

## CHARACTERIZATION OF THE RESISTANCE LOCUS TO ANGULAR LEAF SPOT IN THE COMMON BEAN ACCESS 'JAPONÊS'

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**INTRODUCTION** - The angular leaf spot caused by the fungus *Pseudocercospora griseola* (Sacc.) Crous & U. Braun, is a major diseases that causes large losses to common bean producers (Pastor-Corrales et al., 1998). The allelism test is commonly used to determine whether various phenotypes of a given character, observed in a population of individuals, by participation of a number of alleles or genetic interaction. This test consists of crossing the individuals with the many phenotypes, two by two, in all possible combinations and study the phenotypic segregation in offspring. If a different monogenic inheritance is found, there is a case of gene interaction and not multiple allelic. Thus, this study aimed to characterize the R loci for resistance to angular leaf spot, present in 'Japanese' creole access, in relation to the five other related sources.

**MATERIAL AND METHODS** - For allelic tests, genotypes 'Azulão', 'Carioca Precoce', 'Casquinha', 'Criangu', 'Pardo' and 'Madrepérola' were crossed with 'Japonês'. In all cases, 'Japonês' genotype was used as pollen donor. F<sub>2</sub> populations from each cross were used to test the allelic. To ensure that the F<sub>1</sub> seeds were actually the result of hybridization, we analyzed the color, shape, size and brightness of the F<sub>2</sub> seeds. To support the understanding of allelic relations was executed also heritage studies. The genotypes 'Azulão', 'Carioca Precoce', 'Casquinha', 'Criangu' and 'Pardo' were crossed with 'Madrepérola'. In all cases, 'Madrepérola' was the female parent. Main populations were used in inoculations with races 63.23 and 63.39, which are known to be aggressive and virulent. The suspension of conidia of each race was obtained by scraping the surface of the fungus colonies grown in Petri dishes containing a mixture of distilled water, tomato sauce, agar and calcium carbonate (CaCO<sub>3</sub>), for 12 days at 24°C. This suspension was filtered through cheesecloth and then adjusted to a final concentration of 2.0 x 10<sup>4</sup> conidia/mL (Sanglard et al., 2009). The chi-square test ( $\chi^2$ ) were analyzed using the GENES program (Cruz, 2006).

**RESULTS AND DISCUSSION** - The race 63.63 was inoculated in F<sub>2</sub> populations (Japonês x Azulão), F<sub>2</sub> (Japonês x Casquinha), F<sub>2</sub> (Japonês x Criangu) and F<sub>2</sub> (Japonês x Pardo), yielding the pattern of segregation of two genes typically 15:1 (two independent dominant genes) and genes involved three (63:1, 61:3 and 60:4, respectively). The F<sub>2</sub> population (Japonês x Casquinha) did not indicate gene interaction by presenting a segregation of 63:1 (three independent dominant genes), indicating the simultaneous participation of two genes present in 'Casquinha'. The inheritance study of this population resulted in a segregation of 15:1, which corroborates with this idea. Similar results were observed in inoculation with race 63.39, when the populations F<sub>2</sub> (Japonês x Casquinha) and F<sub>2</sub> (Japonês x Criangu) also showed segregation of 63:1 and 15:1, respectively. The F<sub>2</sub> population (Japonês x Carioca Precoce) segregated in 13:3 for this breed, a typical behavior of digenic inheritance where two epistatic genes, one dominant and one recessive, respectively. From the reviews in this work, it is suggested that the locus genotype present in the 'Japonês', distinct from other sources studied. Allelic tests are particularly important for breeding programs aimed at the pyramiding of different genes that confer resistance to different races of a pathogen. The pyramiding of genes has been suggested as a strategy of obtaining genotypes with

durable resistance. The accumulation of resistance genes with major effects on a genotype delays the appearance of new races of the pathogen (Servin et al., 2004). The basis for the stability of resistance is the reduction of the pathogen avirulence adaptation when multiple genes must be inactivated to "break" host resistance (Van der Plank, 1984). Therefore, the intercrossing of these materials analyzed lines derived from 'Japonês' is justified and possibly would increase the spectrum of resistance to *P. griseola* races.

**Table 1.** Allelism tests and inheritance studies for genetic characterization of resistance to *P. griseola* present in the access 'Japonês'

Cross	Race (isolate)	F <sub>2</sub> plants		<sup>a</sup> Expected ratio		Value of $\chi^2$	P (%)
		R	S	R	S		
Japonês x Azulão	63.63 (158-1)	421	27	15	1	0.0140	97.0072
Japonês x Carioca Precoce	63.39 (29-3)	389	74	13	3	0.0449	83.2113
Japonês x Casquinha	63.63 (158-1)	512	14	63	1	0.2984	58.4875
Japonês x Casquinha	63.39 (29-3)	334	4	63	1	0.0786	77.9149
Japonês x Criangu	63.63 (158-1)	356	16	61	3	0.0232	87.8891
Japonês x Criangu	63.39 (29-3)	345	24	15	1	0.0016	96.7127
Japonês x Pardo	63.63 (158-1)	339	22	60	4	0.0027	95.8442
Japonês x Madrepérola	63.63 (158-1)	226	71	3	1	0.1698	62.8720
Japonês x Madrepérola	63.39 (29-3)	367	123	3	1	0.2661	57.7021
Azulão x Madrepérola	63.63 (158-1)	140	43	3	1	0.0014	65.4243
Carioca Precoce x Madrepérola	63.39 (29-3)	323	102	3	1	0.0712	62.2926
Casquinha x Madrepérola	63.63 (158-1)	376	28	15	1	0.2194	91.4625
Casquinha x Madrepérola	63.39 (29-3)	375	27	15	1	0.0805	94.0584
Criangu x Madrepérola	63.63 (158-1)	367	119	3	1	0.0764	59.3658
Criangu x Madrepérola	63.39 (29-3)	141	43	3	1	0.1802	66.2363
Pardo x Madrepérola	63.63 (158-1)	315	103	3	1	0.0798	58.4486

R: resistance; S: susceptibility; <sup>a</sup>Nine proportions were tested (Table 1 shows the best explain of observed data, i.e., that provided the lower chi-square values -  $\chi^2$ ); P (%): Probability of estimated value.

## REFERENCES

- Cruz, CD. Programa GENES - versão Windows. Editora UFV. Viçosa, MG. 285p. 2006.  
 Pastor-Corrales, MA et al. Euphytica, Wageningen, 103(2), 161-171, 1998.  
 Sanglard, DA; Balbi, BP; Barros, EG; Moreira, MA. BIC 52:62-63, 2009.  
 Servin, B; Martin, OC; Mézard, M; Hospital, F. Toward a theory of marker-assisted gene pyramiding. Genetics, 168:513-523, 2004.  
 Van der Plank, JE. Disease resistance in plants. New York: Academic Press, 1984. 194p.