GENETIC ANALYSIS OF ANTHRACNOSE RESISTANCE IN JALO PINTADO 2 DRY BEAN CULTIVAR

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INTRODUCTION

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). Search for new sources of resistance have been the objective of many breeding programs, since genetic resistance is the most effective and environmentally friendly management strategy for the control of anthracnose disease in common bean. Therefore, this study aimed to investigate the genetic resistance to anthracnose in the Andean cultivar Jalo Pintado 2.

MATERIAL AND METHODS

The experiment was conducted under greenhouse conditions at the Common Bean Breeding and Molecular Biology Laboratory of Núcleo de Pesquisa Aplicada à Agricultura (Nupagri). Previous studies carried out in our laboratory and by Vidigal Filho et al. (2007) demonstrated that the Andean cultivar Jalo Pintado 2 confers resistance to races 2, 7, 9, 31, 65, 73, 95, 453 and 2047. The inheritance test was evaluated on F_2 populations derivate from the cross of Jalo Pintado 2 and Cornell 49-242 (susceptible to race 73). Additionally, allelism tests were conducted on F_2 populations from the crosses (R × R) between Jalo Pintado 2 (JP2) and the cultivars Michigan Dark Red Kidney, Cornell 49-242, Mexico 222, PI 207262, TO, TU, AB 136, G 2333, Ouro Negro, Michelite, Jalo Vermelho, Jalo Listras Pretas, Pitanga, Corinthiano, Crioulo 159, Amendoim Cavalo, Paloma and Perla. The parents, F_1 and F_2 populations from each cross were inoculated with races 2, 65, 73 and 2047 of the *C. lindemuthianum* (Table 1). The spore concentration was adjusted to 1.2 x 10^6 spores.mL^{-1} for each race. After inoculation, plants were maintained in high relative humidity (>95%) for 72h at 20±2°C. After this period, seedlings were evaluated for their disease reaction using a scale of 1 to 9 (Pastor-Corrales et al., 1995) 7 days after inoculations. Plants with disease reaction scores of 1-3 were considered resistant, whereas plants that were rated 4-9 were considered susceptible. The genetics analysis on F_2 populations was performed through Chi- Square Test (χ^2) using Genes Software (Cruz, 2006).

RESULTS AND DISCUSSION

Segregation analysis in the F_2 population of the cross between the cultivars Jalo Pintado 2 (R) and Cornell 49-242 (S) fitted to 3R: 1S ratio (Table 1), indicating the action of one dominant gene present in the cultivar Jalo Pintado 2. Considering that the Mesoamerican cultivar Cornell 49-242 possess the *Co-2* gene, which does not confer resistance to race 73 of *C. lindemuthianum*. The allelism tests involving crosses (R × R) between Jalo Pintado 2 and the cultivars Michigan Dark Red Kidney, Cornell 49-242, Mexico 222, PI 207262, TO, TU, Ouro Negro, Jalo Vermelho, Jalo Listras Pretas, Corinthiano and Crioulo 159 fitted to 15:1 R/S ratio (Table 1). These results suggesting the action of two dominant resistance genes, one of them present in the JP2 cultivar and the another in the remaining cultivars. Segregation in the F_2 population derived

from the cross between JP2 and cultivar Mexico 222 fit a ratio of 63:1 R/S, indicating that there are three dominant genes segregating for resistance to race 2 of *C. lindemuthianum*. The two dominant loci in Mexico 222 confers resistance to race 2.

Table 1. Inheritance and allelism tests for genetic characterization of anthracnose resistance in Jalo Pintado 2. Reaction of F_2 populations observed and expected ratios of resistant (R) and susceptible (S) plants to inoculation with different races of *C. lindemuthianum*

Crosses	Race	Resistance Gene	Observed Ratio		Expected Ratio		*P* Value
			R	S	R:S		
JP 2*× Cornell 49-242	73	*Co-2*	73	27	3:1	0.213	0.644
JP 2 × Mexico 222	2	*Co-3*	98	2	63:1	0.124	0.724
JP 2 × Michelite	2	*Co-11*	89	6	15:1	0.001	0.978
JP 2 × Cornell 49-242	65	*Co-2*	61	4	15:1	0.001	0.974
JP 2 × TO	65	*Co-4*	105	7	15:1	0	1
JP 2 × PI 207262	65	*Co-4*^{3}	97	6	15:1	0.031	0.858
JP 2 × TU	65	*Co-5*	94	5	15:1	0.243	0.621
JP 2 × AB 136	65	*Co-6*	108	7	15:1	0.005	0.942
JP 2 × Jalo Vermelho	65	*Co-12*	94	5	15:1	0.010	0.917
JP 2 × MDRK**	73	*Co-1*	91	6	15:1	0.001	0.979
JP 2 × Ouro Negro	73	*Co-3*^{4}	94	6	15:1	0.010	0.917
JP 2 × Jalo Listras Pretas	73	*Co-13*	80	5	15:1	0.019	0.888
JP 2 × G2333	2047	*Co-4*^{2}	147	10	15:1	0.003	0.950
JP 2 × Pitanga	2047	*Co-14*	111	7	15:1	0.020	0.886
JP 2 × Corinthiano	2047	*Co- 15*	87	6	15:1	0.006	0.936
JP 2 × Crioulo 159	2047	*Co-16*	93	5	15:1	0.220	0.638
JP 2 × A. Cavalo***	2047	NI	94	6	15:1	0.010	0.917
JP 2 × Paloma	2047	NI	90	6	15:1	0	1
JP 2 × Perla	2047	NI	97	6	15:1	0.031	0.858

* Jalo Pintado 2, ** Michigan Dark Red Kidney, ***Amendoim Cavalo, NI: Gene not identified yet

CONCLUSION

These results demonstrated that the Jalo Pintado 2 cultivar possesses one dominant gene segregating independently from those previously characterized: *Co-1, Co-2, Co-3, Co-3*^{4} *, Co- 4, Co-4*^{2}*, Co-4*^{3}*, Co-5, Co-6, Co-11, Co-12, Co-13, Co-14, Co-15* and *Co-16*. This new gene is a valuable source of resistance to anthracnose which can be transferred to commercial cultivars to enhance the effectiveness of resistance gene pyramiding in bean breeding programmes.

REFERENCES

Cruz CD (2006). Editora: UFV, Viçosa.
Pastor-Corrales MA, Otoya MM, Molina A, Singh SP (1995). Plant Disease 79: 63-67.
Pastor-Corrales MA, Tu JC (1989). CIAT, Cali, Colombia, p. 77–104.
Vidigal Filho PS, Gonçalves-Vidigal MC, Kelly JD, Kirk, WW (2007). Phytopathology 155: 108–113.

COMMON BEAN WHITE MOLD RESISTANCE SOURCES IDENTIFIED BY GREENHOUSE SCREENING IN BRAZIL

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INTRODUCTION

White mold (WM) caused by *Sclerotinia sclerotiorum* (Lib.) de Bary is a major disease problem for the common bean crop worldwide (Schwartz and Steadman, 1989). WM can cause severe yield and seed quality losses, which dramatically reduce farmer incomes. In Brazil, *S. sclerotiorum* is widely distributed in the majority of agricultural areas and can cause total yield losses under favorable environmental conditions and without chemical control (Oliveira, 2005). The main goal of the present work was to evaluate the reaction of 39 common bean lines to WM in a greenhouse screening. These bean genotypes include Brazilian cultivars and advanced lines from different market classes, in addition to resistance sources previously reported by CIAT (Cali, Colombia). The effective identification of resistance sources and superior genotypes is a basic and continuous step of breeding efforts aiming to develop/select resistant cultivars to be used in the integrated control of WM.

MATERIAL AND METHODS

Common bean genotypes were grown in a completely randomized design with six replications composed by one plant each. Plants were inoculated at the fourth/fifth node, about 35 days after seedling emergence (R5 stage), using the *S. sclerotiorum* isolate SS 1370, the most virulent one maintained at Embrapa Rice and Beans (Santo Antônio de Goiás, Brazil). Inoculation was accomplished based on the straw test method initially reported by Petzoldt and Dickson (1996), but with modifications. The inoculum (mycelial plugs) was grown for 72 h on PDA medium at 21 ± 1ºC. Plants were inoculated with mycelial plugs using micropipette tips of 200 μL with filter. After inoculation, plants were kept under greenhouse condition (28 ± 1ºC and relative humidity > 85%). WM severity was scored at eight days after the inoculation using a 1-to-9 scale, where 1= no symptoms and 9= dead plants. All six plants of the same genotype were evaluated and the mean scores of disease severity were calculated. Variance analysis was performed followed by the Scott-Knott test.

RESULTS AND DISCUSSION

The results showed significant genetic variation for WM reaction among the 39 screened common bean lines (ANOVA, F test at 1% probability), which were grouped on five resistance levels according to Skott-Knott test at 5% probability. Cultivar BRS Cometa and the advanced line CNFC 9500, both "carioca" seeded genotypes, in addition to the CIAT variety K0407, formed the group with lower severity scores, showing to be potential WM resistance sources to Brazil (Table 1). The "carioca" seeded cultivars BRS Estilo, Pérola, BRS Pontal, BRSMG Madrepérola, and BRS Requinte, in addition to the local variety Bola Cheia, formed the genotype group with high mean severity scores, which range from 6.50 to 8.17 (Table 1). The obtained results are agreed with previous reports from field screening realized in Brazil. The