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ABSTRACT. In Brazil, there is an increasing demand for common bean (*Phaseolus vulgaris* L.) cultivars having Carioca-type (cream-colored seed coat with brown stripes) beans which have a light color that persists for a longer time combined with the most possible upright plant architecture. However, plant breeders are finding it difficult to combine these two traits in the same cultivar. The aim of this study was to compare success in the selection of new common bean lines that combine the two traits in segregating populations with 25%, 50%, or 75% of the alleles from the parents contrasting in upright plant architecture or in bean grains with persistent light color. A biparental cross was performed between a parent with light-colored beans (P_1) and another with upright plants (P_2). Three populations were obtained from the F_1 seeds, with allelic frequencies of 75%, 50%, and 25% of P_1. Subsequently, progenies were evaluated in a similar number in each population in the $F_{2:3}$, $F_{2:4}$, $F_{2:5}$, and $F_{2:6}$ generations. The plant architecture (PA) and grain darkening (GD) traits were visually evaluated using a scoring scale. Genetic and phenotypic parameters were estimated for all generations. There was no expressive advantage in using populations with a greater allele proportion of the parent favorable to upright plant architecture or slow grain darkening either in releasing of variability or in the occurrence of progenies with favorable phenotypes for the two traits.

Keywords: *Phaseolus vulgaris* L.; plant breeding; backcross; allele frequency.

Introduction

Common bean (*Phaseolus vulgaris* L.) of the Carioca type, that is, having a cream-colored seed coat with brown stripes, constitute more than 60% of the common bean production in Brazil (CONAB 2020). The first Carioca cultivar was recommended for growing more than fifty years ago (Chiorato, Carbonell, Vencovsky, Fonseca Júnior, & Pinheiro, 2010). Since then, nearly all common bean breeding programs in Brazil have given emphasis to obtain new cultivars with this type of bean grain, and they have been highly successful (Barili et al., 2016; Lemos, Abreu, Souza, Santos, & Ramalho, 2020). However, over time, the demands of growers and consumers regarding the phenotypic expression of various traits of the plants and of the bean grain have increased.

One of the traits of greatest demand for growers, both for typical family farming and for agricultural corporations, is the most upright plant architecture possible, especially up to the time of flowering. This is because upright plants facilitate operations in the field, both in the vegetative phase and at harvest. Additionally, there is evidence that this type of plant mitigates damage caused by some important pathogens in common bean crops (Miklas, Porter, Kelly, & Myers, 2013; Pereira, Abreu, Vieira Junior, Pires, & Ramalho, 2017; Kader, Balasubramanian, & Chatterton, 2018). Bean breeding programs conducted in Brazil have had substantial success in obtaining new cultivars with good plant architecture (Ramalho et al., 2016; Pereira et al., 2017; Wendland et al., 2018). However, the appearance of bean grains from these cultivars is not that desired by growers, and especially, by consumers.

A trait frequently required by consumers is the shorter cooking time of the bean grains. An aspect of the beans that is often related to longer cooking time is dark coloring because grain darkening is associated with beans that were harvested longer ago and, consequently, require a longer cooking time. Thus, farmers seek to produce the lightest-colored Carioca-type beans possible, with the lighter color that persists for a longer time,

facilitating the sale of beans. One of the cultivars recommended for growing that has a markedly favorable phenotype for this trait is BRSMG-Madrepérola (Carneiro et al., 2012). However, this cultivar is also characterized by a non-upright plant architecture.

In theory, having cultivars with good architecture and others with persistent light-colored bean grains, parents contrasting for these two traits could simply be crossed and the lines that combine the two favorable phenotypes mentioned could be selected. This procedure has been used, although the obtention of lines that combine good plant architecture and persistent light-colored bean grains has not yet been successful. The main reason is that the number of genes involved in the genetic control of these traits evidently is not small, although these genes usually exhibit relatively high heritability (Nienhuis & Singh, 1986; Santos & Vencovsky, 1986; Silva, Menezes Junior, Carneiro, Carneiro, & Cruz, 2013; Pires, Ramalho, Abreu, & Ferreira, 2014). Plant architecture, for example, depends on the expression of various traits, such as hypocotyl diameter, internode length, number of branches, and "stay green", among others (Teixeira, Ramalho, & Abreu, 1999). A complicating factor is that control of the expression of these traits evidently involves some genes that interact with each other.

Various genes are involved in the genetic control of bean grain color (Mcclean, Lee, Otto, Gepts, & Basset, 2002). However, in the case of the lighter persistent color in Carioca-type bean grains, theoretically, few genes are involved and are related to tannin production (Caldas & Blair, 2009; Alvares, Silva, Melo, Melo, & Pereira, 2016; Rodrigues, Rodrigues, Souza, Melo, & Pereira, 2019). However, the study of the metabolome of pinto bean lines contrasting for grain darkening time has shown that the process is not metabolomically simple (Duwadi et al., 2018). Erfatpour, Navabi, and Pauls (2018), also working with pinto beans, found that only one QTL explained 48% of the phenotypic variation for early darkening. Additionally, in that study, 40 candidate genes related to the expression of that trait were identified.

An alternative that has not yet been evaluated is obtaining segregating populations with different allele frequencies from parents differing in plant architecture and in speed of grain darkening. This strategy has already been used in soybean (Vello, Fehr, & Bahrenfus, 1984) in crosses involving commercial lines with non-adapted introduced lines, as well as in crosses between common bean lines from the Mesoamerican and Andean gene pools (Baldoni, Ramalho, & Abreu, 2008).

Given the importance of achieving success in obtaining new common bean cultivars with the phenotypes desired for the traits mentioned, the present study was conducted to compare success in the selection of new lines in segregating populations with 25%, 50%, or 75% of the alleles from the parents contrasting in upright plant architecture or in bean grains with persistent light color.

Material and methods

The experiments were conducted in the Center for Scientific and Technological Development of the Federal University of Lavras (UFLA) in the city of Lavras, southern region of the state of Minas Gerais, Brazil, at 918 m, 21°58′ S, 42°22′ W.

The parents used to obtain the populations were the cultivar BRSMG-Madrepérola (Madrepérola), which has a high yield and is characterized by Carioca-type bean grains with light color and slow darkening and a prostrate type III indeterminate growth habit (Carneiro et al., 2012); and the line RP-8, coming from the recurrent selection for upright plant architecture program at UFLA and has a high yield, type II indeterminate growth habit, upright architecture, and grain darkening similar to that of the original Carioca cultivar.

First, the Madrepérola (P_1) and RP-8 (P_2) parents were crossed. Three populations with different frequencies of alleles for light-colored bean grains and upright plant architecture were obtained from the F_1 generation: i) the F_2 generation with 50% of the alleles from each parent; ii) backcrossing with the Madrepérola cultivar, 75% of the P_1 alleles, light-colored bean grains, and 25% of the P_2 alleles, upright plant architecture; and iii) backcrossing with the RP-8 parent, 25% of the alleles for light-colored bean grains and 75% of the alleles for upright plant architecture.

The F_2 and F_1 seeds (from the backcrosses) obtained were sown in February 2018, and the plants were collected and threshed individually, generating the $F_{2:3}$ progenies. It is noteworthy that in the case of backcrosses, as the allele frequencies of the populations were not ½, it would be correct to use $S_{0:1}$ for the progenies, however, for simplification, the progenies of all populations will be referred to $F_{2:3}$. The steps for obtaining the progenies are shown in Figure 1.
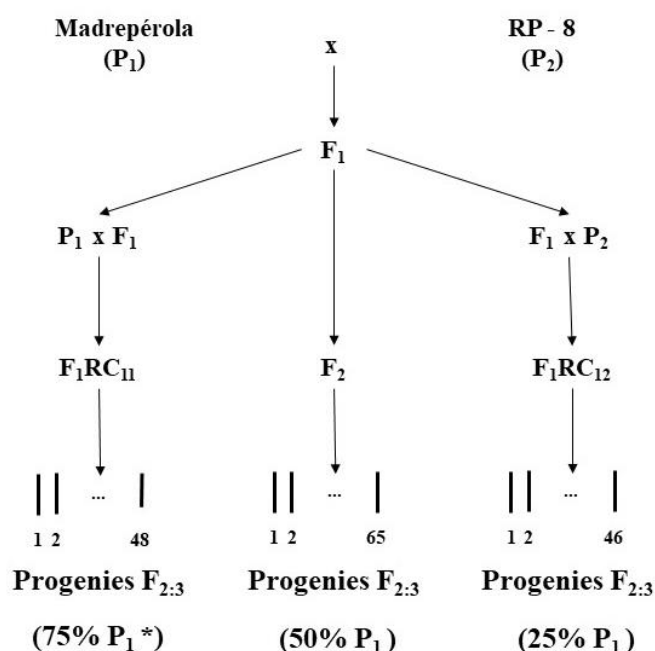
Figure 1. Crossing scheme conducted to obtain the progenies. *Allele proportion of the Madrepérola parent.

A total of 159 progenies were evaluated in a group of experiments with common treatments, which were sown in July 2018. Four experiments were conducted in a randomized complete block design with two replications. In each experiment, 39 or 40 progenies were evaluated, as well as three controls common to all the experiments, the cultivars BRSMG-Madrepérola, BRSMG-UAI, and BRSMG-Estilo. The plots consisted of one 2 m row, with a between-row spacing of 0.6 m. Close to the harvest time, the plant architecture (PA) was evaluated using the scoring scale adopted by Lemos, Abreu, and Ramalho (2020), in which score 1 was attributed to prostrate plants and score 9 to completely upright plants.

The other evaluated trait was grain darkening (GD). After harvest, a sample of the bean grains from each progeny was placed in a 4 × 23 cm transparent plastic bag of, identified, and stored in the dark. At 90 days after harvest, the samples were evaluated by two researchers using a scoring scale from 1 to 5, modified from Silva, Ramalho, Abreu, and Silva (2008), in which 1 referred to the background color of a dark bean grain and 5 referred to a light-colored bean grain. In this generation and the others, the evaluation of this trait was conducted in a completely randomized design with two replications: the two evaluators.

Using the mean values for PA and GD, 142 $F_{2:4}$ progenies were selected, an average of 47 from each population. The progenies were sown in November 2018, together with two controls, the cultivar BRSMG-UAI, a reference for upright plant architecture, and Madrepérola. These two cultivars were used as controls in all subsequent experiments. A 12 × 12 triple lattice experimental design was used, and the plots consisted of two 2-m rows with a between-row spacing of 0.6 m.

Using the same procedure as before, 62 progenies, now $F_{2:5}$, were selected and evaluated in an 8 × 8 triple lattice experimental design, with sowing in February 2019. After obtaining the mean values of PA and GD, 34 $F_{2:6}$ progenies were selected and evaluated in a 6 × 6 triple lattice design, with sowing in July 2019. In both experiments, the plots consisted of two 2 m rows with a between-row spacing of 0.6 m. The crop management practices and the traits evaluated were the same in all generations.

Analysis of variance per generation/environment was performed on the data for each trait according to the experimental design used. Subsequently, a joint analysis of variance was performed using the mean values from the 34 progenies and the 2 controls evaluated in all generations. The model adopted in the joint analyses considered all the random effects, except for the mean and the generations/environments. In these analyses, the source of variation of treatments was decomposed into the effect of progenies, among populations, progenies within each population, among controls, and the progeny *vs.* control contrast.

Considering the adjusted mean values obtained in the joint analysis, the simultaneous selection was conducted for the score of upright plant architecture and slow bean grain darkening. The mean values for each trait were standardized and was estimated the standardized selection index (Z) of each progeny involving the two traits, according to Ramalho, Abreu, Santos, and Nunes (2012).

From the expectations of the mean squares of the individual and joint analyses, estimations were made of heritability for selection in the mean of all progenies (h^2_P) and heritability for selection in the mean of the progenies within each population ($h^2_{P/Pop}$). The proportion of progenies from each segregating population among the best progenies selected was estimated at different selection intensities, considering each trait separately and by the standardized selection index.

Results and discussion

A significant difference was found among the progenies for both traits in all generations (results not shown). Wide variability among all the progenies was observed for the PA and GD traits in the $F_{2:3}$ generation (Figures 2 and 3). When only the progenies within each population were considered, regardless of the generation, wide variability was also observed for the two traits evaluated. Thus, it can be inferred that the selection of progenies with good performance for both desired traits is possible in all populations.
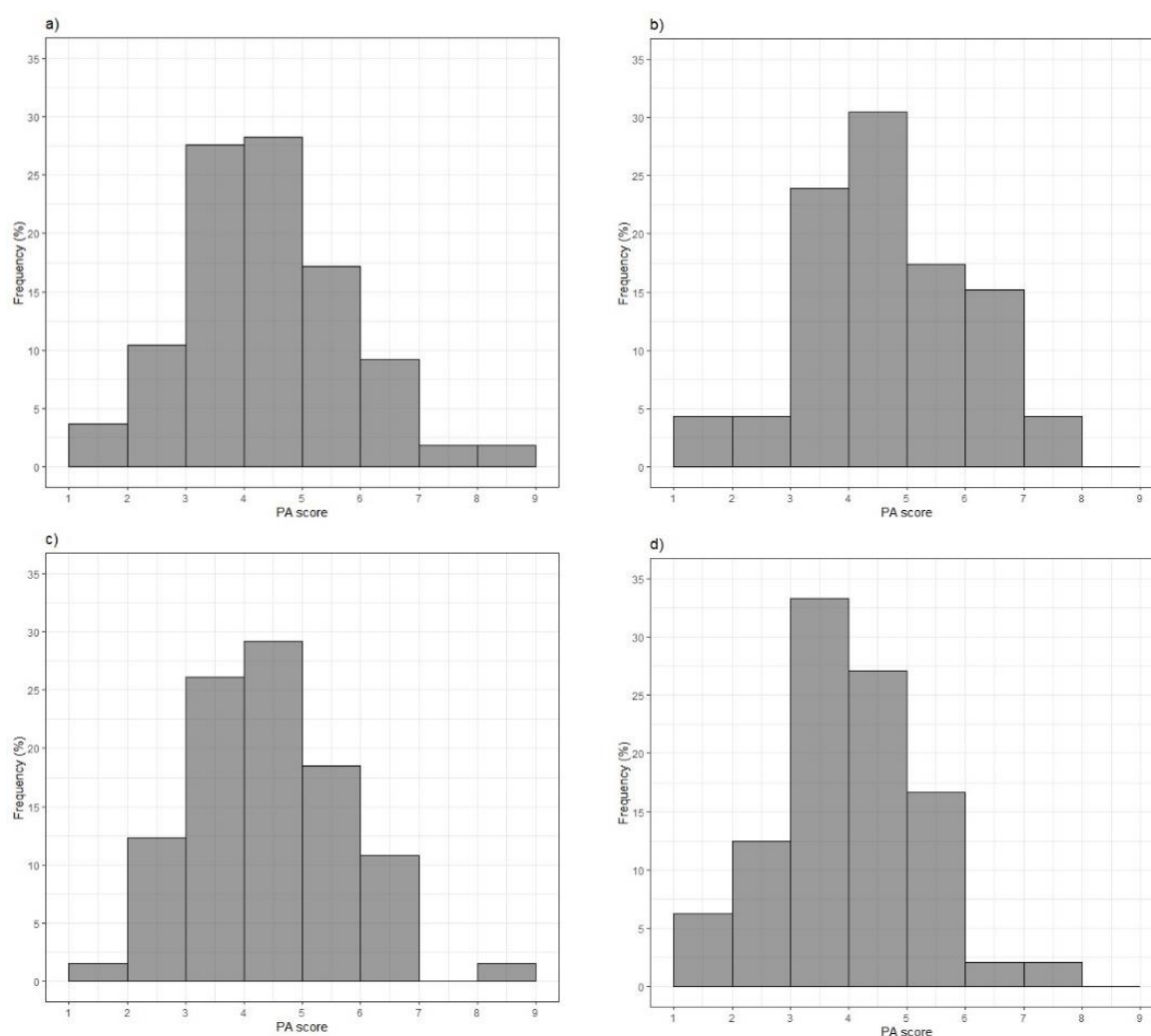

Figure 2. Distribution of frequencies of mean values of the PA score of the progenies in $F_{2:3}$ generation considering: a) all the progenies; b) progenies of the population with 25% of the alleles from the parent favorable to slow grain darkening (GD); c) population with 50% of the alleles from each parent; and d) population with 75% of the alleles from the parent favorable to GD.

It should be emphasized that the estimates of h^2 are in the broad sense; however, the contribution of the dominance variance (V_D) to the genetic variance (V_G) among the progenies is small. Considering, for example, the progenies of the population with 50% of the alleles from each parent, that is, an allele frequency of ½, in $F_{2:3}$, the V_G among progenies is comprised of $V_{G_{F_{2:3}}} = V_A + \frac{3}{4}V_D$, and in $F_{2:4}$ it is comprised of $V_{G_{F_{2:4}}} = V_A + \frac{3}{16}V_D$ (Ramalho, Abreu, Santos, & Nunes, 2012). Additionally, there is no

information in respect to the importance of the dominance allelic interaction for the PA and GD traits given the way they were evaluated. However, it is likely of small magnitude. In the case of the progenies from populations with allele frequencies other than ½, in addition to V_A and V_D, the genetic variance is also comprised of D_1, which corresponds to the covariance between the mean effects (additive) of the alleles and the dominance effects of the homozygotes, and D_2, which is the genetic variance of the dominance effects of the homozygotes. However, for them to be different from zero, the dominance effect must occur, which seems not to be the case for these two traits. Thus, it can be deduced that the h^2 estimated can be considered in the narrow sense. Because of the difficulties in using the h^2 estimate, above all because of the type of progeny evaluated, the selection unit, Bernardo (2020) proposed the term "reliability". However, this would simply be one more term to be used without altering the possible difficulties in the interpretation of the results.
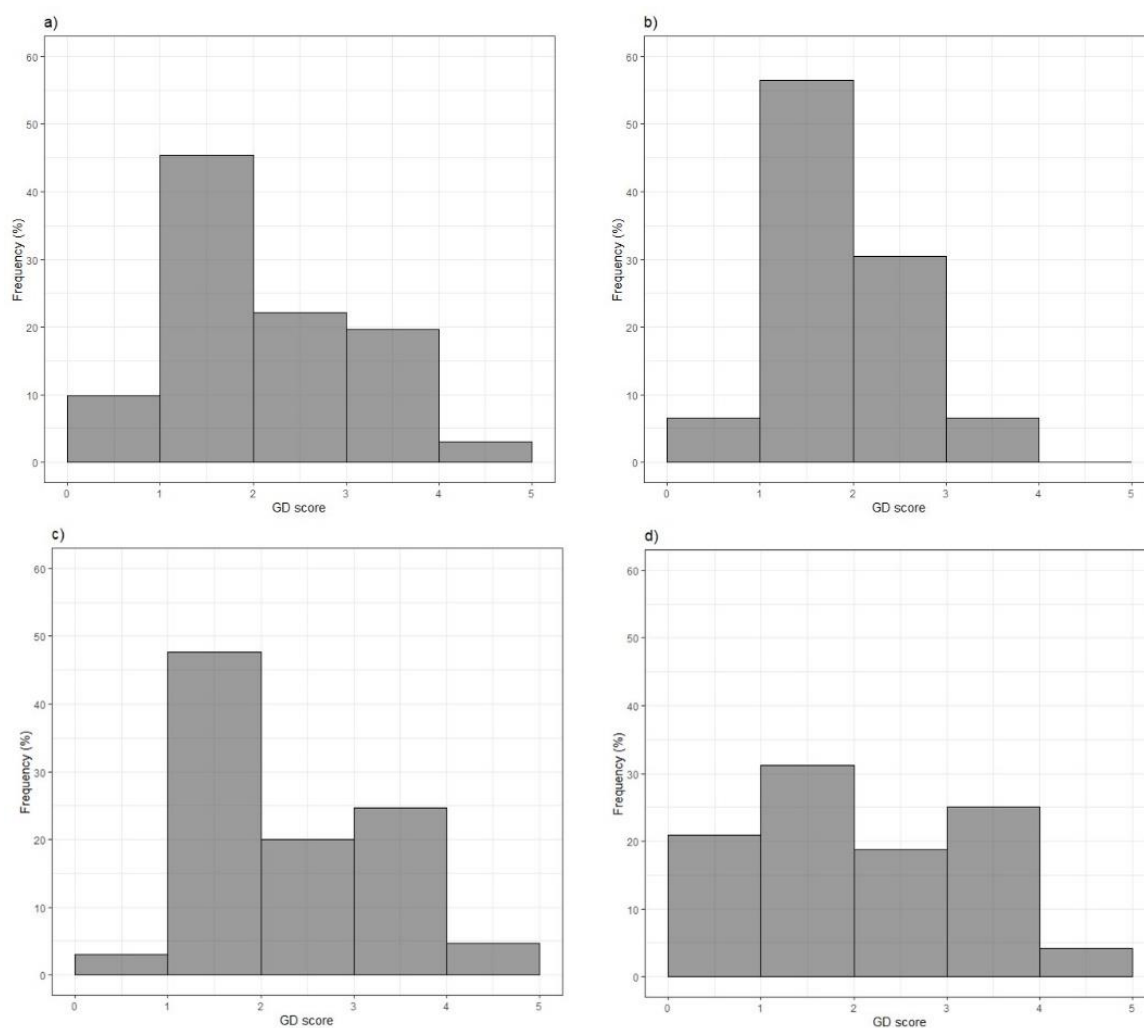

Figure 3. Distribution of frequencies of the mean values of GD score of progenies in the $F_{2:3}$ generation considering: a) all the progenies; b) progenies of the population with 25% of the alleles from the parent favorable to slow grain darkening (GD); c) population with 50% of the alleles from each parent; and d) population with 75% of the alleles from the parent favorable to GD.

In all generations, the accuracy of the GD trait was always superior to the accuracies obtained for PA, which was evidenced by the estimated heritability (h^2) values for each generation (Tables 1 and 2). The way the GD evaluation is performed increases the level of experimental accuracy, although both traits are evaluated visually. In the $F_{2:3}$ generation, when 159 progenies were evaluated, h^2 estimates among the mean values of the progenies of the three populations (with 25%, 50%, and 75% of the alleles from the Madrepérola parent) were practically the same for both PA and GD (Tables 1 and 2). The same observation was valid for the $F_{2:4}$ generation. In the $F_{2:5}$ generation, although the magnitude of h^2 among the mean values of the progenies of different origins for the PA trait varied, there was overlap in the confidence intervals of the estimates; consequently, they could also be considered equivalent (Table 1).

Table 1. Estimates of the heritabilities among all progenies (h^2_P), among progenies of the populations with 25% of the alleles from the parent favorable to slow grain darkening ($h^2_{25\%}$), with 50% of the alleles from each parent ($h^2_{50\%}$), and with 75% of the alleles from the parent favorable to slow grain darkening ($h^2_{75\%}$), for the upright plant architecture (PA), considering the $F_{2:3}$, $F_{2:4}$, $F_{2:5}$, and $F_{2:6}$ generations.

Generation	h^2_P	$h^2_{25\%}$	$h^2_{50\%}$	$h^2_{75\%}$
$F_{2:3}$	55.96 (40.45–67.53)[1]	61.22 (40.17–76.47)	54.31 (32.75–70.16)	49.35 (22.34–68.95)
$F_{2:4}$	77.41 (69.89–83.26)	76.62 (64.5–85.67)	77.64 (66.27–86.15)	78.43 (67.46–86.65)
$F_{2:5}$	61.68 (40.72–75.89)	47.34 (-4.99–79.44)	44.32 (-7.6–76.73)	66.45 (42.38–82.31)
$F_{2:6}$	62.66 (32.3–80.38)	80.51 (52.58–94.86)	55.29 (-2.43–86.07)	35.49 (-38.69–76.38)
Joint[2]	90.7 (84.28–94.92)	76.77 (35.44–94.12)	92.46 (81.06–97.72)	89.8 (76.98–96.34)

[1]Values between parentheses correspond to the confidence intervals of h^2 ($\alpha = 0.05$). [2]Heritabilities estimated by the adjusted mean of the 36 common treatments in the $F_{2:3}$, $F_{2:4}$, $F_{2:5}$, and $F_{2:6}$ generations.

Table 2. Estimates of the heritabilities among all progenies (h^2_P), among progenies of the populations with 25% of the alleles from the parent favorable to slow grain darkening ($h^2_{25\%}$), with 50% of the alleles from each parent ($h^2_{50\%}$), and with 75% of the alleles from the parent favorable to slow grain darkening ($h^2_{75\%}$), for the slow grain darkening (GD) traits, considering the $F_{2:3}$, $F_{2:4}$, $F_{2:5}$, and $F_{2:6}$ generations.

Generation	h^2_P	$h^2_{25\%}$	$h^2_{50\%}$	$h^2_{75\%}$
$F_{2:3}$	89.79 (86.18–92.48)[1]	76.54 (63.78–85.77)	90.35 (85.79–93.7)	92.66 (88.73–95.5)
$F_{2:4}$	89.21 (84.99–92.25)	84.44 (75.64–90.64)	89.04 (82.94–93.34)	89.73 (84.01–93.76)
$F_{2:5}$	84.74 (74.81–90.78)	81.09 (60.63–92.75)	86.38 (72.46–94.42)	84.72 (72.3–92.17)
$F_{2:6}$	91.46 (83.13–95.7)	82.3 (54.33–95.42)	94.43 (86.41–98.3)	89.58 (76.03–96.29)
Joint[2]	49.07 (13.93–72.19)	74.54 (29.24–93.55)	0 (-358.64–44.84)	60.2 (10.16–85.71)

[1]Values between parentheses correspond to the confidence intervals of h^2 ($\alpha = 0.05$). [2]Heritabilities estimated by the adjusted mean of the 36 common treatments in the $F_{2:3}$, $F_{2:4}$, $F_{2:5}$, and $F_{2:6}$ generations

It should be mentioned that in the absence of dominance, additive variance, considering only one locus, is maximum when the allele frequencies are equal, as in the case of F_2 (Falconer & Mackay, 1996). However, it was not observed an expressive difference among the h^2 estimates of the three populations. This was because, although the punctual estimates of h^2 could be different, their confidence intervals overlapped (Table 2). It can be inferred that the differences in the release of genetic variance among the progenies from each population were of small magnitude and were not detected under the conditions in which the experiments were conducted. It could be argued that this occurred because of sampling problems. A small number of progenies were evaluated in the more advanced generations; however, in the $F_{2:3}$ generation, this was not the case. Another hypothesis is related to the error associated with the estimates. In the case of the PA trait, whose phenotyping is more difficult to perform, this may have had an effect. However, for GD, this likely did not occur. A similar result was found by Baldoni et al. (2008) when they evaluated common bean progenies from populations with different allele frequencies for grain yield and number of days to flowering traits.

In the joint analysis of variance of the four generations, involving the 36 common treatments, 34 progenies, and the controls, significant difference was also observed among the treatments. In decomposition of the progeny source of variation, significance was also observed for the progenies from the populations with 25% of the alleles from the Madrepérola parent (backcross of F_1 with RP-8), with 50% of the alleles from both parents (F_2 generation), and with 75% of the Madrepérola alleles (backcross of F_1 with Madrepérola) (Table 3).

Significant difference was detected between the controls for the GD trait; however, the same was not observed for the PA trait. The control *vs.* progeny contrast stood out, which was not significant for either trait (Table 3). Confirming these results, the mean of PA of the controls (5.43) was similar to the mean of the progenies (5.61). For GD, the mean of the controls was 2.66, and of the progenies was 2.95. The effects of the progeny × generation/environment interaction were significant only for PA (Table 3).

Table 3. Summary of the joint analyses of variance for the plant architecture (PA) and grain darkening (GD) traits of the 36 common treatments in the $F_{2:3}$, $F_{2:4}$, $F_{2:5}$, and $F_{2:6}$ generations.

SV	PA		GD	
	DF	MS	DF	MS
Environment/Generation (E)	3	117.25**	3	4.43**
Treatments (T)	35	5.168**	35	9.65**
Progenies (P)	33	4.18*	33	8.94**
Progenies 25% ($P_{25\%}$)	8	7.16**	8	3.29**
Progenies 50% ($P_{50\%}$)	10	1.56^{ns}	10	13.33**
Progenies 75% ($P_{75\%}$)	13	4.62*	13	7.63**
Among Populations (Pop)	2	2.53^{ns}	2	18.11**
Controls (C)	1	42.13^{ns}	1	40.87**
C vs P	1	0.74^{ns}	1	1.79^{ns}
T x E	105	2.40**	105	0.81^{ns}
P x E	99	2.13**	99	0.83^{ns}
$P_{25\%}$ x E	24	1.82^{ns}	24	0.77^{ns}
$P_{50\%}$ x E	30	2.85**	30	1.01^{ns}
$P_{75\%}$ x E	39	1.84*	39	0.78^{ns}
Pop x E	6	1.67^{ns}	6	0.58^{ns}
C x E	3	6.38**	3	0.10^{ns}
C vs P x E	3	7.33**	3	0.63^{ns}
Mean error	592	1.16	419	0.25
Overall mean		5.61		2.93
Mean of Controls		5.43		2.66
Mean of Progenies		5.61		2.95

**, *, and ns: significant (P < 0.01), significant (P < 0.05), and non-significant (p > 0.05) according to the F test, respectively.

The most important aspect for breeders is knowing the best strategy for selecting progenies with superior performance for traits of interest. To provide this information for the traits evaluated, three selection intensities were considered. As expected, in most cases, the greater the proportion of alleles from the parent with the best expression of the trait, the greater the possibility of selecting progenies with a favorable phenotype for that trait (Tables 4 and 5). This is more evident for GD. For example, when the population had 25% of the alleles from the Madrepérola parent, no progeny was selected with slow grain darkening in any of the generations evaluated when the selection intensity applied was 10% (Table 5). It is noteworthy that the results of the progenies containing 50% of the alleles from each parent exhibited a good percentage of progenies with the two phenotypes desired in most cases (Tables 4 and 5).

It should be emphasized that the only generation whose results were entirely random was $F_{2:3}$ (Tables 4 and 5). In the others, the progenies selected were evaluated in the following generation based on the two traits. However, the aim was always to evaluate a similar number of progenies from each population.

Table 4. Percentage of progenies among the best from the populations with 25% of the alleles from the parent favorable to slow grain darkening (GD) ($P_{25\%}$), with 50% of the alleles from each parent ($P_{50\%}$), and with 75% of the alleles from the parent favorable to GD ($P_{75\%}$), selected at the selection intensities of 10, 15, and 20% for the plant architecture trait in each generation.

Generation	10%			15%			20%		
	$P_{25\%}$	$P_{50\%}$	$P_{75\%}$	$P_{25\%}$	$P_{50\%}$	$P_{75\%}$	$P_{25\%}$	$P_{50\%}$	$P_{75\%}$
$F_{2:3}$	56.25	37.5	6.25	41.67	45.83	12.50	36.36	45.45	18.18
$F_{2:4}$	35.71	21.43	42.86	33.33	33.33	33.33	32.14	35.71	32.14
$F_{2:5}$	33.33	33.33	33.33	30.00	40.00	30.00	30.77	38.46	30.77
$F_{2:6}$	75.00	0.00	25.00	60.00	0.00	40.00	57.14	14.29	28.57

Table 5. Percentage of progenies among the best from the populations with 25% of the alleles from the parent favorable to slow grain darkening (GD) ($P_{25\%}$), with 50% of the alleles from each parent ($P_{50\%}$), and with 75% of the alleles from the parent favorable to GD ($P_{75\%}$), selected at the selection intensities of 10, 15, and 20% for the slow grain darkening trait in each generation.

Generation	10%			15%			20%		
	$P_{25\%}$	$P_{50\%}$	$P_{75\%}$	$P_{25\%}$	$P_{50\%}$	$P_{75\%}$	$P_{25\%}$	$P_{50\%}$	$P_{75\%}$
$F_{2:3}$	0.00	56.25	43.75	4.17	50.00	45.83	9.09	48.48	42.42
$F_{2:4}$	0.00	42.86	57.14	4.76	28.57	66.67	10.71	25.00	64.29
$F_{2:5}$	0.00	50.00	50.00	10.00	30.00	60.00	7.69	30.77	61.54
$F_{2:6}$	0.00	75.00	25.00	0.00	80.00	20.00	0.00	57.14	42.86

The simultaneous selection was also carried out on the two traits through the standardization of the variables by the Z index (Ramalho, Abreu, Santos, & Nunes, 2012). Under this condition, it was found that no progeny would be selected if the population with 25% of the alleles from the parent with a good phenotypic expression for GD (Table 6). However, the results showed that the population containing 50% of the alleles from each parent would be the more appropriate strategy.

Table 6. Percentage of progenies among the best from the populations with 25% ($P_{25\%}$) of the alleles from the parent favorable to slow grain darkening (GD), with 50% of the alleles from each parent ($P_{50\%}$), and with 75% of the alleles from the parent favorable to GD ($P_{75\%}$), selected at different selection intensities for the upright plant architecture (PA) and slow grain darkening (GD) traits and the standardized Z index (Z), considering the 36 common treatments in the $F_{2:3}$, $F_{2:4}$, $F_{2:5}$, and $F_{2:6}$ generations.

Selection intensity (%)	PA			GD			Z		
	$P_{25\%}$	$P_{50\%}$	$P_{75\%}$	$P_{25\%}$	$P_{50\%}$	$P_{75\%}$	$P_{25\%}$	$P_{50\%}$	$P_{75\%}$
10	66.67	0.00	33.33	0.00	66.67	33.33	0.00	66.67	33.33
15	60.00	20.00	20.00	0.00	60.00	40.00	0.00	60.00	40.00
20	42.86	42.86	14.29	0.00	42.86	57.14	0.00	57.14	42.86

The results showed that when the trait has low h^2, as was the case for PA, backcrossing with the parent with the best phenotypic manifestation of the trait did not provide an expressive advantage. This was also observed by Baldoni et al. (2008), in which the highest proportion of alleles in the population that generated the progenies was only more advantageous when the trait had a high h^2. There are other reports in the literature, especially with the soybean crop, in which the highest allele proportion of the population was "required" when the cross involved a non-adapted line (Vello et al., 1984). The present study showed that breeders should prefer to obtain progenies from the F_2 generation in crosses involving two parents. The use of populations containing greater frequency of alleles from one of the parents not only demands more time to obtain these populations but also more work during backcrosses to obtain the desired number of seeds, especially in a species such as common bean, which produces a small number of seeds in each artificial hybridization.

The most recommended procedure for working with traits such as plant architecture and slow grain darkening is carrying out a recurrent selection (RS) program. To do so, two groups of lines with a good phenotypic expression for each of the traits should be involved. Visual selection should be performed for plant architecture before flowering, crosses between the plants selected for plant architecture should be made, and after harvest, a new selection should be made considering the slow grain darkening trait. Experience has shown that if the parents that will contribute to the base population are well chosen, that is, with good performance for the traits of interest, within a few selection cycles, it will be possible to achieve the objective of having new lines that combine upright plant architecture and light-colored bean grains with the greatest delay possible in grain darkening.

Conclusion

Using populations with a greater proportion of alleles from the parent favorable to upright plant architecture or slow grain darkening did not show an expressive advantage either in the release of genetic variability or in the occurrence of progenies with favorable phenotypes for the two traits.

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