

## Short Communication

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# Association of Dominant and Recessive Genes Confers Anthracnose Resistance in Stem and Leaves of Common Bean

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### Abstract

Different genes might be involved in *Colletotrichum lindemuthianum* resistance in leaves and stem of common bean. This work aimed to study the genetic mechanisms of the resistance in the leaf and stem in segregating populations from backcrosses involving resistant cultivar AN 910408 and susceptible cultivar Rudá inoculated with spore suspensions of *C. lindemuthianum* race 83. Our results indicate that two genes which interact epistatically, one dominant and one recessive, are involved in the genetic control of leaf anthracnose resistance. As for stem anthracnose resistance, two genes also epistatic, one dominant and one recessive, explain the resistance to *C. lindemuthianum* race 83. The recessive gene is the same for leaf and stem resistance; however, the dominant genes are distinct and independent from each other. The three independent resistance genes of AN 910408 observed in this work could be derived from Guanajuato 31.

### Introduction

Anthracnose caused by the ascomycete *Colletotrichum lindemuthianum* (Sacc. and Magn.) Lams-Scrib. is one of the most important diseases of the common bean (*Phaseolus vulgaris* L.) in Brazil and in other bean growing regions of the world (Balardin et al., 1997). Typical symptoms of common bean anthracnose are observed in the leaf and in pods. However, if the environment favours the development of fungus, injuries in the stem can also be observed. This may weaken the stem and impair its capacity to support the plant. Differential symptoms in leaves and stem were observed in segregating populations derived from backcrosses involving common bean Brazilian cultivar AN 910408, resistant to *C. lindemuthianum* races 64, 67, 73 and 83,

with susceptible recurrent parent cultivar Rudá. This led to the hypothesis that different genes might be involved in resistance in leaves and stem. Thus, this work aimed to study the genetic mechanisms of the resistance in the leaf and stem in segregating populations from backcrosses involving resistant cultivar AN 910408 and susceptible cultivar Rudá.

### Materials and Methods

BC<sub>4</sub>F<sub>2</sub> plants with small 'carioca-type' seeds derived from crosses between cultivars Rudá (Carioca × Rio Tibagi) (recurrent susceptible) and AN 910408 (Carioca × [Carioca (Rio Tibagi × Guanajuato 31)]) (donor resistant) were used. These crosses are part of a common bean backcross breeding programme assisted by molecular markers conducted at the Universidade Federal de Viçosa, Viçosa, MG, Brazil.

Carioca and Rio Tibagi have small cream beige and black seeds, respectively, and are popular cultivars in central and southern Brazil (Singh et al., 2001; Alzate-Marin et al., 2003). Guanajuato 31 is a beige-coloured, medium-seeded (25–40 g/100 seed) landrace from the semi-arid central highlands of Mexico. It is high yielding, has a high harvest index, and is resistant to anthracnose [caused by *C. lindemuthianum* (Sacc. and Magn.) Lams.-Scrib.] (Singh et al., 2001). More specifically, crosses involving this cultivar indicate that it possesses resistance genes to *C. lindemuthianum* races 6, 31, 38, 39 and 357 (Rodriguez-Suarez et al., 2007). Rio Tibagi and Carioca belong to race Mesoamerica, and Guanajuato 31 belongs to race Durango.

One hundred and sixty BC<sub>4</sub>F<sub>2</sub> plants and twelve plants of each genitor (Rudá and AN 910408) were sown in the greenhouse. Fourteen days after sowing the first expanded trifoliolate leaf of each plant was inoculated with spore suspensions of *C. lindemuthianum*

Table 1  
Separate analyses for common bean leaf and stem anthracnose resistance to *C. lindemuthianum* race 83

Hypothesis <sup>a</sup>	Population	Organ	Observed ratio		Expected ratio		Expected frequency		$\chi^2$	Probability (%)
			R	S	R	S	R	S		
1:3 (R:S)	Rudá × AN 910408	Leaf	32	128	40	120	1/4	3/4	2.193	14.41
3:13 (R:S)	Rudá × AN 910408	Leaf	32	128	30	130	3/16	13/16	0.106	68.54
1:3 (R:S)	Rudá × AN 910408	Stem	24	136	40	120	1/4	3/4	8.53	0.349
3:13 (R:S)	Rudá × AN 910408	Stem	24	136	30	130	3/16	13/16	1.477	22.42

<sup>a</sup>1:3 = Resistance is conferred by one recessive gene; 3:13 = Resistance is only conferred when one dominant and one recessive genes are present.

Table 2  
Hypothesis test for combined inheritance of common bean leaf and stem anthracnose resistance in cultivar AN 910408

Reaction		Hypothesis 1 <sup>a</sup>					Hypothesis 2 <sup>b</sup>					Hypothesis 3 <sup>c</sup>			
Leaf	Stem	Observed number	Expected frequency	Expected number	$\chi^2$	P	Expected frequency	Expected number	$\chi^2$	P	Expected frequency	Expected number	$\chi^2$	P	
S <sup>d</sup>	S	125	43/64	107.5	49.93	0%	49/64	122.5	4.48	21.37%	39/64	97.5	63.18	0%	
R <sup>e</sup>	S	11	9/64	22.5			3/64	7.5			13/64	32.5			
S	R	3	9/64	22.5			3/64	7.5			9/64	23.5			
R	R	21	3/64	7.5			9/64	22.5			3/64	7.5			

<sup>a</sup>Hypothesis 1: Anthracnose resistance in leaf and stem is given by  $A\_bbcc$ ; leaf resistance is given by  $A\_bb$  and stem resistance by  $A\_cc$ .

<sup>b</sup>Hypothesis 2: Anthracnose resistance in leaf and stem is given by  $A\_bbC\_$ ; leaf resistance is given by  $A\_bb$  and stem resistance by  $bbC\_$ .

<sup>c</sup>Hypothesis 3: Anthracnose resistance in leaf and stem is given by  $A\_bbC\_$ ; leaf resistance is given by  $A\_$  and stem resistance by  $bbC\_$ .

<sup>d</sup>Susceptible.

<sup>e</sup>Resistant.

race 83. Spores ( $1.2 \times 10^6$  conidia/ml) were sprayed onto the plants with the aid of a DeVilbiss apparatus. The plants were incubated and maintained in a mist chamber (20–22°C, 100% relative humidity) for 7 days. After this period, each plant was scored visually for disease symptoms as described by Alzate-Marín et al. (2007). For evaluation of anthracnose symptoms in the stem, plants with no symptoms or with very small dark brown lesions were evaluated as resistant. Plants with severe symptoms showing depressed and obscure cankers leading or not to stem breakage were considered susceptible. The observed values of resistant and susceptible plants were compared with the expected values, for each tested hypothesis, through the Chi-square test.

## Results and Discussion

Our results indicate that two genes which interact epistatically, one dominant and one recessive, are involved in the genetic control of leaf anthracnose resistance when this cultivar was inoculated with *C. lindemuthianum* race 83 (Table 1). As for stem anthracnose resistance, two genes also epistatic, one dominant and one recessive, explain the resistance to *C. lindemuthianum* race 83 (Table 1). For leaf resistance, the hypothesis of one recessive gene could also be accepted, but the probability associated with this hypothesis shows strong evidence that the leaf resistance is controlled by two epistatic genes (Table 1; hypothesis 3, Table 2).

The combined analysis of anthracnose symptoms in leaves and stems in a BC<sub>4</sub>F<sub>2</sub> population (Rudá × AN

910408) showed that 21 plants did not present any symptoms in leaves or stems, whereas 11 showed symptoms only in stems, 3 showed symptoms only in leaves, and 125 showed symptoms in both organs (Table 2). Although these two characteristics present the same genetic control when analyzed separately (segregation 3:13, Table 1), the hypothesis that both are controlled by the same genes was rejected, because there were individuals that presented leaf resistance but stem susceptibility, and the opposite was also true. Our analyses indicate that the recessive gene is the same for leaf and stem resistance; however, the dominant genes are distinct and independent from each other (hypothesis 2 – Table 2).

Previous molecular works have reported the existence of major effect QTL's associated with specific organs in common bean. Three of them, positioned on linkage groups (LG) B3, B7 and B11, were found to have significant effects on stem resistance, one QTL on LG B2 was associated with leaf resistance and the remaining QTL on the middle of LG B4 was involved in petiole resistance (Geffroy et al., 2000). Possibly the independent *C. lindemuthianum* resistance genes detected in cultivar AN 910408 can be part of the quantitative locus observed by Geffroy et al. (2000). Recently, a LOD score calculation has been developed to map two independent segregating genes (Geffroy et al., 2008). This method could be used to map the resistance genes reported in this work to determine if they are located near the QTL described in Geffroy et al. (2000).

Since Rudá (Carioca × Rio Tibagi) is susceptible to *C. lindemuthianum* race 83, the resistance genes observed in AN 910408 (Carioca × [Carioca (Rio Tibagi × Guanajuato 31)]) could be derived from Guanajuato 31, the other genitor of AN 910408.

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