
B78.5.3	Q008-2	F <sub>5:7</sub>	+	T	5.31	0.3193	0.6738	0.0002
A182.5.3	Q012-1	F <sub>5:7</sub>	+	T	5.36	0.2807	0.7353	0.0003
E120.2.5	Q035-4	F <sub>4:6</sub>	+	T	5.36	0.2807	0.7353	0.0003
E46.4.3	Q028-1	F <sub>4:6</sub>	+	T	5.36	0.4764	0.8237	0.0153
A126.8.7	Q006-1	F <sub>5:7</sub>	+	T	5.42	0.2455	0.7986	0.0004
G207.6.6	Q012-1	F <sub>5:7</sub>	+	S	5.42	0.2455	0.7986	0.0004
G106.1.4	Q004-1	F <sub>5:7</sub>	+	T	5.47	0.2135	0.8632	0.0005
A182.1.2	Q012-1	F <sub>5:7</sub>	+	T	5.47	0.2135	0.8632	0.0005
E229.9.5	Q030-1	F <sub>4:6</sub>	+	T	5.47	0.2135	0.8632	0.0005
G108.9.6	Q004-1	F <sub>5:7</sub>	+	T	5.47	0.2135	0.8632	0.0005
H15.5.4	Q012-1	F <sub>5:7</sub>	+	T	5.50	0.1987	0.8959	0.0006
G44.P9.1	Q002-1	F <sub>5:7</sub>	-	S	5.53	0.1859	0.9259	0.0006
E66.5.2	Q028-1	F <sub>4:6</sub>	+	S	5.53	0.1847	0.9288	0.0006
A182.3.3	Q012-1	F <sub>5:7</sub>	+	T	5.58	0.1588	0.9949	0.0009
D70.3.4	Q020-1	F <sub>4:6</sub>	+	S	5.58	0.1588	0.9949	0.0009
E46.1.4	Q028-1	F <sub>4:6</sub>	+	S	5.58	0.1588	0.9949	0.0009
G110.3.2	Q004-1	F <sub>5:7</sub>	+	T	5.58	0.1588	0.9949	0.0009
G112.1.7	Q004-1	F <sub>5:7</sub>	+	T	5.58	0.1588	0.9949	0.0009
H15.1.4	Q012-1	F <sub>5:7</sub>	+	T	5.64	0.1958	0.9494	0.0046
G110.1.3	Q004-1	F <sub>5:7</sub>	+	T	5.70	0.1155	0.8734	0.0015
D169.7.7	Q017-1	F <sub>4:6</sub>	+	S	5.75	0.0984	0.8114	0.002
G44.P6.4	Q002-1	F <sub>5:7</sub>	-	S	5.75	0.0984	0.8114	0.002
A11.3.1	Q012-1	F <sub>5:7</sub>	-	T	5.75	0.0977	0.8086	0.002
A182.6.3	Q012-1	F <sub>5:7</sub>	+	T	5.75	0.0977	0.8086	0.002
E120.3.1	Q035-4	F <sub>4:6</sub>	+	T	5.75	0.0977	0.8086	0.002
G113.1.3	Q001-1	F <sub>5:7</sub>	+	T	5.80	0.1314	0.7799	0.0087
G141.4.5	Q006-1	F <sub>5:7</sub>	+	S	5.81	0.0821	0.7451	0.0026
G161.5.6	Q008-2	F <sub>5:7</sub>	+	T	5.81	0.0821	0.7451	0.0026
H12.2.2	Q003-1	F <sub>5:7</sub>	-	T	5.81	0.1308	0.7768	0.0089
E97.11.1	Q018-2	F <sub>4:6</sub>	+	T	5.86	0.0692	0.6859	0.0034
E112.3.7	Q035-4	F <sub>4:6</sub>	+	S	5.86	0.0686	0.6832	0.0034

Table A10. (Continued) Straw test least squared (LS) means for spring 2009 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold. (Teran scale<sup>z</sup>)

Line	Cross No.	Generation	SS18	PHAS	Straw Test LS Mean	Check <sup>x</sup>		
						G122	NY6020-5	OR 91G
E229.7.7	Q030-1	F <sub>4:6</sub>	+	S	5.86	0.0686	0.6832	0.0034
D169.3.1	Q017-1	F <sub>4:6</sub>	-	S	5.92	0.0575	0.6261	0.0044
E185.6.7	Q023-1	F <sub>4:6</sub>	-	S	5.92	0.0575	0.6261	0.0044
D70.2.4	Q020-1	F <sub>4:6</sub>	+	T	5.92	0.0575	0.6235	0.0044
E120.1.2	Q035-4	F <sub>4:6</sub>	+	T	5.92	0.0575	0.6235	0.0044
E66.4.1	Q028-1	F <sub>4:6</sub>	+	S	5.92	0.0575	0.6235	0.0044
G112.1.5	Q004-1	F <sub>5:7</sub>	+	T	5.92	0.0575	0.6235	0.0044
H5.5.2	Q012-1	F <sub>5:7</sub>	+	T	5.92	0.0575	0.6235	0.0044
E159.7.3	Q017-3	F <sub>4:6</sub>	+	T	5.96	0.0869	0.627	0.0157
E97.6.1	Q018-2	F <sub>4:6</sub>	+	T	5.97	0.0475	0.5886	0.0056
E258.6.7	Q035-4	F <sub>4:6</sub>	+	T	5.97	0.0471	0.5661	0.0057
A11.1.1	Q012-1	F <sub>5:7</sub>	-	T	5.97	0.0471	0.5661	0.0057
E115.1.7	Q035-4	F <sub>4:6</sub>	+	T	5.97	0.0471	0.5661	0.0057
E185.3.6	Q023-1	F <sub>4:6</sub>	+	T	6.03	0.0391	0.5138	0.0072
E97.6.8	Q018-2	F <sub>4:6</sub>	+	T	6.03	0.039	0.5138	0.0072
A182.4.1	Q012-1	F <sub>5:7</sub>	+	T	6.03	0.0387	0.5114	0.0073
E159.4.7	Q017-3	F <sub>4:6</sub>	+	T	6.08	0.0319	0.4619	0.0091
H15.5.2	Q012-1	F <sub>5:7</sub>	+	T	6.08	0.0316	0.4597	0.0092
H9.2.1	Q012-1	F <sub>5:7</sub>	+	T	6.08	0.0316	0.4597	0.0092
D138.1.2	Q017-2	F <sub>4:6</sub>	+	T	6.13	0.0541	0.4829	0.0276
B167.3.4	Q008-2	F <sub>5:7</sub>	+	S	6.14	0.0257	0.411	0.0117
E84.6.1	Q029-1	F <sub>4:6</sub>	+	T	6.14	0.0257	0.411	0.0117
G110.2.4	Q004-1	F <sub>5:7</sub>	+	T	6.14	0.0257	0.411	0.0117
G141.6.3	Q006-1	F <sub>5:7</sub>	+	S	6.14	0.0257	0.411	0.0117
G49.12.3	Q004-1	F <sub>5:7</sub>	+	T	6.14	0.0257	0.411	0.0117
G44.P4.1	Q002-1	F <sub>5:7</sub>	-	S	6.14	0.0525	0.4748	0.0285
E185.3.3	Q023-1	F <sub>4:6</sub>	+	T	6.19	0.0209	0.3674	0.0145
G44.P7.1	Q002-1	F <sub>5:7</sub>	-	S	6.19	0.0209	0.3674	0.0145
G140.2.4	Q006-1	F <sub>5:7</sub>	+	S	6.20	0.0442	0.4317	0.0338
A182.2.6	Q012-1	F <sub>5:7</sub>	+	T	6.20	0.0207	0.3655	0.0147
H2.4.5	Q012-1	F <sub>5:7</sub>	+	T	6.20	0.0207	0.3655	0.0147
G112.3.5	Q004-1	F <sub>5:7</sub>	+	T	6.25	0.1143	0.5177	0.11777
G4.10.1	Q002-1	F <sub>5:7</sub>	+	S	6.25	0.0168	0.3251	0.0182
B167.4.5	Q008-2	F <sub>5:7</sub>	+	T	6.25	0.0166	0.3233	0.0183
E245.10.6	Q035-4	F <sub>4:6</sub>	+	S	6.25	0.0166	0.3233	0.0183

Table A10. (Continued) Straw test least squared (LS) means for spring 2009 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold. (Teran scale<sup>z</sup>)

Line	Cross No.	Generation	SS18	PHAS	Straw Test LS Mean	Check <sup>x</sup>		
						G122	NY6020-5	OR 91G
G161.1.5	Q008-2	F <sub>5:7</sub>	+	T	6.25	0.0166	0.3233	0.0183
G49.7.4	Q004-1	F <sub>5:7</sub>	+	T	6.25	0.0166	0.3233	0.0183
G113.2.3	Q001-1	F <sub>5:7</sub>	+	T	6.31	0.0133	0.2844	0.0228
E168.10.4	Q017-3	F <sub>4:6</sub>	+	T	6.36	0.0106	0.2504	0.0279
E245.7.6	Q035-4	F <sub>4:6</sub>	+	S	6.36	0.0105	0.2489	0.0282
G44.P5.1	Q002-1	F <sub>5:7</sub>	-	S	6.42	0.0084	0.218	0.0343
E118.1.3	Q035-4	F <sub>4:6</sub>	+	T	6.42	0.0083	0.2166	0.0346
E112.2.8	Q035-4	F <sub>4:6</sub>	+	S	6.47	0.0065	0.1874	0.0423
G44.P9.4	Q002-1	F <sub>5:7</sub>	-	S	6.53	0.0051	0.1624	0.0509
B109.6.5	Q007-1	F <sub>5:7</sub>	+	T	6.56	0.0134	0.2101	0.0979
E55.3.7	Q028-1	F <sub>4:6</sub>	+	T	6.58	0.0039	0.138	0.062
D31.1.1	Q018-1	F <sub>4:6</sub>	-	S	6.63	0.0103	0.1778	0.1184
D31.1.6	Q018-1	F <sub>4:6</sub>	-	T	6.64	0.0031	0.1183	0.0738
E159.7.4	Q017-3	F <sub>4:6</sub>	+	T	6.64	0.0031	0.1183	0.0738
A6.2.2	Q012-1	F <sub>5:7</sub>	+	T	6.64	0.003	0.1174	0.0744
E64.4.3	Q028-1	F <sub>4:6</sub>	+	T	6.64	0.003	0.1174	0.0744
E168.1.1	Q017-3	F <sub>4:6</sub>	+	T	6.64	0.0099	0.1737	0.1216
G141.1.5	Q006-1	F <sub>5:7</sub>	+	T	6.70	0.008	0.152	0.1389
E245.1.6	Q035-4	F <sub>4:6</sub>	+	S	6.70	0.0023	0.0993	0.0887
G141.5.4	Q006-1	F <sub>5:7</sub>	+	T	6.81	0.0013	0.0699	0.1242
G44.P8.3	Q002-1	F <sub>5:7</sub>	-	T	6.86	0.001	0.0586	0.1447
H1.2.1	Q012-1	F <sub>5:7</sub>	+	T	6.86	0.001	0.0581	0.1457
D31.3.5	Q018-1	F <sub>4:6</sub>	-	S	6.89	0.0038	0.0925	0.2203
D31.2.2	Q018-1	F <sub>4:6</sub>	-	S	6.97	0.0006	0.0398	0.1958
E159.3.3	Q017-3	F <sub>4:6</sub>	+	T	6.97	0.006	0.0398	0.1958
G141.3.3	Q006-1	F <sub>5:7</sub>	+	S	7.03	0.004	0.0323	0.2274
G84.5.1	Q004-1	F <sub>5:7</sub>	-	T	7.03	0.0004	0.0323	0.2274
D31.4.2	Q018-1	F <sub>4:6</sub>	-	T	7.31	0.0006	0.0266	0.4619
G44.P2.4	Q002-1	F <sub>5:7</sub>	-	S	7.36	<0.0001	0.0086	0.4749
E256.3.2	Q035-4	F <sub>4:6</sub>	+	T	7.36	0.0077	0.0816	0.6392
E55.2.1	Q028-1	F <sub>4:6</sub>	+	T	7.36	0.0077	0.0816	0.6392
A115.1.3	Q003-1	F <sub>5:7</sub>	+	T	7.39	0.0004	0.0202	0.562
E40.1.3	Q027-1	F <sub>4:6</sub>	+	S	7.47	<0.0001	0.0053	0.5831
A115.4.4	Q003-1	F <sub>5:7</sub>	+	T	7.64	<0.001	0.0024	0.7639
A115.2.1	Q003-1	F <sub>5:7</sub>	-	T	7.86	<0.001	0.0008	0.975

Table A10. (Continued) Straw test least squared (LS) means for spring 2009 families and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold. (Teran scale<sup>z</sup>)

Line	Cross No.	Generation	SS18	PHAS	Straw Test LS Mean	Check <sup>x</sup>		
						G122	NY6020-5	OR 91G
E40.7.1	Q027-1	F <sub>4:6</sub>	+	S	7.86	<0.0001	0.0008	0.975
4.1.3					4.70	0.9325	0.1832	<0.001
5.3.4					6.92	0.0008	0.048	0.17
5.3.8					6.42	0.0215	0.2815	0.0666
5.3.10					6.58	0.0039	0.138	0.062
5.3.18					5.75	0.149	0.8308	0.0072
5.3.24					7.42	0.0004	0.0181	0.5874
8.6.1					4.92	0.7152	0.3863	0.0002
8.6.16					5.75	0.0977	0.8086	0.002
9.12.4					6.25	0.0166	0.3233	0.0183
9.12.8					5.92	0.057	0.6235	0.0044
OSU 5630					7.59	<0.001	0.0002	0.6492
OSU 6229					4.91	0.6124	0.2077	<0.001
OSU 6230					5.21	0.2873	0.4821	<0.001
OSU 6241					6.17	0.0047	0.2826	0.002
M0162					6.36	0.0905	0.4465	0.1468
OR 91G					7.84	<0.001	<0.001	
G122					4.64		0.0778	<0.0001
NY6020-5					5.59	0.0778		<0.0001

<sup>z</sup> Scale of 1-9 where 1=no infection and 9=total plant collapse (Teran *et al.*, 2006 scale).

<sup>y</sup> Probability of LS mean of experimental line equal to LS mean of the check

<sup>x</sup> G122 and NY60205-5 are partially resistant, OR 91G is susceptible

Table A11. Straw test least squared (LS) means for spring 2009 families of NY6020-5 x OR 91G and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold. (Teran scale<sup>z</sup>)

Line	SS18	Phas	Straw Test LS Mean	Check <sup>x</sup>		
				G122	NY6020-5	OR 91G
8.3.55	-	T	4.00	0.8823 <sup>y</sup>	0.7467	0.0027
8.3.41	+	T	4.28	0.8505	0.9893	0.0074
8.3.56	-	T	4.33	0.7981	0.9356	0.0090
8.3.60	-	S	4.33	0.7981	0.9356	0.0090
8.3.67	+	S	4.33	0.7981	0.9356	0.0090
8.3.2	+	S	4.50	0.6473	0.7774	0.0158
8.3.75	+	S	4.56	0.5997	0.7264	0.0188
8.3.26	+	S	4.61	0.5538	0.6765	0.0224
8.3.38	+	S	4.67	0.5097	0.6280	0.0266
8.3.57	+	S	4.67	0.5097	0.6280	0.0266
8.3.1	+	T	4.72	0.4676	0.5811	0.0315
8.3.35	+	S	4.72	0.4676	0.5811	0.0315
8.3.11	+	S	4.78	0.4274	0.5360	0.0371
8.3.10	+	S	4.83	0.3894	0.4926	0.0436
8.3.99	+	S	4.83	0.3894	0.4926	0.0436
8.3.76	+	S	4.94	0.3198	0.4120	0.0593
8.3.34	-	T	5.00	0.2883	0.3748	0.0689
8.3.65	+	S	5.00	0.2883	0.3748	0.0689
8.3.82	+	T	5.02	0.3329	0.4165	0.1079
8.3.88	+	T	5.06	0.2589	0.3397	0.0797
8.3.97	+	S	5.10	0.2900	0.3668	0.1289
8.3.24	+	T	5.11	0.2317	0.3069	0.0918
8.3.22	+	S	5.28	0.1626	0.2215	0.1372
8.3.31	+	S	5.33	0.1434	0.1972	0.1558
8.3.59	+	T	5.33	0.1434	0.1972	0.1558
8.3.74	+	S	5.33	0.1434	0.1972	0.1558
8.3.93	-	T	5.35	0.1844	0.2412	0.2114
8.3.89	+	S	5.47	0.1031	0.1452	0.2105
8.3.66	+	T	5.67	0.0625	0.0910	0.3087
8.3.90	+	S	5.83	0.0392	0.0588	0.4140
8.3.61	+	S	5.89	0.0333	0.0505	0.4536
8.3.83	-	T	5.89	0.0333	0.0505	0.4536
8.3.92	+	S	5.89	0.0333	0.0505	0.4536

Table A11. (Continued) Straw test least squared (LS) means for spring 2009 families of NY6020-5 x OR 91G and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold. (Teran scale<sup>z</sup>)

Line	SS18	Phas	Straw Test LS Mean	Check <sup>x</sup>		
				G122	NY6020-5	OR 91G
8.3.80	-	S	6.11	0.0168	0.0264	0.6308
8.3.4	-	S	6.17	0.0140	0.0222	0.6793
8.3.78	+	T	6.22	0.0116	0.0186	0.7293
8.3.3	-	S	6.22	0.0116	0.0186	0.7293
8.3.53	+	S	6.22	0.0116	0.0186	0.7293
8.3.72	+	S	6.22	0.0116	0.0186	0.7293
8.3.45	-	S	6.28	0.0096	0.0156	0.7804
8.3.13	+	S	6.33	0.0079	0.0130	0.8325
8.3.98	+	T	6.50	0.0044	0.0073	0.9923
8.3.5	-	T	6.62	0.0075	0.0117	0.9072
8.3.49	+	T	6.64	0.0025	0.0044	0.8686
8.3.79	-	S	6.72	0.0019	0.0033	0.7952
8.3.47	+	S	6.83	0.0012	0.0021	0.6935
8.3.40	-	T	6.89	0.0009	0.0017	0.6445
8.3.73	+	T	7.33	0.0001	0.0003	0.3179
OSU 5613			6.76	0.0016	0.0029	0.7623
OSU 5630			6.94	0.0008	0.0014	0.5970
OSU 6229			4.32	0.8086	0.9463	0.0087
OSU 6230			4.39	0.7467	0.8823	0.0109
OSU 6241			4.81	0.4018	0.5069	0.0413
Ex Rico			5.76	0.0484	0.0717	0.3649
M0162			4.94	0.3198	0.4120	0.0593
OR 91G			6.51	0.0042	0.0071	
G122			4.12		0.8611	0.0042
NY6020-5			4.27	0.8611		

<sup>z</sup> Scale of 1-9 where 1=no infection and 9=total plant collapse (Teran *et al.*, 2006 scale).

<sup>y</sup> Probability of LS mean of experimental line equal to LS mean of the check

<sup>x</sup> G122 and NY6020-5 are partially resistant, OR 91G is susceptible

Table A12. Straw test least squared (LS) means for spring 2009 families of NY6020-5 x OSU 5613 and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold. (Teran scale<sup>z</sup>)

Line	SS18	Phas	Straw Test LS Mean	Check <sup>x</sup>		
				G122	NY6020-5	OR 91G
14.3.36	+	T	4.14	0.9839 <sup>y</sup>	0.8770	0.0045
14.3.42	+	S	4.22	0.9036	0.9571	0.0061
14.3.83	-	T	4.27	0.9004	0.9986	0.0568
14.3.1	+	T	4.33	0.7981	0.9356	0.0090
14.3.47	+	S	4.44	0.6963	0.8295	0.0131
14.3.18	+	T	4.50	0.6473	0.7774	0.0158
14.3.52	+	S	4.61	0.5538	0.6765	0.0224
14.3.4	+	T	4.64	0.5315	0.6521	0.0245
14.3.26	+	T	4.94	0.3198	0.4120	0.0593
14.3.75	+	T	5.02	0.3329	0.4165	0.1079
14.3.9	+	T	5.11	0.2317	0.3096	0.0918
14.3.5	+	T	5.31	0.1527	0.2091	0.1463
14.3.16	+	T	5.33	0.1434	0.1972	0.1558
14.3.7	+	T	5.33	0.1434	0.1972	0.1558
14.3.55	+	S	5.39	0.1260	0.1750	0.1762
14.3.46	-	T	5.44	0.1103	0.1547	0.1985
14.3.21	-	T	5.50	0.0962	0.1362	0.2229
14.3.82	+	T	5.50	0.0962	0.1362	0.2229
14.3.19	+	T	5.60	0.1105	0.1496	0.3269
14.3.37	+	T	5.61	0.0724	0.1045	0.2780
14.3.8	+	S	5.72	0.0537	0.0790	0.3417
14.3.63	-	T	5.83	0.0392	0.0588	0.4141
14.3.62	+	S	5.89	0.0333	0.0505	0.4536
14.3.66	-	T	5.89	0.0333	0.0505	0.4536
14.3.60	+	S	6.00	0.0238	0.0368	0.5385
14.3.12	+	T	6.06	0.0200	0.0312	0.5838
14.3.23	+	S	6.11	0.0168	0.0264	0.6308
14.3.81	-	S	6.33	0.0079	0.0130	0.8325
14.3.22	+	S	6.37	0.0159	0.0239	0.8783
14.3.2	+	S	6.44	0.0053	0.0089	0.9387
14.3.20	+	S	6.78	0.0015	0.0026	0.7438
14.3.68	-	S	6.78	0.0015	0.0026	0.7438
14.3.84	-	T	6.78	0.0015	0.0026	0.7438



Table A12. Straw test least squared (LS) means for spring 2009 families of NY6020-5 x OSU 5613 and standard check varieties of *Phaseolus vulgaris* screening for resistance to white mold. (Teran scale<sup>z</sup>)

Line	SS18	Phas	Straw Test LS Mean	Check <sup>x</sup>		
				G122	NY6020-5	OR 91G
14.3.50	+	S	6.80	0.0014	0.0024	0.7235
14.3.17	-	S	6.83	0.0012	0.0021	0.6935
14.3.45	+	S	6.89	0.0009	0.0017	0.6445
14.3.14	+	T	6.97	0.0007	0.0012	0.5739
14.3.65	-	S	6.97	0.0007	0.0012	0.5739
14.3.74	+	S	6.98	0.0023	0.0037	0.6124
14.3.39	-	S	7.00	0.0006	0.0011	0.5512
14.3.11	-	S	7.06	0.0005	0.0009	0.5073
14.3.61	-	S	7.06	0.0005	0.0009	0.5073
14.3.40	-	S	7.11	0.0004	0.0007	0.4652
14.3.32	-	S	7.27	0.0008	0.0013	0.4111
14.3.69	-	S	7.56	<0.0001	<0.0001	0.2053
14.3.85	-	T	7.56	<0.0001	<0.0001	0.2053
OSU 5613			6.76	0.0016	0.0029	0.7623
OSU 5630			6.94	0.0008	0.0014	0.5970
OSU 6229			4.32	0.8086	0.9463	0.0087
OSU 6230			4.39	0.7467	0.8823	0.0109
OSU 6241			4.81	0.4018	0.5069	0.0413
Ex Rico			5.76	0.0484	0.0717	0.3649
M0162			4.94	0.3198	0.4120	0.0593
OR 91G			6.51	0.0042	0.0071	
G122			4.12		0.8611	0.0042
NY6020-5			4.27	0.8611		

<sup>z</sup> Scale of 1-9 where 1=no infection and 9=total plant collapse (Teran *et al.*, 2006 scale).

<sup>y</sup> Probability of LS mean of experimental line equal to LS mean of the check

<sup>x</sup> G122 and NY60205-5 are partially resistant, OR 91G is susceptible