

IDENTIFICATION OF ANTHRACNOSE RESISTANCE GENES IN COMMON BEAN CULTIVARS FROM PARANÁ STATE, BRAZIL

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INTRODUCTION

The anthracnose caused by *Colletotrichum lindemuthianum* is one of the main diseases that occurs in common bean crop. The use of resistant cultivars is characterized as one of the most efficient and economic alternatives in the control of this disease (Mahuku et al., 2002). For this matter, the utilization of assisted selection by molecular markers intimately linked to alleles of interest has shown efficiency on identifying host genotypes of alleles that confer resistance to anthracnose (Kelly and Vallejo, 2004). The allele *Co-4*² can be identified by the molecular marker SCAR SAS13₉₅₀ (Young et al., 1998). The present work had the objective to identify SCARs molecular markers linked to *Co-10* and *Co-4*² genes in common bean accessions and lines derived from the backcross Pérola x G 2333.

MATERIAL AND METHODS

Forty common bean accessions from Germplasm Bank of Núcleo de Pesquisa Aplicada à Agricultura (Nupagri) and 233 lines F₂RC₃ derived from backcross Pérola x G 2333 were analyzed to verify the presence of SCARs SF10₁₀₇₂ markers linked to *Co-10* resistant gene and SAS13₉₅₀, linked to *Co-4*² resistant allele. The DNA extracted from the 40 accessions was used as template for amplification reactions according to a methodology proposed by Edwards et al. (1991). The amplification reactions used the SCAR SAS13₉₅₀ marker. Trust analysis was carried out using data from resistant plants with presence of marker (R+), resistant plants without the marker (R-), susceptible plants with absence of marker (S-), and finally susceptible plants with marker (S+). Through these data trust marker, (T) was calculated for identification of resistance in the accesses utilizing the formula: $T = (R++R-)/(R++R-+S++S-)$.

RESULTS AND DISCUSSION

The combined genotype analysis estimated by markers and race reactions showed that most cultivars possess at least one resistance gene from Mesamerican cultivars (*Co-2*, *Co-3* and *Co-11* or *Co-4*²). Marker OPAS13₉₅₀ was present in three cultivars resistant to races 73 and 2047. The magnitude of the trust analysis was 62 and 59%, respectively for SCARs SF10₁₀₇₂ and SAS13₉₅₀ (Figure 1). The accessions Carioca Claro, Preto III, BGF12 and BGF13 exhibited the presence of the molecular markers SF10₁₀₇₂ and SAS13₉₅₀ (Table 1). The marker linked to *Co-4*² allele was observed in accessions Carioca I, Carioca IV, Jalo Pardo, BGF3, BGF4, BGF6, BGF8, BGF11, BGF14, BGF16, BGF17, BGF19 and BGF20. However, Carioca V, Carioca VI, Carioca Pintado I, Preto I and Preto II showed the presence of marker linked to *Co-10* gene. Out of the 233 F₂RC₃ lines analyzed by molecular markers, 80 of them revealed the presence of SAS13₉₅₀ linked to *Co-4*² allele.

Table 1 - Amplification standard of the SCARs SF10₁₀₇₂ and SAS13₉₅₀ and resistance to races 73 and 2047 in thirty-seven common bean accessions

Accessions	Pathotype of <i>C. lindemuthianum</i>		Presence of molecular marker	
	73	2047	SF10 ₁₀₇₂	SAS13 ₉₅₀
BGF 1	S	R	-	+
BGF 2	S	R	-	-
BGF 3	S	R	-	+
BGF 4	R	S	-	-
BGF 5	S	R	-	-
BGF 6	R	R	-	+
BGF 9	S	R	+	+
BGF 11	R	R	-	+
BGF 12	R	S	+	+
BGF 13	R	S	+	+
BGF 14	S	S	-	+
BGF 16	R	S	-	+
BGF 17	R	S	-	+
BGF 18	S	R	-	-
BGF 19	R	S	-	+
BGF 20	R	R	-	+
Carioca I	S	S	-	+
Carioca II	S	S	-	-
Carioca III	S	S	-	-
Carioca IV	S	S	-	+
Carioca V	S	S	+	-
Carioca VI	S	S	+	-
Carioca Claro	S	S	-	+
Carioca Pintado I	S	S	-	-
Carioca Pintado II	R	S	-	-
Carioca Pitoko	S	S	-	-
Iapar 31	S	S	-	-
Preto I	S	S	+	-
Preto II	S	S	+	-
Preto III	S	S	+	+
Preto IV	S	S	-	-
Rosinha	S	R	-	-
Jalo Listras Pretas	S	S	+	-
Jalo Pardo	S	S	-	+
Jalo Mulato	S	S	-	-
Jalo Pintado I	S	R	-	+
Bolinha	S	S	-	-

(+) Presence of resistance mark; (-) Absence of resistance mark.

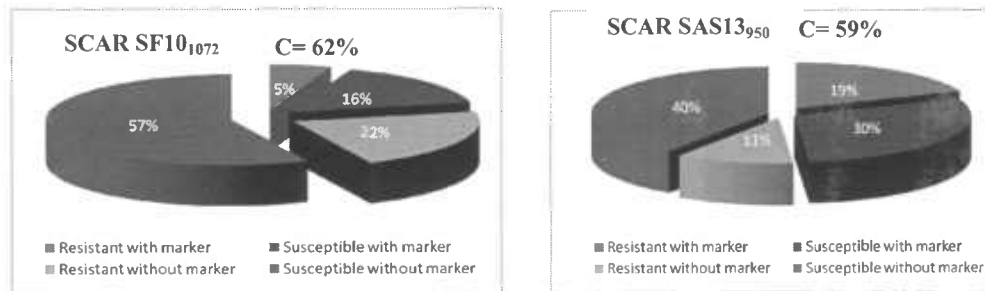


Figure 1. Results of the molecular analyses with the SCAR markers SF10₁₀₇₂ and SAS13₉₅₀ and reaction to races 73 and 2047 of *C. lindemuthianum* in 40 accessions of common bean.

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