# Sources of Resistance to *Colletotrichum lindemuthianum* in the Secondary Gene Pool of *Phaseolus vulgaris* and in Crosses of Primary and Secondary Gene Pools

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**ABSTRACT**

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Use of genetic resistance is the most practical and economic way to manage anthracnose of common bean. *Colletotrichum lindemuthianum,* the causal agent of bean anthracnose, is a highly variabile pathogen, and there are no host resistance genes that are effective against all known races of the pathogen. To diversify sources of resistance, we screened the core collection of the secondary gene pool of *Phaseolus* spp. and interspecific lines derived from simple and complex crosses of primary and secondary genotypes for their resistance to anthracnose. High levels of resistance were observed in the secondary gene pool. None of the 162 accessions tested was susceptible to *C. lindemuthianum*. Of the two species composing the secondary gene pool, *P. polyanthus* displayed higher levels of resistance than *P. coccineus*, and all accessions tested were resistant. The response of *P. coccineus* was more variable, with six genotypes showing an intermediate reaction. Among the 75 lines from interspecific crosses, 49 were resistant to the three races (races 6, 15, and 3481) used in this study, and higher levels of resistance were found in lines that had *P. polyanthus* as one of the parents in the crosses than in the lines derived from *P. coccineus*. These lines constitute a valuable source of resistance and may aid in the development of stable resistance to anthracnose.

Bean anthracnose, caused by *Colletotrichum lindemuthianum* (Sacc. & Magnus) Briosi & Cav., is one of the major diseases of common bean, *Phaseolus vulgaris* L. (18). The disease is particularly important in relatively cool, wet production areas of tropical and temperate regions (18). Crop losses can be severe or total (9), especially when susceptible cultivars are grown in an environment that is conducive to the disease (17,23).

Several strategies can be used to manage anthracnose, but planting genetically resistant cultivars is most effective, least expensive, and easiest for farmers to adopt (17,23). The main drawback to resistant cultivars is the possible breakdown of resistance caused by the adaptation of the pathogen to host resistance (8,13). *C. lindemuthianum* is a highly variable pathogen (1,11,18,19,24,26), and there are no resistance genes that are effective against all known races of this pathogen. One way of making the resistance more stable is to pyramid or incorporate several resistance genes into a single line. This requires a thorough understanding of the population structure of the pathogen, and the nature and effectiveness of the resistance genes. The effectiveness of available resistance genes in *P. vulgaris* rarely has been tested against a large range of pathotypes of the pathogen; therefore, several of the cultivars previously described as resistant were later found to be highly susceptible elsewhere (11,14,27). For example, cultivars that carry the *ARE* or *A* resistance genes have failed in North America (11,12,16,17,27). The protection conferred by single genes is potentially short term; therefore, a need for diverse sources of genetic resistance is widely recognized among bean breeders.

Genetic resistance to some pathotypes of *C. lindemuthianum* is conferred by different single, duplicate, or complementary dominant genes (23,28), and is available in numerous germplasm accessions (6,17,23,25). The available resistance is not effective against all known races from the same or different regions. For example, some of the well-known resistance genes that are effective in Europe (*Co-2, Co-3, Co-4,* and *Co-5*) (7,11) are not effective in Colombia, Brazil, Costa Rica, and Mexico (11,12,14, 27). Although the cultivar G2333, which has three resistance genes (*Co-42, Co-5,* and *Co-7*), is resistant to more than 90% of the races that have been described, it is susceptible to some races (e.g., 3481, 3545, 3977, and 3933) from Costa Rica, Mexico, and Argentina (4). The breakdown of resistance in G2333, once thought to be effective against all races, reflects on the need for diversification of resistance genes.

The secondary gene pool of *P. vulgaris,* which includes the species *P. coccineus* and *P. polyanthus,* has long been known to be a source of interesting agronomic traits (20). There is little or no information on the reaction of the secondary gene pool to *C. lindemuthianum,* although these species have resistance to Ascochyta blight (*Phoma exigua* var. *diversispora*), angular leaf spot (*Phaeoisariopsis griseola*), white mold (*Sclerotinia sclerotiorum*), *Bean golden mosaic virus,* and drought (2,10,20,21). This article reports the results obtained from screening accessions of the secondary gene pool (*Phaseolus coccineus* and *P. polyanthus*) of genus *Phaseolus* and interspecific lines derived from simple and complex crosses of primary and secondary gene pool accessions for their reaction to Andean and Mesoamerican races of *C. lindemuthianum*.

## MATERIALS AND METHODS

**Germplasm.** Accessions of the secondary gene pool of genus *Phaseolus*, *P. vulgaris, P. polyanthus,* and *P. coccineus,* were obtained from the CIAT germplasm bank. A total of 162 accessions (93 *P. coccineus* and 69 *P. polyanthus*) constituted the core collection (Table 1). These were screened for resistance to *C. lindemuthianum* in greenhouse and screenhouse trials. Accessions were chosen to reflect climatic and geographic variability of the

**Table 1.** Geographical origin and number of *Phaseolus coccineus* and *P. polyanthus* accessions in the core collection of the secondary gene pool that were evaluated in this study

| | Number of accessions | |
|---|---|---|
| **Origin** | ***P. coccineus*** | ***P. polyanthus*** |
| Mexico | 49 | 27 |
| Guatemala | 21 | 25 |
| Colombia | 7 | 12 |
| Costa Rica | 1 | 2 |
| Honduras | 1 | … |
| Puerto Rico | 1 | … |
| Portugal | 1 | … |
| Romania | 2 | … |
| Yugoslavia | 3 | … |
| Rwanda | 2 | … |
| Great Britain | 2 | … |
| Turkey | 2 | … |
| Netherlands | 1 | … |
| Venezuela | … | 3 |
| Total | 93 | 69 |

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species, particularly in the primary centers of diversity from Mexico and Central America. In addition, 75 interspecific lines resulting from simple and complex crosses involving *P. polyanthus*, *P. coccineous,* and *P. vulgaris* (3) that were resistant to angular leaf spot (5) were evaluated for resistance to *C. lindemuthianum* (Table 2).

**Fungal isolates.** Isolates of *C. lindemuthianum* obtained from naturally infected common bean cultivars were used in this study (Table 3). Monosporic isolates were characterized using a set of 12 host differential genotypes (5,15,19) and were maintained on potato dextrose agar (PDA) medium at 4°C (short term), or lyophilized and stored at 4°C for long-term storage. Mixtures of local Andean (races 7 and 15) or Middle American (races 137, 521, 385, and 1545) races collected from Popayán, Colombia, were used to inoculate secondary gene pool accessions in the screenhouse (Table 3). To produce inoculum, Erlenmeyer flasks (250 ml) half-filled with sterile young green bean pods were inoculated with a spore suspension of each isolate of *C. lindemuthianum*. The flasks were incubated at 20°C for 10 days in darkness, and then equal proportions of the colonized pods of each isolate were liquefied in sterile distilled water in a blender. A conidial suspension was obtained by filtering the homogenate through two layers of cheesecloth. The spore concentration was estimated using a hemacytometer and adjusted to a final concentration of $1.2 \times 10^6$ conidia/ml using sterile distilled water.

*C. lindemuthianum* races 6, 15, and 3481 (Table 3) were used separately to inoculate

**Table 2.** Reaction of interspecific lines derived from crosses of genotypes from the primary and secondary gene pool to inoculation with three races of *Colletotrichum lindemuthianum* in the greenhouse

| | | | Disease reaction for race of *C. lindemuthianum*[a] | | |
|---|---|---|---|---|---|
| **Genotypes in crosses[b]** | **Family** | **Parents[c]** | **6** | **15** | **3481** |
| BAT 338 × G35252 (1) | F8 | Pv × Pc | 3.4 | 3 | 1 |
| BAT 338 × G35252 (1) | F8 | Pv × Pc | 1 | 2.6 | 1.5 |
| BAT 338 × G35252 (1) | F8 | Pv × Pc | 6.6 | 1.6 | 7.4 |
| BAT 338 × G35252 (1) | F8 | Pv × Pc | 5.9 | 4.3 | 6.7 |
| BAT 338 × G35252 (1) | F8 | Pv × Pc | 5.3 | 3.2 | 1 |
| BAT 338 × G35252 (3) | F8 | Pv × Pc | 1 | 1 | 1 |
| BAT 338 × G35252 (1) | F8 | Pv × Pc | 1 | 1 | 9 |
| BAT 338 × G35252 (1) | F9 | Pv × Pc | 1 | 1 | 1 |
| BAT 338 × G35252 (1) | F9 | Pv × Pc | 8.8 | 7 | 8.5 |
| BAT 338 × G35252 (1) | F9 | Pv × Pc | 1.8 | 1 | 8.2 |
| BAT 338 × G35252 (1) | F9 | Pv × Pc | 1 | 1 | 5.4 |
| BAT 338 × G35252 (1) | F9 | Pv × Pc | 8 | 3.5 | 5.7 |
| BAT 338 × G35252 (1) | F9 | Pv × Pc | 1.9 | 1 | 8.9 |
| BAT 338 × G35252 (1) | F9 | Pv × Pc | 1 | 1 | 8.4 |
| BAT 338 × G35252 (1) | F9 | Pv × Pc | 1 | 1 | 1 |
| BAT 338 × G35252 (1) | F9 | Pv × Pc | 1 | 1.2 | 1 |
| BAT 338 × G35252 (1) | F9 | Pv × Pc | 1.1 | 1 | 9 |
| (G35649 × G3807) × G35023 (1) | F5 | (Pcw × Pv) × Pc | 1 | 1 | 2.3 |
| (G35649 × G3807) × G35023 (1) | F5 | (Pcw × Pv) × Pc | 1 | 1 | 1 |
| ((G35876 × G3807) × G35182) × A 114 (10) | F7 | (Pcw × Pv) × Pp | 1 | 1 | 1.14 |
| ((G35876 × G3807) × G35182) × S31003 (12) | F7 | (Pcw × Pv) ×Pp | 1 | 1 | 1.13 |
| (G35649 × L32) × BAC 24 (1) | F6 | (Pcw × Pv) × Pv | 1 | 1 | 8.6 |
| Mortiño × X7 (2) | F9 | Pv × Pp | 1 | 1 | 1 |
| (ICA PIJAO × G35171)F1× ICA PIJAO) (1) | F8 | (Pv × Pc) × Pv | 1 | 1 | 2.8 |
| (ICA PIJAO × G35171)F1 × ICA PIJAO) (1) | F8 | (Pv × Pc) × Pv | 1.3 | 1 | 6.6 |
| (ICA PIJAO × G35172) × ICA PIJAO) (1) | F8 | (Pv × Pc) × Pv | 1 | 1 | 9 |
| (ICA PIJAO × G35172) × ICA PIJAO) (1) | F8 | (Pv × Pc) × Pv | 1 | 1 | 5 |
| ICA PIJAO × (ICA PIJAO × G35877) (1) | F5 | Pv × (Pv × Pc) | 1.3 | 1 | 8.8 |
| ICA PIJAO × (ICA PIJAO × G35877) (1) | F5 | Pv × (Pv × Pc) | 2.1 | 1 | 9 |
| ICA PIJAO × (ICA PIJAO × G35877) (1) | F5 | Pv × (Pv × Pp) | 2.8 | 1.4 | 6.2 |
| ICA PIJAO × (ICA PIJAO × G35877) (1) | F5 | Pv × (Pv × Pc) | 4.6 | 3.7 | 7.4 |
| ICA PIJAO × (ICA PIJAO × G35877) (1) | F5 | Pv × (Pv × Pc) | 4.5 | 4.7 | 9 |
| ICA PIJAO × (ICA PIJAO × G35877) (1) | F5 | Pv × (Pv × Pc) | 1.1 | 4.3 | 9 |
| ICA PIJAO × (ICA PIJAO × G35877) (1) | F5 | Pv × (Pv × Pc) | 2.7 | 1.8 | 9 |
| ICA PIJAO × (ICA PIJAO × G35877) (1) | F5 | Pv × (Pv × Pc) | 1.1 | 1.8 | 9 |
| ICA PIJAO × (ICA PIJAO × G35877) (1) | F5 | Pv × (Pv × Pc) | 1.7 | 1.9 | 6.7 |
| Anthracnose differential genotypes | … | … | | | |
| Michelite | … | … | 1 | 9 | 9 |
| Michigan dark red kidney | … | … | 9 | 9 | 1 |
| Perry marrow | … | … | 9 | 9 | 1 |
| Cornell 49242 | … | … | 1 | 9 | 9 |
| Widusa | … | … | 1 | 1 | 9 |
| Kaboon | … | … | 1 | 1 | 1 |
| Mexico 222 | … | … | 1 | 1 | 1.8 |
| PI 207262 | … | … | 1 | 1 | 9 |
| TO | … | … | 1 | 1 | 9 |
| TU | … | … | 1 | 1 | 1 |
| AB 136 | … | … | 1 | 1 | 9 |
| G2333 | … | … | 1 | 1 | 6.5 |
| G2338 | … | … | 1 | 1 | 1 |
| La Victorie | … | … | 9 | 9 | 9 |

[a] Disease reactions are based on the 1 to 9 class scale described by Schoonhoven and Pastor-Corrales (22). Ratings of 1 to • 3 were considered resistant, 3 > to 6, intermediate and ratings >6 as susceptible.

[b] Genotypes of lines of *Phaseolus vulgaris* and accessions of *P. coccineus* or *P. polyanthus* used in the crosses and evaluated in this study. The number in parenthesis represents the number of lines for that cross that had the designated response to inoculation with races of *Colletotrichum lindemuthianum*.

[c] Parents are the species that were used in the cross. Pv = *P. vulgaris,* Pc = *P. coccineus*, Pcw = *P. coccineus* wild, and Pp = *P. polyanthus.*

plants in the greenhouse. Inoculum of each isolate was produced by inoculating PDA with a monosporic culture of *C. lindemuthianum*. After incubation at 20°C for 8 days in darkness, plates were flooded with 5 ml of sterile distilled water. The surface of the culture was scraped with a sterile glass rod, and the dislodged spores were filtered through four layers of cheesecloth to remove mycelial fragments. The spore concentration was estimated using a hemacytometer and adjusted to a final concentration of $1.2 \times 10^6$ conidia/ml using sterile distilled water.

**Resistance testing under screenhouse conditions.** All 162 accessions were evaluated in screenhouse infection beds in Popayán, Colombia (1,700 m above sea level, 18°C daily average temperature, 12-hr photoperiod per day) using local races of *C. lindemuthianum* of Mesoamerican (races 137, 521, 385, and 1545) and Andean (races 7 and 15) origin in separate inoculations. Ten seeds per accession were sown in completely randomized 0.40-m rows that were replicated three times. After 3 weeks, plants were inoculated by spraying the stem and leaves until runoff with the aqueous conidial suspensions of each race using a De Vilbiss air compressor at one-third horsepower. Inoculated plants were covered with a plastic tent for 4 days to ensure high humidity. In each test, known susceptible (Michelite and La Victorie) and resistant (G2333, G2338, and Widusa) cultivars were included as controls.

**Resistance testing under greenhouse conditions.** The secondary gene pool core accessions were evaluated in the greenhouse using race 3481, which infects the anthracnose differential cultivar G2333 (resistance genes *Co-4*[2], *Co-5*, and *Co-7*). Because of shortage of seed, only 147 secondary gene pool accessions (61 *P. polyanthus* and 86 *P. coccineus)* were screened. The cultivars La Vicorie, G2333, and Michelite were included as susceptible controls, and the cultivars G2338 and G19833 were included as resistant controls. In addition, 75 interspecific lines with high levels of resistance to angular leaf spot under field and greenhouse conditions (5) were screened using races 6, 15, and 3481. Anthracnose differential cultivars were included to verify the race designation of each isolate. Thirty seeds were used for each accession and there were 10 plants in each replicate. For each accession, the stem and cotyledons of bean seedlings with fully expanded primary leaves were sprayed until runoff with the conidial suspension using a De Vilbiss air compressor of one-third horsepower. Inoculated plants were incubated in a chamber at 19 to 22°C and 90 to 100% relative humidity with a photoperiod of 12 h light, 12 h dark for 8 days.

**Disease assessment.** Plants were rated 19 days after inoculation in the screenhouse test and 8 days after inoculation in the greenhouse test using the 9-class scale described by Schoonhoven and Pastor-Corrales (22). A plant with no visible symptoms or with only a few, very small isolated lesions mostly on the primary leaf veins and covering approximately 1% of the total leaf area was scored as resistant (rating 1 to 3). A plant with several small lesions on the petioles, on primary and secondary veins on the lower surface of the leaf, and on stems and covering approximately 5% of the leaf or stem area was recorded as intermediate (rating 3.1 to 6). A plant with numerous small or enlarged lesions, or with sunken cankers on the lower sides of leaves and stems, covering 25% or more of the leaf and stem area was recorded as susceptible (rating 6.1 to 9). All experiments were repeated and data were statistically analyzed using the Kruskal-Wallis nonparametric variance analysis PROC NPAR1WAY (SAS Institute Inc., Cary, NC).

## RESULTS

**Response of secondary gene pool to Andean and Mesoamerican races.** The response of accessions of *P. polyanthus* and *P. coccineus* to inoculation with Andean and Mesoamerican races of *C. lindemuthianum* were not different ($F = 0.08$; $P = 0.783$). The 69 *P. polyanthus* accessions were rated as resistant (rating ≤ 3) to *C. lindemuthianum*. Of these accessions, 93% displayed no symptoms (immune response), while the remaining accessions were resistant, with only minor symptoms limited to veins on the lower surface of the primary leaf. The reaction of *P. coccineus* to the disease was more variable, but 97% of the accessions were classified as resistant, while three (G35171, G35346, and G35381) were classified as intermediate. Of the 162 materials composing the secondary gene pool, none of the accessions was rated as susceptible (rating > 6.0) to the six races of *C. lindemuthianum* used in this study.

**Response of secondary gene pool accessions to race 3481.** In greenhouse screening, 61 *P. coccineus* and 57 *P. polyanthus accessions* had an immune reaction (no symptoms observed) to pathotype 3481. All *P. polyanthus* accessions were resistant to race 3481, while five *P. coccineus* accessions (G35609, G35381, G35103, G35311, and G35346) had an intermediate response. The highest rating recorded was 4.6 for the *P. coccineus* accession G35311. None of the secondary gene pool accessions were susceptible to race 3481, which demonstrates the high levels of resistance that are present in the secondary gene pool of *Phaseolus* spp. The susceptible genotypes of *P. vulgaris* included as controls (G2333, La Victorie, and Michelite) were all susceptible to this pathotype, and developed large lesions with sunken cankers on stems and the apex of plants was often dead. The resistant genotypes included as controls (G2338 and G19833) were resistant to race 3481.

**Response of interspecific lines to three races of *C. lindemuthianum.*** Of the 75 interspecific lines screened, 49 were resistant to race 3481, and 69 were resistant to races 6 and 15. Among the 58 advanced lines (F5 or higher), 33 were resistant to the three races used in this study (Table 2). The interaction between the interspecific lines and the races of *C. lindemuthianum* used for inoculation was significant ($F =$

**Table 3.** Origin and phenotypes of races of *Colletotrichum lindemuthianum* used to characterize accessions of *Phaseolus coccineus, P. polyanthus*, and interspecific lines derived from crosses of genotypes from the primary and secondary gene pool

| | | Differential cultivar[a] | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Isolate, origin[b] | Race | A | B | C | D | E | F | G | H | I | J | K | L |
| CL 171, Ecuador (2000) | 6 | – | + | + | – | – | – | – | – | – | – | – | – |
| CL 002, Colombia (1989) | 7 | + | + | + | – | – | – | – | – | – | – | – | – |
| CL 056, Colombia (1986) | 15 | + | + | + | + | – | – | – | – | – | – | – | – |
| CL 094, Colombia (1989) | 137 | + | – | – | + | – | – | – | + | – | – | – | – |
| CL 020, Colombia (1987) | 521 | + | – | – | + | – | – | – | – | – | + | – | – |
| CL 043, Colombia (1988) | 385 | + | – | – | – | – | – | – | + | + | – | – | – |
| CL 017, Colombia (1986) | 1545 | + | – | – | + | – | – | – | – | – | + | + | – |
| CL 077, Costa Rica (1992) | 3481 | + | – | – | + | + | – | – | + | + | – | + | + |

[a] Genotypes of common bean differentials used to designate races of *C. lindemuthianum* followed by their binary value: A = Michelite (1), B = Michigan Dark Red Kidney (2), C = Perry Marrow (4), D = Cornell 49242 (8), E = Widusa (16), F = Kaboon (32), G = Mexico 222 (64), H = PI 207262 (128), I = TO (256), J = TU (512), K = AB 136 (1024), and L = G2333 (2047); + = susceptible; – = resistant.

[b] Origin of isolate followed in parentheses by the year of collection. All isolates from Colombia were collected from Popayan, while the isolate from Ecuador was collected from Valle de Chota, and the isolate from Costa Rica was collected from Puriscal.

7.96; $P < 0.0001$). Twenty-two lines were susceptible to race 3481 (rating >6), while two and zero lines were susceptible to races 15 and 6, respectively. All lines that were susceptible to race 15 also were susceptible to race 3481, and all were derived from simple crosses involving *P. vulgaris* and *P. coccineus*. The interspecific lines that had *P. polyanthus* as one of the parents displayed a high level of resistance to the three *C. lindemuthianum* races.

## DISCUSSION

The stability and longevity of resistant cultivars is partially dependent on the variation displayed by the pathogen. For diseases caused by highly variable pathogens, such as *C. lindemuthianum,* it is necessary to diversify the sources of resistance to effectively manage the disease. Identification of genotypes with resistance to anthracnose within the secondary gene pool could contribute to this management strategy. We have shown that the secondary gene pool of *Phaseolus* spp. is highly resistant to a range of *C. lindemuthianum* pathotypes. Furthermore, this resistance has been transmitted successfully to interspecific progeny. This is evident in the number of interspecific lines with the plant type of *P. vulgaris* that are highly resistant to various races of *C. lindemuthianum*, including race 3481, which infects the differential cultivar G2333 that carries three resistance genes, *Co-4*$^2$, *Co-5,* and Co-*7*.

The population of *P. polyanthus* was highly resistant to *C. lindemuthianum*. Most of the entries (93%) were symptomless under greenhouse or screenhouse conditions, while symptoms on the remaining accessions were limited to very small lesions on veins on the underside of leaves. *P. coccineus* did not show the same high degree of immunity, but 98% of the accessions were resistant. In another study, Schmit and Baudoin, (20) observed that 64% of the accessions of *P. polyanthus* tested were immune and 100% were resistant to inoculations with *Phoma exigua* var. *diversispora*, while 72% of the accessions of *Phaseolus coccineus* were resistant. A similar observation also was made for the angular leaf spot pathogen, *Phaeoisariopsis griseola* (2,5). The susceptible interspecific lines reported in this study were derived from *Phaseolus vulgaris* × *P. coccineus,* while interspecific lines that had *P. polyanthus* as one of the parent were highly resistant. These results show that *P. coccineus* does not possess the same level of resistance as *P. polyanthus,* and introgressing resistance from *P. polyanthus* into *P. vulgaris* is likely to provide broad anthracnose resistance.

Stable resistance to plant pathogens with extensive pathological variability, such as *C. lindemuthianum*, requires continual evaluation of germ plasm and eventual introgression of diverse genetic resistance into commercial cultivars. The breakdown of resistance in some cultivars regarded as highly resistant (e.g., G2333) shows that stable resistance to *C. lindemuthianum* might not be found in the primary gene pool and, consequently, alternative sources of resistance must be sought. Although resistance to *C. lindemuthianum* has been found in wild beans (17), the large number of susceptible accessions seems to suggest that wild beans might not provide stable anthracnose resistance. Pastor-Corrales (17) evaluated 510 wild bean accessions and found only 68 (13%) resistant to both Andean and Mesoamerican races of *C. lindemuthianum*. Low levels of resistance in wild beans also have been observed for *P. griseola*, where only 4% of the 350 wild bean accessions evaluated were resistant under field conditions and only four accession (G23477, G23478, G23479, and G23434) were resistant when challenged with the most aggressive and virulent race, 63-63, under greenhouse conditions (5). These results show that stable resistance to angular leaf spot or anthracnose is not likely to come from wild beans.

The high level of resistance to anthracnose observed in the secondary gene pool makes using *P. polyanthus* as a source of resistance a sound strategy for diversifying sources of resistance to *C. lindemuthianum*. In addition to their good disease resistance (2,5,10,21), the secondary gene pool has been a source of many desirable and useful agronomic traits, such as cold tolerance, lodging resistance due to the thick stem at the base of the plant, the presence of a tuberous or fibrous root system that allows a perennial cycle, long epicotyls, and a high number of pods per inflorescence, which all can be used to improve the agronomic characteristics of common bean (20). The feasibility of interspecific hybridization between primary and secondary genotypes has been demonstrated (3); therefore, resistance genes within genotypes of the secondary gene pool can be transmitted to common bean. Using the secondary gene pool will also allow screening for multiple traits simultaneously (20).

The results obtained in this study revealed the potential of *P. coccineus* and *P. polyanthus* as valuable novel sources of broad anthracnose resistance for bean breeding programs in the future. One problem with introgression of resistance from one convariety to another in *Phaseolus* spp. is the difficulty in recovering an acceptable crop type following hybridization. The presence of some interspecific lines with sufficient resistance to anthracnose and with *P. vulgaris* plant type, however, indicates that the time required to transfer this resistance to commercial types of beans can be greatly reduced. The interspecific lines that have been identified also have resistance to angular leaf spot (5); therefore, resistance to these two pathogens can be introgressed simultaneously into commercial types of beans. A clear understanding of the nature and inheritance of resistance in these lines will allow proper selection of genes to transfer to commerial types, as well as develop molecular markers for marker-assisted selection breeding.


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