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YIELD PERFORMANCE OF EXPERIMENTAL MAIZE HYBRIDS IN THE SECOND SEASON OF THE CENTER-SOUTH REGION VIA MIXED MODELS

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ABSTRACT – Phenotypic expression is a function of genotypic variance, environmental variance, and the differential sensitivity of certain genotypes to distinct environmental cues. By estimating genotype-by-environment (GxE) interactions, it is possible to identify superior, stable, and adapted cultivars for different macro-regions with diverse soil and climate (edaphoclimatic) conditions. Based on this, trials were conducted to evaluate stability, adaptability, and selection gains in maize hybrids in the 2019 off-season (second crop) in the regions of Londrina, Paraná state (PR) and Sete Lagoas, Minas Gerais state (MG). Maize grain yield of 144 hybrids was evaluated in a 12x12 lattice design with two replicates. Analyses were performed via mixed models; genetic parameters were estimated by restricted maximum likelihood (REML), and the prediction of breeding values was carried out using the best linear unbiased prediction (BLUP). The yield performance of genotypes at each site was evaluated using the harmonic mean of the relative performance of genotypic values (HMRPGV) method. The genotype effect was significant; however, the effects of environment and the genotype-by-environment interaction were not significant, allowing the selection of the same genotypes for both environments. Mixed modeling allowed the estimation and selection of 20 superior experimental hybrids, considering genotypic values, stability, and adaptability. The best hybrids selected within this group showed estimates of new genotypic and phenotypic means that did not statistically differ from the commercial checks AG 8088 and DKB 310, with averages 50% higher than the national average for the second crop. All selection accuracies ranged from high to moderate, indicating the feasibility of selecting superior genotypes for the second season in the Center-South transition region.

Keywords: *Zea mays L.*, restricted maximum likelihood, HMRPGV, off-season maize, grain yield.

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Maize (*Zea mays* L.) cultivation in Brazil has achieved an increase of over 150% in production and 60% in cultivated area over the last two decades (Associação Brasileira das Indústrias do Milho, 2022). In 2024, the country was the world's third-largest producer (approximately 114 million tons), third-largest in planted area (approximately 22 million hectares), and the second-largest exporter of maize grain (FAO, 2025, Conab, 2026).

One of the key drivers behind these impressive figures is the triple-cropping system (planting in three cropping seasons per year), which leads to high production compared to other countries (Pereira Filho, 2015; Artuzo et al., 2019; Von Pinho et al., 2022). There is a downward trend in the area planted with maize during the summer crop season, accompanied by an increase in areas dedicated to the second crop (off-season), primarily in the Center-West and South regions. In this process, the second-crop maize (commonly known as 'safrinha') has become the main cropping season in Brazil, currently accounting for 70% of national production (Céleres, 2022).

This second season of maize is considered a period of climatic instability for cultivation, due to the risks of prolonged drought or frost/excessive rainfall depending on the region, soil conditions, and sowing time (Sans et al., 2001; Instituto Nacional de Meteorologia, 2022). This heterogeneity of edaphoclimatic conditions across producing regions challenges breeding programs to develop specific hybrids for this period (Von Pinho et al., 2022). To achieve this, through crosses of promising genotypes, studies of their progenies are conducted, and individuals with the best agronomic performance are selected. In the final stage of genetic improvement, candidate genotypes are evaluated in Value for Cultivation and Use (VCU) trials across different locations where the improved cultivar is intended to be recommended (Elias et al., 2016).

When considering yield performance across multiple environments, in addition to genetic and environmental effects, there is an additional effect due to their interaction (Eeuwijk et al., 2016). This genotype-by-environment (GxE) interaction results in differential behavior, meaning the best hybrid in one environment may not perform as well in another. The main genetic mechanisms proposed to explain this phenomenon are overdominance, pleiotropy, epistasis, gene linkage, and epigenetics (Leon et al., 2016). For selection and recommendation purposes, hybrids must exhibit high adaptability and stability—that is, perform favorably and predictably in response to environmental changes (Rezende et al., 2021).

In trials evaluating multiple genotypes across different locations, data imbalance is common due to the variability of the genotypes under evaluation, non-orthogonal experimental design such as lattices, and potential plot losses (Eeuwijk et al., 2016; Elias et al., 2016). In such cases, analysis of variance (ANOVA) is a limited statistical methodology because it does not provide as much genetic information as

mixed model approaches (Resende, 2007). To characterize a model as mixed, it must contain one or more fixed effects, in addition to the overall mean, and one or more random effects, in addition to the experimental error. Mixed modeling allows for the simultaneous modeling of fixed and random effects, facilitating the identification of superior, stable, and adapted genotypes (Resende et al., 2012).

The prediction of random effects and the estimation of fixed effects depend on estimating variance components. The Restricted Maximum Likelihood (REML) methodology estimates variance components obtained by maximum likelihood, which provides the necessary parameters for Best Linear Unbiased Prediction (BLUP), whose function is to predict breeding values (Resende et al., 2012). The use of REML/BLUP in experimental data analysis constitutes a strategy that increases selection accuracy, minimizes prediction errors, and maximizes genetic gain per selection cycle (Resende & Duarte, 2007; Resende, 2016).

The Harmonic Mean of Relative Performance of Genotypic Values (HMRPGV), advocated by Resende (2007), is a method that allows the simultaneous estimation of adaptability and stability based on REML/BLUP. The HMRPGV method can concurrently predict stability, adaptability, and genotype yield performance within the same measurement and scale of the evaluated trait. This methodology can precisely and informatively estimate, at the individual level, how adapted and stable a genotype is within the population. This allows for comparing individuals across time and space in models with complex data networks (Resende, 2007; Resende & Alves, 2020).

All these advantages of statistical estimation using REML/BLUP and HMRPGV reinforce their adoption in maize trials (Mendes et al., 2012; Faria et al., 2017; Oliveira et al., 2017; Santos et al., 2021; Yamamoto et al., 2021) and in many other crops (Resende, 2016). After 2005, the use of mixed modeling in various genotype-by-environment interaction studies surpassed other estimation methodologies, and this trend is expected to continue growing (Eeuwijk et al., 2016). However, of the 75 articles published using adaptability and stability methodologies in maize in Brazil between 1970 and 2017, only four used HMRPGV, and none of these were conducted in the second season (Rezende et al., 2021). Given the above, the objective of this study was to estimate yield adaptability and stability, as well as genetic gains from selecting maize genotypes in the second season in experimental maize hybrids via mixed model analysis.

Material and Methods

A total of 144 maize hybrids were evaluated in the 2019 second season in Londrina, PR, and Sete Lagoas, MG, during the second half of February. Second season maize in Paraná is sown between February and March, in locations suitable for this cultivation system, and is characterized by a gradual reduction in rainfall and an increased probability of frost. In Sete

Lagoas, MG, plantings occur from January to February and historically coincide with periods of irregular rainfall.

The experimental design used was a 12x12 lattice with two replicates. The experimental plots for each hybrid consisted of two 4.2 m rows, with a spacing of 0.7 m between rows. The commercial cultivars AG8088PRO2, DKB310PRO2, DKB390PRO2, BRS1055, and the experimental hybrid 1F640PRO2 (developed by Embrapa) were used as checks.

For planting, 500 kg ha^{-1} of 08-28-16 fertilizer (+1.8% Ca; 1.0% S; 0.3% B) was used, and topdressing was performed with 200 kg ha^{-1} of urea at the V4 vegetative stage. Planting was mechanized, using a plot planter and fertilizer applicator. After planting, foliar fungicides and insecticides were applied as required by pest and disease infestation levels. Other agronomic practices were carried out in accordance with standard recommendations for maize cultivation (Pereira Filho, 2015). Harvesting was performed using a plot harvester, with weight and moisture content measurements. Subsequently, yield data were converted from kilograms per plot to tons per hectare (t ha^{-1}) adjusted to 13% moisture content.

In data analysis, genetic parameters were estimated via restricted maximum likelihood (REML) and breeding values were predicted using the best linear unbiased prediction (BLUP), utilizing the statistical model $y = Xt + Zg + Wb + Ti + e$, where y is the data vector, t is the vector of trial or environment effects (assumed as fixed) added to the overall mean, g is the vector of genotypic effects (assumed as random), b is the vector of block effects (assumed as random), i is the vector of genotype-by-environment interaction effects (random), and e is the vector of error or residual effects (random). Capital letters represent the incidence matrices for their respective effects. The likelihood ratio test (LRT) was applied to infer the significance of the random effects in the model. Adaptability and stability were estimated using the harmonic mean of the relative performance of genotypic values (HMRPGV) method. All analyses were performed using Selegen-REML/BLUP software (Resende, 2007; Resende, 2016).

To present the data relative to the HMRPGV estimates, the methodology proposed by Mendes et al. (2012) was used. In the Cartesian plane: the upper right quadrant represents hybrids with superior performance in all environments, indicating high stability and adaptability; the lower left quadrant represents hybrids with inferior performance across the evaluated environments, indicating low stability and adaptability; the upper left and lower right quadrants represent hybrids with stability and adaptability in specific environments, plotted on the abscissa and ordinate, respectively. The cut-off point for the quadrants was defined as the BLUP mean (5.764 t ha^{-1}) and the HMRPGV*GM mean (5.756 t ha^{-1}).

Results and Discussion

Deviance estimates and their respective

LRT values expressed the significance of the genotype effect in the performance trials conducted in Sete Lagoas, Londrina, and the joint analysis considering both environments (Table 1). These significant effects reveal high genotypic variability and infer differential yield responses of genotypes when facing contrasting environments, which is a premise for studying adaptability and stability (Resende, 2007; Elias et al., 2016; Eeuwijk et al., 2016; Leon et al., 2016; Rezende et al., 2021).

Estimates of phenotypic and genotypic variance were 2 to 5 times higher in the Sete Lagoas trial compared to Londrina. Sete Lagoas also exhibited the highest heritabilities, with 28% for individual broad-sense heritability (h^2g) and 56% for genotype mean heritability (h^2mg) assuming complete survival. In the joint analysis, individual broad-sense heritability (15%) and genotype mean heritability (47%) showed lower values than the average of the two analyzed regions, which highlights the importance of the simultaneous evaluation of all genotypes and locations. Heritabilities can be considered high, given that grain yield is a quantitative, complex trait highly influenced by the environment. Heritability represents the proportion of the total variation in a population that is of genetic origin, meaning it is amenable to selection, allowing breeders to establish selection and genetic control strategies (Resende & Duarte, 2007).

Genotype selection accuracies measure how closely the predicted breeding values align with the true breeding values of the genotypes. In this experiment, AcGEN values ranged from moderate (0.50 - 0.69) to high (0.70 - 0.89). Selection accuracies calculated via PEV (AcPEV) were approximately 16% lower than AcGEN, a reduction expected due to the inclusion of additional parameters in this calculation. This parameter is directly influenced by the number of replicates, the residual variance, and the ratio between residual and genetic variance. Higher accuracies infer a lower risk of error in utilizing the information, denoting greater reliability in prediction and the selection process (Resende, 2007; Resende & Duarte, 2007; Resende & Alves, 2020).

The genotypic correlation between hybrid performance across the various environments was high (0.67), which contributes to gains from direct selection—i.e., selection in one site aiming for gain in another (Eeuwijk et al., 2016; Resende & Alves, 2020). This indicates the feasibility of selecting the same genotypes for both environments, optimizing genotype recommendation for second-crop conditions.

Genotypic coefficients of variation are indicative of the genetic variability present in the population, ranging from 9.33% (Londrina) to 20.11% (Sete Lagoas) in these trials. Experimental coefficients of variation confirm the precision of trial, which ranged from 17.76% to 31.13% in Londrina and Sete Lagoas, respectively. The genotypic and experimental coefficients of variation estimated in individual and joint trials support the idea of differential hybrid behavior in response to interaction with contrasting

Table 1. Estimates of deviance, variance components, and genotypic determination coefficients for maize hybrid performance trials conducted in Londrina, PR, and Sete Lagoas, MG, in the 2019 second season.

	Sete Lagoas		Londrina		Joint	
Efects	**Deviance**	**LRT**	**Deviance**	**LRT**	**Deviance**	**LRT**
Block	527.37	1.32^{ns}	331.42	$0,02^{ns}$	964,84	$1,07^{ns}$
Genotype (G)	543.1	17.05^{**}	346.11	$14,71^{**}$	983,42	$19,65^{**}$
Environment (E)	-	-	-	-	965,91	$2,14^{ns}$
GxE	-	-	-	-	965,02	$1,25^{ns}$
Full model	526.05		331.4		963.77	
Variance Components						
Genotypic variance	1.40		0.28		0.44	
Block variance	0.30		0.01		0.10	
GxE	-		-		0.22	
Residual variance	3.36		1.00		2.17	
Phenotypic variance	5.06		1.28		2.93	
Genotypic Determination Coefficients						
h^2_g	0.28		0.22		0.15	
h^2_{mg}	0.56		0.45		0.47	
Ac_{GEM}	0.75		0.67		0.69	
Ac_{PEV}	0.62		0.57		0.58	
Rgloc	-		-		0.67	
CVg (%)	20.11		9.33		11.49	
CVe (%)	31.13		17.76		25.56	
Média	5.89		5.62		5.76	

*** Tabulated Chi-square: 3.84 and 6.63 at the 5% and 1% levels of significance, respectively; ns: non-significant; GxE = interaction between genotypes and environments; h²mg = genotype mean heritability, assuming complete survival; AcGEN = accuracy of genotype selection, assuming complete survival (AcGEN = $\sqrt{h^2}$); AcPEV = selection accuracy calculated via PEV (AcPEV = $\sqrt{(1 - PEV / \sigma^2 g)}$ where PEV = $(1 - AcGEN^2)\ \sigma^2 g$); Rgloc = genotypic correlation between hybrid performance across environments; CVg = coefficient of genotypic variation; CVe(%) = coefficient of experimental variation.

environments (Resende & Alves, 2020). Mean yields in the two evaluated environments were statistically similar, showing a difference of only 5% in absolute terms. These average yields were analogous to the Brazilian average in the same second-crop period of 2024/25, which reached 5.46 t ha^{-1} (Conab, 2026).

Among the experimental hybrids, 64 genotypes performed above the average for stability and adaptability across the trials (5.76 t ha^{-1}) (Figure 1). Because these hybrids are in the experimental phase, there was a pronounced discrepancy in adaptability and stability, with a difference of 2.71 t ha^{-1} (37%) between the first and last positions of the evaluated hybrids. The hybrids with the highest HMRPGV values were 1F640PRO2 (9.56 t ha^{-1}), AG8088PRO2 (7.23 t ha^{-1}), and HIB3 (7.20 t ha^{-1}). The commercial check BRS1055 ranked 16th in terms of HMRPGV, with 12 experimental hybrids showing superior average performance compared to this hybrid.

The fact that the checks expressed high HMRPGV values can be explained not only by their status as commercial cultivars but also by the advantage conferred by transgenic traits, which does not apply to the other treatments in the trials. Comparing the performance of the commercial checks with the experimental hybrids, it is noteworthy that although the latter category did not carry transgenic insecticidal proteins and was thus exposed to pests and diseases, more than half of them still achieved yield, adaptability, and stability levels close to those of the checks.

The selection of the 35 most productive, adapted, and stable hybrids provided an average selection gain of 0.86 t ha^{-1} in Sete Lagoas and 0.40 t ha^{-1} in Londrina (Table 2). The highest phenotypic means of the selected genotypes in the individual trials were observed in experimental hybrids: in Sete Lagoas, HIB3 and 9-01026 (10.68 and 10.36 t ha^{-1}, respectively), and in Londrina, 9-00953 and 9-00824 (8.90 and 8.21 t ha^{-1}, respectively). These results are promising for the selection of new cultivars for release, since the superiority of these hybrids in yield, adaptability, and stability is confirmed by means that exceed those of commercial hybrids.

Despite the non-significant deviance for environment and GxE interaction effects (Table 1), the Sete Lagoas environment yielded a phenotypic mean (μF) 14% higher than Londrina among the selected hybrids, and 27% higher in the overall average across both environments. The primary explanation for this environmental difference is related to the contrasting microclimates of these regions in Southeast and South Brazil, which provide distinct edaphoclimatic conditions and highlight complex genotype-by-environment interactions. Between planting and harvesting, Londrina experienced sharp temperature fluctuations (maximum of 28.03ºC and minimum of 15.96ºC), which potentially induced abiotic stress and compromised yield performance (Instituto Nacional de Meteorologia, 2022). In contrast, Sete Lagoas maintained high temperatures

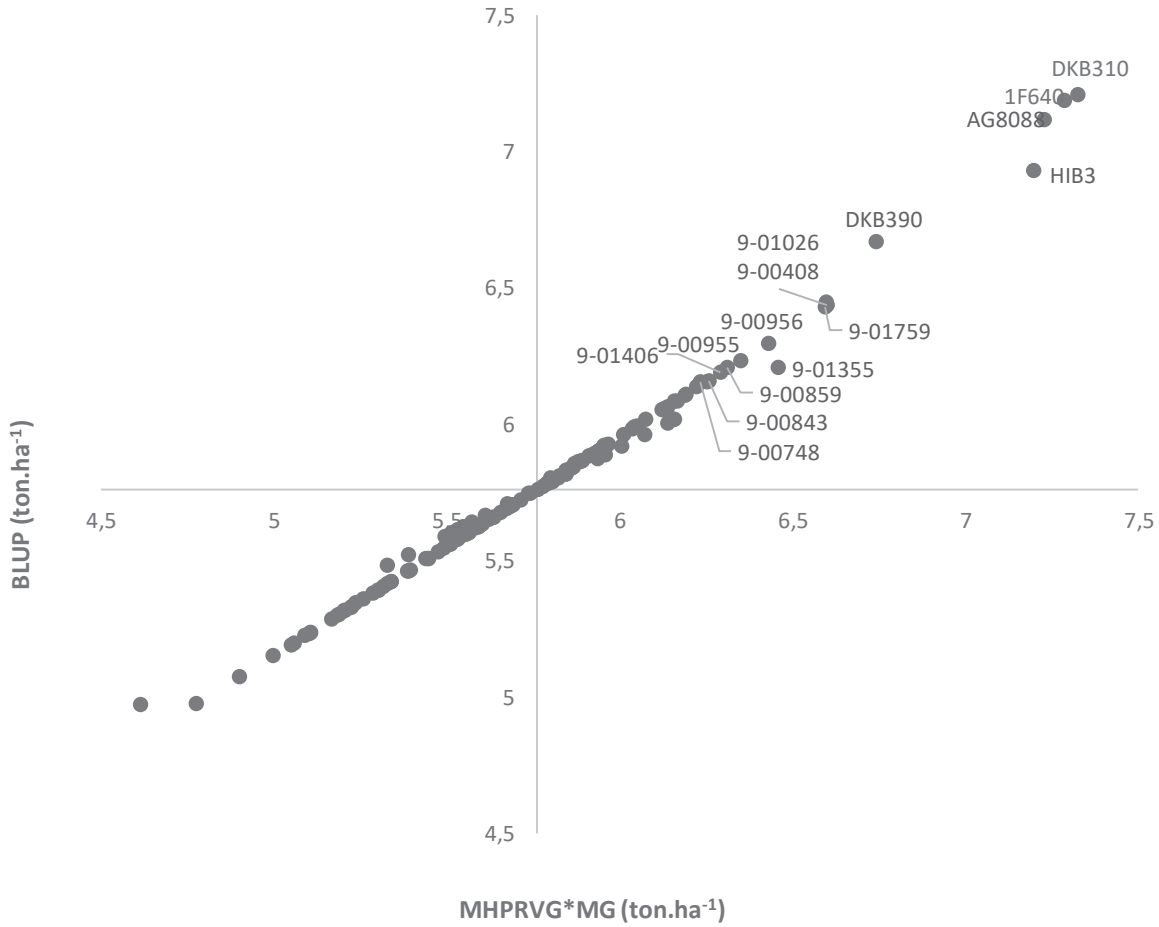


Figure 1. Harmonic mean of the relative performance of predicted genotypic values multiplied by the overall mean yield (HMRPGV*GM) of 139 maize hybrids evaluated in the 2019 off-season in Londrina, PR, and Sete Lagoas, MG.

throughout the developmental cycle (maximum of 22.97ºC and minimum of 21.39ºC), and this low thermal amplitude tends to favor the development of C4 plants, such as maize (Sans et al., 2001; Pereira Filho, 2015).

Another meteorological parameter that contributed to the distinct performance of the hybrids was the precipitation regime, with 0.11 mm in Sete Lagoas and 1.92 mm in Londrina (Instituto Nacional de Meteorologia, 2022). Although this 94% higher rainfall in Londrina was well distributed throughout the crop cycle, it may have caused stress due to waterlogging (excess water). This wet period was atypical compared to the 2018 season, as the off-season period usually demands irrigation across Brazilian territory. Humidity and atmospheric pressure were similar in both cities, with values close to 70% .

There was a selection gain of 0.48 t ha^{-1} at a selection intensity of 25% (Table 3). All

Table 2. Selection gains, selective accuracy and new genotypic means in Londrina, PR, and Sete Lagoas, MG, based on BLUPs from the maize hybrid performance trial conducted in the 2019 second season.

Rank	Sete Lagoas - MG						Londrina – PR					
	Hybrid	μ_F	BLUP	Ac	SG	μ_{G^*}	Hybrid	μ_F	BLUP	Ac	SG	μ_{G^*}
1	1F640PRO2	10,12	8,89	0,83	3,00	8,89	DKB310PRO2	7,86	7,01	0,78	1,39	7,01
2	HIB3	10,68	8,20	0,65	2,65	8,54	9-00824	8,21	6,50	0,59	1,14	6,76
3	AG8088PRO2	8,59	7,87	0,83	2,43	8,32	AG8088PRO2	6,93	6,44	0,78	1,03	6,65
4	9-00408	9,92	7,47	0,66	2,22	8,11	DKB390PRO2	6,88	6,41	0,78	0,97	6,59
5	DKB310PRO2	7,99	7,44	0,83	2,08	7,97	9-00953	8,90	6,30	0,46	0,91	6,53
6	9-01026	10,36	7,14	0,53	1,94	7,83	9-01355	7,20	6,26	0,59	0,87	6,49
7	BRS1055	9,17	7,10	0,66	1,84	7,73	HIB1	7,27	6,16	0,59	0,82	6,44
8	9-00859	8,53	6,96	0,66	1,74	7,63	9-01268	7,13	6,12	0,59	0,78	6,40
9	DKB390PRO2	7,40	6,95	0,81	1,67	7,56	9-00747	7,10	6,10	0,59	0,75	6,37
10	9-00289	8,48	6,90	0,66	1,60	7,49	9-00955	6,61	6,05	0,59	0,72	6,33
11	9-01759	8,16	6,85	0,66	1,54	7,43	9-01759	6,51	6,02	0,59	0,69	6,31
12	9-00956	7,88	6,75	0,66	1,49	7,38	9-01305	6,82	6,00	0,59	0,66	6,28
13	9-00802	8,02	6,72	0,66	1,43	7,32	9-00843	7,49	6,00	0,46	0,64	6,26
14	9-01406	7,55	6,70	0,66	1,39	7,28	9-01011	6,71	5,97	0,59	0,62	6,24
15	9-00702	8,28	6,67	0,53	1,35	7,24	9-00945	6,38	5,97	0,59	0,60	6,22
16	9-00645	7,60	6,61	0,66	1,31	7,20	9-00720	6,71	5,97	0,59	0,58	6,20
17	9-00680	7,47	6,61	0,66	1,28	7,17	9-00678	6,70	5,96	0,59	0,57	6,19
18	9-00748	7,35	6,59	0,65	1,24	7,13	9-01332	6,69	5,96	0,59	0,56	6,18
19	9-00210	7,80	6,54	0,66	1,21	7,10	9-01177	6,66	5,95	0,59	0,55	6,16
20	9-00779	7,64	6,53	0,66	1,18	7,07	9-00934	6,28	5,93	0,59	0,53	6,15
21	9-00926	7,35	6,49	0,66	1,16	7,05	9-00640	7,05	5,90	0,46	0,52	6,14
22	9-01526	7,87	6,47	0,66	1,13	7,02	9-00956	6,18	5,90	0,59	0,51	6,13
23	9-00949	7,48	6,47	0,66	1,11	7,00	9-00423	6,14	5,88	0,59	0,50	6,12
24	9-01466	6,67	6,45	0,65	1,08	6,97	HIB3	6,45	5,87	0,59	0,49	6,11
25	9-01037	7,37	6,40	0,52	1,06	6,95	9-01425	6,41	5,86	0,59	0,48	6,10
26	9-01179	6,63	6,40	0,65	1,04	6,93	9-01178	6,40	5,86	0,59	0,47	6,09
27	9-00683	7,59	6,39	0,66	1,02	6,91	9-00448	6,40	5,85	0,59	0,46	6,08
28	9-00955	7,23	6,34	0,66	1,00	6,89	9-01026	6,39	5,85	0,59	0,45	6,07
29	9-00675	7,35	6,32	0,53	0,98	6,87	HIB2	6,33	5,83	0,59	0,45	6,06
30	9-00843	7,21	6,28	0,66	0,96	6,85	9-00738	6,26	5,81	0,59	0,44	6,06
31	9-01438	6,65	6,16	0,66	0,94	6,83	9-00797	6,24	5,80	0,59	0,43	6,05
32	9-00642	6,41	6,16	0,66	0,92	6,81	9-00748	5,88	5,79	0,59	0,42	6,04
33	9-00750	6,43	6,14	0,53	0,90	6,79	9-01179	6,17	5,78	0,59	0,41	6,03
34	9-00448	6,86	6,12	0,66	0,88	6,77	9-00321	5,83	5,77	0,59	0,41	6,02
35	9-01553	6,84	6,12	0,66	0,86	6,75	9-00279	6,42	5,77	0,46	0,40	6,02
Selected μ		**7,85**	**6,75**	**0,66**	**1,42**	**7,31**		**6,73**	**6,02**	**0,59**	**0,63**	**6,25**
Overall μ		**5,80**	**5,89**	**0,62**	**0,70**	**6,59**		**5,59**	**5,62**	**0,57**	**0,29**	**5,91**

μF: phenotypic mean; Ac: selective accuracy via PEV; SG: selection gain; μG*: new genotypic mean. Unit of measurement in t ha^{-1}, except accuracy which ranges from 0 to 1.

selected hybrids presented estimates of new genotypic and phenotypic means up to 50% higher than the national off-season average (5.3 t ha^{-1}) and the Center-South region average (5.67 t ha^{-1}) (Conab, 2026). The most productive, adapted, and stable experimental hybrids were: HIB3, 9-01026, 9-01759, 9-00956, 9-00748, 9-01179, 9-00955, 9-00843, and 9-00448.

The selection accuracies of the commercial hybrids were close to 0.80, and those of the experimental hybrids were around 0.60, which is in agreement with Faria et al. (2017) and Santos et al. (2021). It is recommended that genotypes with accuracies above 0.80 be selected, and those above 0.90 be recommended (Resende & Duarte, 2007). However, the number of evaluated genotypes and locations resulted in lower accuracies, which justifies applying a rigorous selection intensity on the hybrids. Other authors obtained higher accuracies using mixed models when evaluating genotypes across more environments and replicates (Mendes et al., 2012; Oliveira et al., 2017; Yamamoto et al., 2021).

Predicted genotypic values, in conjunction with the SEP (standard error of predicted genotypic value) estimate, can be used to obtain confidence intervals for genotypic values using the expression $(u + g) \pm t * SEP$, where $t = 1.96$ is the tabulated value from Student's t-distribution. By checking for overlaps among these confidence intervals, multiple comparisons among genotypes can be inferred based on their predicted genotypic values (Resende, 2016).

BLUP is the procedure that maximizes selection accuracy and, therefore, is superior to any other combined selection index, except for one that uses all random effects of the statistical model (multi-effect index), which is BLUP itself in the case of balanced data (Resende, 2007). Within the facets of the BLUP-based selection index, applying individual and joint analyses across environments proves strategic to reveal how the final ranking is constructed. This can be exemplified by the hybrid HIB3, which obtained the second-highest BLUP (8.20) and the highest phenotypic mean (10.68 t ha^{-1}) in Sete Lagoas, whereas in Londrina, it occupied the 24th BLUP position (5.87) with an 18% reduction in yield (6.45 t ha^{-1}); this led it to occupy the 4th BLUP position (6.93 t ha^{-1}) and the highest phenotypic mean (8.56 t ha^{-1}) in the joint analysis. A similar situation occurred with the check 1F640, which had the highest BLUP in Sete Lagoas and ranked 49th in Londrina; despite this, in the joint analysis, this imbalance was corrected, and its BLUP value was the second-largest in the ranking.

Conclusions

HMRPGV analysis was efficient for selecting promising experimental hybrids for the second crop in the southern region, predicting the average behavior of genotypes and simplifying the selection process.

The experimental hybrids that stood out most in terms of grain yield, genotypic values, stability, and adaptability, considering both evaluation environments, were HIB3, 9-00408,

Table 3. Selection gains, selective accuracy and new genotypic means for Londrina, PR, and Sete Lagoas, MG, based on BLUPs from the maize hybrid performance trial conducted in the 2019 second season.

Rank	Hybrid	μ_F	BLUP	Ac	LCL	UCL	SG	μ_G^*	μ_F^*
1	DKB310PRO2	7,92	7,21	0,81	6,44	7,97	1,45	7,21	7,57
2	1F640PRO2	7,92	7,19	0,81	6,42	7,95	1,44	7,20	7,55
3	AG8088PRO2	7,76	7,12	0,81	6,35	7,88	1,41	7,17	7,46
4	HIB3	8,56	6,93	0,62	5,91	7,95	1,35	7,11	7,22
5	DKB390PRO2	7,12	6,67	0,80	5,88	7,45	1,26	7,02	6,90
6	9-00408	7,75	6,45	0,62	5,43	7,46	1,16	6,93	6,62
7	9-01026	7,71	6,44	0,57	5,37	7,50	1,09	6,86	6,61
8	9-01759	7,33	6,43	0,62	5,41	7,45	1,04	6,80	6,60
9	9-00956	7,03	6,30	0,62	5,28	7,32	0,98	6,75	6,43
10	9-00955	6,92	6,23	0,62	5,22	7,25	0,93	6,70	6,35
11	9-01355	7,20	6,21	0,49	5,08	7,34	0,89	6,65	6,32
12	9-00859	7,51	6,21	0,57	5,15	7,27	0,85	6,61	6,32
13	9-01406	6,69	6,19	0,62	5,17	7,21	0,82	6,58	6,30
14	9-00843	7,30	6,16	0,57	5,09	7,22	0,79	6,55	6,26
15	9-00748	6,61	6,16	0,62	5,14	7,17	0,76	6,53	6,25
16	BRS1055	7,04	6,16	0,62	5,14	7,17	0,74	6,50	6,25
17	9-00289	6,93	6,14	0,62	5,12	7,16	0,72	6,48	6,23
18	9-00210	6,65	6,11	0,62	5,09	7,13	0,70	6,46	6,20
19	9-00702	6,47	6,11	0,57	5,04	7,17	0,68	6,44	6,19
20	9-01179	6,40	6,09	0,62	5,07	7,10	0,66	6,42	6,17
21	9-00802	6,80	6,09	0,62	5,07	7,10	0,64	6,41	6,17
22	9-00747	6,79	6,06	0,62	5,05	7,08	0,63	6,39	6,14
23	9-00949	6,47	6,06	0,62	5,04	7,07	0,61	6,38	6,13
24	9-00824	6,89	6,05	0,57	4,99	7,12	0,60	6,36	6,13
25	9-00678	6,70	6,02	0,49	4,89	7,15	0,59	6,35	6,08
26	9-00645	6,57	6,02	0,62	5,00	7,03	0,57	6,34	6,08
27	9-00945	6,38	6,02	0,49	4,89	7,15	0,56	6,33	6,08
28	9-01332	6,69	6,01	0,49	4,87	7,14	0,55	6,31	6,07
29	9-00448	6,63	5,99	0,62	4,98	7,01	0,54	6,30	6,05
30	9-00680	6,17	5,99	0,62	4,97	7,01	0,53	6,29	6,05
31	9-00675	6,43	5,98	0,57	4,92	7,05	0,52	6,28	6,04
32	9-00738	6,55	5,96	0,62	4,94	6,98	0,51	6,27	6,01
33	9-00423	6,14	5,96	0,49	4,83	7,09	0,50	6,26	6,01
34	9-00953	6,83	5,93	0,51	4,81	7,04	0,49	6,25	5,97
35	9-00779	6,40	5,92	0,62	4,91	6,94	0,48	6,24	5,96
Selected μ		**6,95**	**6,24**	**0,61**	**5,23**	**7,26**	**0,80**	**6,56**	**6,36**
Overall μ		**5,69**	**5,76**	**0,58**	**4,71**	**6,82**	**0,36**	**6,13**	**5,76**

μF: phenotypic mean; Ac: selective accuracy via PEV; LCL/UCL: lower and upper confidence limits, respectively; SG: selection gain (GS); μG*: new genotypic mean; μF*: new phenotypic mean capitalizing on the interaction with environments. Unit of measurement in t ha^{-1}, except accuracy which ranges from 0 to 1.

9-01026, 9-00953, 9-00824, and 9-01759.

Despite the efficiency of the joint analysis by the HMRPGV method in predicting the average behavior of genotypes and selecting superior genotypes, the results obtained in this study indicate that individual evaluation per environment enables the identification of superior genotypes in specific environments that may be unfavored in the final average.

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