

Potential of intervarietal maize hybrids from a reciprocal recurrent selection program

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Abstract: We aimed to evaluate the feasibility of intervarietal hybrids (IH) from a reciprocal recurrent selection (RRS) program and determine the optimal number of parents for creating IH. A RRS cycle was conducted, and the top 20 hybrids were selected based on full-sib (FS) evaluation results. Various numbers of S1 progenies were recombined to form improved populations A, B, C, and D. IH populations AB and CD were also created. Evaluations of the IH indicated significant genetic variance among FS progenies, suggesting variability and potential for successful selection. Heterosis estimates were higher with fewer progenies in the parent population. Combining RRS programs with IH production is promising, as it allows for the creation of superior hybrids and continued improvement of heterosis between populations.

Keywords: Zea mays, plant breeding, combining ability, grain yield, heterosis

INTRODUCTION


Advances in maize cultivation have been largely driven by the discovery and application of heterosis in breeding programs for this crop (Grigolo et al. 2021). The use of hybrids allows breeders to exploit heterosis to its full potential. Initially, the low yield of inbred lines made use of single hybrids (SHs) economically unfeasible. As a result, double hybrids became the preferred commercial option. Brazil was the second country to embrace hybrid maize cultivars, initially through the use of double-cross hybrids. In recent years, however, the cost of seeds as a percentage of total agricultural production costs has increased significantly in Brazil. While hybrid and transgenic seeds offer improved production performance, they also come with a high cost. These seeds require significant investments in research and development, as well as advanced production and treatment technologies (Galvão 2014).

An alternative approach is the use of cultivars with lower seed costs that still capitalize on the benefits of heterosis, such as intervarietal hybrids (IH). High-performing IHs can be developed through crosses between commercial SHs that are already widely utilized in maize breeding programs (Resende et al. 2020). Single hybrids with superior combining ability may be incorporated into a reciprocal recurrent selection (RRS) program, particularly to enhance heterosis and develop new lines. Additionally, these SH can be utilized to



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improve IHS through successive cycles of reciprocal recurrent selection, although this application has not yet been extensively pursued.

In the absence of references in the literature, this study aimed to evaluate the feasibility of utilizing IHS derived from populations subjected to RRS. Additionally, the study sought to determine the optimal strategy for the number of S1 progenies to recombine in order to develop high-performing IH.

MATERIAL AND METHODS

Experimental field data collection

Sites

The experiments were carried out at four locations in in Brazil, Minas Gerais state, Lavras, at the Centro de Desenvolvimento Científico e Tecnológico em Agropecuária - Fazenda Muquém (lat 21° 09' S, long 44° 58' W, alt 918 m asl); Ijaci, at the Centro de Desenvolvimento e Transferência de Tecnologia - Fazenda Palmital (lat 21° 09' S, long 44° 54' W, alt 890 m asl); Nazareno, at Fazenda Grupo G7 (lat 21° 15' 27.29" S, long 44° 30' 48.70" O , alt 935 m asl), and Lambari, on the EPAMIG experimental farm (lat 21° 58' 32" S, long 45° 20' 48" O, alt 869 m asl) (Figure 1).

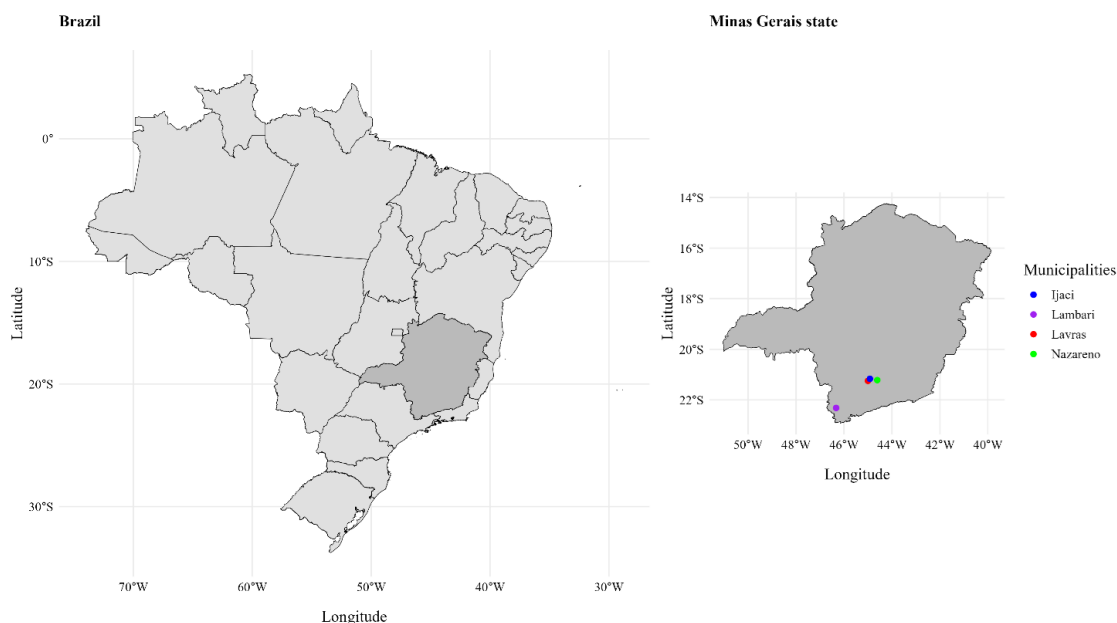


Figure 1. Sites where the experiments were conducted, Minas Gerais, Brazil.

Plant material

Four populations in Hardy-Weinberg equilibrium were used, i.e., populations A, B, C, and D, which originated from single hybrid commercial crosses. Populations A and B are not GMO (genetic modified organisms), and populations C and D are transgenic cultivars, RR (roundup ready) and BT (*Bacillus thuringiensis*). In populations A and B, seven cycles of RRS have already been performed; however, populations C and D have not yet been subjected to RRS. To assess the populations and obtain the progenies, a procedure similar to that presented by Reis et al. (2012) was used.

Full-sib and S1 progenies obtaining

To obtain the progenies for the RRS program, each pair of the A, B populations or C, D populations was initially sown in two contiguous areas under irrigation outside the normal maize crop season for the region. At flowering time,

prolific plants were identified. Thus, S1 and full-sib (FS) progenies were obtained from each plant. FS corresponded to the descendants resulting from the crosses between individuals from population A and B as well as from the crosses between populations C and D. Ninety-six (96) progenies were obtained from the A and B populations with S1 from the same plant. For the C and D populations, 45 FS progenies with corresponding S1 were obtained.

In January 2019, the AB and CD FS evaluation experiments were carried out in two sites: Lavras and Nazareno (MG-Brazil). A triple lattice experimental design was adopted, one being 10×10 (96 progenies + 4 controls) and the other 7×7 (45 progenies + 4 controls). The respective populations and the commercial hybrids DKB 230 PRO3 and SHS 4070 were used as controls. The plots consisted of a three-meter line, 0.60 m apart and 0.25 m between plants, with each plot containing 12 plants after thinning. The following traits were evaluated: i) plant height, in centimeters; ii) first ear height, in centimeters; and iii) grain yield. After standardizing grain moisture to 13%, yield was defined as kg ha^{-1} . Individual analysis was performed for AB and CD populations.

Recombination

Recombination was done manually by crossing the plants two by two. Different numbers (one, two, five, ten, fifteen, and twenty) of S1 progenies were recombined, aiming to obtain intrapopulation (AB or CD). Simultaneously, hybrids derived from them were obtained. That way, six intrapopulations of A or B and six IH (AB) were obtained. The same numbers of intrapopulations were obtained from the C and D populations.

Intervarietal hybrids evaluation

Six AB hybrids (IH) were evaluated. In the field trial, ten treatments were evaluated, including the six hybrids, the intrapopulation from the last RRS cycle (obtained by intercrossing the twenty best progenies) and two commercial hybrids as controls (DKB 230 PRO3 and RB 9077). The same procedure was adopted for the C and D populations. The AB or CD experiments were carried out in a contiguous area, adopting a completely randomized block design with three replicates in the spring-summer crop season of 2020/2021 in four sites: Lavras, Nazareno, Ijaci, and Lambari, in the state of Minas Gerais, Brazil.

To estimate the heterosis of the hybrids, another experiment was conducted in the 2020/2021 crop season in Lavras, MG. A completely randomized block design (CRBD) was adopted, with six replicates, with plots consisting of two 4-meter rows in four contiguous areas as follows: i) composed of the AB hybrids (IH); ii) composed of A and B parental lines obtained by recombination in different proportions (one, two, five, ten, fifteen, and twenty; iii) composed of the CD hybrids (IH); and iv) composed of C and D parental lines.

Statistical analysis

Full-sib progenies analysis

Individual analyses were performed using a mixed model, considering progenies and blocks as random effects and replicates as fixed effects, according to model 1:

$$y_{ijk} = \mu + p_i + r_j + b_{k(j)} + e_{ijk} \quad (1)$$

where,

y_{ijk} : observation referring to progeny i , in repetition j , in block k ;

μ : general constant associated with all observations;

p_i : random effect of progeny i ;

r_j : fixed effect of repetition j ;

$b_{k(j)}$: random effect of block k within repetition j ;

e_{ijk} : random experimental error associated with observation y_{ijk} .

Joint analysis was performed using the model 2. The 20 best FS progenies of both populations were identified, according to model 2:

$$y_{ijkl} = \mu + p_i + r_{j(l)} + b_{k(jl)} + a_l + (ta)_{il} + e_{ijkl} \quad (2)$$

where,

y_{ijkl} : observation referring to progeny i , in repetition j , in block k , in environment l ;

μ : general constant associated with all observations;

p_i : random effect of progeny i ;

$r_{j(l)}$: random effect of repetition j within environment l ;

$b_{k(jl)}$: random effect of block k within repetition j in environment l ;

a_l : fixed effect of environment l ;

$(ta)_{il}$: random effect of the progeny x environment interaction;

e_{ijkl} : random experimental error associated with observation y_{ijkl}

Intervarietal hybrids analysis

Data from each location of the interpopulation full sibling progenies were subjected to joint AB and CD analysis (Pimentel-Gomes 2009), according to model 3:

$$y_{ijl} = \mu + t_i + r_{j(l)} + a_l + (ha)_{il} + e_{ijl} \quad (3)$$

where,

y_{ijl} : observation regarding treatment i , in repetition j , in environment l ;

μ : general constant associated with all observations;

t_i : fixed effect of treatment i ;

$r_{j(l)}$: random effect of repetition j within environment l ;

a_l : fixed effect of environment l ;

$(ha)_{il}$: fixed effect of the hybrid x environments interaction;

e_{ijl} : random experimental error associated with observation y_{ijl} .

Heterosis estimates

The grain yield data (kg ha^{-1}), corrected to 13% moisture content, were subjected to analysis of variance according to model 4:

$$y_{ij} = \mu + t_i + r_j + e_{ij} \quad (4)$$

where,

y_{ij} : observation of the plot that received treatment i in reproduction j ;

μ : general constant associated with all observations;

t_i : fixed effect of treatment i ;

r_j : random effect of repetition j ;

e_{ij} : random experimental error associated with observation y_{ij} .

The heterosis was estimated using the following estimator: $h = \left[F_1 - \left(\frac{P_1 + P_2}{2} \right) \right]$, where F_1 is the average mean of the IH; P_1 is the average of parental lines 1 (Population A or Population C), from the respective IH; P_2 is the average of parental lines 2 (Population B or Population D), from the respective IH.

Analyses for this experiment and the others previously reported were done using the R software (R Development Core Team 2020). The Scott-Knott's (1974) test with a significance level of $p < 0.05$ for mean comparisons was applied. To carry out the test, the partition into two groups with k_1 and k_2 that maximizes the SS (sum of squares) between groups β_0 was first determined in the treatments according to model 5:

$$\beta_0 = \left(\frac{T_1^2}{k_1} + \frac{T_2^2}{k_2} \right) - \frac{(T_1 + T_2)^2}{k_1 + k_2} \quad (5)$$

where,

T : sum of the means in group, $T_1 = \sum_{i=1}^{k_1} \bar{y}_{(i)}$ and $T_2 = \sum_{i=k_1+1}^{k_2} \bar{y}_{(i)}$

K : number of averages in group g , $g = 1, 2$.

Subsequently, it continued with the calculation of the maximum likelihood estimator σ^2 , according to model 5.1:

$$\hat{\sigma}_0^2 = \frac{[\sum_{i=1}^{k_1} (\bar{y}_i - \bar{y})^2 + \nu s^2]}{k + \nu}; s^2 = \frac{MS_E}{n} \quad (5.1)$$

where,

ν : error degrees of freedom;

n : number of observations in treatments (or blocks);

\bar{y}_i : average of treatment k ;

\bar{y} : average of all treatments involved in the comparison.

Next, the λ Test statistics were calculated for the partition that maximized β_0 (model 5.2)

$$\lambda = \frac{\pi}{2(\pi-2)} * \frac{\beta_0}{\hat{\sigma}_0^2} \quad (5.2)$$

if $\lambda > \chi_{\alpha}^2, \frac{K}{(\pi-2)}$, there is evidence to reject the null hypothesis, that is, evidence that the two subgroups differ.

Variation estimation

The variance components were estimated using Restricted Maximum Likelihood (REML) and the estimated significance was evaluated with the Likelihood Ratio Test (LRT) at the 0.05 significance level.

Heritability estimative

Heritability was estimated according to Cullis et al. (2006), using model 6:

$$hc^2 = 1 - \frac{\nu BLUP}{2\sigma_G^2} \quad (6)$$

where,

$\nu BLUP$: mean variance of a difference of two BLUPs for the genotypic effect;

σ_G^2 : Genetic variance.

Accuracy estimation

Accuracy (Resende and Duarte 2007).

$$r_{gg} = \sqrt{1 - \frac{PEV}{\sigma_G^2}} \quad (7)$$

where,

PEV : Prediction error variance of BLUP;

σ_G^2 : Genetic variance.

RESULTS AND DISCUSSION

Selective accuracy r_{gg} estimates ranged from 59.2 to 91.1% in individual data analysis (Table 1). In the joint analysis,

Table 1. Estimates of genetic and phenotypic parameters for the grain yield, plant height and first ear height (Ear) traits. Data for the AB and CD progenies at the Nazareno and Lavras and joint analyses in Brazil, Minas Gerais state

Nazareno	Grain yield (kg ha ⁻¹)		Plant height (cm)		Ear (cm)	
	AB	CD	AB	CD	AB	CD
$\hat{\sigma}_{gp}^2$	1074224**	1024362.7**	83.3 ***	83.3***	66.9***	47.4***
$\hat{\sigma}_{ep}^2$	1260156.6	1279837.1	170.3	133.5	119.9	119.8
H_c^2	0.68	0.71	0.58	0.65	0.60	0.60
r_{gg} %	84.9	84.3	76.8	80.6	78.8	79.4
Lavras	Grain yield (kg ha ⁻¹)		Plant height (cm)		Ear (cm)	
	AB	CD	AB	CD	AB	CD
$\hat{\sigma}_{gp}^2$	1408060.9**	780899.2**	113.7***	33.7	77.3***	28.5*
$\hat{\sigma}_{ep}^2$	862235.7	768629.7	288.4	187.9	140	95.7
H_c^2	0.79	0.70	0.51	0.33	0.60	0.46
r_{gg} %	91.1	84.3	73.5	59.2	78.8	68.6
Joint analyses	Grain yield (kg ha ⁻¹)		Plant height (cm)		Ear (cm)	
	AB	CD	AB	CD	AB	CD
$\hat{\sigma}_{gp}^2$	165197.1*	620804.1	69.2***	68.1**	53.4***	42.9*
$\hat{\sigma}_{GxA}^2$	80248.84	277979.6*	29.9	37.7	18.1*	16.5
$\hat{\sigma}_{ep}^2$	1063961.58	1067435.2	229.5	105.7	131.5	61.6
r_{gg} %	91.7	81.24	75.5	84.9	79.4	85.4
H_c^2	0.81	0.65	0.55	0.70	0.55	0.65

$\hat{\sigma}_{gp}^2$ – residual variance; $\hat{\sigma}_{GxA}^2$ – variance in the genotype × environment interaction; $\hat{\sigma}_{ep}^2$ – environmental variance; H_c^2 – heritability; r_{gg} % – accuracy; *** significant at 0.1% probability, maximum likelihood ratio test; * Significant at 5% probability, maximum likelihood ratio test.

from 75.5 to 91.7%, with the lowest magnitude obtained for plant height with the hybrid AB. For grain yield, rgg estimates ranged from 84.26 to 91.1%, considered high to very high (Resende and Duarte 2007).

The average grain yield of the FS progenies from the AB population, considering the two locations, ranged from 5580 kg ha⁻¹ to 11460 kg ha⁻¹. For population CD, the variation observed was smaller, only 5.4% between limits (Figure 2). Regardless of site, the average grain yield for the FS progenies from the AB population (7994.55 kg ha⁻¹) was 17.25% higher than that for those from the CD population (6817.96 kg ha⁻¹).

For plant height, the phenotypic means ranged from 242 cm to 270 cm in AB progenies and from 212 cm to 249 cm in CD progenies. The average first ear height values for the AB progenies, in turn, ranged from 110 cm to 138 cm. The CD progenies had first ear height values from 101 cm to 126 cm (Figure 2).

The variance of the genotype × environment interactions was significant only for first ear height of the AB progenies, and for the most part, the response of the FS progenies coincided in both environments (Table 1). From the heritability estimates (H_c^2), the existence of genetic variability and the possibility of success from selection can be inferred. For grain yield, considering the joint analysis, the H_c^2 estimates were higher for the AB population than for the CD population.

Intervarietal hybrids may show greater heritability, especially when considering the genetic contribution of the parents. In the joint analysis, the AB population had an H_c^2 of 0.81, which is considered high (Resende and Duarte 2007). Carvalho et al. (2017) reported a difference in the estimated strict-sense heritability between female and male parents for maize production components. However, it is important to note that the present study did not employ any specific criteria for selecting the female parent.

In general, estimates of heterosis among IH with different numbers of parents suggest that the highest heterosis values were always obtained when the smallest number of S1 progenies was used to constitute the parental population of the IH, as previously mentioned (Figure 3). A possible explanation for this is that with a smaller number of S1 progenies, there is a more intense and specific selection of the best genotypes to constitute the hybrid's parents. As a result, there may be a greater genetic contrast between the selected parents, providing an increase in hybrid vigor in the resulting progenies (Hallauer and Miranda 1988).

The h estimates of the hybrids from the AB population were of greater magnitude than those from the CD population, regardless of the number of parents involved. In fact, some h estimates were negative for the CD population. These findings corroborate the fact that the estimates of heterosis depend on and are directly related to the studied populations.

Joint analysis of the four sites, considering data from combined analyses of the two populations, showed a significant difference between the adjusted treatments means. The same was observed for the treatment \times location interaction (data not shown). Using the averages of the four environments, the treatments were classified into four groups using the Scott-Knott (1974)'s test (Figure 3). The performance of population C, *per se*, is noteworthy; and its performance averages are among the best. The widely used commercial hybrid RB 9070 was included in the same group. This result shows that even a population derived from a single cross hybrid, after reaching equilibrium, performs as well as good commercial hybrids.

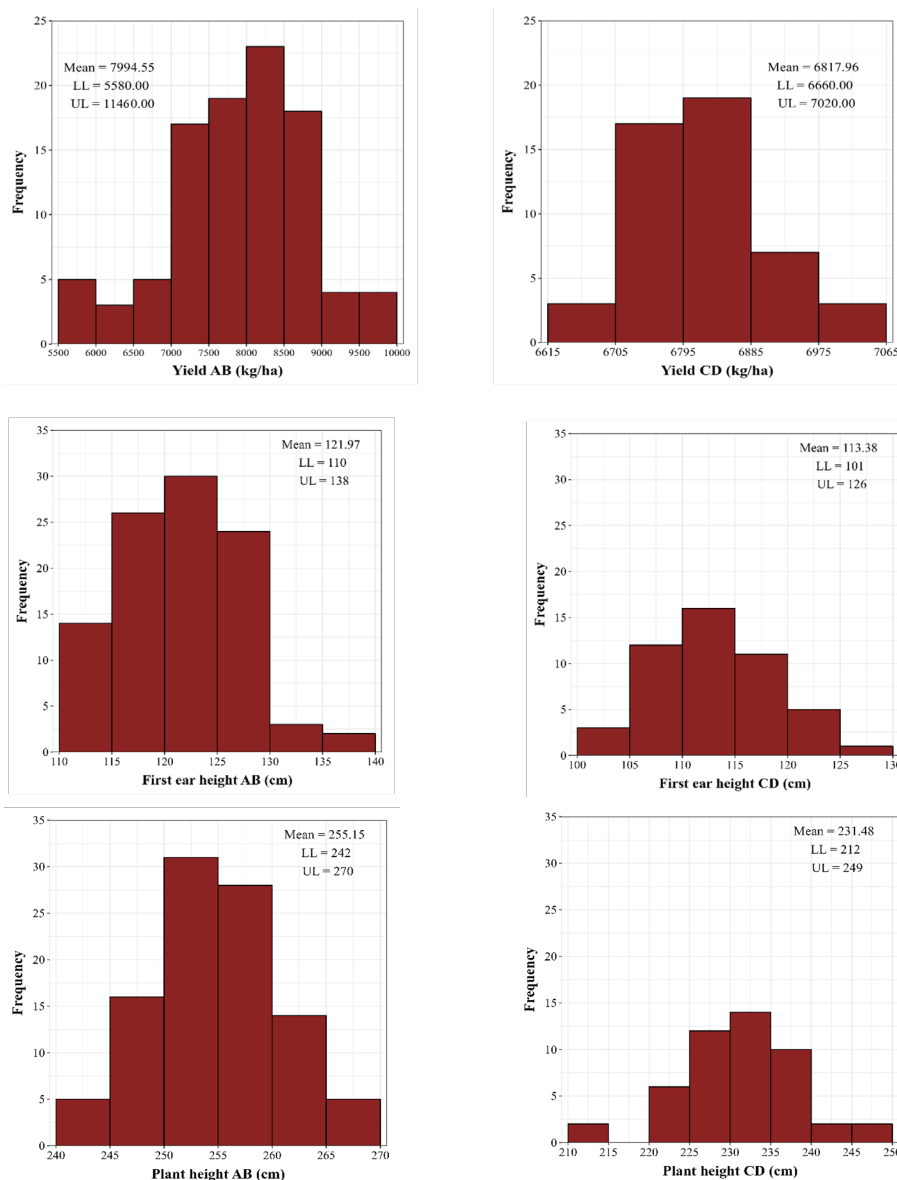


Figure 2. Frequency distribution for BLUP means, lower limit (LL), and upper limit (UL). Data for the AB and CD progenies in joint analysis of Lavras, MG, and Nazareno, MG, Brazil.

Considering the averages of four sites, the six types of IH from AB were classified in the same group; that is, the grain yields of the IH were not significantly affected by the number of parents (S1s) that gave rise to each population. However, it is important to point out that the average yield of the six IHs in AB was 9119.6 kg ha⁻¹, and the average of the two populations (A and B) of the CVII cycle was 7037.1 kg ha⁻¹ (Figure 3). These values indicate that the average yield of the IHs was 22.8% higher than that of the populations that gave rise to the hybrids. The six IHs of the AB population were classified in the same group as the commercial hybrid DKB 230 PRO3. The effect of the number of parents involved in obtaining the six IH of the CD population differed from that in AB. However, the IHs obtained with 1, 2, or 4 parents were also in the same group as DKB 230 PRO3.

To accelerate the RRS cycle, the parental populations were sown in July/August, outside the normal maize growing season in the region, to obtain the FS and S1 progenies. Under those conditions, it was difficult to meet all the water needs of the maize crop, even using irrigation, due to the low relative humidity of the air, especially in the first two months after sowing. Other stresses can occur due to abnormal temperatures at different stages of the crop. Thus, even if the plants are more widely spaced, it is difficult to obtain two ears per plant and simultaneously produce S1

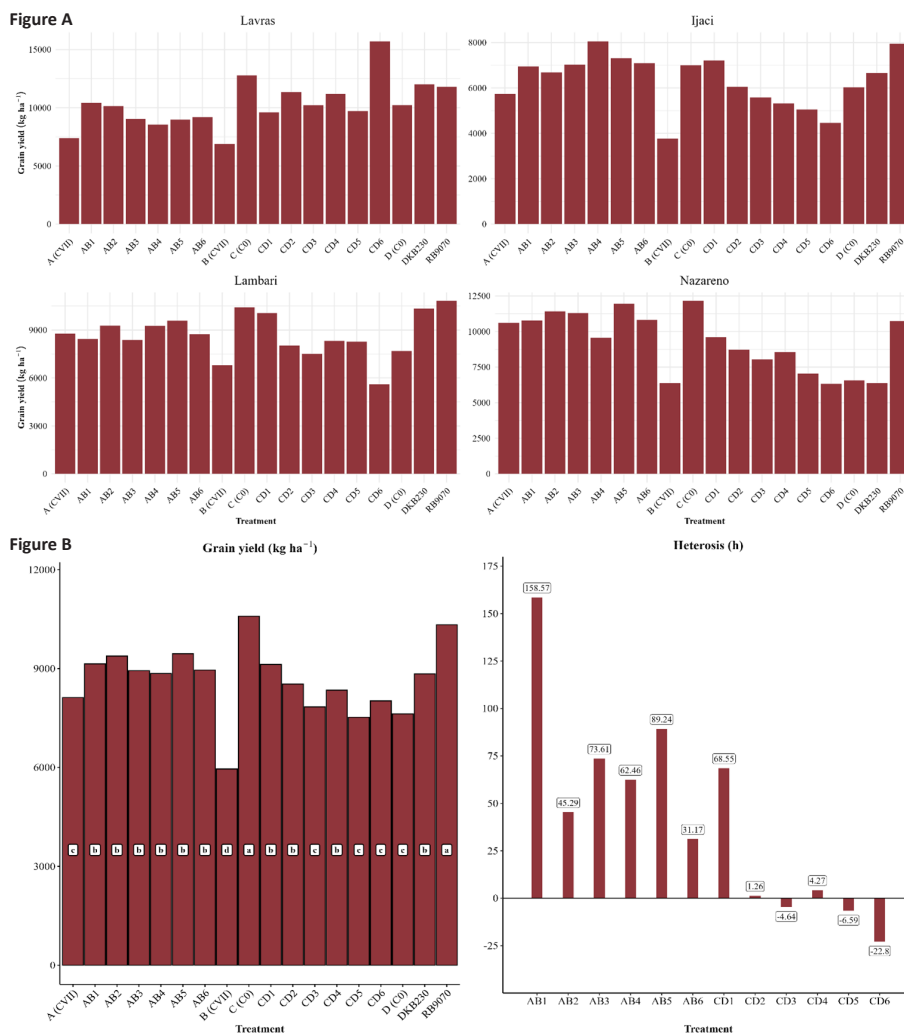


Figure 3. Phenotypic means and heterosis for grain yield in kg ha⁻¹. Data for hybrids IH obtained from populations A, B, C, and D at sites in Lavras, Ijaci, Lambari and Nazareno in Brazil, Minas Gerais state. Figure A shows means for site and Figure B shows overall mean of treatment heterosis. Means followed by the same letter belong to the same group by the Scott-Knott test ($p < 0.05$).

and FS progenies. Even so, for the AB population, 96 progenies were obtained. However, in CD this number was lower (45). The results obtained showed that the FS derived from populations C and D had inferior performance in grain yield compared to populations A and B.

As mentioned, populations A and B were subjected to seven cycles of recurrent selection, whereas C and D were not yet. This fact highlights the efficiency of repeated cycles of selection and recombination (Xue et al. 2017). For characteristics controlled by many genes and strongly influenced by the environment, the recurrent selection arises as an excellent alternative for obtaining consistent gains in long-term selection and maintaining variability in the population (Soares et al. 2020).

Considering the two sites and grain yield, the average grain yield at Nazareno was higher than that obtained at Lavras. This difference is notable despite the fact that the Nazareno experiment was not irrigated, unlike the Lavras experiment. However, in Nazareno, frequent fog may have met the daily moisture needs. Additionally, the Nazareno experiment was conducted in an area with potentially greater availability of macro- and micronutrients, as well as soil cover, which likely improved moisture and water retention in the soil (Peixoto et al. 2018).

The estimates obtained from AB populations, both for the original cycle (C0) and for CIII, confirmed the existence of genotypic variation among the FS progenies (Raposo and Ramalho 2004, Reis et al. 2012). Other studies carried out in Brazil confirm the maintenance of genetic variability even after repeated cycles of selection and recombination (Chen et al. 2019), corroborating the results of the present study.

In the case of population A and B, estimates of genetic parameters were obtained for C0 (Raposo and Ramalho 2004) and CIII (Reis et al. 2012). The estimates of H_c^2 reaffirm the existence of variability; on the other hand, Raposo and Ramalho (2004) and Reis et al. (2012) found that the estimate of H_c^2 was of lower magnitude than that observed in this study. However, it must be emphasized that the trait considered was husked ear weight and the accuracy in evaluating the experiments was lower than in this study.

The main focus of this study was to determine the optimal number of progenies to include in the parents for producing intervarietal hybrids. In evaluating these IHs, emphasis was placed on grain yield, excluding plant height and first ear insertion height. Taking as reference the six types of IHs from both A and B, as well as C and D, it is clear that IHs involving only one parent, in absolute value, showed higher grain yield than the others. However, considering the four environments, the average IHs of the AB populations were classified in the same group, regardless of the number of parents involved. Raposo and Ramalho (2004) and Reis et al. (2012) also demonstrated significant divergence between populations A and B, indicating great heterosis.

The four populations used in the present study are derived from commercial single crosses (SH) widely used in the region. Some combinations of SH from different companies show heterosis when crossed, as observed by Reis et al. (2012), which confirms the results previously discussed in this study. Under these conditions, the use of two populations derived from SH, with significant heterosis between them, is ideal for a RRS program, whose main objective is to increase the heterosis between the two populations (Baretta et al. 2019), as observed in the AB population.

Considering the results obtained in this study, seed production comparisons can be made. For example, if a yield of 2.0 t ha⁻¹ is considered for the female line of the SH, for the female parent of the IH (that is for a population in H&W equilibrium), a yield at least 20% greater than the previous yield should be considered. Furthermore, a breeding program aimed at obtaining IH is less expensive than a breeding program of hybrids obtained from lines, since the time and cost of selecting and obtaining IH are lower. Thus, in tropical regions, where climatic adversities are frequent (Andrea et al. 2019), the use of IH provides an interesting alternative (Baretta et al. 2019).

According to Paterniani and Denucci (2022), the high cost of hybrid seeds results from investments in research and development, complex production processes, multinational market dominance, and limited conventional cultivar options, which leaves farmers with few affordable alternatives.

The obtaining of IH is completely independent of continuation of the recurrent selection program. For instance, every three RRS cycles, a new IH could be created using data from the FSs of the latest RRS cycle, allowing periodic improvements in heterosis. These IH can be produced at a lower cost than hybrids from inbred lines, making IH especially

suitable for high-risk cropping conditions, common in various sowing times across Brazil (Baretta et al. 2019).

Unfortunately, no studies report the number of progenies for obtaining parents to synthesize IH, though there is solid theoretical basis using average forecasting (Vencovsky and Barriga 1992). Reports exist on the number of $S_{0:1}$ progenies for recombination in each cycle to maintain effective population size in RRS (Vieira et al. 2021). Additionally, there is information on variability exploited in hybrid selection at different inbreeding levels (Resende 2015), with variance given by the following equation:

$$VHI = \frac{1}{4}(1+F)V_{A12} + \frac{1}{4}(1+F)V_{A21} + \frac{1}{4}(1+F)^2V_{D12} \quad (7)$$

where V_{A12} and V_{A21} are the interpopulation additive genetic variances, having parents 1 and 2 as references; V_D is the interpopulation dominance variance; and F is the inbreeding coefficient referring to the plant that gave rise to the hybrid parent.

For example, in this study, the intercrossing of $S_{0:1} \times S_{0:1}$ plants was carried out. In this situation, the inbreeding coefficient is not from S1, but from S_0 , that is, $F = 0$. Thus, considering $V_{A12} = V_{A21}$, the variance exploited for selection between $S1 \times S1$ would be $V_{H_{S1 \times S1}} = \frac{1}{2}V_{A12} + \frac{1}{4}V_{D12}$. If, for example, $S_2 \times S_2$ parents were used, the inbreeding coefficient would be $F = 1/2$ (reference generation S1), resulting in $V_{H_{S2 \times S2}} = \frac{3}{4}V_{A12} + \frac{1}{2}V_{D12}$. When considering completely inbred lines, $F = 1$, for example, then $V_{HL} = V_{A12} + V_{D12}$; that is, all possible genetic variance would be used.

Notice that $S_2 \times S_2$ hybrids would be a better option than $S1 \times S1$ hybrids, as they would exploit 75% of the variation regarding the use of inbred lines. The strategy to obtain $S2 \times S2$ hybrids from an RRS program would be to obtain FS from the descendants of S1 plants from the two self-fertilized populations (A and B). The best hybrids would be identified from evaluations of the FSs, as done in the present study. It is evident that, as inbreeding increases, the variation that is available becomes closer to that obtained involving lines. However, the lower the level of inbreeding of the parents, the lower the uniformity of the plants of the hybrid cultivar under the growing conditions. It is important to emphasize that, although less variability is exploited in parents with a lower level of inbreeding, it is possible to obtain IH (non-inbred relatives) with yields similar to those of the hybrid lines, as confirmed by the results of the present study.

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DATA AVAILABILITY

The datasets generated and/or analyzed in this study are available from the corresponding author upon reasonable request.

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