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Optimization of maize hybrids in the Brazilian Northeast: a multi-trait selection and envirotyping techniques in multi-environment trials

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ABSTRACT: The objective of this study was to apply the envirotyping methodology to delineate macroenvironments (MEs) in the Brazilian Northeast. Multivariate analyses were conducted to investigate the relationship between genotype × environment interaction (G × E), stability, and the average performance of maize genotypes, to enhance corn adaptation to diverse environmental conditions. Twenty corn hybrids were cultivated across ten environments over two harvest seasons, with the following characteristics assessed in each environment: grain yield (GY), plant height (PH), ear height (EH), plant density (PD), and number of ears (NE). The target regions were characterized based on 19 environmental covariates (ECs) and a 23-year climatological series (2001-2023), which resulted in the identification of four MEs with similar climatic features. The interaction between genotype × macroenvironment × year significantly influenced the evaluated traits. The top five genotypes for each ME were identified using the multitrait mean performance and stability index (MTMPS) which demonstrated favorable average performance and stability across multiple years seasons. The hybrids G03 and G04 were selected in three out of four MEs, indicating their stability and adaptability as hybrids. Envirotyping revealed a robust correlation between environments, enhancing the precision with which cultivars can be recommended for various locations within the same ME. The multivariate approach utilizing MTMPS proved effectively identified productive and stable genotypes tailored to each ME.

Keywords: agricultural zoning, climate adaptation, ecophysiology, resource optimization, sustainable agriculture

Introduction

Brazil is among the three leading global producers of corn (*Zea mays* L.), ranking behind only the United States of America and China (USDA, 2024). During the 2022/2023 crop season, Brazil cultivated approximately 22,269.2 million hectares, yielding 131,892.6 million tons of corn, with an average yield of 5.9 t ha⁻¹ (CONAB, 2024). However, the northeastern region exhibited below-average productivity, recording 3.5 t ha⁻¹, underscoring the urgent need to develop cultivars adapted to the diverse environments of the Brazilian Northeast. This is becoming increasingly critical in the context of climate challenges characterized by greater rainfall variability and extreme weather events.

Notwithstanding the region's overall belowaverage productivity, a number of northeastern states have exhibited commendable performance. The states of Sergipe, Maranhão, Bahia, and Piauí demonstrated the highest corn productivity during the 2022/2023 crop season. The state of Sergipe recorded the highest productivity at 5.2 t ha⁻¹, followed by Maranhão with 5.1 t ha⁻¹, Bahia with 4.7 t ha⁻¹, and Piauí with 4.5 t ha⁻¹ (CONAB, 2024). These results underscore the resilience of these states in overcoming climatic and agronomic challenges, emphasizing the importance of tailored management strategies and technologies for each regional context.

Furthermore, it is crucial to highlight the pivotal role of phenotypic and biometric analysis in the identification and selection of corn cultivars that are well-suited to a range of environmental conditions. A comprehensive genotype evaluation in multi-environment trials is imperative to gain insight into elucidating genotype \times environment interaction (G \times E) and ascertaining adapted and productive materials with high value for cultivation and use under heterogeneous environmental conditions.

The integration of environmental covariates (ECs) into genomic and phenomic prediction models via "envirotyping" enhances our understanding of G \times E and its implications for crop productivity (Costa-Neto et al., 2021a, b; Millet et al., 2019). By deepening our understanding of G \times E in maize cultivation in the northeastern region of Brazil, we seek to facilitate the development of more efficient and sustainable agricultural practices. This encompasses the optimization of maize hybrid selection, the reduction of the necessity for extensive field trials, and the optimization of resource and time utilization in corn breeding efforts.



Materials and Methods

Study site

The present study was conducted in ten environments distributed across three states in the northeastern region of Brazil (Figure 1) over two consecutive harvest seasons: 2011/2012 and 2012/2013.

Genotypes used

Twenty corn genotypes from public and private companies were utilized in this study. Comprehensive information regarding each genotype, including cultivar, grain texture, grain color, cycle, and the seed company holding the registration, is provided in Table 1. The objective was to encompass various genetic backgrounds and performance characteristics to ensure a comprehensive evaluation across different environments.

Experimental design

The experiments were conducted using a randomized complete block design with two replications. Each plot consisted of four rows measuring 5.0 m in length, with a spacing of 0.70 m between rows and 0.20 m within rows. The seeds were planted manually, and thinning was performed 15 days after emergence, resulting in 100 plants per plot. The fertilization was conducted in accordance with the recommendations based on the soil analysis results from each experimental area. The irrigation was not utilized, and pest and weed control measures were implemented according to the specific crop requirements in each region.

Morphological variables

This study examined five agronomic traits that are related to productivity. The records included plant density (PD, unit), number of ears (NE, unit), and grain yield (GY, t ha⁻¹), which were manually harvested and measured from the two central rows of the plot. Plant height (PH, cm) was measured from the base of the root to the insertion of the flag leaf, while ear height (EH, cm) was measured from the base of the root to the peduncle of the main ear.

Statistical analysis

The methodology employed in the statistical analyses follows the recommendations established by Yue et al. (2022), who pioneered the use of EnvRtype for environmental segmentation and the the multi-trait mean performance and stability index (MTMPS) approach for selecting corn hybrids in mega-environments in China. Each stage is delineated in the following sections.

Macroenvironment (ME)

The macroenvironment (ME) was delineated using the R software (R Core Team, 2023). The get weather() function from the EnvRtype package (Costa-Neto et al., 2021b) was employed to obtain 23 years (2001-2023) of daily meteorological data for 19 ECs (Table 2), with consideration given to the planting and harvesting dates for each environment. The EnvRtype package retrieves raw environmental data from platforms, such as NASA's Prediction of Worldwide Energy Resources (NASA-POWER) (Sparks, 2018). The reliability of NASA-

Figure 1 – Geographic information of the ten experimental sites for the trials carried out during 2012 and 2013. The four macroenvironments (MEs) are delineated based on long-term (23 years) climate information.

Code	Cultivar	Transgenic/ conventional	Type ¹	Cycle ²	Grain color ³	Grain texture⁴	Seed company
G01	20A55HX	Transgenic	TH	E	OR	SMHARD	Morgan
G02	2B433HX	Transgenic	ТН	EE	Y/OR	SMDENT	Dow Agro
G03	2B587HX	Transgenic	SH	Е	Y/OR	SMDENT	Dow Agro
G04	2B604HX	Transgenic	SHm	Е	OR	SMHARD	Dow Agro
G05	2B707HX	Transgenic	SH	Е	OR	SMHARD	Dow Agro
G06	2B710HX	Transgenic	SH	Е	Y/OR	SMHARD	Dow Agro
G07	30A16HX	Transgenic	SH	Е	Y/OR	SMHARD	Morgan
G08	30A37HX	Transgenic	SH	EE	Y/OR	SMHARD	Morgan
G09	30A91HX	Transgenic	SHm	Е	Y/OR	SMHARD	Morgan
G10	30A95HX	Transgenic	TH	Е	OR	SMHARD	Morgan
G11	BRS2022	Conventional	DH	Е	OR	SMDENT	Embrapa
G12	BRS2020	Conventional	DH	Е	OR	SMHARD	Embrapa
G13	BM820	Conventional	SH	Е	R	HARD	Biomatrix
G14	DKB330YG	Conventional	SH	EE	R/OR	SMDENT	Dekalb
G15	DKB370	Conventional	SHm	Е	Y/OR	SMHARD	Dekalb
G16	Statusvip	Transgenic	SH	Е	OR	HARD	Syngenta
G17	30A68HX	Transgenic	SH	EE	OR	SMHARD	Morgan
G18	P4285H	Transgenic	SH	Е	Y/OR	HARD	DuPont
G19	30F53HR	Transgenic	SH	E	OR	SMHARD	DuPont
G20	30K73H	Transgenic	SH	E	Y/OR	SMHARD	DuPont

Table 1 – List of genotypes used, along with the codes used in segmentation, and their respective origins, types, cycles, colors, grain textures, and supplying companies.

¹TH = triple hybrid; SH = single hybrid; SHm = modified single hybrid; DH = double hybrid. ²E = early; EE = extra early. ³OR = orange; Y = yellow; R = reddish. ⁴SMHARD = semi-hard; SMDENT = semi-dent; G = genotype.

POWER for agricultural use was confirmed by Monteiro et al. (2018), and Yue et al. (2022) validated its use in this context. The 19 ECs observed in each locality were utilized to construct the environmental covariate matrix W, which was then employed to compute environmental kinships. This process was carried out using the W_ matrix() function of the EnvRtype R package (Costa-Neto et al., 2021b), in accordance with the methodology proposed by Costa-Neto et al. (2021a).

Six months was deemed an appropriate timescale to capture the temporal variation of environmental information more accurately throughout a year. Consequently, each of the 2,622 variables (23 years \times 19 variables \times 6 periods) was employed as an environmental descriptor to construct environmental relationships. Subsequently, to ensure data quality, ECs that exceeded \pm 3 standard deviations were eliminated (Costa-Neto et al., 2021a). Then, utilizing the W_matrix (10 rows \times 2,622 columns), an enviromic kernel (equivalent to a genomic relationship) was computed using the env_ kernel() function of the EnvRtype R package (Costa-Neto et al., 2021b).

To visualize the relationships between ECs and their linkage to the study location, we conducted a principal component analysis (PCA). For this purpose, we constructed a two-way table comprising the average values of ECs (columns) associated with each location (rows). A biplot was generated using the fviz_pca_biplot() function from the factoextra R package (Kassambara and Mundt, 2020).

Table 2 - List of environmental covariates used to segment the								
environmen	ts ar	nd group	them	according	to	their	distances	
(greater sim	ilarity	/).						

	Cada	Environmental veriable	Linita
	Coue		Units
	WS	Wind speed at 2 m	km h⁻¹
	TMAX	Maximum temperature at 2 m	°C d⁻¹
	TMIN	Minimum temperature at 2 m	°C d⁻¹
Nasa	TMDEW	Temperature of the dew/frost point at 2 m	°C d ⁻¹
POWER ^a	TMED	Average temperature	°C d⁻¹
1 OTTER	PRECTOT	Rainfall precipitation	mm d ⁻¹
	RTA	Extraterrestrial radiation	MJ m ⁻² d ⁻¹
	RH	Relative humidity at 2 m	%
	ASKLW	Downward thermal infrared (longwave) radiative flux	
	ASKSW	All sky insolation incident on a horizontal surface	
	FRUE	Effect of temperature on radiation use efficiency	-
	GDD	Growing degree day	°C d⁻¹
	n	Solar radiation	h
	Ν	Daylight hours	h
Calculated ^b	VPD	Vapor pressure deficit	kPa d⁻¹
	SPV	Slope of saturation vapor pressure curve	kPa °C d⁻¹
	TRANGE	Temperature range	°C d⁻¹
	ETP	Potential evapotranspiration	mm d ⁻¹
	PETP	Deficit by precipitation	mm d ⁻¹

^aEstimated from NASA orbital sensors (Sparks, 2018). ^bProcessed using concepts from Allen et al. (1998) and Soltani and Sinclair (2012). Source: Compiled by the authors, with data extracted from the EnvRtype package (Costa-Neto et al., 2021b). The EnvRtype gathers raw environmental data from public platforms, such as a satellite-based meteorological system known as "NASA's Prediction of Worldwide Energy".

Environmental typing

To analyze the experiment's climatic data, the env_ typing() function from the EnvRtype R package was employed to define environmental types based on the means of the 19 ECs highlighted in Table 2. This was done to gain insight into the temporal variation of environmental information during the development of tropical maize crops.

The crop cycles were classified into five principal phenological stages (PS) based on days after sowing: 0-14 (initial growth), 15-35 (first leaf expansion), 36-65 (second leaf expansion), 66-90 (flowering), and 91-120 (grain filling). A frequency distribution was calculated for each combination of YEAR-ME-PS, with quantiles 0.01, 0.025, 0.50, 0.75, 0.975, and 0.99, thereby enabling a comprehensive analysis of climatic patterns.

Variance component analyses

The impact of ME and year on genotype behavior was assessed using a linear model with random effects (only the intercept was fixed) employing the lmer() function from the lmer4 R package (Bates et al., 2015), according to the Eq. (1):

$$y_{ijkn} = \mu + G_i + M_j + Y_k + GM_{ij} + GY_{ik} + MY_{jk} + GMY_{ijk} + REP_{n(j:k)} + \varepsilon_{ijkn}$$
(1)

where y_{ijkn} are the scores of the characteristics of the *i*-th genotype observed in the *n*-th repetition nested within the *j*-th ME of the *k*-th year; μ is the grand mean; G_{i} , M_{j} , and Y_k are the main effects of genotype, ME, and year, respectively. Interaction effects are represented by GM_{ij} , GY_{ik} , MY_{jk} , GMY_{ijk} , $REP_{n(j:k)}$ denotes the effect of repetition n (likely the combination of location and blocks) nested within the ME and year; and ε_{ijkn} denotes the random error associated with y_{ijkn} .

The variance components and genetic parameters were estimated through the Restricted Maximum Likelihood method, as proposed by Dempster et al. (1977). The significance of the random effects was evaluated through the likelihood ratio test. The broadsense heritability (H^2), based on the genotype mean, was calculated as the ratio of genotypic variance (σ_G^2) to the variance of the genotype mean (σ_P^2) (Schmidt et al., 2019; Yan, 2014) according to the Eq. (2):

$$H^{2} = \frac{\sigma_{G}^{2}}{\sigma_{P}^{2}} = \frac{\sigma_{G}^{2}}{\sigma_{G}^{2} + \frac{\sigma_{GY}^{2}}{K} + \frac{\sigma_{GM}^{2}}{J} + \frac{\sigma_{GMY}^{2}}{JK} + \frac{\sigma_{E}^{2}}{\sum_{k=1}^{K} N}$$
(2)

where *J*, *K*, and *N* are the numbers of MEs, years, and combinations of location/blocks, respectively. σ_{G}^2 , σ_{GY}^2 , σ_{GMY}^2 are the variances of G, G × YEAR interaction, G × ME interaction, and G × YEAR × ME interaction, respectively; σ_{ϵ}^2 is the residual variance.

A H^2 close to 1 indicates that variations in genotypic effects are predominantly attributed to genetic differences. Conversely, an H^2 close to zero suggests that observed genotypic divergences are more influenced by $G \times E$ or experimental errors (Yan, 2014).

Mean performance and stability of individual traits

Genotype selection was conducted independently within each delineated ME, with the objective of selecting genotypes that exhibited the desired performance within the ME while maintaining stability over time. The average performance of genotypes *i* over *k* years (\overline{Y}_{ik}) was calculated for each ME. Subsequently, Wricke's ecovalence (W_i) was employed as a measure of genotypic stability over time and was calculated using the Eq. (3):

$$W_i = \sum_{k=1}^{K} \left(\overline{Y}_{ik} - \overline{Y}_{i.} - \overline{Y}_{.k} + \overline{Y}_{..} \right)$$
(3)

Genotypes with low W_i values demonstrate a reduced tendency to deviate from the mean over time, suggesting enhanced stability. To integrate the mean performance and stability index (*MPS_i*) of the genotypes, we adapted the concept of the weighted average of the stability and yield based on performance (Olivoto et al., 2019a; Yue et al., 2022). In this adaptation, the weighted mean of absolute scores (WAASB) was replaced with W_i as a measure of stability, as calculating WAASB requires at least two axes of principal component interaction. The *MPS_i* was computed using the Eq. (4):

$$MPS_{i} = \frac{(rY_{i} \times \theta_{Y}) + (rW_{i} \times \theta_{S})}{\theta_{Y} + \theta_{S}}$$

$$\tag{4}$$

where *MPS*_i represents the superiority index for genotype *i*, balancing between average performance and stability; θ_Y and θ_s are the weights for average performance and stability, respectively (we chose to use $\theta_Y = 70$ and $\theta_s = 30$ to give greater weight to average performance, as selecting hybrids that are highly stable but with low performance is not desired); rY_i and rW_i are the rescaled values for average performance $\overline{Y_i}$ and W_{ii} , where W_i represents the stability, respectively, of genotype *i*. The rescaled values were calculated as follows, Eq. (5):

$$rY_i = rW_i = \frac{nma - nmi}{oma - omi} \times (o_i - oma) + nma$$
(5)

where *nma* and *nmi* are the new maximum and minimum values after rescaling; *oma* and *omi* are the original maximum and minimum values, and *i* is the original value of the response variable (or ecovalence value) of genotype *i*. For variables where lower values are desired (EH and PH), *nma* = 0 and *nmi* = 100 were used. Thus, the genotype with the lowest mean and lowest W_i would have $rY_i = 100$ and $rW_i = 100$ after rescaling. Higher values were desired for the other three variables (PD, NE, and GY). Therefore, we used *nma* = 100 and *nmi* = 0. After rescaling all features, a twoway table rM_{qp} with q rows (genotypes) and p columns was created. In rM_{qp} , the column ranges from 0 to 100, considering the desired direction of selection (decrease or increase), while maintaining the correlation structure of the original variable set (Olivoto and Nardino, 2021). To calculate these indices, we used the multiperformance score (mps) and weighted stability and multi-performance (wsmp), mps() and wsmp() functions from the R package metan (Olivoto and Lúcio, 2020).

Mean performance and productive stability

The mean performance and stability were calculated using the mgidi() function from the R package metan, which was employed to calculate the MTMPS. The MTMPS is based on the concept of the multi-trait stability index (MTSI) (Olivoto et al., 2019b). The difference between MTMPS and MTSI lies in the methodology employed in this study, wherein MTMPS incorporates W_i instead of the WAASB index. Initially, an exploratory factor analysis was conducted on rM_{qp} to cluster correlated variables into factors and compute factor scores for each genotype, in accordance with the approach proposed by Olivoto and Nardino (2021):

$$X = \mu + Lf + \in \tag{6}$$

where X is a vector of standardized observations of dimension $p \times 1$; μ is a vector of standardized means of dimension $p \times 1$; L is a matrix of factor loadings of dimension $p \times f$; f is a vector of common factors of dimension $p \times 1$; and \in is a vector $p \times 1$ of residuals, where p is the number of traits and f is the number of retained common factors.

The initial loadings were determined by considering only factors with eigenvalues exceeding one. Subsequently, varimax rotation criteria (Kaiser, 1958) were applied to obtain the final loadings, which were then utilized to compute the genotypic scores using the following procedure:

$$F = Z \left(A^T R^{-1} \right)^T \tag{7}$$

where *F* is a matrix of factor scores of dimension $q \times f$; *Z* is a standardization matrix (zero mean and unit variance) rM_{qp} of dimension $q \times p$; *A* is a matrix of canonical loadings of dimension $p \times f$; and *R* is a correlation matrix of dimension $p \times p$ between the MPS values. Here, *q*, *p*, and *f* represent the number of genotypes, traits, and retained factors, respectively. Considering the rescaled values in rM_{qp} , the ideotype would be the genotype with the best performance and stability, achieving 100 for all analyzed traits. Thus, the ideotype was defined by a vector $(1 \times p)$ *I* such that I = [100]. The classification of genotypes was determined by calculating the Euclidean distance between the scores of each genotype and the score of the ideotype, as follows:

$$MTMPS_{i} = \left[\sum_{j=1}^{f} X \left(F_{ij} - F_{j}\right)^{2}\right]^{0.5}$$
(8)

where $MTMPS_i$ is the MTMPS of the *i*-th genotype, F_{ij} represents the *j*-th scores of the *i*-th genotype, and F_i

Selection differentials (SD)

For each delineated ME, the top five genotypes were chosen, considering a selection intensity of 25 %. The selection differential (SD) as a percentage of the population mean (ΔS %) was then calculated by the Eq. (9):

$$\Delta S\% = (X_S - X_O) / X_O \times 100 \tag{9}$$

where X_s represents the mean phenotypic value of the selected genotypes, and X_o represents the population mean.

Results

Environmental similarity

A climatological series spanning the past 23 years, encompassing 19 ECs, delineated four MEs (Figure 2) based on the observed similarity on an "omic" scale. ME1 included the municipalities of Teresina - Piauí state, Brejo - Maranhão state, and Uruçuí - Piauí state. In ME2, the cities of Balsas - Maranhão state, São Raimundo das Mangabeiras - Maranhão state, Colinas - Maranhão state, and Nova Santa Rosa - Piauí state were identified. ME3 was formed solely by the municipality of Umbaúba -

Figure 2 – Illustrates a heatmap displaying delineated macroenvironments (MEs), depicting similarity based on a 23-year dataset across 19 environmental covariates. The correlation scale on the x-axis ranges from 0 (red) to 1 (purple), indicating that the closer the value is to 1, the more similar the environments are, while values closer to 0 represent greater dissimilarity. NSD = Nossa Senhora das Dores; FP = Frei Paulo; UMB = Umbaúba; NSR = Nova Santa Rosa; COL = Colinas; SRM = São Raimundo das Mangabeiras; BAL = Balsas; URU = Uruçuí; BRE = Brejo; TER = Teresina. Sergipe state, while ME4 consisted of the municipalities of Frei Paulo - Sergipe state and Nossa Senhora das Dores - Sergipe state (Figures 1 and 2, Table 3).

Moreover, environmental scores of the PCA Biplot (Figure 4A) were found to be most influenced by the following ECs: growing degree day (GDD), effect of temperature on radiation use efficiency (FRUE), slope of saturation vapor pressure curve (SPV), thermal downward longwave radiative flux (ASKLW), and rainfall precipitation (PRECTOT). These variables were identified as the most influential factors in Figure 3.

Figure 3 – Contribution of environmental covariates (x-axis) in the principal component analysis (averaged over a period of 23 years). Dim = dimension; GDD = growing degree day; FRUE = effect of temperature on radiation use efficiency; SPV = slope of saturation vapor pressure curve; ASKLW = thermal downward longwave radiative flux; PRECTOT = rainfall precipitation; TMDEW = temperature of the dew/frost point; RTA = extraterrestrial radiation; TMIN = minimum temperature; PETP = deficit by precipitation; N = daylight hours; TMAX = maximum temperature; WS = wind speed at 2 m; ETP = potential evapotranspiration; n = solar radiation; TRANGE = temperature range; ASKSW = all sky insolation incident on a horizontal surface; RH = relative humidity; VPD = vapor pressure deficit.

Environmental analysis of the two years of study

A review of the trends of ECs across individual experimental years (Figure 4B and C) reveals distinct correlation patterns, indicating the influence of seasonality. For instance, in 2012, GY exhibited a negative correlation with relative humidity (RH) and a positive correlation with vapor pressure deficit (VPD). In contrast, in 2013, the correlations were reversed, with GY positively correlated with RH and negatively correlated with VPD.

In 2012, when environmental conditions were conducive to maize cultivation, there was a strong positive correlation between genetic variation (var) and GY. This year recorded the highest GY values across all MEs, particularly in ME4 and ME3, with average yields of 10.6 and 10.5 t ha⁻¹, respectively. Genotype G18 exhibited remarkable productivity, yielding 13.7 t ha⁻¹ in ME4 and averaging 11.1 t ha⁻¹ across all MEs (Figure 5).

Conversely, the least productive year, 2013, registered ME3 with the highest yield at 10.2 t ha⁻¹, with ME4 following at 8.3 t ha⁻¹. Genotype G19 exhibited the highest productivity, yielding 11.4 t ha⁻¹ in ME3. Interestingly, G18, in ME4, recorded a yield of 8.6 t ha⁻¹, ranking among the ten least productive genotypes for this ME (Figure 5). These observations suggest that the (G × E) × YEAR interaction may influence phenotypic variation.

Another noteworthy observation pertains to the correlation between VPD \times PRECTOT and VPD \times deficit by precipitation (PETP), which exhibited negative correlations in 2012 and positive correlations in 2013. This suggests that higher VPD correlates with a drier year in 2012 and a wetter year in 2013, or vice versa, indicating that lower VPD correlates with a wetter 2012 and a drier 2013. Such variations in VPD could result in water stress, either due to shortage or excess, which would impact maize growth and development in different ways depending on the phenological stage (Figures 6A-B and 7A-B) at which this stress occurs. This would, in turn, elucidate the variation in GY between different years.

Environmet	Code	State	Longitude	Latitude	Altitude	Corn Yield
					m	t ha ⁻¹
Balsas	BAL	Maranhão	46°01'45" W	07°31'47" S	244	5,161
Brejo	BRE	Maranhão	42°45'00" W	03°40'48" S	68	5,161
Colinas	COL	Maranhão	44°04'12" W	06°01'12" S	302	5,161
Nossa Senhora das Dores	NSD	Sergipe	37°12'45" W	10°29'30" S	180	5,209
Frei Paulo	FP	Sergipe	37°31'42" W	10°33'36" S	435	5,209
Nova Santa Rosa	NSR	Piauí	44°33'30.08" W	08°17'02.8" S	489	4,523
São Raimundo das Mangabeiras	SRM	Maranhão	45°25'10" W	06°49'48" S	327	4,879
Teresina	TER	Piauí	42°46'48" W	05°01'48" S	68	4,523
Umbaúba	UMB	Sergipe	37°40'26" W	11°22'34" S	130	5,209
Uruçuí	URU	Piauí	44°28'10" W	07°13'59" S	50	4,523

Table 3 – List of municipalities in the Brazilian Northeast and corn productivity (2022/2023), according to CONAB (2024), as well as the geographic coordinates in decimal degrees of the ten environments, used for the segmentation of macroenvironments.

Figure 4 – Depicts the biplot for the principal component analysis among environmental variables. A) illustrates long-term pattern data, representing the average of 23 years of climatic information; B) and C) display climatic variables observed during the experiments in 2012 and 2013, respectively; D) presents the average information from the two years of experiments. The variables analyzed include GY = grain yield; var = genotypic variance within the macroenvironment (ME); WS = wind speed; TMAX = maximum temperature; TMIN = minimum temperature; TMDEW = temperature of the dew/frost point; TMED = average temperature; PRECTOT = rainfall precipitation; RTA = extraterrestrial radiation; RH = relative humidity; ASKLW = thermal downward longwave radiative flux; ASKSW = all sky insolation incident on a horizontal surface; FRUE = effect of temperature on radiation use efficiency; GDD = growing degree day; n = solar radiation; N = daylight hours; VPD = vapor pressure deficit; SPV = slope of saturation vapor pressure curve; TRANGE = temperature range; ETP = potential evapotranspiration; PETP = deficit by precipitation. Dim = dimension.

Figure 5 – Heatmap illustrating the mean grain yield of the examined genotypes across each combination of macroenvironment (ME) and year.

With regard to PETP, during the initial growth and leaf expansion I phases of the 2011/2012 season, ME1 and ME2 exhibited the lowest value, indicating a reduction in water availability (Figure 6A). In ME1, the PETP ranged from 80 to 50 % during the initial growth and leaf expansion I phase, respectively, with values between -11.9 and -9.38 mm d⁻¹. A similar trend was observed in ME2, with frequencies declining to approximately 45 and 20 % during the respective phases. Conversely, ME3 and ME4, which exhibited the highest productivity, displayed PETP values that consistently exceeded the range of -11.9 to -9.38 mm d⁻¹ during the initial growth phase. During the leaf expansion I phase, both ME3 and ME4 exhibited PETP values above -9.38 mm d⁻¹, with approximately 25 % of the time falling between -2.75 and 15 mm d⁻¹. This, in conjunction with the average temperature (TMED) (Figure 7B), may elucidate the higher productivities observed in these MEs.

In the 2012/2013 season, these differences in PETP were attenuated. ME3, which achieved the highest GY in 2013, exhibited the PETP values during both the initial growth and leaf expansion phases, with approximately 30 % of the time between -2.75 and 15 mm d^{-1} .

With regarding to VPD (Figure 6B), ME1, characterized by the lowest mean GY in both 2012 and 2013, exhibited the highest VPD levels across diverse growth stages. This, in conjunction with elevated TMED (Figure 7B), resulted in a more stressful environment and, consequently, lower productivity.

Figure 6 – A) Relative frequency for each type of environment regarding precipitation deficit and B) vapor pressure deficit observed across the studied environments and macroenvironments (MEs) at various stages of the crop development and trial years.

Figure 7 – A) Frequency of each environmental type for rainfall and B) mean temperature observed in the studied environments and macroenvironments (MEs) at different stages of the crop development and trial years.

The highest VPD levels were recorded for ME4 during the flowering and grain filling stages in 2012, reaching approximately 70 and 50 % between 0.903 and 1.25 kPa d⁻¹ (during flowering) and between 1.25 and 2.18 kPa d⁻¹ (during grain filling), respectively. However, ME4 exhibited the highest productivity in 2012, indicating that VPD did not significantly impact transpiration rate.

Variance components

The G \times ME \times YEAR interaction was significant for four out of the five analyzed traits, with NE and PD displaying the largest contributions to phenotypic variance (Figure 8A and Table 4). This underscores the direct impact of environmental factors on genotypic responses, emphasizing the necessity for genotype selection tailored to each ME (Heinemann et al., 2019; Mebratu et al., 2019; Singamsetti et al., 2021; Yue et al., 2022). Considering GY, year and ME were identified as the primary contributors to phenotypic variance. As for genetic variance, the interactions $G \times ME$, $G \times ME \times YEAR$, and $G \times YEAR$ collectively accounted for over 50 % of the variance in genotype means for GY, NE, and PD (Figure 8B).

The phenotypic correlations between the traits studied in each ME over the two years exhibited

Figure 8 – A) Percentage of phenotypic mean value variance and B) percentage of genotype mean variance. EH = ear height, GY = grain yield; NE = number of ears; PD = plant density; PH = plant height; ME = macroenvironment; G = genotype; REP = repetition.

Table 4 – Variance components for the main effect of genotypes variance (σ_{σ}^2), macroenvironments variance (σ_{M}^2), cultivation year variance (σ_{γ}^2), and their interactions estimated for five traits assessed in 20 maize hybrids.

Source of variation	EH	GY	NE	PD	PH
σ_M^2	0.804 ^{ns}	0.146 ^{ns}	0.017*	0.008**	0.109 ^{ns}
σ_{G}^{2}	0.000**	0.072 ^{ns}	0.652 ^{ns}	0.707 ^{ns}	0.157 ^{ns}
σ^2_{GY}	1.000 ^{ns}	0.000**	0.008**	0.154 ^{ns}	0.422 ^{ns}
σ^2_{GM}	0.360 ^{ns}	0.001**	0.022*	0.369 ^{ns}	1.000 ^{ns}
σ^2_{GMY}	0.055 ^{ns}	0.006**	0.000**	0.000**	1.000 ^{ns}
$\sigma^2_{REP(M:Y)}$	0.000**	0.000**	0.000**	0.000**	0.000**
σ^2_{MY}	0.158 ^{ns}	0.839 ^{ns}	1.000 ^{ns}	1.000 ^{ns}	1.000 ^{ns}
σ_{γ}^2	1.000 ^{ns}	0.061 ^{ns}	0.376 ^{ns}	1.000 ^{ns}	0.999 ^{ns}

EH = ear height; GY = grain yield; NE = number of ears; PD = plant density; PH = plant height; REP = repetition. * $p \le 0.05$; ** $p \le 0.01$; "*p > 0.05.

notable differences. The ME1 was the only to exhibit negative correlations between EH and PD, EH and GY, and PD and PH (Figure 9A). In the other MEs, all the characteristics were positively correlated with each other, although the degree of Mantel correlation between the matrices was low. This lends support to the use of a multiple characteristics index in each ME to account for the different correlation structures (Figure 9B-D).

Selection differentials for mean performance and stability

The selection process for each ME entailed considering multiple traits, resulting in identifying the top five

F	igure 9 – Phenotypic correlations between the traits evaluated
	in macroenvironments (MEs) A) ME1, B) ME2, C) ME3, and D)
	ME4 in the two years studied. PH = plant height; NE = number
	of ears; EH = ear height; PD = plant density; GY = grain yield.

genotypes for each ME (Figures 10A-D and 11). The hybrids G04 and G03 were selected in three MEs (ME1, ME3, and ME4), which serves to illustrate their commendable performance and stability across diverse environments. In addition, certain hybrids were selected for two specific MEs: G17 (ME1 and ME2), G10 (ME1 and ME3), G08 (ME2 and ME3), and G06 (ME2 and ME4).

The five selected genotypes (ranked by MTMPS) within ME1 were identified as G14, G04, G10, G03, and G17 (Figure 10A). For ME2, the selected hybrids were G06, G08, G01, G07, and G17 (Figure 10B). In ME3, the selected hybrids were G08, G03, G02, G04, and G10 (Figure 10C). Within ME4, the top-performing hybrids were G06, G03, G04, G05, and G20 (Figure 10D).

Three factors remained consistent in all MEs, collectively explaining 83, 82, 93, and 97 % of the total variance for ME1, ME2, ME3, and ME4, respectively. The multivariate selection demonstrated a 100 % success rate (five out of five traits) for the desired SD in ME1, ME3, and ME4, and 80 % (four out of five traits) for ME2 (Figure 12).

The SD for PD was positive for all MEs, except ME2, where it was at -0.13. The GY exhibited a positive SD across all MEs, ranging from 3 % in ME2 to 15 % in ME4 (Figure 12). Upon analysis of stability over the two years of cultivation, the majority of the studied characteristics exhibited negative SD values (Figure 13), with the exceptions of EH in ME1 and ME2, which demonstrated SD values of 9.4 and 30.5, respectively, and PH in ME1, which exhibited an SD value of 9.6. GY, NE,

Figure 10 – The genotypic ranking and the chosen genotypes (G) for the multi-trait mean performance and stability index (MTMPS), considering a selection intensity of 25 % within A) macroenvironment (ME)1, B) ME2, C) ME3, and D) ME4. The highlighted red circles indicate the five selected genotypes for each respective macroenvironment.

and PD exhibited negative SD across the MEs. Notably, ME1 and ME2 demonstrated the lowest SD values for GY, at -32.9 and -45.7, respectively. This confirms that the selected hybrids exhibit superior average performance and remain stable across diverse environments and contrasting cultivation years.

Classification of MEs

The Genotype and Genotype \times Environment Biplot (GGE biplot) (Figure 14) illustrates the categorization of the four delineated MEs in relation to an ideal ME. With regard to the mean productivity of each ME, ME4 (Nossa Senhora das Dores and Frei Paulo) is the most proximate the "ideal" environment, exhibiting a mean productivity of 9.5 t ha⁻¹. Conversely, ME2, with mean yields of 8.5 t ha⁻¹, appears to be the most distant from the "ideal" environment depicted in Figure 14.

Genotype classification

The GGE Biplot is a graphical representation that depicts the ranking of genotypes in relation to an ideal genotype (Figure 15A) and illustrates the means of each genotype along with their stability (Figure 15B). Genotypes G17, G08, and G07 were identified as the hybrids that most closely approximated the ideal genotype, as indicated by their proximity to the center of concentric circles (Figure 15A). With regard to stability, G08, G09, and G14 exhibited greater stability, whereas G16 displayed the highest level of instability among the evaluated hybrids (Figure 15B). A comparison of GGE with MTMPS revealed that hybrids G07, G08, G14, and G17 (Figure 10A-D) were also selected as the most productive and stable among the different MEs.

Discussion

The climate variability in the northeastern region of Brazil is complex and diverse. This is evidenced by the grouping of distant cities from different states into the same ME (ME1 and ME2), while closer cities within the Figure 11 – A Venn diagram illustrating the five selected genotypes (G) in each macroenvironment (ME).

same state (Sergipe) formed two distinct MEs (ME3 and ME4) (Figure 1).

The observed complexity in climatic patterns within the northeastern region of Brazil is consistent with similar findings of Yue et al. (2022), who documented comparable ME dynamics in the Huanghuaihai Plain of China. Furthermore, the high spatio-temporal variability and irregular rainfall patterns observed in northeastern Brazil (Brito et al., 2021) are highlighted, particularly in the context of major atmospheric phenomena such as El Niño and La Niña (Nóia Júnior and Sentelhas, 2019). These parallels underscore the significance of our study in understanding climatic variability and optimizing genotype selection and agricultural planning. Our research offers valuable insights that can enhance the resilience and productivity of agricultural systems in similar environments globally.

These findings prompt a more comprehensive exploration of the distinctive attributes associated with each ME identified in this study. The PCA biplot (Figure 4A) offers insights into the characteristics of each ME in the study. ME1 is distinguished by elevated values of GDD, which signify the accumulated temperature for plant development. Additionally, ME1 exhibits a higher Figure 12 – Selection gains for average performance within each macroenvironment (ME) were calculated considering the top five selected genotypes. EH = ear height; PH = plant height; GY = grain yield; NE = number of ears; PD = plant density.

Figure 13 – Selection gains for stability within each macroenvironment (ME) were calculated based on the top five selected genotypes. EH = ear height; GY = grain yield; NE = number of ears; PD = plant density; PH = plant height.

ratio of radiation use efficiency (FRUE), indicating that plants in this ME utilize solar radiation (n) for photosynthesis and biomass production. Moreover, ME1 is associated with elevated values of mean temperature of the dew point (TMDEW) and daylight hours (N), indicating favorable conditions for plant growth. Conversely, ME2 is characterized by elevated values of maximum temperature (TMAX), ASKLW, PRECTOT, and PETP. The increased precipitation levels and higher values of PETP suggest that ME2 is experiencing greater water availability. In contrast, ME3 exhibits higher values of wind speed (WS) and n, indicating stronger winds and longer sunlight duration, as well as a lower temperature range (TRANGE), with a TMAX of 28.1 °C and a minimum temperature (TMIN) of 22.5 °C. These conditions are optimal for maize development and may influence the growth and development of plants in ME3. Finally, ME4 is distinguished by higher values of VPD and TRANGE, with a TMAX of 29.4 °C and a TMIN of 19.3 °C. This association suggests that drier environmental conditions are characterized by higher evapotranspiration rates and greater temperature fluctuations. This observation aligns with the findings of Yue et al. (2022), who reported similar characteristics for drier environments.

Similar findings were reported, indicating that the most productive ME exhibited the highest VPD levels. This led to the conclusion that VPD alone was not sufficient to diminish productivity (Yue et al., 2022). This is likely due to the influence of other environmental variables, including TMAX, TMED, and TMIN, as well as RH, WS, and PRECTOT. These variables can significantly influence the phenotypic expressions of the hybrids studied.

An understanding of the environmental dynamics across diverse locations and years, in conjunction with $G \times E$, is of heightened significance (Gauch et al., 2008; Olivoto et al., 2019a; Yan et al., 2007). The identification of maize genotypes capable of effectively navigating water stress and other climatic fluctuations, particularly within specific MEs and aligned with growth stages, is of paramount importance for sustaining productivity over successive years (Carcedo et al., 2022; Rezende et al., 2020; Xu, 2016; Yue et al., 2022). These findings underscore the reliance of genotype phenotyping expressions on environmental cues (Guo et al., 2020; Krause et al., 2020; Rezende et al., 2020), thus emphasizing the significance of genotype selection within MEs (Sampaio Filho et al., 2023; Yue et al., 2022). Such tailored selection strategies have the potential to yield greater selection gains, particularly in cases where

Figure 14 – Genotype and Genotype × Environment Biplot (GGE Biplot) of environmental ranking, displaying the classification of macroenvironments (MEs) concerning an ideal ME. The analysis uses Single Value Projection (SVP) = 2, the singular value is entirely partitioned into the environment eigenvectors. PC = principal component.

the primary traits for genotype enhancement are matric in nature, and involve multiple genes in phenotypic expressions (Borém et al., 2017; Ceballos et al., 2020; Jarquín et al., 2014; Sampaio Filho et al., 2023).

This information is of paramount importance for the classification of environments into distinct ME categories and the selection of genotypes within these categories, as opposed to the use of broadly adapted genotypes for all MEs (Abakemal et al., 2016; Gauch and Zobel, 1997; Sampaio Filho et al., 2023; Yue et al., 2022).

Nevertheless, genotypes have been developed and demonstrated to be productive in a range of MEs. The selection of hybrids G04 and G03 in three out of four MEs (ME1, ME3, and ME4) underscores their robust performance and stability across diverse environmental conditions. Furthermore, ME4 emerged as the most favorable environment, aligning closely with the optimal conditions for the studied hybrids.

The MTMPS, a novel form of multivariate selection, may be regarded as an adaptation of MTSI (Olivoto et al., 2019b; Yue et al., 2022). The MTMPS index identified five hybrids for each ME using a selection intensity of 25 % (Figure 10A-D). The selected hybrids exhibited reduced MTMPS values, suggesting their proximity to the ideotype when considering all evaluated traits (Olivoto et al., 2019b; Sampaio Filho et al., 2023). The MTMPS methodology has demonstrated efficacy in assessing G × E in maize breeding, enhancing performance and stability across all evaluated traits. Nevertheless, despite its potential for improving genotype selection, the MTMPS methodology is not widely utilized.

In conclusion, envirotyping has been demonstrated to be an effective method for establishing robust correlations

Figure 15 – Genotype and Genotype × Environment Biplot (GGE Biplot): mean × stability for grain yield (t ha–1) of 20 maize genotypes grown in four macroenvironments (MEs) of the Brazilian Northeast and their respective production stabilities. The analysis uses Single Value Projection (SVP) = 1, the singular value is entirely partitioned into the genotype eigenvectors. Env = environments and Gen = genotypes. PC = principal component; G = genotype.

between environments, thereby enhancing the accuracy of cultivar recommendations across different locations within the same ME trial. The multivariate approach, specifically the MTMPS index, has demonstrated effectiveness in selecting productive and stable genotypes for each ME. By integrating envirotyping techniques with multivariate selection strategies for average performance and stability, this study has provided valuable insights into genotypeenvironment interaction within multi-environment trials. These advancements are poised to significantly enhance breeding programs and contribute to the development of more resilient and productive crop varieties tailored to specific environmental contexts.

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Declaration of conflict of interest

The authors declared that there is no conflict of interest that could constitute an impediment to the publication of this article.

Data availability statement

All data generated or analyzed during this study are included in this paper or will be made available for publication.

Declaration of use of AI Technologies

The authors used AI technologies only to assist with English language corrections in the preparation of this paper.

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