

Progress in transferring *Sclerotinia* resistance from runner bean to common bean

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ABSTRACT:

Our overall goal is to develop white mold resistant dry and snap beans using partially resistant accessions of *Phaseolus coccineus* as a source. Resistance is quantitatively inherited within *P. coccineus*, while there appears to be a qualitative factor for resistance in interspecific crosses to *P. vulgaris*. This year, we focused on developing backcross inbred populations for several different interspecific cross combinations. The populations were chosen from a much larger set of initial crosses based on cross compatibility of the parents and fertility of the progeny. Backcross populations will be evaluated for resistance and for appropriate molecular markers. Initially, the population (OR91G x PI 255956) BC₂F₂ has been evaluated for *Sclerotinia* resistance in the greenhouse using the straw test. Lines were evaluated four times at approximately one week intervals. The population showed a bimodal distribution that is associated with whether the infection passes through a node. We find that with *P. coccineus* derived materials, the standard eight day period used for evaluating common bean with the straw test is inadequate, with at least a two-week interval needed for disease development after inoculation.

INTRODUCTION:

•What limited genetic variability common bean (*Phaseolus vulgaris*) has for white mold (*Sclerotinia sclerotiorum*) resistance is quantitatively inherited with low to moderate heritability (Fuller et al., 1984, Kolkman and Kelly, 1999, Miklas & Grafton, 1992). QTL for resistance have been identified in the common bean accessions Buns1, G 122, NY 6020-4, PC 50. The QTL account for 12 - 38% of the genetic variation for resistance in various cross combinations (Park et al. 2001, Miklas et al., 2001, Kolkman & Kelly, 2003, Miklas et al., 2003).

•The Scarlet Runner Bean (*Phaseolus coccineus*) is the best source identified to date for resistance to white mold (Abawi et al., 1978, Adams et al., 1973, Gilmore and Myers 2000, Gilmore et al., 2002, Hunter et al., 1982, Schwartz et al., 2004).

•Previous researchers have partially transferred resistance, but the resulting germplasm appears not to have been widely used to develop elite common bean cultivars. A process is needed that moves complete resistance without linkage drag bringing along deleterious factors associated with interspecific hybridization.

•By the use of molecular tools that were not available to previous researchers, we will develop an understanding of the genetic architecture of white mold resistance and to transfer it into a common bean background.

OBJECTIVES:

To develop white mold resistant dry and snap bean (*Phaseolus vulgaris*) germplasm and cultivars by:

•Transferring resistance from *P. coccineus* into *P. vulgaris* using advanced backcross QTL analysis (Tanksley, 1996).

•Determining if markers associated with white mold resistance in the Woven Pole x PI 255956 are present in the interspecific backcrosses, and can be used to transfer resistance into common bean.

MATERIALS AND METHODS:

•Preliminary work was done with a 91G x PI 255956 cross. In the BC₂F₂ generation, the material was evaluated for *Sclerotinia* resistance in the greenhouse after straw test inoculation approximately once per week for four weeks. Disease severity was rated on a 1-9 scale with 1 being disease-free, and 9 being total plant death. Resistance was measured over four readings and area under the disease progress curve (AUDPC) was calculated. AUDPC integrates disease severity over time.

•We have selected several additional BC₂F₂ combinations that have high compatibility and produce sufficient quantities of seed (Table 1). Beginning with the first backcross, we attempted to get at least one seed on each of 50 plants, with the same being done with the second backcross. DNA isolation will begin in the BC₂F₂ and lines will be selfed from that generation 3-4 times. The 91G x PI 255956 population has been advanced to the BC₂F₄.

•We have selected several additional F₁ combinations that have high compatibility and produce sufficient quantities of seed (Table 1).

•The recurrent parents chosen are:

- MO 162 – Yellow seeded line developed by H. Lamprecht from interspecific crosses with *P. coccineus*.
- PC 50 – Caribbean red mottle accession with QTL for white mold resistance.
- Spinel – Great northern cultivar that despite a bush growth habit, is highly susceptible to WM.
- 5-593 – Small black seeded bush genetic stocks line; susceptible to WM.
- OR 91G – bush blue lake green bean with high degree of WM susceptibility.
- G122-3 Cranberry type dry bean accession with QTL for WM resistance.

•These have been advanced to the BC₁ generation using the protocol shown in figure 1. The next round of backcrosses is currently in progress.

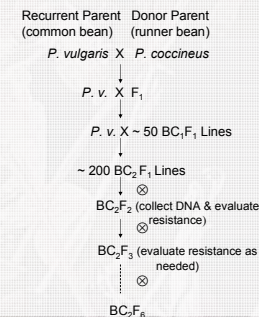
Table 1. Number of seed obtained from backcrosses between common bean and runner bean parents used to create backcross-inbred populations for advanced backcross QTL analysis.

P. coccineus accession	Recurrent parent (P. vulgaris)					
	MO 162	PC 50	Spinel	5-593	OR 91G	G122-3
PI 255956	0	0	0	0	62 ^a	0
PI317551	12	0	0	7	8	24
PI433245	0	10	0	0	7	0
PI433246B	8	13	0	0	0	0
PI433247A	0	5	0	0	0	26
PI433247B	0	22	0	0	0	0
PI433251A	0	29	0	51 ^b	47	38
PI433251B	99 ^a	82 ^a	53 ^a	0	70 ^a	41 ^a
PI 58554B	0	57	0	0	0	39 ^a

^aIn BC₂F₂ generation; all other crosses in BC₂F₁.

^bIndicates crosses with sufficient seed (or expected to soon have sufficient seed) to be carried on to the next generation.

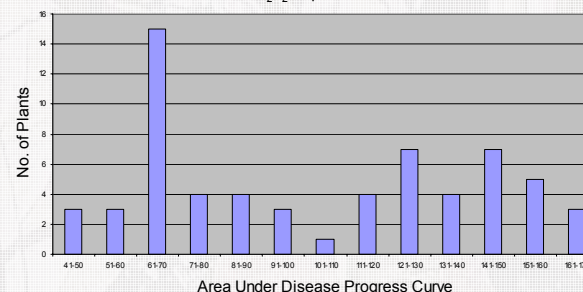
Figure 1: Advanced Backcross QTL Analysis



RESULTS AND DISCUSSION:

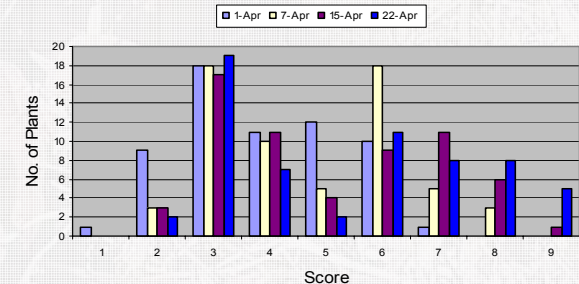
Area under the disease progress curve was plotted from the data obtained from evaluation of the OR91G x PI 255956 BC₂F₂ for white mold resistance (Figure 2). AUDPC gives a good summarization of the multiple reading data, and takes into account the rate of disease development as well as the severity.

Figure 2: Sclerotinia Area Under Disease Progress Curve for 91G/PI255956 E BC₂F₂ Population



P. coccineus derived material requires a longer timeframe for evaluation, since infection does not progress as rapidly as with common bean. Figure 3 shows a shifting distribution of average disease ratings for the population over time.

Figure 3: Sclerotinia Score for 91G/PI255956 E BC₂F₂ Population



Both sets of graphs show a bimodal distribution. The shape of the distribution is influenced by the barrier that a node creates to the rate of growth of *Sclerotinia*. In particular, partially resistant lines tend to limit the infection at the node.

Distributions are skewed toward resistance, although this is less apparent over time. Table 2 shows the number of resistant versus susceptible observations for each evaluation date.

Table 2: Numbers of resistant versus susceptible observations, by date.

	1-Apr	7-Apr	15-Apr	22-Apr
Resistant (WM score <= 4)	39	31	31	28
Susceptible (WM score > 4)	23	31	31	34

In earlier readings, our data would support the hypothesis of a dominant gene with major effect, but this is less apparent as the disease progresses. Implications are that disease ratings should be done after allowing longer time for disease progression, and that although there are two reports of interspecific resistance behaving as a single dominant gene (Abawi et al., 1978, Schwartz et al., 2004), resistance is best manipulated as a quantitative trait.

Our plan, based on advanced backcross QTL analysis (Tanksley and Nelson, 1996), requires that our analysis of QTL is delayed until the BC₂F₂ or later generations. DNA will be isolated from young leaf tissue of single plants as described by Kobayshi et al. (2000), as modified for beans (Myers et al. 2004). At the same time that molecular marker studies commence, lines will be advanced to homozygosity by single seed descent and single plant selection to produce introgression lines and germplasm for release.

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