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Research Article

Genetic control of orange hilum corona of carioca beans (*Phaseolus vulgaris*)

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Abstract

The purpose of this research was to elucidate the genetic control of orange corona color in carioca common beans (*Phaseolus vulgaris*). We made four crosses between carioca group cultivars that differed in respect to the presence or absence of an orange hilum corona color. The F_2, F_3, F_1BC_{11}, F_1BC_{21}, F_2BC_{11} and F_2BC_{21} phenotypic segregations were evaluated with a chi-square test which fitted with the hypothesis that one gene with a dominant allele is responsible for the orange corona color. All generations resulting from the four different crosses showed segregation patterns which agreed with the expected proportions. Our results show that the dominant *G* allele controls orange corona color in the carioca bean group.

Key words: carioca bean group, corona color, *G* locus, genetic inheritance.

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Introduction

The bean market is influenced by bean characteristics such as coat color, size and shape, cooking time, texture, flavor, taste and bean broth color. Studies on the genetic control of the testa color of beans have been carried out for more than seventy years, and a review of the genes studied until now had been published by Basset (2004).

Brazil is the most important producer of beans and has an annual production of around three millions tonne (FAO, 2006), the most widely cultivated beans belonging to the carioca bean (*Phaseolus vulgaris*) commercial bean group. Carioca beans generally have a cream-colored testa, or seed coat, with clear brown stripes, but some have an orange hilum corona (Figure 1), which has been erroneously correlated with low grain cooking quality so that beans with this type of corona have a low market price and farmers avoid cultivating seeds with this trait. Disagreement occurs in regard to the genetic mechanism responsible for the presence of a corona, however the number of genes involved in the inheritance of this trait is lower than the genes involved in the genetic control of seed coat color (Barigozzi and Conti, 1981; Bassett, 1995; Mendonça *et al.*, 1998; Bassett, 2003). A knowledge of the genetic control mechanisms responsible for the presence of an orange corona in carioca beans is important for the development of breeding programs for the development of carioca cultivars with high commercial acceptance.

The presence of a hilum corona in beans is controlled by the *Cor* locus, but the color of the corona depends of the expression of other genes (Leakey, 1988). The phenotypic segregation observed in the F_2 offspring of some *P. vulgaris* crosses (P45 x Embrapa 201-Ouro, P45 x Carioca 300V and Carioca 300V x Embrapa 201-Ouro) has shown that at least two genes control the corona color trait, the *Cor* locus being responsible for the presence of a corona and the corona color being controlled by the interaction of three other loci (*B*, *D*, and *G*), the dark corona having the *BBDDCorCorgg* genotype and the yellow corona the *BbddCorCorGG* genotype (Mendonça *et al.*, 1998). Basset (1995) suggested that beans with a dark hilum corona resulted from the pleiotropic effect of V^{lae} alleles, which are also responsible for pink flowers, so that plants with pink flowers would produce beans with dark corona while plants with white flowers would produce beans with no corona. Basset (1995) also suggested that another possible explanation for the genetic control of this trait could be strong genetic linkage between the genes for dark corona and pink flowers. However, the data obtained by Mendonça *et al.* (1998) disagree with this conclusion because the genotypes studied by these authors showed plants with white flowers and dark corona, which did not agree with a pleiotropic effect of the V^{lae} gene or a genetic linkage between the loci for flower color and dark hilum corona color.

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The purpose of our research was to clarify the genetic control of orange hilum corona color in the commercial carioca bean group and assess the utility of this information for the genetic improvement of carioca-type beans.

Material and Methods

Plant material and crossing method

We investigated commercial carioca-group bean cultivars (*Phaseolus vulgaris*) contrasting in respect to the presence of an orange corona around the hilum ring (Figure 1), the cultivars being the orange corona cultivars Aporé, IAPAR-14 and IAPAR-57 which were used as female parents (P_1) and the Carioca, FT-Paulistinha and Rudá cultivars which had no orange corona and were used as male parents (P_2). Seed material for these plants was obtained from bean germplasm bank of the Paraná State Agronomic Institute (Instituto Agronômico do Paraná, IAPAR) and all the generations of the plants were grown in the greenhouse of the IAPAR, Londrina, PR, Brazil. The crosses were made according to Bliss (1980) and we evaluated the progenies of the crosses IAPAR-14 x Carioca, IAPAR-14 x FT-Paulistinha, IAPAR-57 x Carioca and Aporé x Rudá.

The presence or absence of an orange hilum corona is determined prior to fertilization (Ramalho *et al.*, 2000) because the testa develops from the maternal ovule tegument (Esau, 1966) and its phenotype is thus determined by the genetic constitution of the female parent plant. We evaluated the phenotypic segregation of the orange corona trait in the P_1, P_2, F_1, F_2 and F3 generations and the backcross generations F_1BC_{11}, F_1BC_{21}, F_2BC_{11} and F_2BC_{21}. The F_1 seeds were used as female parents to get the BC_{11} and BC_{21} backcrosses. A random sample of 300 F_1 beans and 90 BC_1 beans were sown, then a random sample of 150 plants from each F_1 population and a random sample of 15 plants from each BC_{11} and BC_{21} populations were selected and their F_2, F_1BC_{11} and F_1BC_{21} progenies evaluated for the presence of orange hilum corona. To obtain the F_3, F_2BC_{11} and F_2BC_{21} progenies we planted samples of 50 beans from each individual F_2, F_1BC_{11} and F_1BC_{21} plant and when the plants were at the physiological maturation stage one pod from each F_1BC_{11}, F_1BC_{12}, F_2, F_3, F_2BC_{11} and F_2BC_{21} plant was evaluated for the presence of orange corona.

Statistical analysis

A chi-square test (Steel *et al.*, 1997) was used to verify if the F_2, F_3, F_1BC_{11}, F_1BC_{21}, F_2BC_{11} and F_2BC_{21} phenotypic segregations fitted the hypothesis that one gene with a dominant allele controls the orange hilum corona trait. The Genes software (Cruz, 2001) was used to calculate the chi-square tests. The chi-square results were subjected to an homogeneity test (Strickberger, 1968) to check whether or not each generation was uniform and verify that the results could only be explained by the dominant monogenic inheritance genetic hypothesis.

Figure 1 - The commercial carioca bean group (*Phaseolus vulgaris*). A. beans without an orange corona. B. beans with an orange corona; C. Diagram showing the orange corona region of the testa.

Results and Discussion

All the F_1 plants showed an orange hilum corona (Figure 1), while in the F_2 generation the proportion of orange corona to non-orange corona segregates was 3:1 and in the F_3 generation the segregant ratio was 5:3 for orange corona to non-orange corona segregates (Table 1). In the backcrosses the segregation ratio for orange corona to non-orange corona segregates was 1:0 for the F_1BC_{11} generation, 1:1 for the F_1BC_{21} generation, 7:1 for the F_2BC_{11} generation and 3:5 for the F_2BC_{21} generation

(Table 1). These results indicate that a single gene with a dominant allele controls the orange hilum corona trait in the carioca bean group. In the four different crosses (IAPAR-14 x Carioca, IAPAR-14 x FT-Paulistinha, IAPAR-57 x Carioca, and Aporé x Rudá) all the evaluated progenies (F_1 F_2, F_3, F_1BC_{11}, F_1BC_{21}, F_2BC_{11} and F_2BC_{21}) showed segregation ratios supporting the hypothesis of a dominant allele controlling the presence of orange corona trait (Table 1). The chi-square homogeneity test for each generation demonstrated that the data obtained for each cross grouped in only one population (Table 2).

As discussed in the introduction, the hilum corona trait is controlled by the *Cor* locus and the *G* locus determines the presence of yellow-brownish pigments in the seed coat and its expression may be epistatic in relation to the *C* or *J* loci responsible for the color of the testa (Leakey, 1988), Mendonça *et al.* (1998) having shown that at least two independent genes are responsible for the presence of the orange corona trait and that in addition to the *Cor* locus three other loci (*B*, *D*, and *G*) must interact in the expression of corona color. Mendonça *et al.* (1998) also reported that interaction between the *B* and *G* loci is important for the expression of orange corona color in the carioca bean group,

Table 1 - Phenotypic segregation of orange hilum corona color of seven generations of four crosses between different cultivars of the commercial carioca bean (*Phaseolus vulgaris*).

Cross and generations	Observed phenotype		Expected proportions	Expected phenotype		χ^2 value
	(+)*	(-)†		(+)*	(-)†	
IAPAR 14 x Carioca						
F_1	596	0	1:0	596.00	0.00	0.000^{ns}
F_2	114	37	3:1	113.25	37.75	0.020^{ns}
F_3	1993	1125	5:3	1948.75	1169.25	2.679^{ns}
F_1BC_{11}	15	0	1:0	15.00	0.00	0.000^{ns}
F_1BC_{21}	4	10	1:1	7.00	7.00	2.571^{ns}
F_2BC_{11}	390	57	7:1	391.13	55.88	0.026^{ns}
F_2BC_{21}	124	203	3:5	122.63	204.38	0.025^{ns}
IAPAR 14 x FT Paulistinha						
F_1	268	0	1:0	268.00	0.00	0.000^{ns}
F_2	109	41	3:1	112.50	37.50	0.436^{ns}
F_3	2543	1531	5:3	2546.25	1527.75	0.011^{ns}
F_1BC_{11}	15	0	1:0	15.00	0.00	0.000^{ns}
F_1BC_{21}	8	7	1:1	7.50	7.50	0.067^{ns}
F_2BC_{11}	351	54	7:1	354.38	50.63	0.257^{ns}
F_2BC_{21}	181	264	3:5	166.88	278.13	1.913^{ns}
IAPAR 57 x Carioca						
F_1	428	0	1:0	428.00	0.00	0.000^{ns}
F_2	104	40	3:1	108.00	36.00	0.593^{ns}
F_3	2148	1253	5:3	2125.63	1275.38	0.628^{ns}
F_1BC_{11}	15	0	1:0	15.00	0.00	0.000^{ns}
F_1BC_{21}	6	9	1:1	7.50	7.50	0.600^{ns}
F_2BC_{11}	294	36	7:1	288.75	41.25	0.764^{ns}
F_2BC_{21}	142	224	3:5	137.25	228.75	0.263^{ns}
Aporé x Rudá						
F_1	700	0	1:0	700.00	0.00	0.000^{ns}
F_2	113	37	3:1	112.50	37.50	0.009^{ns}
F_3	2739	1566	5:3	2690.63	1614.38	2.319^{ns}
F_1BC_{11}	15	0	1:0	15.00	0.00	0.000^{ns}
F_1BC_{21}	7	8	1:1	7.50	7.50	0.067^{ns}
F_2BC_{11}	403	72	7:1	415.63	59.38	3.068^{ns}
F_2BC_{21}	168	283	3:5	169.13	281.88	0.012^{ns}

*Beans with orange corona. †Beans without orange corona. ^{ns}Non-significant at $p = 0.05$.

Table 2 - Homogeneity tests for phenotypic segregation of orange hilum corona color of seven generations of four crosses between different cultivars of the commercial carioca bean (*Phaseolus vulgaris*).

Crosses	Observed phenotype		Degrees of freedom	χ^2 value
	(+)*	(-)†		
F_2 generation, expected ratio 3:1				
IAPAR 14 x Carioca	114	37	1	0.020^{ns}
IAPAR 14 x FT Paulistinha	109	41	1	0.436^{ns}
IAPAR 57 x Carioca	104	40	1	0.593^{ns}
Aporé x Rudá	113	37	1	0.009^{ns}
Total	440	155	4	1.057^{ns}
Deviation from the expected ratio 3:1	446.25	148.75	1	0.350^{ns}
Homogeneity			3	0.707^{ns}
F_3 generation, expected ratio 5:3				
IAPAR 14 x Carioca	1993	1125	1	2.679^{ns}
IAPAR 14 x FT Paulistinha	2543	1531	1	0.011^{ns}
IAPAR 57 x Carioca	2148	1253	1	0.628^{ns}
Aporé x Rudá	2739	1566	1	2.319^{ns}
Total	9423	5475	4	5.638^{ns}
Deviation from the expected ratio 5:3	9311.25	5586.75	1	3.576^{ns}
Homogeneity			3	2.061^{ns}
F_2BC_{11} generation, expected ratio 7:1				
IAPAR 14 x Carioca	390	57	1	0.026^{ns}
IAPAR 14 x FT Paulistinha	351	54	1	0.257^{ns}
IAPAR 57 x Carioca	294	36	1	0.764^{ns}
Aporé x Rudá	403	72	1	3.068^{ns}
Total	1438	219	4	4.115^{ns}
Deviation from the expected ratio 7:1	1449.88	207.12	1	0.778^{ns}
Homogeneity			3	3.337^{ns}
F_2BC_{21} generation, expected ratio 3:5				
IAPAR 14 x Carioca	124	203	1	0.025^{ns}
IAPAR 14 x FT Paulistinha	181	264	1	1.913^{ns}
IAPAR 57 x Carioca	142	224	1	0.263^{ns}
Aporé x Rudá	168	283	1	0.012^{ns}
Total	615	974	4	2.213^{ns}
Deviation from the expected ratio 3:5	595.88	993.12	1	0.982^{ns}
Homogeneity			3	1.231^{ns}

*Beans with orange corona. †Beans without orange corona. ^{ns}Non-significant at p = 0.05.

which presents the recessive allele *b* in the homozygote. Our data shows that only the *G* and *Cor* loci are needed for the expression of orange corona color in the commercial carioca bean group. This agrees with the findings of Basset *et al.* (2002), who reported that the orange corona phenotype occurs in Wagenaar and Enola common bean plants with the *G-bb* genotype.

In our study, the cultivars used as parents belonged to the carioca group and differed regarding the presence or absence of an orange hilum corona. In fact, all the plants analyzed by us had the same genotype for the corona trait (*bbddCorCor*—), differing only regarding the presence of the *G* allele. Thus, the genotype of the parents with an orange corona (IAPAR-14, IAPAR-57, and Aporé) is *bbdddCorCorGG* and the genotype of the parents without the orange corona trait (Carioca, FT-Paulistinha, and Rudá) is *bbddCorCorgg*.

Our conclusion that the presence of an orange corona color in the carioca bean group is controlled by only one gene with a dominant allele is an important contribution for future breeding programs of this commercial bean group. The orange corona trait, wrongly supposed to correlate to low grain-cooking quality, is an undesirable characteristic because it is used by grain traders to justify a lower price for beans with this characteristic. Our results show that backcrossing can easily eliminate this trait from cultivars with otherwise good agronomic performance. The genotypes of desirable plants can be identified using progeny testing. In conclusion, the presence of orange corona trait in commercial carioca bean group may be controlled by only two genes, the *Cor* locus responsible for the presence of the hilum corona trait and the *G* locus for the orange corona color. These data are important for future breeding programs of carioca bean group market classes.

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