ARTICLE

Selection of maize lines and prediction of hybrid and synthetic means using intergroup topcrosses

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Abstract: *Topcrosses are routinely used in maize-hybrid programs. This study aimed to evaluate heterosis components and combining ability to predict hybrid means between synthetics from two groups of S_1 maize lines using the intergroup topcrosses model that includes S_2 lines. Two groups, each with 30 S_1 maize lines, were crossed using an intergroup topcross system, with a mixture of lines from one group as a tester for the contrasting group. Simultaneously, 30 S_2 lines from each group were generated via self-pollination. Lines and topcrosses were experimentally evaluated and the data were analyzed using a model adapted to the study design. The results showed the suitability of the proposed model for studying heterosis components and general combining ability, detailing additive and dominance effects. Prediction of hybrid means between synthetics showed the potential of the lines to generate base populations for an interpopulation breeding program.*

Keywords: *Testcross, diallel crossing, inbreeding depression, heterosis, combining ability*

INTRODUCTION

In maize breeding, diallel analyses are one of the most common methods for generating genetic information that can be used to develop breeding strategies (Nardino et al. 2020, Onofri et al. 2021). It is possible to make inferences about the genetic control of the traits of interest from the information provided by the diallels, evaluate the heterotic potential and genetic values of the parents by their combining abilities, and predict the best crosses between the parents (Hallauer et al. 2010, Coelho et al. 2020).

One of the main restrictions imposed by the diallel usage is the number of hybrid combinations to be obtained and evaluated. This greatly increases with an increase in the number of parents, making breeding programs more expensive (Inocente et al. 2021). To reduce the number of crosses for evaluation, breeders have opted to use topcrosses (Rodrigues et al. 2016, Rosa et al. 2020). This method evaluates the lines in crosses with common testers, allowing the assessment of the genetic values of individuals from the population to be improved (Miranda Filho 2018).

The use of intragroup topcrosses was suggested by Chaves and Miranda

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Filho (1997) with the objective of reducing evaluation costs and allowing the estimation of genetic parameters for parent selection, in addition to predicting the means of composite or synthetic populations. This method consists of crossing each parent with a mixture of pollen from the entire set of parents. The parameter estimates are obtained according to an adaptation of the model by Gardner and Eberhart (1966), and the prediction of means is made using data from the evaluation of the parents and crosses. The intragroup topcross methodology was adapted by Moreira Júnior et al. (2022) at the interpopulation level, with the aim of evaluating two groups of lines from distinct heterotic groups; thereby, reducing the number of combinations to be evaluated for a given number of parents. In this case, a mixture of parents from each heterotic group acts as a tester for the other.

In a diallel design, where only the parents and their crosses are evaluated, the additive and dominant effects are confounded; therefore, they must be jointly estimated. To discretely estimate the additive and dominant effects, one option is to include the generation from the self-fertilization of the parents in the experiment (Gardner and Eberhart 1966). Knowledge of the magnitude of these effects can provide better knowledge about the genetic control of quantitative traits (Chaves 2021), in addition to estimating inbreeding depression and the means of all potential lines in the homozygotic generation (Vencovsky and Barriga 1992).

The objectives of this study were to evaluate the heterosis components and combining ability of two groups of S_1 maize lines, to adapt the heterosis component analysis procedure based on the use of intergroup topcrosses (including S_2 lines), and to predict the performance of potential synthetic crosses from the two groups of lines.

MATERIAL AND METHODS

The S_1 maize lines derived from the UFG–Samambaia population were used. The population was synthesized at the Federal University of Goiás from recombination by three cycles of nine commercial hybrids (C-901, C-701, G-85, AG-951, AGX 7391, P3041, Z-8452, BR-201, and PL-3012), selected for their high productivity and adaptation to the climatic conditions of the State of Goiás. S_1 lines were obtained by the self-pollination of S_0 plants in the summer of 2016/2017, resulting in 390 lines with great variation in grain type. From the set of lines, 30 with dent grains (group A) and 30 with flint grains (group B) were selected for use in the present study.

The lines were crossed in autumn 2018 in an intergroup reciprocal topcross scheme, as proposed by Moreira Júnior et al. (2022), in the experimental area of the School of Agronomy of the Federal University of Goiás. In an isolated area, the lines of each group were sown in individual rows of 4 m in length and 0.80 m spacing (female rows), interspersed by tester rows (male rows) composed of a balanced mixture of seeds of the inbred lines of the contrasting group. Male rows were sown every three female rows on two dates spaced one week apart to ensure uniformity in pollen supply. To avoid coincidence between the flowering phases, the planting of the lines of each group was carried out 25 days apart. At flowering, the female rows were detaselled and pollinated freely by the pollen mixture of the contrasting group. The seeds collected in each row constituted two groups of topcross hybrids ($A_{♀} \times B_{♂}$ and $B_{♀} \times A_{♂}$). Three crosses of the A × B group were not included in the experiments because there were insufficient seeds for sowing. At the same time, a 2 m row of each line was sown with 10 seeds to proceed with self-fertilization to advance the lines from S_1 to S_2, with 75% inbreeding. Due to seed insufficiency, some genotypes could not be evaluated in the field.

The genotypes were evaluated in six trials (first trial: 21 S_1 lines from group A, second trial: 16 S_1 lines from group B, third trial: 30 S_2 lines from group A, fourth trial: 30 S_2 lines from group B, fifth trial: 27 hybrids from the A × B crosses, and sixth trial: 30 hybrids from the B × A crosses) in a randomized complete block design with four replications and plots of 2.88 m^2 (a 3.6 m row with 18 plants and a row spacing of 0.8 m), totaling 62.500 plants ha^{-1}. The experiments were conducted in March 2019 in the experimental area of the School of Agronomy of the Federal University of Goiás, Goiânia, Goiás, Brazil (lat 16° 3’ 48” S, long 49° 16’ 39” W, alt 730 m asl). The soil in the experimental area was a dark red latossol (Embrapa 2018). In each trial, three common genotypes were included as control treatments: AG 1051 (double-cross hybrid), BM 3061 (three-way cross hybrid), and UFG–Samambaia (open-pollinated variety). For some S_1 lines (eight from group A and four from group B), three replications were performed according to seed availability.

The agronomic traits evaluated were male flowering (days), female flowering (days), plant height (m), ear height (m), ear yield (t ha^{-1}), and grain yield (t ha^{-1}). The ear and grain yield traits were adjusted for 13% moisture and for the ideal stand using analysis of covariance, as described by Vencovsky and Barriga (1992).

The data for each variable were subjected to analysis of variance (ANOVA) according to the randomized complete block design. The homogeneity of variance among the six trials was tested using the relationship between the intrablock errors of the individual analyses. The values obtained did not exceed seven units, indicating that the assumption of the joint ANOVA was met. The pooled residual mean square was obtained by the average of the mean squares of the individual trials, weighted by their respective degrees of freedom. The means of the genotypes from different trials were adjusted using the multiplicative model and the means of the common control genotypes (Chaves et al. 1989), as the additive correction of the data could cause an overestimation of the means of the S_1 and S_2 lines because of the differences in productive potential between the lines and controls.

Analysis of the table data from the reciprocal topcrosses was performed using an adaptation of the model provided by Moreira Júnior et al. (2022). As S_1 (parents), S_2, and topcross hybrids were evaluated, it was possible to replace the effects of lines in groups A and B, v_i and v_j, respectively, by additive effects (a_i and a_j) and dominant effects (d_i and d_j). In this way, the analysis of the table provided by the topcross method with intergroup reciprocal testers with the inclusion of the S_2 generation can be performed from the model:

$T_i = \mu + c + \left(\frac{1}{2}\right)a_i + \left(\frac{1}{2}\right)d_i + \bar{h} + h_i$, for the topcrosses of group A;

$T_j = \mu - c + \left(\frac{1}{2}\right)a_j + \left(\frac{1}{2}\right)d_j + \bar{h} + h_j$, for the topcrosses of group B;

$S_{1_i} = \mu + k + a_i + d_i$, for S_1 lines of group A;

$S_{1_j} = \mu - k + a_j + d_j$, for S_1 lines of group B;

$S_{2_i} = \mu + k + a_i + \left(\frac{1}{2}\right)d_i$, for S_2 lines of group A; and

$S_{2_j} = \mu - k + a_j + \left(\frac{1}{2}\right)d_j$, for S_2 lines of group B

where T_i, T_j is the observed means of topcrosses from groups A and B, respectively; S_{1_i} , S_{1_j} is the observed means of S_1 lines of groups A and B, respectively; S_{2_i} , S_{2_j} is the observed means of S_2 lines of groups A and B, respectively; μ is the average of means of the potential homozygotic lines from groups A and B; *c* is the deviations of the mean of each group of topcrosses from the mean of the two groups; a_i , a_j is the additive effects of lines from groups A and B, respectively; d_i , d_j is the dominance effects of lines from groups A and B, respectively; $\bar{h}$ is the average heterosis of the potential crosses between lines from groups A and B; h_i, h_j is the heterosis effect of lines from groups A and B, respectively; and *k* is the deviation of the means of the potential homozygotic lines from groups A and B, from the mean of the two groups (μ). In this study, the adjusted means of T_i, T_j, S_{1_i} , S_{1_j} S_{2_i} and S_{2_j} were used according to the aforementioned adjustment procedure.

The estimates of the parameters and the sums of squares for the ANOVA were obtained using the least-squares method. The parameters were estimated using $\hat{\beta} = (X'X)^{-1}(X'Y)$ and the sum of the squares of the model using $SQ = \hat{\beta}'(X'Y)$, where $\hat{\beta}$ is the vector of the parameter estimates of the model, X is the incidence matrix of the parameters, and Y is the vector of observations. The calculation of the sum of squares for each effect was performed sequentially by the difference in the sum of squares of the model with and without the inclusion of each effect. To solve this system, the following restrictionsh were imposed:

$\sum_{i=1}^{I} a_i = \sum_{j=1}^{J} a_j = \sum_{i=1}^{I} h_i = \sum_{j=1}^{J} h_j = 0.$

The inbreeding depression (ID) of the S_2 generation relative to S_1 was estimated using the following formula:

$ID_i = \left(\frac{1}{2}\right)d_i$, for the lines of group A; and

$ID_j = \left(\frac{1}{2}\right)d_j$, for the lines of group B.

The general combining ability (GCA) was estimated by:

$GCA_i = \frac{1}{2}(a_i + d_i - \bar{d}_A) + h_i$, for lines of group A; and

$GCA_j = \frac{1}{2}(a_j + d_j - \bar{d}_B) + h_j$, for lines of group B where $\overline{d}_A$ is the mean of the dominance effects of group A and $\overline{d}_B$ is the mean of the dominance effects of group B. The ANOVA and estimations of parameters were performed in R software, using the features of the 'Matrix' package (R Core Team 2019).

The means of the single-cross hybrids between the lines of groups A and B were predicted using the model described by Miranda Filho and Geraldi (1984), reduced for the specific heterosis:

$\hat{C}_{ij} = \mu + (1/2)v_i + (1/2)v_j + \overline{h} + h_i + h_j$, where $\hat{C}_{ij}$ is the predicted mean of the hybrid of lines *i* and *j*.

Replacing the parameters by their estimators as a function of parents and topcrosses, it follows that (Moreira Júnior et al. 2022):

$\hat{C}_{ij} = T_i + T_j - (1/2)(\overline{T}_{.(A)} + \overline{T}_{.(B)})$, where $\overline{T}_{.(A)}$ and $\overline{T}_{.(B)}$ are the general means of the topcrosses of groups A and B, respectively.

The predicted mean of the cross between the two synthetics formed by subsets of parents from each group was obtained as follows:

$MC_{(i...i' x j...j')} = \frac{1}{K_1}\sum_{i=1}^{K_1} T_i + \frac{1}{K_2}\sum_{j=1}^{K_2} T_j - \frac{1}{2}(\overline{T}_{.(A)} + \overline{T}_{.(B)})$, where K_1 and K_2 are the number of lines that participate in the formation of synthetics from groups A and B, respectively.

Owing to the high number of possible combinations (more than 1 billion), only predictions of hybrids between synthetics with the same number of lines in both groups were performed ($k_1 = k_2$). The ten best lines of each group were selected according to the highest estimates of the general combining ability (GCA) for grain yield (Miranda Filho and Chaves 1991). Predictions were made for all synthetics of the same size (from two to ten) and for all traits, using the values obtained from the topcrosses.

RESULTS AND DISCUSSION

ANOVA by intergroup topcross model

There was a significant difference ($p \leq 0.05$) among the genotypes for male and female flowering and plant height in all trials. For ear height, the genotypes differed from each other ($p \leq 0.05$) in trials involving the S_1 lines of groups A and B, the S_2 lines of group B, and the topcrosses of group B. For ear and grain yields, there was a significant difference among the genotypes in the trials with S_1 lines from group B and topcrosses from group B. These results indicated the presence of genetic variability in these traits among the evaluated genotypes.

When using two groups of lines with distinct heterotic patterns and one group as a tester for the other, a mixture of single-cross hybrids was obtained. Therefore, information about a line used in crosses with reciprocal testers must correspond to the average performance of this line in hybrid combinations (Moreira Júnior et al. 2022). For this purpose, the values of the topcrosses were assumed to correspond to the marginal mean of the intergroup diallel table. In this situation, it is not possible to estimate the specific combining abilities of particular crosses, and it is possible to estimate only the general combining ability of the evaluated lines.

The partitioning of genotype effects according to the topcross model showed significance for the effects of additivity and dominance of groups A and B, between and within the line groups (Table 1). These results indicate the possibility of selecting parents from both groups to form base populations for recurrent selection at intrapopulation and interpopulation levels. In the latter case, one population from each group was obtained, maintaining heterotic groups.

For the traits related to flowering, it was observed that the additive gene effects had greater expression than the dominance effects (Table 1). The predominance of additive effects in the genetic control of traits related to flowering indicates the easy identification of superior genotypes with a higher concentration of favorable alleles. There was no significant difference in the dominance effects ($p > 0.05$) for plant height and ear height in group A (Table 1), which indicated that the lines of this group were similar in terms of the contribution of dominance effects for these traits. Furthermore, for these traits, greater contributions of additive effects were observed for total variation in relation to dominance effects. Other studies have also reported a predominance of additive effects and partial dominance in the genetic control of plant and ear height (Senhorinho et al. 2015, Coelho et al. 2020). For ear and grain yields, no significant

Table 1. Mean squares of analysis of variance according to intergroup reciprocal topcrosses model for the following traits: male flowering (MF - days), female flowering (FF – days), plant height (PH – m), ear height (EH – m), ear yield (EY – t ha^{-1}), and grain yield (GY – t ha^{-1})

Sources of variation	df[1]	MF	FF	PH	EH	EY	GY
Genotypes	153	7.159^{**}	8.570^{**}	0.026^{**}	0.010^{**}	3.609^{**}	2.300^{**}
Additivity GA[2]	29	9.386^{**}	8.686^{**}	0.020^{**}	0.010^{**}	0.660^{**}	0.410^{**}
Additivity GB[3]	29	8.093^{**}	10.059^{**}	0.043^{**}	0.022^{**}	0.559^{**}	0.289^{**}
Dominance GA	21	1.133^{*}	1.229	0.006	0.003	0.324	0.193
Dominance GB	16	2.287^{**}	4.394^{**}	0.010^{**}	0.006^{*}	1.409^{**}	0.895^{**}
Between groups (lines)	1	62.200^{**}	47.900^{**}	0.168^{**}	0.018^{*}	0.019	0.001
Average heterosis	1	404.200^{**}	512.700^{**}	1.306^{**}	0.210^{**}	427.298^{**}	274.478^{**}
Heterosis GA	26	0.581	1.273	0.006	0.004	0.718^{**}	0.487^{**}
Heterosis GB	29	1.383^{**}	2.517^{**}	0.005	0.003	0.689^{**}	0.430^{**}
Between groups (topcrosses)	1	5.900^{**}	5.100^{*}	0.037^{**}	0.001	21.529^{**}	13.569^{**}
Error	f[4]	0.689	1.239	0.004	0.003	0.231	0.146

*, **: significant at the 5% and 1% levels, respectively, by the F test. [1] Degrees of freedom; [2] Group A (dent grains); [3] Group B (flint grains); [4] Error degrees of freedom varied from 422 to 432 for different traits.

differences were observed ($p > 0.05$) in the dominance effects for the lines of group A. It is worth mentioning that the absence of significance within a group does not mean the absence of dominance effects but that the contribution of parents to these effects is similar.

The contribution of average heterosis was predominant in relation to the other effects, being significant ($p \leq 0.05$) for all evaluated traits (Table 1). The traits grain yield, ear yield, female flowering and male flowering showed the highest percentages of participation of the average heterosis in the total variation, which were 78.01%, 77.38%, 39.09% and 36.92%, respectively. These results demonstrated that the topcrosses were significantly superior in relation to the mean of the parental lines. Significant participation of average heterosis in grain yield has also been reported in other studies (Doná et al. 2011, Laude and Carena 2014).

No significant differences ($p > 0.05$) were observed in line heterosis for plant height and ear height between the two groups, which shows that the parents of both groups contributed similarly to the crosses (Table 1). Male and female flowering traits showed significant values ($p \leq 0.05$) only for line heterosis in group B (Table 1). These results indicate that there is variability in the manifestation of hybrid vigor, in other words, genetic divergence between the parents in the contribution to heterosis only for the lines of group B. Ear yield and grain yield showed significant mean squares ($p \leq 0.05$) for line heterosis for both groups (Table 1), which indicates the dispersion of allelic frequencies of the lines (Oliveira et al. 2004). Significant values ($p \leq 0.05$) were found for the deviations of the line groups in relation to the means of the two groups for male and female flowering, ear height, and plant height (Table 1). These results showed that there were statistical differences between the groups of lines S_1 and S_2 of group A, and lines S_1 and S_2 of group B, in relation to the average of the two groups for these traits.

The deviations in the means of each group of topcrosses in relation to the mean of the two groups were significant ($p \leq 0.05$) for male and female flowering, plant height, ear yield, and grain yield (Table 1), which were unexpected. These results may be due to an imbalance in pollination to obtain topcrosses, causing some parents to contribute differently to their development (Moreira Júnior et al. 2022). However, it is most likely that the correction of the genotype means using the means of the common controls caused a reduction in the means of one of the groups of topcross hybrids, since the productivity of the controls was considerably lower in one of the tests containing hybrids.

Estimates of parameters

There were large variations between the minimum and maximum values for the additive and dominance effects of parents in groups A and B (Table 2). For additivity effects, a restriction was imposed such that the sum of all effects must be zero, implying positive and negative values. No restrictions were imposed on dominance effects. These results suggest the feasibility of selection among parents aimed at genotypes with higher frequencies of favorable alleles for the formation of new base populations for breeding programs (Senhorinho et al. 2015).

Table 2. Range of variation of additive effects ($\hat{a}_i$) and ($\hat{a}_j$), dominance effects ($\hat{d}_i$) and ($\hat{d}_j$), line heterosis ($\hat{h}_i$) and ($\hat{h}_j$), inbreeding depression ($\widehat{ID}_i$) and ($\widehat{ID}_j$) , general combining ability ($\widehat{GCA}_i$) and ($\widehat{GCA}_j$), means of the groups of lines ($\hat{\mu}$), average heterosis ($\hat{\bar{h}}$), difference between groups of lines ($\hat{k}$), and difference between groups of topcrosses ($\hat{c}$). MF: male flowering (days); FF: female flowering (days); PH: plant height (m); EH: ear height (m); EY: ear yield (t ha^{-1}), and GY: grain yield (t ha^{-1})

Estimates	**Groups**	**Traits**					
		MF	**FF**	**PH**	**EH**	**EY**	**GY**
$\hat{a}_i$ minimum	A (dent)	-5.84	-6.49	-0.29	-0.19	-1.31	-1.08
$\hat{a}_i$ maximum		9.17	7.90	0.32	0.29	1.68	1.28
$\hat{a}_j$ minimum	B (flint)	-6.50	-6.86	-0.46	-0.25	-1.60	-1.28
$\hat{a}_j$ maximum		9.65	5.01	0.36	0.40	1.67	1.15
$\hat{d}_i$ minimum	A (dent)	-9.53	-7.27	-0.56	-0.49	-1.95	-1.42
$\hat{d}_i$ maximum		2.14	4.69	0.23	0.13	1.96	1.46
$\hat{d}_i$ mean		-2.06	-1.64	-0.08	-0.08	0.50	0.40
$\hat{d}_j$ minimum	B (flint)	-10.70	-9.02	-0.16	-0.34	0.93	0.93
$\hat{d}_j$ maximum		3.35	3.76	0.48	0.21	4.76	3.73
$\hat{d}_j$ mean		-3.38	-1.92	0.18	-0.01	2.79	2.19
$\hat{h}_i$ minimum	A (dent)	-1.61	-2.49	-0.18	-0.16	-1.72	-1.47
$\hat{h}_i$ maximum		2.76	2.00	0.12	0.13	2.43	1.98
$\hat{h}_j$ minimum	B (flint)	-2.96	-3.95	-0.15	-0.07	-2.09	-1.60
$\hat{h}_j$ maximum		2.13	2.78	0.14	0.12	1.67	1.44
$\widehat{ID}_i$ minimum	A (dent)	-4.76	-3.64	-0.28	-0.25	-0.97	-0.71
$\widehat{ID}_i$ maximum		1.07	2.34	0.12	0.06	0.98	0.73
$\widehat{ID}_j$ minimum	B (flint)	-5.35	-4.51	-0.08	-0.17	0.47	0.46
$\widehat{ID}_j$ maximum		1.67	1.88	0.24	0.11	2.38	1.86
$\widehat{GCA}_i$ minimum	A (dent)	-1.76	-3.05	-0.20	-0.12	-1.68	-1.45
$\widehat{GCA}_i$ maximum		2.52	2.79	0.12	0.17	2.40	1.94
$\widehat{GCA}_j$ minimum	B (flint)	-2.17	-3.35	-0.23	-0.13	-2.55	-1.92
$\widehat{GCA}_j$ maximum		2.73	3.34	0.15	0.16	2.06	1.71
$\hat{\mu}$	-	60.52	62.99	1.63	0.89	1.07	0.63
$\hat{\bar{h}}$	-	-3.79	-4.28	0.21	0.08	3.84	3.07
$\hat{k}$	-	-0.94	-0.84	0.09	0.02	0.56	0.44
$\hat{c}$	-	0.46	0.39	0.03	0.00	0.88	0.70

The high estimates of $\mu + a$ (Table 2) indicate that the genotypes derived from the selected lines had a high mean after self-fertilization. On the other hand, high estimates of *d* indicate the existence of a greater number of segregating loci, which will generate genetic variability among the lines in the S_∞ generation. This effect is lost during self-fertilization but manifests in the hybrids obtained from these lines (Cruz et al. 2012). Thus, it is recommended to select genotypes that associate desirable values for the estimates of additive and dominance effects, according to the desired traits. Some negative estimates for the expected means for yield traits occur because, as dominance effects are closely related to inbreeding, the values of the additive effects and means of all homozygous lines ($\mu + a$) may be underestimated (Simon et al. 2004). The estimates of dominance effects that were significant ($p \leq 0.05$) were higher than the estimates of additive effects for ear and grain yield (Table 2). These results indicate that the contribution of heterozygous loci is greater for these traits, which present greater genetic complexity in relation to other traits (Botelho et al. 2016).

The average heterosis values ($\hat{\bar{h}}$) reflect the potential of the parents of each group in hybrid combinations and indicate the superiority of the mean of the hybrids over the mean of the parents (Oliveira et al. 2004). For traits related to flowering, the manifestation of heterosis was predominant in the sense of increasing earliness (Table 2). For the other traits, heterosis increased the average number of topcross hybrids. The *k* component, which reveals the expected deviations between the means of the homozygous lines of groups A and B in relation to the mean of the two groups, was small for most traits (Table 2). The *c* component measures the deviations of topcross groups A and B in relation to the average of the two groups and presented, in general, low values.

Table 3. Estimates of $\mu + a$ for grain yield (t ha^{-1}) of synthetics of different sizes (k) from groups A (dent) and B (flint), and predicted means of the single-cross hybrid ($k = 1$) and of hybrids between synthetics ($k = 2$ to $k = 10$) formed by subsets of parents of groups A and B for the following traits: male flowering (MF – days), female flowering (FF – days), plant height (PH – m), ear height (EH – m), ear yield (EY – t ha^{-1}), and grain yield (GY – t ha^{-1})

Size (k)	Predicted means (GY) of homozygous lines		Predicted means of hybrids between lines ($k = 1$) or synthetics ($k = 2$ to $k = 10$)					
	Group A $\mu + a_{i(k)}$	Group B $\mu + a_{j(k)}$	MF	FF	PH	EH	YE	GY
1	0.56	1.18	54.19	52.94	1.96	0.98	8.91	6.99
2	1.16	1.24	54.06	53.44	1.97	0.95	8.31	6.64
3	1.01	1.42	54.69	54.68	1.86	0.92	7.70	6.04
4	0.84	1.33	54.87	55.67	1.90	0.93	7.45	5.77
5	0.74	1.11	55.53	56.47	1.94	0.98	7.51	5.78
6	0.70	0.94	55.64	56.75	1.93	0.98	7.52	5.80
7	0.55	0.98	56.04	57.09	1.92	0.99	7.33	5.63
8	0.66	1.03	56.06	57.04	1.89	0.97	7.15	5.48
9	0.59	1.02	55.99	56.99	1.89	0.98	6.99	5.36
10	0.70	0.93	55.98	57.09	1.90	0.99	7.01	5.35

Estimates of inbreeding depression for groups A ($\widehat{ID}_i$) and B ($\widehat{ID}_j$) showed wide variation for all traits (Table 2). The ear and grain yield traits showed the highest estimates of inbreeding depression. This is because the effects of dominance are more important for these traits because of their greater genetic complexity. The general combining ability estimates for groups A ($\widehat{GCA}_i$) and B ($\widehat{GCA}_j$) showed large variations between minimum and maximum values. Low GCA values indicate that the averages of the hybrids in which one parent participates do not differ significantly from the general average of the diallel (Cruz and Vencovsky 1989). On the other hand, the high estimates, both positive and negative, indicate that the population is much better or worse than the others included in the diallel in relation to the average of its hybrids.

For grain yield, when simultaneously considering the estimates of $\mu + a$, parent heterosis, inbreeding depression, and general combining ability, the line GA21 (group A) stands out. It was among the five best for all the mentioned parameters, showing that it is suitable for use in breeding programs aimed at the formation of hybrids or synthetics. For group B, line GB41 stood out, which was highlighted for the estimates despite not being among the best for the $\mu + a$ estimates.

Prediction of hybrid means

An index for the selection of parents to obtain composites or synthetics based on the effects of variety (v_i) and heterosis of varieties (h_i) was proposed by Miranda Filho and Chaves (1991). The larger the size of the composite (k), the closer the index is to the values of general combining ability ($\widehat{GCA}$). Therefore, this estimate is adequate for the selection of the best parents to obtain synthetic populations. Thus, the average predictions obtained in this work were performed by selecting ten lines from each group according to the best estimates of the general combining ability for grain yield.

As expected, the predicted means of the single-cross hybrid between the two lines with the best general combining ability in each group were higher than those of the hybrids between synthetics with two or more lines for ear and grain yield. The mean values for the other traits were similar (Table 3). This occurs because all heterosis of the two best lines is computed in the prediction of the single-cross hybrid, resulting in the manifestation of hybrid vigor, which can be increased if the two lines present high specific combining ability (Hallauer et al. 2010, Xiao et al. 2021). In general, the greater the number of lines involved in the formation of the synthetic ($k = 2$ to $k = 10$), the lower the predicted hybrid means for several traits (Table 3). Prediction of hybrid means between synthetics from different groups is important, especially when the objective of the program is the formation of base populations for reciprocal recurrent selection.

The estimates of $\mu + a$ for groups A and B decreased with an increase in the size of the synthetics (Table 3). Although the lines of group A presented lower estimates, all were adequate. This indicates that the synthetics of both groups have the potential to produce lines with good performance per se, with the aim of conducting a program of reciprocal recurrent selection.

The results indicate variability in heterosis components and general combining ability between the lines, demonstrating the feasibility of selecting parents for a hybrid breeding program or for reciprocal recurrent selection. The adaptation of the topcross method with intergroup testers (including the S_2 lines) proved to be efficient for data analysis, separately estimating additive and dominance effects. In addition, the inclusion of S_2 lines allows the estimation of inbreeding depression and the prediction of the potential of homozygous lines derived from the tested genotypes. Finally, the prediction of hybrid means allows for the selection of superior lines for the formation of synthetic populations with better yield potential when crossed.

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