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Scientific Article

Genetic potential of maize populations derived from commercial hybrids for interpopulation breeding

Potencial genético de populações de milho derivadas de híbridos comerciais para o melhoramento interpopulacional

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ABSTRACT – Our objective was to evaluate the genetic potential of two maize populations derived from commercial hybrids for beginning a reciprocal recurrent selection (RRS) program. For this, 280 interpopulation half-sib (HS) progenies were produced from two populations (140 HS from each population), which were derived from the selfing of the commercial hybrids AS1598 (Pop1) and RB9210 (Pop2). We then evaluated the 280 HS progenies, the two base populations, and the two hybrids for grain yield (GY) and ear and plant architecture traits in southwestern Goias during the 2020 winter season. Variance components and genetic values of each progeny were estimated using the REML/BLUP (Restricted Maximum Likelihood/Best Linear Unbiased Prediction) methodology. Genetic gains by selection of the top 20% of progenies were predicted using two strategies: i) selection for GY and ii) selection for GY and days to silking (DTS) simultaneously. We observed genetic variability in both populations for all tested traits; therefore, it is possible to obtain genetic gains from the interpopulation improvement of both Pop1 and Pop2. The genetic gain estimates with the selection based on GY were 9.03 and 3.45% for Pop1 and Pop2, respectively. Simultaneous selection for GY and DTS resulted in positive (>4%) genetic gains for GY in both populations and decreased the cycle in Pop1, but we did not observe any alteration of the cycle in Pop2. We concluded that both populations derived from commercial hybrids have genetic potential for interpopulation improvement using RRS.

Keywords: *Zea mays* L. Genetic Parameters. Selection Index. Reciprocal Recurrent Selection.

RESUMO – O objetivo deste trabalho foi avaliar o potencial genético de duas populações de milho derivadas de híbridos comerciais para iniciar um programa de seleção recorrente recíproca (SRR). Para isso, 280 progênies de meios-irmãos (PMI) interpopulacionais foram obtidas de duas populações (140 PMI de cada população) derivadas da autofecundação dos híbridos comerciais AS1598 (Pop1) e RB9210 (Pop2). As 280 PMI, as duas populações e os dois híbridos foram avaliados para produtividade de grãos (PG) e seis caracteres de arquitetura de planta e de espiga em dois locais no Sudoeste de Goiás, na segunda safra de 2020. Os componentes de variância e os valores genéticos de cada progênie foram estimados pela metodologia REML/BLUP (*Restricted Maximum Likelihood/Best Linear Unbiased Prediction*). Os ganhos genéticos com a seleção de 20% das progênies superiores foram preditos usando duas estratégias: i) seleção truncada para PG e ii) seleção simultânea para PG e florescimento feminino (FF). Observou-se variabilidade genética nas duas populações para todos os caracteres avaliados. Consequentemente, é possível obter ganhos genéticos a partir do melhoramento interpopulacional das Pop1 e 2. As estimativas de ganhos com a seleção truncada para PG foram de 9,03% e 3,45% para as Pop1 e Pop2, respectivamente. A seleção simultânea para PG e FF resultou em ganhos positivos (>4%) para PG em ambas populações e redução no ciclo na Pop1, mas não houve alteração para ciclo na Pop2. Conclui-se que as duas populações derivadas de híbridos comerciais de milho têm potencial genético para o melhoramento interpopulacional com emprego de SRR.

Palavras-chave: *Zea mays* L. Parâmetros Genéticos. Índice de Seleção. Seleção Recorrente Recíproca.

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INTRODUCTION

Maize is a cereal extensively adapted to a variety of environments and used for various purposes. Notably, it plays a crucial role in human and animal nutrition, along with its contribution to fuel production (MORÔ; FRITSCHE-NETO, 2017). Brazil is the world's third largest maize producer and the second largest exporter (ERENSTEIN et al., 2022). During the 2021/2022 growing season, Brazilian maize production reached 112.81 million metric tons of harvested grain across 21.60 million hectares (CONAB, 2022). Approximately 37.00 million metric tons of this volume were exported, mainly to Vietnam, Iran, Japan, and Egypt. Currently, maize hybrids derived from crossing among inbred lines account for approximately 90% of the maize production area of Brazilian maize farmers (FRITSCHE-NETO; MÔRO, 2017). Consequently, both public and private maize breeding programs target their efforts toward the development of hybrids, specifically single and triple crosses.

Inbred lines have been developed through generations of recurrent selfing and/or haploid induction (GUIMARÃES et al., 2018; CHAIKAM et al., 2019). These lines are derived from different germplasm sources, such as synthetics and biparental populations derived from elite lines within each heterotic group, composites, open-pollinated varieties, and advanced generations of commercial hybrids (HALLAUER; CARENA; MIRANDA FILHO, 2010; GUIMARÃES et al., 2018). In Brazil, commercial hybrids serve as the primary germplasm source for the development of new lines in many breeding programs (GUIMARÃES et al., 2018; TREVISAN, 2018). Due to their development from crossing among elite inbred lines and extensive exposure to high selection pressure by farmers, they exhibit a high frequency of favorable alleles for many agronomic traits and, consequently, contain a high concentration of alleles ‘adapted’ to diverse environmental conditions. Therefore, commercial hybrids have been used with great success in the development of base populations and, consequently, new inbred lines and hybrids (OLIBONI et al., 2013; SENHORINHO et al., 2015; TOLENTINO et al., 2017; FARIA et al., 2022).

Populations derived from commercial hybrids are constituted by a mixture of germplasm from different origins, thereby presenting a highly complex genetic background (TREVISAN, 2018; FARIA et al. 2022). Consequently, they must be allocated into divergent groups to explore the non-additive effects of crossing them and to develop well-defined heterotic groups (HALLAUER; CARENA; MIRANDA FILHO, 2010; VIANA et al., 2013; SOUZA JÚNIOR, 2018). The clustering of populations derived from commercial hybrids has been carried out based on the specific combining ability effects of grain yield (GY) estimated from the diallel mating of commercial hybrids or their advanced generations (OLIBONI et al., 2013; TOLENTINO et al., 2017; COELHO et al., 2020). Subsequently, those with a higher frequency of favorable and divergent alleles have been used as base populations in reciprocal recurrent selection (RRS) programs, aiming to increase heterosis and crossing between them and to develop elite lines that exhibit high genetic complementation in crosses and high-yielding hybrids derived from these interpopulation lines (RAPOSO; RAMALHO; RIBEIRO, 2004; REIS et al., 2009; 2013; SOUZA JÚNIOR, 2018; KOLAWOLE et al., 2019). Nevertheless, populations derived from a single commercial hybrid have a narrow genetic base, and it is essential to monitor their genetic variability during RRS cycles to prevent genetic narrowing (inbreeding) and, consequently, the absence of genetic gains in initial cycles. Moreover, although RRS has been proposed to improve the crossing between two populations with a broad genetic base, it is successfully applicable in the interpopulation improvement of populations with a narrow genetic base (REIS et al., 2009; 2013).

Considering the foregoing, the objective of our study was to evaluate the genetic potential of two maize populations derived from commercial hybrids to begin a RRS program.

MATERIALS AND METHODS

Genetic materials

Two base maize populations derived from the advanced generation of two commercial hybrids, AS1598 (Pop1) and RB9210 (Pop2), were used. These two populations were selected based on their performance in crosses and the genetic divergence manifested between them from a pool of 13 populations (COELHO et al., 2020). They were employed to begin a RRS program based on interpopulation half-sib (HS) progenies (HALLAUER; CARENA; MIRANDA FILHO, 2010; SOUZA JÚNIOR, 2018). The phase of obtaining interpopulation HS progenies was carried out in the Genetic Resources field at the Federal University of Jataí between August and December 2019. Additionally, prolific plants were used in each population, as the first ear was pollinated with pollen from the other population to produce interpopulation HS progenies (selection unit), and the second ear was selfed and constituted the recombination unit. A total of 140 interpopulation HS and 140 S_1 inbred progenies were obtained from each population.

Experimental procedure

The 140 interpopulation HS progenies of each population, along with AS1598 and RB9210 single crosses and the two base populations, were evaluated between February and July 2020 (second season) at two locations in southwestern Goiás State, Brazil. The evaluation sites were the experimental station of the Federal University of Jataí – environment 1 (17°52’53” S, 51°42’52” W, and altitude of 696 m) and a farm located 10 km from the city of Jataí, GO – environment 2 (17°51’46” S, 51°38’51” W, and altitude of 808 m).

In all environments, the trial was laid out in a randomized complete block with three replications. Each plot consisted of a row of 4 m, with rows spaced at 0.90 m apart. Approximately 25 days after sowing, thinning was carried out in the plots to stands of 61 thousand plants per hectare. In both environments, the experiments were on under no-tillage conditions. Fertilizer rates and other agricultural practices were performed following the technical recommendations for maize farming in the region.

Trait measurements

We measured the following traits: days to pollen (DTP, days), days to silking (DTS, days), plant height (PH, cm), ear height (EH, cm), ear length (EL, cm), ear diameter (ED, mm), and grain yield (GY, kg ha^{-1}). GY data were adjusted to 13% moisture.

Statistical analysis

Variance components and breeding values of each progenies were estimated using the REML/BLUP (Restricted Maximum Likelihood/Best Linear Unbiased Prediction) framework with the “lme4” (BATES et al., 2015) and “lmerTest” (KUZNETSOVA; BROCKHOFF; CHRISTENSEN, 2017) packages in the R software. The genetic parameters and BLUP were estimated and predicted, respectively, by environment and based on the means of the two environments. Thus, the phenotypic values were modeled according to Equations 1 (individual analysis) and 2 (joint analysis), as follows: $y_{ij} = \mu + g_i + b_j + \varepsilon_{ij}$ (1); and $y_{ijk} = \mu + g_i + E_k + b/E_{jk} + gl_{ik} + \varepsilon_{ijk}$ (2), where μ is the overall mean; g_i is the genotype effect, which was split into the random effects of progenies and fixed effect of checks; b_j is the random block effect; E_k is the fixed effect of environments; b/l_{jk} is the random block effect within an environment; gl_{ik} is the random effect of genotype × environment interaction; and ε_{ijk} is the random effect of error. Random effects were tested using the likelihood ratio test with 1 degree of freedom, and fixed effects were tested based on the F-test.

Estimates of the heritability coefficients on a progenies-mean basis were estimated according to the following equation (HALLAUER; CARENA; MIRANDA FILHO, 2010): $h_{\bar{x}}^2 = \frac{\hat{\sigma}_G^2}{\hat{\sigma}_G^2 + \frac{\hat{\sigma}_{GE}^2}{E} + \frac{\hat{\sigma}^2}{rE}}$, where $\hat{\sigma}_G^2$ is the estimate of the genetic variance component; $\hat{\sigma}_E^2$ is the estimate of the progenies × environment interaction variance component; $\hat{\sigma}^2$ is the estimate of the error variance component; and E and r correspond to the number of environments and replicates, respectively. The coefficient of experimental variation was calculated according to the following equation: $CV\,(\%) = 100\,\frac{\sqrt{\hat{\sigma}^2}}{\bar{x}}$, where $\hat{\sigma}^2$ is the estimate of the residual variance; and $\bar{x}$ is the mean of the progenies. Additionally, Pearson correlations between the traits were estimated using BLUP. The correlations were estimated with the aid of the "agricolae" package implemented in the R software.

Genetic gains

In both populations, 20% of the superior progenies (28 progenies from each population) were selected using two selection strategies: truncated selection for GY and simultaneous selection for GY and DTS, based on the FAI-BLUP index proposed by Rocha, Machado, and Carneiro (2018). It consists of a multi-trait index based on factor analysis and ideotype-genotype distance. To establish the ideotype, the maximum genotypic values for GY and the genotypic mean for DTS were set. When GY presented a significant ($P<0.05$) progeny × environment interaction variance component ($\hat{\sigma}_{GE}^2$), the BLUP of the evaluated trait in different environments was considered a new trait to capitalize on the genotype × environment interaction in the improvement of populations. The genetic gain with the selection of superior progenies was calculated in each population based on the following equation (FALCONER; MACKAY, 1996; HALLAUER; CARENA; MIRANDA FILHO, 2010): $GS\% = c * \left(\frac{DS}{\mu}\right) * 100$, where μ is the population mean, DS is the selection differential, expressed as the deviation of the mean value of the selected progenies from the population mean, and c is the parental control. This was set to one (c=1) because HS progenies were used as the selection unit, and S_1 progenies were used as the recombination unit in the improvement of populations (SOUZA JÚNIOR, 2018).

The predicted gain in the interpopulation hybrid, considering trait GY, was calculated based on the following equation (HALLAUER; CARENA; MIRANDA FILHO, 2010; SOUZA JÚNIOR., 2018): $RSH_{(12)} = \frac{i_1 c \hat{\sigma}_{G12}^2}{\hat{\sigma}_{F12}} + \frac{i_2 c \hat{\sigma}_{G21}^2}{\hat{\sigma}_{F21}}$, where: i_1 and i_2 are the standardized selection differentials applied to the interpopulation progenies from populations 1 and 2, which were 1.4 (20%) for both populations; $\hat{\sigma}_{G12}^2$ and $\hat{\sigma}_{G21}^2$ are the estimates of interpopulation genetic variance components associated with populations 1 and 2, respectively; and $\hat{\sigma}_{F12}$ and $\hat{\sigma}_{F21}$ are the phenotypic standard deviations of the selection units related to populations 1 and 2, respectively e; and c is the parental control with a value equal to one.

RESULTS AND DISCUSSION

In general, the coefficients of variation were of low magnitude and below the levels considered satisfactory for maize experimentation (FRITSCHE-NETO et al., 2012). They ranged from 1.27 (PH) to 13.45% (GY) and from 1.64 (DTP) to 11.39% (GY) in the trials of Pop1 and Pop2, respectively (Table 1). Both populations *per se*, Pop1 and Pop2, had longer cycle means than the means of the founder hybrids, while for the other traits, there was a pronounced loss of vigor in the populations, especially for GY. For this trait, Pop1 and Pop2 showed a reduction in the mean of 2,483 kg ha^{-1} (−26%) and 4,827 kg ha^{-1} (−52%), respectively, compared to their respective founder hybrids. The loss of vigor in the advanced generation (referred to as F_2) of commercial hybrids is associated with the loss of beneficial effects of genetic complementarity among the lines involved in hybrid formation (HALLAUER; CARENA; MIRANDA FILHO, 2010; SENHORINHO et al., 2015; SOUZA NETO et al., 2015; TOLENTINO et al., 2017). Thus, hybrids that show lower vigor losses, such as AS1598, are formed from the crossing of lines with a high frequency of favorable alleles with additive effects and have a higher genetic potential for developing improved populations. In contrast, maize hybrids that exhibit a higher loss of vigor (>50%), such as RB9210, are usually formed by highly divergent lines that show high genetic complementarity in crossing, and therefore, there is a greater contribution of heterosis to the performance in this type of hybrid than in those with lower loss of vigor (COVARRUBIAS-PRIETO; HALLAUER; LAMKEY, 1989; HALLAUER; CARENA, 2009).

The means of the interpopulation HS progenies derived from Pop1 and Pop2 were nearly identical to the means of their founder hybrids (AS1598 and RB9210) for almost all traits, except GY (Table 1). For this trait, the means of HS from Pop1 (8,185 kg ha^{-1}) and Pop2 (8,140 kg ha^{-1}) were 1,215 (−13%) and 1,090 (−12%) kg ha^{-1} lower than the means of the founder hybrids, respectively. However, there was considerable variation among the genotypic values of HS for all traits. For GY, the variations among HS from Pop1 and Pop2 ranged from 9,348 to 4,607 and from 8,698 to 7,648 kg ha^{-1}, respectively, indicating the presence of HS with similar potential to the founder hybrids. The components of genetic variance associated with the HS of both populations were highly significant ($P<0.01$) according to the likelihood ratio test for all evaluated traits based on the mean across environments (joint analysis). Consequently, there is genetic variability in both maize populations for all evaluated traits, and it is possible to achieve genetic gains through interpopulation breeding of Pop1 and Pop2 formed from the advanced generations of the commercial hybrids AS1598 and RB9210. Populations derived from the advanced generation of commercial maize hybrids have been successfully used in RRS programs to develop elite inbred lines that exhibit genetic complementarity in crosses and, consequently, produce hybrids with high yield potential (RAPOSO; RAMALHO; RIBEIRO, 2004; REIS et al., 2009). According to Reis et al. (2013), populations derived from commercial maize hybrids have genetic potential for interpopulation breeding and, therefore, must be used in RRS programs.

However, these populations have a narrow genetic base since they are formed by only two inbred lines; thus, it is essential to monitor the genetic variability of these populations during recurrent selection cycles. Additionally, it is recommended to correctly sample during the phase of obtaining interpopulation HS progenies to avoid genetic drift and to use larger effective population sizes (lower selection intensity) in the recombination of selected progenies to prevent narrowing of the genetic variability in these populations.

Table 1. Estimates of variance components, heritability on a progenies-mean ($\hat{h}^2_{\bar{x}}$), coefficient of variation (CV %), and mean of interpopulation half-sib progenies ($\bar{x}_{HSP}$), check hybrids ($\bar{x}_{CH}$), and maize populations Pop1 (AS1598) and Pop2 (RB9210) for seven agronomic traits.

Parameters	DTP[1] days	DTS days	PH cm	EH cm	ED mm	EL cm	GY kg ha^{-1}
				Pop1 (AS1598)			
$\hat{\sigma}^2_G$[2]	1.30**[3]	1.46**	48.43**	33.66**	0.20**	0.36**	510,849**
$\hat{\sigma}^2_A$	5.20**	5.84**	193.72**	134.64**	0.80**	1.44**	2,043,396**
$\hat{\sigma}^2_{GxL}$	0.20**	0.15*	4.76**	9.54**	0.23	~0.00	95,949
$\hat{\sigma}^2_{B/E}$	0.08**	0.07**	2.61**	0.80*	0.07	0.01*	47,936**
$\hat{\sigma}^2$	0.97	1.09	8.14	48.71	0.03	0.92	1,212,896
Φ_E	1.26**	1.43**	0.02	0.02	0.20**	0.36	0.02
$\hat{h}^2_{\bar{x}}$	0.83	0.85	0.85	0.72	0.76	0.70	0.67
CV(%)	1.64	1.75	1.27	6.14	3.19	6.00	13.45
$\bar{x}_{HSP}$	60.08	59.76	225.09	113.71	49.73	16.00	8,185
$\bar{x}_{CH}$	60.08	59.58	232.50	119.17	51.00	16.55	9,400
$\bar{x}_{Pop1}$	62.67	62.00	222.17	107.83	49.00	14.90	6,917
				Pop2 (RB9210)			
$\hat{\sigma}^2_G$	0.46**	0.49**	35.89**	25.16**	0.01**	0.23**	117,870*
$\hat{\sigma}^2_A$	1.84**	1.96**	143.56**	100.64**	0.03**	0.92**	471,480*
$\hat{\sigma}^2_{GxL}$	0.18**	0.05	3.30	1.70	~0.00	0.09	163,956**
$\hat{\sigma}^2_{B/L}$	0.15**	0.17**	30.62**	16.43**	~0.00	~0.00	85,858**
$\hat{\sigma}^2$	0.97	1.05	61.81	43.44	0.03	0.90	858,965
Φ_E	0.62**	1.53**	0.02	0.02	0.04	0.06	0.03
$\hat{h}^2_{\bar{x}}$	0.64	0.71	0.75	0.76	0.51	0.55	0.34
CV(%)	1.64	1.70	3.53	5.79	3.48	5.82	11.39
$\bar{x}_{HSP}$	59.89	60.29	222.88	113.76	49.70	16.25	8,140
$\bar{x}_{CH}$	59.58	59.83	222.13	111.47	51.33	16.67	9,230
$\bar{x}_{Pop2}$	60.33	60.33	190.50	95.00	44.67	14.27	4,403

[1] DTP: days to pollen; DTS: days to silking; PH: plant height; EH: ear height; EL: ear length; ED: ear diameter; and GY: grain yield. [2] $\hat{\sigma}^2_G$, $\hat{\sigma}^2_A$, $\hat{\sigma}^2_{GxL}$, $\hat{\sigma}^2_{B/E}$, $\hat{\sigma}^2$ e Φ_E correspond to the estimates of genetic, additive variance, progeny x environment interaction, blocks within environment, residual and quadratic component of environment variance, respectively. [3] **; *, significant at 1% and 5% probability, respectively, by the F-test for fixed effects and by the likelihood ratio test (LRT) for random effects.

For GY and DTP in Pop2 and cycle and plant stature in Pop1, the HS progenies showed different performance due to variations among environments. For these traits, the components of variance for progeny × environment interaction were statistically significant (P<0.05; Table 1). However, the progeny × environment interaction was predominantly simple, and the ranking of HS progenies did not show alterations between environments. Additionally, there was a significant effect of environment (P<0.01) for the plant cycle in both populations and for ED in Pop1, highlighting the differences among environments in the evaluation of HS for these three traits.

The heritability estimates with the evaluation of HS progenies are in the narrow sense, as the genotypic variance component among HS corresponds to ¼ of the additive genetic variance component of the reference population from which the progenies were derived (FALCONER; MACKAY, 1996; HALLAUER; CARENA; MIRANDA FILHO, 2010). The heritability estimates ranged from moderate to high magnitude and were higher in the evaluation of HS for Pop1 compared to HS for Pop2 (Table 1). For HS evaluation, they ranged from 0.67 (GY) to 0.85 (DTS, PH) in Pop1 and from 0.34 (GY) to 0.76 (EH) in Pop2. Consequently, more than half of the observed phenotypic variation among HS progenies was of a genetic nature for almost all traits, except for GY in HS of Pop2. Therefore, the use of some selection strategies will provide satisfactory genetic gains for all traits in both populations. These heritability values are consistent with those found in the evaluation of interpopulation progenies in maize recurrent selection programs (DONÁ et al., 2012;

BERILLI et al., 2013; REIS et al., 2013; KOLAWOLE et al., 2019).

The HS from both Pop1 and Pop2 exhibited significant positive correlation estimates between plant stature (PH and EH) and cycle (DTP and DTS) (P<0.05, Figure 1). However, the correlations involving EH in Pop1 and between cycle and stature in Pop2 were of low magnitude (r<0.35). The EL showed a significant and positive correlation of moderate magnitude (r>0.35) with plant stature, indicating that taller plants tend to produce longer ears in HS from both populations. Regarding GY, it exhibited a significant (P<0.05) positive correlation of moderate magnitude (>0.35) with plant stature, ED, and EL in HS of both populations. Additionally, GY negatively correlated with DTS in HS derived from Pop1 and did not correlate with the cycle in HS derived from Pop2.

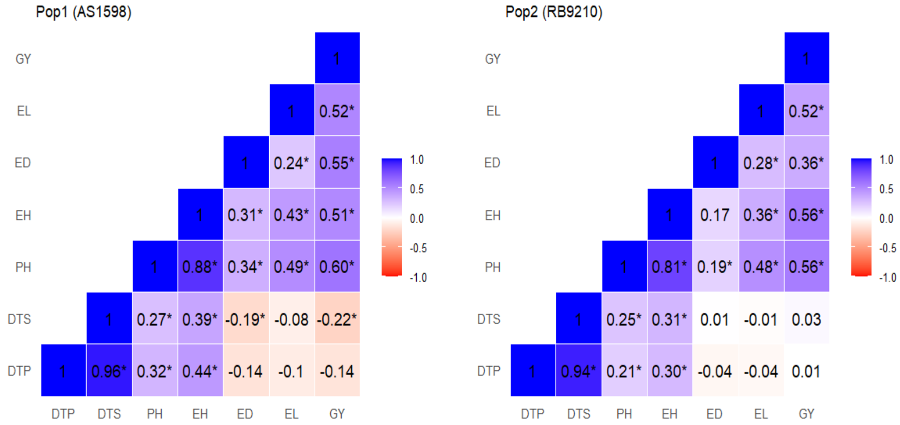

Figure 1. Heat map of the estimates of correlation coefficients between pairs of vectors of genetic values for agronomic traits measured in the interpopulation half sib progenies. The color assigned to a point in the Heat map grid indicates the strength of a correlation between two traits. The level of correlation is indicated by red for positive correlations and blue for negative correlations, as depicted in the color key. *Significant at a 5% probability level by the t-test.

The estimates of genetic gain with truncated selection for GY were 9.03 (739 kg ha^{-1}) and 3.45% (281 kg ha^{-1}) for Pop1 and Pop2, respectively (Table 2). The strategy of simultaneous selection for all traits, using the FAI-BLUP index to reduce the cycle (DTP and DTS) and plant stature (AP and AE) and increase ED, EL, and GY, resulted in negative estimates of genetic gains for GY, which is not desirable in the development of maize cultivars (results not shown). However, simultaneous selection to increase GY and reduce DTS using the FAI-BLUP index resulted in estimates of gains of 7.19% for GY, a reduction in cycle (DTP and DTS), and little change in other traits in Pop1. In Pop2, the inclusion of BLUP from each environment for GY allowed the selection of a single set of HS with favorable performance for both environments, capitalizing on the interaction between progenies and environments (YAN, 2016; ROCHA; MACHADO; CARNEIRO, 2018; PEIXOTO et al., 2021). In this population, the genetic gains for GY using the BLUP from each environment (4.18 and 4.90% for environments 1 and 2, respectively) were higher than the gains based on the average of environments (3.00%). According to Peixoto et al. (2021), selecting genotypes based on the BLUP from each environment results in higher gains for all environments compared to selection based on the average of environments, especially when the progeny × environment interaction is significant.

Table 2. Prediction of genetic gain for seven agronomic traits in both populations *per se* and the interpopulation hybrid (HI) of maize.

Populations	DTP[1/] days	DTS days	PH cm	EH cm	ED cm	EL cm	GY kg ha^{-1}
			Truncated selection (GY)				
Pop1 (AS1598)	0.77%	0.66%	1.94%	3.53%	1.11%	1.07%	9.03%
Pop2 (RB9210)	0.13%	0.17%	1.97%	3.18%	0.41%	1.30%	3.45%
			FAI-BLUP*				
Pop1 (AS1598)	-0.10%	-0.12%	0.54%	0.79%	0.59%	0.03%	7.19%
Pop2 (RB9210)	0.21%	0.29%	2.16%	3.08%	0.51%	1.03%	3.00%
Pop2 (RB9210)[E1]	0.34%	0.21%	1.45%	2.72%	0.30%	1.27%	4.18%
Pop2 (RB9210)[E2]	0.10%	0.27%	2.27%	3.07%	0.72%	0.65%	4.90%
Estimated gain in the interpopulation hybrid - GY							656.83 kg ha^{-1} (8.05%)

[1/] DTP: days to pollen; DTS: days to silking; PH: plant height; EH: ear height; ED: ear diameter; EL: ear length; and GY: grain yield. [E1] and [E2] Selection based on the mean of the two environments and response in environment 1 and 2, respectively. * Simultaneous selection for GY and DTS.

Regarding the interpopulation hybrid (HI), the estimated genetic gain in HI after one cycle of RRS was 656.83 kg ha^{-1} (8.05%; Table 2). Raposo, Ramalho and Ribeiro (2004) reported genetic progress for GY of 5.7% in the interpopulation hybrid of two populations derived from commercial hybrids after one cycle of RRS. In another study, Reis et al. (2009) assessed genetic progress in interpopulation hybrids of populations derived from improved commercial hybrids with RRS. They found progress of 7.9% per cycle after three cycles of RRS. Since the equation used to estimate gains considers only additive effects and as RRS also capitalizes on non-additive effects, it was expected that the genetic progress in the HI derived from the improved versions of both populations would be higher than the estimated gain in the present study (COMSTOCK; ROBINSON; HARVEY, 1949; VIANA et al., 2013; SOUZA JÚNIOR., 2018).

CONCLUSION

We conclude that the two populations derived from commercial single-cross maize hybrids have genetic potential for interpopulation breeding using RRS. The estimates of genetic gains are satisfactory in both populations *per se* and in the interpopulation hybrid after one cycle of RRS.

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