

Full Length Research Paper

Combining ability of double-cross maize hybrids derived from single-cross parents and their interaction across planting dates and crop seasons in Brazil

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Received 26 February, 2026; Accepted 30, April, 2026

The success of maize breeding programs depended on the development of base populations with high genetic variability and yield potential. This study aimed to identify superior parents and crosses for incorporation into the genetic base of a maize breeding program at the Federal University of Goiás. Six single-cross hybrids were intercrossed in a complete diallel scheme, generating 15 populations. Parents and populations, along with five commercial controls, were evaluated for agronomic traits across four planting seasons, two during the first Brazilian crop season and two during the second crop season of 2018/2019. Diallel analyses were conducted across different planting dates to evaluate combining ability, while genotype $\times$ environment ($G \times E$) interaction was assessed using the GGE biplot methodology. Hybrid G1 was identified as a promising parent for reducing the growth cycle, while G2, G3, and G4 showed favourable effects for yield-related traits. The crosses $G1 \times G4$, $G3 \times G6$, and $G1 \times G6$ showed high stability and performance for grain yield. These results indicated that these parents and crosses were strong candidates for the development of base populations in maize breeding programs.

Key words: *Zea mays* L., diallel analysis, grain yield, $G \times E$, GGE Biplot.

INTRODUCTION

The choice of suitable parents in maize breeding programs requires combining a high frequency of favourable alleles with broad genetic variability across multiple traits (Zhang et al., 2017; Coelho et al., 2020). Using commercial hybrids as parents is an interesting strategy because they combine desirable phenotypic traits with a high frequency of favourable alleles, saving time and resources in developing base populations (Guimarães et al., 2018; Luz

et al., 2024). Diallel analysis enables the identification of promising hybrid combinations based on general combining ability (GCA) and specific combining ability (SCA) estimates, which reflect additive and non-additive effects (Fasahat et al., 2016; Zhang et al., 2017). Such parameters are particularly useful for selecting crosses with higher probabilities of transmitting desirable traits to their progeny (Ramadan et al., 2021; Mukri et al., 2022).

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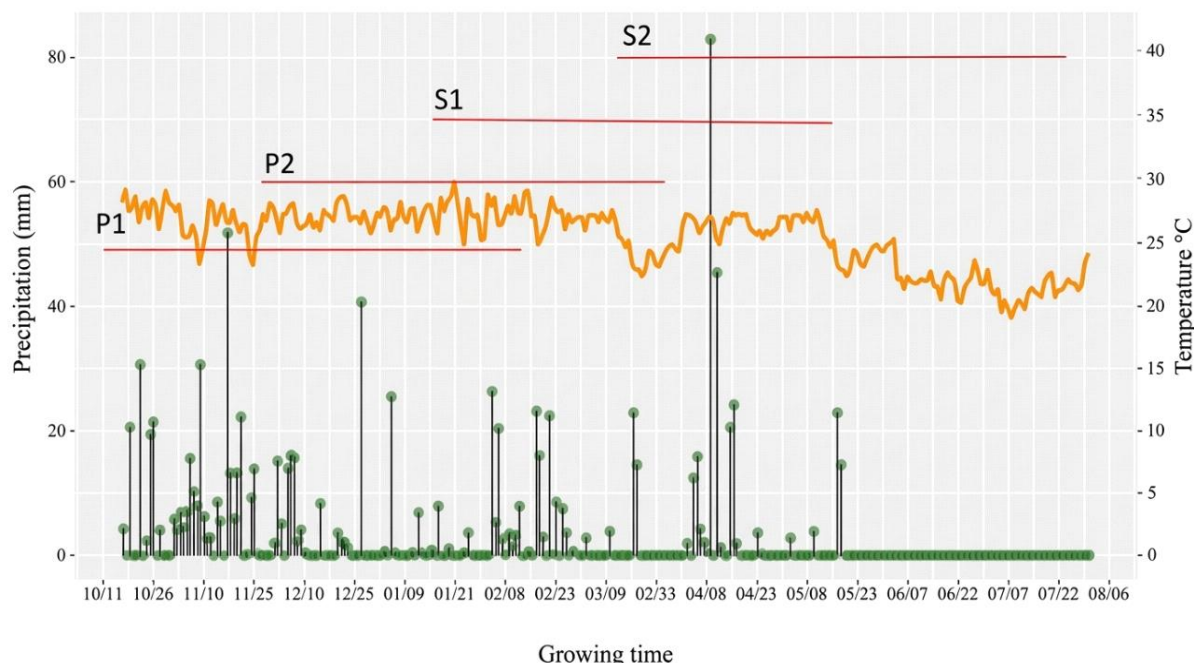


Figure 1. Precipitation (mm) and average ambient temperature (°C). Daily totals occurred throughout the period of evaluation in environments P1, P2, S1 and S2, during the 2018/2019 growing season, in Goiânia-GO.

However, the expression of quantitative traits is strongly influenced by the environment, making it necessary to assess genotype $\times$ environment ($G \times E$) interactions to ensure both performance and stability (Nyombayire et al., 2018; Mekonnen et al., 2023). In Brazil, where both first- and second-season maize crops are predominant, the environmental variability across planting seasons is considerable (Rezende, 2020; Miranda et al., 2021). This reinforces the importance of evaluating the stability and adaptability of genotypes not only across growing seasons but also at different sowing dates within the same season. Moreover, recent studies indicate that climate change has intensified and lengthened drought periods, negatively affecting maize phenology and yield (Nyombayire et al., 2018; Sah et al., 2020; Silva et al., 2021).

Given these challenges, it is crucial to evaluate hybrid performance in terms of stability and adaptability, not only between crop seasons but also across planting dates within each season. Such evaluations help identify parents and crosses that are more suitable for specific environmental conditions, thus supporting more precise decision-making in breeding programs (Coelho et al., 2020; Lima et al., 2023; Akintunde et al., 2025). The objective of this study was to identify promising parents and crosses, based on GCA and SCA estimates, for the development of base populations in the maize breeding program at the Federal University of Goiás, evaluating their performance across four different planting dates during the 2018/2019 growing season in the Brazilian Cerrado.

MATERIALS AND METHODS

Six single-cross hybrids: 30F53 (G1), DKB 310 PRO3 (G2), LG 3055 PRO3 (G3), P4285 YHR (G4), 30F35 (G5), and AS 1575 (G6), were crossed in a complete diallel design during the 2017/2018 summer season at the experimental station of the School of Agronomy at the Federal University of Goiás, resulting in 15 double-cross hybrids. These hybrids are widely cultivated in the state of Goiás and are suitable for both grain and silage production. Four commercial double-cross hybrids BM 207 (T1), SHS 4080 (T3), SHS 4070 (T4), AG 1051 (T5), and one triple-cross hybrid, BM 3061 (T2), were included as controls for mean comparison and were not included in the diallel analyses.

The genotypes were evaluated during the 2018/2019 harvest season across four planting dates (environments): P1 (first planting in the first season, 10/17/2018), P2 (second planting in the first season, 11/28/2018), S1 (first planting of the second season, 01/15/2019), and S2 (second planting of the second season, 03/01/2019). Daily precipitation (mm) and average temperature (°C) were recorded at the UFG weather station (Figure 1).

The experiments were conducted in a randomized complete block design with three replications. Each plot consisted of a single 4 m row, spaced 0.80 m between rows and 0.20 m between plants, totaling 20 plants per plot (62,500 plants ha^{-1}). The following traits were evaluated: female flowering (FF, days): number of days from sowing until 50% of the plants in the plot had silk emergence; male flowering (MF, days): number of days from sowing until 50% of the plants in the plot were shedding pollen; ear production (EP, t ha^{-1}); and grain yield (GY, t ha^{-1}), adjusted to 13% moisture. Grain moisture was determined using a Gehaka Agri G650 meter. Ear and grain yields were corrected to the ideal stand of 20 plants per plot, according to Vencovsky and Cruz (1991), using the Genes software (Cruz, 2006). When significant differences were detected, means were grouped using the Scott-Knott test at a 5% probability level.

Individual diallel analyses were performed according to Griffing's

(1956) Method 2. For these analyses, a fixed-effect model was adopted, in which only the effect of the experimental error is considered random. The genotype effect was treated as fixed because the single-cross hybrids were specifically selected based on their agronomic performance and relevance to the maize market in the State of Goiás, representing a specific set of interest rather than a random sample of the population. Therefore, the inferences are restricted to these genotypes.

The following parameters were estimated: overall mean ($\bar{m}$), general combining ability ($\hat{g}_i$), and SCA ($\hat{s}_{ij}$), as described by Cruz et al. (2012). Coefficients of determination (R^2) were calculated as follows:

$$R^2(\text{GCA}) = (\text{SQ}_{\text{GCA}} / \text{SQ}_{\text{Treat}}) \times 100$$

$$R^2(\text{SCA}) = (\text{SQ}_{\text{SCA}} / \text{SQ}_{\text{Treat}}) \times 100$$

where SQ_{GCA} and SQ_{SCA} are the sums of squares for general and SCA, respectively, and SQ_{Treat} is the sum of squares for treatments. Quadratic components ($\hat{\phi}$), were also estimated to express genetic variability (Cruz et al., 2012). All analyses were performed using the Genes software (Cruz, 2006). Genotype $\times$ environment (G $\times$ E) interaction was evaluated for grain yield, considering both general and SCA estimates. The GGE Biplot model (Yan et al., 2007) was implemented using the “GGE BiplotGUI” package in R software (R Core Team, 2016). The JK scaling (row metric preserving) was adopted for the “Mean vs. Stability” analysis, as it preserves genotype main effects, facilitating the comparison of mean performance and stability. In contrast, the GH scaling (column metric preserving) was used for the “Which-Won-Where” biplot, as it emphasizes genotype $\times$ environment interaction patterns and aids in identifying mega-environments. Both analyses used a genotype-centered model without scaling, since all traits were measured in the same unit.

RESULTS AND DISCUSSION

Individual diallel analyses

In this study, the identification of superior crosses was based on the combined evaluation of GCA and SCA estimates. Crosses were considered promising when they exhibited positive SCA effects associated with at least one parent presenting high GCA for the trait of interest, indicating favorable additive effects combined with advantageous dominance deviations. The joint diallel analysis revealed significant effects ($p < 0.05$) for the interaction between GCA and planting dates for the most relevant traits, including grain yield and ear weight. This significant interaction indicates that parent performance was not consistent across environments, which statistically justifies the decision to analyze planting dates individually and subsequently apply the GGE biplot methodology to identify genotypes with superior stability and adaptability.

Significant differences were observed for GCA ($p < 0.01$) in ear production and grain yield across all environments; for SCA in the first planting of the second season (S1) for EP; and in both plantings of the second season (S1 and S2) for GY (Table 1). In all cases, GCA effects accounted for the largest proportion of variance, with coefficients of

determination exceeding 60%, reaching up to 82.68% in S2. These results indicate variation in the contribution of favorable alleles from the parental lines in the expression of EP and GY (Mogesse et al., 2020).

In all environments, GCA accounted for the largest proportion of the treatment sum of squares (Table 1), indicating that additive effects were more relevant than non-additive effects in trait expression. This result is consistent with several studies that also reported the predominance of additive over dominance effects for ear weight and grain yield (Lemos et al., 2002; Oliboni et al., 2013; Melo et al., 2017; Mogesse et al., 2020; Rezende, 2020). According to these authors, such predominance can be explained by the heterogeneity of the parental lines, thereby evidencing the presence of genetic variability among them.

The superiority of GCA for both traits was also confirmed by the estimates of the ratio between quadratic components ($\hat{\phi}_g / \hat{\phi}_s$), which exceeded 1.26 (Table 1). According to Bernardo (2020), the variance associated with additive effects generally outweighs that of dominance effects, even when the latter contribute to trait control, as is the case for grain yield in maize. In maize breeding, the predominance of additive effects is highly relevant, as it ensures the consistent transmission of favorable alleles across generations, increasing the efficiency of recurrent selection and accelerating genetic gain (Hallauer et al., 2010). GCA effects were prioritized in the identification of parental lines for the formation of the base populations in this study.

Parents G2, G3, and G4 contributed most to the performance of the hybrids, with parent G4 standing out due to its highest GCA estimates in three of the four experiments (P1, S1, and S2), both for EP (1.44 to 1.79) and grain yield (0.98 to 1.29) (Table 2), indicating that these parents carry a high frequency of favorable alleles and are promising candidates for the development of base populations (Oliboni et al., 2013). In contrast, parents G1, G5, and G6 showed the lowest estimates, reducing the mean performance of the crosses in which they were involved.

In environment S1, the G3 $\times$ G4 cross proved highly favorable, as it exhibited positive SCA estimates (Table 3) combined with high GCA values (Table 2). This combination indicates desirable gene flow between the parents, suggesting the simultaneous presence of additive and positive dominance effects capable of producing superior hybrids (Wuhaib, 2016; Fasahat et al., 2016; Mukri et al., 2022), which was prioritized in this study. However, in environment S2, for grain yield, the G3 $\times$ G4 cross displayed a negative SCA estimate ($\hat{s}_{34} = -1.23$) (Table 3). Although parents G1, G5, and G6 had positive SCA values in this environment, they showed low GCA values (Table 2).

The purpose of the crosses between commercial hybrids in this study was not to generate new commercial hybrids, but rather to evaluate their potential for composing base

Table 1. Summary of individual diallel analyses, coefficients of determination (R^2), general means and quadratic components for ear production (EP, t ha⁻¹) and grain yield (GY, t ha⁻¹). evaluated in the first (P1) and second (P2) sowing times of the first growing season, and first (S1) and second (S2) sowing times of the second growing season of 2018/2019.

SV	df	Mean square							
		EP				GY			
		P1	P2	S1	S2	P1	P2	S1	S2
Treat.	20	10.31**	6.35**	12.00**	11.39**	5.29**	3.26**	5.34**	7.37**
GCA	5	27.26**	17.62**	35.79**	37.68**	13.03**	8.22**	16.3**	23.95**
SCA	15	4.66	2.60	4.07**	2.63	2.71	1.60	1.68**	1.84*
Error	40	2.43	1.77	0.62	1.47	1.57	0.98	0.25	0.95
R2 (GCA)		66.08	69.32	74.55	82.68	61.58	63.06	76.41	81.27
R2 (SCA)		33.92	30.68	25.45	17.32	38.42	36.94	23.59	18.73
Mean		10.51	3.82	3.60	4.84	7.74	2.39	1.95	3.57
Quadratic components									
$\hat{\phi}_g$ (Fixed)		1.03	0.66	1.46	1.51	0.48	0.30	0.67	0.96
$\hat{\phi}_s$ (Fixed)		0.74	0.28	1.15	0.39	0.38	0.21	0.48	0.30
$\hat{\phi}_g/\hat{\phi}_s$		1.39	2.36	1.27	3.87	1.26	1.43	1.40	3.2

SV: Source of variation; df: degree of freedom; Treat.: treatment **, *: Significant at 1 and 5% probability by F test; $\hat{\phi}_g$: quadratic components of GCA; $\hat{\phi}_s$: quadratic components of SCA.

Table 2. Estimates of general combining ability ($\hat{g}_i$) of the crosses and standard deviation (SD) of these estimates for ear production (EP, t ha⁻¹) and grain yield (GY, t ha⁻¹) in the first (P1) and second (P2) sowing times of the first season, and first (S1) and second (S2) sowing times of the second season of 2018/2019.

Effect	Estimates of general combining ability (GCA)							
	EP				GY			
	P1	P2	S1	S2	P1	P2	S1	S2
$\hat{g}_1$	-1.66	-1.51	-1.70	-1.75	-1.19	-0.99	-1.06	-1.41
$\hat{g}_2$	0.42	0.22	0.28	0.95	0.32	0.20	0.23	0.84
$\hat{g}_3$	0.57	1.04	0.43	0.61	0.32	0.80	0.25	0.44
$\hat{g}_4$	1.44	0.45	1.79	1.59	0.98	0.15	1.29	1.22
$\hat{g}_5$	-0.27	0.01	0.21	-0.71	-0.07	0.00	-0.01	-0.55
$\hat{g}_6$	-0.50	-0.22	-1.03	-0.69	-0.36	-0.15	-0.70	-0.55
SD ($\hat{g}_i$)	0.29	0.25	0.15	0.23	0.23	0.18	0.09	0.18
SD ($\hat{g}_i - \hat{g}_j$)	0.45	0.38	0.23	0.35	0.36	0.29	0.14	0.28

populations. The main advantage of using these hybrids lies in the fact that they have already undergone breeding processes, ensuring a high frequency of favorable alleles (Guimarães et al., 2018; Coelho et al., 2020) and sufficient genetic variability to enable gains through selection (Oliboni et al., 2013; Crispim-Filho et al., 2020).

Accordingly, by crossing three hybrids in pairs, three promising combinations were identified ($G2 \times G3$, $G2 \times G4$, and $G3 \times G4$), which are derived from four inbred lines. Overall, the means of these crosses were higher than

those of the others, suggesting that the populations derived from them combine both genetic variability and a high frequency of favorable alleles, thus exhibiting strong potential for grain yield (Table 4).

Another alternative for forming base populations would be the cross $[(G2 \times G3) \times G4]$, since parent $G4$, in addition to showing the highest GCA estimates (Table 2), consistently ranked among the highest-performing genotypes across planting dates, not differing statistically from the superior group in all environments (Table 4). This

Table 3. Estimates specific combining ability ($\hat{s}_{ii}$) of the crosses and standard deviation (SD) of these estimates for ear production (EP, t ha⁻¹) and grain yield (GY, t ha⁻¹) in the first (P1) and second (P2) sowing times of the first season, and first (S1) and second (S2) sowing times of the second season of 2018/2019.

Effect	Estimates specific combining ability (SCA)							
	EP				GY			
	P1	P2	S1	S2	P1	P2	S1	S2
$\hat{s}_{12}$	2.37	0.11	-0.54	-0.88	1.64	0.11	-0.34	-0.84
$\hat{s}_{13}$	-0.15	-1.24	-0.65	-0.45	-0.08	-0.96	-0.41	-0.29
$\hat{s}_{14}$	0.01	0.82	-0.71	-0.94	0.11	0.40	-0.55	-0.72
$\hat{s}_{15}$	-1.20	-0.19	-0.54	-0.28	-1.26	-0.06	-0.29	-0.41
$\hat{s}_{16}$	0.35	0.61	0.37	0.27	0.11	0.52	0.30	0.27
$\hat{s}_{23}$	-1.32	0.33	0.15	-0.20	-1.01	0.22	0.10	-0.14
$\hat{s}_{24}$	-0.92	0.58	-0.31	-0.54	-0.81	0.47	-0.79	-0.43
$\hat{s}_{25}$	-0.87	-0.91	-1.14	-0.21	-0.52	-0.71	-0.60	-0.14
$\hat{s}_{26}$	-0.21	-1.46	0.25	-0.84	-0.16	-0.98	0.90	-0.72
$\hat{s}_{34}$	-0.88	-0.68	0.26	-1.53	-0.87	-0.42	0.14	-1.23
$\hat{s}_{35}$	-1.04	-1.00	-0.75	0.12	-0.65	-0.78	-0.42	0.12
$\hat{s}_{36}$	0.26	0.19	-0.19	0.24	0.05	0.09	-0.09	0.15
$\hat{s}_{45}$	-1.20	0.26	-1.74	0.31	-0.83	0.41	-1.02	0.33
$\hat{s}_{46}$	0.22	-1.12	0.05	-0.21	0.24	-0.90	-0.28	-0.27
$\hat{s}_{56}$	0.42	-0.27	-1.40	-0.87	0.35	-0.63	-0.60	-0.70
SD ($\hat{s}_{ii}$)	0.66	0.56	0.33	0.51	0.53	0.42	0.21	0.41
SD ($\hat{s}_{ij}$)	0.80	0.68	0.40	0.62	0.64	0.51	0.25	0.50
SD ($\hat{s}_{ii}\hat{s}_{jj}$)	0.90	0.77	0.46	0.70	0.72	0.57	0.29	0.56
SD ($\hat{s}_{ii}\hat{s}_{ik}$)	1.19	1.02	0.60	0.93	0.96	0.76	0.38	0.74
SD ($\hat{s}_{ij}\hat{s}_{kl}$)	1.10	0.94	0.56	0.86	0.89	0.70	0.35	0.69

scheme would allow greater contribution of alleles from G4 to the base population, especially if SCA effects are also considered in the selection process. According to Cruz et al. (2012), the most promising hybrid combinations should exhibit high SCA estimates and include at least one parent with strong GCA effects for the trait under evaluation. The greater the magnitude of SCA, the more advantageous the combination, as it indicates the presence of favorable dominance deviations (Hallauer et al., 2010; Zhang et al., 2017).

The importance of SCA estimates lies in the fact that, when the goal is to develop populations for interpopulation recurrent selection, it is desirable that they be contrasting (Oliboni et al., 2013). In this context, one alternative would be the formation of two populations from hybrids G3 and G4, which, as previously discussed, showed positive SCA estimates in environment S1. However, the results indicate that populations derived from these hybrids would not present sufficient contrast to ensure consistent progress

through reciprocal recurrent selection.

The poor performance of genotypes in the second planting of the first season (P2) was likely related to drought (Figure 1), which negatively affected the pre-flowering period, tasseling, and early grain filling. Water stress during flowering compromises tasseling and grain filling, significantly reducing yield (Sah et al., 2020; Silva et al., 2021). In contrast, environments P1 and S2 presented more favorable conditions, allowing greater uniformity in the expression of the genotype's genetic potential. This fluctuation across planting times reinforces the importance of evaluating genotypes within the same crop season, and not only across seasons, since water instability may occur randomly between planting periods and even between weeks within the same growing cycle (Sah et al., 2020; Mekonnen et al., 2023).

The individual diallel analysis for female (FF) and male (MF) flowering revealed significant differences for GCA in both environments of the first season (P1 and P2) and in

Table 4. Means and mean test for the traits ear production (EP, t ha⁻¹) and grain yield (GY, t ha⁻¹) of the six single-crosses (parents) and 15 populations evaluated in the first (P1) and second (P2) sowing times of the first season, and first (S1) and second (S2) sowing times of the second season of 2018/2019.

Genotype	EP				GY			
	P1	P2	S1	S2	P1	P2	S1	S2
G1	6.51 ^c	3.59 ^b	1.25 ^e	2.49 ^d	5.10 ^b	0.39 ^b	0.47 ^e	1.74 ^d
G2	11.83 ^b	4.94 ^a	4.97 ^c	8.09 ^a	8.82 ^a	3.23 ^a	3.18 ^b	6.40 ^a
G3	13.23 ^a	7.11 ^a	5.06 ^c	6.98 ^b	9.66 ^a	4.91 ^a	2.79 ^c	5.16 ^b
G4	14.79 ^a	4.80 ^a	8.41 ^a	9.49 ^a	10.78 ^a	2.71 ^a	5.78 ^a	7.18 ^a
G5	11.91 ^b	4.91 ^a	6.81 ^b	3.89 ^c	9.06 ^a	3.27 ^a	3.40 ^b	2.88 ^c
G6	8.99 ^c	4.41 ^a	2.00 ^e	4.18 ^c	6.74 ^b	3.03 ^a	0.84 ^e	3.11 ^c
G1 × G2	11.64 ^b	2.64 ^b	1.65 ^e	3.17 ^d	8.51 ^a	1.70 ^b	0.77 ^e	2.17 ^d
G1 × G3	9.27 ^c	2.12 ^b	1.69 ^e	3.26 ^d	6.78 ^b	1.23 ^b	0.72 ^e	2.32 ^d
G1 × G4	10.30 ^c	3.59 ^b	2.99 ^d	3.74 ^c	7.63 ^a	1.94 ^b	1.62 ^d	2.66 ^c
G1 × G5	7.38 ^c	2.14 ^b	1.57 ^e	2.11 ^d	5.23 ^b	1.34 ^b	0.58 ^e	1.21 ^d
G1 × G6	8.70 ^c	2.70 ^b	1.25 ^e	2.68 ^d	6.30 ^b	1.76 ^b	0.49 ^e	1.88 ^d
G2 × G3	10.19 ^c	5.42 ^a	4.47 ^c	6.21 ^b	7.38 ^a	3.60 ^a	2.53 ^c	4.72 ^b
G2 × G4	11.46 ^b	5.07 ^a	5.36 ^c	6.85 ^b	8.23 ^a	3.21 ^a	2.69 ^c	5.20 ^b
G2 × G5	9.79 ^c	3.15 ^b	2.94 ^d	4.87 ^c	7.48 ^a	1.88 ^b	1.57 ^d	3.73 ^c
G2 × G6	10.22 ^c	2.37 ^b	3.10 ^d	4.28 ^c	7.54 ^a	1.45 ^b	1.57 ^d	3.15 ^c
G3 × G4	11.65 ^b	4.63 ^a	6.08 ^c	5.52 ^b	8.17 ^a	2.92 ^a	3.63 ^b	4.00 ^b
G3 × G5	9.77 ^c	3.87 ^a	3.49 ^d	4.87 ^c	7.34 ^a	2.41 ^a	1.77 ^d	3.59 ^c
G3 × G6	10.84 ^b	4.83 ^a	2.82 ^d	5.02 ^c	7.75 ^a	3.12 ^a	1.41 ^d	3.62 ^c
G4 × G5	10.48 ^c	4.55 ^a	3.86 ^d	6.04 ^b	7.82 ^a	2.95 ^a	2.21 ^c	4.57 ^b
G4 × G6	11.68 ^b	2.94 ^b	4.42 ^c	5.54 ^b	8.60 ^a	1.48 ^b	2.26 ^c	3.97 ^b
G5 × G6	10.16 ^c	3.34 ^b	1.38 ^e	2.58 ^d	7.67 ^a	1.60 ^b	0.64 ^e	1.78 ^d
General mean	10.51	3.96	3.60	4.85	7.74	2.88	1.95	3.57

Means followed by the same letter in the same column do not differ statistically among themselves by Scott-knott test ($p < 0.05$).

the second environment of the second season (S2) (Table 5). Parents G1 and G6 showed negative GCA estimates for both flowering traits in most environments, indicating their potential to reduce the crop cycle. For instance, G1 presented negative estimates for FF and MF in P1 (-0.82 and -0.47, respectively) and P2 (-0.13 and -0.89), while G6 showed even more pronounced negative effects, particularly for MF in P1 (-0.76) and P2 (-1.06) (Table 6).

Although both parents contribute to earlier flowering, G6 demonstrated greater consistency and magnitude in reducing the flowering period across environments compared to G1. This suggests that G6 has a higher potential for developing early-maturing genotypes. However, these parents were also associated with lower grain yield (Table 4), indicating a possible trade-off between earliness and productivity. This is likely due to a shorter grain-filling period and reduced photoassimilate accumulation in earlier genotypes (Mekonnen et al., 2023), which should be carefully considered in breeding strategies.

The highest SCA values for female (FF) and male (MF) flowering traits were observed in P2 and S1 (Table 5), which may be attributed to the water stress recorded in

these environments (Figure 1). Previous studies have shown that floral synchronization is highly sensitive to water deficit (Amaral et al., 2016; Sah et al., 2020; Mekonnen et al., 2023), which may enhance the expression of non-additive effects under stress conditions. In this context, although G2, G3, and G4 were identified as the most promising parents for yield-related traits, some crosses involving these genotypes stood out for flowering earliness. In particular, G1 × G4 and G2 × G3 showed the most negative SCA estimates for FF and MF (Table 6), indicating that these combinations, through dominance effects, contributed to reducing the flowering cycle across planting periods.

The SCA estimates indicated that the crosses G1 × G5, G3 × G4, and G5 × G6 were the least favorable for flowering traits, as each presented ten positive values out of twelve possible, considering three flowering traits across four planting periods (Table 6). In other words, these combinations tend to prolong the maize growth cycle and increase the interval between female and male flowering under most growing conditions.

As previously discussed, environments P2 and S1 were affected by water deficiency. In S1, precipitation was

Table 5. Summary of individual diallel analyses, coefficients of determination (R^2), general means and quadratic components for the flowering traits: female flowering (FF, days) and male flowering (MF, days), evaluated in the first (P1) and second (P2) sowing time of the first season, and first (S1) and second (S2) sowing time of the second season of 2018/2019.

SV	df	Mean Squares							
		FF				MF			
		P1	P2	S1 ¹	S2	P1	P2	S1 ¹	S2
Treat.	20	5.73*	711.43**	87.03	5.55	5.92**	11.08**	78.16	4.72
GGA	5	7.56**	224.67**	87.55	13.19*	8.89**	27.89**	53.20	6.74*
SCA	15	5.12	486.76**	86.86	3.00	4.92**	5.47	86.48*	4.05
Error	40	2.87	427.05	58.37	4.11	1.32	3.23	43.47	2.73
R^2 (GCA)		32.99	31.58	25.15	59.44	37.59	62.95	17.02	35.72
R^2 (SCA)		67.01	68.42	74.85	40.56	62.41	37.05	82.98	64.28
Mean		59.41	65.43	70.88	60.32	59.21	62.11	70.33	58.83
Quadratic components									
$\hat{\Phi}_g$ (Fixed)		0.20	1.43	1.22	0.38	0.32	1.03	0.41	0.17
$\hat{\Phi}_s$ (Fixed)		0.75	7.26	9.50	-0.37	1.20	0.75	14.34	0.44

SV: source of variation; df: degree of freedom; Treat.: treatment; **, *: significant at 1 and 5% probability by the F test; $\hat{\Phi}_g$: quadratic components of the general combining ability; $\hat{\Phi}_s$: quadratic components of the specific combining ability; 1: degree of freedom of the residuals equal to 39 due to the loss of experimental plot.

Table 6. Estimates of general combining ability ($\hat{g}_i$) for the six parents, specific combining ability ($\hat{s}_{ij}$) of the crosses and standard deviation (SD) of these estimates for the flowering traits: female flowering (FF, days), male flowering (MF, days), evaluated in the first (P1) and second (P2) sowing time of the first season, and first (S1) and second (S2) sowing time of the second season of 2018/2019.

Effect	FF				MF			
	P1	P2	S1	S2	P1	P2	S1	S2
Estimates of general combining ability (GCA)								
$\hat{g}_1$	-0.82	-0.13	1.58	-0.19	-0.47	-0.89	0.65	-0.39
$\hat{g}_2$	0.60	1.71	-0.65	-0.28	0.94	1.49	-0.29	0.94
$\hat{g}_3$	0.68	-2.08	2.14	-0.36	-0.14	-0.89	2.26	-0.43
$\hat{g}_4$	-0.07	0.50	-3.23	-0.74	0.36	0.69	-2.33	-0.01
$\hat{g}_5$	-0.15	0.96	0.44	0.18	0.07	0.65	-0.04	-0.35
$\hat{g}_6$	-0.24	-0.96	-0.29	1.39	-0.76	-1.06	-0.26	0.24
SD ($\hat{g}_i$)	0.32	0.61	1.42	0.38	0.21	0.33	1.23	0.31
SD ($\hat{g}_i - \hat{g}_j$)	0.49	0.94	2.21	0.59	0.33	0.52	1.90	0.48
Estimates of specific combining ability (SCA)								
$\hat{s}_{12}$	-1.86	-5.35	1.18	0.82	-1.35	-1.71	0.31	-0.71
$\hat{s}_{13}$	0.39	0.11	-1.28	-0.43	0.07	0.00	-1.23	0.66
$\hat{s}_{14}$	-1.52	-2.47	-2.23	-1.39	-1.43	-0.58	-1.32	-1.42
$\hat{s}_{15}$	2.23	4.74	7.77	0.70	1.86	2.46	8.06	0.58
$\hat{s}_{16}$	-0.36	-2.68	3.33	-0.51	0.03	-0.83	4.79	-0.34
$\hat{s}_{23}$	0.64	-2.72	-1.05	-0.01	-0.01	-1.04	-0.97	-0.34
$\hat{s}_{24}$	0.73	-1.64	10.33	-0.30	-0.18	-0.29	9.96	0.24
$\hat{s}_{25}$	0.48	2.24	-1.34	-0.89	0.11	1.42	-1.34	-0.09

Table 6. Contd

$\hat{s}_{26}$	-0.77	2.49	-5.94	1.24	-1.72	1.13	-5.11	1.66
$\hat{s}_{34}$	0.98	3.49	2.21	1.78	0.24	0.75	1.41	0.95
$\hat{s}_{35}$	0.39	1.36	-4.13	1.20	0.53	0.79	-5.22	-0.71
$\hat{s}_{36}$	0.48	-1.05	0.60	-0.01	1.03	0.17	0.35	2.04
$\hat{s}_{45}$	-0.19	0.45	-6.76	0.57	0.36	0.54	-5.63	1.20
$\hat{s}_{46}$	1.89	3.70	2.64	0.36	2.20	1.92	2.93	0.62
$\hat{s}_{56}$	0.64	1.24	-7.36	0.45	0.49	-1.71	-7.36	-1.38
SD ($\hat{s}_{ii}$)	0.72	1.38	3.23	0.86	0.49	0.76	2.79	0.70
SD ($\hat{s}_{ij}$)	0.87	1.67	3.91	1.04	0.59	0.92	3.37	0.85
SD ($\hat{s}_{ii}, \hat{s}_{jj}$)	0.98	1.89	4.41	1.17	0.66	1.04	3.81	0.95
SD ($\hat{s}_{ii}, \hat{s}_{ik}$)	1.29	2.50	5.83	1.55	0.88	1.37	5.04	1.26
SD ($\hat{s}_{ij}, \hat{s}_{kl}$)	1.20	2.31	5.40	1.43	0.81	1.27	4.66	1.17

insufficient during the initial germination stage. In P2, rainfall during the critical flowering period was extremely limited, with virtually no precipitation recorded. In addition, the crop faced a pronounced dry spell during the flowering window (late December to mid-January), when daily precipitation remained near zero for approximately 15 consecutive days (Figure 1).

In P2, drought stress directly impacted the flowering interval, widening the gap between female and male flowering, an effect also reported by Amaral et al. (2016), Sah et al. (2020), and Mekonnen et al. (2023). Water deficit not only compromises pollination efficiency but also increases the risk of yield losses (Sah et al., 2020; Silva et al., 2021), reinforcing the need to assess genotype adaptability across different planting dates within the same season.

Environment S1 showed higher coefficients of variation for flowering traits, likely due to the lack of precipitation during the initial growth stage. Some genotypes were able to germinate using the residual soil moisture before the rainfall interruption, while others experienced delayed emergence. Since the calculation of the flowering interval in this study was based on the planting date, these differences in emergence resulted in more divergent values in this environment.

GGE Biplot analysis

The GGE Biplot analysis revealed consistent patterns of genotype $\times$ environment interaction. The first two principal axes explained 97.1% of the total variation for GCA and 75.5% for SCA in grain yield (Figure 2A), values were considered adequate for a reliable interpretation (Shojaei et al., 2022). The “Mean vs. Stability” plot analysis for grain yield, based on GCA estimates, showed that genotypes

G4, G3, and G2 had higher means compared to the others (Figure 2A). However, although G4 exhibited the highest mean grain yield (Table 5), it was also the most unstable.

In the GGE biplot context, the greater the absolute distance of a genotype from the ATC horizontal axis (represented by magnitude of the PC2 score), the more unstable it is across environments (Yan et al., 2007). Thus, G4's position, characterized by the largest projection onto the ATC ordinate among the high-yielding genotypes, indicates a high contribution to the Genotype $\times$ Environment interaction, despite its high yield potential. Similar variation in the productive performance of different maize genotypes under changing environmental conditions has also been reported by Coelho et al. (2020), Lima et al. (2023), and Akintunde et al. (2025).

Although this study was based on the evaluation of a single crop season (2018/2019), the GGE biplot methodology proved to be an effective tool for identifying mega-environments and genotypes with specific adaptation. This enabled a more precise parental selection for the different planting dates analyzed.

Higher SCA estimates for grain yield were observed in the crosses G1 $\times$ G2, G1 $\times$ G6, G1 $\times$ G4, G3 $\times$ G6, and G5 $\times$ G6 (Table 3). Among them, the G3 $\times$ G6 cross stood out, showing the highest stability (Figure 2B), followed by G1 $\times$ G6. Although G3 $\times$ G6 presented low SCA values (-0.19 to 0.26), its superiority is primarily driven by the high GCA of parent G3 and exceptional environmental stability. This indicates that additive genetic effects and favorable G $\times$ E interactions were more decisive than non-additive effects (SCA) for its consistent performance (Habiba et al., 2022). Furthermore, both crosses involved the top-performing genotypes (Table 5), confirming their potential for breeding programs focused on high yield and stability.

In the “Which Won Where/What” plot, used to identify grain yield potential, the four environments were grouped

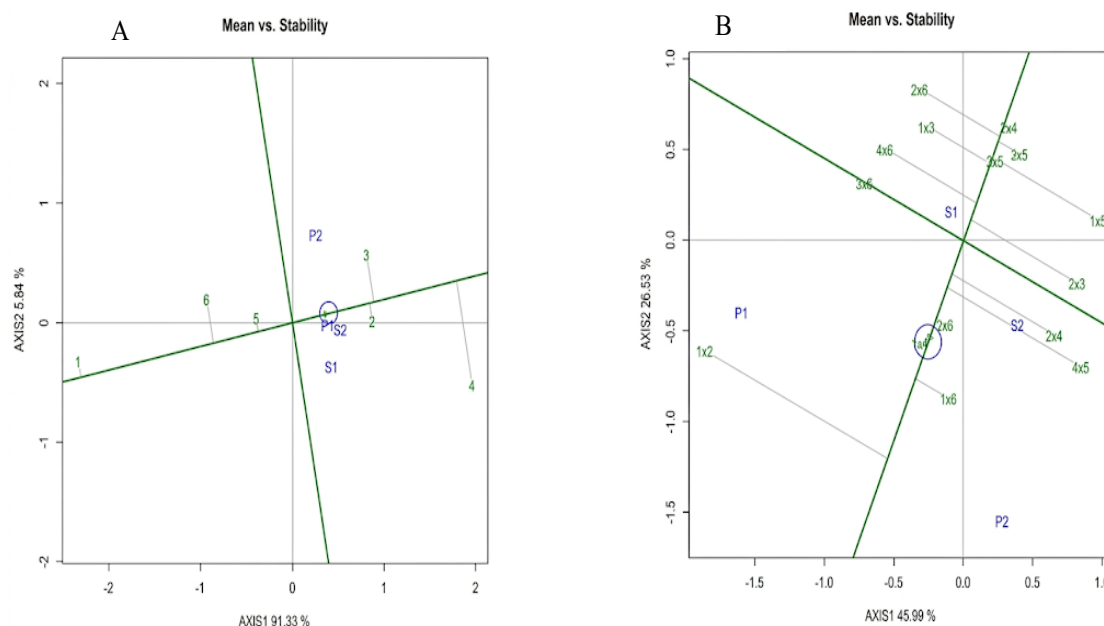


Figure 2. Genotype-by-environment interaction analysis using the GGE Biplot. A: Relationship between trait mean and genotype stability (Mean vs. Stability) of general combining abilities (GCA); B: Relationship between trait mean and genotype stability (Mean vs. Stability) of specific combining abilities (SCA) for grain yield in a complete diallel scheme with six single-crosses parents in P1, P2, S1, and S2 environments during the 2018/2019 season in Goiânia-GO.

into two mega-environments (Yan et al., 2007). The polygonal view highlighted the most productive hybrids within each group and indicated that these materials can guide the choice of the most suitable planting time (Liu et al., 2022). Environment P2 was placed separately into one mega-environment, with G3 identified as the winning genotype, while P1, S1, and S2 were clustered into another mega-environment, where G4 emerged as the winner (Figure 3A). Similarly, Nyombayire et al. (2018), when analyzing maize hybrids using the “Which Won Where/What” plot, emphasized the importance of this approach for identifying genotype adaptation not only across contrasting environments but also within regional contexts.

In the “Which Won Where/What” analysis, G1 and G6 were included in the polygon but had no environments associated with them, thus being considered unfavorable due to their low yield performance (Figure 3A). Previous studies have also identified genotypes without specific adaptation using the GGE Biplot approach (Santos et al., 2016; Lima et al., 2023).

To adapt maize hybrids to different yield environments, it is essential to understand the interaction between genotypes and locations (Akintunde et al., 2025). In the analysis of SCA estimates for grain yield, the four environments were grouped into four mega-environments (Figure 3B). The G1 × G2 cross was the winning genotype in P1, followed by G2 × G6 in S1, G4 × G5 in S2, and G1 × G6 in P2. The polygon connected the crosses G1 × G2,

G2 × G6, G3 × G4, G1 × G5, G4 × G5, and G1 × G6, placing them at the vertices of the GGE Biplot. This indicates that these crosses showed longer vectors, reflecting greater sensitivity and differential response to the environments (Yan et al., 2007; Akintunde et al., 2025). Therefore, these hybrids stood out for their specific adaptation, with stronger responses to the environments where they were allocated.

Overall, the results demonstrate that additive genetic effects play a major role in the expression of grain yield, supporting the use of selected parents in breeding strategies focused on population improvement. In addition, the presence of significant genotype × environment interaction reinforces the importance of multi-environment evaluation, particularly across planting dates within the same season. The identification of stable and high-performing crosses such as G1 × G4, G3 × G6, and G1 × G6 highlights their potential for use in breeding programs targeting both productivity and adaptability under Cerrado conditions.

Conclusion

The G1 parent has the potential to reduce the corn cycle, while the G2, G3, and G4 parents stand out for their high GCA and yield stability, making them excellent candidates for breeding programs focused on increasing average grain yield. The G1 × G4, G3 × G6, and G1 × G6 crosses

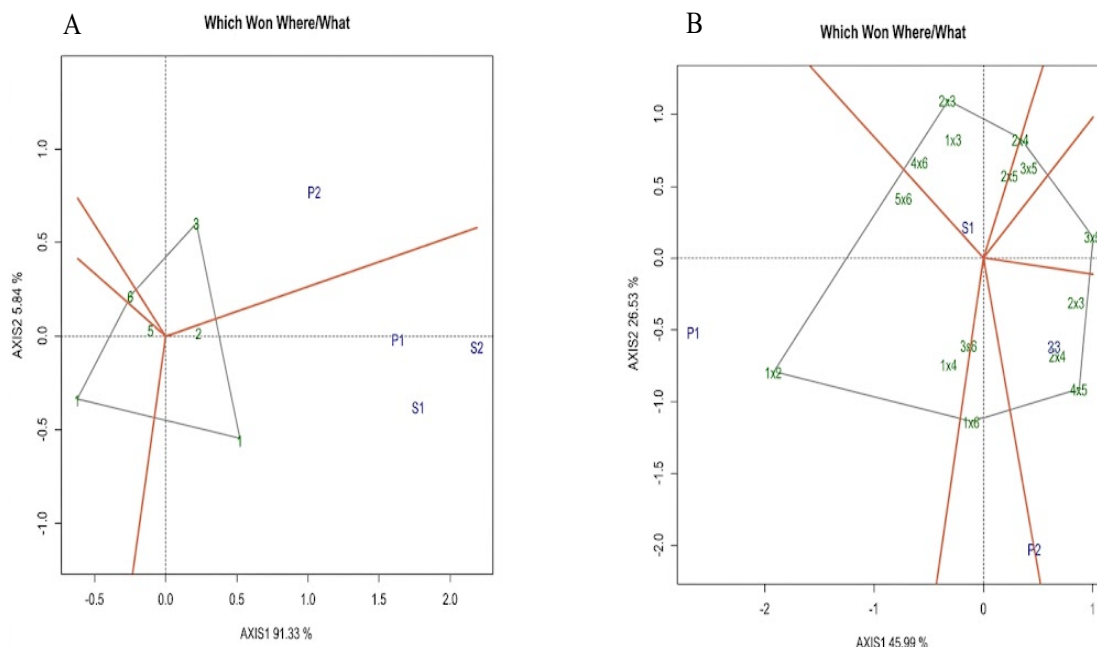


Figure 3. Genotype-by-environment interaction analysis using the GGE Biplot. A: “Which Won Where/What” of general combining abilities (GCA); B: “Which Won Where/What” of specific combining abilities for grain yield in a complete diallel scheme with six single-crosses parents in P1, P2, S1, and S2 environments during the 2018/2019 season in Goiânia-GO.

exhibit high stability and complementarity, indicating their potential for use in breeding programs targeting grain yield. However, these findings are based on a single-season evaluation (2018/2019) and a restricted genetic base. Therefore, while these results provide a solid foundation for local breeding, further multi-year trials with broader germplasm are recommended to confirm the generalizability of these findings across diverse environmental conditions.

ACKNOWLEDGEMENTS

The authors appreciate the Coordination for the Improvement of Higher Education Personnel (CAPES) - Financial Code 001, the Foundation for Research Support of the State of Goiás (FAPEG) for their financial support, and the Federal University of Goiás for the support and infrastructure provided for this research.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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