

Relative importance of *per se* and topcross performance in the selection of popcorn S_3 families

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ABSTRACT – *The objective of this paper was to discuss the relative importance of per se and topcross performance in the selection of inbred families. The analyses, considering expansion volume and yield, were based on two trials of S_3 progenies from the popcorn population Beija-Flor, and six experiments with the corresponding topcross hybrids, derived from crosses with the tester Viçosa, another popcorn population. With respect to the estimates of heritabilities (assessment of the selection efficiency), predicted genetic gains, genotypic correlations and the percentages of coincidence between selected and non selected families, the equivalence with the selection procedures based on per se and topcross performance was good. The correspondence would certainly be greater if the genotypic correlations were of higher magnitude. The selection based simultaneously on the phenotypic values of progenies and hybrids tends to be satisfactory when the weights of the per se and topcross merits are proportional to the heritabilities.*

Key words: topcross, testcross, inbred families.

INTRODUCTION

The topcross or testcross, proposed by Davis (1927) to evaluate the combining ability of inbred families for the development of hybrids, is equivalent to the factorial mating design II of Comstock and Robinson or partial diallel. One group of parents contains the inbred progenies (normally S_3) and the other at least one tester. In view of the satisfactory results it achieved since it was proposed, it is commonly used by maize breeders nowadays (Bauman 1981).

Except for the identification of QTL (Quantitative Trait Loci) (Austin et al. 2001, Mihaljevic et al. 2005, Papst et al. 2004), the recent uses of testcross in maize improvement are not new: (i) in the tester evaluation (Duarte et al. 2003); (ii) in the evaluation of single-cross hybrids as inbred line sources (Koutsika-Sotiriou and Karagounis 2005); (iii) in studies into the association between inbred line per se and testcross performance (Mihaljevic et al. 2005, Papst et al. 2004, Presterl et al. 2002); (iv) in the investigation of the potential of tropical germplasm under temperate climate conditions in maize improvement

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(Goodman 2004, Tarter et al. 2003); (v) in maize improvement for forage (Frey et al. 2004), for nutritional grain quality (Thomison et al. 2001, 2002, 2003) and targeting resistance to mites (Bynum et al. 2004) and European corn borer (Bohn et al. 2003, Papst 2004); and (vi) in sweet corn improvement, considering vigor and adaptation degree (Malvar et al. 2001).

Duarte et al. (2003) evaluated three elite inbred lines as testers of inbred lines, hybrids and populations. One tester provided the best hybrid combinations, but not the best discrimination in all situations. Comparing the yields of three single-cross hybrids with their corresponding F_2 generations, with those of the populations obtained by means of a diallel and with those of the testcrosses with an inbred line, Koutsika-Sotiriou and Karagounis (2005) selected the most adequate hybrid as source of inbred lines, considering a lower inbreeding depression and a positive effect of general combining ability.

In the study of Mihaljevic et al. (2005) the QTL analysis showed that it is possible to conduct molecular marker-assisted selection in testcross hybrids, based on QTL detected in the F_3 to F_6 progenies for traits whose genotypic variance is to a large extent explained by QTL. Using testcross progenies, Papst et al. (2004) identified six QTL for resistance to European corn borer, three of which were detected in the $F_{2.3}$ *per se* families as well. Austin et al. (2001) evaluated *per se* and testcross $F_{2.3}$ and $F_{6.8}$ progenies with three tester inbred lines. A larger number of QTL was identified in $F_{6.8}$. Approximately 40 to 70% of those identified in $F_{2.3}$ were verified in $F_{6.8}$. Of the QTL determinant for plant and ear height and for three flowering-related traits two to 11 were detected in all generations, independent of the tester.

One aspect of topcrosses that is worth investigating is that superior inbred progenies can be identified in the *per se* family test. With a view to gaining new insights in this area, the objective of our study was to evaluate the relative importance of the *per se* and testcross performance in the selection of S_3 families of a popcorn population, targeting population improvement and the establishment of inbred lines.

MATERIAL AND METHODS

The 305 S_3 families were derived from the popcorn population Beija-Flor. They were evaluated in two trials conducted in Viçosa, MG, one in the growing season 1999/00, with 176 progenies (Program 1) plus the control ISLA

208 (open-pollinated population), and the other in the growing season 2000/01, with 129 progenies (Program 2) plus control IAC 112 (modified single-cross hybrid). In both, only the controls were repeated, a similar procedure to the one breeders of autogamous species use. ISLA 208 was repeated at every 16 progenies and the IAC 112 at each 12 progenies, in the mean. In the two experiments, sown on separate areas, all control plants were detasseled, to restrict recombination to among-families only, aiming at population improvement. Three to five plants were selfed in each progeny to establish S_4 progenies. The grain weight and expansion volume (EV) of the selfed plants and the three sampled IAC 112 plants of each plot in the progeny test of program 2 were measured.

With the progenies of Program 1 four topcross trials were conducted in the growing season 2000/01. The hybrids had been obtained in the previous growing season, using the population Viçosa as tester. One experiment was conducted at the Empresa de Pesquisa Agropecuária do Estado do Rio de Janeiro (PESAGRO), in Campos dos Goytacazes, in a 10 x 10 lattice with four replicates. Another trial was conducted at the Central de Experimentação, Pesquisa e Extensão do Triângulo Mineiro (CEPET/UFV), in Capinópolis, in a 9 x 9 lattice with four replicates. The other two experiments, in an 8 x 8 lattice, were conducted on an experimental area of the Universidade Federal de Viçosa, in Coimbra, one with three and the other with two replicates. All of them included the populations Viçosa and Beija-Flor Cycle 1 (obtained by half-sib selection) and the hybrids IAC 112 and Zélia as controls.

The topcross progeny trials of Program 2 were performed in the growing season 2001/02, one at the Universidade Estadual de Maringá (UEM) and the other at the CEPET. The hybrids were also derived from crosses with Viçosa, performed in the growing season 2000/01 and the experiments were set up in a 12 x 12 lattice design with three replicates. The populations Viçosa and Beija-Flor, the hybrids IAC 112 and Zélia and the variety Ângela were used as controls.

In the progeny and hybrid trials, each plot consisted of one 5 m long row, with 30 plants, with a spacing of 0.9 m between plots. Of the measured traits only yield and EV were analyzed. The EV of the families and hybrids was assessed in one 30 g grain sample per plot in all experiments, popped in a 1.250 watt hot air popcorn popper. In the trials conducted at the CEPET, in Coimbra (2000/01) and the UEM, the EV of the hybrids was also measured in

the Metric Weight Volume Tester (MWVT) popper in 250 g samples. The EV of the selfed and the IAC 112 plants was assessed based on 10 g samples in the hot air popper. The phenotypic values of IAC 112 plants were used to estimate the environmental variances at the plant level since it is a single-cross hybrid.

Before the analyses, the yield was corrected to a moisture of 14.5% and to an ideal stand of 30 plants per plot. The genetic analyses included the estimation of genotypic variances among and within families, of heritabilities and of genotypic correlations as well as the gain prediction, using selection differential (Hallauer and Miranda Filho 1988). The selection strategies were direct selection for EV and selection based on the index of Mulamba and Mock (1978) with weights 3 for EV and 1 for yield, or 1.5 for EV evaluated in the hot air popper and in the MWVT and 1 for yield. Independently of the selection strategy, approximately 57% of the families were selected. A parental control of one was admitted to establish the S_4 families. In the case of selection based on the testcross performance, the selection differential was calculated based on the phenotypic values of the S_3 progenies. In the gain predictions, however, heritability at the topcross hybrid level was used, which is the measure of accuracy of the phenotypic value to indicate superior S_3 families.

In order to select S_3 families, using the information on the per se and testcross performance, the Mulamba and Mock index was used, given by

$$I_i = p_1 r_{1i} + p_2 r_{2i} + p_3 r_{3i} + p_4 r_{4i} + p_5 r_{5i}$$

where p_1 is the weight of the per se family merit for EV measured in a hot air popper; p_2 is the weight of the per se family merit in relation to yield; p_3 is the weight of the testcross family merit in relation to EV measured in a hot air popper; p_4 is the weight of the testcross family merit in relation to EV measured in the MWVT; p_5 is the weight of the testcross family merit in relation to yield; and r indicates the corresponding rank (classification after ranking).

To calculate the indices, the followings sets of weights were attributed:

Index 1: $p_1 = 3, p_2 = 1, p_3 = 1.5, p_4 = 1.5$ and $p_5 = 1$

Index 2: $p_1 = 3, p_2 = 1, p_3 = 0.75, p_4 = 0.75$ and $p_5 = 0.5$

Index 3: $p_1 = 3, p_2 = 1, p_3 = 0.5, p_4 = 0.5$ and $p_5 = 1/3$

In these indices, the weight of the quality merit is three times higher than the weight of the yield merit, in the per se as much as testcross performance. There are, however, differences between the indices regarding the weights of the ranks of the per se and testcross

performances. In index 1, the sum of weights of the ranks regarding the individual merit is equal to the sum of ranks of the testcross performance. The proportions in relation to the indices 2 and 3 are of 2 for 1 and 3 for 1, respectively.

Combined selection indices for EV evaluated in hot air popper and yield were generically calculated by

$$I = \hat{b}_1(\bar{Y}_i - \bar{Y}_*) + \hat{b}_2(\bar{Y}_{i \times T} - \bar{Y}_{* \times T}),$$

where $\hat{b}_1 = \frac{v_2 c_2 - c_1 c_3}{v_1 v_2 - c_1^2}$ is the weight of the individual merit,

and $\hat{b}_2 = \frac{v_1 c_3 - c_1 c_2}{v_1 v_2 - c_1^2}$ the weight of the testcross family

merit, with

$$v_1 = \left(\frac{F_e - 1}{F_e} \right) \hat{\sigma}_{GSnF}^2 + \left(\frac{F_e - 1}{r_1 F_e} \right) \hat{\sigma}_1^2,$$

$$v_2 = \left(\frac{F_t - 1}{F_t} \right) \hat{\sigma}_{GTH}^2 + \left(\frac{F_t - 1}{r_2 F_t} \right) \hat{\sigma}_2^2,$$

$$c_1 = \left(\frac{F_e F_t - F_e - F_t - F}{F_e F_t} \right) \text{cov}(S_n F, S_n F_x T),$$

$$c_2 = \left(\frac{F_e - 1}{F_e} \right) \hat{\sigma}_{GSnF}^2, \text{ and}$$

$$c_3 = \left(\frac{F_t - 1}{F_t} \right) \text{cov}(S_n F, S_n F_x T)$$

where: $\bar{Y}_i$ is the mean of family i ; $\bar{Y}_*$ is the mean of all families; $\bar{Y}_{i \times T}$ is the mean of topcross family i ; $\bar{Y}_{* \times T}$ is the mean of all topcross families; F_e is the number of progenies in the test; F_t is the number of topcross hybrids; F is the number of common families of the test and the topcross; r_1 is the number of replicates in the family test; r_2 is the number of replicates in the topcross trial; $\hat{\sigma}_{GFSn}^2$ is the estimator of genotypic variance among S_n families; $\hat{\sigma}_{GHT}^2$ is the estimator of genotypic variance among topcross hybrids; $\hat{\sigma}_1^2$ is the estimator of environmental variance in the family test; $\hat{\sigma}_2^2$ is the estimator of environmental variance in the topcross; and $\text{cov}(S_n F, S_n F_x T)$ is the estimator of the covariance between the phenotypic values of S_n family and the topcross hybrid.

The weights $\hat{b}_1$ and $\hat{b}_2$ are those that minimize the variance of the difference between the genotypic value of a S_n topcross family and its genotypic value predicted by

the combined selection index. The values of the combined selection indices were used to compute the index of Mulamba and Mock, with weights 3 and 1 for the family ranks in relation to the combined selection indices of EV and yield, respectively.

RESULTS AND DISCUSSION

Selection based on *per se* performance

The tests in the analyses of variance of the family trials evidenced genetic variability in S₃ for EV and yield (Table 1). Even though there was no common control of the two experiments, conducted in different growing seasons, the EV means of the progenies of both programs can be considered equivalent since IAC 112 was used as common treatment in the quality evaluations. Once the residual variances were homogenous for EV and yield (maximum ratio of 3.1 between the highest and the lowest) it is possible to take a greater genotypic variability in the

families of program 1 into consideration, mainly regarding yield. In spite of the lower number of progenies in program 2 this had been expected since they were the result of two selection processes based on EV and yield, while those of the other program resulted from only one (Santos et al. 2004, Vilarinho et al. 2003). The heritability estimates are generally high, evidencing that the phenotypic value accurately indicates the superiority of a family in relation to the frequency of the favorable genes that are determinant for EV and yield. Only in relation to progenies of program 2 a positive genotypic correlation was verified between EV and yield, probably due to the selection processes based on the two traits, performed by Santos et al. (2004) and Vilarinho et al. (2003).

The analysis of the predicted gains evidenced superiority of the selection based on the index of Mulamba and Mock in both programs, in comparison to direct selection for EV (Table 2). The EV gains represented 96.3% of the maximum gain and were generally associated to higher yield gains.

Table 1. Estimates of the means of S₃ families and topcross hybrids (μ_i and μ_h), of the genotypic variances among progenies and among topcrosses (σ_{Gf}^2 and σ_{Gh}^2), of the broad-sense heritabilities for progenies and topcrosses (h_f^2 and h_h^2 , %), for EV (mL g⁻¹) evaluated in the MWVT and in a hot air popper (HA), and yield (kg ha⁻¹), and of the genotypic correlations (r) between EV and yield, in the progeny and hybrid tests of the two programs¹

Parameter		Program 1			Program 2		
		EV _{MWVT}	EV _{HA}	Yield	EV _{MWVT}	EV _{HA}	Yield
μ_i		-	22.7	1.194.7	-	23.8	701.8
σ_{Gf}^2		-	23.6830*	452.781.98**	-	18.6482**	71.660.77*
h_f^2		-	64.8	81.8	-	81.9	69.0
ρ		-	0.014		-	0.265	
μ_h	Minimum	19.0	16.0	2.179.5	24.2	20.5	1.811.8
	Maximum	27.0	28.9	3.944.9	24.8	21.4	1.983.6
	Joint analysis	23.3	22.4	3.064.7	24.5	-	1.898.7
σ_{Gh}^2	Minimum	5.6870**	5.3030**	83.682.5**	3.5070**	3.4430**	67.528.7**
	Maximum	6.4820**	7.3650**	175.204.1 ^{ns}	4.2300**	5.7080**	70.590.7**
	Joint analysis	5.1320**	5.4360**	66.562.8**	2.0580**	-	21.364.8 ^{ns}
h_h^2	Minimum	60.6	54.0	36.1	59.4	36.9	30.0
	Maximum	87.6	81.8	63.9	71.0	61.3	60.9
	Joint analysis	68.1	80.2	60.948.4	-	20.2	

¹ **, * and ^{ns}: significant at 1% and 5% and non-significant at 5%

Table 2. Predicted gains with direct selection for expansion volume (EV, mL g⁻¹) (DSEV) and with selection based on the index of Mulamba and Mock (MMSI), for EV evaluated in the MWVT and in a hot air popper (HA) and for yield (kg ha⁻¹), in the family and hybrid tests of the two programs¹

Unit of Selection	Strategy	Local	Program 1				Program 2			
			EV	Yield	EV _{AQ}	Yield	EV _{MWVT}	Yield	EV _{AQ}	Yield
S ₃ family	DSEV		-	-	2.7	- 13.5	-	-	2.7	27.2
	MMSI		-	-	2.6	59.5	-	-	2.6	42.5
Hybrid	DSEV	PESAGRO	-	-	1.5	- 29.3	-	-	-	-
		CEPET	1.7 (1.5)	- 199.2	1.6 (1.3)	- 238.2	1.2 (0.6)	24.5	0.8 (0.4)	27.3
		COIMBRA	1.2 (0.8)	83.9	1.1 (0.7)	104.2	-	-	-	-
			1.1 (0.9)	- 38.2	1.2 (0.8)	- 24.3	-	-	-	-
	MMSI	UEM	-	-	-	-	1.8 (1.5)	9.2	1.3 (1.0)	- 1.4
		Joint An.	1.1	-	1.2	- 64.3	0.7	10.4	-	-
		PESAGRO	-	-	1.5	55.5	-	-	-	-
		CEPET	1.7	-	1.4	- 184.0	0.8	-	0.3	40.1
		COIMBRA	1.0	-	1.1	122.0	-	-	-	-
			0.9	-	1.1	- 0.9	-	-	-	-
		UEM	-	-	-	-	1.7	-	1.2	30.9
		Joint An.	-	-	1.2	- 42.7	0.7	20.8	-	-

¹The values in brackets are the indirect gains in EV evaluated in one device, with EV based selection evaluated in the other device

Selection based on the testcross performance

In the topcross hybrids of the progenies of program 1, genotype x environment interaction was only stated in relation to EV evaluated in a hot air popper (at 5%). In the joint analyses with hybrids of program 2, the tests regarding the interaction were both statistically significant (at 1%). The tests of absence of genetic variability in S₃ were significant at 1% in the individual and joint hybrid analyses, with two exceptions (Table 1). Only in relation to the yield of the hybrids of program 1, in one of the experiments conducted in Coimbra, and to the yield of the hybrids of program 2, in the joint analysis, no evidence of variability was observed. The estimates of genotypic variance in topcross hybrids may generally be considered homogenous, mainly regarding EV. Although discrepant in relation to the estimates of genotypic variance among S₃ families, mainly for EV, the estimates obtained with the topcross hybrids of program 2 were the lowest. The analysis of the hybrid means in comparison to the means of Beija-Flor and Viçosa presented positive relevant heterosis for yield, and negative, low-magnitude heterosis for EV evaluated in a hot air popper or the MWVT. The estimates for yield varied from - 7.9% (the only negative estimate) to 27.3%, with a mean heterosis of 12.6%. In relation to EV evaluated in hot air popper and the MWVT

the estimates varied from - 6.2 to 1.3% and from - 6.7 to 3.6, with means of - 2.6 and - 2.1%.

The heritability estimates at the level of topcross hybrid were higher for EV evaluated in a hot air popper and the MWVT than values obtained with yield, which are, in general, higher for hybrids of the families of program 1 (Table 2). The selection efficiency of superior S₃ families, based on the hybrid means therefore tends to be a little higher in quality than yield. The predicted gains in the individual and joint analyses also showed that the use of the index was, in general, more effective than direct selection for EV. The use of the index attained, with one single exception, a quality gain of at least 66.7% of the maximum gain.

Selection based on the *per se* and testcross performance

The selection efficiency of S₃ families, considering the phenotypic values of the progenies and their hybrids, was evaluated based on 109 and 97 progenies of programs 1 and 2, assessed for *per se* and testcross performance. Each subgroup represents a sample of the respective total of families since the means of EV evaluated in a hot air popper and of yield are equivalent (23.5 mL g⁻¹ and 1.310.3 kg ha⁻¹, and 24.4 mL g⁻¹ and 699.4 kg ha⁻¹). The predicted gains are higher due to the lower number of selected progenies (Table 3). In both programs, the indices 2

Table 3. Predicted gains for EV (mL g⁻¹) and yield (kg ha⁻¹) with selection based on the *per se* performance, using direct selection for expansion volume (DSEV) and the Mulamba and Mock index (MMSI), and with selection based on the *per se* and testcross performances, based on the indices 1, 2, and 3, and with combined selection¹

Strategy	Program 1		Program 2	
	EV	Yield	EV	Yield
DSEV	2.8	- 48.4	2.5	15.0
MMSI	2.7	45.1	2.5	28.7
Index 1	2.0	91.7	2.1	18.5
Index 2	2.6	62.6	2.3	41.6
Index 3	2.6	42.7	2.3	41.7
Combined selection	0.6	- 29.2	2.4	31.4

¹Program 1: selection of 62/109 families; Program 2: selection of 55/97 families; Index 1: equal weights for the ranks of the *per se* and testcross performances; Index 2: weights 2 and 1 for the ranks of the *per se* and testcross performances; and Index 3: weights 3 and 1 for the ranks of the *per se* and testcross performances

and 3, which attribute higher weight to the individual merit, were more effective than the best selection strategy of S₃ families, based on the *per se* performance. The predicted gains in EV correspond to, at least, 92% of the gains predicted with selection based on the index of Mulamba and Mock, usually associated to higher yield gains. The use of combined selection was not satisfactory with the progenies of program 1, determining irrelevant predicted gain in EV and yield loss. This is probably due to the estimated weights of the individual and testcross merits. For EV as much as for yield, the weight of the testcross merit was higher than the weight of the individual merit (0.00110605 and 0.00003270 for EV, and 0.00024483 and 0.00013574 for yield, respectively). In the progeny selection of program 2 the use of combined selection was equivalent to the use of the indices 2 and 3, probably because the *per se* merit was considered more important. The weight estimates of the individual and testcross merits were 0.00045994 and -0.00021293 for EV, and 0.00013468 and -0.00000811 for yield.

Genotypic correlations between *per se* and testcross performances

The estimates by local for EV evaluated in a hot air popper were -0.15, 0.03, 0.26, 0.33, 0.34, and 0.41. The means of all trials attained 0.23 and 0.26 in programs 1 and 2. The values for yield were -0.01, 0.03, 0.07, 0.10, 0.14, and 0.17 in the analyses by environment, and 0.12

and 0.11, using the means of all tests. A perfect coincidence is therefore not expected of the families identified as superior based on the *per se* and testcross performances.

Mihaljevic et al. (2005) used F₃ to F₆ progenies and estimated genotypic correlations between *per se* and testcross performances. The estimates for yield varied from low (0.28) to intermediate (0.56), increasing continuously for the other traits (0.52 to 0.87). Papst et al. (2004), using F_{2:3} progenies, estimated low-magnitude correlations for resistance to European corn borer. Bohn et al. (2003), who evaluated S₁, S₃ and S₅ *per se* progenies and S₂, S₄ and S₅ testcross families, claimed that the selection of inbred progenies based on resistance to European corn borer and the selection of testcross families based on yield and maturation would not result in simultaneous improvement, when using conventional improvement methods. Based on the testcrosses of 48 S₂ families, using two elites inbred lines as testers, Presterl et al. (2002) verified low, medium and high genotypic correlations between the *per se* and testcross performances, depending on the trait and the nitrogen level. Under low availability of this nutrient, the relative correlation to yield was high. The results indicated that the selection of the inbred lines at low N levels can indirectly improve the nitrogen use efficiency of the testcross hybrids.

In the trial conducted at PESAGRO, 35.1% of the families selected based on testcross performance, using the Mulamba and Mock index, were also selected based on the performance *per se*, by the use of the same index. Nevertheless, considering that 25.5% of the testcross families that were evaluated and not selected were not selected either by *per se* performance, a coincidence of 60.6% between the two experiments was inferred. In the trials conducted in the CEPET the coincidence values of selected and of non-selected families were 59.5 and 68.1. In the tests realized in Coimbra, 56.1 and 53.6% were obtained. In the experiment conducted at the UEM the coincidence was 60.5%. Using the hybrid means of all trials, the coincidence values were 58.4% and 59.3%, respectively, in programs 1 and 2. Considering only those selected based on the *per se* performance, 51.8% to 68.8% were also selected based on the hybrid performance, depending on the trial. Considering the overall hybrid means, 64.4 and 60.2% were obtained in programs 1 and 2.

The analysis of non-coincidence of selected families demonstrated that the progeny test was a little

more effective for the identification of superior families, probably because the EV and yield heritabilities were higher, compared to the hybrid trials. Considering the two programs jointly and selection based on the overall hybrid mean, 34% (16/47) of the S_3 families selected based on the per se performance but not selected considering the testcross performance, generated S_4 progenies evaluated in the growing season 2001/02. Of these, 75% (12/16) originated at least one selected S_4 family. In relation to the non-selected S_3 progenies based on per se performance but considering the testcross performance, 16.3% (8/49) provided S_4 families evaluated in the growing season 2001/02. Of these, 50% (4/8) originated at least one selected S_4 progeny (Arnhold and Viana 2006).

CONCLUSIONS

The results obtained for the heritabilities (evaluation of selection efficiency), predicted gains, genotypic correlations and percentages of coincidence

between selected and non-selected families demonstrated that the selection processes based on the per se and testcross performances were largely equivalent. The correspondence would certainly be higher if the genotypic correlations were higher. So, if heritabilities at the progeny and the hybrid level are of the same magnitude and if the genotypic correlations between the per se and testcross performances are high, the identification of superior families tends to be the same, considering the per se and testcross performances. The selection based, simultaneously, on the phenotypic means of families and hybrids tends to be adequate if the weights of the individual and testcross gains are proportional to the heritabilities.

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Importâncias relativas dos desempenhos *per se* e em cruzamento na seleção de famílias S_3 de milho-pipoca

RESUMO - O objetivo deste trabalho foi discutir o mérito do testcross em permitir identificar progênies endógamas superiores, avaliando as importâncias relativas dos desempenhos *per se* e em cruzamento na seleção. Foram considerados dois testes de progênies S_3 da população de milho-pipoca Beija-Flor e seis ensaios dos correspondentes híbridos testcrosses, obtidos usando-se a população Viçosa como tester. As análises consideraram capacidade de expansão e produção. Os resultados relativos às herdabilidades (avaliação da eficiência de seleção), aos ganhos preditos, às correlações genotípicas e às porcentagens de coincidência entre famílias selecionadas e não selecionadas, evidenciam boa equivalência dos processos de seleção com base nos comportamentos *per se* e em cruzamento. A correspondência seria certamente maior se as correlações genotípicas fossem mais elevadas. A seleção com base, simultaneamente, nas médias fenotípicas das famílias e dos híbridos tende a ser adequada se os pesos dos méritos individual e em cruzamento forem proporcionais às herdabilidades.

Palavras-chave: topcross, testcross, famílias endógamas.

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