

Efficiency of S_2 progeny selection strategies in popcorn

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ABSTRACT - Selection among and within inbred families is a common procedure for developing corn inbred lines. The only alternative methods are selection among families, mass selection, or combined selection. Main objective of this work was to assess the relative efficiency of these selection strategies with S_2 popcorn progenies, evaluated in an experiment that included 13 rows of the control IAC 112. The predicted gains indicated that selection of families and plants based on yield and expansion volume using the Mulamba and Mock index was superior to direct selection based on expansion volume, in all selection strategies. Mass and combined selection presented the highest predicted quality and yield gains. On the contrary, there was no difference between the realized gains from direct selection and the Mulamba and Mock index based on expansion volume. The best strategy was selection among and within families, providing a mean quality gain of 1.5 mL g⁻¹ with positive alteration in yield.

Key words: expansion volume, inbred line selection, popcorn breeding.

INTRODUCTION

Main objective of popcorn breeding is to simultaneously improve quality and grain yield, although improvements in pest and disease resistance and in ear and grain size are also desirable (Ziegler and Ashman 1994). Hybrid production, used in popcorn breeding since the 1930s, has been responsible for the great grain yield and quality progresses obtained in the United States (Ziegler and Ashman 1994). Popcorn hybrid breeding is recent in Brazil, although common maize hybrid breeding started as early as 1932 at the Agronomic Institute, Campinas (Krug et al. 1943). Popcorn population breeding is necessary to develop

improved open pollinating populations for small maize farmers. Such populations may also be sources for the development of elite inbred lines due to increased frequencies of the favorable genes brought about by recurrent selection (Pacheco et al. 1998).

Several studies with corn employed recurrent selection methods with inbred progenies. Yield gains per cycle of 2.0% and 4.6% were observed in a S_2 and S_1 progeny selection (Sprague and Eberhart 1977). Weyrich et al. (1998) compared the response of the BS11 population to six intra- and one inter-population methods; among the intra-population breeding methods, S_2 progeny selection attained the strongest response for yield, with 4.5% per cycle.

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The use of inbred families in recurrent selection programs should also minimize inbreeding depression. According to Vasal et al. (1995), reduction was in the mean 4% for yield, for four maize populations. The estimates of means of the inbred lines that can be derived from the population showed that recurrent selection based on S_3 families should be efficient at increasing the probability of obtaining vigorous and high yielding inbred lines.

Direct selection for expansion volume was the method used by Vilarinho et al. (2002) to select thirty S_1 families for intra-population improvement. A gain of 1.08 mL g⁻¹ for expansion volume was predicted. The expected indirect gain for grain yield was irrelevant, mainly because of the negative genotypic correlation between these traits. The Mulamba and Mock (1978) index was used for the selection of thirty S_2 progenies, with weights three and one for expansion volume and yield, respectively. A predicted gain of 0.81 mL g⁻¹ was obtained for expansion volume. When aiming at the identification of superior S_2 and S_3 families, satisfactory concordance occurred only between the predicted and realized gains in respect to expansion volume for the S_1 progenies (Vilarinho et al. 2003). The four criteria with the highest predicted gains (2.04 to 2.17 mL g⁻¹) were the same that provided the four highest realized gains (1.03 to 1.56 mL g⁻¹), although not in the same order. In relation to S_2 progenies, the coincidence between the four superior selection procedures was one for expansion volume (predicted and realized gains of 1.06 mL g⁻¹ and 0.92 mL g⁻¹) and three for yield (predicted gains of 31.29 to 34.64 kg ha⁻¹ and realized gains of 140.69 to 193.02 kg ha⁻¹).

Selection among and within inbred families is the common procedure to develop corn inbred lines. The only alternative methods are selection among families, mass selection, and combined selection. Objectives of this study were to assess the efficiency of these selection strategies for popcorn S_2 progenies, to identify superior S_3 families, and to achieve population improvement.

MATERIALS AND METHODS

One hundred and eighty-nine S_2 families from the popcorn population Beija-Flor were assessed on an isolated area in Viçosa, State of Minas Gerais, in the crop 1999/2000. The families were sown in blocks of 50 five-meter rows with the modified single-cross hybrid IAC 112 as control, intercalated among the progenies. Spacing between rows was 0.9 m and twenty-five plants per row were left after thinning (density of 55555 plants per hectare). Three to five plants with a superior development within each progeny were selfed. The experiment

was also a recombination area, since the control was detasseled. The improved population was obtained from seeds of the selected S_2 families.

The experimental assessment of the progenies with replication of the control(s) only has advantages from the practical point of view. The main advantage is that at least two equivalent studies can be carried out in the area required for the replicated experiment, with similar expenditure of human labor. Therefore, the number of experiments could be increased without increasing the area or labor resources. Furthermore, the overall program costs are generally lower.

The assessed traits per plot were plant and ear height, numbers of stalk-lodged and root-lodged plants, stand, number of ears, weight of one hundred grains, yield, grain moisture, number of poorly hulled ears, of ears attacked by pests and diseases, and expansion volume (relationship between popcorn volume in milliliters and grain weight in grams). Samples of 30 g and 10 g were used to determine family and selfed plant expansion volume, respectively, in a 1,250 watt Proctor Silex Hot Air Popcorn Pumper, model H7340. The samples were stored in a cold chamber for at least three weeks before determining the expansion volume. The grain weight of all selfed ears was assessed. Grain weight data were corrected to 14.5% standard moisture before proceeding with the statistical analyses. Covariance analysis was used to adjust yield to ideal stand, as suggested by Vencovsky and Cruz (1991).

The variance analyses followed a completely randomized design with control in thirteen replications. The variance among control replications was assumed as the estimated residual variance. Modified single-cross hybrid IAC 112 was chosen as control to provide estimates of total, among and within residual variances and covariances, assuming a negligible genetic variability within population.

Only selection among S_2 families was taken into consideration for the Beija-Flor improvement. To obtain superior S_3 families, the following strategies were applied: among-family selection, among and within-family selection, mass selection, and combined selection. The selection criteria were direct selection based on expansion volume and selection based on the Mulamba and Mock (1978) index with expansion volume and yield, adopting weights of three and one, respectively. Direct selection based on yield was considered only for comparison, because it is not generally a strategy applicable to popcorn breeding. Approximately 30% of the progenies were selected in the among-progeny selection strategy. In the among and within-family selection strategy, the proportions of selected S_2 progenies and plants were 57.7% and 47%, respectively, resulting in 109 S_3 families. In the mass and combined selection strategies, 30% of the S_2 plants were selected, also resulting in 109 S_3 families.

The usual function of parental control (1/2 or 1), selection differential, and broad-sense heritability was used to compute predicted gains. The combined selection index was (Viana and Cruz 1997):

$$I = \hat{b}_1(Y_{ij} - \bar{Y}_j) + \hat{b}_2(\bar{Y}_j - \bar{Y}_{..})$$

where

$$\hat{b}_1 = \left[\frac{(1+F)\sigma_A^2}{\sigma_{PwF}^2} \right] (1-r_1) \text{ is the individual merit weight;}$$

$$\hat{b}_2 = \left[\frac{(1+F)\sigma_A^2}{\sigma_{Gaf}^2 + \sigma^2 + \frac{\sigma_{PwF}^2}{p}} \right] \cdot \frac{1}{p} [1 + (p-1)r_1] \text{ is the family merit}$$

weight;

$r_1 = \frac{\sigma_A^2}{(1+F)\sigma_A^2} = \frac{1}{(1+F)} = \frac{4}{7}$ is the correlation between the additive genetic values of plants within S_2 family;

Y_{ij} is the phenotypic value of the i -th plant of the j -th family;

p is the average number of selfed plants (2.5); and

σ_{Gaf}^2 , σ_{PwF}^2 and σ^2 are the among-family genotypic variance, within-family phenotypic variance and residual variance.

The realized gains were computed based on the expansion volume and yield of the S_3 families, assessed in 2000/2001, also in Viçosa, as the difference between the progenies mean derived from selected S_2 plants and the S_3 generation mean.

RESULTS AND DISCUSSION

The F tests of the variance analyses indicated genetic variability in the population, except for prolificacy index, weight of one hundred seeds, and proportion of ears attacked by pests (Table 1). Therefore, selection is likely to produce genetic progress. Since the population is inbred, the discussion on mean values loses relevance, and any comparison with IAC 112 should be treated with care. The control plants were detasseled and, consequently, the plant height, ear height, and yield trait means were certainly lower than the corresponding means from plants not submitted to emasculation, which removes four to six leaves. It is important to emphasize that there were high yield and high quality families with over 4000 kg ha⁻¹ and 38 mL g⁻¹, respectively. The proportions of ears with pests and diseases were not negligible. The absence of prolific plants must be due to selfing. The weight of one hundred grains was typical for the Beija-Flor population.

Heritability estimates were generally high (Table 1) and, therefore, S_2 family selection should be efficient, aiming at the identification of superior S_3 families and breeding the population, using expansion volume in direct selection or the expansion volume and yield index. The highest genotypic correlation was between plant height and ear height, which is a customary result (Table 2). Direct selection based on expansion volume should not determine relevant indirect changes in other traits because of the reduced magnitude of the genotypic correlations, including yield. The same result is expected from selection based on the Mulamba and Mock index, because of the reduced correlation of expansion volume and yield with the other traits or because some traits showed small correlations of similar magnitude but opposite signs with expansion volume and yield.

Among-family selection

The expected gains from selection for superior S_3 families correspond to twice the gains expected from recombination of selected and non-selected progenies. The expected gains from direct selection for expansion volume were 6.09 mL g⁻¹ and 102.06 kg ha⁻¹ for quality and yield, respectively (Table 3). The changes in the means of the other traits were negligible. The use of the Mulamba and Mock index resulted in expected gains for expansion volume and yield of 5.89 mL g⁻¹ and 205.45 kg ha⁻¹, respectively (96.7 and 47.3% of the maximum gains). This strategy is therefore superior to direct selection for expansion volume. The indirect responses in the other traits were, as expected, negligible.

The magnitudes of these predicted gains are higher than those estimated by Vilarinho et al. (2003), with another group of S_2 progenies from the Beija-Flor population (1.02 mL g⁻¹ and 27.20 kg ha⁻¹). When the purpose was intra-population breeding, the predicted gains were 0.8 mL g⁻¹ and 0.36 kg ha⁻¹. One probable reason was the high heritability observed in this experiment.

Among and within-family selection

Family selection based on expansion volume resulted in an expected quality gain of 3.77 mL g⁻¹ and indirect yield alteration of 59.06 kg ha⁻¹ (Table 3). The mean changes in the other variables were negligible. The use of the index resulted in an expected expansion volume and yield gains of 3.63 mL g⁻¹ and 111.96 kg ha⁻¹, respectively. The expansion volume gain is equal to 96.3% of the maximum gain. The Mulamba and Mock index was once more superior to direct selection for expansion volume because it resulted in a practically maximum quality gain associated to a greater yield gain.

Table 1. Analyses of variance and estimates of genotypic variance among families ($\hat{\sigma}_{GaF}^2$) and heritability (h^2)

Source of variation	df	Mean Squares				
		PH ¹	EH ²	PEAP ³	PSL ⁴	PRL ⁵
		m	m			
Family	188	0.05803**	0.0396**	0.0323	0.00725**	0.0089**
Family vs. Control	1	0.00001	0.0003	0.1407	0.0723	0.0735
Error	12	0.01184	0.01152	0.04712	0.00201	0.00038
Maximum		2.42	1.55	1.00	0.45	0.50
Mean		1.68	0.92	0.46	0.10	0.09
Minimum		1.10	0.48	0.00	0.00	0.00
Control mean		1.68	0.92	0.34	0.02	0.007
CV (%)		6.48	11.69	48.20	44.86	24.24
$\hat{\sigma}_{GaF}^2$		0.04620	0.02804	0.0	0.00514	0.00856
h^2 (%)		79.59	70.88	0.0	71.91	95.71

PPHE ⁶	PI ⁷	WG ⁸	PEAD ⁹	Y ¹⁰	EV ¹¹
		g		kg ha ⁻¹	mL g ⁻¹
0.0138**	0.1844	2.0420	0.04596*	415273.7419*	53.72**
0.0267	6.3534	7.7875	0.5206	20000363.7208	3450.31
0.00096	0.10576	1.91881	0.01678	178915.65840	15.05
1.00	2.00	19.24	1.00	4107.34	38.33
0.09	0.92	13.12	0.48	1452.90	19.10
0.00	0.10	6.17	0.00	359.30	3.33
0.03	1.64	12.31	0.27	2735.20	35.94
37.43	33.58	10.59	27.86	27.54	19.21
0.01293	0.07864	0.12321	0.02917	236358.0835	38.67
93.01	42.64	6.03	63.47	56.92	71.98

¹plant height; ²ear height; ³proportion of ears attacked by pests; ⁴proportion of stalk-lodged plants; ⁵proportion of root lodged plants; ⁶proportion of poorly hulled ears; ⁷proliferacy index; ⁸weight of one hundred grains; ⁹proportion of ears attacked by disease; ¹⁰yield; and ¹¹expansion volume

*, **P<0.05; P<0.01, respectively

Table 2. Genotypic correlations between eight traits of popcorn

Traits ¹	PH	EH	PSL	PRL	PEAD	PPHE	Y	EV
PH		1.00	-0.33	-0.34	0.08	0.03	0.34	-0.17
EH			-0.24	-0.27	0.15	0.01	0.48	-0.19
PSL				0.20	0.36	-0.03	0.11	0.28
PRL					0.19	0.18	-0.06	-0.03
PEAD						0.03	-0.04	-0.25
PPHE							-0.15	-0.10
Y								-0.14

¹coded as in Table 1

Genetic parameter estimates from self-pollinated plants

Grain weight of self-pollinated ears of plants with best development in the families corresponded approximately to the yield of the selfed plants, as they were not usually prolific. The estimates of the phenotypic, genotypic, and residual variances between families (Table 4) were not very different from those obtained in data analyses involving all individuals in the families (Table 1). The among-family genotypic variance was larger than the within-family genotypic variance for yield. This superiority is always expected, regardless of gene frequency and dominance degree (Hallauer and Miranda Filho 1988). The same was not observed for expansion volume since the ratio of these variances is approximately 1.0. Heritabilities at S₂ plant level and within-family plant level (Table 4) indicated that within-family selection based on expansion volume or selection alone or on the Mulamba and Mock index should be highly efficient. The phenotypic correlation between expansion volume and yield plant values was of small magnitude (0.13). This fact allowed the inference that indirect alteration in yield due to direct selection on expansion volume should be small. Index-based selection should allow gains in both traits.

Total Predicted gains from among and within-family selection

Quality and yield gains of 7.84 mL g⁻¹ and 17.06 kg ha⁻¹, respectively, are expected from direct selection based on expansion volume (Table 3). The expected expansion volume and yield gains with the use of the index are 7.98 mL g⁻¹ and

191.33 kg ha⁻¹, respectively. The expected results with among-family selection showed that direct selection for expansion volume and the use of the Mulamba and Mock index should improve quality. Similarly, within-family selection is expected to improve quality. However, the estimated expected yield gains from within-family selection based on direct selection for expansion volume were negative. Positive results of larger magnitude were estimated with selection based on the index.

The expected quality gains from among and from within-family direct selection for expansion volume were 48.1% and 51.9% of the estimated total gain, respectively. The predicted yield gain was negative in the within-family selection method (-42 kg ha⁻¹). The predicted quality gains from selection based on the Mulamba and Mock index were 45.5% and 54.5% for among and within-family selection, respectively. Similar proportions for yield were 58.5 and 41.5%, respectively. Once again, the use of the Mulamba and Mock index was superior to direct selection for expansion volume. The estimated quality gains using the index were equivalent to those expected from direct selection and the yield gains were superior.

Mass selection

The expected quality and yield gains from direct selection for expansion volume and from the index selection were 9.69 mL g⁻¹ and 256.92 kg ha⁻¹, and 9.31 mL g⁻¹ and 457.14 kg ha⁻¹, respectively (Table 3). These results indicated

Table 3. Expected Selection methods Selection strategies gains to obtain superior S₃ families for yield (Y) and expansion volume (EV) by means of several strategies

Selection methods	Selection strategies	Y	EV
		kg ha ⁻¹	mL g ⁻¹
FS ¹	DSY ⁵	434.74	1.23
	DSEV ⁶	102.06	6.09
	MM ⁷	205.45	5.89
AW ²	Among		
	DSEV	59.06	3.77
	MM	111.96	3.63
	Total		
	DSEV	17.06	7.84
	MM	191.33	7.98
MS ³	DSEV	256.92	9.69
	MM	457.14	9.31
CS ⁴	DSEV	240.43	9.68
	MM	458.93	9.30

¹among-family selection; ²among and within-family selection; ³mass selection; ⁴combined selection; ⁵direct selection for yield; ⁶direct selection for expansion volume; ⁷selection based on the Mulamba and Mock index, with EV and yield

Table 4. Estimates of total, among and within phenotypic ($\hat{\sigma}_P^2$, $\hat{\sigma}_{PaF}^2$ and $\hat{\sigma}_{PwF}^2$), genotypic ($\hat{\sigma}_G^2$, $\hat{\sigma}_{GaF}^2$ and $\hat{\sigma}_{GwF}^2$) and residual ($\hat{\sigma}_E^2$, $\hat{\sigma}$ and $\hat{\sigma}_w$) variances, and of heritabilities at the S_2 plant, family and plant within-family levels (h^2 , h_a^2 and h_w^2), for grain yield (Y) and expansion volume (EV)

Estimators	Y	EV
	— kg ha ⁻¹ —	— mL g ⁻¹ —
$\hat{\sigma}_P^2$	1241186.5864	76.9952
$\hat{\sigma}_{PaF}^2$	809764.2890	54.7143
$\hat{\sigma}_{PwF}^2$	738946.0296	55.8925
$\hat{\sigma}_G^2$	924240.4610	72.7877
$\hat{\sigma}_{GaF}^2$	733785.5521	52.4153
$\hat{\sigma}_{GwF}^2$	464175.3446	53.9835
$\hat{\sigma}_E^2$	316946.1254	4.2075
$\hat{\sigma}^2$	75978.7369	2.2990
$\hat{\sigma}_w^2$	274770.6850	1.9090
h^2	74.46	94.53
h_a^2	90.61	95.79
h_w^2	62.81	96.58

a clear superiority of Mulamba and Mock selection index. The expected quality gain corresponds to 96.1% of the maximum and the predicted yield gain is 77.9% greater than that of the former method, which was practically the maximum quality gain and the largest yield gain, respectively.

Combined selection

For yield and expansion volume, the individual and family merit weights did not differ considerably (0.5360 and 0.6211 for yield, and 0.5581 and 0.7015 for expansion volume). The family merit weight was slightly greater than the individual merit weight. This slight superiority should not determine the selection of all individuals in the best families, that is, the selection of an inferior individual in an exceptional family, in detriment of a superior individual in an inferior family. The 109 plants belong to at least 71 and at most 73 families (Table 5), comparable numbers to those obtained by mass selection, but larger than those of the among-family selection. The predicted gains from direct selection for expansion volume were 9.68 mL g⁻¹ and 240.43 kg ha⁻¹, in expansion volume and yield, respectively (Table 3). Using the index, expected gains of 9.30 mL g⁻¹ and 458.93 kg ha⁻¹ in expansion volume and yield were estimated. The expansion volume gain corresponded to 96.1% of the maximum gain. The predicted quality gains for selection based on the Mulamba and Mock index were very close to the maximum and the yield gain was

the largest, which confirms this method's superiority for expansion volume, compared to direct selection for expansion volume.

Comparison of the selection strategies based on predicted gains

Results showed that for all the selection strategies (among-families, among- and within-families, mass and combined selection), the expected gains obtained by the Mulamba and Mock index were superior to those expected from direct selection for expansion volume. Magnitudes of the predicted quality gains were higher for all selection strategies. This was not observed for yield, where gains from mass and combined selection were largest, followed by expected gains from selection among families and among and within families. The within-family selection method was not efficient to promote yield gains.

The estimates for the four selection strategies using the index showed that mass and combined selection produced best results (Table 3), but it was not possible to tell any difference among these strategies. Among and within-family selection methods resulted in intermediate quality and yield gains, among-family selection was less expressive, and among and within-family selection method were superior to among-selection.

It is further of interest to take the number of families from which the selected plants were derived into consideration (Table 5). There is no difference between the number of selected families for selection based on the index or for direct selection on expansion volume strategies. Among and within-family methods selected the largest number of families (86 in the mean). The mean was 73.5 families for combined and mass selection, and the lowest mean was obtained by among-family selection (44.5 progenies).

Therefore, there is no doubt that based on predicted gains and the numbers of advanced S_2 families, mass selection and combined selection were the best strategies. As mass selection is easy to use, it should be preferred for selecting superior S_2 plants based on the Mulamba and Mock expansion volume and yield index.

Realized gains

The realized gains were much smaller than the predicted ones (Table 6), presenting a linear relationship of only 0.18 for yield and 0.41 for expansion volume. According to Vencovsky and Barriga (1992), although genetic gains estimates are not exact and approximations are generally used,

Table 5. Numbers of S₂ families and plants selected based on expansion volume and on the Mulamba and Mock index, considering four selection methods

Selection methods ¹	Selection strategies ¹	Families	Plants
FS	DSEV	43	114
	MM	46	129
AW	DSEV	85	109
	MM	87	109
MS	DSEV	74	109
	MM	76	109
CS	DSEV	71	109
	MM	73	109

Coded as in Table 3

Table 6. Realized gains with among S₂ family selection (FS), among and within-family selection (AW), mass selection (MS) and combined selection (CS), for expansion volume (EV) and yield (Y), considering direct selection for EV (DSEV) and selection based on the Mulamba and Mock index, with EV and yield (MM)

Selection methods ¹	Selection strategies	Number of S ₂ families	Y	EV
			— kg ha ⁻¹ —	— mL g ⁻¹ —
FS	DSEV	58 (44.6%)	-15.9	1.18
	MM	69 (53.1%)	-13.1	0.58
AW	DSEV	52 (40.0%)	-13.4	1.54
	MM	61 (46.9%)	15.1	1.56
MS	DSEV	64 (49.2%)	8.1	1.18
	MM	64 (49.2%)	13.1	1.21
CS	DSEV	64 (49.2%)	-4.7	1.23
	MM	66 (50.8%)	10.1	1.24

Coded as in Table 3

predicted and realized progresses have been in reasonable agreement and largest deviations are normally attributed to genotype x environment interaction.

The realized expansion volume and yield gains from among-family selection based on expansion volume were 1.18 mL g⁻¹ and -15.9 kg ha⁻¹, respectively. The realized gain for quality using the Mulamba and Mock index was fifty percent lower. The values estimated by Vilarinho et al. (2003), with another group of S₂ progenies from the Beija-Flor population, were greater (2.52 mL g⁻¹ and 97.10 kg ha⁻¹). The realized expansion volume and yield gains from among and within family direct selection for expansion volume were 1.54 mL g⁻¹ and -13.4 kg ha⁻¹, respectively. The index selection resulted in expansion volume gains equivalent to those expected from direct selection for expansion volume, without relevant alteration in yield. Mass selection for expansion volume

resulted in realized gains of 1.18 mL g⁻¹, and the index selection resulted in a quality gain of 1.21 mL g⁻¹. The yield gains from direct and index selection were positive, but small. The realized gains from combined selection were also smaller than the predicted ones. Direct selection based on expansion volume resulted in a gain of 1.23 mL g⁻¹ with no relevant indirect alteration in yield. The realized gains using the index were 1.24 mL g⁻¹ and 10.1 kg ha⁻¹ for expansion volume and yield, respectively.

The among-family selection was the worst method, with the smallest gains for expansion volume. The largest gain was obtained from direct selection for expansion volume (1.18 mL g⁻¹). It is interesting to observe that direct selection for expansion volume was superior to the index. Results from mass and combined selection were similar. Among and within-family selection with the index was shown to be the best

selection strategy. The progress in quality resulting from direct selection for expansion volume and the index are numerically superior to the others. Therefore, based on the realized gains and on the number of advanced S_2 families, there is no doubt that the best strategy is among and within-family selection, while superior S_3 families should be selected by the Mulamba and Mock expansion volume and yield index.

CONCLUSIONS

The existence of genetic variability for yield and expansion volume was confirmed by variance analyses. The maximum family values for yield and expansion volume were greater than the respective values of the control. Heritabilities ranged from moderate to high for yield and expansion volume. Genotypic correlations between yield and expansion volume were of low magnitude. The predicted gains

evidenced that selection of families and plants based on yield and expansion volume using the Mulamba and Mock index was superior to direct selection based on expansion volume, in all selection strategies. Mass and combined selection presented the highest predicted quality and yield gains. On the contrary, there was no difference between realized gains obtained from direct selection based on expansion volume and by the Mulamba and Mock index. Among and within-family selection was the best selection strategy, resulting in a mean quality gain of 1.5 mL g^{-1} with positive alteration in yield.

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Eficiência das estratégias de seleção de progênies S_2 em milho-pipoca

RESUMO - Seleção entre e dentro de famílias endogâmicas é um procedimento usual no desenvolvimento de linhagens de milho. Métodos alternativos são apenas seleção entre, seleção massal e seleção combinada. O objetivo principal deste trabalho foi avaliar a eficiência relativa destas estratégias de seleção com progênies S_2 de milho-pipoca, avaliadas em experimento com 13 parcelas da testemunha IAC 112. Os ganhos preditos evidenciaram que a seleção de famílias e plantas para capacidade de expansão e produção, com base no índice de Mulamba e Mock, foi superior à seleção direta para capacidade de expansão, independente da estratégia de seleção. Seleção massal e combinada proporcionaram os maiores ganhos preditos em qualidade e produção. Em relação aos ganhos realizados, não se verificou superioridade do índice. Seleção entre e dentro foi a melhor estratégia, proporcionando ganho médio em qualidade de $1,5 \text{ mL g}^{-1}$, associado à alteração positiva em produção.

Palavras-chave: capacidade de expansão, seleção de linhagens, melhoramento de milho-pipoca.

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