

Breeding potential of single, double and multiple crosses in common bean

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ABSTRACT

This common bean study was carried out to improve the understanding of the several strategies that can be used to obtain segregant populations in self-pollinating plant breeding programs. Eight inbred lines were crossed in a pyramidal form, and four single, two double and one multiple hybrid were obtained. The potential of the different hybrids was investigated based on the performance of the F_2 and F_2 plus F_3 segregant populations. The potential for obtaining superior inbred lines was estimated by $(m + a)$, which is the average of the F_{∞} inbred lines, and by the probability of a given population producing inbred lines that outperform the yield of the Pérola cultivar by 20%. It was shown that the use of multiple crosses is not advantageous when breeders have well defined objectives and experimental conditions to assess and identify the most promising segregant populations.

KEY WORDS: *Phaseolus vulgaris* L., choice segregant populations, quantitative genetics.

INTRODUCTION

Hybridization is a widely used breeding procedure in self pollinating plants. Breeding common bean using hybridization requires important decisions at certain stages of the program, such as, parent choice for obtaining the cross derived segregant populations and increasing homozygosity for inbred line extraction.

The choice of parents and segregant populations has received a lot of attention from research for some time (Ramalho et al., 1988; Cruz, 1990; Takeda et al., 1991; Oliveira et al., 1996; Otubo et al., 1996; Abreu, 1997; Mendonça, 2001). Similarly, the procedures to increase homozygosity have received attention (Fouilloux and Bannerot, 1988; Silva et al., 1994; Ranalli et al., 1996; Corte et al., 1998; Rosal, 1999; Raposo, 1999; Gonçalves, 2000; Santos, 2001). However, the strategies for obtaining the populations have not been extensively studied.

Biparental crosses are most frequently used to obtain the segregant populations. Therefore, the derived population will have 50% of the alleles of each parent. The main problem in this case is the difficulty in finding two parents that completely complement each other, that is, together express the desirable phenotypes for all traits under selection. To minimize this restriction, breeding is carried out in stages crossing two inbred lines that express part of the

desirable phenotypes. Their derived population is advanced for several generations and individuals are obtained that accumulate the favorable alleles involved in the cross. These individuals are then crossed with other inbred lines containing favorable alleles not involved in the previous cross and so forth. The main problem of this strategy is the time required to attain the goal, which requires above all program continuity and persistency.

An alternative solution is to carry out multiple crosses involving simultaneously all parents carriers of desirable alleles. This is a common strategy in some common bean breeding programs (Fouilloux and Bannerot, 1988; Singh, 1997, 2001; Kelly et al., 1997).

However, as most of the traits of economic importance such as grain yield are controlled by many genes, many parents are required to accumulate the majority of the favorable alleles. Large number of parents require large number of cross cycles and large F_1 population sizes to avoid loss of the favorable alleles from the parents (Ramalho et al., 1993). Also, involving a large number of parents reduces the probability of obtaining a genotype with all the desirable alleles (Ramalho, 1997).

The present study was carried out to compare the potential of populations derived from biparental,

double and multiple crosses to produce superior inbred lines. Although these different alternatives to obtain the segregant population are commonly used in the Brazilian common bean breeding programs, little information on their relative efficiency is available.

MATERIAL AND METHODS

The experiments were carried out in Lavras and Coimbra, Minas Gerais state, Brazil. Lavras is located at 918 meters altitude, 21°14' S latitude and 45°00' W longitude and Coimbra at 690 meters altitude, 20°45' S latitude and 42°51' W longitude.

Eight parents with 'carioca' type grain, two cultivars and six experimental inbred lines (Table 1), were used. They will be referred to as inbred lines without distinction.

The eight inbred lines were crossed using the pyramid method (Fehr, 1987; Fouilloux and Bannerot, 1988). Four single or biparental F_1 were obtained in the first crossing cycle: HS1/3 - (Pérola x FEB 200), HS6/8 - (MAR 2 x H4-10), HS2/4 - (IAPAR 31 x AN 9022180) e HS5/7 - (A 805 x PF 9029975). In the second cycle the four F_1 's were crossed to obtain two double crosses: HD1/3//6/8 - [(Pérola x FEB 200) x (MAR 2 x H4-10)] and HD2/4//5/7 [(IAPAR 31 x AN 9022180) x (A 805 x PF 9029975)]. In the third crossing cycle, the two double F_1 were crossed to obtain the multiple hybrid HM1/3//6/8///2/4//5/7 - {[(Pérola x FEB 200) x (MAR 2 x H4-10)] x [(IAPAR 31 x AN 9022180) x (A 805 x PF 9029975)]}.

The F_2 populations derived from the single, double and multiple hybrids were assessed with the eight parents, in Lavras and Coimbra in the Winter of 1999,

using a randomized complete block design with five replications with plots of four five-meter rows spaced at 0.5 m and sowing density of 15 seeds per meter. Twenty plots were assessed per block, that is, eight plots of parents, four of single hybrids, four (two in each of two replicates) of double hybrids and four of the multiple hybrid. This procedure was adopted to ensure that all hybrid types were assessed using the same number of plants. In the following season (the year 2000 dry season), the parents and the F_2 and F_3 generations were simultaneously assessed in a randomized complete block design, using an arrangement similar to that previously adopted for the F_2 generation assessment.

The grain yield (kg/ha) data were initially submitted to individual (experiment) analysis of variance considering the treatment effects and the mean as fixed. Later, joint analyses of variances of locations were performed for the F_2 and F_2 plus F_3 generations (Ramalho et al., 2000). All the effects, except the average error, were considered as fixed.

In the Lavras experiments, yield per plant was obtained using a random sample of 25 plants from each plot. From these data the phenotypic variance (σ_F^2), the genetic variance ($\sigma_{G_i}^2$) and the broad sense heritability (h_a^2) were estimated, using the following expression:

$$\sigma_{G_{2i}}^2 = \sigma_{F_{2i}}^2 - \sigma_{E_i}^2 \text{ and } \sigma_{G_{3i}}^2 = \sigma_{F_{3i}}^2 - \sigma_{E_i}^2$$

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

where: $\sigma_{F_{2i}}^2$: phenotypic variance of the *i*th population F_2 generation; $\sigma_{F_{3i}}^2$: phenotypic variance of the *i*th population F_3 generation; $\sigma_{E_i}^2$: environmental

Table 1. Inbred lines used as parents in crosses to obtain the segregant populations.

Inbred lines	Growth habit	Plant type	AN ^{1/}	ALS ^{2/}	OI ^{3/}	Grain Type	Origin
1. Pérola	II/III	Semi-prostrate	S ^{4/}	MR ^{5/}	R ^{6/}	Carioca/pattern	Embrapa
2. IAPAR 31	II	Semi- upright	MR	MR	S	Carioca/spotted	IAPAR
3. FEB 200	II	Upright	MR	S	R	Carioca/dark	CIAT
4. AN 9022180	II	Semi- upright	S	MR	S	Carioca/pattern	Embrapa
5. A 805	II	Upright	MR	S	R	Carioca/pattern	CIAT
6. MAR 2	III	Prostrate	-	R	S	Carioca/shining	CIAT
7. PF 9029975	II	Upright	S	S	R	Carioca/ dark	UFLA
8. H-4-10	II/III	Semi-prostrate	MR	S	MR	Carioca/pattern	UFLA

^{1/}AN: Anthracnosis; ^{2/}ALS: Angular Leaf Spot; ^{3/}OI: Oidium; ^{4/}S: Susceptible; ^{5/}MR: Moderately Resistant and ^{6/}R: Resistant.

variance of the *i*th population estimated from the average of the phenotypic variance of the parents involved in the crosses.

The estimates of the (**m + a**) and **d** components were obtained using a procedure similar to that adopted by Oliveira et al. (1996), where (**m + a**) is the mean of all possible F_{∞} inbred lines obtained by the contrast $2\bar{F}_{3i} - \bar{F}_{2i}$, and **d** is the algebraic sum of the effects of the heterozygous loci, that is, it is the deviation of the heterozygous individuals around the mean, given by the expression $4(\bar{F}_{2i} - \bar{F}_{3i})$.

The probability of a population to produce inbred lines outperforming a given control was obtained using the property of the standard normal distribution, according to the expression presented by Jinks and Pooni (1976). In the expression $Z = (\bar{L} - \bar{X})/s$, \bar{L} is the mean of the inbred line used as control, and, in the present case, was the mean of the Pérola cultivar increased by 20%; $\bar{X} = \mathbf{m} + \mathbf{a}$ is the mean of the F_{∞} inbred lines that in a model without dominance, which is the present case, corresponds to the mean of the F_2 or F_3 generation and *s* is the standard phenotypic deviation among the inbred lines ($s = \sqrt{\sigma_{F_i}^2}$). The genetic variance among the inbred lines ($\sigma_{G_L}^2$) is twice the additive genetic variance (σ_A^2) of the F_2 generation. Considering a model without dominance the phenotypic variance of F_2 ($\sigma_{F_2}^2$) is equal to $\sigma_A^2 + \sigma_E^2$. Thus, $2\sigma_A^2 = 2\sigma_{F_2}^2 - 2\sigma_E^2$. Assuming the environmental variance among inbred lines similar to the environmental variance of the F_2 generation, the following expression holds $s = \sqrt{\sigma_{F_i}^2} = \sqrt{2\sigma_A^2 + \sigma_E^2} = \sqrt{2\sigma_{F_2}^2 - \sigma_E^2}$. Therefore, for a given *i*th population $Z_i = (\bar{L} - \bar{F}_{2i})/\sqrt{2\sigma_{F_2}^2 - \sigma_E^2}$. In the case of the F_3 generation, the phenotypic variation ($\sigma_{F_3}^2$) contains $1,5\sigma_A^2 + \sigma_E^2$. Thus, $\sigma_A^2 = \frac{\sigma_{F_3}^2 - \sigma_E^2}{1,5}$. Assuming the environmental variance among the inbred lines similar to the environmental variance of the F_3 generation, results $\sqrt{\sigma_{F_i}^2} = \sqrt{2\sigma_A^2 + \sigma_E^2} = \sqrt{1,33\sigma_{F_3}^2 - 0,33\sigma_E^2}$. Therefore, for a given *i*th population, $Z_i = (\bar{L} - \bar{F}_{3i})/\sqrt{1,33\sigma_{F_3}^2 - 0,33\sigma_E^2}$.

RESULTS AND DISCUSSION

Significant differences among the parent inbred lines were observed in all experiments, indicating that although showing similar grain types the parents expressed variability for grain yield (Tables 2 and 3). The mean yield ranged from 2537 kg/ha (MAR 2) to 3172 kg/ha (PF 9020075) in the F_2 generation assessed in the winter 1999 season. In the dry 2000 season, the mean yield ranged from 2440 kg/ha (FEB 200) to 3193 kg/ha (IAPAR 31) in the simultaneous F_2 and F_3 generations assessment.

The parent x location interaction was significant ($P < 0.01$) in the two growing seasons. In the winter 1999 assessment (Table 2), the interaction was mainly due to the different behavior of the IAPAR 31 and H4-10 inbred lines, which performed better in Coimbra than in Lavras. However, in the 2000 dry season (Table 3) assessment, the parent x location interaction was mainly due to the different performances of the A 805, MAR 2 and FEB 200 inbred lines. This non-coincident performance was mainly due to the different pathogen incidence in the two locations, especially *Erysiphe polygoni* and *Phaeoisariopsis griseola*.

Significant differences were observed for the parent versus hybrid contrast in all generations. The mean performance of the segregant F_2 and F_3 populations was always superior to the mean of the parents (Tables 2 and 3). This fact alone indicates the presence of heterosis (Vencovsky, 1987). In the mean of all assessments, heterosis corresponded to 10% of the mean of the parents. The existence of heterosis for grain yield in the common bean has already been reported (Gutiérrez and Singh, 1985; Nienhuis and Singh, 1986; Abreu, 1997; Mendonça, 2001).

The presence of heterosis depends on the existence of genetic divergence among the parents and on the

Table 2. Grain yield means (kg/ha) of the F_2 populations derived from single (HS), double (HD) and multiple (HM) hybrids. Lavras and Coimbra, winter 1999 ^{1/}.

Parents/populations	Yield		
	Lavras	Coimbra	Mean
1. PÉROLA	3495 B ¹	2321 B	2908
2. IAPAR 31	3159 C	2579 A	2869
3. FEB 200	3499 B	2374 B	2936
4. AN 9022180	3364 B	2314 B	2839
5. A 805	3531 B	2469 B	3000
6. MAR 2	3030 C	2044 B	2537
7. PF 9029975	3679 A	2665 A	3172
8. H4-10	2743 D	2579 A	2661
Parents mean	3313	2418	2865
HS1/3	3877 a ¹	2673 a	3275
HS6/8	3341 b	2281 b	2811
HS2/4	3884 a	3019 a	3451
HS5/7	3749 a	2898 a	3323
HD1/3//6/8	3783 a	2809 a	3296
HD2/4//5/7	3705 a	2971 a	3338
HM1/3//6/8//2/4//5/7	3702 a	2820 a	3261
Hybrids mean	3720	2782	3251
Mean - HS	3713 1 ¹	2718 1	3215
Mean - HD	3744 1	2890 1	3317
Mean - HM	3702 1	2820 1	3261

^{1/} Means followed by the same letter in a column belong to the same similarity group by the Scott and Knott test ($P < 0.05$).

presence of dominant allelic interaction in the control of the trait (Falconer and Makay, 1996). The existence of divergence among the parents has been previously reported. As already pointed out, the assumption of dominance effect in the control of the trait implies the presence of inbreeding depression, that is, the mean of the F_2 generation should be superior to that of the F_3 generation. However, endogamy depression was not detected since the contrast F_2 versus F_3 generation was not significant. On the other hand, Lamkey and Edwards (1999) commented that heterosis dependent on additive x additive type epistasis and may occur without the presence of depression from endogamy. Unfortunately there are only a few reports of the occurrence of epistasis in the genetic control of common bean traits.

No significant difference among hybrid types was detected in either generation, that is, the mean yield of the four single hybrids did not differ from the mean of the double or multiple hybrids. It is pointed out that averaging the six experiments, which included assessments of the F_2 populations in two seasons and two locations and the F_3 in two locations, resulted in means of 3078 kg/ha, 3148 kg/ha and 3157 kg/ha for the single, double and multiple hybrids, respectively. Thus the mean alone did not allow inferences on the advantage of using multiple crosses.

The performance of the single hybrid derived populations differed significantly in the various environments. In the experiments carried out in 1999, for example, the worst performance was from the population derived from the single hybrid HS6/8 (MAR 2 x H4-10) in both locations (Table 2). In the experiments involving two locations and two generations (Table 3) in 2000, the population derived from the HS2/4 single hybrid (IAPAR 31 x AN 9022180) was outstanding.

Considering these previously discussed results, other alternatives to compare the potential of the populations for inbred line extraction and to infer on the most appropriate type of cross were sought. Assuming that the ideal population associates high means and variances, the variances of individual plants within each segregant population and the parents were obtained. From these estimates the genetic variances and among plant heritabilities were obtained (Tables 4 and 5). The values obtained in the different generations did not agree, probably because of the presence of interaction and to the low accuracy of individual plant assessments. The results, however, were consistent when the relative values were compared. The heritability estimates were larger than 20% in most cases. As the parents used in this study were of different origin, these results indicated that the various carioca-type common bean

Table 3. Grain yield means (kg/ha) of parents and the F_2 and F_3 segregant populations derived from single (HS), double (HD) and multiple (HM) hybrids. Lavras and Coimbra, dry season 2000 ^{1/}.

Parents/populations	Grain mean yield (kg/ha)								
	Lavras			Coimbra			Mean		
	F_2	F_3	Mean	F_2	F_3	Mean	F_2	F_3	Mean
1. PÉROLA			3255 B ¹			3001 A			3128 A
2. IAPAR 31			3496 A			2889 A			3193 A
3. FEB 200			2226 E			2653 B			2440 C
4. AN 9022180			3005 C			2367 B			2686 C
5. A 805			2428 E			2800 A			2614 C
6. MAR 2			2887 C			2853 A			2870 B
7. PF 9029975			3239 B			2816 A			3028 B
8. H4-10			2705 D			2497 B			2601 C
Parents mean			2905			2735			2820
HS1/3	2882	2922	2902 c	2921	2773	2847 a	2901	2848	2874 b
HS6/8	2999	2782	2891 c	3143	2889	3016 a	3071	2835	2953 b
HS2/4	3686	3492	3589 a	2967	3053	3010 a	3326	3272	3299 a
HS5/7	2794	2863	2829 c	3030	2960	2995 a	2912	2912	2912 b
HD1/3//6/8	3091	3093	3092 c	2911	2975	2943 a	3001	3034	3017 b
HD2/4//5/7	3191	3140	3165 b	3115	2997	3056 a	3152	3068	3110 a
HM1/3//6/8//2/4//5/7	3328	3137	3233 b	2954	3002	2978 a	3141	3070	3105 a
Hybrids mean	3139	3061	3100	3006	2950	2978	3072	3006	3039
Mean - HS	3090	3015	3053	3015	2919	2967	3053	2967	3010
Mean - HD	3141	3117	3129	3013	2986	3000	3077	3051	3064
Mean - HM	3328	3137	3233	2954	3002	2978	3141	3070	3105

^{1/} Means followed by the same letter in a column belong to the same similarity group by the Scott and Knott test ($P < 0.05$).

breeding programs used different breeding strategies in spite of having practically the same goal. This result contradicts to a certain extent those of authors such as Nienhuis and Singh (1988) and Singh and Urrea (1995) who found restricted genetic variability for grain yield in crosses carried out within the same gene pool.

The mean heritability of the multiple hybrid derived population was slightly higher than the mean heritability of the single and double hybrid populations. This suggests that the segregant population derived from the multiple hybrid is superior for inbred line extraction. However, individual comparisons of populations derived from single hybrids showed that the HS2/4 single hybrid (IAPAR 31 x AN 9022180) population presented similar heritability to that derived from the multiple hybrid, that is, they showed the same potential for selection.

Another option for comparing segregant populations is the $(m + a)$ and d estimates. The $(m + a)$ value predicts the mean of the lines in the F_{∞} generation and the d value, as already mentioned, quantifies the contribution of the heterozygous loci (Kearsey and Pooni, 1998). Assuming that all loci have the same contribution, the population with the largest d estimate must possess the greatest number of heterozygous loci, which will, therefore, segregate. Consequently, the ideal population associates the largest $(m + a)$ and d estimates (Abreu, 1997). On the other hand, the contribution of the heterozygous loci (d), which

is a measure of dominance, explained on average only 8.3% of the mean performance of the population (Table 6). For other species, such as maize, the contribution of the heterozygous loci for grain yield is higher than 50% (Ferreira et al., 1995; Pacheco et al., 1998; Lima et al., 2000; Souza Sobrinho, 2001). This result indicates that additive effects predominate in the control of grain yield in common bean, which is in agreement with reports by (Nienhuis and Singh, 1988; Ramalho et al., 1988; Abreu et al., 1990; Takeda et al., 1991; Vizgarra, 1991).

Although the d estimate contribution was small, it could be inferred that the population with larger number of segregating loci was derived from the HS6/8 (MAR 2 x H4-10) single hybrid (Table 6). Unfortunately, however, this population presented one of the lowest $(m + a)$ estimates. The HS2/4 (IAPAR 31 x AN 9022180) single hybrid is again highlighted for associating high $(m + a)$ and d estimates, on the average of the two environments. The multiple hybrid and the double hybrids HD2/4//5/7 were also promising.

The probability of the segregant populations of producing inbred lines outyielding the Pérola cultivar by at least 20% was assessed. In the F_2 generation assessment in winter 1999, these estimates ranged from 25.2% for the HS5/7 single hybrid to 43.7% for the HS2/4 single hybrid derived populations (Table 4). According to these estimates, the HS2/4, HD1/3//6/8 and HM derived populations were the most

Table 4. Grain yield means (g/plant) and estimates of phenotypic variance (σ_{Fi}^2), environmental variance (σ_{Ei}^2), genetic variance (σ_{Gi}^2), heritability (h^2) and percentage of inbred lines outperforming the Pérola cultivar by at least 20% (OPP) referent to the F_2 single (HS), double (HD) and multiple (HM) hybrid derived populations. Lavras, winter/1999.

Parents/populations	g/plant	σ_{Fi}^2	σ_{Ei}^2	σ_{Gi}^2	h^2	OPP
1. PÉROLA	14.2	63.1	63.1	-	-	-
2. IAPAR 31	13.6	48.4	48.4	-	-	-
3. FEB 200	13.8	32.0	32.0	-	-	-
4. AN 9022180	12.4	37.3	37.3	-	-	-
5. A 805	13.9	37.7	37.7	-	-	-
6. MAR 2	13.1	37.6	37.6	-	-	-
7. PF 9029975	13.7	58.1	58.1	-	-	-
8. H4-10	12.7	36.5	36.5	-	-	-
Parents mean	13.4	43.8	43.8	-	-	-
HS1/3	15.4	52.9	47.5	5.3	9.9	37.6
HS6/8	13.8	52.0	37.0	11.8	22.8	34.9
HS2/4	15.4	74.7	42.9	31.8	42.6	43.7
HS5/7	14.0	43.4	47.9	-4.5	0	25.2
HD1/3//6/8	14.8	64.1	42.3	20.3	39.0	40.8
HD2/4//5/7	14.5	56.0	45.4	10.6	19.0	38.1
HM	15.2	64.5	43.8	29.8	46.3	42.2

promising. In the 2000 dry season, these estimates, on the average of the two generations (F_2 and F_3), ranged from 9.8% for the HS1/3 single hybrid to 42.2% for the multiple hybrid (Table 5). As already reported in the previous F_2 generation assessment, the HS2/4, HD1/3//6/8, HD2/4//5/7 and HM derived populations were superior to the others in potential to generate superior inbred lines. These estimates were coherent with the previously reported estimates

of (m + a) and d. Considering the three conditions under which the estimates were obtained, the single HS2/4 hybrid, the double hybrids and the multiple hybrid derived populations showed greater probability of producing superior inbred lines.

There are some reports in the literature on the advantages of multiple crosses. One of these was based on the use of RAPD analysis (Bai et al., 1998). The authors showed that polymorphic loci are more

Table 5. Grain yield means (g/plant) and estimates of phenotypic variance ($\sigma_{F_i}^2$), environmental variance ($\sigma_{E_i}^2$), genetic variance ($\sigma_{G_i}^2$), heritability (h^2) and percentage of inbred lines outperforming the Pérola cultivar by at least 20% (OPP) referent to the F_2 and F_3 single (HS), double (HD) and multiple (HM) hybrid derived populations. Lavras, dry season 2000.

Parents/populations	g/plant	$\sigma_{F_{ij}}^2$	$\sigma_{E_i}^2$	$\sigma_{G_i}^2$	$h^2(\%)$	OPP
1. PÉROLA	14.2	48.7	48.7			
2. IAPAR 31	14.6	47.8	47.7			
3. FEB 200	11.7	27.0	27.0			
4. AN 9022180	13.3	37.3	37.3			
5. A 805	12.8	29.8	29.8			
6. MAR 2	12.9	43.1	43.1			
7. PF 9029975	13.7	52.3	52.3			
8. H4-10	14.7	47.1	47.1			
Parents mean	13.5	41.6	41.6			
F_2 -HS1/3	12.3	30.9	37.8	-7.0	0	0
F_2 -HS6/8	13.3	56.2	45.1	11.1	19.8	32.5
F_2 -HS2/4	15.7	64.1	42.5	21.6	33.6	44.2
F_2 -HS5/7	13.8	50.9	41.0	9.9	19.4	33.9
F_2 -HD1/3//6/8	14.6	69.1	41.5	27.6	40.0	40.3
F_2 -HD2/4//5/7	15.6	67.6	41.8	25.8	38.2	44.1
F_2 -HM	15.8	71.9	41.6	30.3	42.1	45.4
F_3 -HS1/3	11.4	40.9	37.8	3.0	7.4	19.5
F_3 -HS6/8	13.7	69.4	45.1	24.3	35.0	35.5
F_3 -HS2/4	14.4	69.0	42.5	26.4	38.3	38.2
F_3 -HS5/7	12.3	36.8	41.0	-4.2	0	0
F_3 -HD1/3//6/8	14.1	65.6	41.5	24.1	36.8	37.0
F_3 -HD2/4//5/7	14.4	46.3	41.8	4.5	9.8	35.4
F_3 -HM	14.5	71.6	41.6	30.0	41.8	39.1

Table 6. Estimates of the (m + a) and d mean components of segregant populations derived from single (HS), double (HD) and multiple (HM) hybrids, assessed simultaneously in the F_2 and F_3 generations. Lavras and Coimbra, dry season/2000.

Populations (hybrids)	Lavras		Coimbra		Mean	
	m+a _i	d _i	m+a _i	d _i	m+a _i	d _i
HS1/3	2962	-160	2625	592	2794	214
HS6/8	2565	868	2635	1016	2599	944
HS2/4	3298	776	3139	-344	3218	216
HS5/7	2932	-276	2890	280	2912	2
HD1/3//6/8	3096	-10	3038	-254	3066	-131
HD2/4//5/7	3090	202	2880	470	2984	336
HM1/3//6/8//2/4//5/7	2946	764	3050	-192	2998	286

frequent in multiple crosses. Unfortunately the investigated loci were not associated with any trait of economic importance, which restricts the use of the information for plant breeding.

The probability of success from selection is proportional to the number of segregating loci for a given trait (Fouilloux and Bannerot, 1988). Thus, it was expected that the probability of success would be greater in populations derived from crosses involving a larger number of parents. However, the results from the present study did not provide information on the number of loci segregating in the populations. No inference could be made that more loci were segregating in double hybrid or especially multiple hybrid derived populations than in the single hybrid populations.

The use of multiple crosses was proposed by Singh (2001) considering the advantage of associating several traits at the same time. However, if these traits are controlled by many genes it is practically impossible to associate all the favorable alleles at the same time. If the required objective is well defined, that is, if attention is focused on one or a few traits, the use of multiple crosses is questionable. Singh (2001) also reached this conclusion when emphasizing that it is possible to obtain substantial progresses in a biparental crosses among well-performing inbred lines.

It should not be forgotten that obtaining multiple crosses also has some restrictions of a practical nature, such as the longer time required to perform the intercrosses and the need to carry out further hybridization with the advance of the intercross cycles, to have a chance of maintaining the majority of the favorable alleles (Ramalho et al., 1993). In the case of the common bean, even considering that there are relatively simple and efficient artificial hybridization techniques available (Peternelli and Borém, 1999), the difficulty in obtaining a sufficient quantity of hybrid seeds in the various intercross cycles is mentioned as the main limitation to this strategy.

Therefore, breeders have two options for traits with low heritability. The first is to carry out the greatest number of biparental crosses and identify one or a few of the segregant populations that are most promising using any of the selection methods for segregant populations. In these populations, the largest possible number of families should be assessed to increase the range of variation of the trait and increase the probability of obtaining lines with superior performance (Comstock, 1964). In this case

it would suffice to assess the F_2 and following segregant generations in replicated experiments. If the bulk method is adopted, the assessments would be made in all generations, preferably in different locations and sowing seasons, and those populations identified as superior would be more intensely exploited.

The second option, performing multiple crosses and assessing the largest possible number of families would be used when no other method were suitable for selecting among the segregant populations. As previously reported, this procedure would require more work and time to obtain the population. However, this would be compensated by the greater range of variation available to the breeder when a larger number of families is assessed from a given cross. The results obtained in this study confirm that these strategies are pertinent in breeding programs.

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RESUMO

Potencial de cruzamentos simples, duplos e múltiplos no melhoramento do feijoeiro comum

Nos programas de melhoramento de plantas autógamas várias estratégias para obtenção de populações segregantes podem ser utilizadas, e como há pouca informação sobre a eficiência relativa das mesmas, foi realizado o presente trabalho com a cultura do feijoeiro. Oito linhagens foram cruzadas de forma piramidal, obtendo-se quatro híbridos simples, dois duplos e um múltiplo. O potencial dos diferentes híbridos foi avaliado com base no desempenho das populações segregantes, gerações F_2 e $F_2 + F_3$ simultaneamente. O potencial de obtenção de linhagens superiores foi estimado por meio da estimativa de $m+a$, que fornece a média das linhagens na geração F_{∞} , e pela probabilidade de uma dada população produzir linhagens que superem a produtividade da cultivar Pérola em 20%. Ficou evidenciado que quando os melhoristas têm objetivos bem definidos e condições de avaliar suas populações segregantes para identificar as mais promissoras, o emprego de cruzamentos múltiplos não é vantajoso.

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