PROGENY TESTS FOR COMMON BEAN ISOLINES RESISTANT TO DISEASES WITH THE AID MOLECULAR MARKERS

Sanglard, D. A.^{1*}; Machado, M. A. M.¹; Batista, F.E.R.¹; Rocha, F. S.¹; Souza, T. L. P. O.² and Barros, E. G.³

¹ICA/UFMG, Montes Claros, MG 39.404-547, Brazil; ²Embrapa Arroz e Feijão (CNPAF), Santo Antônio de Goiás, GO 75375-000, Brazil; ³UCB, Brasília, DF 70.790-160 Brazil demerson.ufmg@gmail.com

INTRODUCTION - Bean (*Phaseolus vulgaris* L.) is one of the most important vegetables in the human diet, mainly due to their nutritional qualities (Maldonado, 2002). One of the major factors limiting their productivity are the fungi that cause rust (*Uromyces appendiculatus*), anthracnose (*Colletotrichum lindemuthianum*) and angular leaf spot (*Pseudocercospora griseola*) in common bean. The aim of this study was progeny tests in segregating populations for resistance genes to these three diseases.

MATERIAL AND METHODS - From the F_2 population [(MAR-138A-1-11-4 x BAT-67-15-8) x Rudá R] carrier resistance genes to angular leaf spot, anthracnose and rust (Sanglard et al., 2007); were advanced two generations in the greenhouse using the pedigree method (*bulk* within families). During this process, tests were conducted for the presence of resistance gene using molecular markers. Evaluations of disease (angular leaf spot, anthracnose and rust) followed the methodology proposed by Pastor-Corrales & Jara (1995), Pastor-Corrales (1992) and Stavely et al. (1983).

RESULTS AND DISCUSSION - Of the 292 individuals F₂ [(MAR-138A-1-11-4 x BAT-67-15-8) x Ruda R], were selected 63 in the presence of SCAR (Sequence Characterized Amplified Regions) molecular markers: SF101050c, SBA08560c, SY20830c, SAZ20845c, SH13520c, SAO12950c, SAA07950c and SE04_{640c} (Sanglard et al., 2007). For planting the next generation, grains were selected within the standard "carioca" genetic *background* 'Ruda'. According to Santos et al. (2001), the early selection of the characteristic type of grain is very efficient due to its high heritability. In F₃ generation [(MAR-138A-1-11-4 x BAT-67-15-8) x Ruda R] were obtained 50 genotypes carrying all molecular markers amplified in the previous generation. Also in the greenhouse, the F₄ generation [(MAR-138A-1-11-4 x BAT-67-15-8) x Ruda R] was sown in family structure for conducting progeny tests. Fifty families were inoculated F_{3:4} [(MAR-138A-1-11-4 x BAT-67-15-8) x Ruda R] sequentially with 21-3 races of U. appendiculatus, 65 of C. lindemuthianum and 63.23 of P. griseola (Table 1). Nine segregating families were discarded, seven to rust and two for anthracnose. Segregating families to rust have not been evaluated for the other diseases (families underlined in Table 1). In addition the evaluations through inoculations, five plants were chosen randomly from each of 41 families segregating for molecular analysis. Were used the same molecular markers described above. We selected 39 common bean families "carioca" containing resistance genes to angular leaf spot, anthracnose and rust. The combined use of phenotypic and molecular evaluations increases reliability in the selection processes.

REFERENCES

Pastor-Corrales, MA. In: Pastor-Corrales, MA. (Ed.), La Antracnosis del Frijol Común, *Phaseolus vulgaris*, en América Latina, p.212-239 (Doc de trabajo, 113). CIAT, Cali. 1992.

Maldonado, SHG et al. Agricultura Técnica en Mexico, 28(2):159-173, 2002.

Pastor-Corrales, MA; Jara, CE. La evolución de *Phaeoisariopsis griseola* com el frijol común em América Latina. Fitopatologia Colombiana, 19:15-24, 1995.

Sanglard, DA et al. Introgression of angular leaf spot resistance genes in common bean isolines. BIC, v.50, p.101-102, 2007.

Santos, VS et al. Implications of early selection for grain type in common bean breeding. BIC, 44:13-14, 2001. Stavely, JR et al. The 1983 Bean Rust Workshop. BIC, 26:4-6, 1983.

Families 21-3 R S R3-4-20-4 15 0 R3-4-20-11 13 0 R3-4-20-16 15 0 R3-4-20-27 15 0	65 R 15 13 15 15 15	5 S 0 0 0 0	63. R 15 13	23 <u>S</u> 0	Families	21- R	-3 S	6	5	63.	23
R S R3-4-20-4 15 0 R3-4-20-11 13 0 R3-4-20-16 15 0 R3-4-20-27 15 0	R 15 13 15 15	S 0 0 0	R 15 13	S 0	- 	R	S				
R3-4-20-4150R3-4-20-11130R3-4-20-16150R3-4-20-27150	15 13 15 15	0 0 0	15 13	0	D2 14 26 15		0	R	S	R	S
R3-4-20-11130R3-4-20-16150R3-4-20-27150	13 15 15	0 0	13		R3-14-26-15	13	0	13	0	13	0
R3-4-20-16150R3-4-20-27150	15 15	0		0	R3-15-25-7	12	2				
R3-4-20-27 15 0	15		15	0	R3-15-25-10	13	0	13	0	13	0
		0	15	0	R3-15-25-13	15	0	15	0	15	0
R3-7-23-10 14 0	14	0	14	0	R3-16-17-4	14	0	13	1		
R3-8-2-5 15 0	15	0	15	0	R3-16-17-9	15	0	15	0	15	0
R3-8-2-18 15 0	15	0	15	0	R3-16-17-12	12	0	12	0	12	0
R3-8-2-22 12 2					R3-16-17-13	13	0	13	0	13	0
R3-8-2-23 10 5					R3-21-18-3	14	0	14	0	14	0
R3-10-11-5 15 0	15	0	15	0	R3-21-18-5	15	0	15	0	15	0
R3-10-11-9 15 0	15	0	15	0	R3-21-18-9	14	0	14	0	14	0
R3-10-11-15 15 0	15	0	15	0	R3-21-18-11	15	0	15	0	15	0
R3-10-11-24 15 0	15	0	15	0	R3-21-18-17	15	0	15	0	15	0
R3-12-42-6 8 5					R3-21-18-19	15	0	15	0	15	0
R3-12-42-14 8 7					R3-21-18-22	15	0	15	0	15	0
R3-12-42-15 14 0	14	0	14	0	R3-21-18-25	11	0	11	0	11	0
R3-12-43-1 0 11					R3-27-11-18	12	0	12	0	12	0
R3-12-43-6 12 0	12	0	12	0	R3-27-11-26	15	0	15	0	15	0
R3-12-43-8 10 3					R3-35-6-2	15	0	15	0	15	0
R3-14-26-2 15 0	15	0	15	0	R3-35-6-8	14	0	14	0	14	0
R3-14-26-8 15 0	15	0	15	0	R3-35-6-10	15	0	15	0	15	0
R3-14-26-9 15 0	14	1			R3-35-6-13	14	0	14	0	14	0
R3-14-26-12 15 0	15	0	15	0	R3-35-6-17	15	0	15	0	15	0
R3-14-26-13 12 0	12	0	12	0	R3-35-6-20	13	0	13	0	13	0
R3-14-26-14 15 0	15	0	15	0	R3-35-6-21	14	0	14	0	14	0

Table 1. Progeny tests performed for families $F_{3:4}$ [(MAR-138A-1-11-4 x BAT-67-15-8) x Ruda R] inoculated with the races 63.23 of *P. griseola*, 65 of *C. lindemuthianum* of 21-3 de *U. appendiculatus*

R: resistant; S: susceptible; Underlined lines refer to families segregating.