

Procedures for identification of superior progenies in successive generations of evaluation in common bean

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ABSTRACT: When breeding the common bean in Brazil, the best progenies are chosen, normally, from solely the generation under analysis at the conclusion of the evaluation, without considering what occurred in the past. However, a number of recently published studies show that if an evaluation were to consider all relevant generations, the gain from selection could be higher, especially when an index that involves information from the population that gave rise to the progenies is used. Thus, the aim of this study was to compare three selection procedures in the evaluation of successive generations and to discuss the implications of the progeny \times environment interaction in terms of success of selection. Cycle XV progenies from a bean recurrent selection program were used. The traits evaluated were grain yield, plant architecture and grain type. Analysis of variance was carried out and the variance components and heritabilities were estimated. The same analyses were made using mixed models. A selection index weighted by the effect of populations and progenies within populations (WSI) was also obtained. We estimated the correlations between the classification of the progenies using the three procedures and the coincidence of the best progenies evaluated in $S_{0.4}$ with the progenies in the previous generations. We found that the classification of the progenies by the BLUP's and WSI did not expressively differ from that obtained when using only the mean, even when a number of generations were considered in the selection. None of the procedures used effectively mitigated the effect of the progeny \times environment interaction.

Keywords: *Phaseolus vulgaris*, recurrent selection, selection index, mixed model approach

Introduction

Common bean breeding strategies (*Phaseolus vulgaris*) have been very effective in improving grain yield. However, differences detected between policies are ever fewer, with the result that breeders have deployed all the strategies available to increase success in selection. Normal practice in Brazil is to select the best progenies only in the generation under analysis at the conclusion of the evaluation process, without considering what had occurred in the past.

Over the last few years, certain proposals have emerged aimed at improving the selection process through analyses, primarily through the use of mixed models, drawing on information from all the progenies evaluated in previous generations (Piepho et al., 2008). In the same vein, Resende et al. (2015) proposed a selection index that considers all generations and the covariance between successive generations for the purpose of identifying the best progenies. Through simulation, they showed that the process was effective. Subsequently, Resende et al. (2016) complemented their previous study with a proposal to carry out selection using the merit of the progenies in all the generations and the performance of the populations from which they were obtained. However, Resende et al. (2015 and 2016) considered that the allelic frequency was equal to $\frac{1}{2}$, which, evidently, might not apply to recurrent selection since the allele frequency is rarely equal. In this situation, in addition to additive variance (V_A) and dominance variance (V_D), D_1

and D_2 components play a role. Given that it is a covariance, D_1 , especially, can be negative (Souza and Ramalho, 1995; Morais et al., 1997). Consequently, its effect on future generations might run contrary to breeders' aims.

In a recurrent selection program it would be possible to obtain a selection deriving performance information of the population that gave rise to each progeny throughout the inbred generations, as recommended by Resende et al. (2016). Then the allelic frequency would not be $\frac{1}{2}$, and an index working with heritability among populations and between progenies within populations could be used.

Considering the foregoing, this study was undertaken for the purpose of evaluating selection efficiency using the adjusted means, the mixed models approach, estimating the BLUPs as influenced by the population effect, and the selection index weighted by the of populations and progenies/populations (WSI) for identifying superior bean progenies using data from a recurrent selection program. In addition, we sought to evaluate the effect of the progeny \times environment interaction on the selection efficiency of the three procedures adopted through coincidence of the best progenies selected in one or more generations on a future generation.

Materials and Methods

The experiments were conducted in the city of Lavras in southern Minas Gerais, Brazil, situated at an altitude of 918 m, 21°58' S and 42°22' W. The progenies

used in this study came from cycle XV of the recurrent selection program for bean yield at UFLA. In the $S_{0:3}$ generation of the XIV cycle, 19 progenies with the best performance were selected. These progenies were recombined in a manner similar to a top cross method; that is, each progeny was used as a female in a cross with all the others (18 progenies). The "F₁" seeds obtained from each female parent were mixed and multiplied to obtain the S_0 population of the XV cycle. Consequently, 19 populations were obtained with the number of progenies within each population ranging from 14 to 29 giving a total of 439 progenies.

The 439 $S_{0:1}$ progenies obtained were evaluated together with two controls in a 21×21 simple lattice design, sown in July 2015. The plots in this generation consisted of one 2-m row, with between-row spacing of 0.6 m. The main common bean traits were evaluated. A plant architecture score was attributed via a modified scoring scale, proposed by Collicchio et al. (1997), in which the score 1 was attributed to prostrate plants and score 9 to completely upright plants. Grain type score was also attributed by three evaluators on a scoring scale from 1 to 9, modified from Ramalho et al. (1998), in which 1 refers to the carioca grain type with a dark cream grain color and dark brown streaks, with a halo, 100-seed weight less than 22 g, and flat grains, and score 9 indicates carioca grain type with a light cream grain color, light brown streaks, no halo, mean 100-seed weight of about 27 g, and non-flat grains. Grain yield was determined in kg ha^{-1} .

Using the adjusted mean values of grain yield, plant architecture score, and grain type score, 322 $S_{0:2}$ progenies were selected. These progenies were sown in Nov 2015, together with the two controls. The same progenies, now $S_{0:3}$, were once more evaluated, with sowing in Feb 2016. In these two generations, an 18×18 simple lattice design was adopted, and the plots consisted of two 2-m rows, with between-row spacing of 0.6 m.

Using the same procedure described above, the 79 progenies with the highest yield were selected. These $S_{0:4}$ progenies and the controls were evaluated once more, with sowing in July 2016. A 9×9 triple lattice experimental design was used and the plots also consisted of two 2-m rows, with between-row spacing of 0.6 m. In all the experiments, the management and traits evaluated were the same as for the $S_{0:1}$ generation.

Three procedures to identify the best progeny were compared: i) using the means derived from the progenies from one or more generations evaluated; ii) estimating a selection index (WSI), which considers not only the performance of the progeny, but also the population of origin, similar to what Resende et al. (2016) evaluated by simulation; and iii) using the mixed models approach in which BLUPs were estimated considering the effect of populations on one or more generations evaluated.

Initially, data on each characteristic evaluated were subjected to analysis of variance by generation/environment. Subsequently, joint analysis of variance

was carried out using the adjusted mean values of the 322 common progenies and the two controls in the $S_{0:1}$, $S_{0:2}$, and $S_{0:3}$ generations, initially using the least squares method (LSM). Joint analysis was also carried out considering the 81 common treatments evaluated in all the generations, $S_{0:1}$, $S_{0:2}$, $S_{0:3}$, and $S_{0:4}$. The model adopted in the joint analyses, considering all the random effects, except for the mean and generations/environments, was the following: $\bar{y}_{ik} = m + t_i + a_k + ta_{ik} + \bar{e}_{ik}$, in which \bar{y}_{ik} is the value observed of the mean of progeny i , in environment/generation k ; m the overall mean of the experiment; t_i the effect of treatment i , in which $i = 1, 2, 3, \dots, q$, in which q is the number of progenies/controls evaluated, where $t_i \sim N(0, \sigma_{t_i}^2)$; a_k the effect of the environment/generation k ; ta_{ik} the effect of the interaction between treatment i and the environment/generation k , where $ta_{ik} \sim N(0, \sigma_{ta}^2)$; and \bar{e}_{ik} the mean error associated with the observation \bar{y}_{ik} , where $\bar{e}_{ik} \sim N(0, \sigma_e^2)$.

In individual and joint analyses of variances, the source of variation of treatments was separated into the effect of progenies, between populations, progenies within each population, between controls, and the progeny vs. control contrast. The variance components and heritabilities were estimated from the expectations of the mean squares of the analyses. Estimates of h^2 were obtained among populations by the estimator

$$h_{Pop}^2 = \frac{MS_{Pop} - MSE}{MS_{Pop}},$$

in which MS_{Pop} is the mean square between populations; the MSE the mean square of the error, obtained by analysis of variance by generation; and the h^2 among progenies/population by the estimator

$$h_{P|Popn}^2 = \frac{MSP_{Pro} - MSE}{MSP_{Pro}},$$

in which MS_{Pro} is the mean square between progenies within the population obtained in the individual analysis. The h^2 among all the progenies in each generation and all the evaluated generations were also estimated.

The confidence intervals of both the estimates of the variance components and the confidence intervals of the heritabilities were obtained using the expressions presented by Knapp et al. (1985), where $\alpha = 0.05$.

A weighted selection index (WSI) was estimated using the adjusted means of the individual analyses and, subsequent combination of the generations/environments. This index was obtained by the following estimator: $WSI = \bar{Y}_{Popn} h_{Pop}^2 + \bar{Y}_{P|Popn} h_{P|Popn}^2$, in which \bar{Y}_{Popn} is the mean of the population n that gave rise to progeny i ; $\bar{Y}_{P|Popn}$ the mean of progeny i from population n ; h_{Pop}^2 the heritability between means of the populations; and $h_{P|Popn}^2$ the heritability between means of the progenies within the population n . This value was considered the mean value obtained in the n populations involved. In the analyses considering the generations evaluated, the WSI was also obtained from the sum of the WSI values of each generation involved.

The data were also analyzed by the mixed models method. The effect of the population on the model was considered, and in each generation of evaluation, analysis was carried out according to the model $y = X\beta + Z_1p + Z_2t + Z_3b + e$, in which y is the vector of the mean phenotypic data; β the vector of the fixed effects, mean and replication; p the random effect of the population, where $p \sim N(0, I\sigma_p^2)$; t the random effect of the progeny within the population, where $t \sim N(0, I\sigma_t^2)$; b the random effect of the block within the replication, where $b \sim N(0, I\sigma_b^2)$; X , Z_1 , Z_2 , and Z_3 are incidence matrixes for β , p , t , and b , respectively; and e the vector of the residual effects (random), where $e \sim N(0, I\sigma_e^2)$.

A sequential procedure analysis was also carried out, considering the population effect on the model and recovering the information from the generations evaluated. The $S_{0.1}$, $S_{0.2}$, and $S_{0.3}$ generations were considered with all the progenies evaluated, adopting the mean, replication, and effect of generations as a fixed effect. This sequential analysis was carried out according to the model, in which y is the vector of the mean phenotypic data; β the vector of the fixed effects, mean, replication within generation and generation; p the random effect of the population, with $p \sim N(0, I\sigma_p^2)$; t the random effect of the progeny within the population, where $t \sim N(0, I\sigma_t^2)$; b the random effect of the block within the replication, where $b \sim N(0, I\sigma_b^2)$; g the random effect of the interaction between progenies and generations/environments, where $g \sim N(0, I\sigma_g^2)$; d the random effect of the interaction between progenies within the population and generations/environments, where $d \sim N(0, I\sigma_d^2)$. X , Z_1 , Z_2 , Z_3 , Z_4 and Z_5 were incidence matrixes for β , p , t , b , g and d , respectively; and e the vector of the residual effects (random), where $e \sim N(0, I\sigma_e^2)$.

For estimating the variance components, the restricted maximum likelihood (REML) method was used. The BLUE estimates of the fixed effects and the BLUP predictions of the random effects were obtained.

The three procedures adopted were compared considering the three traits separately. Initially, the Spearman correlation of these methods was estimated, two by two, aiming to compare classification of the progenies under the different selection procedures adopted. To evaluate the effect of the methodology on the success of selection in future generations, coincidence between the best 10 % of progenies selected in the k generation was estimated for each trait, considering the successive generations $k + 1$ and $k + 2$. This same procedure was adopted considering the common progenies in the $S_{0.1}$, $S_{0.2}$, and $S_{0.3}$ generations, and the same progenies in the $S_{0.4}$ generation.

Results

In the joint analyses of variances considering the 322 common progenies and the two checks in the $S_{0.1}$, $S_{0.2}$, and $S_{0.3}$ generations, a significant difference was found in the effects of progenies on yield and grain type ($p \leq 0.05$), results not shown, confirming that there was

a difference between the progenies stemming from the different populations for these characteristics. The contrast between progenies vs. controls was not significant for either yield or plant architecture, indicating that progenies and control mean was similar for these two characteristics. When the environmental source of variation (generation/crop season) was considered, significant differences were detected for all traits ($p \leq 0.01$). The effects of the environment \times treatment, environment \times progeny, and environment \times population interactions were significant ($p \leq 0.01$) in all cases, showing that the response of the progenies evaluated did not coincide in the different environments. No significant differences were detected between populations that gave rise to the progenies for the traits evaluated, except for the grain type trait. The significance of the progenies/population source of variation varied according to trait.

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The estimates of the genetic and phenotypic variance components corroborated the results of analysis of variance. The progeny \times environment interaction (V_{PE}) component for yield was high (Table 1). The estimate of V_{PE} was 2.2 times that obtained for V_p , showing the pronounced interaction effect for this trait.

Joint analyses of variances were carried out for 81 treatments in the four generations of evaluation, $S_{0.1}$, $S_{0.2}$, $S_{0.3}$, and $S_{0.4}$ (Table 2). Once more, a significant difference was observed between the environments ($p \leq 0.01$). In this case, there was a significant difference between the treatments for the grain type trait only ($p \leq 0.01$). The same was found for the sources of variations between progenies and between controls. The progenies vs. controls contrast was significant ($p \leq 0.01$) for yield only, indicating that the mean values of the progenies and controls were different for this trait. The environment \times treatment and environment \times progeny interactions were also significant for all the characteristics evaluated.

One of the aims of this study was to compare the analyses carried out using the least squares method (LSM) and considering mixed models, in the case of the latter using the effect of the progenies' origin population as an additional source. The comparisons were initially made between the variance components (Table 2). Note that both the estimate of the variances between progenies (V_p) and that between populations (V_{Pop}) were of a higher magnitude when using the least squares method. The comparison between the h^2 varied according to generation. In the $S_{0.1}$ and $S_{0.2}$ the result was very similar in both cases; however, in the $S_{0.3}$ generation and the joint analysis, the magnitude of the h^2 estimate was higher in the LSM.

Table 1 – Estimates of genetic variance between progenies (V_p), phenotypic variance (V_F), variance between populations (V_{Pop}), variance of the progeny \times environment interaction (V_{PE}), heritability among progenies (h^2), for grain yield (kg ha⁻¹), estimated by the least squares (LSM) and the mixed models methods in the $S_{0:1}$, $S_{0:2}$, and $S_{0:3}$ generations and jointly in the three generations.

	$S_{0:1}$	
	LSM	Mixed models
V_F	311562.09	294894.00
V_p	69988.33 (61647.03-73371.09) ¹	60642.00
V_{Pop}	19277.16 (16979.68 - 20208.89)	13262.00
$h^2(\%)$	22 (6-36)	21
	$S_{0:2}$	
	LSM	Mixed Models
V_F	281179.85	240172.00
V_p	136489.62 (118094.79-144597.91)	98994.00
V_{Pop}	46106.25 (39892.47 - 48845.24)	35330.00
$h^2(\%)$	48 (35-59)	41
	$S_{0:3}$	
	LSM	Mixed Models
V_F	218214.51	187983.50
V_p	46098.81 (39886.03 - 48837.35)	25150.00
V_{Pop}	26001.99 (22497.68 - 27546.66)	22082.00
$h^2(\%)$	21 (1-36)	13
	$S_{0:1}$, $S_{0:2}$, and $S_{0:3}$	
	LSM	Mixed Models
V_F	93590.99	52401.08
V_p	18136.39 (15692.13 - 19213.80)	23711.00
V_{Pop}	4686.79 (4055.15 - 4965.21)	0.00
V_{PE}	40268.63	38677.00
$h^2(\%)$	19 (3 - 33)	23

¹Values between parentheses correspond to the confidence intervals for the variance components and h^2 .

The estimates of the correlations involving the data obtained from the means, the BLUPs, and the WSI are shown in Table 3. Note that they were all of high magnitude except for the plant architecture score in the $S_{0:2}$ generation, involving the mean and the WSI. In general, regardless of the trait, the progenies classification was similar under the three methodologies considered.

As the progenies were evaluated simultaneously for three generations, coincidence in classification of the best 10 % of the progenies was estimated by considering the mean, the BLUPs, and the weighted index. Note in Table 4 that the coincidence, in all cases, was of small magnitude - even when the means of the $S_{0:1}$, $S_{0:2}$ generations and the response in $S_{0:3}$ was considered. It should be highlighted that the magnitude of coincidence varied between the traits, and it was higher for the grain type score. However, in none of the cases considering the best 10 % of progenies was it higher than 50 %, which is a very small coincidence.

In the $S_{0:4}$, 79 progenies and two controls were evaluated, and thus the combined effect of the generations ($S_{0:1}$, $S_{0:2}$, and $S_{0:3}$) to increase coincidence with

Table 2 – Summary of the analyses of variances of the traits yield (kg ha⁻¹), plant architecture score (PA), and grain type score (GT) of the common treatments in the $S_{0:1}$, $S_{0:2}$, and $S_{0:3}$ and $S_{0:4}$ generations.

SV	DF	MS		
		Yield	PA	GT
Environment/Generation (E)	3	17167735.78**	59.03**	11.29**
Treatments (T)	80	714351.80 ^{ns}	2.19 ^{ns}	13.02**
Progenies (P)	78	712750.10 ^{ns}	2.23 ^{ns}	9.29**
Checks (C)	1	2083.48 ^{ns}	0.88 ^{ns}	10.21 *
C vs P	1	1551552.90**	0.79 ^{ns}	206.10**
E \times T	240	628292.04**	2.24**	4.56**
E \times P	234	635250.36**	2.17**	4.66**
E \times Cont	3	674553.17 ^{ns}	0.47 ^{ns}	0.41 ^{ns}
E \times Cont vs P	3	39282.26 ^{ns}	90.94**	1.13 ^{ns}
	1012	386858.73	-	-
Error	1042	-	1.456	-
	1569	-	-	0.85
Overall mean		2961.41	5.49	4.86
Mean of Checks		2668.19	5.27	1.81
Mean of Progenies		2968.84	5.49	4.94
Range of variation of the mean of the progenies		1182.83	2.3	6.96

**, * and ^{ns} = significant ($p < 0.01$), significant ($p < 0.05$), and non-significant ($p > 0.05$) by the F test, respectively; SV = Source of variation; DF = Degrees of freedom; MS = Mean square.

Table 3 – Correlation between the BLUPs and the means, the values weighted by heritability (WSI), and the means and between the BLUPs and the weighted values (WSI), for yield (Yield) (kg ha⁻¹), plant architecture score (PA), and grain type score (GT).

	BLUP			WSI			BLUP/WSI		
	Yield	PA	GT	Yield	PA	GT	Yield	PA	GT
$S_{0:1}$	0.99	0.93	0.96	0.81	0.89	0.96	0.79	0.71	0.91
$S_{0:2}$	0.94	0.89	0.96	0.86	0.46	0.88	0.81	0.22	0.75
$S_{0:3}$	0.96	0.88	0.97	0.82	0.72	0.94	0.78	0.72	0.81

performance with the same progenies in $S_{0:4}$ could be verified (Table 5). In the coincidence of the 10 best progenies, now considering the last generation of evaluation, that is the $S_{0:4}$, the efficiency of selection was low, regardless of whether only the data of each generation were used individually or jointly in an analysis of the generations two by two or three by three. The results were similar, regardless of the method of analysis.

Discussion

Progenies were randomized regardless of the population of origin. According to Piepho and Williams (2006) the genetic effects can be efficiently estimated when the resolvable incomplete block design is employed, with either restricted or unrestricted progenies randomization.

Table 4 – Coincidence (%) of the best 10 % of the progenies selected by the means per se of the progenies, by the BLUPs, and by the WSI (weighted selection index) for the traits of yield (kg ha⁻¹), plant architecture, and grain type (GT), in the same generations of evaluation and in a later generation.

Generations	Coincidence (%)								
	Yield			Plant architecture			GT		
	Mean	BLUP	WSI	Mean	BLUP	WSI	Mean	BLUP	WSI
S _{0.1} /S _{0.2}	9.09	11.36	4.55	6.82	4.55	0.00	20.45	20.45	18.18
S _{0.1} /S _{0.3}	6.82	6.82	2.27	2.27	2.27	9.09	18.18	20.45	15.91
S _{0.2} /S _{0.3}	12.12	9.09	15.15	24.24	18.18	27.27	18.18	21.21	42.42
S _{0.1} and S _{0.2} /S _{0.3}	9.09	-	12.12	6.06	-	42.42	21.21	-	36.36

As emphasized in the literature, in balanced experiments, there is no difference between the use of the least squares method and the mixed models method (Thompson, 2008; Bernardo, 2010). However, in this study, there was an imbalance between the number of progenies evaluated within each population and the incomplete blocks in the specific lattice design adopted. In addition, the effect of populations and progenies within populations was considered in the model, which leads to an imperfect association between the two methods of analysis. In spite of this, the results obtained by the two methods of analysis were similar (Table 4). In other studies, with eucalyptus (Reis et al., 2011) and common bean (Mendes et al., 2012), there were also small unbalanced results similar to those found in this study.

It should also be highlighted that when the effect of the populations that gave rise to the progenies is considered, it may contribute in such a way that there is a difference in the mixed models analysis, as was affirmed by Resende et al. (2016). In other words, the information between populations and also between progenies within populations should be used in the weightings to obtain the BLUPs. Even in this situation, the estimates of the correlations between the means and the BLUPs, considering the effect of populations, were slightly lower, though still of high magnitude (Table 4). The estimates of correlation between the mean and the BLUPs in most cases were higher than 0.90. It should be emphasized that the effect of populations that gave rise to the progenies was not expressive, especially for yield and the plant architecture score, which may have contributed to the results observed.

It is expected that the estimates of the variance components will be more robust when analyzing the data using mixed models (Lynch and Walsh, 1998; Thompson, 2008). The reason for this is the use of the restricted maximum likelihood method (REML) and the process is iterative. In this study, the estimates of h² for grain yield obtained from the least squares methods and the mixed models with the inclusion of the effect of populations were practically the same in the S_{0.1} and S_{0.2} generations and in joint analysis. In the S_{0.3} generation, although the point estimate of h² is different in the two methods, from the confidence interval of h² it can be inferred that they may be equal.

Table 5 – Coincidence (%) of the 10 best progenies among the selection generations and the final S_{0.4} generation for the yield trait (kg ha⁻¹).

	Coincidence (%)		
	Mean	BLUP	WSI
S _{0.1}	20	20	10
S _{0.2}	10	10	10
S _{0.3}	20	10	0
S _{0.1} and S _{0.2}	10	-	10
S _{0.2} and S _{0.3}	10	-	10
S _{0.1} , S _{0.2} , and S _{0.3}	10	20	0

WSI = weighted selection index.

A new selection strategy, by which the merit of the progeny is evaluated not only by performance “per se” in the generation evaluated, but also by the population from which it was derived and the kinship coefficients of the different inbreeding generations used to construct this index, was presented by Resende et al. (2016). Using this procedure, they simulated various situations and showed that using the information from past populations and generations increases the efficiency of the selection process, compared to what is normally used, which is the mean values of the last generation evaluated only. The methodology of Resende et al. (2016) places kinship in the model considering an allelic frequency of ½, which may not be appropriate when there are populations from a recurrent selection program, in which allelic frequency would rarely be ½. In this case, as has already been mentioned, D₁, as a covariance, can be negative. Moreover, the few estimates of D₁ available in autogamous plants were negative (Souza and Ramalho, 1995; Morais et al., 1997). To use a procedure similar to that proposed by Resende et al. (2016) for a condition in which the allelic frequency is not ½, a weighted index was chosen, using the mean h² between the populations and h² between the means of the progenies/populations. With this adjustment they reflect what truly occurred, regardless of whether the allelic frequency was ½ or not.

The Spearman correlations between the means and the WSI proposed were of high magnitude, especially for yield (r ≥ 0.81) and the grain type scores (r ≥ 0.88). As a result, classification of the progenies was similar in

the three methodologies adopted in most cases (Table 4). In general, the estimates of the correlations between the weighted means and the BLUPs were also high. Spearman correlation is a nonparametric correlation that measures the variation in ranking the materials, and it is important that it be as high as possible (Bhering et al., 2015). Although the correlation between different methods suffers from the limitation of not identifying which method is the best, this parameter was used to compare the classification of the progenies by the different procedures adopted, since it is the main aim of the breeders. Another statistical approach that can be adopted for the evaluation of competing methods is a cross-validation of simulation, but it was not the focus of this work.

The measures of efficiency of the multigenerational indexes reported in the literature (Resende et al., 2015; Resende et al., 2016) are pertinent and also the efficiency of the BLUPs by generation or the involvement of various generations (Nunes et al., 2008; Piepho et al., 2008). However, little has been evaluated of the effective contribution of these indexes when considering future generations under growing conditions. For this reason, in this study, we sought to estimate the coincidence of the best progenies in the generation of reference and in future generations. In all the methods adopted, coincidence was low (Table 5), even when the three generations of evaluation ($S_{0.1'}$, $S_{0.2'}$, and $S_{0.3}$) were considered in relation to the $S_{0.4}$ (Table 5). The progeny \times environment interaction (crop seasons and/or generations) was expressive in Brazil. This has been a common finding in experiments with bean crops (Lima et al., 2012; Barili et al., 2015; Lima et al., 2015). The variance component associated with the progeny \times environment interaction (V_{PE}) was higher than the estimate of variance between progenies (V_p) for grain yield (Table 2). For yield, V_{PE} was 2.2 times greater than the effect of V_p , thus showing the pronounced effect of the interaction for this trait. The low coincidence in the best progenies identified in the successive generations is due to the progeny \times environment interaction. The possible benefit of adopting the multigenerational index or similar procedure does not necessarily mitigate the effect of the interaction that almost always occurs.

The greatest challenge of the breeder is to identify the best progenies/lines or hybrids that will continue to be the best in future years and under management conditions different from those in experimental stations. This has already been proven with the bean crop (Lima et al., 2012; Ferreira et al., 2015). The alternative for increasing the efficiency of the selection process that has been adopted above all by the large seed companies is evaluation of the lines/hybrids in the greatest number of environments possible (Gaffney et al., 2015).

It is clear that to be sure in deciding which line/hybrid to recommend, considering that the differences that may be detected are ever fewer, the number of replications/environments must be as large as possible. Modern methods of biometry can improve the efficiency of the

selective process, as has been shown, but they will only be truly effective if the data to be analyzed are of good quality and with the effect of the interaction mitigated through the largest number of replications/environments possible. It is possible to improve efficiency using mixed models with additional information from kinship and genomics according to a number of simulation studies (Resende et al., 2016; Nunes et al., 2008; Ramalho et al., 2013). However, these studies must be validated considering future generations to verify if, even with the interaction, they continue to be the most efficient.

Conclusion

The classification of the progenies by the BLUPs and the WSI did not differ significantly from the average only, even when considering several generations in the selection.

None of the procedures used managed to effectively mitigate the effect of interaction progenies \times environments, since coincidence in the selection efficiency of one or more generations with a future generation was small and varied very little between the three procedures adopted.

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