

Selection of maize genotype using multi-trait index and ideotype design for semi-arid regions

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Abstract: *The selection of maize genotypes using multivariate analysis enhances breeding programs by combining adaptability and performance in challenging environmental conditions, such as low water availability and irregular, poorly distributed rainfall. This study aimed to select the most suitable maize genotypes for semi-arid regions using selection indices. Twenty-seven genotypes were evaluated in a randomized block design. The analyzed variables were post-harvest and morphophysiological traits. Analysis of variance, a multi-trait index based on factor analysis and ideotype-design (FAI-BLUP), and the multi-trait genotype-ideotype distance index (MGIDI) were performed. Thus, it can be concluded that the genotypes differ in relation to the variables and conditions studied. The FAI-BLUP and MGIDI indices selected genotypes AG 8780, GNZ 40, GNZ 15, and KWS 9606 Vip3 as the most aligned with the ideal ideotype for maize cultivation in semi-arid regions.*

Keywords: Factorial analysis, genetic gain, selection index, yield, Zea mays L.

INTRODUCTION

Maize (*Zea mays* L.) is one of the most widely cultivated crops in the world, playing a key role in global food security and agricultural economics. Its versatility makes it essential across various sectors, including human food, raw material for several industries, and animal feed. The adaptability to different growing conditions makes maize a crucial crop in many countries, including Brazil (Yue et al. 2022, Zembrato et al. 2024).

The importance of maize is reflected in Brazil's annual production records, which reached 131,892.6 million tons. The Northeast region accounted for 11,691.5 million tons, with the states of Bahia, Maranhão, Piauí, and Sergipe standing out for their contributions to increased productivity. Sergipe, although ranking fourth with a production of 932.3 thousand tons, stood out for its high productivity, reaching 5,209 kg ha⁻¹ within the region (CONAB 2023).

Maize cultivation is essential in the semi-arid region, with significant cultural and socioeconomic importance, although adverse conditions affect its growth (Singamsetti et al. 2023). Nevertheless, production in Sergipe has shown great resilience, attributed to a combination of the genetic potential of the seeds and the region's soil and climate conditions, as pointed out by Prado et al. (2023) and Silva et al. (2021).

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The main challenge faced by breeding programs in the semi-arid region is water scarcity, which is intensified by the irregular and poor distribution of rainfall. To facilitate the selection of ideal genotypes that combine multiple traits, Rocha et al. (2018) introduced the FAI-BLUP index, which integrates factor analysis and the genotype-ideotype concept (Costa et al. 2023). Olivoto and Nardino (2021) developed the multi-trait genotype-ideotype distance index (MGIDI), aiming to enhance strategic decisions for the efficient selection of genotypes.

The FAI-BLUP and MGIDI indices facilitate the selection of genotypes based on multiple traits, thereby optimizing the efforts of breeding programs in the region. Therefore, selecting better-adapted genotypes is essential to improve genetic gain (Guimarães et al. 2019). This study aimed to select the most suitable maize genotypes for the semi-arid region using multivariate techniques, including factor analysis and ideotype design.

MATERIAL AND METHODS

Genetic material and experimental procedure

The experiment was conducted in 2021 at the Embrapa's Semiárido Experimental Farm (Embrapa Semiárido; lat 10° 13' 06" S, long 37° 25' 13" W, alt 291 m asl), in Nossa Senhora da Glória, State of Sergipe, located in the Upper Sertão. According to the Köppen classification, the region has a type As climate, characterized as tropical hot and humid, with hot, dry summers and rainfall concentrated in the winter (Alvares et al. 2013). During the experiment, the total precipitation recorded was 344 mm, and the average air temperature was 22.98 °C (Figure 1).

In this study, a total of 27 promising maize genotypes were used, including commercial and experimental genotypes (Table 1). The experimental design was a randomized complete block design with two replications; each experimental plot consisted of two rows measuring 5.0 m in length, with a spacing of 0.20 m between plants and 0.70 m between rows, totaling 54 experimental plots and forming a population of 71,428 plants ha⁻¹.

The soil for planting was prepared using a four-row cultivator, creating furrows. The genotypes were sown manually, using 50 seeds per plot. Fertilization was divided into two stages: basal fertilization, using 833 kg ha⁻¹ of NPK (6-24-12), equivalent to 50 kg ha⁻¹ of N, 200 kg ha⁻¹ of P₂O₅, and 100 kg ha⁻¹ of K₂O; and topdressing fertilization, with 100 kg ha⁻¹ of 46% N urea applied at the V4 phenological stage. These recommendations were based on soil analysis and the crop's requirements, according to the guidelines of Sobral et al. (2007).

The following traits were assessed: male flowering (MF, days): conducted daily, counting from the planting date, until 50 % of the plants in the plot exhibited pollen dispersal; female flowering (FF, days): conducted daily, counting from the planting date, until 50% of the plants in the plot showed stigma emergence; ear height (EH, cm): average of five randomly selected plants in the plot, measured upwards from ground level to the insertion point of the first ear; relative ear position (REP, cm): obtained by the ratio of ear height to plant height; number of ears per plot (NEP): total number of ears counted from all plants per plot; ear weight (EW, kg): weight of ears from all plants per plot, without husk, measured using a precision scale; total grain weight per plot (TGW, kg): quantification of the total grain weight per plot after threshing, measured using a precision scale.

Statistical analyses

An analysis of variance was performed at the 5% significance level, using the ExpDes.pt package, with comparisons made using the F-test. Subsequently, calculations were performed using the FAI-BLUP (Rocha et al. 2018) and MGIDI

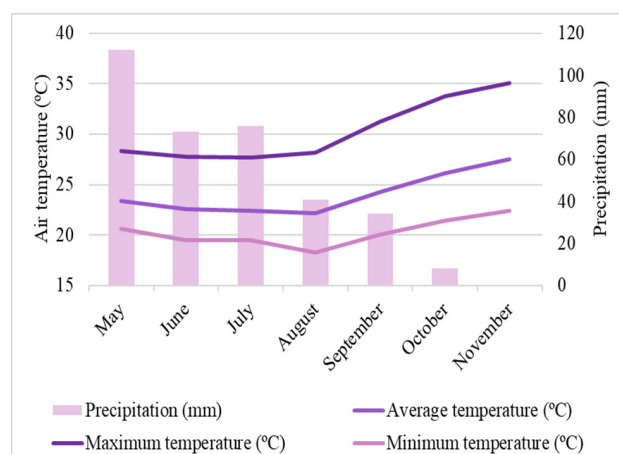


Figure 1. Air temperature (°C) and precipitation (mm) during the experiment conducted in the 2021 crop season.

(Olivoto and Nardino 2021) indices to identify superior genotypes based on genetic values. The Metan package (Olivoto and Lúcio 2020) was used, and all analyses were conducted using R software (R Core Team 2023).

The weights assigned to the traits in the FAI-BLUP and MGIDI indices were based on desirable and undesirable agronomic attributes, according to the study's objective. For traits such as ear number, ear weight, and total grain weight, higher values were preferred, while for male and female flowering, ear height, plant height, and ear position, lower values were ideal. The selection intensity was set at 20% for both indices.

RESULTS AND DISCUSSION

Analysis of variance

According to the analysis of variance presented in Table 2, the significance of the F-test indicates that at least one genotype differs from the others, revealing significant differences between the genotypes for the variables evaluated under the studied conditions. According to Fritsche-Neto et al. (2012), the coefficient of variation (CV) is an important tool for evaluating experimental precision. For crops such as soybean, wheat, beans, sorghum, and corn, the CV should be $\leq 20\%$ (Gurgel et al. 2013). The analyzed variables ranged from 1.93% to 16.59%, falling within the acceptable limits, which indicates a precise experiment.

Exploratory factor analysis

Table 3 shows the eigenvalues and accumulated variance of the seven main components from the genetic correlation matrix. According to Kaiser's (1958) criteria, only the first two components have values greater than one, explaining 80.78% of the data variability. Alves et al. (2021) emphasize that an accumulated variance of 70% is necessary to ensure the reliability of the results. The eigenvalue of the first principal component (PC1) was 4.55, representing a significant portion of the total variability (sum of eigenvalues = 7.00). This result aligns with Kaiser (1958)'s assertion that the higher

Table 1. Description of the 27 maize genotypes evaluated in the experiment conducted at the Embrapa's Semi-arid Experimental Farm (Embrapa Semiárido), in Nossa Senhora da Glória, State of Sergipe, in the agricultural year of 2021

Code	Name	Phase	Origin
1	KWS 9555 Vip3	Cm	KWS
2	GNZ 17(Ex3W06L Vip3-INV)	Ex	GNZ
3	GNZ 7280 Pro2	Cm	GNZ
4	GNZ 15	Ex	GNZ
5	AG 1088 x JM2M77	Ex	IAC
6	IAC Airan	Cm	IAC
7	GNZ 9501 Pro	Cm	GNZ
8	GNZ 7740 Vip3	Cm	GNZ
9	BM 709 x PopTol 2	Ex	IAC
10	IAC 8053	Ex	IAC
11	GNZ 59	Ex	GNZ
12	GNZ 7280 (Convencional)	Cm	GNZ
13	GNZ 16(Ex3W07L Vip3)	Ex	GNZ
14	GNZ 76	Ex	GNZ
15	GNZ 7720 Vip3	Cm	GNZ
16	KWS 9606 Vip3	Cm	KWS
17	AG 8780	Cm	AG
18	IAC 46 x PopTol 2	Ex	IAC
19	IAC 8046	Cm	IAC
20	AG 8088 x PopTol 2	Ex	IAC
21	BM 703 x JM21177	Ex	IAC
22	GNZ 96	Ex	GNZ
23	GNZ 40	Ex	GNZ
24	KWS 9960 Vip3	Cm	KWS
25	GNZ 19(Ex3W06L Vip3)	Ex	GNZ
26	KWS 9822 Vip3	Cm	KWS
27	GNZ 18(Ex3W05L Vip3)	Ex	GNZ

Cm = Commercial; Ex = Experimental; KWS = KWS Seeds; GNZ = Geneze Seeds; IAC = Agronomic Institute of Campinas; AG = Agrocerees Seeds.

Table 2. Summary of the analysis of variance with mean squares (MS) and environmental coefficient of variation (CV%) of the variables evaluated in the field experiment, at Embrapa's Semi-arid Experimental Farm (Embrapa Semiárido), in Nossa Senhora da Glória, State of Sergipe

SV	df	MS								
		NEP	EW	TGW	PH	EH	REP	MF	FF	Y
Gen.	26	57.897**	1.955**	0.948**	0.056*	0.041**	0.031**	6.262**	10.282**	1373104
Block	1	20.167	0.019	0.004	0.008	0.009	0.001	18.963	10.667	33211
Residual	26	19.744	0.701	0.303	0.026	0.012	0.001	1.425	1.744	3558289
CV (%)		11.99	16.01	16.59	6.88	9.14	4.28	1.93	2.15	14.69
Mean		38	5.135	3.258	2.35	1.20	0.51	62	62	6338.99

MS = mean square; FV = source of variation; Gen. = genotype; DF = degrees of freedom; CV = coefficient of variation; NEP = number of ears per plot; EW = ear weight; TGW = total grain weight per plot (kg); PH = plant height (cm); EH = ear height (cm); REP = relative ear position; MF = male flowering; FF = female flowering; Y = grain yield (kg ha⁻¹); **, * significant at 1% and 5% probability by F-test, respectively.

the eigenvalue, the greater its capacity to summarize the variables, highlighting it as a key factor.

In Table 4, after applying the Varimax method, the first factor was named “phenograin” due to the strong genetic correlation between the number and weight of ears, total grain weight, and male and female flowering, with factor loadings of -0.84, -0.89, -0.89, 0.76, and 0.82, respectively. The second factor, “harvestability,” was formed by the variables ear height and position, showing a significant negative correlation between them, with loadings of -0.94 and -0.88, respectively (Table 4). According to Lorentz and Nunes (2013), communalities above 0.7 indicate reduced environmental influence, suggesting more consistent associations. In factor analysis, the relevance of each variable is highlighted by genetic correlations (Murakami and Cruz 2004, Oliveira et al. 2005, Peixoto et al. 2021).

The selection of genotypes can be based on morphological traits such as increased prolificacy (NEP), greater ear weight (EW), greater total grain weight (TGW), precocity (MF and FF), and lower ear position, which suggests better harvesting efficiency. These traits are crucial for the semi-arid region, aiding in the identification of adapted varieties. Guimarães et al. (2019) highlight the importance of high-quality genotypes that are adaptable.

Table 5 shows the genetic gain of selected genotypes based on the selection index. Heritability ranged from 0.64 to 0.85, and according to Rodrigues et al. (2011), this parameter is essential for the success of selection. Additionally, a reduction of -2.66% in male flowering and -3.54% in female flowering is recommended. These reductions contribute to the selection of early-maturing genotypes, as highlighted by Berchembrock et al. (2021). Ear height decreased by -7.66% and relative ear position by -7.10%, facilitating harvesting, as emphasized by Freitas et al. (2013) and Azrai et al. (2023). Positive genetic gains were observed for the number of ears per plot (6.61%), ear weight (8.67%), and total grain weight (10.8%) (Table 5), indicating the selection of superior progenies for breeders.

FAI-BLUP index

The FAI-BLUP index identified genotypes 17 (AG 8780), 23 (GNZ 40), 4 (GNZ 15), and 16 (KWS 9606 Vip3) as the most aligned with the desired ideotype in this study (Figure 2). As highlighted by Volpato et al. (2020), selecting genotypes

Table 3. Estimates of eigenvalues and proportion of cumulative variance by principal component analysis

Principal Component	Eigenvalue	Cumulative Variance (%)
PC1	4.55	65.05
PC2	1.1	80.78
PC3	0.65	90.06
PC4	0.34	94.88
PC5	0.17	97.34
PC6	0.12	99.06
PC7	0.07	100

Table 4. Factor loadings after Varimax rotation and communalities

Traits	Factor		Communalities
	Phenograin	Harvestability	
NEP	-0.84	0.14	0.73
EW	-0.89	0.22	0.84
TGW	-0.89	0.26	0.86
EH	0.21	-0.94	0.92
REP	0.32	-0.88	0.88
MF	0.76	-0.29	0.67
FF	0.82	-0.29	0.76
Mean	-	-	0.81

NEP = Number of ears per plot; EW = Ear weight; TGW = Total grain weight per plot (kg); MF = Male flowering; FF = Female flowering; EH = Ear height (cm); REP = Relative ear position.

Table 5. Predicted genetic gain based on direct selection.

Factor	Variable	Xs	SD	SD (%)	h ²	SG	SG (%)
Phenograin	NEP	40.8	3.72	10.0	0.659	2.45	6.61
	EW	5.94	0.707	13.5	0.641	0.454	8.67
	TGW	3.85	0.527	15.9	0.68	0.359	10.8
	MF	59.7	-2.13	-3.44	0.773	-1.64	-2.66
	FF	58.9	-2.62	-4.26	0.83	-2.18	-3.54
Harvestability	EH	1.07	-0.13	-10.8	0.707	-0.092	-7.66
	REP	0.465	-0.042	-8.35	0.85	0.036	-7.10

Xs = mean of selected genotypes; SD = selection differential; SD% = selection differential in percentage; h² = heritability; SG = selection gain; SG% = selection gain in percentage; NEP = Number of ears per plot; EW = Ear weight; TGW = Total grain weight per plot (kg); MF = Male flowering; FF = Female flowering; EH = Ear height (cm); REP = Relative ear position.

with multiple traits is essential for optimizing genetic gain in the semi-arid region. These results underscore the importance of identifying specific traits to develop well-adapted populations.

View of strengths and weaknesses by the MGIDI Index

Figure 3 shows the strengths and weaknesses of the genotypes selected by the MGIDI index (Olivoto and Nardino 2021). A lower proportion in a factor indicates greater alignment with the ideotype. Genotypes 4 (GNZ 15), 16 (KWS 9606 Vip3), and 23 (GNZ 40) performed well in FA1, with favorable post-harvest traits (NEP, EW, TGW) and precocity (lower FF and MF). Genotype 4 (GNZ 15) stands out as a promising candidate for optimizing Phenograin.

FA2 shows a significant impact on genotypes 17 and 16, which exhibit the desired traits, particularly in terms of ear height and relative position. Genotype 17 is a promising option for optimizing harvest efficiency. Singamsetti et al. (2023) applied a similar methodology and they observed comparable patterns in tropical corn hybrids under varying moisture conditions, noting that MGIDI enhances genotype selection based on multiple traits, including secondary characteristics and grain yield.

CONCLUSIONS

The genotypes differ in relation to the variables and conditions studied, which is favorable for gain through selection.

The FAI-BLUP index highlighted genotypes AG 8780, GNZ 40, GNZ 15, and KWS 9606 Vip3 as promising for a breeding population in the semi-arid region.

The MGIDI index emphasized GNZ 15 for its potential in Phenograin, with higher productivity and precocity, while AG 8780 stood out in terms of harvestability, with lower ear height and better ear position.

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DATA AVAILABILITY

The datasets generated and/or analyzed during the current research are available from the corresponding author upon reasonable request.

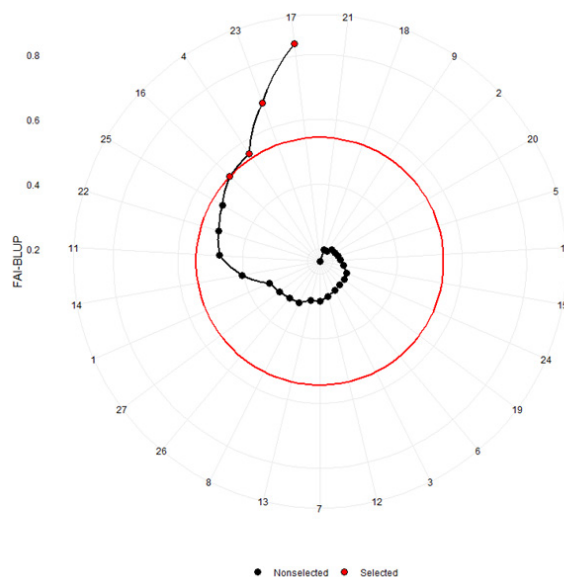


Figure 2. Classification of the 27 maize genotypes and selected genotypes using the FAI-BLUP index.

Strengths and weaknesses view

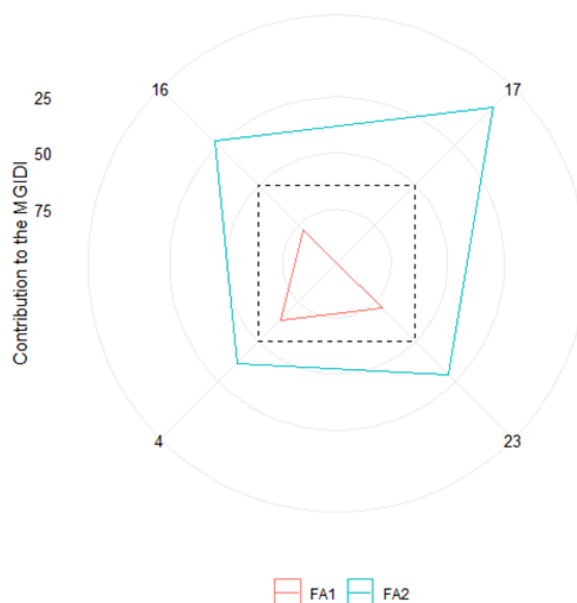


Figure 3. The view of strengths and weaknesses of the selected genotypes is shown in the proportion of each factor computed from multiple traits (MGIDI).

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