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PLANT BREEDING - Article

Hybrid maize selection through GGE biplot analysis

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ABSTRACT: The cultivation of genotypes non-adapted to the cultivation region of interest is among the main factors responsible for low yield. The aim of the present study is to select hybrid maize through GGE biplot analysis and to assess its adaptability and stability in different environments in Northeastern Brazil. Twenty-five hybrid maize cultivars were assessed in ten different environments in Northeastern Brazil in 2012 and 2013 based on the randomized block design, with two replications. The analysis of variance and assessment of genotype adaptability and stability were made through GGE biplot analysis, based on grain yield. Analysis of variance results showed different performances depending on the genotype, as well as genotype/environment interaction. The biplot analysis was efficient on data interpretation and represented 63.73% of the total variation in the first two main components, it also allowed classifying the ten environments into three macro-environments. Most environments were positively correlated. Hybrids 2 B 604 HX, 30 A 95 HX, 2 B 587 HX and 2 B 710 HX were responsive and stable. Hybrid 30 A 16 HX was recommended for macro-environments 2 and 3. Cultivar 30 A 68 HX was recommended to environment 1. São Raimundo das Mangabeiras and Nova Santa Rosa counties were discriminating and representative. Nossa Senhora das Dores, Umbaúba, Teresina, Brejo, Frei Paulo, Colinas and Balsa counties were ambiguous and non-recommended for further evaluations.

Key words: G × E interaction, multivariate analysis, *Zea mays L*.

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INTRODUCTION

Maize (*Zea mays L.*) is an important culture worldwide due to its several applications and economic relevance. Farmers in Northeastern Brazil count on low technological level during maize cultivation because, in this region, it is mainly grown in small farms (Carpentieri-Pípolo et al. 2010). The lack of genotypes adapted to the soil and weather in the region has resulted in low and instable yield (Oliveira et al. 2017).

It is difficult to identify superior genotypes due to the genotypes × environments (G × E) interaction, but assessing such interaction is extremely important, since it is the number one factor responsible for changing genotype performance in different environments. This feature impairs the recommendation of adaptable and stable cultivars (Mohamed 2013; Oliveira et al 2017). G × E studies allow identifying the ideal location to each genotype, which would maximize the grain yield potential and reduce production costs (Oyekunle et al. 2017).

Maize producers use different analyses to assess cultivar adaptability and stability based on biometric concepts (Camargo-Buitrago et al. 2011; Silva and Benin 2012). The GGE biplot analysis derives from the first two main components (MCs), the first one regards the yield ratio, which is associated with genotypic characteristics; and the second one concerns the yield related to the G × E interaction (Yan and Holland 2010; Yan 2001).

The GGE biplot analysis is efficient because it enables predicting the mean genotype yield per specific environment, as well as helps identifying the most stable genotype for the region of interest (Santos et al. 2017; Yan 2014). According to Badu-Apraku et al (2012), this analysis is more versatile and flexible than other models based on simple linear regression and on segmented linear regression, as well as than non-parametric methods, because it allows better understanding the G × E interaction.

Studies about the adaptability and stability of different cultures based on biplot graphics corroborate the efficiency of the analysis to recommend genotypes and to group favorable and unfavorable environments (Silva et al. 2011; Santos et al. 2016; Paramesh et al. 2016; Yokomizo et al. 2017).

The aim of the present study was to select hybrid maize through the GGE biplot analysis and to evaluate its adaptability and stability in different environments in Northeastern Brazil.

MATERIALS AND METHOD

We assessed 25 hybrids from private and public companies during the agricultural years 2012 and 2013 (Table 1) in Maranhão (Balsas, Brejo, Colinas and São Raimundo das Mangabeiras counties), Piauí (Nova Santa Rosa, Teresina and Uruçuí counties) and Sergipe states (Nossa Senhora das Dores, Frei Paulo and Umbaúba counties) (Table 2).

Our study followed the randomized block design, with two repetitions. The plots comprise five lines (5.0 m long) each, and the pits in the rows were spaced 0.70 m and 0.20 m from each other. Fertilization procedures were based on results of soil analyses applied to the soil in each experimental area.

Were sowed 15 seeds per linear meter (75 plants per line). The seedlings were thinned 15 days after emergence (five plants per linear meter remained after thinning) and assessed all lines in each plot at harvest time in order to find the yield rates.

The needs of the culture (in each region) guided the weed and pest control procedures, but we did not irrigate the plants.

The analysis of variance was conducted to each location in 2012 and 2013 in order to assess residual variance homogeneity. The multivariate analysis of variance included genotypes, year and local, finding the GE matrix. The analysis assessed each location as an environment.

Information about the phenotypic mean substantiated the multivariate GGE biplot analysis. We took the following model into consideration (Eq. 1):

$$\bar{Y}_{ij} - \mu = G_i + E_j + GE_{ij} \qquad (1)$$

where $\bar{Y}_{ij}$ is the phenotypic mean of genotype *i* in environment *j*; μ is the general constant; G_i is the random effect of genotype *i*; E_j is the fixed effect of environment *j*; and GE_{ij} is the random effect of the interaction between genotype *i* and environment *j* (Yan 2001).

The GGE biplot model does not dissociate the genotype effect (G) from the genotypse × environments effect (GE). It keeps G and GE together in two multiplicative terms in the Eq. 2:

$$Y_{ij} - \mu - \beta j = g_{i1}e_{1j} + g_{i2}e_{j2} + \varepsilon_{ij} \qquad (2)$$

where Y_{ij} is the expected performance of genotype *i* in environment *j*; μ is the general constant of observations; β_j is the main effect of environment *j*; g_{1i} and e_{1j} are the main

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scores of the i^{th} genotype in the j^{th} environment, respectively; and ε_{ij} is the non-explained residue of both effects ("noise").

The biplot graphs in the GGE model were generated through the simple dispersion of g_{i1} and g_{i2} to assess the

Table 1. List of hybrid maize cultivars and their respective origins, types, cycles, colors, grain textures and companies.

No.	Cultivar	Transgenic/ conventional	Type[1]	Cycle[2]	Grain color[3]	Grain texture[4]	Seed company
1	20 A 55 HX	Transgenic	TH	E	OR	SMHARD	MORGAN
2	20 A 78 HX	Transgenic	SH	E	OR	SMHARD	DOW
3	2 B 433 HX	Transgenic	TH	EE	Y / OR	SMDENT	DOW
4	2 B 587 HX	Transgenic	SH	E	Y / OR	SMDENT	DOW
5	2 B 604 HX	Transgenic	SHm	E	OR	SMHARD	DOW
6	2 B 688 HX	Transgenic	TH	E	OR	SMHARD	DOW
7	2 B 707 HX	Transgenic	SH	E	OR	SMHARD	DOW
8	2 B 710 HX	Transgenic	SH	E	Y / OR	SMHARD	DOW
9	30 A 16 HX	Transgenic	SH	E	OR	SMHARD	MORGAN
10	30 A 37 HX	Transgenic	SH	EE	Y / OR	SMHARD	MORGAN
11	30 A 68 HX	Transgenic	SH	EE	OR	SMHARD	MORGAN
12	30 A 91 HX	Transgenic	SHm	E	Y / OR	SMHARD	MORGAN
13	30 A 95 HX	Transgenic	TH	E	OR	SMHARD	MORGAN
14	30 F 53 HR	Transgenic	SH	E	OR	SMHARD	DU PONT
15	30 K 73 H	Transgenic	SH	E	Y / OR	SMHARD	DU PONT
16	AG 8041 YG	Transgenic	SH	E	Y / OR	SMHARD	SEMENTES
17	AS 1555 YG	Transgenic	SH	E	OR	SMHARD	AGROESTE
18	AS 1596 R2	Transgenic	SH	E	R	SMDENT	AGROESTE
19	BM 820	Conventional	SH	E	R	HARD	BIOMATRIX
20	BRS 2020	Conventional	DH	E	OR	SMHARD	EMBRAPA
21	BRS 2022	Conventional	DH	E	OR	SMDENT	EMBRAPA
22	DKB 330 YG	Conventional	SH	EE	R / OR	SMDENT	DEKALB
23	DKB 370	Conventional	SHm	E	Y / OR	SMHARD	DEKALB
24	P 4285 H	Transgenic	SH	E	Y/ OR	HARD	DU PONT
25	STATUSVIP	Transgenic	SH	E	OR	HARD	SYNGENTA

[1] DH = Double hybrid; TH = Triple hybrid; SHm = Modified single hybrid; [2] EE = Extra early; E = Early; [3] OR = Orange; R = Reddish; Y = Yellow; [4] SMDENT = Semi-dent; SMHARD = Semi-hard.

Table 2. Geographic coordinates of counties where the experiments were installed in Northeast Brazil, 2012 and 2013.

County	Latitude (S)	Longitude (W)	Altitude (m)	Soil type	Mean temperature (°C)
Colinas/MA	06°01	44°4	141	Argisol DR	27
São Raimundo das Mangabeiras/MA	07°22'	45°36'	225	Argisol Y	26
Brejo/MA	03°41	42°45	55	Latosol Y	27
Balsas/MA	07°32'	46°02'	247	Argisol Y	29
Uruçuí/PI	03°11	41°37	70	Argisol Y	25
Teresina/PI	05°05'	42°49'	72	Argisol Y	28
Nova Santa Rosa/PI	08°24	45°55	469	Latosol Y	23
Frei Paulo/SE	10°55'	37°53'	272	Cambisol	26
Nossa Sra das Dores/SE	10°30	37°13	200	Latosol Y	25
Umbaúba/SE	12°22'	37°40'	109	Argisol Y	24

DR = dark red; Y = yellow.

genotypes; and of e_{j1} and e_{j2} to evaluate the environments based on the Singular Value Decomposition (SVD), in Eq. 3:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{1j} + \lambda_2 \xi_{i2} \eta_{2j} + \varepsilon_{ij} \qquad (3)$$

where λ_1 and λ_2 are the highest self-values of the first and second main components: ACP_1 and ACP_2, respectively; ξ_{i1} and ξ_{i2} are the self-vectors of the i^{th} genotype of ACP_1 and ACP_2, respectively; and η_{1j} and η_{2j} are the self-vectors of the j^{th} environment of ACP_1 and ACP_2, respectively (Yan 2001). The R (R Development Core Team 2014) software and the GGEbiplotGUI package (Wickham 2009) were our tools to conduct the GGE biplot analysis.

RESULTS AND DISCUSSION

Based on the coefficient of variation (CV%), the recorded measurements evidenced good experimental precision, because they stayed inside the acceptable limits set for maize cultures (Fristche-Neto et al. 2012) (Table 3).

The significant environment × year result ($p \leq 0.01$) showed weather and soil differences both in 2012 and in 2013. On the other hand, based on the significant cultivar × environment, and cultivar × year effect ($p \leq 0.01$) interaction, crops presented different behavior in the assessed environments during the evaluated years. According to this result, genotypes recorded different performances due to environmental changes. Therefore, maize cultivar classification can change depending on the assessed environment, corroborating the results recorded by Faria et al. (2017) and Oliveira et al. (2017).

Table 3. Joint analysis of the mean grain production of 25 hybrids maize cultivars tested in 10 locations in Northeastern Brazil, 2012 and 2013.

Variation sources	DF	Mean squares
Repetition (Environment (Year))	20	18133220
Genotype	24	15132886**
Environments	9	112119936**
Years	1	1175065583**
Genotype × Environments	216	2667319**
Genotype × Years	24	7132006**
Environments × Years	9	21294325**
Genotype × Environments ×Years	216	1606177**
Error	480	694624
CV(%)		10.08
Mean (kg·ha^{-1})		8623.77

** indicates 1% significance.

The genotype classification instability caused by environmental variations highlighted the need of future and detailed studies about the behavior of this cultivar during the selection of the best genotypes.

The first two main components (MCs) of the biplot analysis applied to the genotypes × environments GGE biplot analysis explained 60.01% of the total variation (Fig. 1). This result suggests that biplot graphics explain most sums of squares and GE interaction in the genotype. This outcome made it possible to have a safe genotype selection based on the multivariate analysis (Yan 2001).

A set of perpendicular lines divided the *which-won-where* biplot into many groups. Genotypes in the vertex of the biplot were farther from the origin than all other genotypes inside the sector limited by them. Therefore, these genotypes were classified as the ones showing the best performance in one or more environments (Yihunie and Gesesse 2018). These genotypes could be used to identify possible macro-environments (Santos et al. 2017; Yan 2001); the ones located inside the polygon were less responsive to environment stimuli (Fig. 1).

Environments grouped inside the same polygon had similar influence on the genotypes. Environment groups deriving from the 10 assessed environments highlighted three macro-environments; the first one encompassed São Raimundo das Mangabeiras, Nossa Senhora das Dores, Frei Paulo, Colinas and Balsas (presented genotype 11 in the vertex), and recorded the highest mean grain yield. This outcome corroborated the results recorded by Cardoso et al. (2014). Hybrid 9 stayed in the vertex of macro-environments 2 (Nova Santa Rosa, Umbaúba, Teresina and Brejo) and 3 (Uruçuí) and reached the best yield rate in environments inside these macro-environments – similar results were found in previous studies (Carvalho et al. 2013; Carvalho et al. 2017).

Genotypes from the polygon vertex did not group in any environment and were not favorable for the tested environment groups – which recorded low yield. Genotypes 12, 14, 18 and 25 were non-responsive because, based on the environments, they were outside the groups.

The assessed genotype yield and stability based on the mean environment coordination (MEC), was represented by the circle around the image in Fig. 2 (means × stabilities). The line cutting the origin and passing cross the ideal environment was the axis of the ideal environment. We used the main-component scores of all environments to define

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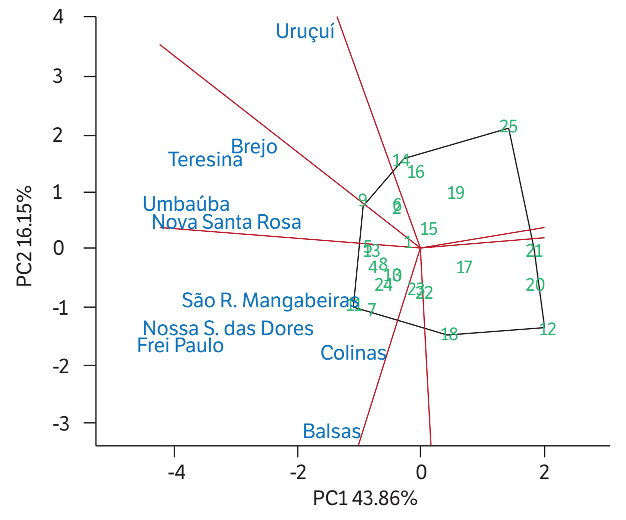

Figure 1. GGE biplot representing the *which-won-where* graph indicating the yield rankings of 25 hybrids.

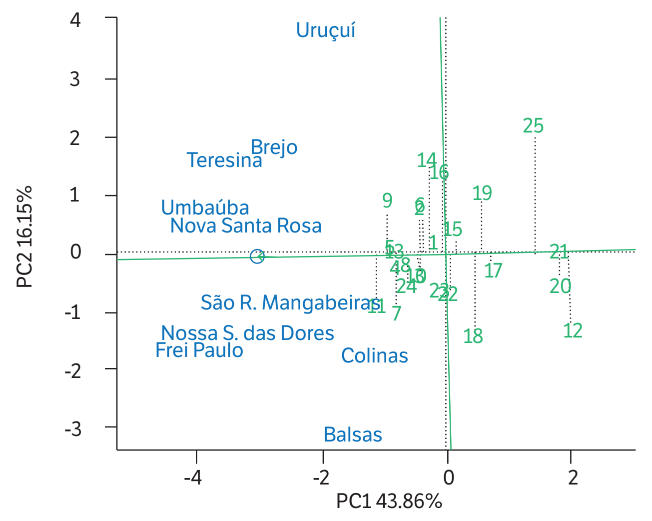

Figure 2. GGE biplot representing the means × stabilities indicating the yield rankings of 25 hybrids, and their respective production stabilities.

the ideal environment (the arrow highlighted the highest genotypic value).

The axis of the coordinate, perpendicular to the abscissas, indicated the genotypes mostly affected by the genotypes × environments interaction, as well as their lower stability. It also separated the genotypes presenting records below and above the average (Yan and Tinker 2006). Therefore, genotypes 11, 9, 5, 13, 4, 7, 8, 24, 6, 10, 2, 3, 14, 1, 16 and 23 recorded yield rates higher than the general mean. The yield of Hybrid 22 was close to the general mean; the other genotypes recorded lower yield. These results were confirmed by the mean test (Table 4).

The higher the genotype projection on the axis, the better the genotype and environment interaction and, consequently, the more stable the genotype. Genotypes 25 and 18 were the most instable ones.

Based on the GGE biplot analysis, the ideal genotype is the one presenting the longest vector and no G × E interaction (arrow in the center of the smallest circle – Fig. 3). Although this genotype was just symbolic, it was the reference to assess other genotypes. Plant breeding programs search for genotypes close to the ideal. The other concentric circles in the figure helped visualizing the distance between genotypes. Yet, ideal hybrids were the ones presenting high PC1 (high yield) and low PC2 (high stability) values in the biplot generated to estimate the best genotype.

Based on the genotypes for grain yield ranking, cultivars 5, 13, 4 and 8, were the closest ones to the ideal

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Table 4. Means yield values of 25 maize hybrids.

Genótypes	Yield*
30A68HX	9461.9 a
30A16HX	9318.2 ab
2B707HX	9257.1 abc
30A95HX	9229.1 abc
2B604HX	9182.0 abc
2B710HX	9096.9 abcd
2B587HX	9087.3 abcd
P4285H	9020.0 abcd
30A37HX	8979.2 abcd
2B433HX	8862.7 abcde
30F53HR	8816.1 abcde
20A55HX	8810.0 abcde
2B688HX	8745.6 bcdef
AG8041YG	8736.8 bcdef
DKB370	8694.5 bcdef
20A78HX	8677.8 bcdef
DKB330YG	8637.8 bcdef
30K73H	8612.2 cdef
AS1596R2	8431.0 def
BM820	8261.8 efg
AS1555YG	8081.3 fgh
STATUSVI	7610.6 ghi
BRS2022	7488.4 hi
BRS2020	7384.2 i
30A91HX	7352.1 i

* Means with different letters in the column differ by 5% probability by the Tukey test.

genotype, because they recorded both high yield means and phenotypic stability. Genotypes 12 and 25 were the lesser productive and most unstable ones.

Discriminating the tested environments is an important measure, since environments unable to discriminate themselves do not provide information about genotypes; therefore, they are useless. It is also essential measuring the ability of a tested environment to represent the target environment. When the environment is not representative, it is not just useless but also biased, because it can provide inaccurate information about the assessed genotypes. The graphic Discrimination × Representativeness showed the environment ability to discriminate itself and its representativeness (Fig. 4).

Concentric calculations in the biplot helped visualizing environment vector length – which is proportional to the standard deviation inside the respective environment – and environment ability to discriminate itself. Thus, the test environments showing long vectors were the ones better separating the genotypes, whereas the shorter vectors provided little, or none, information about differences between genotypes (Yan et al. 2007). The mean environment (represented by the small circle at the end of the arrow on the line) held the mean coordinates of all test environments (Fig. 4). The axis of the mean environment (AME) is the line crossing the mean environment and the origin of the biplot. The test environments presenting shorter angles with AME were the most representative ones (Yan and Tinker 2006).

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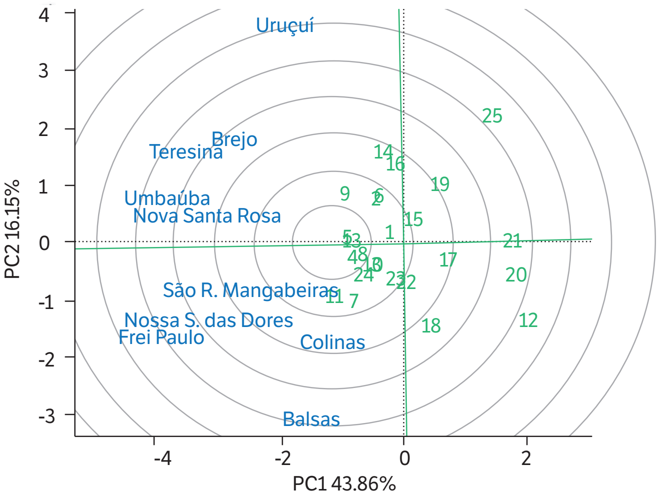

Figure 3. GGE biplot comparing 25 hybrids evaluated according to the estimate of an ideal genotype.

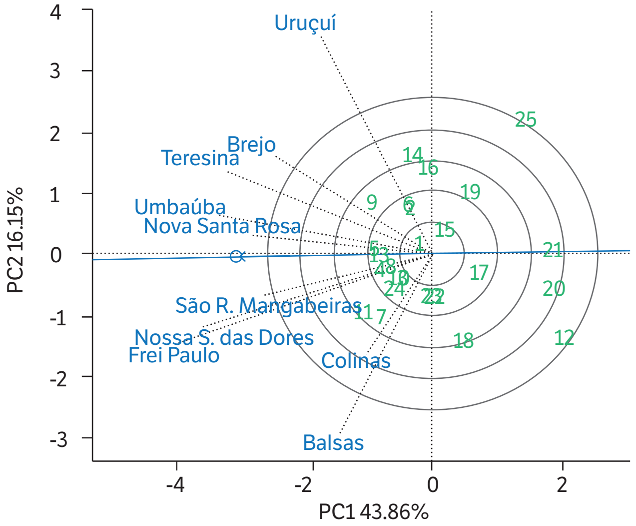

Figure 4. GGE biplot comparing 25 hybrids evaluated according to the discrimination and representativeness of environments for grain yield (kg·ha^{-1}).

Uruçui and Balsas was highly discriminating and non-representative. Such condition could have been useful for genotype selection, mainly to select the adaptable genotypes. Target environments could be divided into macro-environments or help excluding unstable genotypes, when the environment of interest was a single macro-environment. Genotype 7 had good adaptability to environments in macro-environment 1 (Balsas County).

São Raimundo das Mangabeiras and Nova Santa Rosa counties recorded the best representativeness and genotypes with good discriminating ability; this outcome favored the selection of widely adaptable genotypes. Colinas County was non-representative and had the less discriminating genotype; therefore, it was excluded (Yan and Tinker 2006; Yan et al. 2007).

Lines connecting the origin of the biplot to environment markers are the environment vectors. The angle between vectors of the two environments is related to the coefficient of correlation of the two angles. The cosine between vectors of the two environments indicates their coefficient of genetic correlation. Sharp, obtuse and straight angles evidence positive and negative correlation and lack of correlation, respectively.

The widest angle (shorter than 90°) was between Colinas and Balsas with Uruçuí; therefore, these counties had strong GE interaction. Although Colinas and Balsas belong to Maranhão State, and Uruçuí to Piauí State, they are relatively close to each other. Assumingly, their interaction resulted from environmental factors specific to each location. This outcome allowed selecting the most adaptable genotypes to each region.

The 90° angles between Colinas and Balsas, and between Brejo and Teresina, evidenced that the weather and soil differences in Maranhão State were responsible for the lack of correlation between environments. Similar results were recorded between Uruçuí and São Raimundo das Mangabeiras, and between Nossa Senhora das Dores and Frei Paulo. Environmental differences were responsible for the genotypes × environments interaction, reduced the correlation between phenotype and genotype, and influenced cultivar selection.

The other environments were positively correlated, because they presented angles shorter than 90° (the prevailing interaction was of the simple type). Differences between hybrids only concerned genotype variability in the environments they were assessed in. Our result made it easier to accurately select more productive hybrids, because the hierarchic pattern related to genotypes (associated with performance in different environments) still match.

Therefore, information about genotypes can be extrapolated to other environments, because they reduce assessment costs (Yan and Holland 2010; Yihunie and Gesesse 2018). Uruçuí represented macro-environment 1; Nova Santa Rosa, macro-environment 2; and Nossa Senhora das Dores represented macro-environment 3. Umbaúba, Teresina, Brejo, Frei Paulo, Colinas and Balsas counties could be excluded from the evaluations.

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CONCLUSION

Hybrids 30 A 68 HX (11), 30 A 16 HX (9), 2 B 604 HX (5), 30 A 95 HX (13), 2 B 587 HX (4), 2 B 707 HX (7), 2 B 710 HX (8), P 4285 H (24), 2 B 688 HX (6), 30 A 37 HX (10), 20 A 78 HX (2), 2 B 433 HX (3), 30 F 53 HR (14), 20 A 55 HX (1), AG 8041 YG (16) and DKB 370 (23) were the most responsive ones.

Hybrids 20 A 55 HX (1), 2 B 587 HX (4), 2 B 604 HX (5), 2 B 710 HX (8), 30 A 95 HX (13), BRS 2020 (20) and BRS 2022 (21) were stable.

Hybrid 30 A 68 HX (11) was recommended for macro-environment 1. Environments 2 and 3 should use cultivar 30 A 16 HX (9).

AUTHORS' CONTRIBUTION

Conceptualization, T. R. A. Oliveira and R. D. Santos; Methodology, T. R. A. Oliveira, H. W. L. Carvalho and G. H. F. Oliveira; Investigation, T. R. A. Oliveira, G. H. F. Oliveir and G. A. Gravina; Writing – Original Draft, T. R. A. Oliveira and G. H. F. Oliveira; Writing – Review and Editing, T. R. A. Oliveira and G. H. F. Oliveira; Funding Acquisition, H. W. L. Carvalho, E. F. N. Costa and J. L. Carvalho Filho; Resources, H. W. L. Carvalho, E. F. N. Costa and J. L. Carvalho Filho; Supervision, T. R. A. Oliveira.

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