

INTROGRESSION AND PYRAMIDING OF WHITE MOLD RESISTANCE from the SECONDARY GENE POOL OF DRY BEAN

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ABSTRACT:

OT21 *P. coccineus* from Spain evaluated in greenhouse in Idaho using the petiole test only ZJ 1198 (with disease score 3.5) and P1A-0669 (with score 3.4) had a high level of white mold resistance. Of ~400 interspecific breeding lines from crosses of ICA Pijao with *P. coccineus*, *P. costaricensis*, and *P. polyanthus* sequentially evaluated in greenhouse in Idaho using the petiole test and in Colorado using the straw test, and in the field in Washington thus far four (IS115, IS198, WM32, and WM60) entries, with moderate to high resistance were identified. A single dominant gene controlled resistance in *P. coccineus* PI 433246 and PI 439534 in greenhouse in Colorado. A total of 463 F₂ from two single crosses, 2029 F₂ from two first-backcrosses, and 318 F₂ from two second-backcrosses of susceptible Othello and UI 320 with PI 433246 and PI 439534 were produced in greenhouse in Idaho. Four single crosses (MO162/19365-25, ICA Bunsu/G122, 19365-25/BelDakMi-RMR-20, and USPT-CBB-1/CORNN601) and their two double-crosses involving five different sources of resistance were made in Idaho. Inheritance of resistance will be repeated in greenhouse in Idaho. All interspecific breeding lines involving ICA Pijao will be evaluated in greenhouse in Idaho and Colorado and in the field in Idaho and Washington. The F₂ and F₃ from new interspecific crosses and backcrosses will be advanced to the next generation in greenhouse in Idaho. Recurrent selection will be initiated in two double-crosses in Idaho.

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INTRODUCTION

White mold is the most devastating disease of dry bean (*Phaseolus vulgaris* L.) in the U.S. For every percent unit increase in white mold incidence, seed yield was reduced by an average of 12 kg ha⁻¹ in pinto and by 23 kg ha⁻¹ in navy bean even in nonirrigated conditions in North Dakota (del Rio et al., 2004). The fungus produces sclerotia that survive in soil for years and spread from field to field by internally infected seeds, sclerotia mixed with seed, contaminated soil on equipment, and irrigation runoff water, in addition to wind-blown ascospores. Adequate control of white mold, using disease management and fungicides, has been difficult to achieve (del Rio et al., 2004).

Dry bean germplasm with only partial physiological resistance have been reported (Gratton et al., 2002; Steadman et al., 2002). The highest levels of resistance occur in the common bean's secondary gene pool such as *P. coccineus* L. (Gilmore et al., 2002). Resistance in dry bean is quantitatively inherited with low (Park et al., 2001), or moderate to high (Kolkman and Kelly, 2003; Miklas et al., 2004), heritability. Abawi et al. (1978) reported a single dominant allele controlling resistance in a *P. vulgaris* x *P. coccineus* population. Park et al. (2001) reported random amplified polymorphic DNA (RAPD) markers linked with as many as nine quantitative trait loci (QTL) in dry bean. Miklas et al. (2001) reported one amplified fragment length polymorphism (AFLP) marker linked with a QTL for the greenhouse straw test in the A 55/G 122 dry bean population. The same and one additional AFLP linked with a QTL for physiological resistance in the field, and another AFLP linked with a QTL responsible for canopy porosity were also identified. In addition to G 122, 'ICA Bunsu' (Kolkman and Kelly, 2003), 'PC 50' (Park et al., 2001), and NY6020-4 (Miklas et al., 2003) have major QTL for resistance. But recently developed pinto AN 37, 'Chase', and CO 75944 have demonstrated limited effectiveness against white mold.

The major hypotheses and questions to be answered through this research are the following:

- Can the high level of resistance from *P. coccineus* and other secondary gene pool species be introgressed into common bean?
- Is resistance in the secondary gene pool species heritable, if so which alleles and QTL control it? Furthermore, can they be tagged and mapped for molecular marker assisted selection?
- Are alleles and QTL controlling resistance in the greenhouse the same or different from those imparting resistance in the field environments?
- Is the resistance from the secondary gene pool species effective and stable across different field and greenhouse environments?
- Is there any association between resistance introgressed from the secondary gene pool species and growth habit, maturity, and plant age?
- Is resistance in the secondary gene pool complementary and additive to that found in common bean?
- Is it possible to develop early, as well as late maturing, high yielding, equally white mold resistant pinto bean cultivars with indeterminate upright Type II and prostrate Type III growth habits?

GOALS and OBJECTIVES:

Our goal is to introgress and pyramid high levels of white mold resistance from the primary and secondary gene pools of common bean to provide a low input, sustainable, and ecosystem-friendly solution to this most devastating disease in the U.S. Our specific objectives are to:

- Sequentially screen previously developed interspecific breeding lines from crosses of 'ICA Pijao' with *P. coccineus*, *P. costaricensis*, and *P. polyanthus* in greenhouse using the petiole (Idaho) and straw tests (Colorado), and in the field (Idaho and Washington).
- Periodically screen new *P. coccineus* accessions in the greenhouse for resistance.
- Introgress resistance from *P. coccineus* accessions PI 433246 and PI 439534.
- Determine inheritance and identify and tag resistance in PI 433246 and PI 439534.
- Pyramid alleles and QTL imparting resistance from the primary and secondary gene pools of dry bean.

Resulting white mold resistant genotypes will be used in subsequent genetics and breeding studies, and for development of improved dry bean cultivars and germplasm.

This research will permit for the first time a comparison and identification of white mold resistance from all the three species in the common bean's secondary gene pool and facilitate broadening of the genetic base of dry bean cultivars for resistance. The uniqueness of this project is that it encourages inter-state, inter-institutional, and interdisciplinary collaboration, integration of field and greenhouse screening methods, and uses both conventional and molecular techniques.

MATERIALS AND METHODS:

Screening of New *P. coccineus* Accessions. Twenty-one *P. coccineus* accessions introduced from Spain were evaluated for white mold in greenhouse in Idaho using the petiole test (del Rio et al., 2000) in 2004. An average of six plants per genotype were screened. Of 21 genotypes, ZJ 1198 (with disease score 3.5) and P1A-0669 (with score 3.4) had a high level of resistance. It will be worth determining their response to long photoperiod and white mold in other environments before using in breeding programs.

Screening of Previously Developed Interspecific Breeding Lines. Approximately 400 interspecific breeding lines derived from crosses of ICA Pijao with *P. coccineus*, *P. costaricensis*, and *P. polyanthus* along with ICA Pijao, and known white mold susceptible (e.g., Bill Z, Othello, and UI 114) and resistant (e.g., 92 BG-7, B7354), Bunsu, CORN 601, G 122, 19365-25, MO 162, and NY6020-4) genotypes were evaluated in greenhouse in Idaho using the petiole test. An average of six plants per breeding line were screened. Subsequently, approximately 150 interspecific breeding lines were evaluated in greenhouse using the straw test (Petzoldt and Dickson, 1996) in Colorado. An average of 10 plants per breeding line were screened. Of these, 19 were evaluated in the field in Washington. Each plot consisted of a single row 10 ft long with three replicates. White mold pressure in the greenhouse in Idaho (disease scores ranged from 1.0 to 9.0, where 1 = no visible white mold symptoms on stem and pods, and 9 = severely damaged) and Colorado (disease scores ranged from 1.7 to 9.0), and in the field in Washington (disease scores ranged from 2.7 to 9.0) was very severe. Reaction to white mold was recorded on a single plant basis in the greenhouse, and on a plot-basis in the field. Thus, four interspecific breeding lines (IS115, IS198, WM32, and WM60) with moderate to high resistance were identified for seed increase and further evaluation (Table 1).

Inheritance of White Mold Resistance in *P. coccineus*. White mold susceptible pinto Othello and UI 320 and resistant *P. coccineus* PI 433246 and PI 439534 and their F₁, F₂, and backcrosses were evaluated for white mold in greenhouse in Colorado using the straw test to determine inheritance of resistance (Table 2). A single dominant gene controlled resistance in both PI 433246 and PI 439534 (Schwartz et al., 2004).

Development of New Interspecific Breeding Lines. A total of 463 F₂ from two single-crosses, 2029 F₂ from two first-backcrosses, and 318 F₂ from two second-backcrosses of white mold susceptible pinto Othello and UI 320 with resistant *P. coccineus* PI 433246 and PI 439534 were produced in greenhouse in Idaho (Table 3).

Table 1. Mean white mold scores for four breeding lines derived from crosses of ICA Pijao with *Phaseolus* species in the secondary gene pool screened in greenhouse in Idaho (petiole test) and Colorado (straw test) and in the field in Washington in 2004.

Identification	Greenhouse-Colorado*	Greenhouse-Idaho	Field-Washington†
IS 115	-	3.5	5.7
IS 198	-	1.7	4.3
WM 32	3.0	1.0	5.7
WM 60	6.2	2.8	2.7
Range	1.7-9.0	1.0-9.0	2.7-9.0
19365-25	5.2	1.0	9.0
Othello (Susceptible)	8.7	3.9	8.7

*Scored on a 1 to 9 scale where 1=symptomatic, and 9=severely diseased.

†Courtesy of Dr. P.N. Miklas.

Table 2. White mold reaction of Othello and UI 320 and *P. coccineus* PI 433246 and PI 439534, and their F₁, F₂, and backcrosses evaluated in the greenhouse using the straw test in Colorado in 2004.

Genotype	White mold reaction*		No. plants	Ratio	P value-
	Range	Mean			
Othello	3-9	7.91	33	---	0.7558
PI 433246	1-9	3.38	21	---	
Othello/PI 433246	1-7	4.00	16	---	
F ₁	1-9	4.74	31	24R:7S	0.7558
Othello/PI 433246	3-9	7.35	34	7R:27S	
UI 320	1-9	3.22	36	---	
PI 439534	1-5	2.05	38	---	0.8209
UI 320/PI 439534	1-3	2.60	10	---	
F ₁	1-9	4.23	26	20R:6S	
UI 320/PI 439534	1-9	3.13	31	27R:1S	

*Scored on a 1 to 9 scale where 1= symptomless, and 9= severely diseased.

†Three plants with a disease score of 7 probably were the female Othello self, and not hybrids!

Table 3. Number of F₂ and F₃ plants produced from new interspecific crosses between selected white mold resistant *P. coccineus* and susceptible pinto bean cultivars Othello and UI 320 in 2004.

Interspecific crosses	No. of plants produced
Othello/PI 433246	196 F ₂
Othello/PI 433246	495 F ₃
Othello/Othello/Othello/PI 433246	151 F ₃
UI 320/PI 439534	267 F ₂
UI 320/UI 320/PI 439534	1,534 F ₃
UI 320/UI 320/UI 320/PI 439534	167 F ₃
Total	2810

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