



Phenotypic characterization of elite maize genotypes under semi-arid conditions of Sergipe, Brazil

Caracterização fenotípica de genótipos elite de milho em condições semiáridas de Sergipe

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Maize has economic, social, and food importance; however, its productivity in semi-arid regions remains below its productive potential due to irregular rainfall, making it a major focus of breeding programs. Thus, this study aimed to characterize the productive performance of elite maize genotypes and identify genotypes that can serve as parental lines for the genetic improvement of drought-tolerant maize in semi-arid regions. Thirty-four elite maize genotypes were evaluated at the Experimental Farm of Embrapa Semi-arid Region, located in Nossa Senhora da Glória, Sergipe, Brazil. A randomized block design with two replicates was employed. The plots consisted of two 5-meter rows spaced 0.80 m x 0.20 m apart. The following variables were evaluated: final stand, number of ears per plot, weight of ears per plot, plant height, ear height, initial stand, relative position of the ear, female flowering in days, male flowering in days, flowering interval, ear length, ear diameter, number of rows per ear, number of grains per row, and grain yield. Data were subjected to analysis of variance, genetic divergence, and principal component analysis. The genotypes 1R2536, 2R2642, 1Q2400, 1Q2370, 1Q2473, 1S2694, 3S2755, 1S2748, 1S2728, 1S2747, 3S2731, SHS 7930 PRO2, 2S2697, BM 270 PRO2, and 1S2746 exhibited superior grain yield performance and were located in divergent groups of Mahalanobis Distance, indicating their potential for selection as base populations.

Keywords: *Zea mays* L., plant breeding, genetic variability.

O milho apresenta importância econômica, social e alimentar, todavia, apresenta produtividade aquém do seu potencial produtivo em regiões de clima semiárido devido às irregularidades das chuvas, tornando-se, assim, objeto de estudos dos programas de melhoramento. Dessa forma, objetivou-se caracterizar o desempenho produtivo de genótipos elite de milho e identificar os genótipos que podem servir como linhagens parentais para o melhoramento genético de milho tolerante à seca em regiões semiáridas. Para isso, foram avaliados 34 genótipos elite de milho na Fazenda Experimental da Embrapa Semiárido, no município de Nossa Senhora da Glória, Sergipe, Brasil. Utilizou-se o delineamento de blocos ao acaso com duas repetições. As parcelas foram constituídas por duas linhas de 5 metros com espaçamento de 0,80 m x 0,20 m. Foram avaliadas as variáveis estande final, número de espigas na parcela, peso de espigas, altura de planta, altura da espiga, estande inicial, posição relativa da espiga, florescimento feminino em dias, florescimento masculino em dias, intervalo de florescimento, comprimento da espiga, diâmetro da espiga, número de fileiras por espiga, número de grãos por fileira e produtividade de grãos. Os dados foram submetidos à análise de variância, divergência genética e de componentes principais. Os genótipos 1R2536, 2R2642, 1Q2400, 1Q2370, 1Q2473, 1S2694, 3S2755, 1S2748, 1S2728, 1S2747, 3S2731, SHS 7930 PRO2, 2S2697, BM 270 PRO2 e 1S2746 mostraram maior desempenho para rendimento de grãos, e estão em grupos divergentes da Distância de Mahalanobis, sendo os indicados para serem selecionados para formação das populações bases.

Palavras-chave: *Zea mays* L., melhoramento de plantas, variabilidade genética.

1. INTRODUCTION

Brazil ranks third globally in maize production, behind the United States and China [1]. Maize cultivation in the country occurs across three distinct growing seasons. The first, known as the main season (*harvest*), takes place during summer; the second is the off-season (*second crop*); and the third, referred to as the winter crop, is cultivated in the states of Sergipe, Alagoas, and the coastal region of Bahia (SEALBA), as well as in Pernambuco and Roraima. Sowing for the winter crop typically occurs between April and August, during the rainy season [2].

Although maize is grown throughout Brazil, productivity varies considerably due to climatic and edaphoclimatic conditions. In semi-arid regions, irregular rainfall is a major constraint, often resulting in yields below the national average. Variability in water availability directly affects plant development and food security, underscoring the importance of breeding for drought tolerance and adopting management practices that enhance water-use efficiency [3].

Among climatic constraints, irregular rainfall stands out as one of the most critical limiting factors for maize cultivation. Water deficits are a primary cause of reduced agricultural productivity in tropical regions [4]. To promote sustainable agriculture, it is crucial to develop and disseminate genotypes resistant to abiotic stresses, capable of maintaining stable yields under drought conditions, one of the main drivers of yield instability in maize production [5].

In Sergipe, municipalities located in the upper hinterland region, characterized by more challenging climatic conditions, recorded the lowest average maize yields in the state. In such semi-arid areas, maize both grain and forage, play a vital role as a nutritional reserve for animal feed during the dry season [6]. The region is also a notable milk-producing area, where maize represents the second most important agricultural sector [7, 8].

An effective strategy to mitigate yield reductions under adverse environmental conditions is the use of maize hybrids with high adaptability and productivity under water stress. However, due to variability in drought tolerance within and among genotypes, it is crucial to evaluate the performance of different genetic materials under water-deficit conditions prior to their recommendation for commercial cultivation [9].

Conventional breeding uses recurrent selection, backcrossing, and genealogical methods, including secondary traits related to water stress tolerance and traits directly linked to yield. The process involves identifying donor parents with drought-adaptive alleles and incorporating them into elite strains. From this integration, more tolerant inbred populations are formed, allowing the development of pure lines tolerant to water stress [10, 11].

Identifying superior genotypes for the development of new cultivars and commercial hybrids remains a key challenge in maize breeding programs. Elite genotypes are selected based on desirable agronomic traits such as high yield potential, disease resistance, and adaptability to suboptimal environments [12-14].

These materials may include advanced breeding lines, experimental hybrids, or improved varieties, all of which are essential to the success of genetic improvement efforts. Additionally, such evaluations support the identification of hybrids with strong commercial potential [15]. The incorporation of elite maize genotypes contributes to the introduction of favourable alleles and to the increase in genetic divergence, a fundamental condition for expanding heterosis in hybrid programs [16].

In view of the above, studies have shown that the elite genotypes of CKH10080 and CKH08051 corn have greater yield stability under environmental and management variations, which are characterized by an intermediate cycle and drought tolerance, bringing together important attributes for the adaptation of corn to adverse conditions [17]. In general, they stand out for their ability to express high yield in favourable environments and reduce losses under stress, which reinforces their agronomic potential in systems subject to climatic instabilities.

Inbred lines evaluated by Dube et al. (2023) [18] show wide phenotypic variation supported by genetic diversity, reflected in highly significant differences for agronomic traits. This set of evidence demonstrates the potential of these lines to support the selection and development of corn hybrids that are more tolerant to stress conditions.

Evaluating these genotypes contributes both to their direct adoption in agricultural systems and to their strategic use in breeding crosses aimed at developing new lines and hybrids better

adapted to semi-arid conditions. It is hypothesized that elite maize genotypes differ in yield and morphological characteristics under semi-arid conditions, making it possible to identify and select superior parents and direct breeding aiming at greater drought tolerance.

Thus, this study aimed to assess the phenotypic performance of elite maize genotypes under semi-arid conditions to identify those with greater yield stability and superior adaptation to regional constraints.

2. MATERIAL AND METHODS

2.1 Location and climate

The experiment was carried out at the Embrapa Semi-arid Experimental Farm, located in the municipality of Nossa Senhora da Glória, Sergipe, Brazil (latitude 10°12'48.44" S, longitude 37°19'1.68" W, altitude 291 m), during the 2020/2021 growing season.

The region's climate is predominantly classified as As, a tropical climate with hot and dry summers, covering approximately 73.7% of Sergipe's territory [19]. Climatic data for the experimental period, obtained from the agrometeorological station at the Embrapa Semi-Arid Farm, are presented in Figure 1. In the period between planting and harvesting, the accumulated precipitation was 253.20 mm.

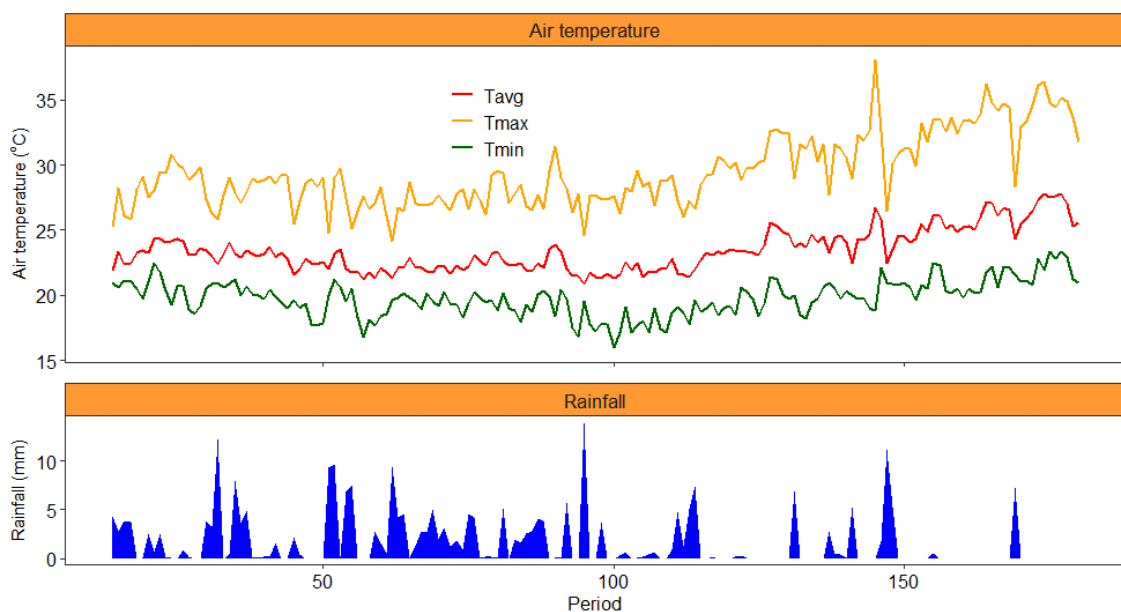


Figure 1: Maximum, average, minimum temperatures, and rainfall from May to October 2021, obtained by the agrometeorological station of the Experimental Farm of Embrapa Semi-Arid Region, Nossa Senhora da Glória, SE, Brazil.

The temporal dynamics of the climatic variables reveal a pattern typical of hot, semi-arid regions. Maximum air temperatures ranged from approximately 27 °C to 37 °C, showing a gradual increase over time, with peaks exceeding 35 °C after period 140. Average temperatures fluctuated between 22 °C and 27 °C, while minimum temperatures remained between 18 °C and 23 °C, resulting in a mean thermal amplitude of 8 °C to 12 °C.

Rainfall exhibited a highly irregular distribution, varying from 0 to 12 mm per period, with a predominance of dry days and most rainfall events (6–10 mm) concentrated between periods 1 and 50, followed by only a few isolated events after period 120. The progressive decline in rainfall coincided with rising maximum temperatures, indicating a transition toward hotter and drier conditions. Together, these patterns highlight the pronounced climatic seasonality of the

experimental area, a factor that strongly influences the agronomic performance and physiological responses of the genotypes evaluated.

2.2 Experimental design and genotypes

The experiment was conducted in a randomized complete block design with two replications and 34 treatments. The use of only two replications was justified by the fact that this number provided the required degrees of freedom for the experiment, as well as by limitations in the experimental area, which restricted the number of replications that could be implemented. Plots were arranged with a spacing of 0.80×0.20 m and consisted of two 5-m rows, under rainfed conditions. The characteristics of the evaluated genetic materials are presented in Table 1.

Table 1: Description of the treatments of the Elite Experiment, carried out in Nossa Senhora da Glória, SE, Brazil, in 2021.

Treatment	Genotype	Phase	Source
1	1R2536	EXPERIMENTAL	EMBRAPA
2	2R2642	EXPERIMENTAL	EMBRAPA
3	1R2620	EXPERIMENTAL	EMBRAPA
4	1Q2427	EXPERIMENTAL	EMBRAPA
5	1Q2400	EXPERIMENTAL	EMBRAPA
6	1Q2425	EXPERIMENTAL	EMBRAPA
7	1Q2370	EXPERIMENTAL	EMBRAPA
8	1Q2473	EXPERIMENTAL	EMBRAPA
9	BRS 1055	COMMERCIAL	EMBRAPA
10	1P2206	EXPERIMENTAL	EMBRAPA
11	1S2719	EXPERIMENTAL	EMBRAPA
12	1S2694	EXPERIMENTAL	EMBRAPA
13	3S2761	EXPERIMENTAL	EMBRAPA
14	3S2755	EXPERIMENTAL	EMBRAPA
15	1S2722	EXPERIMENTAL	EMBRAPA
16	BRS 3042 PRO2	COMMERCIAL	EMBRAPA
17	1S2748	EXPERIMENTAL	EMBRAPA
18	1S2747	EXPERIMENTAL	EMBRAPA
19	3S2731	EXPERIMENTAL	EMBRAPA
20	SHS7930 PRO2	COMMERCIAL	HELIX SEM.
21	3S2777	EXPERIMENTAL	EMBRAPA
22	2S2697	EXPERIMENTAL	EMBRAPA
23	1S2718	EXPERIMENTAL	EMBRAPA
24	3S2734	EXPERIMENTAL	EMBRAPA
25	BM270 PRO2	COMMERCIAL	HELIX SEM.
26	BRS 3042	COMMERCIAL	EMBRAPA
27	1S2746	EXPERIMENTAL	EMBRAPA
28	1S2726	EXPERIMENTAL	EMBRAPA
29	3S2772	EXPERIMENTAL	EMBRAPA
30	3S2770	EXPERIMENTAL	EMBRAPA
31	AG8061 PRO2	COMMERCIAL	MONSANTO
32	1S2728	EXPERIMENTAL	EMBRAPA
33	3S2730	EXPERIMENTAL	EMBRAPA
34	1F640 PRO2	EXPERIMENTAL	EMBRAPA

SH – Single hybrid; TH – Triple hybrid; SME – Semi-early; E - Early

2.3 Experimental procedures and evaluated traits

Soil preparation was carried out using conventional methods with plowing and leveling by harrowing for corn cultivation. Fertilization was applied according to the recommendations of the soil analysis (Table 2), manually applying 833 kg ha^{-1} of NPK (6-24-12) at planting and

100 kg ha⁻¹ of ammonium sulfate (21-0-0) as topdressing at the V4 stage, as recommended for corn cultivation in Sergipe [20].

Sowing was done manually, using tools to ensure uniform seed spacing. The crop was monitored throughout its growth cycle, and pest, disease, and weed management practices were implemented as needed.

Table 2: Chemical analysis of the soil where the experiment was carried out, performed by the Sergipe State Technological and Research Institute (ITPS).

pH	Ca ²⁺	Ca ²⁺ + Mg ²⁺	Al	CTC	Na ⁺	K ⁺	P	V	OM
Water		cmol _c /dm ³				mg/dm ³		%	g/dm ³
5.30	2.09	3.25	0.16	5.56	45.7	112	3.70	67.3	11.6

Ca²⁺: calcium; Mg²⁺: Magnesium; Al: Aluminum; Na⁺: Sodium; K⁺: Potassium; P₃₋: Phosphorus (Mehlich-1); V: Base saturation; OM: Organic matter.

In this study, morphological, phenological, and post-harvest traits were evaluated. These parameters are critical for assessing the agronomic performance of hybrids under the semi-arid conditions of Sergipe.

Morphological characteristics: Initial Stabilization (IS): total number of emerged plants per plot, recorded ten days after it is planting; Final Stabilization (FS): total number of surviving plants per plot at harvest; Plant Height (PH): distance from the soil surface to the panicle insertion point, measured in centimeters (cm) with a graduated ruler; Ear Height (EH): distance from the soil surface to the primary ear insertion point, measured in centimeters (cm); Relative Ear Position (REP): ratio between ear height (EH) and plant height (PH), expressed as a percentage.

Physiological characteristics: Female Flowering in Days (FFD): number of days from planting until 50% of the plants in the plot show stigma on the ear; Male Flowering Days (MFD): number of days from planting until 50% of the plants in the plot show pollen release; Flowering Interval (FI): difference in days between male and female flowering.

Post-harvest characteristics: Number of Ears per Plot (NEP): total number of ears harvested per plot; Ear Weight per Plot (EWP): total mass of ears (with husk) harvested per plot, expressed in kilograms (kg); Ear Length (EL): average ear length per plot, based on five randomly selected ears, measured in centimeters (cm) with a caliper; Ear Diameter (ED): average ear diameter per plot, based on five randomly selected ears, measured in centimeters (cm); Number of Rows per Ear (NFE): average number of grain rows per ear, based on five randomly selected ears; Number of Grains per Row (NGF): average number of grains per row, based on five randomly selected ears; Grain yield (RG, kg/ha): estimated according to the equation described by Zuber (1942) [21].

2.4 Statistical analyses

The selection of statistical packages in RStudio was based on their efficiency and suitability for analyses commonly applied in plant breeding. Data were subjected to analysis of variance (ANOVA), followed by mean grouping using the Scott-Knott clustering test, performed with the AgroR package [22], due to its functions specifically designed for agricultural experimentation. Pearson correlation analysis was conducted using the Corrplot package [23], due to its ability to produce clear and interpretable correlation matrices, while principal component analysis (PCA) and morphological divergence analysis were performed using the Metan package [24], a package developed for multivariate procedures in breeding programs. All statistical analyses were performed in the RStudio software [25], chosen for its reproducibility and seamless integration of specialized packages.

For PCA, the variables were standardized using the Z-score method, ensuring uniform variance among the descriptors and allowing equal contribution to the formation of the principal components. The selection of retained components followed three well-established criteria: (i) eigenvalues greater than 1, according to Kaiser's criterion; (ii) desirable minimum cumulative

variance between 70% and 80%; and (iii) identification of the inflection point in the sedimentation plot, ensuring the retention of only the components with the greatest biological and statistical relevance.

3. RESULTS AND DISCUSSION

3.1 Analysis of variance and means grouping

The reliability of the means for the experimental variables was assessed using the coefficient of variation (CV%). According to Gurgel et al. (2013) [26], CV values below 20% are considered acceptable for maize experiments. All evaluated variables exhibited CVs within this threshold, indicating reliable mean estimates and increased confidence in the results.

Significant differences were observed among genotypes for GY, ED, MFD, FFD, NFE, and NEP, indicating genetic variability and the potential for genetic gain through selection (Table 3).

Table 3. Summary of the analysis of variance of the 34 genotypes for the variables analyzed in the Elite experiment, carried out in Nossa Senhora da Glória, SE, in 2021.

SV	DF	Mean square						
		FS	EWP	PH	EH	MFD	FFD	GY
Treatment	33	42.91	0.75	248.07	205.32	4.59**	8.06**	65837.9*
Block	1	78.37	2.13	147.06	19.06	5.31	6.48	6174305
Residual	33	29.43	0.34	138.09	74.00	1.07	1.27	289358.5
CV (%)		18.25	14.36	5.14	7.24	1.7	1.86	11.69
Mean		29.72	4.04	228.41	118.85	60.63	60.69	4599.09
h ²		0.19	0.38	0.28	0.47	0.62	0.73	0.39
Com. M.		27.36a	3.60a	224a	118.21a	59.64a	59.64a	4328.93a
Exp. M.		30.33a	4.15a	229.56a	119.02a	60.89a	60.96a	4669.90a

SV	DF	Mean square						
		EL	ED	NEP	NGR	NRE	RPE	IS
Treatment	33	1.53	0.19**	64.63**	9.44	5.06**	1.91e-03	51.26
Block	1	3.81	0.29	4.76	9.49	0.12	3.97e-05	91.78
Residual	33	0.95	0.02	26.91	9.04	0.54	1.30e-03	28.96
CV (%)		6.02	3.48	15.75	8.06	4.68	6.92	18.14
Mean		16.15	4.41	32.94	37.30	15.66	0.52	29.66
h ²		0.24	0.78	0.41	0.02	0.80	0.19	0.28
Com. M.		15.64a	4.42a	28.5a	36.67a	15.43a	0.53a	25.86a
Exp. M.		16.33a	4.42a	34.09a	37.47a	15.73a	0.52a	30.65a

Means followed by the same letter did not differ statistically by the t-test. *, **: significant at 5% and 1% probability levels, respectively, by the F test. Characteristics evaluated: FS-final stand, EWP -Ear Weight per Plot (kg), PH - plant height (cm), EH - ear height (cm), MFD - male flowering (days), FFD - female flowering (days), GY - grain yield (kg/ha), EL - ear length (cm), ED - ear diameter (cm), NEP - number of ears in the plot, NGR - number of grains per row, NRE - number of rows per ear, RPE - relative ear position and IS - initial stand.

The average grain yield of 4,599.09 kg/ha during the 2021 experimental season exceeded the national average of 4,366 kg/ha recorded in the 2020/21 harvest [27]. No significant differences were observed among the elite genotypes using Student's t-test, inferring that these experimental hybrids are promising candidates for the development of base breeding populations with high performance for traits such as grain yield.

In the mean comparison analyses, the traits grain yield, male flowering, female flowering, ear diameter, number of ears per plot, and number of rows per ear were classified into multiple homogeneous groups. This grouping method enhances between-group variability while minimizing within-group variation, as indicated by the sum of squares [28].

Among the experimental hybrids, the highest grain yields were recorded for 1R2620 (5,745 kg/ha), 3S2755 (5,615 kg/ha), 1S2747 (5,515 kg/ha), 1R2536 (5,506 kg/ha), 1S2748 (5,288 kg/ha), 3S2731 (5,214 kg/ha), 1S2694 (5,061 kg/ha), 1Q2370 (4,994 kg/ha), 1Q2473 (4,982 kg/ha), 2S2697 (4,965 kg/ha), 2R2642 (4,963 kg/ha), 1Q2400 (4,870 kg/ha), and 1S2746 (4,727 kg/ha). Among the commercial hybrids, BM 270 PRO2 (4,950 kg/ha) and SHS 7930 PRO2 (4,827 kg/ha) stood out (Figure 2).

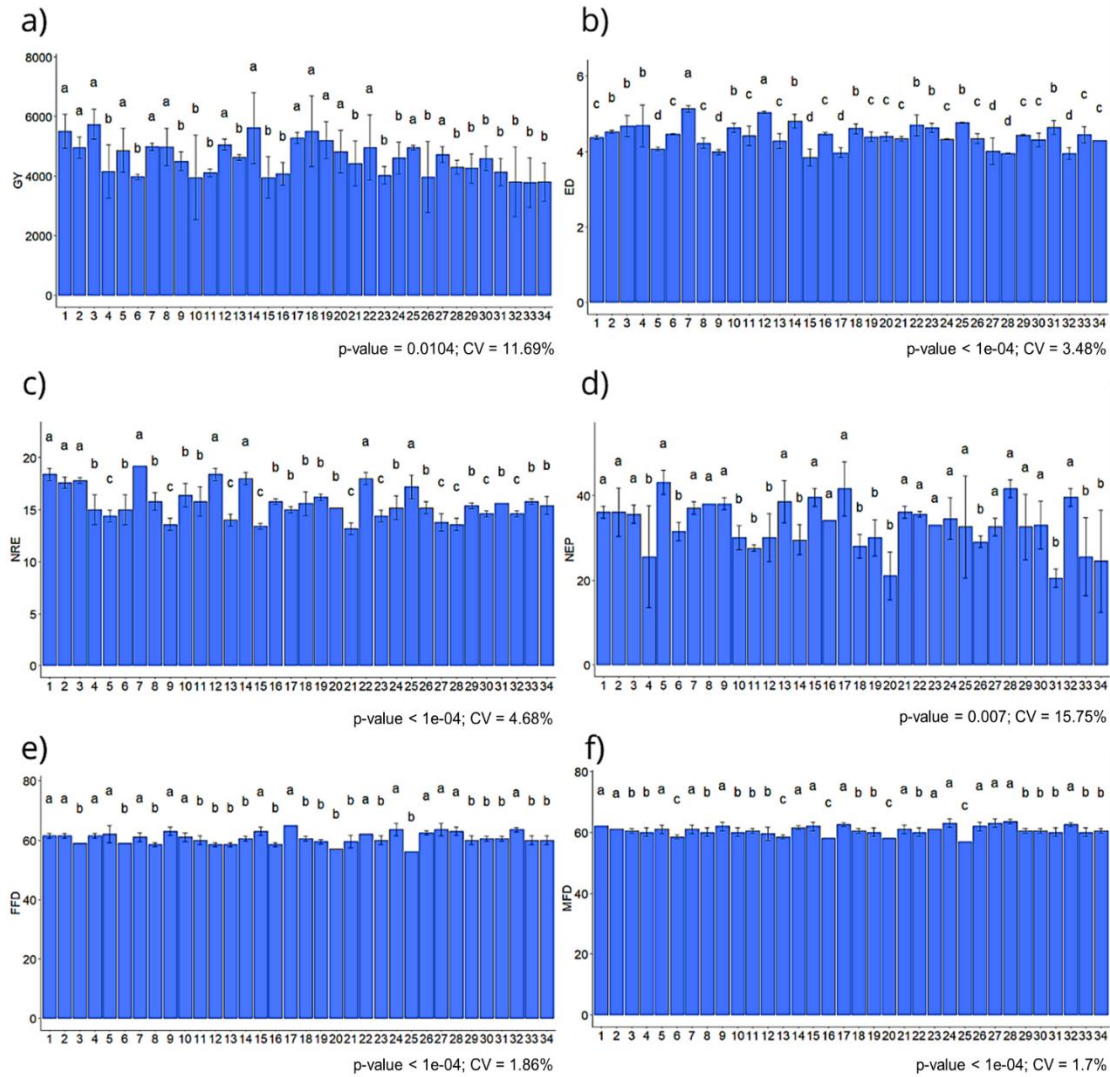


Figure 2. Scott-Knott mean cluster test of the genotypes evaluated for the variables GY (a), ED (b), NRE (c), NEP (d), FFD (e), and MFD (f).

The superior grain yield of these genotypes is largely attributed to favorable morphological traits that enhance adaptation to semi-arid conditions. These include higher prolificacy (1R2536, 1S2748, 1S2746, 2S2697, 1Q2473, 1Q2400, BM 270 PRO2), as shown in Figure 2d; larger ear diameter (1S2694, 1Q2370), as illustrated in Figure 2b; a greater number of rows per ear (3S2755, 1R2620, 2R2642, BM 270 PRO2), presented in Figure 2c; and a higher precocity (3S2731, 1S2747, SHS 7930 PRO2, BM 270 PRO2), as shown in Figures 2e and 2f. Notably, the commercial hybrid BM 270 PRO2 exhibited above-average productivity combined with desirable traits for cultivation in semi-arid environments, such as early maturity and adequate ear morphology.

Such traits are advantageous under the environmental conditions of the study region and support the formation of a potential base population, as well as the possibility of using this genotype in future recombination events to increase genetic diversity.

The results indicate that the experimental genotypes are the most productive, highlighting their potential for cultivation in semi-arid regions. Recombining these materials could generate base populations with a high frequency of alleles associated with increased productivity. This reinforces the importance of breeding programs adapted to the conditions of the high hinterland region of Sergipe, allowing the identification of superior genotypes compatible with the reality of local producers. Selecting genotypes adapted to local environmental conditions is essential to increase the income of the population, while also contributing to the regional economy and food security [29].

3.2 Correlation analysis

The Pearson correlation matrix (Figure 3) illustrates the classification of correlation magnitudes, which range from null to perfect, being positive when both traits increase simultaneously and negative when one trait increases while the other decreases. The Pearson coefficient quantifies this linear association between two continuous variables, with values ranging from -1 to $+1$, where numbers near the extremes indicate strong associations and values close to zero reflect weak relationships. This metric is essential for identifying association patterns and supporting decision-making in genetic and agronomic research [30, 31].

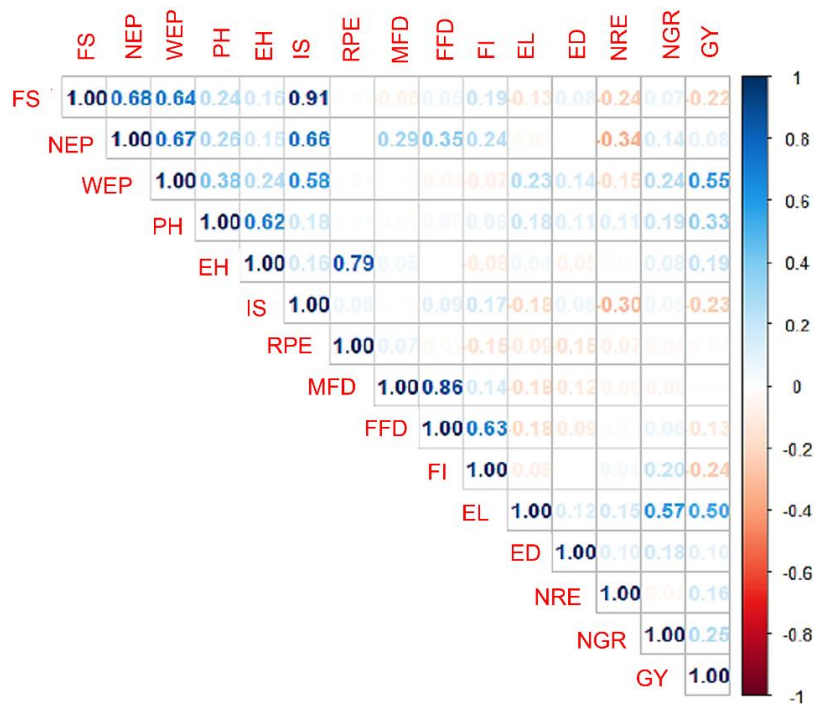


Figure 3. Pearson's correlation plot for the variables analysed in the Elite experiment, carried out in Nossa Senhora da Glória, SE, in 2021.

Correlation enables the identification of association patterns between variables by indicating whether changes in one trait coincide with corresponding changes in another, thereby enhancing prediction and the understanding of relationships in genetics and agricultural sciences. Its interpretation must account for statistical significance and sample size to ensure that observed associations are robust and not the result of spurious relationships in inherently variable biological systems [30].

Among the variables analyzed, the strongest positive correlations were observed between IS and FS (0.91), NEP (0.68), and EWP (0.64). PH showed a positive correlation with EH (0.62), as expected, since taller plants typically develop ears at higher positions [32]. However, this trait may affect lodging resistance and should be carefully considered in breeding programs. Furthermore, phenological traits such as MFD and FFD were highly correlated (0.86), as expected in well-adapted genotypes.

For grain yield (GY), the highest correlations were observed with WEP (0.55) and EL (0.50), indicating that longer ears directly contribute to increased grain production. This result highlights ear length as a relevant selection criterion for identifying superior genotypes, consistent with the findings of Ferreira et al. (2021) [33]. According to Shengu (2017) [34], the direct effects on yield tend to decrease in magnitude. Overall, this association suggests that hybrids expressing higher values for these traits generally exhibit greater productive potential, demonstrating the combined contribution of these attributes to agronomic performance [35, 36].

Conversely, negative correlations such as that between FS and NRE (-0.13) suggest that increased internode thickness may be associated with a reduced number of fertile ears, potentially impacting overall productivity. In the context of indirect selection, it is important to prioritize genotypes with superior ear morphological traits, as grain yield typically exhibits low heritability and is controlled by numerous genes with small phenotypic effects [37, 33].

In this study, the indirect selection of genotypes based on trait correlations with yield may contribute to the formation of a base population characterized by longer and heavier ears, given that ear length and ear weight showed the strongest positive correlations with productivity.

3.3 Principal component analysis and contribution of the first components

Principal component analysis (PCA) is a statistical technique that linearly transforms a set of correlated variables into a smaller set of uncorrelated (independent) components while retaining most of the original information [38]. Each principal component is a linear combination of all the original variables, ordered to capture the greatest variability [38, 39].

In this study, the variables showing the highest positive correlations NEP, WEP, PRE, MFD, FFD, PH, EH, and GY were selected for analysis. The first three principal components together explained 81.50% of the total variance, with the first two components accounting for 65.2%, as shown in Table 4. Similar findings were reported by Téllez et al. (2013) [40], Babić et al. (2024) [41] and Cruz et al. (2020) [42], who also observed that more than two components were required to adequately explain the total variance.

Table 4: Data of eigenvalue, explained variance, and cumulative variance of the Elite Experiment, carried out in Nossa Senhora da Glória, SE, Brazil, in 2021.

PC	Eigenvalue	Explained variance (%)	Cumulative variance (%)
1	3.13	39.06	39.06
2	2.09	26.13	65.19
3	1.30	16.30	81.50
4	0.67	8.41	89.91
5	0.59	7.32	97.23
6	0.12	1.53	98.76
7	0.10	1.23	99.99
8	0.00	0.00	100.00

PC: Principal components

The principal component analysis indicated that PC1 was strongly associated with plant morphological traits, particularly EH (0.46), WEP (0.45), PH (0.44), NEP (0.40), and GY (0.33). In contrast, PC2 was primarily influenced by phenological variables, with greater contributions from female flowering (0.64) and male flowering (0.60), as shown in Table 5 [43].

Each principal component represents a linear combination of the original variables, with components being mutually independent and ordered to sequentially explain the largest possible proportion of total variance in the dataset. These findings align with recent studies demonstrating that components associated with structural traits play a central role in distinguishing superior maize genotypes and predicting yield performance, whereas components related to phenology reflect adaptive strategies to environmental conditions [44-48].

Table 5. Contributions of the variables used for principal components 1 and 2.

Variable	PC1	PC2
NEP	0.40	0.29
WEP	0.45	-0.03
RPE	0.18	-0.24
MFD	0.17	0.60
FFD	0.12	0.64
PH	0.44	-0.12
EH	0.46	-0.24
GY	0.33	-0.16

PC: Principal components

The PCA biplot integrates both variables and genotypes into a single graphical representation. Genotypes and variables positioned within the same quadrant exhibit stronger positive associations. The genotypes 1R2620, 3S2761, 3S2755, 1Q2473, BRS 3042 PRO2, and BM 270 PRO2 were most closely associated with the variables contributing to the first principal component WEP, PH, EH, RPE and GY indicating superior performance in key agronomic traits relevant to the region, particularly earliness and productivity. In contrast, the genotypes 1S2722, 1S2748, and 1S2728 were more strongly associated with phenological variables such as FFD and MFD, which contributed most to PC2 (Figure 4).

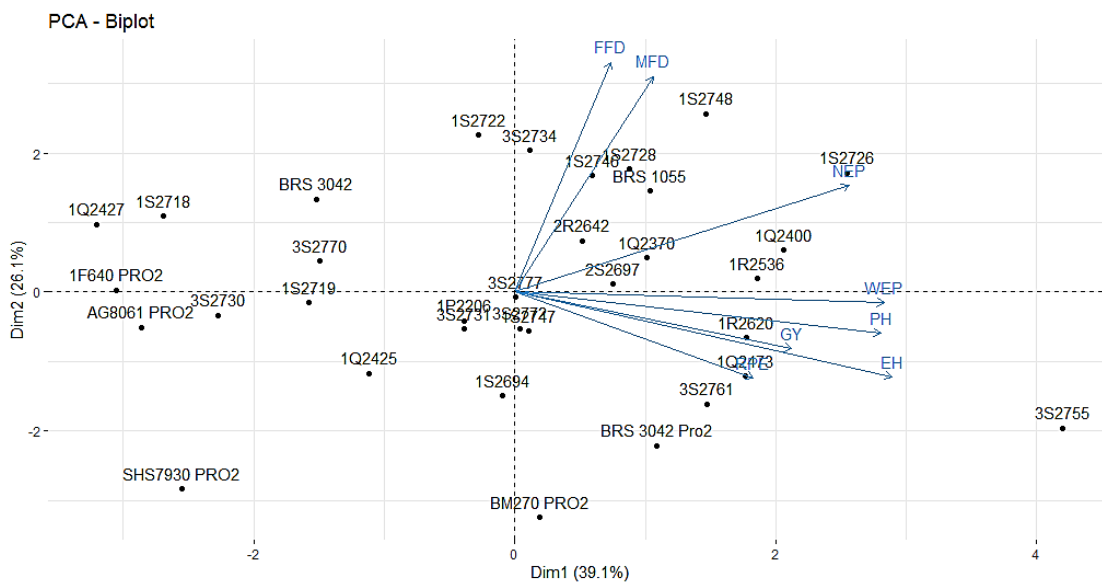


Figure 4. PCA Biplot chart of the 34 genotypes analysed in the Elite experiment, carried out in Nossa Senhora da Glória, SE, in 2021.

3.4 Morphological divergence analysis

The generalized Mahalanobis distance (D^2) is one of the most widely used metrics for quantifying dissimilarity between populations, particularly in analyses involving repeated measures. It is recommended for experimental designs where the variables are correlated [49]. Using the Mahalanobis distance matrix, a dendrogram was constructed for the 34 maize genotypes under study, revealing four distinct groups based on the defined cut-off threshold.

Genotypes positioned closer in the dendrogram exhibit greater phenotypic similarity, whereas those separated by larger distances display more substantial differences. These findings are essential for identifying promising genetic materials and guiding breeding strategies, as they enable the selection of genotypes with desirable traits suited to specific cultivation conditions (Figure 5).

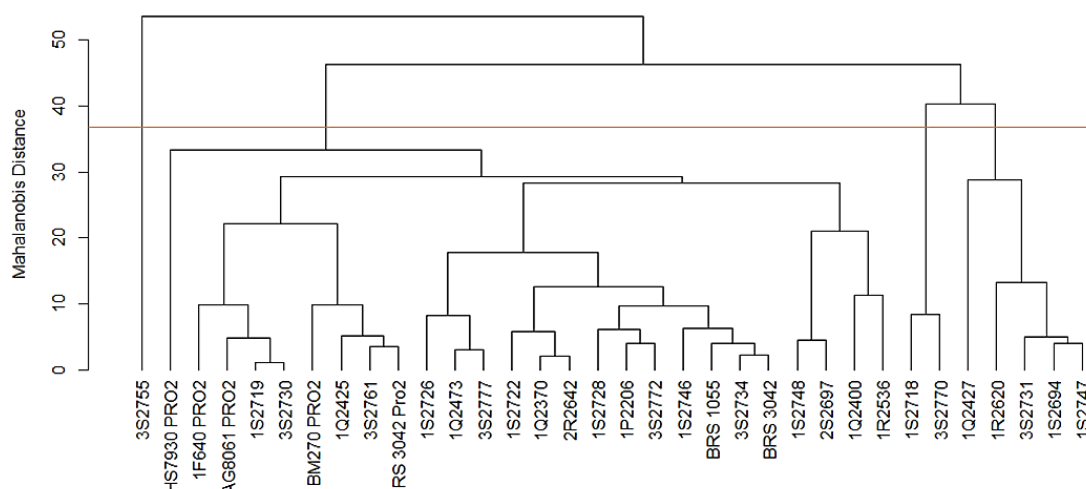


Figure 5. Dendrogram of the Mahalanobis distance of the 34 maize genotypes analysed in the Elite experiment, carried out in Nossa Senhora da Glória, SE, in 2021.

The cut-off point adopted in the dendrogram, at approximately $D \approx 35$, defines the most appropriate number of genetically distinct groups. This choice follows established principles in the literature, such as the method proposed by Cruz et al. (2012) [50], which determines clustering limits based on statistical parameters derived from node heights. This criterion enables the formation of biologically meaningful groups, avoiding artificial subdivisions and ensuring adequate within-group homogeneity and between-group differentiation, as recommended in multivariate analyses applied to plant breeding [51].

The first group (G1) consisted solely of the experimental genotype 3S2755. The second and largest group (G2) included the genotypes 1S2748, 2S2697, SHS 7930 PRO2, 1Q2370, 2R2642, 1P2206, 1S2719, 1S2722, BRS 1055, 1Q2425, 3S2761, BRS 3042 PRO2, 1Q2473, BM 270 PRO2, AG8061 PRO2, BRS 3042, 1S2746, 3S2734, 1Q2400, 1R2536, 1S2726, 3S2777, 1F640 PRO2, 3S2722, 1S2728, and 3S2730. The third group (G3) comprised 1S2718 and 3S2770, while the fourth group (G4) included 1Q2427, 1R2620, 3S2731, 1S2694, and 1S2747.

The experimental genotype 3S2755 (G1) was the most divergent based on the Mahalanobis distance and demonstrated strong performance in grain yield, ranking among the most productive genotypes. This highlights its potential as a promising candidate for developing base populations adapted to the Alto Sertão region of Sergipe. According to [51], selection should prioritize genotypes that combine genetic divergence with superior performance in key agronomic traits.

The highest-yielding genotypes were distributed across different groups: in G2, these included 1R2536, 2R2642, 1Q2370, 1S2748, SHS 7930 PRO2, BM 270 PRO2, 2S2697, 1S2746, 1Q2400, and 1Q2473, while in G4, they included 1R2620, 1S2694, 3S2731, and 1S2747. This distribution

enables strategic crosses between genotypes from G1, G2, and G4, maximizing the combination of high productivity with genetic divergence. Selecting genotypes from distinct groups is recommended to promote contrasting crosses and exploit heterosis, thereby enhancing the potential for obtaining superior hybrids.

Although the study was conducted in a single semi-arid environment, this setting enabled precise characterization of genotype performance under water stress, strengthening the identification of key traits for selection. Expanding the trials to multiple environments remains a valuable opportunity to validate material stability and deepen the understanding of genotype × environment interactions. Similarly, the multivariate analyses provided an integrative assessment of trait performance, and future research should incorporate multi-environment experiments, high-throughput phenotyping, advanced analytical tools, and predictive modeling to further enhance selection efficiency. Thus, the limitations observed do not represent barriers but rather promising avenues for expanding scientific impact and advancing the development of superior materials adapted to semi-arid conditions.

4. CONCLUSION

The genotypes 3S2755, 1R2536, 2R2642, 1Q2370, 1S2748, SHS 7930 PRO2, BM 270 PRO2, 2S2697, 1S2746, 1Q2400, 1Q2473, 1R2620, 1S2694, 3S2731 and 1S2747 demonstrated superior productivity and morphological adaptability, indicating potential as parental lines for the development of drought-tolerant maize populations in the Brazilian semi-arid region.

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