Predicted and realized gains of different selection strategies in soybean populations: a comparative study

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ABSTRACT

Genetic gains from selection on yield were predicted in three soybean populations using original data and data corrected by the variation in agronomic traits of check cultivars. Predicted gains were compared to realized gains after correction for agricultural season effects - caused by environmental differences during the prediction and checking growing seasons - to indicate the best selection strategy and check the influence on yield of selection on the other traits assessed in the field. Individual selection, selection among and within families and combined selection were used for grain yield alone and for simultaneous selection on grain yield, plant height and number of days to maturity traits. Selection was made on F5 generation plants grown in an experimental field in Viçosa, Minas Gerais State during the 1997/98 agricultural season. The experiment used intercalated check cultivars. The results indicated lower within family heritabilities compared to the other types. Little variation was detected in gain prediction due to data correction. At field level, simultaneous selection performed better for grain yield improvement. Simultaneous gains for number of pods per plant, number of seeds per pod and mean weight of one seed, which are primary yield components, were obtained only when selection for the three components was balanced.

KEY WORDS: *Glycine max*, heritability, gain from selection.

INTRODUCTION

Soybean is one of the most important grain crops in Brazil and generates indispensable resources for development. Breeding programs carried out by public and private research institutions have certainly contributed to the development and expansion of the crop in various Brazilian states. However, techniques capable of increasing the genetic gains from selection in segregant generations are needed for greater efficiency in breeding programs.

Genetic progress in any species is associated with the existence of genetic variability, natural or artificial selection and the adaptation of genotypes to the prevailing environments. Once the presence of variability has been ascertained, selection becomes very important for genetic progress. Selection provides the accumulation in a determined population of genes favorable to the trait in question and is a process linked to constant and permanent renovation.

The possibility of the breeder to predict the expected gain from selection is one of the greatest contributions of quantitative genetics (Vencovsky, 1987; Hallawer and Miranda Filho, 1981; Ramalho et al., 1993). Cruz and Regazzi (1997) stated that the procedures adopted in a breeding program can be chosen based on scientifically sound predicted gains provided by the several selection strategies.

Genetic progress refers to alterations observed in the traits of interest during a selection cycle, which involve recombination and multiplication of the units selected. Such modifications will happen in variable magnitudes and directions depending on the strategy and the selection criteria adopted. Thus, one of the most important attributions of the plant breeder is to identify the selection criteria that can promote the desirable alterations in the traits of interest within a breeding program.

The breeder can predict and compare the response of different selection strategies applied to the population of interest (base population) (Nyquist, 1991) and can, therefore, check the efficiency of these strategies.

The breeder uses several procedures to identify superior genotypes in a population. Some methods consider individual performance while others are based primarily on family performance with less emphasis placed on individuals within the family. There is also a strategy that simultaneously uses the data of the individual and its parents called combined selection (Falconer, 1987). Silva (1982) and Falconer (1987) further stated that combined selection is always superior to the individual, family and within and among family selection methods. Lush (1964) found that, theoretically, combined selection gives a response superior or at least equivalent to family or mass selection. Weber (1982) pointed out that selection response can be maximized if all the information obtained from the parents is also used in the selection process.

The present study was carried out to compare the predicted and realized gain from selection for increased soybean grain yield, using data corrected by performance of check cultivars distributed within the experiment. The agreement between predicted and realized gain after correction for agricultural season effects and the influence of selection on the other assessed traits were also verified.

MATERIAL AND METHODS

Experimental Material

Three F5 populations from crosses CR1, CR2 and CR3 were used for the gain predictions. The increase of homozygosity was obtained using the bulk method in the Soybean Breeding Program of the Plant Technology Department at the Federal University of Viçosa (UFV).

CR1: 'CEPS 77-16' x 'Doko RC'

CR2: 'CEPS 89-26' x 'IAC-8'

CR3: 'CEPS 89-26' x 'FT-Cristalina'

Field installation and conduction of experiments for line extraction

The field experimental design was F5 line rows with intercalated check cultivars, which is useful when the small quantity of seeds available from each segregant material precludes designs with replications. The experiment started with a row sown with seeds of one of the check cultivars followed by five rows with seeds from plants (progenies from selected plants) derived from the crosses; in the next line (7th line), seeds of another check cultivar were sown; rows 8th to 12th were sown with another five lines of the cross; seeds from the first check cultivar were sown again in the next line (13th line), and thus successively, until

all seeds from the selected plants were sown. One of the parents and the BR 16 cultivar were used as check cultivars. The lines CEPS 77-16 and CEPS 89-26 were replaced by the BR 16 cultivar, which has similar agronomic traits since their seeds were not available in the required quantities.

Each plot consisted of a one-meter row. Inter-row spacing was 0.70 cm and 30 seeds were used in each row. Rows were thinned to 15 plants per plot 15 to 20 days after emergence.

The experiment was carried out in the Prof. Diogo Alves de Mello experimental Field, at the Crop Science Department at UFV, in Viçosa, Minas Gerais, in the 1996/97 agricultural season (gain prediction). The same experimental procedures were adopted in the 1997/98 agricultural season (realized gains were obtained).

The following traits were assessed in six competitive plants per plot: number of days to flowering (NDF); plant height at flowering (SPF); number of nodes at flowering (NNF); number of days to maturity (NDM); plant height at maturity (APM); number of nodes at maturity (NNM); number of pods per plant (NVP); number of seeds per plant (NSP); mean number of seeds per pod (NSV); grain yield (PRO) and mean weight of one seed (PIS).

Estimation of genotypic variances

According to the experimental design used and based on Ramalho and Vencovsky (1978), the variances were obtained by:

$$\hat{\sigma}_{Ge}^2 = \hat{\sigma}_{Fe}^2 - \hat{\sigma}_e^2$$

$$\hat{\sigma}_{Gw}^2 = \hat{\sigma}_{Fw}^2 - \hat{\sigma}_{ew}^2$$

where,

 $\sigma_{\it Ge}^2$: genotypic variance among family means;

 σ_{Gw}^2 : genotypic variance within families

 σ_{Fe}^2 : phenotypic variance among family means;

 σ_{Fw}^2 : phenotypic variance within families;

 σ_e^2 : environmental variance among family means, obtained from the variance among the means of the check cultivar replications;

 σ_{ew}^2 : environmental variance within families, obtained from the mean variation within the check cultivar replications.

Considering the additive-dominant genetic model, the additive variance (σ_A^2) was estimated by:

$$\sigma_A^2 = \frac{\sigma_{Ge}^2 - I_n \sigma_{Gw}^2}{I_n (1 + I_n)}$$

Where,

 I_n : endogamy coefficient in the generation considered.

Narrow sense heritability estimates

- Among family heritability

$$h_{\text{Re}}^2 = \frac{2I_n \sigma_A^2}{\sigma_{Fe}^2}$$

- Within family heritability

$$h_{Rd}^2 = \frac{(1 - I_n)\sigma_A^2}{\sigma_{Ew}^2}$$

- Heritability at individual level

$$h_{RI}^2 = \frac{(1+I_n)\sigma_A^2}{\sigma_{F_{Total}}^2}$$

Within experiment environmental correction

The 1996/97 data was corrected for environmental variation using the differences between the values of each check cultivar in relation to the general mean of the check cultivars for the given trait, maintaining the field experiment design that at each five segregant lines (rows), one of the check cultivars was sowed.

The matrix composed by the correction factors for each trait was obtained as follows:

- The general mean of each check cultivar was obtained;
- The mean of each check cultivar replication was obtained;
- The correction factor was obtained by subtracting from the mean of the check cultivar 1 or check cultivar 2 in each replication, the corresponding general mean.

The number of rows in the correction matrix was equal to the sum of the number of replications of the

check cultivars. The correction by made by subtracting the correction factor in the kth replication of the zth check cultivars from the value of the three previous and two posterior segregant lines.

$$V_{C_{ij}} = V_{O_{ij}} - F_{C_{zk}}$$
 where,

 $V_{C_{ij}}$ = corrected value for the jth individual within the Ith segregant line;

 $V_{O_{ij}}$ = observed value of jth individual in Ith line; and $F_{C_{zk}}$ = correction factor derived from the zth check cultivars in the kth replication.

The corrected data were used to obtain a second estimate the heritability coefficients. Only the denominators of the expressions presented in item 2.4 of Material and Methods were altered. The phenotypic variances were estimated using the corrected data.

Selection

The best genotypes were selected according to different strategies using the obtained data. The selection for grain yield was based on the individual, on the family and also on the individual and family simultaneously. Another selection strategy took into account minimum yield levels and plant height and number of days to maturity. All selection procedures were carried out on the data corrected by the environmental factor obtained from the variation of the check cultivars.

The selection strategies used in the F₅ populations of the three crosses and the number of individuals selected in each one were:

- i) Selection among and within families for grain yield. The proportions of families selected in each cross were: CR1 = 26.4%, CR2 = 35.8% and CR3 = 44.5%. Within each superior family, 33.4% of the plants were selected totaling 40 superior individuals. This number was fixed for the other strategies.
- ii) Combined selection for grain yield: 40 individuals showing the greatest genetic values obtained from the combination of the deviation of the individual from the family mean and the deviation of the family mean from the general mean were selected.
- iii) Individual selection for grain yield: 40 highest yielding individuals were selected, disregarding family information.
- iv) Simultaneous selection using the 'weight-free' and 'parameter-free' index: 40 individuals were selected

taking into account the number of days to maturity (NDM), plant height at maturity (APM) and grain yield (PRO) simultaneously. The selection limits were: NDM superior to 125 days, APM superior to 65 cm and PRO above the average yield.

The 40 individuals chosen in each selection strategy corresponded to different selection percentages, due to the different size of the populations. This number of selected individuals corresponded to the following selection percentages per cross: CR1: 8.772%, CR2: 11.905% and CR3: 14.815%. Due to the choice of the same individual in the different selection strategies, the following number of individuals were selected in each population: CR1: 84; CR2: 81 and CR3: 75.

Gain prediction

Selection among and within families

According to Vencovsky (1987), once the families and the individuals within families that will compose the bred population are defined, the gain by selection can be estimated by the following expression:

$$GS = \frac{2I_n \sigma_A^2}{\sigma_{Fe}^2} DS_1 + \frac{(1-I_n)\sigma_A^2}{\sigma_{Fw}^2} DS_2$$

where,

GS =expected gain from selection;

 I_n = endogamy coefficient;

 σ_A^2 = additive variance;

 σ_{Fe}^2 = phenotypic variance of the family means;

 DS_1 = mean selection differential for families;

 σ_{Fw}^2 = within family phenotypic variance; and

 DS_2 = within family average selection differential.

Combined selection

The combined selection was carried out using an index obtained taking into account the deviation of the individual from its family mean and the deviation of the family from the general mean. A weight was given for each deviation to minimize the differences among the elements of the selection indices *I* vector, and the elements of genetic values *G* vector.

The gain from selection is given by : $GS = DS_I$

where.

 DS_I = difference between the largest and smallest index in the selected individuals;

The expression for the combined selection index is:

$$I_{ij} = b_1(Y_{ij} - \overline{Y}_{i.}) + b_2(\overline{Y}_{i.} - \overline{Y}_{..})$$
 where,

 I_{ij} = combined selection index;

 $b_{\rm l}$ = weight given to the deviation of the value of the individual (Y_{ij}) from its family mean ($\overline{Y_{i.}}$);

 b_2 = weight given to the deviation of the mean of the family $(\overline{Y}_{i.})$ from the general mean of the population (\overline{Y}) .

The estimator of b_1 and b_2 is:

$$\hat{b}_{1} = \frac{Cov\left[(Y_{ij} - \overline{Y}_{i.}), g_{ij}\right]}{V(Y_{ij} - \overline{Y}_{i.})}$$

$$\hat{b}_2 = \frac{Cov\left[(\overline{Y}_{i.} - \overline{Y}_{..}), g_{ij}\right]}{V(\overline{Y}_{i.} - \overline{Y}_{..})}$$

 g_{ij} = genetic value of jth individual of the ith family.

Individual selection

The response to individual selection was estimated using the following expression:

$$GS_{PRO} = DS_{PRO} \times h_{rPRO}^2$$
 where,

 GS_{PRO} = predicted direct gain for grain yield (PRO);

 h_{rPRO}^2 = narrow sense heritability at the individual level; and

 DS_{PRO} = selection differential, given by

$$DS_{PRO} = \overline{X}_{SPRO} - \overline{X}_{OPRO}$$
 where,

 \overline{X}_{SPRO} = mean of selected individuals; and

 \overline{X}_{OPRO} = mean of the base population.

Simultaneous selection using the 'weight free 'and 'parameter-free' index

Individuals were selected using the 'weight free' and 'parameter free' index, which is expressed by the formula of Elston (1963):

$$I_e = \prod_{j=1}^n w_j$$
 where,

$$w_i = X_i - k_i$$

 X_i = value observed in the jth trait; and

 k_j = minimum or maximum value, stipulated by the breeder for the jth trait (culling level).

After selecting the individuals based on the index, the response to selection for grain yield was estimated using a formula similar to that of individual selection:

For all the strategies, the expected gains from selection were obtained from the corrected and original data. Selection performed based on the corrected data.

Quantification of the realized gains

The lines originated from each selection strategy were identified and the grain yield means of the field experiment (agricultural season 1997/98) obtained. The gain of each strategy was obtained from the difference between the mean of the selected individuals and the mean of the population where the selection was made. The percentage gain was obtained from the ratio between the strategy gain over the original mean multiplied by 100. All traits assessed in the 1996/97 field experiment were reassessed in 1997/98 although the gain was only predicted for grain yield. This allowed the verification of the behavior of the different traits submitted to selection under field conditions.

Correction of the realized gain for agricultural season effect

In this study, the correction of the realized gain for the effect of agricultural year was used to prevent environmental variation from year to year from biasing the gain prediction efficiency comparisons.

The correction was performed as follows: a) the grain yield mean of the check cultivars was obtained in 1996/97 (the prediction agricultural season) and in 1997/98 (the realized gain season); b) a coefficient was obtained from the ratio between the mean of the check cultivars in the prediction year and in the realized gain year; c) this coefficient was used to correct the realized gain grain yield means obtained in each selection strategy and reduce the influence of the agricultural season effect.

RESULTS AND DISCUSSION

Table 1 shows the means and the among families,

within family and individual level heritabilities for the original and corrected grain yield data of the three crosses. The largest mean and heritability estimates were observed for the CR3 cross ('CEPS 89-26' x 'FT-Cristalina'), which made it the most promising cross for expected gain among those studied. The alteration in the magnitude of the heritability values due to data correction was small, which is obviously associated to a small discrepancy among the phenotypic variances for original and corrected data.

Regarding the magnitudes of the heritabilities in the different selection units, the lowest scores were found within family. This may be associated to the lower proportion of the additive variance exploited in this selection unit $(1-I_n)$. The within family heritability did not change with the data correction proposed in this study. The same constant is added or subtracted from all the individuals within a family and, consequently, there is no alteration in the variance. Thus, the difference in response to within family selection for the corrected data depended only on the selection differential.

Table 2 shows the comparison of predicted grain yield gains (agricultural season 1996/97) and realized gains

Table 1. Original mean estimates (\overline{X}_O) for heritabilities of the restricted sense among family means (h_{RE}^2) within family means (h_{RD}^2) and at the individual level (h_{RI}^2) for data corrected by the variation of patterned cultivars among family means (h_{REC}^2) , within family means (h_{RDC}^2) , and at the individual level (h_{RIC}^2) , in the three crosses studied for the production of soybean grains in the 1996/97 agricultural year.

Parameters	Crosses 1/					
Parameters	CR1	CR2	CR3			
\overline{X}_O	12.545	9.337	14.404			
h_{RE}^2	0.523	0.258	0.770			
h_{RD}^2	0.126	0.053	0.377			
h_{RI}^2	0.432	0.206	0.720			
h_{REC}^2	0.634	0.192	0.844			
h_{RDC}^2	0.126	0.053	0.377			
h_{RIC}^2	0.499	0.164	0.780			

^{1/} CR1: 'CEPS 77-16' x 'Doko RC'; CR2: 'CEPS 89-26' x 'IAC-8' and CR3: 'CEPS 89-26' x 'FT-Cristalina'.

(agricultural season 1997/98) for crosses CR1, CR2 and CR3 in the four selection strategies. The table also shows the percentages of predicted gains from selection, the predicted gains corrected for environmental effect, the realized gains in the field and the realized gains corrected for the agricultural season.

The correction for environmental effect reduced the percentage of gain prediction for the CR1 cross (Table 2). The correction for the agricultural year reduced the realized gain, which may be associated to better environmental conditions for the experiment in the 1997/98 agricultural season compared to the 1996/97. Grain yield individual selection resulted in greater expected gain compared to the other strategies. However, this was not observed in the field, since individual selection resulted in the worst realized gain performance. This showed that the single individual is not a good selection unit. Simultaneous selection, combined selection and selection among and within

Table 2. Predicted gain ,in the original mean percentile, for the original data (GS%), and corrected by the cultivar-pattern variation ($GS_C\%$) vs realized gain, in the original mean percentile for the experimental data ($GS_R\%$) and corrected for the prediction agricultural year ($GS_{RC}\%$), in the CR1, CR2 e CR3 crosses, in the four selection strategies used for soybean production in the 1996/97 agricultural years.

Cross. 1/	% gains	Strategies ^{2/}					
C1088.		i	ii	iii	iv		
,	GS%	33.009	41.031	60.768	30.440		
CR1	$GS_C\%$	30.664	31.757	62.549	21.949		
	$GS_R\%$	42.835	48.408	41.429	50.089		
	$GS_{RC}\%$	15.835	20.359	14.698	21.723		
	GS%	11.865	14.298	20.398	12.851		
CD2	$GS_C\%$	10.218	11.085	16.772	10.571		
CR2	$GS_R\%$	63.784	68.862	62.795	71.725		
	$GS_{RC}\%$	10.886	14.323	10.212	16.260		
	GS%	48.187	72.889	80.507	42.022		
CD 2	$GS_C\%$	54.829	74.083	82.828	50.779		
CR3	$GS_R\%$	24.229	20.761	19.059	27.465		
	$GS_{RC}\%$	15.903	12.671	11.078	18.928		

^{1/} CR1: 'CEPS 77-16' x 'Doko RC'; CR2: 'CEPS 89-26' x 'IAC-8' e CR3: 'CEPS 89-26' x 'FT-Cristalina'; ^{2/} i: selection among and within families; ii:combined selection; iii: individual selection; iv: simultaneous selection seleção.

family were more efficient in identifying the individuals with better genetic performance, which was confirmed by the lower discrepancy among predicted and realized gain for data corrected for agricultural season effect. The agreement between predicted and realized gains for simultaneous selection was almost complete.

The data correction practically did not change the efficiency of gain prediction in the CR2 cross (Table 2). The realized gain corrected for agricultural season was very close to the expected, whether corrected or not by the environmental factor. However, this table also shows a large difference in environmental conditions between the prediction and the realized gain year.

Greater discrepancy between predicted and realized gains was found for all the selection strategies for the CR3 cross (Table 3).

Data correction for both environmental effect and agricultural season did not alter the gains significantly. However, the population from this cross, which was the most promising for gain prediction, did not show the expected performance in the field. This may be due to inefficient estimation of the non-genetic factors. For this cross, the realized gain from combined selection was less efficient than from among and within family selection. This may be associated with a low within family error that points to a smaller original b2/b1 ratio, an indicator of the relationship of the heritability coefficients. A large b2/b1 ratio indicates a large influence of non-genetic factors within families. The smaller variation of nongenetic factors within families characterizes one of the main disadvantages of this combined selection index, because an exceptionally good individual belonging to a bad family can be selected, as pointed out by Viana and Cruz (1997). The procedure used to estimate the variance components can be another factor that increases the possibility of discarding the best individuals when using the combined index under the condition of high within family heritability. This results from an underestimation of the within family error, which increases the importance of the deviation of the individual compared to the mean of the family in detriment of the deviation of the mean of the family in relation to the general mean of the population.

The grain yield data correction proposed in the present study did not change the rank of the selection strategies regarding gain prediction comparatively to that obtained with the original data (Table 2). This indicated that this method of population experiment in the field is efficient as it is easy to carry out and allows genetic parameter estimation in any selfing generation. New forms of data correction should be assessed to further improve the method.

Although the yield data correction did not improve the gain prediction compared to the original data, better realized gain performance was obtained for the three crosses when simultaneous selection for two traits less influenced by the environment (number of days to maturity and plant height at maturity) was used. As shown in Table 2,the greater efficiency of the correction was obtained for traits less influenced by the environment. The lower efficiency of the strategies that used only grain yield as selection criteria can be associated with an increase in the correction factor that does not correspond to the variation in the environmental effect.

Alterations in the response to selection due to data correction can occur because of changes in the accuracy of the data, that is, the correction factor may provide better control of the variations due to nongenetic causes, reflecting positively in the response to selection when there is an increase in the magnitude of the genetic component. However, increase in the variation in the data due to correction by the environmental effects tends to reduce the heritability, and it is therefore necessary to increase the selection differential allowing for the reduction in heritability. Thus the efficiency of the correction is measured by the capacity of the correction factor in creating a balance between the two main forces of the response to selection that can be modified: heritability and the

selection differential.

Tables 3, 4 and 5 show, respectively, the real gains corrected for agricultural season effect for the CR1, CR2 and CR3 crosses. They involve all assessed traits in the F6 progenies derived from individuals obtained by different selection criteria in the F5 progeny. In all the crosses, simultaneous selection involving grain yield, plant height and number of days to maturity, using the cutting point as the minimum selection limit, promoted the greatest real gains compared to the other strategies used in all the secondary traits assessed (NDF, APF, NNF, NDM, APM and NNM). As already shown in Table 2, simultaneous selection had direct influence on grain yield, making this the most efficient strategy in the field. For the primary components (NVP, NSV and P1S), the referred tables show differences in the real gains in the crosses assessed for all the selection strategies. There is a competitive effect among the three components, that is, an excessive increase in one causes reduction in the others, probably due to competition for the same physiological site. Table 3 shows a substantial increase in NVP, which was the main component responsible for the increase in grain yield, and a decrease in NSV and P1S compared to the mean of the population under selection. On the other hand, Table 4 shows real gains in NVOP and P1S, which were responsible for the increase in grain yield, while NSV was reduced. Table 5 shows the gains evenly distributed among the three components, which were responsible for the increase in grain yield.

Table 3. Weighted mean coefficient estimates for the agricultural year of prediction (\hat{c}), of the original (\overline{X}_O), of the realized gain percentiles corrected for the agricultural year, in relation to the original mean (GS_{RC} %) in all the characteristics assessed, and in all the selection strategies in the CR1 cross ('CEPS 77-16' x 'Doko RC'), in the 1997/98 agricultural year.

Characteristics	ĉ	\overline{X}_o	$GS_{RC}\%$ per strategy $^{1/}$				
	C		i	ii	iii	iv	
NDF	0.973	61.456	3.941	6.874	6.320	7.784	
APF	0.656	47.561	17.407	26.256	24.157	39.687	
NNF	0.863	11.478	9.730	12.000	11.879	18.575	
NDM	0.972	135.239	2.451	2.612	3.579	3.537	
APM	0.686	63.274	12.389	22.082	19.890	41.250	
NNM	0.890	13.961	7.100	10.652	11.080	21.124	
NVP	0.995	44.825	62.858	70.515	61.668	72.253	
NSV	0.994	1.745	-9.299	-9.299	-10.097	-10.325	
P1S	0.847	0.169	-21.793	-22.294	-20.790	-21.292	
PRO	0.811	12.545	15.835	20.359	14.698	21.723	

¹/ i: selection among and within families; ii: combined selection; iii: individual selection and iv: simultaneous selection.

Table 4. Weighed mean coefficient estimates for the agricultural year of prediction (\hat{c}), for the original means (\overline{X}_O), of the realized gain percentiles and corrected for the agricultural year, in relation to the original mean (GS_{RC} %) in all the characteristics assessed in the different selection strategies used in the CR2 cross: ('CEPS 89-26' x 'IAC-8'), in the 1997/98 agricultural years.

Charact.	ĉ	\overline{X}_o	$GS_{RC}\%$ per strategy $^{1/}$				
Charact.	C	Λ_{o}	i	ii	iii	iv	
NDF	0.869	62.259	-12.111	-10.482	-11.412	-6.095	
APF	0.560	49.128	-5.398	-3.733	-8.407	9.636	
NNF	0.669	10.229	-18.470	-16.265	-15.964	-15.722	
NDM	0.951	131.065	-3.932	-2.707	-3.088	-0.638	
APM	0.620	67.929	-1.554	-0.691	-5.696	11.900	
NNM	0.759	13.232	-9.960	-8.312	-8.479	-7.497	
NVP	0.570	29.926	5.661	10.440	9.750	11.037	
NSV	1.036	2.078	-16.509	-17.107	-15.312	-16.808	
P1S	1.178	0.172	12.280	10.226	9.541	11.595	
PRO	0.677	9.337	10.886	14.323	10.212	16.260	

¹/ i: among and within families selection; ii: combined selection; iii: individual selection; iv: simultaneous selection.

Table 5. Weighted media coefficient estimates for the agricultural year of prediction (\hat{c}), of the original means (\overline{X}_{O}), of the realized gain percentiles corrected for the agricultural year,in relation to the original mean (GS_{RC} %) in all characteristics assessed, in different selection strategies in CR3 cross: ('CEPS 89-26' x 'FT-Cristalina'), for the 1997/98 agricultural years.

Caract.	ĉ	\overline{X}_o	GS_{RC} % per strategy $^{1/}$				
Caract.	ι	21 ₀	i	ii	iii	iv	
NDF	1.024	60.248	5.243	7.444	6.277	8.826	
APF	0.754	44.156	30.316	40.226	36.420	46.437	
NNF	0.895	11.848	9.208	14.426	12.002	15.815	
NDM	0.960	132.10	1.161	1.997	1.516	2.164	
APM	0.784	58.93	32.101	38.679	36.050	45.529	
NNM	0.954	14.378	17.216	19.765	18.159	20.867	
NVP	0.765	53.967	3.837	0.055	-1.287	2.998	
NSV	1.125	1.856	4.400	3.309	3.933	4.885	
P1S	1.032	0.146	0.353	4.594	3.180	4.594	
PRO	0.933	14.404	15.903	12.671	11.078	18.928	

¹/i: selection among and within families; ii: combined selection; iii: individual selection; iv: simultaneous selection.

CONCLUSIONS

- Lower heritability values were detected among individuals assessed within F5 families;
- Gain prediction using corrected or uncorrected data showed little variation;
- Simultaneous selection performed best in the field;
- Simultaneous selection promoted greater plant height and longer cycle compared to the other selection strategies used in the studied crosses;
- Excessive gain in one of the primary grain yield components caused reduction in the others. Equilibrium in the among trait selection is needed

for simultaneous gain in the three components.

RESUMO

Comparação de ganhos preditos e realizados para diferentes estratégias de seleção em populações de soja

O presente trabalho teve como objetivos predizer o ganho genético em três populações de soja, utilizando-se dados originais e corrigidos pela variação de caracteres agronômicos em cultivares-padrão, e compará-los com ganho realizado corrigido para ano

agrícola da predição; indicar a melhor estratégia de seleção, assim como verificar a influência da seleção nos demais caracteres avaliados em campo. Foram utilizadas, considerando apenas produção de grãos, seleção individual, seleção entre e dentro de famílias e seleção combinada, e considerando além da produção de grãos, altura de planta e número de dias para maturação, a seleção simultânea. A seleção foi feita na geração F₅ e os indivíduos conduzidos em campo no esquema cultivares-padrão intercalares às linhas segregantes, no ano agrícola 1997/98, em Viçosa, Minas Gerais. Os resultados indicaram menores herdabilidades dentro de famílias, comparado às demais unidades. Quanto à predição de ganhos, foi verificado pouca variação em virtude da correção dos dados. Em nível de campo, a seleção simultânea apresentou melhor "performance" quanto a produção de grãos, e a obtenção de ganhos em todos componentes primários da produção, só foi conseguido quando houve equilíbrio entre os três componentes (número de vagens por planta, número de sementes por vagem e peso médio de uma semente).

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