

Adaptability and stability of corn hybrids for the south of the Amazon biome via GGE biplot

Abstract – The objective of this work was to select maize hybrids using the GGE biplot analysis, as well as to evaluate their stability and adaptability in different environments of the North and Midwest regions of Brazil. Thirty-six maize hybrids were evaluated in 2018, in the following five environments in the Northern and Midwestern regions, respectively: in the municipality of Vilhena, in the state of Rondônia; and in the municipalities of Sorriso, Sinop, Alta Floresta, and Carlinda, in the Northern region of the state of Mato Grosso. The experimental design was a randomized complete block design. The analysis of variance was performed, and adaptability and stability were estimated by the GGE biplot method based on grain yield performance. A significant interaction between genotypes and environments was detected, and the biplot analysis was efficient in explaining 62.74% of the total variation in the first two principal components, with the formation of three macroenvironments. The 1P2227, 'BRS 3042', and 1P2265 hybrids showed high yield, responsiveness, and stability in the evaluated environments. The DKB310VTPRO2 hybrid was the most unstable genotype. The recommended hybrids are: DKB310 for the Sorriso and Vilhena macroenvironment; 1M1810 and 1O2106 for the Carlinda environment; and 1M1807 for the Sinop environment.

Index terms: *Zea mays*, G×E interaction, multivariate analysis, multienvironments.

Adaptabilidade e estabilidade de híbridos de milho para o sul do bioma Amazônia via GGE biplot

Resumo – O objetivo deste trabalho foi selecionar híbridos de milho, por meio da análise GGE biplot, bem como avaliar sua estabilidade e adaptabilidade em diferentes ambientes das regiões Centro-Oeste e Norte do Brasil. Trinta e seis híbridos de milho foram avaliados em 2018, nos seguintes cinco ambientes das regiões Norte e Centro-Oeste, respectivamente: no município de Vilhena, no estado de Rondônia; e nos municípios de Sorriso, Sinop, Alta Floresta e Carlinda, na região norte do estado de Mato Grosso. O delineamento experimental foi em blocos completos ao acaso. Realizou-se a análise de variância, e estimaram-se a adaptabilidade e a estabilidade pelo método GGE biplot com base na produtividade. Detectou-se interação significativa entre genótipos e ambientes, e a análise biplot foi eficiente para explicar 62,74% da variação total nos dois primeiros componentes principais, com a formação de três macroambientes. Os híbridos 1P2227, 'BRS 3042' e 1P2265 apresentam alta produtividade, capacidade de resposta e estabilidade nos ambientes avaliados. O híbrido DKB310VTPRO2 foi o genótipo mais instável. Os híbridos recomendados são: DKB310 para o macroambiente Sorriso e Vilhena; 1M1810 e 1O2106 para o ambiente Carlinda; e 1M1807 para o ambiente Sinop.

Termos para indexação: *Zea mays*, interação G×E, análise multivariada, multiambientes.

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Introduction

Corn is one of the most important and cultivated cereals in the world, ranking third after wheat and rice. In the 2020 season, the total area for corn production worldwide was approximately 200 million hectares with a total production of 1.1 billion tonnes (FAO, 2022). Currently, Brazil is the third largest corn producer in the world, with a production of about 102 million tonnes in approximately 18 million hectares, in the 2020/2021 season (Anuário..., 2019).

In the state of Mato Grosso, areas located mainly in the north region show a great potential for grain production, where corn yield has been gradually increasing (Pereira et al., 2020). Therefore, it becomes essential to develop research activities aiming at the regional evaluation of cultivars for the selection of adapted materials with desirable agronomic and productive characteristics for a specific region.

The major challenge in the recommendation of cultivars is the different behavior of genotypes between locations, due to the genotype \times environment (G \times E) interaction, especially for quantitative traits such as grain yield. Quantitative traits and economic interests such as grain yield are most influenced by G \times E interaction (Mohammadi et al., 2020). Therefore, from a plant breeding perspective, identifying superior genotypes for different conditions is a complex task. Thus, it is extremely important to know the nature of these interactions because this phenomenon makes it difficult to recommend varieties adapted to specific environments, as several studies on corn for

Brazilian regions have addressed (Cargnelutti Filho & Guadagnin, 2018; Oliveira et al., 2019, 2020; Ceccon et al., 2021; Shojaei et al., 2022).

Traditional analyses of the G \times E interaction based on regression analysis – such as the method of Eberhart & Russell (1966) – are widely used for corn evaluations (Faria et al., 2017; Eckardt et al., 2022); however, these analyses have the disadvantage that the mean values of the environments and the mean values of the genotypes are not independent (Aarthi et al., 2020). Therefore, the multivariate analysis is a more appropriate model, when there are a sufficient number of environments (Yan et al., 2019).

In this sense, the GGE biplot analysis is another useful tool in the plant breeding for the evaluation of genotypes in different environments, and it has been used in stability and adaptability studies on corn (Pagliosa et al., 2015; Kaplan et al., 2017; Oliveira et al., 2019; Božović et al., 2020; Santos et al., 2021).

The objective of this work was to select maize hybrids using the GGE biplot analysis, as well as to evaluate their stability and adaptability in different environments of the North and Midwest regions of Brazil.

Materials and Methods

Thirty-six corn hybrids were evaluated, including 32 experimental hybrids developed by the plant breeding program of Embrapa Milho e Sorgo and four control cultivars – two commercial ones (DKB310 VTPRO2, and DKB390 VTPRO2) developed by Dekalb (Bayer, São Paulo, SP, Brazil), and two developed by Embrapa (the three-way cross 'BRS 3042', and the single cross hybrid IF640). The 32 evaluated hybrids are part of a cultivation and use value (VCU) test promoted by the Embrapa Milho e Sorgo, in 2017/2018 cropping season (Table 1).

The experiments were carried out in 2017/2018 – in the spring-summer crop season, and in the fall-winter off-season – at five sites, in the northern region of Mato Grosso (MT) state, in the municipalities of Sorriso, Sinop, Alta Floresta, and Carlinda, and at one site in Rondônia (RO) state, in the municipality of Vilhena (Table 2).

A randomized complete block experimental design was carried out with two replicates. The experimental plots consisted of two 4 m long rows spaced at 0.7 m

apart. Twenty seed were sown per row 0.20 m spacing between plants.

Two fertilizations were applied, one of which was a basal fertilization at the time of sowing, as follows: 500 kg ha⁻¹ of 08-28-16 N-P-K formula (40 kg ha⁻¹ N, 140 kg ha⁻¹ P₂O₅, and 80 kg ha⁻¹ K₂O); and two post-fertilizations with 350 kg ha⁻¹ of 20-00-20 N-P-K formula (70 kg ha⁻¹ N and 70 kg ha⁻¹ K₂O), and 200 kg ha⁻¹ urea (90 kg ha⁻¹ N) applied 20 and 30 days after

sowing, respectively. There was no irrigation, and the crop needs in each region determined the control of weeds and pests.

The grain yield was determined by weighing the harvested grains from each plot. Data were subjected to a stand correction by analysis of covariance with correction for ideal stand (Schmidt et al., 2001) corrected to 13% moisture, and converted to kilograms per hectare.

For each environment, an individual analysis of variance was performed to test the homogeneity of variances – the ratio between the highest and lowest mean squares of the residue (MSR) –, using the following model: $Y_{ij} = \mu + g_i + b_j + \varepsilon_{ij}$, in which: Y_{ij} is the observed value of the i^{th} genotype evaluated in the j^{th} block; μ is the general constant; g_i is the fixed effect of the i^{th} genotype ($i = 1, 2, \dots, 36$); b_j is the random effect of the j^{th} block ($j = 1, 6$); and ε_{ij} is the random error associated with the observation Y_{ij} .

A joint analysis of variance was then performed to test for the presence and significance of the G×A interaction, according to the following statistical B model: $Y_{ijk} = \mu + g_i + (b/a)_{jk} + a_j + g_{a_{ij}} + \varepsilon_{ijk}$, in which: Y_{ijk} is the observed grain yield of the i^{th} genotype grown in the k^{th} block of the j^{th} environment; μ is the overall mean; g_i is the fixed effect of the i^{th} genotype ($i = 1, 2, \dots, 36$); $(b/a)_{jk}$ is the random effect of block k in environment j ; a_j is the random effect of environment j ; $g_{a_{ij}}$ is the random effect of interaction between genotype i and environment j ; and ε_{ijk} is the experimental error associated with observation Y_{ijk} .

The information from the averages of the genotypes in the environments were used to implement the GGE biplot analysis. The following model was considered: $\bar{Y}_{ij} - \mu = G_i + E_j + GE_{ij}$, in which: \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 random 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 genotype × environments (GE) effect. It holds G and GE together in two multiplicative terms, using the following model: $Y_{ij} - \mu - \beta_j = g_{i1}e_{j1} + g_{i2}e_{j2} + \varepsilon_{ij}$, in which: Y_{ij} is the expected performance of genotype i in the environment j ; μ is the general constant of the observations; β_j is the main effect of the environment j ; g_{i1} and e_{j1} are the scores

Table 1. Description of the 36 corn (*Zea mays*) hybrids evaluated in five environments, in the north of Mato Grosso state and in the southeast of Rondônia state, Brazil.

Genotype	Class ⁽²⁾	Origin	
1	1L1411	HS	Embrapa/CNPMS
2	1M1804	HS	Embrapa/CNPMS
3	1M1810	HS	Embrapa/CNPMS
4	1M1807	HS	Embrapa/CNPMS
5	1M1782	HS	Embrapa/CNPMS
6	1N1958	HS	Embrapa/CNPMS
7	1O2034	HS	Embrapa/CNPMS
8	1O2106	HS	Embrapa/CNPMS
9	1O2112	HS	Embrapa/CNPMS
10	⁽¹⁾ DKB310VTPRO2	HS	Dekalb
11	1O2073	HS	Embrapa/CNPMS
12	1O2008	HS	Embrapa/CNPMS
13	1O2018	HS	Embrapa/CNPMS
14	1P2224	HS	Embrapa/CNPMS
15	1P2227	HS	Embrapa/CNPMS
16	1N1906	HS	Embrapa/CNPMS
17	1P2216	HS	Embrapa/CNPMS
18	⁽¹⁾ DKB390VTPRO2	HS	Dekalb
19	1P2193	HS	Embrapa/CNPMS
20	1P2237	HS	Embrapa/CNPMS
21	1P2203	HS	Embrapa/CNPMS
22	⁽¹⁾ BRS3042	HT	Embrapa/CNPMS
23	1P2184	HS	Embrapa/CNPMS
24	1P2175	HS	Embrapa/CNPMS
25	1P2214	HS	Embrapa/CNPMS
26	1P2188	HS	Embrapa/CNPMS
27	1P2212	HS	Embrapa/CNPMS
28	1P2273	HS	Embrapa/CNPMS
29	1M1752	HS	Embrapa/CNPMS
30	1P2255	HS	Embrapa/CNPMS
31	1P2265	HS	Embrapa/CNPMS
32	1P2247	HS	Embrapa/CNPMS
33	⁽¹⁾ 1F640	HS	Embrapa/CNPMS
34	1P2231	HS	Embrapa/CNPMS
35	1P2267	HS	Embrapa/CNPMS
36	1P2215	HS	Embrapa/CNPMS

⁽¹⁾Commercial controls. ⁽²⁾HS, single cross hybrid; HT, three-way cross hybrid. Embrapa/CNPMS, Embrapa Milho e Sorgo (Sete Lagoas, Brazil).

of the i^{th} genotype in the j^{th} environment, respectively; and ε_{ij} is the unexplained error of the two effects.

The graphs of the GGE model were generated through the simple dispersion of g_{i1} and g_{i2} to access the genotypes; e_{j1} and e_{j2} to evaluate the environments, based on the singular value decomposition (SDV), in accordance with the following model: $Y_{ij} - \mu - \beta_j = \lambda_1 \zeta_{i1} \tau_{1j} + \lambda_2 \zeta_{i2} \tau_{2j} + \varepsilon_{ij}$, in which: λ_1 and λ_2 are the highest values of the first and second principal components (PC1 and PC2, respectively); ζ_{i1} and ζ_{i2} are the eigenvectors of the i^{th} genotype of PC1 and PC2, respectively; and τ_{1j} and τ_{2j} are the eigenvectors of the j^{th} environment of PC1 and PC2, respectively (Yan, 2001). To perform the GGE biplot analysis, the R Studio software (R Core Team, 2021) and the GGE biplot GUI package (Yan, 2001) were used.

Results and Discussion

The experimental precision was adequate, since the coefficient of variation value was below the limits defined for experiments with corn (Fritsche-Neto et al., 2012) (Table 3).

The genotypes showed different behaviors in the studied environments with significant GEI (Table 3), due to the environmental characteristics of each site (Table 2). In this sense, the classification of each cultivar may change depending on the environment (Oliveira et al., 2019; Ceccon et al., 2021).

The first two principal components (PCs) of the biplot analysis applied to genotypes \times environments explained 62.74% of the total variation (Figure 1). To obtain a reliable analysis of the results, it is necessary

that the graphs of the biplot analysis explain most of the sums of squares and GEI among genotypes (Yan et al., 2007). Therefore, it is possible to make a reliable selection of genotypes for the most stable environments.

In the “which-won-where biplot”, a set of perpendicular lines divide the plot into several groups. As to productive performance, genotypes that are further away from the center of origin and that form the vertex of the polygon are more responsive to stimuli from the environments, thus, they can be classified as those that present the best performance for one or more environments (Yihunie & Gesesse, 2018) and can be used to form possible macroenvironments (Santos et al., 2017; Oliveira et al., 2019). In contrast, genotypes located within the polygon are those with the lowest average performance for the studied characteristics.

In this sense, the genotypes 10 (DKB310 VTPRO2), 3 (1M1810), 8 (102106), and 4 (1M1807) represent the vertices of the polygon in which the environments are contained. Thus, they were used to identify at least three macroenvironments. The first one was composed by Sorriso and Vilhena with genotype 10 (DKB310 VTPRO2) at the vertex of the polygon and with better yield performance in the environments within this macroenvironment; the second consisted of Carlinda with two genotypes at the vertex of the polygon – hybrids 3 (1M1810) and 8 (102106) –, that achieved a higher average grain yield; and the third was composed by Sinop with genotype 4 (1M1807) forming the vertex of the polygon. However, the genotypes 7 (1O2034), 15 (1P2227), 26 (1P2188), and 32 (1P2247), at the vertices of polygons, did not group in any of

Table 2. Identification of the experimental cultivation sites of corn (*Zea mays*), cropping season, geographic location, climate, average temperature, precipitation, and altitude.

Environment	Cropping season	Coordinate	Climate ⁽¹⁾	Temperature (°C)	Annual precipitation (mm)	Altitude (m)	Soil type ⁽²⁾
Vilhena	Fall-winter 2017/2018	60°09'38"W/12°78'98"S	Am	25.2	252	615	Oxisols
Sorriso	Fall-winter 2017/2018	55°42'39"W/12°32'42"S	Aw	25.0	194	365	Oxisols
Sinop	Fall-winter 2017/2018	55°35'51"W/11°52'17"S	Am	25.8	220	384	Oxisols
Alta Floresta	Spring-summer 2017/2018	56°20'90"W/10°09'86"S	Am	26.3	253	283	Oxisols
Carlinda	Spring-summer 2017/2018	55°49'52"W/09°49'52"S	Am	25.0	251	290	Oxisols

⁽¹⁾Climate classification of Köppen-Geiger. ⁽²⁾International classification according to Soil Survey Staff (2015).

the studied environments and were not considered responsive to any of these environments. These results corroborate those by Oliveira et al. (2019), with 25 corn cultivars in North of Brazil, where the biplot delimited three sectors (macroenvironment). It is important to highlight that, even though Alta Floresta formed a group in the biplot, no genotype constituted its vertex,

Table 3. Analysis of variance of the grain yield of 36 corn (*Zea mays*) hybrids evaluated in five locations, in the North and Midwest regions of Brazil, in the 2017 crop year.

Source of variation	Degree of freedom	Mean square
Block	1	509,066.41
Genotype	35	993,018.73*
Environment	4	48,072,992.61**
Genotype × environment	140	636,010.95**
Error	175	245,041.46
Mean yield (Mg ha ⁻¹)		9.97
Coefficient of variation (%)		8.87

** , *Significant at 1% and 5%, respectively, by the F-test.

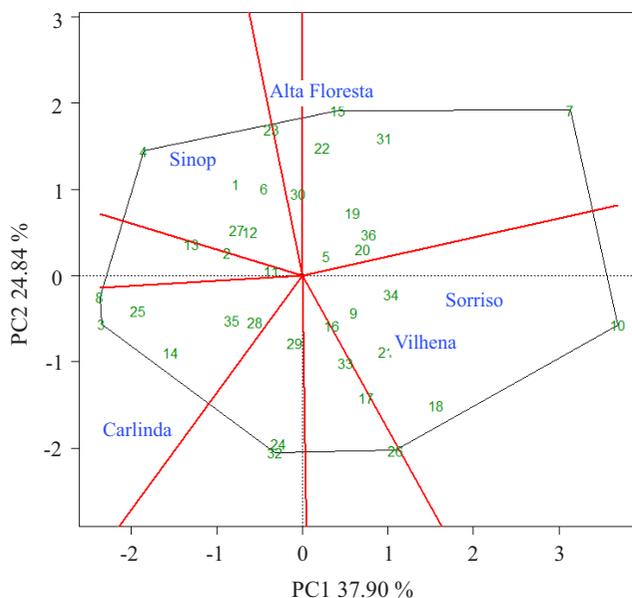


Figure 1. A “which-won-where” view of the genotypic main effects and genotype × environment interaction (GGE) biplot of 36 corn (*Zea mays*) genotypes for the grain yield trait in five environments.

indicating that there was no responsive hybrid to the stimulus of this environment.

From these results, it is possible to affirm that these genotypes are highly productive and excellent alternatives for the regional agriculture, ensuring their recommendations for the different corn production systems practiced in the Midwest of Brazil, especially in systems where modern production technologies are adopted.

The visualization of the biplot means × stability of the GGE biplot is an effective tool for the evaluation of genotypes regarding their grain yield and stability. In Figure 2, the abscissa axis with a small circle that represents the environment-mean axis is defined based on the average coordinates of all environments in the biplot. The arrow on the line that passes through the origin of the biplot and the mean-environment points to a higher average performance of the genotypes. Therefore, genotypes located to the right of the arrow have higher values than the general average of grain yield in the evaluated environments and those to the left of the arrow have lower values (Li et al., 2018). The stability of the genotypes can be observed through the arrangement in the graph and, in this case, the smaller the projection of the dashed line of a given genotype, the closer it goes to the center of the biplot, showing a greater stability for the evaluated characteristic (Yan, 2001; Yan et al., 2007).

Based on the previous description, the genotypes 27 (1P2212), 12 (1O2008), 34 (1P2231), 5 (1M1782), 4 (1M1807), 20 (1P2237), 1 (1L1411), 6 (1N1958), 36 (1P2215), 30 (1P2255), 19 (1P2193), 10 (DKB310 VTPRO2), 23 (1P2184), 22 (BRS3042), 31 (1P2265), 15 (1P2227), and 7 (1O2034) had the highest grain stability and performance and are characterized as the best genotypes. Furthermore, the genotype 10 (DKB310 VTPRO2) was the most unstable genotype due to its distance from the horizontal line, while the genotypes 11 (1O2073), 9 (1O2112), 2 (1M1804), 13 (1O2018), 16 (1N1906), 21 (1P2203), 33 (1F640), 18 (DKB390VTPRO2), 28 (1P2273), 29 (1M1752), 35 (1P2267), 17 (1P2216), 25 (1P2214), 8 (1O2106), 26 (1P2188), 14 (1P2224), 3 (1M1810), 24 (1P2175), and 32 (1P2247) had the lowest grain performance and were characterized as undesirable. These results are relevant and corroborate with the findings by Shojaei et al. (2022) for 12 corn hybrids evaluated in four environments in Iran, evidencing that these studies should be carried

out continuously, to provide information on new genotypes which can be increasingly productive and with high stability, in order to make them available to farmers in the Midwest and North regions of Brazil.

The ideal hybrid is the genotype with the best average performance and stability in all tested environments (Kendal et al., 2019). In this sense, an ideotype has high average performance and high stability. As this ideotype is only symbolic, it serves as a reference to compare the other genotypes. Therefore, based on the GGE biplot genotype ranking plot (Figure 3), the ideotype should have a long vector and low $G \times E$ interaction (arrow inside the smaller circle in the graph area). Thus, genotypes 15 (1P2227), 22 ('BRS 3042'), and 31 (1P2265) were the closest to the ideal, bringing together high grain yield and stability, and genotype 32 (1P2247) is considered the most undesirable.

In the discriminativeness \times representativeness biplot (Figure 4), the ability of an environment to discriminate a genotype is highlighted by the size of the vector (dashed line), thus, the longer is the vector, the more discriminating is this environment (Yan et al., 2007). The representativeness of an

environment can be visualized in the angle formed by the dashed line of an environment with the environment-average axis (EAM). Therefore, an environment that shows a smaller angle with the EAM is considered as more representative, and therefore it shows a great potential for genotype selection for the other environments.

The concentric circles on the graph help visualize the size of the room vectors, which are proportional to the standard deviation within the respective room. Therefore, the Carlinda and Alta Floresta environments were the most discriminating and most representative environments, which are able to efficiently separate the genotypes, in addition to allowing of the selection of hybrids that are broadly adaptable to other environments. Sinop and Sorriso also showed a satisfactory discrimination, but low representation. According to Yan et al. (2007), discriminating but not representative environments are useful to select genotypes adapted to specific conditions, if the target environments can be divided into megaenvironments. Such discrimination can also be used to eliminate

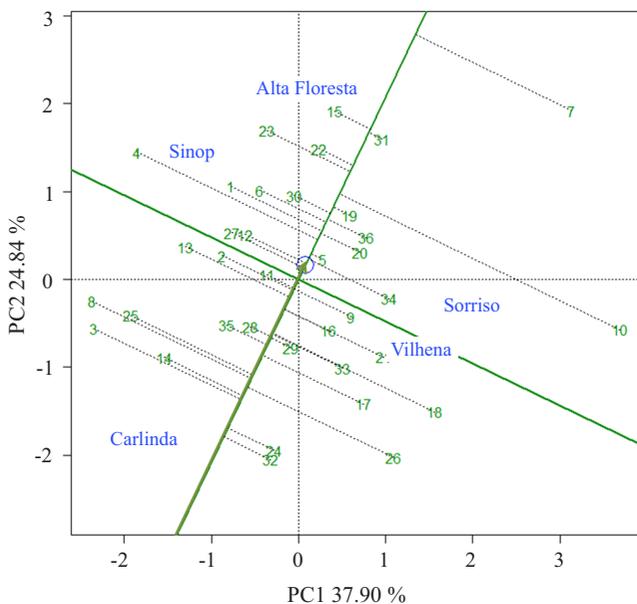


Figure 2. The “mean \times stability” of the genotypic main effects plus genotype \times environment interaction (GGE) biplot view of 36 corn (*Zea mays*) genotypes for the grain yield trait in five environments.

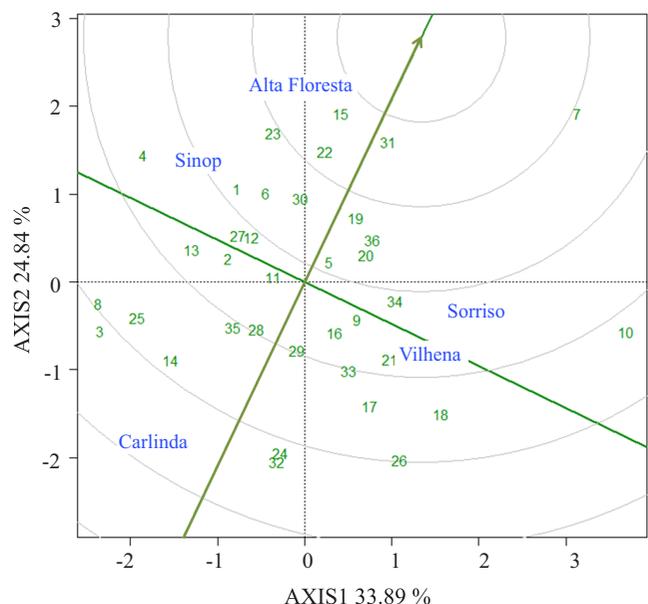


Figure 3. The genotypic main effects plus genotype \times environment interaction (GGE) biplot view showing the ranking of 36 corn (*Zea mays*) genotypes for the grain yield trait in five environments.

unstable genotypes, if the target environment is a single megaenvironment, as is the case of Sinop.

In addition to the possibility of analyzing discrimination and representativeness, in the discriminativeness \times representativeness biplot, the vectors of environments allow us to infer the correlation between these environments. The cosine of the angle between two environments approximates the correlation between them. In this sense, if the angle between vectors of two environments is $< 90^\circ$, both are positively correlated; if the angle is $> 90^\circ$, there is a negative correlation; and if the angle is 90° , the absence of correlation between the environments is evident (Al-Naggar et al., 2020). In this sense, the smallest angles observed ($< 90^\circ$) were between Sorriso and Vilhena, and between Sinop and Alta Floresta. The correlation between these environments indicates that differences for hybrid behaviors in these specific conditions are associated with their genetic variability in particular, and less related to correlations in these environments (Oliveira et al., 2018). The other pairs of environments showed a negative correlation ($> 90^\circ$), which indicates that different environmental

conditions can influence the behavior of genotypes in these environments, reducing the correlation between genotype and phenotype, which therefore affects the selection of cultivars.

The results obtained here allow of a more reliable selection of more productive hybrids, since it is possible to indicate genotypes both for specific environments and for macroenvironments, as it was the case of Sorriso and Vilhena, which will contribute a greater yield per unit of area.

Conclusions

1. The most responsive corn (*Zea mays*) genotypes to the evaluated environments are the following hybrids: 27 (1P2212), 12 (1O2008), 34 (1P2231), 5 (1M1782), 4 (1M1807), 20 (1P2237), 1 (1L1411), 6 (1N1958), 36 (1P2215), 30 (1P2255), 19 (1P2193), 10 (DKB310 VTPRO2), 23 (1P2184), 22 (BRS3042), 31 (1P2265), 15 (1P2227), and 7 (1O2034).

2. The most unstable genotype is the hybrid 10 (DKB310 VTPRO2).

3. Because of their lower yield performance the following genotypes are characterized as undesirable hybrids, as follows: 11 (1O2073), 9 (1O2112), 2 (1M1804), 13 (1O2018), 16 (1N1906), 21 (1P2203), 33 (1F640), 18 (DKB390VTPRO2), 28 (1P2273), 29 (1M1752), 35 (1P2267), 17 (1P2216), 25 (1P2214), 8 (1O2106), 26 (1P2188), 14 (1P2224), 3 (1M1810), 24 (1P2175), and 32 (1P2247).

4. The hybrids 15 (1P2227), 22 (BRS 3042), and 31 (1P2265) show high grain yield, responsiveness, and stability in the evaluated environments.

5. The hybrid 10 (DKB3910 VTPRO2) is indicated for Sorriso and Vilhena macroenvironments; the hybrids 3 (1M1810) and 8 (1O2106) are indicated for Carlinda; and the hybrid 4 (1M1807) is indicated for Sinop.

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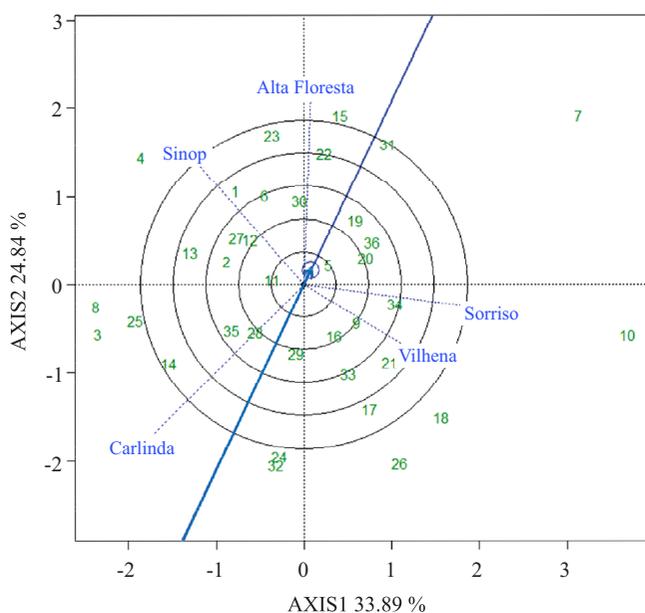


Figure 4. GGE biplot “discriminativeness \times representativeness” of 36 corn (*Zea mays*) genotypes evaluated in accordance with the discrimination and representativeness of environments for grain yield.

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