

# Selection of common bean segregating populations using genetic and phenotypic parameters and RAPD markers

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## ABSTRACT

In an attempt to identify strategies for choosing common bean segregating populations, the diallel parameters, the contribution of homozygous ( $m+a'$ ) and heterozygous ( $d$ ) loci, the heritability ( $h_a^2$ ), the genetic distance (RAPD), and the selection potential ( $Z$ ) were estimated in a study carried out in two stages. In the first, 30 hybrid combinations (partial diallel) were assessed in the  $F_2$  and  $F_3$  generations. Increasing grain yield was due dominance effect ( $d$ ) although, both GCA and SCA were significant.  $d$  varied greatly and gave an information like SCA, however  $h_a^2$  alone was not indicative of success in a breeding program. In the second stage, five populations with lesser  $d$  and five with higher were selected, and twenty-seven families were taken from each, which were assessed with the parents and seven controls. The estimated parameters were used to check those from the first stage. There was partial agreement among the estimates and the percentages of lines superior to Pérola cultivar, which suggests that two or more estimates are needed to identify the promising segregating populations.

**KEY WORDS:** *Phaseolus vulgaris*, mean components, partial diallel, genetic and phenotypic parameters, molecular marker.

## INTRODUCTION

With the yield levels currently obtained for most cultivated species, new advances will only be possible if breeders are more efficient. Thus efforts should be concentrated only on assessing families from the most promising segregating populations, that is, those that associate high mean yield and greater variability. There are many options among segregating populations so the most promising must be identified as early as possible. Some procedures are suggested in the literature such as diallel crosses (Ramalho et al., 1993; Cruz and Regazzi, 1994), the  $m+a$  estimate (Vencovsky, 1987) and the genetic divergence obtained by morphological or molecular markers (Ferreira et al., 1995; Machado, 1999).

These methodologies supply information about the mean performance or variability, but not both simultaneously. The methodology by Jinks and Pooni (1976), which estimates the probability of obtaining superior lines to the standard in the  $F_\infty$  generation, and the estimates of the contribution of the heterozygous loci ( $d$ ) with that of loci in homozygous ( $m+a'$ ) are some of the few methodologies which associate the two parameters. All these methodologies have been used singly in common bean but there are few data which compare their efficiency.

Carioca cultivar is the most used in Brazil, which has cream colored seeds with brown stripes. Practically all breeding programs are directed toward obtaining this phenotype. There are already many commercial lines available with this type of grain, but there is little information on the potential of the segregating populations derived from them. Thus the present study was carried out to assess the efficiency of methods for selecting common bean segregating populations and to identify the ones most promising for the extraction of new lines with the Carioca grain type.

## MATERIAL AND METHODS

The study was carried out in two stages. In the first, 12 bean cultivars/lines, differing in some traits (Table 1), were intercrossed in a partial diallel design, resulting in 30 hybrid combinations, five from each parent. The segregating populations of each hybrid were evaluated in the  $F_2$  and  $F_3$  generations.

The sixty segregating  $F_2$  and  $F_3$  populations were assessed, together with the twelve parents, in the randomized complete block design, with three replications in plots with two 4m rows, 0.5m apart and 15 seeds per meter. Grain yield per plot was analyzed. The analysis of variance of the grain yield (g/plot) and

the partial diallel parameters (general combining ability – GCA – and specific combining ability – SCA) were estimated from the mean data, following the methodology presented by Cruz and Regazzi (1994) using the Genes program (Cruz, 1997).

The mean yield,  $m+a'$  and  $d$  genetic components were also estimated using the minimum square method, using the following equations:  $(\bar{P}_{1_i} + \bar{P}_{2_i})/2 = m + a'_i$ ;  $\bar{F}_{2_i} = m + a'_i + 1/2 d_i$ ;  $\bar{F}_{3_i} = m + a'_i + 1/4 d_i$  where  $m+a'_i$  is the mean of all the possible lines which can be derived from a cross, in the  $F_{\infty}$  generation;  $d_i$  is the deviation of the heterozygous genotypes compared to the mean;  $\bar{P}_{1_i}$  and  $\bar{P}_{2_i}$  are the means of parents 1 and 2, of the  $i_{th}$  population;  $\bar{F}_{2_i}$  and  $\bar{F}_{3_i}$  are the means of the  $i_{th}$  population, in the  $F_2$  and  $F_3$  generations.

Ten competitive plants were sampled in all the plots to assess the yield per plant. The phenotypic variance ( $\sigma_{F_i}^2$ ) and the genetic variance ( $\sigma_{G_i}^2$ ) were estimated for each population using the data from the sampled plants. The genetic variance of one given population  $i$ , for the  $F_2$  or  $F_3$  generation was estimated by the expression  $\sigma_{G_{2_i}}^2 = \sigma_{F_{2_i}}^2 - \sigma_{E_i}^2$  or  $\sigma_{G_{3_i}}^2 = \sigma_{F_{3_i}}^2 - \sigma_{E_i}^2$ .

Wide sense heritability was estimated for each population in the  $F_2$  and  $F_3$  generations, using the following expression

$$h_{a_i}^2 = \frac{\sigma_{G_i}^2}{\sigma_{F_i}^2} \times 100$$

The potential of the populations for superior lines was also assessed by the Jinks and Pooni (1976) procedure using the expression  $Z = (x - m_i)/s$ , where  $x$ : is the mean of the line taken as standard, which in the present case was the Pérola cultivar;  $m_i$ : mean of any segregating populations ( $i$ );  $s$ : standard phenotypic deviation among the lines ( $s = \sqrt{\sigma_{F_i}^2}$ ). Considering a model without dominance, the phenotypic variance of  $F_2$  ( $\sigma_{F_2}^2$ ) contains  $\sigma_A^2 + \sigma_E^2$ . And also considering that environmental variance among the lines is similar to the environmental variance in the  $F_2$  generation, we have  $\sqrt{\sigma_{F_i}^2} = \sqrt{2\sigma_A^2 + \sigma_E^2} = \sqrt{2\sigma_{F_2}^2 - \sigma_E^2}$ .

Five populations with lower values of  $d$  and five with higher values were selected at the second stage of the study to check the efficiency of the procedures. From those populations twenty-seven families were taken from each, and assessed together with the 12

**Table 1.** Origin, genealogy, growth habit, seed coat color and weight of 100 seeds of the twelve common bean cultivars/lines.

Cultivars	Origin	Genealogy <sup>1/</sup>	Growth habit <sup>2/</sup>	Seed coat color	Weight of 100 seeds (g)
ESAL 693	UFLA	(Carioca TU/Line 3272)	I	Cream with dark brown stripes	30
Carioca 300V	UFLA	Selection on Carioca	III	Cream with dark brown stripes	24
CI-21	UFLA	Recurrent selection	III	Cream with dark brown stripes	22
H-4-7	UFLA	(EMGOPA 201 Ouro/ Carioca)	III	Cream with dark brown stripes	22
CI-128	UFLA	Recurrent selection	III	Cream with dark brown stripes	29
Carioca MG	UFLA	(Carioca 80/Rio Tibagi)	II	Cream with dark brown stripes	22
Ouro Negro	CIAT	Introduction from Honduras (Honduras 35)	III	Black	26
PF 9029975	CNPAF	Selection on ESAL 582 (Carioca 80/Rio Tibagi)	II	Cream with dark brown stripes	21
Pérola	CNPAF	Selection on Aporé	II/III	Cream with dark brown stripes	26
IAC Carioca Aruã	IAC	(Cornell 49-242/AB 136)	II/III	Cream with dark brown stripes	23
Aporé	CNPAF	(Carioca/México 168)// (Carioca/Bat 76)	III	Cream with dark brown stripes	24
A-285 Rudá	CIAT	(Carioca/Rio Tibagi)	II	Cream with dark brown stripes	24

<sup>1/</sup> /: simple cross and //: double cross; <sup>2/</sup> I: determined growth habit; II: undetermined growth habit with short branches and III: undetermined growth habit with long branches.

parents and seven controls in a simple 17 x 17 lattice experimental design, in plots of one 1 m line 0.5m apart, and 15 seeds per meter. Grain yield, in g/plot, was assessed. Wide sense heridity ( $h_s^2$ ) was estimated using the methodology of Vencovsky and Barriga (1992) along with the lower and upper limits of the confidence intervals at the levels of  $1-\alpha = 0.95$  probability (Knapp et al., 1985).

The estimates of the genetic distances of the parents were obtained by Machado (1999), using RAPD molecular markers.

Rank correlations were estimated (Steel and Torrie, 1980) between SCA,  $d$  and the genetic distance obtained by RAPD markers of the segregating populations in the  $F_2$ ,  $F_3$  generations and the  $F_{3:4}$  families of the selected populations.

## RESULTS AND DISCUSSION

All the variation sources were significant ( $P \leq 0.01$ ) in the grain yield (g/plot) analysis of variance of the segregating populations in the  $F_2$  and  $F_3$  generations, except for the populations vs parents contrast. These results indicate that there were differences among the parents, among the  $F_2$  generation populations and among the  $F_3$  generation populations. The significance of the  $F_2$  generation vs  $F_3$  generation contrast showed that the mean of the populations in the  $F_2$  and  $F_3$  generations differed for grain yield, indicating, at least in principle, the presence of dominance in the direction of increasing grain yield. This could be proved by the superiority of the mean yield of most of the populations in the  $F_2$  generation compared to the mean yield of the populations in the

$F_3$  generation (Table 2), by the superiority of the general  $F_2$  mean yield (1576.03 g/plot) compared with the general  $F_3$  mean yield (1576.70 g/plot) and by the mean heterosis (356.32 g/plot).

The fact that some  $F_2$  populations presented inferior yields to the  $F_3$  generation is probably due to sampling problems in the segregating populations in the  $F_3$  generation. According to Ramalho et al. (1993), the number of plants to be used in each generation for having success in selection is an aspect to be considered during the selfing generations. In the present study, the number of individuals used in the  $F_3$  generation (360 plants) was proportionally lower compared to that used in the  $F_2$  generation and may not have been enough to sample all the variation existing in the segregating populations.

The diallel analysis showed that the general combining ability (GCA) and the specific combining ability (SCA) effects of the  $F_2$  and  $F_3$  populations were significant. Although there was a poor concordance among GCA and SCA estimates of the  $F_2$  and  $F_3$  generation, the parents which had greatest GCA were CI-21 and A-285 Rudá while Aporé and H-4-7 had the lowest GCA. The crosses which had the lowest and highest SCA were Ouro Negro x A-285 Rudá and Carioca 300V x Ouro Negro (Table 3). The ideal is to choose those crosses with high positive SCA values which derive from parents with the greatest GCA magnitudes (Veiga et al., 1998). The availability of such crosses implies that they should release enough variability for selection, because a greater SCA value presumes a greater number of lines after complete homozygosis and, consequently, greater variance among the lines, considering that all the loci

**Table 2.** Mean grain yield (g/plot) of the parents (diagonal), the segregating populations in the  $F_2$  generations (above the diagonal) and  $F_3$  (below the diagonal) <sup>1/,2/</sup>.

	1	2	3	4	5	6	7	8	9	10	11	12
1	1244.00 <sup>b</sup>				1386.33 <sup>b</sup>	1666.67 <sup>a</sup>	1674.33 <sup>a</sup>	1492.67 <sup>b</sup>	1645.00 <sup>a</sup>			
2		1684.67 <sup>a</sup>				1447.67 <sup>b</sup>	1601.67 <sup>a</sup>	1581.00 <sup>a</sup>	1698.67 <sup>a</sup>	1632.00 <sup>a</sup>		
3			1464.67 <sup>a</sup>				1764.33 <sup>a</sup>	1421.00 <sup>b</sup>	<b>1867.33<sup>a</sup></b>	1535.00 <sup>b</sup>	1850.33 <sup>a</sup>	
4				<b>1189.67<sup>b</sup></b>				<b>1150.00<sup>b</sup></b>	1460.00 <sup>b</sup>	1415.00 <sup>b</sup>	1364.67 <sup>b</sup>	1760.00 <sup>a</sup>
5					1588.67 <sup>a</sup>				1511.67 <sup>b</sup>	1458.67 <sup>b</sup>	1770.33 <sup>a</sup>	1689.00 <sup>a</sup>
6						1677.33 <sup>a</sup>				1605.00 <sup>a</sup>	1679.33 <sup>a</sup>	1755.33 <sup>a</sup>
7							1530.67 <sup>a</sup>				1510.33 <sup>b</sup>	1408.33 <sup>b</sup>
8								1573.67 <sup>a</sup>				1479.33 <sup>b</sup>
9									1616.67 <sup>a</sup>			
10										1245.67 <sup>b</sup>		
11											<b>1795.67<sup>a</sup></b>	
12												1593.00 <sup>a</sup>

<sup>1/</sup> 1: ESAL 693; 2: Carioca 300V; 3: CI-21; 4: H-4-7; 5: CI-128; 6: Carioca MG; 7: Ouro Negro; 8: PF 9029975; 9: Pérola; 10: IAC Carioca Aruã; 11: Aporé and 12: A-285 Rudá; <sup>2/</sup> Means followed by the same letter are of the same group according to Scott-Knott test at 1% level of probability.

give the same contribution to the phenotype. High GCA estimates should generate populations with greater mean yield.

The Carioca MG x Aporé and CI-128 x Aporé populations had the greatest  $m+a'$  estimates and H-4-7 x IAC Carioca Aruã and ESAL 693 x PF 9029975 had the lowest estimates (Table 4). The H-4-7 x A-285 Rudá and ESAL 693 x Ouro Negro populations showed higher  $d$  estimates (contribution of the heterozygous loci) and Carioca 300V x Carioca MG and H-4-7 x PF 9029975 showed the lowest estimates (Table 4). The  $d$  estimates emphasize the presence of dominance in the expression of the grain yield, confirming the results obtained in the analysis of variance of the populations in the  $F_2$  and  $F_3$  generations and the diallel analyses in the same generations.

The  $m+a'$  estimate is very useful, but it does not permit inference on the expected variability of the lines. Thus, two populations can generate lines with the same mean; however, the variation range in the performance of these lines may be very different. Obviously, a population which generate lines with a greater variation range among them will be preferred.

The phenotypic variance present in the early generations of segregating populations is normally used as an indication of the potential variability among the lines of the  $F_{\infty}$  generation. The phenotypic variance estimate is generally obtained from individual plant data. However, this estimate is time consuming and normally associated with large errors. An alternative is to obtain the  $d$  estimate, which can indicate the variability among the lines. Presuming that all the loci have the same contribution to the phenotype, higher  $d$  estimates imply a higher frequency of heterozygous loci and thus greater variance will be expected among the lines at the end of the selection process (Abreu, 1997).

The rank correlations between  $d$  and SCA in the  $F_2$  and  $F_3$  generations were  $r = 0.66^{**}$  and  $r = 0.37^*$ . These results indicate that the  $d$  and SCA estimates supply similar informations about the variability of the populations. It should be pointed out that the  $d$  estimate is less time consuming than that of the SCA as it can be obtained for any number of crosses, and the only restriction is the need to assess two generations simultaneously, which can be  $F_1$  and  $F_2$  or  $F_2$  and  $F_3$ .

The wide sense heritability estimates at the individual

**Table 3.** General combining ability (diagonal), specific combining ability (above the diagonal) of the populations in the  $F_2$  generation, general combining ability (diagonal, in parenthesis) and specific combining ability (below the diagonal) of the populations in the  $F_3$  generation, for grain yield (g/plot) <sup>1/</sup>.

	1	2	3	4	5	6	7	8	9	10	11	12
1	66.96 (-89.58)				-180.06	39.24	125.25	60.41	-44.84			
2		79.65 (4.16)				-192.45	39.89	136.05	-3.86	20.37		
3			<b>152.63</b> (14.64)				129.57	-96.93	91.83	-149.61	25.14	
4				-154.33 (-66.94)				-60.96	-8.54	37.36	-153.56	<b>185.70</b>
5	-81.96				-76.61 (31.52)				-34.60	3.30	174.38	36.98
6	-43.46	-119.53				-15.57 (66.69)				88.60	22.35	42.27
7	168.03	<b>246.30</b>	-35.85				-93.91 (-54.47)				-68.32	<b>-226.40</b>
8	-29.15	128.78	-187.70	-45.46				<b>-210.74</b> (-131.29)				-38.56
9	-13.46	-222.87	218.32	-63.77	81.77				46.84 (35.03)			
10		-32.68	2.84	174.42	-58.71	-85.88				-44.06 (-35.16)		
11			2.39	-146.71	79.20	58.33	6.82				96.52 (129.67)	
12				81.51	-20.28	190.54	<b>-385.30</b>	133.52				152.60 (95.42)

<sup>1/</sup> 1: ESAL 693; 2: Carioca 300V; 3: CI-21; 4: H-4-7; 5: CI-128; 6: Carioca MG; 7: Ouro Negro; 8: PF 9029975; 9: Pérola; 10: IAC Carioca Aruã; 11: Aporé and 12: A-285 Rudá.

level of the populations varied from 0 to 59.33% in the  $F_2$  generation and from 0 to 67.33% in the  $F_3$  generation (Table 5). The Carioca 300V x IAC Carioca Aruã ( $F_2$  generation) and ESAL 693 x Ouro Negro ( $F_3$  generation) populations had the highest estimates. Some populations in the  $F_2$  generation which showed greater mean grain yield showed nil heritability (Table 2). The same can be observed in the  $F_3$  generation. Furthermore, populations which showed lower mean grain yield showed high heritability estimates, both in the  $F_2$  and the  $F_3$  generations. Thus, this isolated estimate is not indicative of success in a breeding program, as it may be associated with lower mean yields. Furthermore, because it is dependent on the genetic variance estimates at the individual level, it may be associated with large errors.

The potential of each segregating  $F_2$  population for superior line selection was estimated using the grain yield per plant, by the methodology of Jinks and Pooni (1976). The most promising populations were Carioca MG x A-285 Rudá and CI-21 x Aporé and the least promising were PF 9029975 x A-285 Rudá and Ouro Negro x A-285 Rudá (Table 6).

It should be pointed out that to apply this methodology, the  $F_2$  generation mean is assumed to represent the  $F_\infty$  inbred lines mean. Additive genetic action must predominate for this to be valid. Although

there was dominance for grain yield in the present study, the inference using the  $F_2$  generation may be valid, because even when inflated, the probability estimate is relative and probably does not interfere in the choice of the best populations.

Table 6 shows the estimates of the molecular distances obtained by RAPD. The smallest distances were obtained among the crosses Carioca 300V x Carioca MG and Carioca MG x A-285 Rudá, and the greatest distances between the crosses ESAL 693 x Carioca MG and ESAL 603 x Pérola.

It should be pointed out that the smallest distances were associated with the more genetically similar parents and the greatest with the most divergent, thus it was expected that the greater the molecular distance between two parents, the greater the variability of the cross. The greatest molecular distances were obtained when the ESAL 693 parent was involved. This parent showed low yield mainly because it is the only one which has type I growth habit (Table 2).

The correlations among the molecular distances and SCA from  $F_2$  and  $F_3$  ( $r = 0.006$  and  $r = -0.04$ ) and  $d$  ( $r = 0.23$ ) indicated that *a priori*, the molecular distance does not supply the same information as those estimates. However, the estimates of the molecular distances obtained by RAPD markers are based on a set of DNA fragments, representative but random of the genome (Skroch et al., 1992). Thus, the

**Table 4.**  $m+a'$  estimates (above the diagonal) and  $d$  estimates (below the diagonal) of the populations for grain yield, using the  $F_2$  and  $F_3$  generations <sup>1/</sup>.

	1	2	3	4	5	6	7	8	9	10	11	12
1	-				1397.75 <sup>2/</sup>	1409.25	1380.25	1337.00	1390.25			
2		-				1638.17	1633.33	1589.75	1526.33	1423.25		
3			-				1424.00	1422.75	1557.33	1362.75	1594.42	
4				-				1373.67	1389.25	<b>1298.17</b>	1483.67	1397.92
5	-61 <sup>3/</sup>				-				1628.17	1412.08	1690.42	1574.67
6	413	<b>-466</b>				-				1427.08	<b>1747.25</b>	1682.33
7	573	-12	532				-				1656.92	1447.00
8	168	-97	-197	-464				-				1600.42
9	429	96	652	113	-182				-			
10		333	359	394	83	287				-		
11			439	-256	155	-115	-307				-	
12				<b>737</b>	196	240	-308	-209				-

<sup>1/</sup> 1: ESAL 693; 2: Carioca 300V; 3: CI-21; 4: H-4-7; 5: CI-128; 6: Carioca MG; 7: Ouro Negro; 8: PF 9029975; 9: Pérola; 10: IAC Carioca Aruã; 11: Aporé and 12: A-285 Rudá; <sup>2/</sup> standard error of the  $m+a'$  estimates: 96.1833; <sup>3/</sup> standard error of the  $d$  estimates: 298.2201.

associations among markers and genes which control agronomic characteristics are not known. It is expected that many genes that control grain yield are spread throughout the genome, so it is probable that the random markers do not sample the genes related to grain yield efficiently.

Five populations were selected, based on the  $d$  estimates, which showed the highest estimates (H-4-7 x A-285 Rudá, CI-21 x Pérola, ESAL 693 x Ouro Negro, CI-21 x Aporé and H-4-7 x IAC Carioca Aruã) and five populations which presented the lowest estimates (Carioca 300V x Carioca MG, H-4-7 x PF 9029975, Ouro Negro x Aporé, H-4-7 x Aporé and ESAL 693 x CI-128), to check the efficiency of the

estimates used. In the analysis of variance of the 270  $F_{3:4}$  families of the selected populations, there were significant differences for grain yield among the families of each population ( $P \leq 0.01$  or  $P \leq 0.05$ ), except among the families of the ESAL 693 x CI-128 and H-4-7 x IAC Carioca Aruã populations. Table 7 shows the mean yield (g/plot) and the wide sense heritability of the  $F_{3:4}$  families of each population, together with the lower and upper limits. Grain yield varied from 140.22 to 219.44 g/plot obtained by the families of the ESAL 693 x CI-128 and CI-21 x Pérola. The  $h_a^2$  varied from 0, obtained by the families of the H-4-7 x IAC Carioca Aruã population, to 59.56%, obtained by the families of the CI-21 x Pérola

**Table 5.** Wide sense heritability estimates at the individual level (%) for grain yield (g/plant) of the population in the  $F_2$  generation (above the diagonal) and  $F_3$  generation (below the diagonal) <sup>1/</sup>.

	1	2	3	4	5	6	7	8	9	10	11	12
1	-				55.22	0	52.57	36.32	0			
2		-				0	13.20	40.50	5.95	<b>59.33</b>		
3			-				42.73	40.14	0	53.10	9.91	
4				-				1.99	0	54.88	0	0
5	2.4				-				0	41.49	0	30.05
6	0	0				-				30.18	0	0
7	<b>67.33</b>	0	6.68				-				3.14	0
8	32.85	0	0	0				-				0
9	0	0	0	0	0				-			
10		0	40.11	27.86	63.26	23.36				-		
11			42.79	0	0	34.12	2.47				-	
12				32.61	7.59	3.30	9.45	0				-

<sup>1/</sup> 1: ESAL 693; 2: Carioca 300V; 3: CI-21; 4: H-4-7; 5: CI-128; 6: Carioca MG; 7: Ouro Negro; 8: PF 9029975; 9: Pérola; 10: IAC Carioca Aruã; 11: Aporé and 12: A-285 Rudá.

**Table 6.** Probability of the populations for selecting lines which surpass the Pérola cultivar, using the  $F_2$  generation mean yield (g/plot) (above the diagonal) and estimates of the genetic distances obtained by RAPD markers (below the diagonal) <sup>1/,2/</sup>.

	1	2	3	4	5	6	7	8	9	10	11	12
1	-				45.22	40.42	43.41	31.91	27.52			
2		-				13.67	23.67	37.03	38.96	36.56		
3			-				36.82	29.41	34.78	27.03	48.66	
4				-				28.25	-	24.92	25.87	41.87
5	0.51				-				21.21	37.06	19.81	32.63
6	<b>0.59</b>	<b>0.07</b>				-				19.82	22.06	<b>55.18</b>
7	0.48	0.30	0.27				-				22.31	12.73
8	0.53	0.21	0.22	0.20				-				<b>1.89</b>
9	<b>0.57</b>	0.11	0.19	0.17	0.15				-			
10		0.22	0.27	0.28	0.30	0.27				-		
11			0.24	0.21	0.22	0.12	0.36				-	
12				0.19	0.18	<b>0.07</b>	0.28	0.19				-

<sup>1/</sup> 1: ESAL 693; 2: Carioca 300V; 3: CI-21; 4: H-4-7; 5: CI-128; 6: Carioca MG; 7: Ouro Negro; 8: PF 9029975; 9: Pérola; 10: IAC Carioca Aruã; 11: Aporé and 12: A-285 Rudá; <sup>2/</sup> Source: Machado (1999).

**Table 7.** Wide sense heritability ( $h_a^2$ ) of the  $F_{3,4}$  families derived from the selected populations and their respective confidence intervals, mean grain yield (g/plot) and their respective amplitudes, estimated percentage of families superior to the Pérola cultivar (EPFSP) in the  $F_2$  generation and percentage of  $F_{3,4}$  families superior to the Pérola cultivar (POFSP) of the selected populations.

Families	$h_a^2$ (%)	L.L. <sup>1/</sup>	U.L. <sup>2/</sup>	Mean grain yield	L.L. <sup>1/</sup>	U.L. <sup>2/</sup>	EPFSP (%) $F_2$	POFSP (%) $F_{3,4}$
H-4-7 x PF 9029975	36.61	-21.36	62.02	163.78	72.00	269.00	28.25	3.70
Carioca 300V x Carioca MG	36.59	-21.40	62.01	213.19	116.00	276.00	13.67	40.74
Ouro Negro x Aporé	59.28	22.03	75.60	175.74	88.00	293.00	22.31	18.52
H-4-7 x Aporé	38.03	-18.65	62.87	172.37	87.00	263.00	25.87	3.70
ESAL 693 x CI-128	31.87	-30.44	59.18	140.22	69.00	211.00	45.22	0.00
H-4-7 x IAC Carioca Aruã	0	-	-	172.07	105.00	229.00	24.92	3.70
H-4-7 x A-285 Rudá	48.11	-0.64	68.91	182.78	78.00	262.00	41.87	22.22
CI-21 x Aporé	43.65	-7.89	66.24	185.96	116.00	268.00	48.66	11.11
CI-21 x Pérola	59.56	22.58	75.77	219.44	146.00	337.00	34.78	40.74
ESAL 693 x Ouro Negro	54.66	13.20	72.84	165.33	92.00	247.00	43.41	14.81

<sup>1/</sup> lower limit; <sup>2/</sup> upper limit.

population. Although the rank correlation between the  $d$  and  $h_a^2$  estimates of the  $F_{3,4}$  families of the selected populations was not significant ( $r = 0.45$ ), the families of the selected populations with lower  $d$  estimates showed lower  $h_a^2$  than that of the families of the populations with higher  $d$  estimates, except in the case of the Ouro Negro x Aporé and H-4-7 X IAC Carioca Aruã crosses. However, for the breeder, when assessing several populations, the interest is in the extreme, that is, the populations most promising for the trait in question. When only the extreme values are considered,  $d$  and  $h_a^2$  were partially in agreement. This result was similar to that reported by Abreu (1997), who obtained high and positive correlation between  $d$  and  $h_a^2$  in  $F_{5,7}$  families ( $r=0.97$ ) when studying four bean populations. It should be pointed out that the  $d$  and  $h_a^2$  estimates were obtained simultaneously in the study of Abreu (1997).

When the observed probability of the selected populations was compared with the estimated probability in the  $F_2$  generation for obtaining lines superior to the Pérola cultivar, it was found that there was no coherence in the result obtained (Table 7). The rank correlation among these probabilities was  $r = -0.28$  indicating that the Jinks and Pooni (1976) method was not efficient in predicting the potential of the populations for superior line extraction. Although this method is theoretically correct, it has the inconvenience of using the estimate of variance obtained from individual plants, which creates problems of low experimental accuracy and difficulty in obtaining data.

Among the choices of promising segregating populations for line selection it is noted that the

populations with greater  $m+a'$  and/or  $d$  estimates identify the more promising segregating populations (Tables 4 and 7). When the observed probability in superior line selection for families that outyield the Pérola cultivar (Table 7) is compared with the GCA and SCA of the populations in the  $F_2$  generation (Table 3) it can be concluded that the mean GCA of the population is equivalent to its  $m + a'$  and that SCA is equivalent to the  $d$  estimate, as expected based on the genetic constitution of these parameters. Therefore, the breeder can select the ideal population by the  $m+a'$  and  $d$  estimates which are easier to obtain.

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## RESUMO

### Seleção de populações segregantes em feijoeiro comum usando parâmetros fenotípicos e genéticos e marcadores RAPD

Visando identificar estratégias de escolhas de populações segregantes de feijoeiro, foram utilizados os parâmetros do dialelo, a contribuição dos locos em homozigose ( $m+a'$ ) e em heterozigose ( $d$ ), a herdabilidade ( $h_a^2$ ), a distância genética (RAPD) e o potencial de seleção ( $Z$ ) obtidos em um estudo conduzido em duas etapas. Na primeira, 30 populações

híbridas (dialelo parcial) foram avaliadas nas gerações  $F_2$  e  $F_3$ . Constatou-se que o efeito de dominância ( $d$ ) contribuiu para aumentar a produção e que tanto a CGC como a CEC foram significativas. As estimativas de  $d$  exibiram ampla variação e deram informação similar a CEC, no entanto, a  $h_a^2$  isolada não foi um indicativo de sucesso no programa da melhoramento. Na segunda etapa foram selecionadas cinco populações com as menores estimativas de  $d$  e cinco com as maiores e, dentro de cada foram tomadas 27 famílias, as quais foram avaliadas juntamente com os genitores e sete testemunhas visando verificar a eficiência das estimativas empregadas. Constatou-se que a porcentagem de linhas superiores à cultivar Pérola foi parcialmente prevista pelas estimativas, sendo que duas ou mais são necessárias para identificar as populações mais promissoras quanto a produção de grãos.

## REFERENCES

- Abreu, A. de F.B. 1997. Predição do potencial genético de populações segregantes do feijoeiro utilizando genitores inter-raciais. Ph.D. Diss. Universidade Federal de Lavras, Lavras.
- Cruz, C.D. 1997. Programa GENES: aplicativo computacional em genética e estatística. UFV, Viçosa.
- Cruz, C.D. and Regazzi, A.J. 1994. Modelos biométricos aplicados ao melhoramento genético. UFV, Viçosa.
- Ferreira, D.F.; Oliveira, A.C. de; Santos, M.X. dos and Ramalho, M.A.P. 1995. Métodos de avaliação da divergência genética em milho e suas relações com os cruzamentos dialélicos. Pesquisa Agropecuária Brasileira. 30:1189-1194.
- Jinks, J.L. and Pooni, H.S. 1976. Predicting the properties of recombinant inbred lines derived by single seed descent. Heredity. 36:253-266.
- Knapp, S.J.; Stroup, W.W. and Ross, W.M. 1985. Exact confidence intervals for heritability on a progeny mean bases. Crop Science. 25:192-194.
- Machado, C. de F. 1999. Procedimentos para a escolha de genitores de feijão. M.S. Thesis. Universidade Federal de Lavras, Lavras.
- Ramalho, M.A.P.; Santos, J.B. dos and Zimmermann, M.J.O. 1993. Genética quantitativa em plantas autógamas: aplicações no melhoramento do feijoeiro. UFG, Goiânia.
- Skroch, P.W.; Santos, J.B. dos and Nienhuis, J. 1992. Genetic relationships among *Phaseolus vulgaris* genotypes based on RAPD marker data. Annual Report of the Bean Improvement Cooperative. 35:23-24.
- Steel, R.G.D and Torrie, J.H. 1980. Principles and procedures of statistics: a biometrical approach. 2.ed. McGraw-Hill, New York.
- Veiga, R.D.; Nunes, G.H.S. and Santos, J.B. dos. 1998. Associação de parâmetros do dialelo com a variabilidade de populações segregantes avaliada por simulação. p.56. In: Anais do Encontro Mineiro de Geneticistas, 5., Viçosa, 1998. Sociedade Brasileira de Genética, Regional Minas Gerais, Viçosa.
- Vencovsky, R. 1987. Herança quantitativa. p.137-209. In: Paterniani, E. and Viegas, G. (Eds.). Melhoramento e produção de milho no Brasil. 2.ed. Ed. Fundação Cargill, Campinas.
- Vencovsky, R. and Barriga, P. 1992. Genética biométrica no fitomelhoramento. Sociedade Brasileira de Genética, Ribeirão Preto.

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