Common Bean Landrace Jalo Listras Pretas Is the Source of a New Andean Anthracnose Resistance Gene

M. C. Gonçalves-Vidigal, Pedro S. Vidigal Filho, A. F. Medeiros, and M. A. Pastor-Corrales*

ABSTRACT

Novel sources of resistance are continuously needed to combat anthracnose disease in common bean (Phaseolus vulgaris L.) caused by the hypervariable pathogen Colletotrichum lindemuthianum (Sacc. and Magnus) Briosi and Cavara. We sought to characterize the novel anthracnose resistance in Andean common bean landrace ‘Jalo Listras Pretas’ (JLP). Jalo Listras Pretas is resistant to races 9, 64, 65, and 73 of the anthracnose pathogen used in this study. To examine inheritance of anthracnose resistance in JLP, F2 populations JLP/Mexico 222 and JLP/Cornell 49242 were inoculated with discriminating races of the pathogen. Segregation for resistance in both F2 populations fit a 3:1 resistant/susceptible ratio suggesting that the anthracnose resistance in JLP is controlled by a single dominant gene. To establish independence of the resistance gene in JLP from other published resistance genes, allelism tests were conducted with 14 F2 populations derived from crossing JLP with Andean cultivars carrying anthracnose resistance genes Co-1, Co-12, Co-13, Co-15, and Co-12, and with Middle American cultivars with Co-2, Co-3, Co-43, Co-5, Co-6, Co-7, Co-9, Co-10, and Co-11. Results revealed the resistance gene in JLP was independent of the Andean loci Co-1 and Co-12, and the nine Middle American anthracnose resistance genes. The symbol Co-13 was assigned to this newly discovered anthracnose resistance gene in Brazilian Andean common bean landrace JLP.

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Abbreviations: JLP, Jalo Listras Pretas; R, resistant; S, susceptible.

ANTHRACNOSE, caused by the fungus Colletotrichum lindemuthianum (Sacc. and Magnus) Briosi and Cavara, is one of the most widespread and economically important diseases of common bean (Phaseolus vulgaris L.) worldwide (Pastor-Corrales and Tu, 1989; Balardin et al., 1997; Pastor-Corrales, 2005). This disease is particularly important and recurrent in cooler subtropical and temperate bean production regions (Pastor-Corrales and Tu, 1989).

Genetic resistance is the most effective and environmentally friendly management strategy for the control of anthracnose disease in common bean (Phaseolus vulgaris L.) worldwide (Pastor-Corrales and Tu, 1989; Balardin et al., 1997; Pastor-Corrales, 2005). This disease is particularly important and recurrent in cooler subtropical and temperate bean production regions (Pastor-Corrales and Tu, 1989).

Several anthracnose resistance genes have been characterized in common bean (Kelly and Young, 1996; Bassett, 2004; Kelly and Vallego, 2004). These genes, and their alleles, include Co-1, (McRostie, 1919), Co-12 (Melotto and Kelly, 2000), Co-13...
(Melotto and Kelly, 2000), Co-1^h, (Alzate-Marin et al., 2003a), Co-1^t (Gonçalves-Vidigal and Kelly, 2006), Co-2 (Mastenbroek, 1960), Co-3, Co-3^2 (Bannerot, 1965; Fouilloux, 1976, 1979), Co-4 (Fouilloux, 1976, 1979), Co-4^t (Young et al., 1998), Co-4^t (Alzate-Marin et al., 2007), Co-5 (Young and Kelly, 1996; Young et al., 1998; Alzate-Marin et al., 2007), Co-6 (Schwarz et al., 1982; Gonçalves-Vidigal, 1994; Kelly and Young, 1996; Young and Kelly, 1996), Co-7 (Pastor-Corráles et al., 1994; Young et al., 1998), co-8 (Alzate-Marin et al., 1997), Co-9 originally described as Co-3^3 (Geffroy et al., 1999; Rodriguez-Suárez et al., 2004; Méndez-Vigo et al., 2005; Alzate-Marin et al., 2007), Co-10 (Alzate-Marin et al., 2003b), Co-11 (Gonçalves-Vidigal et al., 2007b), and Co-12 (Gonçalves-Vidigal et al., 2008). Thus, resistance to anthracnose in common bean is conditioned mostly by single independent genes. Only the co-8 gene is recessive; all the other genes are dominant. In addition, multiple alleles exist at the Co-1, Co-3, and Co-4 loci (Kelly and Vallejo, 2004). Furthermore, the great majority of anthracnose resistance genes in P. vulgaris (Co-2, Co-3, Co-3^2, Co-4, Co-4^t, Co-4^h, Co-5, Co-6, co-8, Co-9, Co-10, and Co-11) are from beans belonging to the Middle American gene pool. The Co-1 locus and the recently described Co-12 gene are the only anthracnose resistance genes originating from beans of the Andean gene pool.

The resistance alleles at the Andean Co-1 have been very valuable in breeding Middle American beans with anthracnose resistance, particularly in production countries where Mesoamerican races of the anthracnose pathogen are dominant (Pastor-Corráles, 1996; Kelly and Vallejo, 2004). Conversely, when controlling Andean races, anthracnose resistance loci from Middle American beans are very important. It has been posited that the Andean and Mesoamerican races of C. lindemuthianum have evolved separately; Andean races with Andean beans in South America and Mesoamerican races with Middle American beans. The previous discussion highlights the need to identify and characterize additional resistance genes in Andean beans to complement the many anthracnose resistance genes available in Middle American common beans.

Twenty-six landrace cultivars collected in the State of Paraná, Brazil, which were inoculated with 12 different Brazilian races of C. lindemuthianum, were identified as new sources of anthracnose resistance (Vidigal Filho et al., 2007). These accessions included the Andean bean Jalo Listras Pretas (JLP) that was resistant to the Mesoamerican races 9, 31, 65, 69, 73, 81, 89, and 95 of C. lindemuthianum and susceptible to races 7, 19, and 55 that appeared to be Andean (Vidigal Filho et al., 2007). These results revealed that the race resistance spectrum of JLP was different from ‘Michigan Dark Red Kidney’, ‘Perry Marrow’, ‘Kaboon’, and ‘Widusa’; the Andean anthracnose differential cultivars that carry different alleles of the Co-1 locus for anthracnose resistance. These results also revealed that JLP was a potential new source of resistance to anthracnose. A seed sample of common bean landrace JLP presently cultivated by farmers in Paraná state was collected and multiplied in 2001. Previous work conducted by our group showed that the JLP cultivar, obtained from a single plant selection, has morphological characteristics similar to bean cultivars from the Nueva Granada race of the Andean gene pool (Singh et al., 1991). Jalo Listras Pretas has a Type I growth habit, and large seeds (~40.0 g 100^-1 seeds). Recent analysis of the phaseolin seed protein, through SDS-PAGE gel electrophoresis conducted by Gonçalves-Vidigal et al. (2007a), showed that JLP has a band that corresponds to the “T” phaseolin, which is characteristic of beans of Andean origin.

The objectives of this study were to elucidate the inheritance of anthracnose resistance in the Andean bean landrace JLP and to establish the genetic relationship between the anthracnose resistance in JLP and other anthracnose resistance genes characterized previously.

**MATERIALS AND METHODS**

**Genetic Material and Crosses**

Jalo Listras Pretas studied here, along with Jalo Vermelho (Co-12), belong to the Andean gene pool and are two of 26 Andean and Middle American common bean landraces collected in the north and northwest regions of the state of Parana in Southern Brazil (Vidigal Filho et al., 2007). A sample of 30 seeds was obtained from a single plant selection and multiplied to get enough seeds for further experiments. This landrace, JLP, was evaluated for anthracnose resistance with 12 races of C. lindemuthianum and it exhibited resistance to races 9, 31, 65, 69, 73, 81, 89, and 95 and susceptibility to races 7, 19, 55, and 453 (Vidigal Filho et al., 2007).

The 12 common bean differential cultivars proposed by Pastor-Corráles (1991) for characterizing the virulence diversity of C. lindemuthianum, in addition to Middle American common bean cultivars MSU 7-1 (Co-5, Co-7), BAT 93 (Co-9), and Ouro Negro (Co-10) were also used in this study. Seeds of the anthracnose differentials and other commercial cultivars were obtained from the Nupagri Bean Gene Bank of the Universidad Estadual de Maringá, Paraná, Brazil. Seeds from the cultivar MSU 7-1 were provided by Dr. James D. Kelly (Michigan State University). All crosses used in this study were performed in the greenhouse.

The inheritance studies were conducted in two F₂ populations derived from the crosses JLP (resistant [R]) × Mexico 222 (susceptible [S]) and JLP (R) × Cornell 49242 (S). The resulting segregating F₂ populations were inoculated with races 64 and 73 of C. lindemuthianum, respectively. Mexico 222 and Cornell 49242 are susceptible to races 64 and 73, respectively, while JLP is resistant to both.

To determine the independence of the anthracnose resistance allele present in JLP from other previously characterized anthracnose resistance alleles, JLP was crossed with Andean bean
cultivars Michigan Dark Red Kidney (Co-1), Kaboon (Co-18), Perry Marrow (Co-16), Widusa (Co-1), and Jalo Vernelho (Co-12), and Middle American cultivars Cornell 49242 (Co-2), Mexico 222 (Co-3), PI 207262 (Co-4, Co-9), TU (Co-5), AB 136 (Co-6 and co-8), MSU 7-1 (Co-5, Co-7), BAT 93 (Co-9), Ouro Negro (Co-10), and Michelite (Co-11). In all cases JLP was used as the female parent. The F1 seeds were planted and self-pollinated to obtain the corresponding F2 seeds. F1 seedlings were inoculated with an isolate of *C. lindemuthianum* to which JLP was susceptible and the male parent was resistant to ensure that the progeny was the product of a cross. F1 seeds derived from each cross were planted in pots with soil previously sterilized and fertilized. Pots were kept in a greenhouse until pod maturation and F2 seeds were harvested. The F2 generation seeds were sown in trays containing soil (approximately 100 seeds from each cross per tray). Plants were maintained in the greenhouse until first trifoliate leaves were fully developed.

Races 9, 64, 65, and 73 *C. lindemuthianum* were chosen for the allelism tests, because all parental cultivars inoculated with these races yielded R × R type of reaction in the parents (Table 1). Isolates of race 9 were provided by Dr. James D. Kelly from Michigan State University. Cultures of each *C. lindemuthianum* race were incubated on petri dishes containing Mathur’s medium (Mathur et al., 1950). The identification of the races was confirmed by inoculation of the isolates on a set of 12 common bean anthracnose differential cultivars (Pastor-Corrales, 1992).

### Inoculation and Disease Evaluation

Monosporic cultures of each race of *C. lindemuthianum* used in this study were prepared in young green common bean pod medium and incubated at 25°C for 14 d. The inoculation of the parents, F1, and F2 populations from each cross, was performed separately to prevent contamination. Seedlings were grown under natural light in greenhouses supplemented by 400-W high-pressure sodium lamps giving total light intensity of 115 μmol m⁻² s⁻¹ for 7 to 10 d until they reached the first trifoliate leaf stage. Twelve parental seedlings from each cross were inoculated and the number of F1 and F2 seedlings inoculated varied by cross ranging from 10 to 365 plants. Seedlings with fully developed first trifoliate leaves of parents, F1, F2, and backcross populations were inoculated with spores of select races of *C. lindemuthianum*. Spore suspensions containing 1.2 × 10⁹ spores mL⁻¹ were spray-inoculated on seedlings using a De Vilbiss number 15 atomizer powered by an electric air compressor (Schulz, SA, Joinville, Santa Catarina, Brazil). For each cross, the F1 seeds and those of the respective parents and one susceptible control (Michelite, Mexico 222, or Cornell 49242) were inoculated. After inoculation, plants were placed in a mist chamber for 2 d and maintained at >95% relative humidity at 21 to 23°C and 16-h daylength (light intensity of 300 μmol m⁻² s⁻¹ at 1 m height). After misting, plants were transferred to benches in a greenhouse with suitable environment at 22°C with artificial light (12-h daylength at 25°C) for 7 d. Anthracnose disease reactions were rated visually using a scale of 1 to 9 (Pastor-Corrales et al., 1995). Plants with disease reaction scores between 1 and 3 were considered resistant, whereas plants with scores from 4 to 9 were considered susceptible.

### Table 1. Reaction of Andean common bean landrace Jalo Listras Pretas (JLP), four other bean genotypes, and the 12 bean anthracnose differential cultivars to four races of *Colletotrichum lindemuthianum* used in this study.

<table>
<thead>
<tr>
<th>Bean genotypes</th>
<th>Host genes</th>
<th>Gene pool†</th>
<th>Binary no.‡</th>
<th>Reaction to races§</th>
</tr>
</thead>
<tbody>
<tr>
<td>JLP</td>
<td>Unknown</td>
<td>A</td>
<td>9</td>
<td>64 65 73</td>
</tr>
<tr>
<td>MSU 7-1</td>
<td>Co-5, Co-7</td>
<td>M</td>
<td>R</td>
<td>R R R R R</td>
</tr>
<tr>
<td>BAT 93</td>
<td>Co-9</td>
<td>M</td>
<td>R</td>
<td>R R S R R</td>
</tr>
<tr>
<td>Ouro Negro</td>
<td>Co-10</td>
<td>M</td>
<td>R</td>
<td>R R S R R</td>
</tr>
<tr>
<td>Jalo Vernelho</td>
<td>Co-12</td>
<td>A</td>
<td>R</td>
<td>R R S R S</td>
</tr>
<tr>
<td><strong>Differential cultivars</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Michelite</td>
<td>Co-11</td>
<td>M</td>
<td>1</td>
<td>S R S S</td>
</tr>
<tr>
<td>MDRK†</td>
<td>Co-1</td>
<td>A</td>
<td>2</td>
<td>R R R R</td>
</tr>
<tr>
<td>Perry Marrow</td>
<td>Co-18</td>
<td>A</td>
<td>4</td>
<td>R R R R</td>
</tr>
<tr>
<td>Cornell 49242</td>
<td>Co-2</td>
<td>M</td>
<td>8</td>
<td>S R S S</td>
</tr>
<tr>
<td>Widusa</td>
<td>Co-16</td>
<td>A</td>
<td>16</td>
<td>R R R R</td>
</tr>
<tr>
<td>Kaboon</td>
<td>Co-12</td>
<td>A</td>
<td>32</td>
<td>R R R R</td>
</tr>
<tr>
<td>Mexico 222</td>
<td>Co-3</td>
<td>M</td>
<td>64</td>
<td>R S S S</td>
</tr>
<tr>
<td>PI 207262</td>
<td>Co-4†, Co-9</td>
<td>M</td>
<td>128</td>
<td>R R R R</td>
</tr>
<tr>
<td>TO</td>
<td>Co-4</td>
<td>M</td>
<td>256</td>
<td>R R R R</td>
</tr>
<tr>
<td>TU</td>
<td>Co-5</td>
<td>M</td>
<td>512</td>
<td>R R R R</td>
</tr>
<tr>
<td>AB 136</td>
<td>Co-6, Co-8</td>
<td>M</td>
<td>1024</td>
<td>R R R R</td>
</tr>
<tr>
<td>G 2333</td>
<td>Co-4†, Co-5, Co-7</td>
<td>M</td>
<td>2048</td>
<td>R R R R</td>
</tr>
</tbody>
</table>

†M, Middle American; A, Andean.
‡The sum of the binary numbers of bean cultivars with susceptible reaction gives the race denomination. Race 9 which is virulent on Michelite (1) and Cornell 49242 (8) results from adding the binary numbers 1+8 (Pastor-Corrales, 1991).
§R, resistant; S, susceptible.
†MDRK, Michigan Dark Red Kidney.

### Statistical Analysis

Segregation analysis of the disease reaction of 137 F2 plants from the cross JLP × Mexico 222, and 365 F2 plants from the cross JLP × Cornell 49442 were performed by the chi-square (χ²) test, according to the Mendelian segregation hypothesis of a 3:1 R/S ratio. Similarly the BCF1 to Mexico 222 and Cornell 49422 were tested for goodness of fit to a 1:1 R/S ratio. For the allelism tests, segregation analysis of 14 F2 populations from crosses between the JLP and Andean (Michigan Dark Red Kidney, Kaboon, Perry Marrow, Widusa, and Jalo Vernelho) and Middle American (Cornell 49424, Mexico 222, PI 207262, TU, AB 136, MSU 7-1, BAT 93, Ouro Negro, and Michelite) *P. vulgaris* cultivars were also performed by the chi-square test, according to the Mendelian segregation hypothesis of a 15:1 or 63:1 R/S ratio.

### RESULTS AND DISCUSSION

#### Inheritance of Anthracnose Resistance in Jalo Listras Pretas

All F2 plants from JLP × Mexico 222 and JLP × Cornell 49424 crosses exhibited the same resistant reaction as JLP when inoculated with races 64 and 73 of *C. lindemuthianum*; suggesting that anthracnose resistance in JLP is a dominant trait (Table 2). Similarly, all anthracnose resistant plants in
Table 2. Response of the parental lines Jalo Listras Pretas (JLP), Mexico 222, Cornell 49242, and the F1 and F2 plants from the crosses JLP × Mexico 222 and JLP × Cornell 49242 and the backcross F1 progenies inoculated with Colletotrichum lindemuthianum, races 64 and 73, respectively.

<table>
<thead>
<tr>
<th>Parent/cross</th>
<th>Race</th>
<th>Generation1</th>
<th>Observed ratio (R:S)</th>
<th>Expected ratio (R:S)</th>
<th>( \chi^2 )</th>
<th>( P ) value</th>
</tr>
</thead>
<tbody>
<tr>
<td>JLP</td>
<td>64</td>
<td>PR</td>
<td>20:0</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mexico 222</td>
<td>64</td>
<td>PS</td>
<td>0:20</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>JLP × Mexico 222</td>
<td>64</td>
<td>F1</td>
<td>10:0</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>JLP × Mexico 222</td>
<td>64</td>
<td>F2</td>
<td>104:33</td>
<td>3:1</td>
<td>0.061</td>
<td>0.81</td>
</tr>
<tr>
<td>JLP × F1</td>
<td>64</td>
<td>BC0 F1</td>
<td>20:0</td>
<td>1:0</td>
<td>0.00</td>
<td>1.00</td>
</tr>
<tr>
<td>Mexico 222 × F1</td>
<td>64</td>
<td>BC0 F1</td>
<td>20:20</td>
<td>1:1</td>
<td>0.00</td>
<td>1.00</td>
</tr>
<tr>
<td>JLP</td>
<td>73</td>
<td>PR</td>
<td>20:0</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cornell 49242</td>
<td>73</td>
<td>PS</td>
<td>0:20</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>JLP × Cornell 49242</td>
<td>73</td>
<td>F1</td>
<td>10:0</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>JLP × Cornell 49242</td>
<td>73</td>
<td>F2</td>
<td>275:90</td>
<td>3:1</td>
<td>0.023</td>
<td>0.88</td>
</tr>
<tr>
<td>JLP × F1</td>
<td>73</td>
<td>BC0 F1</td>
<td>20:20</td>
<td>1:1</td>
<td>0.00</td>
<td>1.00</td>
</tr>
<tr>
<td>Cornell 49242 × F1</td>
<td>73</td>
<td>BC0 F1</td>
<td>20:20</td>
<td>1:1</td>
<td>0.00</td>
<td>1.00</td>
</tr>
</tbody>
</table>

1PR, resistant parent; PS, susceptible parent; BCs F1, backcross to susceptible; BC R F1, backcross to resistant parent.

The F2 populations exhibited the same reaction as JLP. Segregation for resistance in the F2 populations was consistent with a 3:1 R/S ratio for Mexico 222 × JLP (\( \chi^2 = 0.061, P = 0.81 \)) and Cornell 49242 × JLP (\( \chi^2 = 0.023, P = 0.88 \)) indicating monogenic dominant inheritance. All plants of the backcross population with the resistant parent JLP revealed the same type of resistant reaction as JLP while segregation among plants in the backcrosses with susceptible parents Mexico 222 and Cornell 49242 showed segregation consistent with 1:1 anthracnose R/S ratio (Table 2). Altogether, these results provide evidence that anthracnose resistance in Andean common bean cultivar Jalo Listras Pretas is conferred by a single dominant gene.

Allelism Tests

We present here the results from studies of the allelic relationship between the anthracnose resistance gene in Andean common bean landrace JLP and other known anthracnose resistance genes present in four Andean and nine Middle American common bean cultivars. Segregation for anthracnose resistance in these 14 allelism tests fit a 15:1 R/S ratio (Table 3). These results support the hypothesis that two independent dominant genes confer resistance to C. lindemuthianum in these F2 populations; one anthracnose resistance gene present in Andean bean JLP used as the female parent and the other gene present in the male parent. In short, the anthracnose resistance dominant gene in JLP is independent of Andean anthracnose resistance genes Co-1, Co-2, Co-3, Co-4, Co-5, Co-6, Co-7, Co-9, Co-10, and Co-11. The segregation in the F2 population derived from the cross between JLP and Middle American bean cultivar PI 207262, fit a ratio of 63:1 R/S (\( \chi^2 = 0.036, P = 0.85 \)) indicating that there are three dominant genes segregating for resistance to race 73 C. lindemuthianum used to evaluate this population (Table 3). The two dominant loci in PI 207262 Co-4 and Co-9 confer anthracnose resistance to races 23, 64, and 73 of C. lindemuthianum (Gonçalves-Vidigal et al., 1997, 2007b; Gonçalves-Vidigal and Kelly, 2006; Alzate-Marín et al., 2007). Since race 73 elicits an R × R reaction in the JLP and PI 207262 parents (Table 1), the third gene in the F2 JLP × PI 207262 population is from JLP which is located at a distinct locus from Co-4 and Co-9.

The combined results of the monogenic inheritance and the allelism tests presented here support the hypothesis that only a single dominant locus confers resistance to C. lindemuthianum in Andean common bean landrace JLP, and that this locus is independent from other Andean and Middle American bean anthracnose resistance loci previously reported. The authors propose that this single dominant anthracnose resistance locus in JLP cultivar be named Co-13, according to gene symbol guidelines set forth by the Bean Genetics Committee (Myers and Weeden, 1988; Bassett and Myers, 1999).

The data obtained in the present research provides breeders with an anthracnose resistance gene of Andean origin that can be deployed in commercial cultivars providing the opportunity for improving the effectiveness of anthracnose resistance gene pyramiding in common bean breeding programs while at the same time broadening the germplasm base of common bean.

CONCLUSIONS

In this study we elucidated the inheritance of anthracnose resistance in the Andean bean landrace JLP and established the genetic relationship between this resistance and other known anthracnose resistance genes. The segregation analysis of F1, F2, and backcross populations resulting from crossing JLP with Mexico 222 and Cornell 49242 provided strong evidence that anthracnose resistance in JLP was conferred by a single dominant gene. Additional segregation analysis in populations derived from crossing JLP with 14 Andean and Middle American bean cultivars, each carrying different anthracnose resistance genes, revealed that the resistance to anthracnose in JLP is conferred by a new gene that is distinct from all other previously reported anthracnose resistance genes in common bean. Based on the evidence, the authors are proposing that the single dominant anthracnose resistance locus in JLP cultivar be named Co-13.

The great majority of anthracnose resistance genes in P. vulgaris are from beans that belong to the Middle American common bean germplasm base of common bean.
American gene pool. The Co-1 locus and the recently described Co-12 gene are the only anthracnose resistance genes originating from beans of the Andean gene pool. Thus discovering the new anthracnose resistance gene Co-13 in JLP, a bean from the under-utilized Andean gene pool, is very valuable in several ways. First of all, Co-13 will contribute to a more effective management of anthracnose, one of the most widespread and economically important diseases of common bean worldwide. Disease resistance genes from the Andean gene pool of common bean have been very valuable in breeding Middle American beans for resistance to pathogens possessing high virulence diversity such as those that cause rust [Uromyces appendiculatus (Pers.: Pers.) Unger], anthracnose, and angular leaf spot [Phaeosariopsis griseola (Sacc.) Ferrari] of common bean. Resistance genes from Andean beans provide resistance to many Middle American races of this highly variable bean pathogens including Colletotrichum lindemuthianum. Additionally, and perhaps more importantly, the discovery, elucidation, and use of novel anthracnose resistance genes such as Co-13 also contribute to broadening the genetic base of the common bean and to reducing the vulnerability of this important leguminous crop to the hypervirulent bean anthracnose pathogen.

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**References**


