

MOLECULAR MARKER ASSISTED INTRODUCTION OF RESISTANCE GENES FOR RUST, ANTHRACNOSE AND ANGULAR LEAF SPOT INTO COMMON BEAN CULTIVAR BRSMG TALISMÃ

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The new common bean (*Phaseolus vulgaris* L.) cultivars released in Brazil must present a high disease resistance spectrum, as diseases are among the main causes for the low productivity of this crop in the country. BRSMG Talismã is a “carioca-type” cultivar which meets the market demands. The seeds are medium sized, beige with light brown stripes, with clear background, and colorless hylum). In addition, field evaluations demonstrate that BRSMG Talismã surpasses the most cultivated “carioca-type” varieties in Brazil by approximately 10%. However, this cultivar is highly susceptible to several races of *Uromyces appendiculatus*, *Colletotrichum lindemuthianum* and *Pseudocercospora griseola* (SOUZA et al., 2005). A “carioca-type” line Pérola “R” was developed by the Bean Breeding Program of BIOAGRO/UFV with the following resistance genes and respective linked molecular markers: *Ur-ON* (SCF10_{1050a} and SCBA08_{560a}), *Co-4* (SCY20_{830a}), *Co-6* (SCAZ20_{845a}), *Co-10* (SCF10_{1050a} and SCBA08_{560a}) and *Phg-1* (SCH13_{520a}). The objective of this work was to simultaneously transfer the resistance genes to rust (*Ur-ON*), anthracnose (*Co-4*, *Co-6* and *Co-10*) and angular leaf spot (*Phg-1*) present in Pérola “R” to the cultivar BRSMG Talismã with the aid of molecular markers.

In a previous work, DNA samples from BRSMG-Talismã and Pérola “R” amplified with those molecular markers showed they were polymorphic indicating that those markers could be used to assist the breeding process (Table 1). Crossings were made between the Pérola “R” and BRSMG Talismã in the greenhouse. The hybrid nature of the F₁ plants was confirmed with molecular marker SCF10_{1050a}. Molecular markers linked to the resistance genes were used in the F₂ and F₃ generations (Figure 1). For each generation analyzed, a leaf of each plant was collected and stored at -80°C for DNA extraction (DOYLE & DOYLE, 1990). From 17 F₁ plants, 476 F₂ seeds were produced. Out of those, 300 were sown, yielding 276 plants, which were inoculated with *P. griseola* race 63.23. Out of the 276 plants, 78 were susceptible to angular leaf spot, suggesting that they did not possess the resistance allele *Phg-1*. The 198 F₂ plants left were analyzed with the molecular markers mentioned in Table 1. These analyses showed that 18 plants harbored all the molecular markers for the three diseases. These plants were used to produce the F₃ generation. They were planted in a structure of families so progeny tests could be performed with the use of molecular markers. For the formation of each family, 15 seeds of each one of the 18 F₂ plants were sown. Two non-segregating families for all the molecular markers were identified.

The material to be reached at the end of the breeding process started in this work, after being tested for resistance and agronomic performance, may be released as a new cultivar and be used as a resistance gene source.

Table 1. Molecular markers linked to resistant genes to rust, anthracnose and angular leaf spot used in the transfer process

Marker	Distance ^a (cM)	Resistance gene	Resistance Sources	Reference
SCAR-Y20 _{830a}	1.20	<i>Co-4</i>	TO	QUEIROZ et al. (2004b)
SCAR-AZ20 _{845a}	7.10	<i>Co-6</i>	AB 136	QUEIROZ et al. (2004b)
SCAR-BA08 _{560a}	2.20	<i>Co-10</i> and <i>Ur-ON</i>	Ouro Negro	CORRÊA et al. (2000)
SCAR-F10 _{1050a}	6.50	<i>Co-10</i> and <i>Ur-ON</i>	Ouro Negro	CORRÊA et al. (2000)
OPX11 _{550a}	5.80	<i>Co-10</i> and <i>Ur-ON</i>	Ouro Negro	FALEIRO et al. (2000)
SCAR-H13 _{520a}	5.60	<i>Phg-1</i>	AND 277	QUEIROZ et al. (2004a)

^acM: genetic distance (centiMorgan) from the molecular marker to the resistance gene.

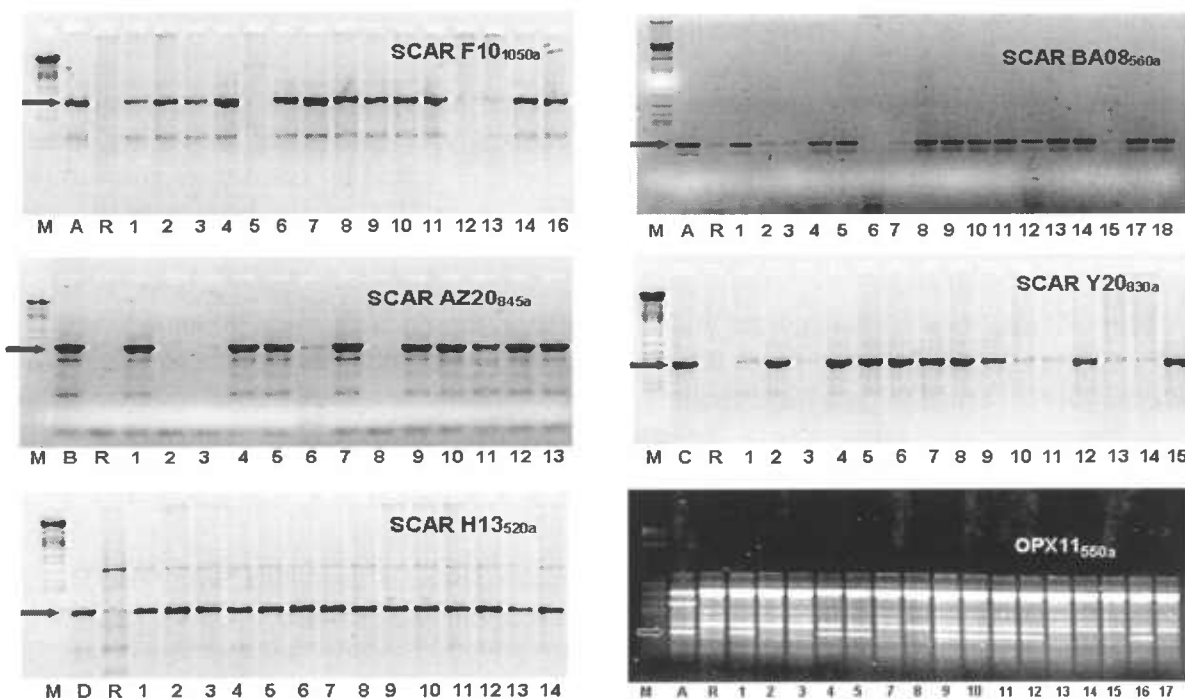


Figure 1. Amplification products obtained with markers SCARF10_{1050a}, SCBA08_{560a}, SCAZ20_{845a}, SCY20_{830a}, SCH13_{520a} and OPX11_{550a}. Lane M: Lambda phage DNA digested with *EcoRI*, *BamHI*, *HindIII* (size markers). Lanes R, A, B, C and D: Rudá, Ouro Negro, AB136, TO and AND 277, respectively, followed by part of the F₂ population (Pérola “R” x BRSMG Talismã). The arrows indicate the bands linked to the resistance loci.

REFERENCES

- CORRÊA, R.X., et al. Sequence characterized amplified regions linked to rust resistance genes in the common bean. *Crop Science*, 40: 804-807, 2000.
- DOYLE, J.J. and DOYLE, J.L. Isolation of plant DNA from fresh tissue. *Focus*, 12: 13-15, 1990.
- FALEIRO, F.G. et al. RAPD markers linked to a block of genes conferring rust resistance to the common bean. *Genetics and Molecular Biology*, 23: 399-402, 2000.
- QUEIROZ, V. T., et al. Development of SCAR markers linked to common bean angular leaf spot resistance genes. *Annual Report of the Bean Improvement Cooperative*, 47: 237-238, 2004a.
- QUEIROZ, V. T., et al. Development of SCAR markers linked to common bean anthracnose resistance genes *Co-4* and *Co-6*. *Annual Report of the Bean Improvement Cooperative*, 47: 249-250, 2004b.
- SOUZA, T.L.P.O., et al. Phenotypic and molecular characterization of cultivar BRSMG-Talismã regarding the principal common bean pathogens. *Crop Breeding and Applied Biotechnology*, 5: 247-252, 2005.