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CROP BREEDING AND
APPLIED BIOTECHNOLOGY

Selection aiming at upright growth habit common bean with carioca type grains

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ABSTRACT - *Aiming at common bean lines with a high grain yield, upright growth habit and carioca type grains, ten common bean lines were crossed in a diallel scheme. The resulting populations were evaluated as to their capacity of generating superior lines. Eleven of the 42 evaluated populations were chosen to form the base population (S_0) of the first cycle (C-0). The resultant families were evaluated up to the $S_{0:5}$ generation for yield, plant architecture and grain type. In this generation, a total of 14 families was evaluated with two controls to estimate the genetic gain considering the three traits of interest together. The obtained genetic gain was 3.1% after one selection cycle, confirming the efficiency of the realized selection. The estimates of genetic and phenotypic parameters in the different generations associated to the mean family performance allow a prediction of the success of recurrent selection in future cycles.*

Key words: recurrent selection, genetic gain, common bean, upright growth habit, yield.

INTRODUCTION

Genetic improvement of common bean, along with the incorporation of technologies and investment in the productive sector has stimulated the grain yield in Brazil to an increase of about 45% in the last 15 years (Conab 2005). However, the pressure to achieve more productive lines, associated to the needs for headway in management and regarding consumer demands in relation to grain type is on the rise.

In several regions of the country farmers and consumers clearly prefer carioca type grains, in other words, medium-sized cream-colored grains with brown stripes. The principal objective of most improvement programs in Brazil has therefore been the establishment of new carioca grain type lines which are up to commercial standards and substitute the cultivars recommended earlier

advantageously. The greatest difficulty breeders find in the development of lines with grains of high commercial quality is the number of genes involved in the expression of the grain type. For color only there are at least 12 genes that control the trait expression (Bassett and McClean 2000, Beninger et al. 2000).

Besides the focus on the grain type, more upright plants need to be obtained. This trait makes the management easier and diminishes harvest loss and the incidence of some pathogens. Research into the genetic control of plant architecture has demonstrated that various morphological traits are involved in the phenotypic expression of plant architecture of common bean (Teixeira et al. 1999). The complexity and number of genes involved in the genetic control of each one of these traits, along with the environment influence make the breeder's work of developing carioca cultivars with a high yield potential,

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upright growth habit and grains of good commercial quality even more difficult.

It was concluded that the development of upright plants with the commercially accepted carioca grain type and high yield potential will only be successful when done in successive selection cycles, in other words, recurrent selection. Several reports in literature demonstrate its efficiency in common bean for diverse quantitative traits, including the acquirement of upright plants with larger grains (Kelly and Adams 1987). Objective of our study was to obtain common bean lines with high yield, upright growth habit and carioca type grains according to commercial standards and to predict the success of recurrent selection in future cycles.

MATERIAL AND METHODS

Ten common bean lines of upright growth habit, nine of which belong to the group Carioca (Carioca MG, LP 9876, CNFC 9454, CNFC 9455, CNFC 9458, CNFC 9466, CNFC 9471, CNFC 9484, IAPAR 81) and one to Black group (IPR Uirapuru), were crossed in a greenhouse in the complete diallel design. Forty-two hybrids were obtained from 45 possible combinations. Seeds of the 42 F_1- generation hybrids were sown in Lavras, MG (lat 21° 14' S, long 45° 00' W and alt 918 m asl), in order to obtain seeds of the F_2 (S_0) populations. The 42 S_0 populations were evaluated together with the 10 parents for grain yield (g plot^{-1}) in the dry season of 2002, in a randomized complete block design with two replications. The plots consisted of two four-meter long rows spaced 50 cm apart, in a planting density of 15 seeds per meter.

The data obtained for grain yield per plot were subjected to analysis of variance (ANOVA). The estimates of variance were obtained using yield data of 10 randomly collected competitive plants from each plot. The phenotypic variance of each population ($\sigma^2_{F_{ij}}$) was estimated by the mean of variances of the plots that had received the same treatments in the different replications. The genetic variance ($\sigma^2_{G_{ij}}$) of each population was estimated by the following expression: $\sigma^2_{G_{ij}} = \sigma^2_{F_{ij}} - \sigma^2_{E}$, where σ^2_{E} is environmental variance of the experiment estimated based on the mean of the phenotypic variances of the parents (lines) involved in the crossings. The potential of F_2 populations that brought forth lines that exceeded a certain standard was determined according to the methodology of Jinks and Pooni (1976).

Later, 190 plants were taken from amongst the 11 selected S_0 populations. The seeds obtained from each one of these plants constituted a $S_{0:1}$ family. A total of 190 $S_{0:1}$ families was obtained to begin the process of evaluation of the segregating families of the first cycle (C-0). These families were evaluated for grain yield (g 2m^{-2}) and plant architecture and the best selected for the next phase of evaluation. The process was repeated up to the $S_{0:5}$ generation. From the $S_{0:3}$ generation on, the grain type was also evaluated. Families with superior performance regarding the traits evaluated in each generation were advanced by the bulk-within-family method.

The plant architecture was evaluated according to a scale of scores used by Collicchio et al. (1997), where score 1 refers to plants of upright growth habit and score 5 very prostrated plants. The grain type was evaluated according to the scale of scores described by Ramalho et al. (1998b), where score 1 refers to the typical carioca grain type, i.e., cream-colored grains with light brown stripes, light underground, white halo, mean 100-seed weight of 22 to 24 g and unflattened grains and score 5 is given to cream-colored grains with dark brown stripes, dark underground, colored halo, mean 100-seed weight of less than 22 g and flattened grains.

Table 1 shows the number of evaluated families and controls, season and crop year of evaluation, design and number of replications, plot size and evaluated traits in each generation. The controls evaluated in the $S_{0:1}$ and $S_{0:2}$ generations were the ten parents used to obtain the base population. In $S_{0:3}$ generation, the controls were the parents CNFC 9455, CNFC 9458, CNFC 9466, and CNFC 9471. Finally, in the $S_{0:4}$ and $S_{0:5}$ generations, the controls were the parents CNFC 9455 and CNFC 9471. The different number of controls was used to adjust the required number of treatments in each square lattice used.

The data obtained for the grain yield, plant architecture and grain type of each generation were processed by ANOVA. The analysis of the data of generations $S_{0:1}$, $S_{0:2}$, $S_{0:3}$, and $S_{0:4}$ considered all random effects, except for the mean. In generation $S_{0:5}$, the treatment effect was considered fixed because an intensive selection had been realized in the previous generations. The broad-sense heritability ($\hat{h}^2$) of the families evaluated in the $S_{0:1}$, $S_{0:2}$, $S_{0:3}$, and $S_{0:4}$ generations was estimated for the traits under study, using a similar methodology to the one presented by Ramalho et al. (2000). The confidence intervals of heritabilities were obtained through the

Table 1. Details of the family evaluation experiment in the first recurrent selection cycle

	$S_{0:1}$	$S_{0:2}$	$S_{0:3}$	$S_{0:4}$	$S_{0:5}$
Families number	190	134	60	34	14
Controls number	10	10	4	2	2
Crop year	2002	2002/03	2003	2003	2004
Season	Winter	Wet	Dry	Winter	Dry
Design	Rand. block	12x12 Lattice	8 x 8 Lattice	6 x 6 Lattice	4 x 4 Lattice
Replications number	2	3	3	3	3
Plot	1 row of 1m	2 rows of 2m	2 rows of 2m	2 rows of 2m	2 rows of 2m
Evaluated traits	Yield	Yield	Yield	Yield	Yield
	Plant	Plant	Plant	Plant	Plant
	architecture	architecture	architecture	architecture	architecture
			Grain	Grain	Grain

expressions presented by Knapp et al. (1985).

Using the adjusted means of the common treatments with the generation of reference, the joint analysis of the generations for the grain yield and plant architectures was realized as described by Ramalho et al. (2000), using the common progenies in the generations included in each analysis: $S_{0:2}$ and $S_{0:3}$; $S_{0:2}$, $S_{0:3}$ and $S_{0:4}$; $S_{0:2}$, $S_{0:3}$, $S_{0:4}$, and $S_{0:5}$. The heritability estimates of the joint analyses $S_{0:2}$ and $S_{0:3}$, $S_{0:2}$, $S_{0:3}$, and $S_{0:4}$ were obtained by the following expression

$$h^2 = \frac{\hat{\sigma}_G^2}{\hat{\sigma}_{\bar{F}}^2} \times 100$$

where $\hat{\sigma}_G^2$ is the genetic variance of the families in the joint analysis. It was obtained based on the estimate of the covariance between the mean performance of the families in the generations involved. When more than two generations were involved, the mean of the covariances was used pairwise; $\hat{\sigma}_{\bar{F}}^2$ is the mean phenotypic variance, obtained by dividing the mean square of families of the joint analysis by the number of replications multiplied by the number of seasons.

The genetic gain obtained after the first selection cycle was estimated considering the three traits of interest simultaneously. As the unity of yield was g $2m^{-2}$ and the plant architecture and grain type scores varied from 1 to 5,

a data adjustment was necessary to make them directly comparable (Steel et al. 1997). Variable Z was therefore estimated by the following estimator

$$Z = \frac{x - m}{s}$$

where x is the mean of the considered trait of family i and m is the mean of all families and controls of $S_{0:5}$ generation. For yield and plant architecture it is the mean performance of the family in generations $S_{0:2}$, $S_{0:3}$, $S_{0:4}$, and $S_{0:5}$ and for the grain type only the performance of $S_{0:5}$ generation; s is the standard deviation of the mean performance of the cited families.

To calculate variable Z, the standard of scores attributed to growth and grain type was inverted, that is, score 5 now corresponded to value 1 of the aforementioned scale and vice-versa. Constant 3 was added to value of Z to make all values positive. The genetic gain was obtained considering the five best families of the $S_{0:5}$ generation. The following estimator was used for this purpose

$$GS = \frac{\bar{Z}_i - \bar{Z}_J}{\bar{Z}_J} \times 100$$

where $\bar{Z}_i$ is the mean of the sums of the standardized variable

Z, obtained for each one of the evaluated traits of the five best families; z_j is the mean of the sums of the standardized variable Z, obtained for each one of the evaluated traits of the controls CNFC 9455 and CNFC 9471.

RESULTS AND DISCUSSION

Jinks and Pooni (1976)'s methodology has been applied successfully in common bean crop (Abreu et al. 2002, Carneiro et al. 2002). The methodology has the advantage of allowing the prediction in early generations of the potential a population has to bring forth lines that exceed a certain standard, through estimates of mean and variance. According to the estimates obtained with the methodology, the crossing between the lines LP 9876 and CNFC 9458 created the most promising segregating population. This crossing also presented the second-highest yield mean. The genetic variance of this population was however practically zero. The crossing between the parents CNF 9484 and IAPAR 81 and CNFC 9455 and CNFC 9471 were also considered promising.

Since this is a program of recurrent selection, in which the maintenance of the genetic variability is of extreme importance, we also decided to choose the populations so that all parents involved in the diallel would still be represented in similar proportions. Besides the capacity of bringing forth superior lines, the selected populations were thus chosen according to the mean yield value, to the capacity of producing variability and, moreover, according to the maintenance of the alleles originated from their parents.

The selected populations and their estimates of mean yield, genetic variance and the potential to bring forth superior lines according to the method of Jinks and Pooni (1976) are presented in Table 2. The other traits of interest besides the yield (growth and grain type) were observed in the choice of the populations. Populations that were promising according to the previously considered estimates but with undesirable traits of growth and grain type were discarded.

A decomposition of the sum of squares of the treatments of grain yield and plant architecture showed the existence of variability between the families in the different generations of evaluation ($P < 0.05$). The source of variation controls which involved the parents was however not significant ($P > 0.10$). This result shows that the parents presented similar performance. The contrast families *vs* controls was not significant ($P > 0.10$) in nearly all generations of evaluation. This fact indicates that the mean family performance was similar to the control means. The variability between the families lets one expect that plants with a better performance than the controls can be selected.

The interaction genotypes x environments is one of the main difficulties breeder face when working with common bean. The possibility of planting the crop in three distinct seasons throughout the year calls for the creation of more stable cultivars towards environmental variations through improvement. It is therefore imperative that the trials of evaluation be conducted in different seasons.

In the present paper, the study of the interaction between genotypes and seasons was realized by the joint analysis of the common families of the $S_{0:2}$, $S_{0:3}$, $S_{0:4}$ and $S_{0:5}$ generations of the first recurrent selection cycle for the traits yield and plant architecture. For grain yield, the mean squares of the interaction families x seasons (generations) were generally not significant ($P > 0.25$). This result suggests that the evaluated families and controls had a coincident performance in the different seasons, which is a selection-favorable condition.

The absence of interaction for grain yield is contradictory to the great majority of studies realized with common bean which, besides detecting the presence of significant interaction, verified that there is predominance of the complex part (Abreu et al. 1990, Carneiro et al. 2002). Besides, results obtained in other studies with this leguminous plant showed that the interaction genotypes x seasons is more expressive than the interaction genotypes x locals (Ramalho et al. 1993, Ramalho et al. 1998a). In this case, we suggest that the families are evaluated in more seasons rather than in more locations.

The joint analyses of generations, considering the scores for the plant architecture, revealed the presence of significant interaction ($P < 0.01$) of treatments x seasons and families x seasons when considering the selected plants up to generation $S_{0:4}$. The performance of the families was not coincident in the different generations (seasons) for this trait. Similar results were reported by Collicchio et al. (1997). However, the discrimination by plant architecture of the best and worst families is more precise than of the intermediate ones. Since interaction is result of the mean of the pairwise interactions, it may be stated that probably the greatest part of the interaction is originated by families with intermediate scores.

At this point it was verified that, despite the

Table 2. Means and genetic variance estimates of the grain yield (g 4m^{-2}) and probability (%) to obtain lines that exceed the IPR Uirapuru standard, referring to the populations selected for the development of the recurrent selection program

Populations	Yield	Genetic variance	Probability
Carioca MG (1) x CNFC 9454 (3)	1019	0.000	*[1]
Carioca MG (1) x CNFC 9466 (6)	918	18.555	33.586
LP 9876 (2) x CNFC 9458 (5)	1278	1.963	53.777
LP 9876 (2) x CNFC 9466 (6)	92	0.423	23.466
CNFC 9454 (3) x CNFC 9484 (8)	1186	0.000	*
CNFC 9455 (4) x CNFC 9471 (7)	1031	69.759	41.091
CNFC 9455 (4) x IAPAR 81 (9)	1145	0.000	*
CNFC 9455 (4) x IPR Uirapuru (10)	1094	4.569	30.045
CNFC 9458 (5) x IPR Uirapuru (10)	1052	7.787	20.813
CNFC 9471 (7) x IPR Uirapuru (10)	1330	14.269	37.369
CNFC 9484 (8) x IAPAR 81 (9)	1141	40.964	44.498

[1] The probability could not be estimated by the methodology in use since the genetic variance of these populations was zero

occurrence of interaction between families x seasons for the plant architecture which suggests the need of realizing the selection considering the evaluation mean of three seasons, the result obtained with the joint analysis of the $S_{0:2}$, $S_{0:3}$, $S_{0:4}$, and $S_{0:5}$ generations indicates that this interaction was principally result of the oscillating scores attributed to families of intermediate scores. So, the low intensity selection realized in the first generations offers a better discrimination of the most promising families in more advanced generations, since under these conditions the families could be evaluated on larger plots and in experiments with a larger number of replications.

From the $S_{0:3}$ generation on, besides the yield and the plant architecture, scores were attributed to the grain type of the evaluated families and controls. As much as for yield and plant architecture, the score means attributed to the grain type of treatments differed significantly (P < 0.05) in all generations. The decomposition of the sum of squares of treatments manifested the existence of variability between the families. However, as expected, when the generations of selection advance, there was a reduction in the variability of the aforesaid trait and a bottleneck towards the lower scores. This is evidence of a higher probability of success with selection for this trait.

The heritability estimates (h^2) prove the existence of

genetic variability between families for the evaluated traits (Table 3). For the trait yield, the heritability estimates varied from 18.7% to 53.5% and for plant architecture from 9.0% to 58.3%. The inferior heritability limit for the $S_{0:1}$ and $S_{0:4}$ generations was negative, indicating that the heritability may have been zero in these generations. This result can be explained by the fact that the experimental precision was lower in these two generations.

The selection for the grain type was only initiated in the $S_{0:3}$ generation after an intense selection process of the best families for yield and plant architecture. Nevertheless, the heritability estimates were high, demonstrating that the previous selective process did not use all genetic variability for grain type in the population. This result is important since it indicates the independence of the genes controlling grain yield and plant architecture from the genes that determine the grain type. Similar results in relation to the absence of linkage between genes that control the yield and those that control grain types were obtained by Santos et al. (2002) and Carneiro et al. (2002).

The heritability estimate of the plant architecture in the joint analysis of the $S_{0:2}$ and $S_{0:3}$ generations was lower than the one obtained in the $S_{0:3}$ generation (Table 3). This result is due to the exclusion of the component of the variance of the interaction (σ^2_{FxS}) from the estimate of the

Table 3. Coefficient of variation (CV) and heritability (h^2) estimates and the lower (LL) and upper limits (UL) of the heritability of the grain yield (g 2m^{-2}) and of the scores attributed to the plant architecture and grain type obtained in the analyses of each generation (season) and of the joint analyses of the generations of the first cycle of recurrent selection

Generations	Yield				Plant architecture				Grain type			
	CV	h^2 %	LL	UL	CV	h^2 %	LL	UL	CV	h^2 %	LL	UL
$S_{0:1}$	28.4	18.7	-7.9	38.6	26.6	9.0	-20.7	31.4	-	-	-	-
$S_{0:2}$	19.7	36.0	13.2	52.2	21.2	52.6	35.4	64.4	-	-	-	-
$S_{0:3}$	22.8	53.5	25.7	70.1	16.2	58.3	33.4	73.2	16.0	57.7	33.1	72.3
$S_{0:4}$	22.4	19.5	-53.2	55.6	23.4	36.0	-21.8	64.7	9.7	82.8	67.9	90.2
$S_{0:5}$	21.8	-	-	-	22.3	-	-	-	15.9	-	-	-
$S_{0:2} - S_{0:3}$	21.0	40.7	-	-	21.7	13.2	-	-	-	-	-	-
$S_{0:2} - S_{0:3} - S_{0:4}$	19.9	0.0	-	-	22.1	52.4	-	-	-	-	-	-
$S_{0:2} - S_{0:3} - S_{0:4} - S_{0:5}$	22.1	-	-	-	23.7	-	-	-	-	-	-	-

Table 4. Grain yield (g 2m^{-2}) and plant architecture scores referring to the joint analysis of the generations $S_{0:2}$, $S_{0:3}$, $S_{0:4}$ and $S_{0:5}$, grain type scores of the $S_{0:5}$ generation of the first cycle of recurrent selection (C_0), values of the standardization variable Z and the estimate of the gain with selection in relation to the control means, considering the mean of the five selected families

Genotypes[1]	Yield	Z	Plant architecture	Z	Grain type	Z	$\sum Z$
1 x 3 – 120	441	2.6	3.9	2.8	4.2	4.4	9.7
2 x 6 – 162	419	1.9	4.1	3.5	3.8	3.2	8.6
3 x 8 – 133	445	2.7	4.1	3.4	4.2	4.4	10.4
4 x 9 – 81	423	2.0	4.0	2.9	3.8	3.2	8.1
4 x 9 – 82	471	3.5	4.1	3.4	3.8	3.2	10.2
5 x 10 – 42	516	5.0	3.9	2.9	3.5	2.0	9.9
8 x 9 – 100	469	3.5	3.8	2.2	3.7	2.6	8.3
8 x 9 – 101	419	1.9	4.2	3.8	4.0	3.8	9.4
8 x 9 – 107	466	3.4	3.7	1.9	4.0	3.8	9.0
8 x 9 – 108	429	2.2	3.6	1.7	3.8	3.2	7.1
8 x 9 – 111	433	2.3	4.0	3.2	4.0	3.8	9.3
8 x 9 – 93	470	3.5	4.3	4.2	3.3	1.4	9.1
8 x 9 – 94	474	3.6	3.3	0.7	3.7	2.6	6.9
8 x 9 – 99	507	4.7	3.9	2.7	3.3	1.4	8.8
CNFC 9455	416	1.8	4.3	4.3	4.0	3.8	9.8
CNFC 9471	472	3.6	4.4	4.4	3.3	1.4	9.4
Family mean	456	3.1	3.9	2.8	3.8	3.1	8.9
Mean of the five selected families	458	3.1	4.0	3.3	3.9	3.6	9.9
Control means	444	2.7	4.4	4.4	3.7	2.6	9.6
Gain (%)	3.24	14.81	-9.09	-25.00	5.41	38.46	3.13

[1] Parent identification shown in Table 2

genetic variance (σ_G^2) (Cruz and Regazzi 2001). In this case, the component of the interaction was nearly 6.5 times greater than the component of the genetic variance.

Finally, we point out that eight of the evaluated 14 families in the $S_{0:5}$ generation were originated by the crossing between the parents CNFC 9484 and IAPAR 81. This crossing was the one that presented the second-greatest probability among the chosen populations of bringing forth lines with a better performance than line IPR Uirapuru in the recurrent selection program (Table 2). Note that the population that presented the greatest probability had a low estimate of genetic variance (1.96), while the population resulting from the crossing between the parents CNFC 9484 and IAPAR 81 had the second-highest estimate (40.96).

Only two of the 14 families evaluated in the $S_{0:5}$ generation were selected in the $S_{0:2}$ generation for the recombination process. This result had already been expected since the families to be recombined had not only been chosen by the mean performance of the evaluated traits. The selection initiated in the $S_{0:3}$ generation for grain type may also have contributed to the non-coincidence of the families chosen for recombination and those evaluated in the $S_{0:5}$ generation. Finally, the presence of interaction families x seasons for the trait plant architecture must have further contributed to this fact, which must be quite frequent in recurrent selection programs with autogamous plants. The strategy to be used to alleviate the effect would be to include families (lines) obtained at the end of each cycle with an authenticated superior performance in future recombination cycles. This procedure should be used in the continuation of this recurrent selection program.

Literature presents some alternatives for the evaluation of the gain with recurrent selection in common bean. One of them is based on the comparison of the means of the best families obtained during the first segregating generations of the selection program. This strategy provides an early estimate of the selection gain and was used by Singh et al. (1999) and Ranalli (1996). Another alternative is the evaluation of the lines of best performance obtained at the end of each cycle, as used by Ramalho et al. (2003).

Since the objective of this program is the selection of lines that associate high yield, upright growth habit and commercially acceptable grain types, the main interest is to verify the gain obtained after the selection of the best families (lines) evaluated in the $S_{0:5}$ generation, considering the three traits jointly. Table 4 displays the obtained means and Z values for the 14 families and two controls evaluated in the $S_{0:5}$ generation. In the mean of the 14 families, the sums of Z presented a value of 8.9, while the control means attained a value of 9.6. The 5 best families however presented 3.1% higher means than the controls. One may therefore conclude that it was already possible to obtain lines with a better performance than the controls in the first selection cycle.

The selection was effective at developing common bean lines that associate high grain yield potential, upright growth habit and commercially acceptable carioca type grains. The estimates of genetic and phenotypic parameters, obtained in the different generations and associated to the mean performance of the families, allow a prediction of the gain with recurrent selection in future cycles.

Seleção visando a obtenção de plantas de feijoeiro de porte ereto e grãos tipo carioca

RESUMO - *Com o objetivo de obter linhagens de feijoeiro com grãos tipo carioca, boa produtividade e porte ereto da planta, dez linhagens foram cruzadas em um esquema dialélico. As populações obtidas foram avaliadas quanto à capacidade de gerar linhagens superiores. Das 42 populações avaliadas foram selecionadas 11 para formar a população base (S_0) do primeiro ciclo (C-0). As famílias resultantes foram avaliadas até a geração $S_{0:5}$ para produtividade e tipo de grãos e arquitetura da planta. Nessa geração, 14 famílias foram avaliadas com duas testemunhas para se estimar o ganho genético considerando as três características em conjunto. O ganho obtido foi de 3,1% após um ciclo de seleção, confirmando a eficiência da seleção realizada. As estimativas dos parâmetros genéticos e fenotípicos nas diferentes gerações associadas ao desempenho médio das famílias permitem predizer o sucesso com a seleção recorrente em ciclos futuros.*

Palavras-chave: seleção recorrente, ganho genético, feijoeiro comum, arquitetura da planta, produção.

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