

# Using the best linear predictor (BLP) in the selection between and among half-sib progenies of the CMS-39 maize population

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## ABSTRACT

Data of corn ear production (kg/ha) of 196 half-sib progenies (HSP) of the maize population CMS-39 obtained from experiments carried out in four environments were used to adapt and assess the BLP method (best linear predictor) in comparison with to the selection among and within half-sib progenies (SAWHSP). The 196 HSP of the CMS-39 population developed by the National Center for Maize and Sorghum Research (CNPMS-EMBRAPA) were related through their pedigree with the recombined progenies of the previous selection cycle. The two methodologies used for the selection of the twenty best half-sib progenies, BLP and SAWHSP, led to similar expected genetic gains. There was a tendency in the BLP methodology to select a greater number of related progenies because of the previous generation (pedigree) than the other method. This implies that greater care with the effective size of the population must be taken with this method. The SAWHSP methodology was efficient in isolating the additive genetic variance component from the phenotypic component. The pedigree system, although unnecessary for the routine use of the SAWHSP methodology, allowed the prediction of an increase in the inbreeding of the population in the long term SAWHSP selection when recombination is simultaneous to creation of new progenies.

## INTRODUCTION

Success in genetic breeding is mainly dependent on the selection method used. Several methods have been suggested and modified in recent years for greater selection efficiency using the statistical properties most suitable for different experimental situations. Among known methods, selection among and within half-sib progenies (SAWHSP) is one of the most used for maize because of its proven efficiency along with its easy handling and simplicity in estimating genetic parameters (Paterniani and Miranda Filho, 1978).

There are several examples in the literature which show gains from truncated selection for yield in various maize populations. Three cycles of SAWHSP were carried out on the CMS-39 population, with the following expected gains: 10.3% (Aguiar, 1986), 4.0% (Pacheco, 1987), and 7.3% (Arriel, 1991). The realized gain estimated by Arriel *et al.* (1993b) in the assessment of these three cycles was 3.6% per cycle, half the arithmetical mean of the expected gains in the three cycles.

Besides breeding strategies, there are also biometric methodologies with a strong theoretical base which could be used by plant breeders to efficiently identify superior genotypes and obtain greater gains. Among these are BLUP (best linear unbiased predictor), which classifies individuals submitted to selection using a function of the observed data and a matrix of

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genetic and residual variances and covariances of previously known traits (Henderson, 1963, 1973, 1975). Thus, an observable random vector  $y$  ( $n \times 1$ ) is used to estimate a non-observable vector of genetic values  $g$  ( $n \times 1$ ), where  $y$  and  $g$  are not independently distributed. The best progenies are selected based on the estimated genetic vector.

According to Henderson (1963), the BLUP of  $g$  is defined as the regression coefficient of the genetic values ( $g$ ) in function of the observations ( $y$ ) corrected for the fixed effects ( $X\beta$ ). To estimate the genetic value without inverting the variance and covariance matrices of the observed data, a time-consuming computer operation, since this matrix is frequently non-diagonal and very large, Henderson (1973) proposed an alternative computer method using mixed model equations for obtaining the BLUP. More details of this method are given by Martins et al. (1993).

The objective of the present study was to adapt and assess Henderson's alternative method in the selection among half-sib maize progenies.

## MATERIAL AND METHODS

In the agricultural years of 1990/91 (90) and 1991/92 (91) 196 half-sib progenies (HSP) from the CMS-39 maize population were assessed. Sowing densities were 25,000 plants/ha (25) and 50,000 (50), totaling four experiments, taken as four environments identified as: 9025, 9050, 9125 and 9150. The experiments were carried out in a 14 x 14 simple lattice design at the National Center for Maize and Sorghum Research (CNPMS-EMBRAPA), at Sete Lagoas, MG. Sowings were done on the recommended date in soil fertilized with 400 kg/ha of 4-14-8 NPK plus Zn, and 100 kg/ha of urea was added at 30 days after emergence. No supplementary irrigation was used.

The seeds of the HSP assessed in these experiments were obtained from the harvest of the 10 best plants selected within each of the 20 female rows, in an isolated recombination plot from remnant seeds of the HSP selected by Arriel et al. (1993a), concluding the third SAWHSP cycle in this population. The modified Irish

method was used (Figure 1) for recombination with simultaneous creation of new HSP, keeping track of the female rows (old progenies) to establish a pedigree relationship among the new and old progenies.

This genealogical structure is disregarded in the original methodology quoted by Paterniani and Miranda Filho (1978), based on two assumptions. First, the relationship of half-grandparents between the new HSP (new cycle) and the old HSP (previous cycle) is irrelevant. Second, it assumes that the gametes of all HSP in the recombination plot have the same frequency, resulting in equal chances of fertilization and in a balanced contribution of each progeny to the next cycle. From cycle to cycle, from each one of the 20 old progenies, 10 new ones would be obtained and submitted to a selection intensity of 10% (only one would be selected), without affecting the original effective size.

The variance analyses (ANOVA) of the 14 x 14 simple lattices were carried out using Cochran and Cox's model (1957) with recuperation of interblock information, to obtain the variance of the effective error and of the adjusted means. The adjusted treatments sum of squares was obtained and a joint ANOVA was carried out. The mathematical expectations to estimate the variance components of the total yield per plot (kg of ears/ha) for the individual and joint analyses were obtained using the randomized complete block model, following Vianna and Silva (1978).

The BLUP determination for selection among half-sib progenies adapted to mixed model methodologies, revised by Martins et al. (1993), was used. The fixed

Old progeny	Plants
A	Y Y Y Y Y Y Y Y Y Y Y Y ... Y Y Y Y Y Y Y Y Y Y Y Y
B	I <sub>1</sub> I <sub>2</sub> I <sub>1</sub> I <sub>3</sub> I <sub>1</sub> I <sub>4</sub> I <sub>1</sub> I <sub>5</sub> ... I <sub>6</sub> I <sub>7</sub> I <sub>1</sub> I <sub>8</sub> I <sub>9</sub> I <sub>1</sub> I <sub>10</sub> I <sub>1</sub>
C	I <sub>1</sub> I <sub>1</sub> I <sub>2</sub> I <sub>1</sub> I <sub>3</sub> I <sub>1</sub> I <sub>4</sub> I <sub>1</sub> I <sub>5</sub> ... I <sub>6</sub> I <sub>1</sub> I <sub>1</sub> I <sub>7</sub> I <sub>1</sub> I <sub>8</sub> I <sub>9</sub> I <sub>10</sub> I <sub>1</sub>
D	I <sub>1</sub> I <sub>1</sub> I <sub>1</sub> I <sub>2</sub> I <sub>1</sub> I <sub>3</sub> I <sub>4</sub> I <sub>1</sub> I <sub>1</sub> I <sub>1</sub> ... I <sub>5</sub> I <sub>6</sub> I <sub>1</sub> I <sub>7</sub> I <sub>8</sub> I <sub>1</sub> I <sub>1</sub> I <sub>9</sub> I <sub>10</sub> I <sub>1</sub>
...	Y Y Y Y Y Y Y Y Y Y Y Y ... Y Y Y Y Y Y Y Y Y Y Y Y
Q	Y Y Y Y Y Y Y Y Y Y Y Y ... Y Y Y Y Y Y Y Y Y Y Y Y
R	I <sub>1</sub> I <sub>2</sub> I <sub>1</sub> I <sub>1</sub> I <sub>3</sub> I <sub>1</sub> I <sub>4</sub> I <sub>1</sub> ... I <sub>5</sub> I <sub>6</sub> I <sub>1</sub> I <sub>7</sub> I <sub>8</sub> I <sub>9</sub> I <sub>10</sub> I <sub>1</sub>
S	I <sub>1</sub> I <sub>1</sub> I <sub>1</sub> I <sub>2</sub> I <sub>3</sub> I <sub>1</sub> I <sub>4</sub> I <sub>1</sub> ... I <sub>5</sub> I <sub>1</sub> I <sub>6</sub> I <sub>1</sub> I <sub>7</sub> I <sub>8</sub> I <sub>9</sub> I <sub>10</sub> I <sub>1</sub>
T	I <sub>1</sub> I <sub>1</sub> I <sub>1</sub> I <sub>2</sub> I <sub>1</sub> I <sub>3</sub> I <sub>4</sub> I <sub>5</sub> I <sub>1</sub> ... I <sub>6</sub> I <sub>7</sub> I <sub>1</sub> I <sub>8</sub> I <sub>1</sub> I <sub>9</sub> I <sub>10</sub> I <sub>1</sub>
	Y Y Y Y Y Y Y Y Y Y Y Y ... Y Y Y Y Y Y Y Y Y Y Y Y

A to T → HSP selected (AMONG) at the 3rd selection cycle - old HSP;  
 I<sub>1</sub> to I<sub>10</sub> → HSP selected (WITHIN) to start 4th selection cycle - new HSP;  
 I → detasseled plants - female rows - consisting of 100 plants;  
 Y → tasseled plants - male rows - consisting of 100 plants;  
 Y: I = relation male rows: female rows = 1:4.

Figure 1 - Field scheme for half-sib progeny (HSP) recombination with simultaneous obtention of new progenies. Modified Irish method.

effect components of the  $\beta$  vector, which are devised to correct the phenotypic values in function of the different environments, were not included in the calculations to estimate the  $g$  random vector because of the computational difficulties in obtaining their values from the original data. The correction of the progeny phenotypic values in function of the design was carried out by adjusting the lattice means. This second option brought a great simplification in the calculations because it reduced the dimension of the  $y$  vector to the number of treatments. However, this second option still keeps the genetic effects biased by the fixed effects, as characterized by the BLP (Best Linear Predictor) methodology.

Thus, the BLP of  $g$ , in a univariate analysis, could be obtained from the following expression:

$$\hat{g} = (I + A^{-1}K)^{-1} y$$

where:

$y$  = vector of  $n$  treatment adjusted means;

$n$  = number of treatments (196).

$$K = \frac{\hat{\sigma}_e^2}{b\hat{\sigma}_A^2} \text{ for individual analyses}$$

$$K = \frac{\hat{\sigma}_e^2 + b\hat{\sigma}_{g \times a}^2}{ba\hat{\sigma}_A^2} \text{ for joint analysis}$$

In the expressions to obtain  $K$ ,

$b$  = number of repetitions;

$a$  = number of environments

and the variance components are:

$\hat{\sigma}^2$  = estimate of residual error variance;

$\hat{\sigma}_A^2 = 4\hat{\sigma}_g^2$  = estimate of the additive genetic variance among half-sib progeny means;

$\hat{\sigma}_{g \times e}^2$  = estimate of genotype x environment interaction variance.

The kinship matrix ( $A$ ), of  $n \times n$  dimension, has a diagonal-block structure when the observations are grouped according to the ancestor in the  $y$  vector, allowing independent calculation of the inverse in each block, facilitating the inversion of the  $A$  matrix.

$$A = \begin{bmatrix} [A_1] & \phi & \dots & \phi \\ \phi & [A_2] & \dots & \phi \\ \dots & \dots & \dots & \dots \\ \phi & \phi & \dots & [A_{20}] \end{bmatrix}_{196}$$

where:

the sub-matrices  $A_i$ 's (blocks) have the same kinship structure, of  $10 \times 10$  order, except for four sub-matrices which are of  $9 \times 9$  dimension to fit the number of assessed treatment into the  $14 \times 14$  lattice.

$$A_i = \begin{bmatrix} 0.25 & 0.0625 & \dots & 0.0625 \\ 0.0625 & 0.25 & \dots & 0.0625 \\ \dots & \dots & \dots & \dots \\ 0.0625 & 0.0625 & \dots & 0.25 \end{bmatrix}$$

For assembling the twenty  $A_i$ 's matrices the covariances among progeny means were estimated for the experiments with sowing densities of 25,000 plants/ha ( $p = 25$ ) and 50,000 plants/ha ( $p = 50$ ). In the joint analysis, where the means of the treatments were estimated based on two experiments of 25,000 and two of 50,000 plants/ha,  $p = 150$ . Thus, the diagonal of the kinship sub-matrices is 0.28, 0.265 and 0.255, respectively. Off the diagonal, the kinship among the progenies, which had a common half-maternal grandmother, is  $1/16$  and is not affected by the number of plants ( $p$ ) in the plots.

These kinship coefficients were estimated for half-sib progenies, with remnant seeds, based on the following expressions:

a) Covariance between the mean ( $T_i$ ) of a progeny with itself:

$$\begin{aligned} Cov(T_i, T_i) &= Cov\left(\frac{il+i2+\dots+ip}{p}, \frac{il'+i2'+\dots+ip'}{p}\right) \\ &= \frac{1}{p^2} [p^2 Cov(p_{ip}, p_{ip'})] \\ &= Cov(p_{ip}, p_{ip'}) \end{aligned}$$

where

$$Cov(p_{ip}, p_{ip'}) = \frac{1}{4} \sigma_A^2, \text{ if the } p_{ip} \text{ and } p_{ip'} \text{ plants were half sibs;}$$

$$Cov(p_{ip}, p_{ip'}) = \frac{1}{2} \sigma_A^2 + \frac{1}{4} \sigma_D^2, \text{ if the } p_{ip} \text{ and } p_{ip'} \text{ plants were full sibs;}$$

$$Cov(p_{ip}, p_{ip'}) = \sigma_A^2 + \frac{1}{4} \sigma_D^2, \text{ if the } p_{ip} \text{ and } p_{ip'} \text{ plants were } S_1 \text{'s.}$$

The additive genetic variance ( $\sigma_A^2$ ) is the most important because it represents the inheritable part of the genotypic variance (Falconer, 1978).

b) covariance among the mean ( $T_i$ ) of a progeny with the mean ( $T_j$ ) of other progeny from the same half-grandmother:

$$\begin{aligned} Cov(T_i, T_j) &= Cov\left(\frac{i1+i2+\dots+ip}{p}, \frac{j1+j2+\dots+jp}{p}\right) \\ &= \frac{1}{p^2} [p^2 Cov(ip, jp)] \\ &= Cov(ip, jp) = 2r_{ip, jp} \sigma_A^2 \end{aligned}$$

where:  $r$  = Malécot kinship coefficient. Considering that the inbreeding coefficients of the half-grandmothers of the half-sib progenies were nil,  $r = 1/32$ .

In spite of the deductions shown above, the value of  $1/4$  was used in the diagonal of the A matrix because: a) there is a simplification of computer operations; b) in the literature the number of plants ( $p$ ) is considered large enough to reduce the covariance among HSP to  $1/4$  of the additive variance, and c) comparison of gains is obtained by selection using the two methodologies.

The estimate of the components of variance and of the genetic parameters was carried out according to Vencovsky (1978). For the comparison between the selection methodologies, truncated selection based on the vectors  $y$  and  $g$  was performed on the 20 superior progenies in each environment and for the four environments (joint) analysis. The coefficients of coincidence (percentage of common HSP selected by each methodology) and the expected gains from selection were estimated.

## RESULTS AND DISCUSSION

Table I shows the individual and joint variance analyses for the four environments, where the importance of the genotype x environment interaction is apparent. Its size was approximately 40% greater than the genotypic variance component among the HSP, and reflected the low agreement among the selected progenies in each environment (Tables II and III). This also occurred in the previous selection cycles (Aguiar, 1986; Pacheco, 1987; Arriel, 1991). The efficiency of the lattice shows that the use of this design was correct, mainly in the experiments carried out in the agricultural year 1991/92. The environment variation coefficients are within the variation limits found by Ramalho (1977) for this type of progeny.

Tables II and III show the progenies selected by the SAWHSP and BLP methods, respectively, for the four environments. The influence of the genotype x environment interaction when selection was made considering the environments individually was evident, and some superior progenies in a given environment were not selected in others. For example, sib number 78-101, which achieved the highest yield when assessed as 25,000 plants/ha in agricultural year 1990/91, was not among the 20 most productive progenies in the other experiments.

The pedigree analyses of the selected HSP in the fourth among progeny selection cycle (Tables II and III) show that truncated selection caused an imbalance in the expected frequency of new and old progenies. For example, in the 9125 experiment (Table II) the old progeny number 34 contributed four new progenies, when it was expected to contribute only one. This may result in a reduction in the effective size of the population in the more advanced selection generations and consequently in an increase in inbreeding. Among 20 progenies selected for their phenotypic value in experiments 9025, 9050, 9125 and 9150, the following old progenies contribution were quantified: 15, 12, 15 and 12, respectively.

Except for experiment 9125, the estimated selection gain in the individual analyses of the two methodologies was high, around 15%, due to the

**Table I** - Summary of analyses of individual and joint variances of experiments 9025, 9050, 9125, 9150 of corn ear production data (kg/ha).

SV	d.f.	MS				d.f.	MS
		9025	9050	9125	9150		
P	195	392249**	1224760**	330445**	539245**	195	920922**
P x E	-	-	-	-	-	585	534714**
Ef. error	169	233388	786262	251277	328482	676	399852
$\hat{\sigma}_g^2$		79430.9	219249.1	39584.1	105381.6		48276.1
$\hat{\sigma}_F^2$		196124.7	612380.0	165222.5	269622.6		115115.3
$\hat{\sigma}^2$		233387.6	786261.8	251276.8	328482.0		399852.0
$\hat{\sigma}_{g \times e}^2$		-	-	-	-		67430.8
VC (%)		21.51	23.88	22.24	26.36		24.38
LE (%)		128.88	119.38	175.18	190.85		-

P = Half-sib progenies; P x E = progenies x environments interaction; Ef. Error = effective error of lattice (median effective error in joint analysis); VC = variation coefficient; LE = lattice efficiency.

\*,\*\*Significant by the F-test, at 5 and 1% level of probability, respectively.

SV = Source of variation; d.f. = degrees of freedom; MS = mean square.

**Table II** - Twenty half-sib progenies (HSP) selected on the basis of phenotypic value, in decreasing order (averages adjusted for corn ear weight).

Rank	9025	9050	9125	9150
1	78-101*	171-87	180-100	193-7
2	96-109	69-40	141-102	4-77
3	46-115	129-25	179-100	62-161
4	125-163	106-176	136-25	46-115
5	136-125	130-25	159-162	5-77
6	82-101	165-162	120-163	45-115
7	74-40	155-93	13-18	83-101
8	193-7	153-93	40-115	2-77
9	110-34	161-162	18-18	49-2
10	90-109	111-34	108-34	25-126
11	57-2	68-40	110-34	113-34
12	171-87	70-40	116-34	171-87
13	85-101	14-18	62-161	34-74
14	155-93	124-163	49-2	90-109
15	36-74	115-34	79-101	173-87
16	5-77	66-161	111-34	172-87
17	18-18	61-161	150-93	31-74
18	30-74	193-7	5-77	50-2
19	145-102	166-162	76-40	6-77
20	130-25	35-74	169-87	120-163
$\bar{X}_S$	3086.25	5324.16	2922.71	3164.98
$\bar{X}_0$	2245.86	3713.44	2253.62	2173.98
SD	840.40	1610.73	669.09	991.00
EG	340.36	576.69	160.30	387.33
%EG	15.16	15.53	7.11	17.82
$h^2$ (%)	40.50	35.80	23.96	39.08

$\bar{X}_S$  = Phenotypic average of 20 selected HSP;

$\bar{X}_0$  = phenotypic average of 196 HSP;

SD =  $\bar{X}_S - \bar{X}_0$ ;

$$\%EG = \frac{EG \times 100}{\bar{X}_0};$$

EG(SAHSP) = expected gain with selection among HSP =  $h^2 \cdot SD$ ;  
 $h^2$  = heritability in strict sense.

\*Pedigree (new progeny-old progeny).

capitalized genotype x environment interaction (Tables II and III). BLP considers the relationships among the assessed HSP that are not considered in the conventional SAWHSP method and the use of the two methods indicated a greater expected genetic gain for BLP. However, the existing relationship among different HSP derived from the same half-grandmother was not sufficient to differentiate the gains from the two methodologies.

The BLP methodology emphasized the descendance for the HSP selection. This may be seen in the reduction of the number of old progenies in the pedigree of the new selected progenies, which in experiments 9025, 9050, 9125 and 9150 was 13, 9, 9 and 8,

**Table III** - Twenty half-sib progenies (HSP) selected on the basis of genetic value, in decreasing order.

Rank	9025	9050	9125	9150
1	78-101*	171-87	108-34	4-77
2	96-109	69-40	110-34	5-77
3	82-101	129-176	116-34	2-77
4	125-163	130-25	111-34	193-7
5	46-115	165-162	112-34	46-115
6	85-101	155-93	180-100	6-77
7	90-109	68-40	120-163	45-115
8	136-25	70-40	179-100	62-161
9	196-7	153-93	76-40	7-77
10	110-34	106-176	115-34	83-101
11	74-40	111-34	159-162	34-74
12	79-101	161-162	74-40	31-74
13	171-87	115-34	39-74	1-77
14	81-101	66-161	49-2	171-87
15	36-74	61-161	57-2	173-87
16	57-2	77-40	13-18	172-87
17	155-93	72-40	101-176	8-77
18	5-77	14-18	106-176	113-34
19	30-74	71-40	69-40	40-115
20	177-87	166-162	119-163	38-74
$\bar{X}_{BS}$	1868.06	2974.18	1294.00	1875.91
$\bar{X}_{BO}$	1539.48	2381.55	1131.65	1462.32
EG	328.57	592.63	162.36	413.59
%EG	14.63	15.96	7.20	19.02
K	0.3673	0.4483	0.7935	0.3896

$\bar{X}_{BS}$  = Average of the predicted genetic value of the 20 HSP selected;

$\bar{X}_{BO}$  = average of the predicted genetic value of the 196 HSP;

EG(BLP) =  $\bar{X}_{BS} - \bar{X}_{BO}$  = expected gain with selection among HSP;

$$K = \frac{\hat{\sigma}^2}{r\hat{\sigma}_A^2}, \text{ for individual analyses.}$$

\*Pedigree (new progeny-old progeny).

respectively. In experiment 9150, seven HSP descending from the 77th progeny were selected (Table III). In other words, the BLP conferred greater importance to the mean of the related progenies with the same half-grandmother than to the means of the isolated HSP, a process that results in the screening out of the high mean progenies descending from low mean families, which would be selected based on their phenotype.

On the other hand, it can be seen that the BLP was influenced by extreme phenotypic values, because it distributes this influence equally to all the progenies of the same family. This fact was observed with the HSP numbered 78-101 in experiment 9025, the adjusted mean of which, far superior to the others, contributed to the selection of other HSP of the 101 family, even when they had lower phenotypic values than other

discarded HSP. This fact was minimized when the discrepant value was arbitrarily substituted by a measurement nearer to the mean of the family (data not shown).

The comparison between the two methodologies can be better visualized based on the coincidence coefficients for the experiments 9025, 9050, 9125, 9150 and joint analysis, which were, respectively, 85, 85, 55, 75 and 75%. An inverse relation of 84.93% among these coincidence coefficients and the estimated values of K was found (Table III and IV). This shows that as the genetic variance increases in relation to the residual variance, the BLP tends to select the same individuals that would be selected based on greater phenotypic values. A negative correlation of 99.36% was also shown among the values of K and  $h^2$ , showing that as the heritability values increased the selection, results of the two methodologies would be closer. With large  $h^2$  the phenotypic value is a good predictor of the genetic value.

The joint analysis of the four environments was used to select the 20 HSP which were recombined in the summer of 93 to produce, simultaneously, 196 new progenies to start the fifth cycle of SAWHSP in the CMS-39 population. As in the first three cycles, selection was based on the means over the environments to improve the genetic adaptability of the population, including those with lower densities, by giving priority to prolificacy. However, the data show that there was sufficient variability to select progenies adapted to low population densities (25,000 plants/ha), which seems promising for the development of a population adapted to crop rotation with common bean. Table IV shows the selected progenies.

Table IV also shows that the BLP selected a greater number of progenies stemming from the same ancestor, totaling 11 different maternal half-grandmothers. Selection based on the phenotypic value, however, resulted in 15 different ancestors as noted by the pedigree.

When the relationship among progenies descending from the same half-grandmother was discounted for the HSP selection by the BLP methodology, i.e., the A matrix was considered diagonal, there was a coincidence of 100% with the progenies selected by the SAWHSP method (Table IV), with identical expected percentual gains (9.26%). Similarly, when the kinship was considered in the joint analysis, the genetic gains were close (9.07%).

The expression  $(I + A^{-1}K)^{-1}$ , which originated the BLP of  $g$  without kinship, corresponded to an identity matrix (196 x 196) multiplied by a constant which is the heritability value. This means that the BLP

**Table IV** - Twenty half-sib progenies (HSP) selected on the basis of phenotypic value (SAWHSP) and of the genetic value (BLP), in decreasing order, with and without kinship among the progenies originating from a common maternal half-grandmother.

	Joint analysis		
	SAWHSP	BLP	
		Without kinship	With kinship
1	171-87*	171-87	171-87
2	193-7	193-7	5-77
3	46-15	46-15	193-7
4	5-77	5-77	111-34
5	155-93	155-93	46-15
6	62-161	62-161	62-161
7	111-34	111-34	74-40
8	96-109	96-109	155-93
9	78-101	78-101	129-25
10	74-40	74-40	115-34
11	129-25	129-25	71-40
12	67-161	67-161	110-34
13	120-163	120-163	173-87
14	25-126	25-126	116-34
15	173-87	173-87	2-77
16	79-101	79-101	67-161
17	106-176	106-176	120-163
18	18-18	18-18	78-101
19	130-25	130-25	130-25
20	71-40	71-40	72-40
	$\bar{X}_S = 3166.69$	$\bar{X}_{BS} = 1328.02$	$\bar{X}_{BS} = 2046.49$
	$\bar{X}_0 = 2594.16$	$\bar{X}_{BO} = 1087.92$	$\bar{X}_{BO} = 1811.27$
SD	572.53		
EG	240.10	240.10	235.22
%EG	9.26	9.26	9.07
K		0.3461	0.3461
$h^2$ (%)	41.9372	100.00	100.00

$$K = \frac{\hat{\sigma}^2 + r\hat{\sigma}_{g \times e}^2}{ra\hat{\sigma}_A^2}, \text{ for joint analysis.}$$

\*Pedigree (new progeny-old progeny).

genetic values, together with the mean of the selected HSP and the original mean of the 196 HSP, are obtained multiplying the respective phenotypic values of SAWHSP by  $h^2$  (see Table IV). Thus, the gain of selection (GS) obtained with the BLP is the selection differential (SD) among the means of the genetic values of the selected progenies in relation to all the assessed ones.

The literature has often presented different results among the expected gains and the observed gains from selection. This lack of agreement is partially due to the fact that the estimates of the expected gains are based on phenotypic values, which suffer from

environmental influences and from genotype  $\times$  environment interaction. In the majority of cases the expected gains are overestimated, which was also shown for this population by Arriel *et al.* (1993b), who found an observed gain of 3.6% per selection cycle, while the mean of the expected gains was 7.2%. This difference was attributed to the genotype  $\times$  environment interaction, whose component  $\sigma_{g \times e}^2$  was large in the three cycles, being larger than the estimate of genetic variance among the HSP in this cycle (Table I). On the other hand, when dealing with genetic values, this should not happen and the expected gains should be nearer the observed gains. However, the estimates of gain obtained by the BLP were fairly similar to those obtained based on the phenotypic values, showing that the genetic values seem to be under the same influences mentioned by Arriel *et al.* (1993b).

In these results, it was shown that the original SAWHSP, quoted by Paterniani and Miranda Filho (1978), is an efficient method, even when the relationship of the selected progenies is not considered. In this method, the genetic gains were identical to those obtained based on the BLP, showing its efficiency in isolating the additive component, responsible for the heritability and the expected gain, from the phenotypic variance. It also contributed less to the reduction in the effective size of the population, and consequently reduced future problems with inbreeding.

Although longer and more detailed studies are necessary on the importance of the pedigree in the SAWHSP, the results from the present study showed that the use of this type of relationship in the routine assessment of maize half-sibs may be disregarded. However, the indication of a reduction in the effective size of the population caused by an imbalance in the contribution of the selected progenies, as shown by the pedigree structure, draws attention to the problem of an increase in the level of inbreeding.

Thus, after every three SAWHSP cycles the new HSP should be used for a second recombination, instead of beginning a new selection cycle. One should continue with the same structure of the modified Irish method, shown in Figure 1, but with a balanced mixture of seeds from ears selected within the female row used for recombination, to sow the female rows. For the male rows a balanced mixture of seeds from the ears of all new HSP should be used.

When dealing with full sib and  $S_1$ 's progenies where the relationship among the progenies is more accentuated, the suggested double recombination becomes even more important in maintaining the rates of inbreeding within levels that do not damage future gains from selection.

## CONCLUSION

The methods used for selection of the 20 best half-sibs, SAWHSP and BLP led to similar values of expected genetic gains. There was a tendency for the BLP methodology to select a greater number of related progenies (pedigree) than the SAWHSP method, which implies greater care with the effective size of the population. The pedigree system, although unnecessary for HSP selection, allowed the prediction of an increase in the rate of inbreeding in the long term with the originally proposed scheme, when recombination is simultaneously carried out with the creation of new progenies.

Sufficient genetic variability was observed in the fourth selection cycle of the CMS-39 population allowing the continuation of the breeding program, with an expected gain of 9.26% in this cycle, with selection based on the mean of the four environments. After four SAWHSP continuous cycles, no reduction in the genotype  $\times$  environment interaction was observed.

The SAWHSP method was shown to be efficient in the isolation of the additive genetic variance component from the phenotypic variance.

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## RESUMO

Com os objetivos de adaptar e avaliar a metodologia do BLP (melhor preditor linear) em comparação com o método de seleção entre e dentro de progênies de meios-irmãos (SAWHSP), foram analisados dados de produção de espigas (kg/ha) de experimentos conduzidos em quatro ambientes, onde foram avaliadas 196 progênies de meios-irmãos (HSP), relacionadas através do seu "pedigree" com as progênies recombinadas no ciclo de seleção anterior, da população de milho CMS-39, desenvolvida pelo Centro Nacional de Pesquisa de Milho e Sorgo (CNPMS-EMBRAPA). Pode-se chegar à conclusão que as duas metodologias utilizadas para a seleção das 20 melhores progênies de meios-irmãos, SAWHSP e BLP, levaram a ganhos genéticos esperados com a seleção bastante similares. Houve uma tendência da metodologia do BLP em selecionar um maior número de

progênies relacionadas em função da geração anterior ("pedigree") do que o outro método, implicando maiores cuidados com o tamanho efetivo da população. A metodologia de SAWHSP mostrou-se eficiente no isolamento do componente da variância genética aditiva da variância fenotípica. O sistema de "pedigree", embora tenha se mostrado desnecessário para a utilização rotineira da metodologia de SAWHSP, permitiu a previsão de um aumento na taxa de endogamia a longo prazo no esquema originalmente proposto, quando é feita a recombinação com obtenção simultânea das novas progênies.

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