

Inheritance of White Mold Resistance in the Interspecific Crosses of Pinto Cultivars Othello and UI 320 and *Phaseolus coccineus* L. Accessions PI 433246 and PI 439534

Howard F. Schwartz¹, K. Otto¹, Henry Terán², Margarita Lema² and Shree P. Singh²

¹Colorado State University, Fort Collins, CO 80523; and ²University of Idaho, Kimberly, ID 83341

Introduction

White mold (caused by *Sclerotinia sclerotiorum* Lib de Bary) is an endemic and one of the most devastating diseases of the common bean in the U.S. Chemical control is often inadequate, and it increases production cost for growers and minimizes their competitive edge in the national and international market. Use of resistant cultivars is pivotal to any effective and economical long-term strategy to control white mold. However, only low to moderate level of resistance to white mold exists in the common bean. On the other hand, some accessions of *Phaseolus coccineus* L. are known to possess much higher level of resistance than the common bean (Gilmore et al., 2002). White mold resistance from *P. coccineus* has been introgressed into common bean (Miklas et al., 1998). Although comparative data is not available, there is a general feeling that the level of white mold resistance introgressed in common bean, in general, is lower than that of *P. coccineus*. Our interest in *P. coccineus* resistance for white mold was rejuvenated because of the USDA-Sclerotinia Initiative. As part of our project we screened all *P. coccineus* accessions that were reported to be resistant to white mold by Gilmore et al. (2002). Moreover, we selected *P. coccineus* accessions PI 433246 and PI 439534 to study the inheritance and introgress their white mold resistance into dry bean.

Materials and Methods

Pinto bean cultivars Othello and UI 320 were selected for the inheritance study. Both Othello and UI 320 are early maturity in the Western U.S. Moreover, Othello is widely adapted despite its susceptibility to anthracnose, common bacterial blight, rust, and white mold. On the other hand, UI 320 is resistant (*I* gene) to bean common mosaic virus (BCMV) and some races of the pathogen causing rust. Othello was crossed with PI 433246, and the resulting interspecific F₁ was backcrossed on to Othello and allowed to produce F₂ seed. Similarly, UI 320 was crossed with PI 439543. The F₁ was backcrossed on to UI 320 and allowed to produce F₂ seed. The four parents, two F₁, two F₂, and two backcrosses were grown in the greenhouse, and inoculated with *S. sclerotiorum* isolate, using the straw-test at the Colorado State University Fort Collins, Colorado (Myers et al., 1999; Petzoldt and Dickson, 1996) and cut-stem branch test at the University of Idaho Kimberly, Idaho (Terán et al., 2006). Individual plants were rated for their reaction to white mold. The frequency distribution and mean disease scores for each genotype were determined. Also, the frequencies were grouped into resistant (receiving scores of 1 to 5) and susceptible (6 to 9), and subjected to the χ^2 test. The data from both locations were similar, hence a pooled analysis was performed.

Table 1. White mold reaction of pinto bean cultivars Othello and UI 320 and *Phaseolus coccineus* L. accessions PI 433246 and PI 439534, and their F₁, F₂, and backcrosses evaluated in the greenhouse at Fort Collins, Colorado in 2004 using the straw-test, and Kimberly, Idaho using the cut-branch test in 2005.

Genotype	White Mold Reaction [†]		No. Plants	Ratio	P value
	Range	Mean			
Othello	3-9	8.45	39		
PI 433246	1-7	3.79	18		
Othello / PI 433246					
F ₁	1-7	3.67	15		
F ₂	1-9	4.68	46	36R:10S	0.61
Othello // Othello / PI 433246	3-9	7.57	28	5R:23S	
UI 320	1-9	5.20	42		
PI 439534	1-5	2.80	44		
UI 320 / PI 439534					
F ₁	1-3	2.60	10		
F ₂	1-9	4.31	41	32R:9S	0.63
UI 320 / UI 320 / PI 439534	1-9	3.07	28	27R:1S	

[†] Scored on a 1 to 9 scale, where 1=symptomless, and 9= severely diseased.

Results and Discussion

Othello with mean white mold score of 8.45 was the only susceptible parental genotype. To our pleasant surprise UI 320 with a mean disease score of 5.20 was intermediate (Table 1). Nonetheless, both Othello and UI 320 had a wide range. For example, out of 39 plants scored for Othello, six showed a resistant reaction. Similarly, three out of 42 plants for UI 320 were susceptible. Both *P. coccineus* accessions were resistant to white mold. Similarly, the two interspecific F₁ hybrids had a resistance reaction suggesting that the resistance to white mold in the two accessions is controlled by dominant allele(s). Furthermore, the F₂ of Othello/PI 433246 segregated into 36 resistant to 10 susceptible, giving a good fit to 3 resistant to 1 susceptible ratio ($P=0.61$). This suggested that the white mold resistance in PI 433246 is controlled by a single dominant allele. However, in the backcross to Othello, one would have expected a 1 resistant to 1 susceptible ratio. Instead, there was an excess of the susceptible plants. This might have occurred because of an excess of Othello gametes and/or the tendency of the interspecific hybrid to revert to the parental genotype, especially when backcrossed on to common bean.

Out of 41 F₂ plants of UI 320 / PI 439534, nine were susceptible to white mold, and all others had a resistant reaction. Thus, giving a good fit to 3 resistant to 1 susceptible ratio, indicating that the resistance in PI 439534 was also controlled by a single dominant allele. But, only one out of 28 plants in the backcross to UI 320 was susceptible, whereas one would have either expected a 1 resistant to 1 susceptible ratio supporting the F₂ segregation, or else all resistant if the same dominant allele controlled white mold resistance in both UI 320 and PI 439534. Abawi et al. (1978) also reported a single dominant allele controlling resistance to white mold in a *P. vulgaris* / *P. coccineus* population.



References

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