Adaptability and stability of maize genotypes in growing regions of central Brazil

Euriann Lopes Marques Yamamoto[1]*, *Manoel Carlos Gonçalves*[2], *Livia Maria Chamma Davide*[2],
Adriano dos Santos[2], *Liliam Silvia Candido*[3]

10.1590/0034-737X202168030006

ABSTRACT

This study aimed to estimate and compare parameters of adaptability and stability for maize grain yield in a variety of environments by different projection methods. Data from experiments on 36 maize genotypes, in simple lattice 6x6, in 2012/13 season performed at nine growing locations in central Brazil were used. Adaptability and stability analyses were performed using the methods of Lin & Binns (1988) with decomposition, MHPRVG through REML/BLUP, AMMI-Biplot, and GGE-Biplot analysis. These methods have similarities in terms of genotype ordering but differ in precision and amount of information provided on genotype-environment (GxE) interactions. When compared to GGE-Biplot, AMMI method retained a good percentage of the total square sum, based on pattern of GxE interaction. The method of Lin & Binns with decomposition is similar to MHPRVG, but these one is more accurate, practice and informative. MHPRVG and GGE-Biplot methods should be used together to select the most promising genotypes. The genotypes G5 and G8 can be recommended for cultivation in central Brazil due to their adaptability, stability, and yield.

Keywords: *Zea mays* L.; Lin & Binns with decomposition; REML/BLUP; GGE-Biplot; AMMI-Biplot.

INTRODUCTION

The Genotype x Environment interaction reflects the way genotypes behave in different environments (Rezende *et al*., 2020). This is because the most effective traits for improvement of genotypes are of metric nature and have continuous distribution and polygenic inheritance when under the constant influence of environmental changes (Borem *et al*., 2017).

Over the last two decades, several studies have been performed to develop stability indices for quantification and selection of promising genotypes. These methods use multivariate parametric models, such as additive main effects and multiplicative interaction analysis (AMMI-Biplot) (Bocianowski *et al*., 2019), as well as genotype + genotype-by-environment biplots (GGE-Biplot) (Machado *et al*., 2019), harmonic mean of relative performance of genetic values (MHPRVG) method through REML/BLUP (Oliveira *et al*., 2017), and non-parametric models (Lin & Binns, 1988; Cargnelutti Filho & Guadagnin, 2018). The selection among the existing methods depends on the ability to explain the sum of squares of GxE interactions.

Some studies with maize have compared several methods for GxE interaction analysis (Faria *et al*., 2017, Machado *et al*., 2019, Santos *et al*., 2019, Rezende *et al*., 2020). However, few of them have assessed parametric and non-parametric or even mixed models, such as REML/BLUP. Furthermore, the number of publications has been decreased over the last several decades in Brazil. Eberhart and Russel was the traditional predominant method in the study of adaptability and stability in maize and soybean. Other methods as AMMI, GGE Biplot and MHPRVG had their used increased (Rezende *et al*., 2021).

To improve selection accuracy and hence the recommendation of superior maize genotypes, studies comparing traditional and recent statistics should be carried out. In this line, this study aimed to estimate and

---

Submitted on February 18th, 2020 and accepted on January 04th, 2021.

[1]Universidade Federal da Grande Dourados, Faculdade de Ciências Agrárias, Dourados, Mato Grosso do Sul, Brazil. euriann@outlook.com; manoelgoncalves@ufgd.edu.br; liviadavide@ufgd.edu.br

[2] Embrapa Agroenergia, Brasília, Distrito Federal, Brazil. adriano.agro84@yahoo.com.br

[3]Universidade Federal da Grande Dourados, Faculdade de Ciências Biológicas e Ambientais, Dourados, Mato Grosso do Sul, Brazil. liliamcandido@ufgd.edu.br

*Corresponding author: euriann@outlook.com

compare parameters of adaptability and stability for maize grain yield in a variety of environments by different projection methods.

MATERIAL AND METHODS

Data grain yield were used to evaluate 36 maize genotypes in experiments conducted in the 2012/13 season at nine growing locations in central Brazil (E1: Sete Lagoas/MG, E2: Londrina/PR, E3: Goiânia/GO, E4: Janaúba/MG, E5: Planaltina/DF, E6: Paragominas/PA, E7: Altamira/PA, E8: Campo Grande/MS, and E9: Manduri/SP). All the experiments were conducted using a 6 x 6 simple lattice design. Each experimental unit consisted of two four-meter rows with an interrow spacing of 0.8 meters (1.6 x 4 m) and a useful plot area of 4.8 m^2.

Maize plants were sown in October and November and harvested 120 days thereafter. Planting and topdressing fertilizations followed crop recommendations and were performed based on soil analysis of each growing site. Grain yield (GY) estimates (kg ha^{-1}) were made by rescaling harvested grain mass per experimental unit to grain mass per hectare, and moisture correction to 13%.

Intra-block variance analysis with adjusted treatments and blocks within unadjusted repetitions was performed for each environment and significance tested by the F-test. After confirming homogeneity of variances by the Hartley F-max test, a joint analysis was carried out to test the significances of effects of genotype (G), environment (E), and GxE interaction. The environmental effect was considered random and the genotype one as fixed. Selection accuracy was calculated as described by Resende & Duarte (2007).

Adaptability and stability parameters were estimated using the following methods: Lin & Binns (1988) with decomposition (Cruz *et al*., 2012), harmonic mean of relative performance of genetic values (MHPRVG) by a mixed model method with restricted maximum likelihood and best linear unbiased prediction (REML/BLUP) (Resende, 2016), additive main effects and multiplicative interaction biplots (AMMI-Biplot) (Zobel *et al*., 1988), and genotype + genotype-by-environment (GGE-Biplot) (Yan & Tinker, 2006). The statistical software used for these analyses were GENES (Cruz, 2013), SELEGEN (Resende, 2016), and R (R Core Team, 2018).

In Lin & Binns (1988) with decomposition, adaptability P_i was measured by the mean-square distance between genotype *i* and the genotype with maximum response to the environment *j*, using the following equation: $P_i = \frac{\sum_{j=1}^{a}(Y_{ij} - M_j)^2}{2a}$; wherein: P_i is the superiority index of genotype *i*, Y_{ij} is the yield of the i$^{\text{-th}}$ genotype in the j$^{\text{-th}}$ environment, M_j is the maximum response observed among all genotypes in the j$^{\text{-th}}$ environment, and *a* is the number of environments. However, Carneiro (1998) suggested decomposition of statistics to favorable and unfavorable environments by the following equations: $P_{i(f)} = \frac{\sum_{j=1}^{f}(Y_{ij} - M_j)^2}{2f}$; wherein: *f* is the number of favorable environments, and $P_{i(d)} = \frac{\sum_{j=1}^{d}(Y_{ij} - M_j)^2}{2d}$; wherein: *d* is the number of unfavorable environments.

An additive main effect and multiplicative interaction (AMMI-Biplot) model is a combination of analysis of variance (ANOVA) and principal component analysis (PCA). The equation used for this method is $\bar{Y}_{ij} = \mu + g_i + a_j + \sum_{k=1}^{n} \lambda_k \gamma_{ik} \alpha_{jk} + r_{ij} + \varepsilon_{ij}$; wherein: $\bar{Y}_{ij}$ is the mean yield of the genotype i (i = 1. 2, …, 36) in the environment j (j = 1, 2, … 9); μ is the overall mean of experiments; g_i is the effect of the genotype i; a_j is the effect of the environment j; $\sum_{k=1}^{n} \lambda_k \gamma_{ik} \alpha_{jk}$ is the effect of multiplicative G x E interaction, wherein: λ_k is the singular value, γ_{ik} and α_{jk} are the PCA scores of k axis for genotype and environment, respectively, and n is the number of axes or principal components retained to describe the pattern of GxE interaction; r_{ij} is the residual effect of AMMI model (noise); and ε_{ij} is the experimental error of random effect. As a measure of stability, the first component (IPCA1) scores of each genotype, obtained from AMMI1 analysis, were used. In addition, AMMI stability value (ASV) was used as a statistical parameter to replace graphical analysis by AMMI2. ASV is defined in terms of the Euclidean distance between the Cartesian plane origin and the coordinate of genotype or environment point (Purchase *et al*., 2000), as in the equation $ASV = \sqrt{\left[\frac{SSIPCA1}{SSIPCA2}(IPCA1\ score)\right]^2 + [IPCA2\ \text{score}]^2}$; wherein: SS IPCA1 is the sum of squares of IPCA1 and SS IPCA2 is sum of squares of IPCA2.

As proposed by Yan (2011), the analysis by GGE method was made by the equation: $Y_{ij} - \mu - E_j = Y_1\varepsilon_{i1}P_{i1} + Y_2\varepsilon_{i2}P_{j2} + \varepsilon_{ij}$; wherein: Y_{ij} is the yield of the i$^{\text{-th}}$ genotype in the j$^{\text{-th}}$ environment, μ is the overall mean, E_j is the environment effect, Y_1 and Y_2 are the singular values of IPCA1 and IPCA2, respectively, ε_{i1} and ε_{i2} are the IPCA1 and IPCA2 scores for the i$^{\text{-th}}$ genotype, respectively, P_{j1} and P_{j1} are the IPCA1 and IPCA2 scores for the j$^{\text{-th}}$ environment, respectively, and ε_{ij} is the residual effect not explained by any of the factors (noise). After constructing the plot of PCA scores associated with environments and genotypes, the following parameters were analyzed: which-won-where pattern, genotype mean performance and stability, environment discriminating-ability and representativeness, and ideal-genotype ranking (Yan & Tinker, 2006).

Mixed linear model analyses were carried out by REML/BLUP method using model 52 of SELEGEN software, by the following equation (Resende, 2016): $y = Xr + Z_g + W_b + T_i + e$; wherein: y is the data vector; r is the vector of fixed effects of repetition added to the overall mean; g is the vector of genotypic random effects; b is the vector of random effects of blocks; i is the vector of random effects of genotype x environment interactions; e is the error vector, considered random; and X, Z, W, Y, and Z represent the incidence matrices for these effects. Simultaneous measures of adaptability and stability for each genotype were obtained by means of MHPRVG, as in the following equation: $MHPRVG = {}^{n}\!/\Sigma_{i=1}^{j} \frac{1}{PRVG_{ij}}$; wherein: n is the number of environments and $PRVG_{ij} = VG_{ij}/VG_j$, in which VG_{ij} is the genetic value of the genotype i in the environment j and VGj is the genotypic mean in the environment j.

For a better interpretation of results, the MHPRVG values were multiplied by the overall mean of all environments (MHPRVG*MG), representing the results in the same magnitude of the studied variable. Subsequently, environments were grouped into favorable and unfavorable as a function of the overall yield mean of all environments, and separate analyses were conducted for each group. The environments showing averages above the overall mean were considered as favorable and those with values below as unfavorable, according to Mendes *et al*. (2012).

RESULTS AND DISCUSSION

The analysis indicated significant effects ($p < 0.01$) for genotypes, environment and the G x E interaction. The effect of the environment was responsible for more than 38% of the variation sum of squared, as observed by Faria *et al*. (2017) with commercial maize hybrids in five locations em Minas Gerais. Most of environment variations effect is due the differences between locations. During the period of conducting the experiments were observed monthly rainfall volumes is a range of 62 to 323,9 millimeters (INMET, 2017). The growing locations also differed em relation to altitude (90 to 971 meters), and consequently in the mean temperature. This implies that the performance of genotypes was influenced by environments conditions, what justifies the study of adaptability and phenotypic stability (Table 1).

For the method of Lin & Binns (1988) with decomposition, the genotypes G1, G34, G31, G8, and G5 presented the lowest P_i value for the overall environment (Table 2). These genotypes, except for G1 (only 11.11% of genetic variation), contributed little to the GxE interaction, reflecting considerable participation of the genetic variance to express grain yield.

Twelve, out of the 13 genotypes with the highest grain yield, showed the lowest P_i value for overall environment (G1, G34, G31, G8, G30, G5, G21, G7, G12, and G20). This is because P_i statistics considers as highly adaptable and stable (low P_i) genotypes those whose yields are closer to maximum for each environment (Cruz *et al*., 2012) as a comparison between genotypes and an ideotype. Therefore, higher stability will always be associated with higher yields (Lin & Binns, 1988). Currently, this method has been recommended to study adaptability and stability in maize when the number of experiments analyzed does not exceed nine (Cargnelutti Filho & Guadagnim, 2018).

Besides recommended for general environment, G1 also proved adaptability to favorable environments, as did G5 and G8. To unfavorable environments, the three best-performing genotypes were G1, G34 and G31. G1 is a simple hybrid developed for high-medium investment fields with a history of high-medium yields. According to Oliveira *et al*. (2020) this genotype had greater performance under harvest season and off-season in Amazonas.

The method Lin & Binns (1988) with decomposition does not allow the detection of the predominant type of

Table 1: Summary of joint variance analysis of grain yield (kg ha^{-1}) in 36 maize genotypes at nine different environments of central Brazil

SV	DF	MS	%SS$_F$$^{(1)}$
Replication	1	6803899**	
Block (Replication)	10	6610551**	
Genotype (G)	35	14050219**	30.00
Environment (E)	8	79444006**	38.00
G x E	280	1899783*	32.00
Residual	313	1004964	
Mean		6853.14	
CV%		14.63	
$\hat{r}_{\hat{g}g}$		0.96	

$^{(1)}$: percentage of sum of squared factors: genotype, environment, and GxE interaction. *Significant by the F-test ($P < 0.05$),**Significant by the F-test ($P < 0.01$). CV%: coefficient of variation. $\hat{r}_{\hat{g}g}$: accuracy.

GxE interaction. But it can select productive, adapted, and stable genotypes to the environments, under a interaction predominant simple.

The decomposition of the sum of squares of GxE interaction was decomposed into eight principal component axes (IPCAs) by the AMMI-Biplot method, which four showed significance. The first (IPCA1) and second (IPCA2) were highly significant ($P < 0.01$) by the Gollob (1968) F-test (Table 3).

The lack adjustment of AMMI models evidenced by Cornelius test denotes that AMMI1 residuals were not significant, confirming the selection of AMMI1. This model explained 35% of the total variation (pattern), using only about 15% of the original degrees of freedom (Table 3). About one-third of the changes in grain yield related to deviations of the main effects (genotypes and environments) could be explained by the first component (IPCA1). And about 65%, in others axis, corresponds to a large amount of noise.

The AMMI method has the objective of capturing the pattern of the variation of the GxE interaction and discarding the noise (random variation that little explains the GxE interaction). As more parameterized models are considered (AMMI2, AMMI3), noise can distort the interpretation of the performance of genotypes and environments regarding stability in

Table 2: Estimates of overall P_i, favorable P_i ($P_{i(f)}$), and unfavorable P_i ($P_{i(u)}$), and genetic value (GV) by the Lin & Binns (1988) method with decomposition regarding grain yield (kg ha^{-1}) of 36 maize genotypes grown in nine environments of central Brazil in the 2012/2013 season

Genotype	Mean	P_i	$P_{i(f)}$	$P_{i(u)}$	%GV
G1	10817.7	3353.81	6036.85	0.00	11.11
G2	6294.13	12070812.80	9112900.04	15768203.75	85.79
G3	6082.55	12322237.00	11449907.47	13412648.91	92.03
G4	6568.73	11552043.01	7304913.23	16860955.24	79.15
G5	7932.03	6445160.04	2382057.03	11524038.79	65.83
G6	6909.75	9222527.99	7537902.12	11328310.33	83.96
G7	7395.88	7370106.76	5382267.76	9854905.52	80.71
G8	7701.63	5862180.92	3504298.75	8809533.63	84.28
G9	6994.61	9664839.59	8074860.63	11652313.28	76.70
G10	6303.22	13179694.02	10913636.63	16012265.75	78.26
G11	7066.88	9039410.05	4983765.17	14108966.16	78.96
G12	7251.99	8186980.81	5468002.44	11585703.77	78.84
G13	6657.36	9942158.27	6635300.92	14075729.94	88.19
G14	6871.67	8485670.12	7101066.34	10216424.86	93.02
G15	7033.31	9022388.20	6476189.38	12205136.74	80.52
G16	6686.04	10065849.35	8241981.91	12345683.65	85.92
G17	6193.47	12628804.53	8444391.05	17859321.39	85.66
G18	5353.55	18115438.96	13759096.90	23560866.54	83.23
G19	6558.24	11120866.32	8721562.90	14119995.59	82.62
G20	7026.20	8406863.83	7542001.33	9487941.95	86.74
G21	7305.50	6593532.81	5218815.80	8311929.07	95.00
G22	6784.99	9977037.15	7087094.63	13589465.29	82.61
G23	5387.09	16466759.99	14229730.97	19263046.26	90.45
G24	6266.63	12889252.67	7366311.15	19792929.58	81.31
G25	5565.02	15883993.99	10057407.52	23167227.07	87.76
G26	6188.53	13372557.11	7899649.03	20213692.22	81.07
G27	6674.15	9824825.43	7649637.59	12543810.23	88.53
G28	6180.25	13147607.30	10605437.64	16325319.37	82.75
G29	7043.75	8428907.79	7088005.17	10105036.06	85.71
G30	7556.21	6280188.29	5222370.96	7602459.95	86.11
G31	7780.03	5477440.40	4285832.88	6966949.79	85.75
G32	6734.88	9366677.87	6622362.68	12797071.86	90.18
G33	5921.91	14284812.69	11293048.07	18024518.47	84.83
G34	7915.18	4927469.04	4133240.30	5920254.96	87.10
G35	6807.73	10475095.71	7142561.48	14640763.49	77.80
G36	6902.21	10148469.43	8815773.16	11814339.77	76.59
Overall mean	6853.14				

graphics analysis. Thus, it is inferred that the high value for noise in this analysis (65%) has no relevant content. Similar results were observed by Oliveira *et al*. (2010), 21.8%; Hongyu *et al*. (2014), 56,2%; and, Machado *et al*. (2019), 45.4%.

Despite the selection of an axis, it is only expected to select the highest percentage of the G x E interaction pattern. Therefore, AMMI1 biplot is enough to explain the real G x E interactions, disregarding the rest of the variation that has the most noise. The graphical analysis of AMMI1 shows that the control G1 (1) contributed the most to GxE interaction since it had the greatest range of scores in the interaction axis (Figure 1). Even with the highest yield, this genotype showed no specificity in terms of adaptability to any of the evaluated environments, attesting its instability.

Still, this method demonstrates that the most stable genotypes should also be the most productive in the studied environments, among which G11 and G6 stood out.

Another way to interpret an AMMI-Biplot model is through ASV analysis. It measures how much each genotype contributed to GxE interactions considering the first two IPCAs. For this reason, these statistics can be used as a measure equivalent to biplot AMMI2 (IPCA1 x IPCA2), for classification purposes (Abate, 2020). In accordance with AMMI1 graphical analysis, G1 and G10 remained as the most unstable genotypes by ASV analysis (Table 4). Conversely, G3, G9, G32, G7, and G5 contributed less to GxE interaction and were the most stable by AMMI1 biplot. ASV analysis also indicated that G8 and G23 presented the lowest values of ASV but not confirmed by AMMI1.

Table 3: Analysis of variance with interaction GxE decomposition for the AMMI model and the explained variance for grain yield (kg ha^{-1}) variable

Source	DF	S S	MS	F_G	F_C	Explained (%)
IPCA1 (pattern)	42	93093078	2216502	3.70^{**}	-	35.3
AMMI1 error (noise)	238	170925721	718175.3	-	1.20^{*}	-
IPCA2	40	55520332	1388008	2.32^{**}	-	21
AMMI2 error	198	115405389	582855.5	-	0.97^{ns}	-
IPCA3	38	35949509	946039.7	1.58^{*}	-	13.6
AMMI3 error	160	79455872	496599.2	-	0.83^{ns}	-
IPCA4	36	32201802	894494.5	1.49^{*}	-	-
AMMI4 error	124	47254069	381081.2	-	0.64^{ns}	-
Error	450	269299169	598442.6	-	-	-

G: Gollob (1968), C: Cornelius *et al* (1992),**, *, and ^{ns}: significant ($P < 0.01$), significant ($P < 0.05$), and non-significant by the F-test, respectively.

Table 4: Genotype rank by AMMI stability value (ASV) for grain yield (kg ha^{-1}) of 36 maize genotypes grown in nine environments of central Brazil in the 2012/2013 season

Rank	Genotype	IPCA1	IPCA2	ASV	Rank	Genotype	IPCA1	IPCA2	ASV
1	G8	12.01	-0.15	5.07	19	G17	-5.91	-6.28	22.89
2	G23	-10.54	-20.59	6.26	20	G29	14.52	4.03	24.09
3	G26	-15.11	11.17	7.71	21	G16	-3.68	-1.73	24.70
4	G3	0.55	-6.22	8.35	22	G25	-8.86	11.36	25.15
5	G9	-4.91	25.93	9.90	23	G6	0.25	-27.48	25.62
6	G32	5.22	-3.70	10.11	24	G21	26.13	-2.02	25.68
7	G7	-8.30	7.64	12.45	25	G20	9.38	15.37	25.70
8	G34	35.65	-5.46	13.18	26	G36	-21.83	-16.16	26.70
9	G5	-6.65	5.29	13.28	27	G33	-11.45	-25.12	27.48
10	G24	-14.76	12.60	14.16	28	G27	15.40	-16.21	29.17
11	G35	-17.52	-8.09	15.56	29	G15	-5.58	-10.14	30.28
12	G18	-31.61	-14.87	16.15	30	G30	10.86	1.68	32.56
13	G11	0.73	-8.29	16.56	31	G14	19.78	0.12	33.90
14	G31	19.41	-0.99	17.48	32	G4	-13.29	3.07	35.77
15	G22	1.28	30.24	19.23	33	G2	-12.22	-12.64	40.92
16	G13	9.61	-4.62	19.58	34	G10	-21.30	30.24	43.55
17	G12	17.32	27.86	20.26	35	G28	-19.83	-0.19	46.49
18	G19	-6.33	14.39	22.53	36	G1	41.56	-10.03	54.74

IPCA: Interaction principal component axes.

Considering both AMMI1 and ASV analyses, the results of AMMI analysis pointed G9, G7, and G5 as the most productive and stable genotypes. ASV analysis has the purpose to assist breeders in selecting promising genotypes, avoiding using solely visual graphical analysis.

In the GGE-Biplot method, the first two principal components (IPCA1 and IPCA2) accounted for 71.88% of the total variance of maize yield in the genotypes. Thus, this method explained a good part of the sum of squares of genotypes and GxE interaction, but this percentage may be related by noise. This value is within the range of 60–83.12% showed by other authors when evaluating maize genotypes (Hongyu *et al*., 2015; Machado *et al*., 2019, Oliveira *et al*., 2019).

The GGE-Biplot method has a series of graphical tools for effective genotype selection. Regions limited by red lines were created by *which-won-where* plot (Figure 2), which groups evaluated environments into mega-environments, representing the most similar environments. Genotypes located at the vertex of the polygon are more distant from the origin and classified as more responsive to environmental stimulus; yet, those within the polygon are less responsive.

The nine environments were cut into two groups of mega-environments: Sector 1 composed by E1, E2, E3, E4, E5, E7, E8, and E9; Sector 2 composed by E6 (Figure 2). The vertex genotype was G1 and presented the highest mean yield in Sector 1. When the genotypes are at vertices where it is not possible to define which sector they belong to and does not have related environments, it can be assumed that these genotypes were not responsive to any of the grouped environments. They are considered unfavorable and have low productivity.

E6 was the most different environment when compared to the others. Therefore, different genotypes should be selected and developed specifically for such mega-environment. E6 is located to the north of the Brazilian territory and, among the evaluated environments, it is at a lower altitude (90 m) and has an average annual maximum temperature of 33 °C (INMET, 2017). These factors may have influenced its classification as the most different from the others by the GGE-Biplot method.

Another analysis enabled by GGE-Biplot method is investigating the relationship between grain yield and genotype stability, represented by a mean x stability graph (Figure 3).

When considering yield and stability, G8 and G31 were the most stable and productive among the genotypes. On the other hand, G10 was the most unstable, followed by G22, G6, and G33. By contrast, G1 and G18 were not highly unstable as seen through the AMMI-Biplot method. This might have occurred due to the way statistical calculations were set up for each method. In the AMMI-Biplot, the

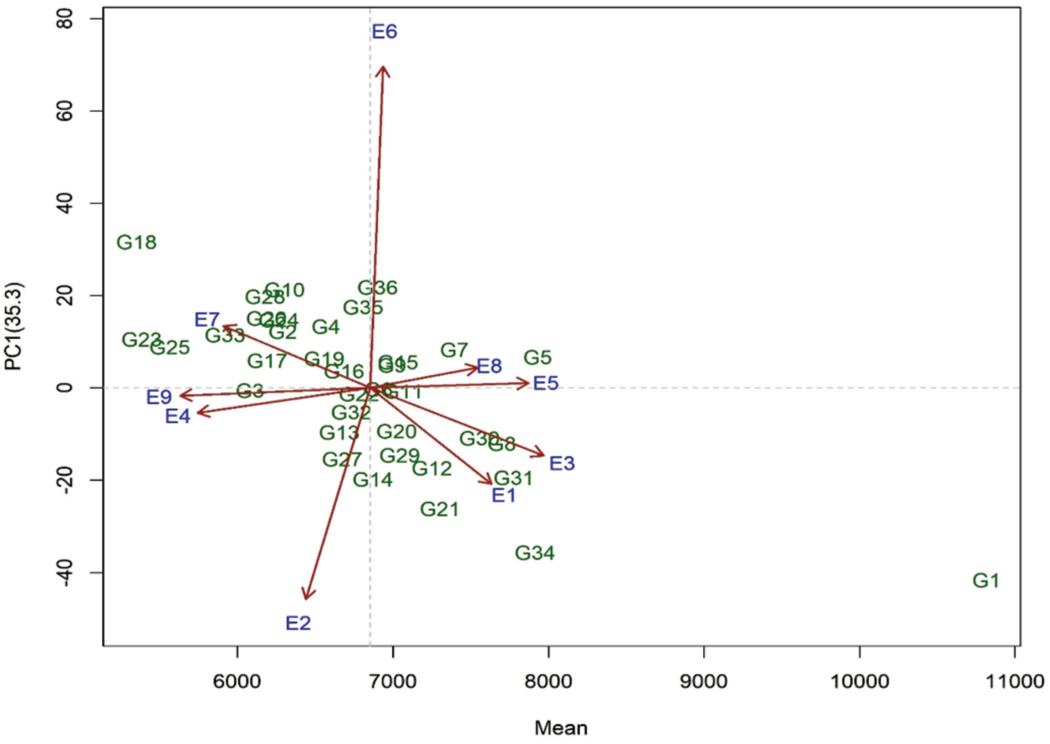

Figure 1: Biplot of AMMI1 analysis for grain yield (kg ha^{-1}) of 36 maize genotypes grown in nine environments of central Brazil in the 2012/2013 season.

effects of genotypes, environments, and GxE interaction are subtracted from the matrix of means, while in the GGE-Biplot, only the environmental effects are deducted from this matrix. In this way, the environmental effect was mitigated in the graphic representation of genotypes by GGE-Biplot.

An ideal genotype must have both high productivity and high stability in every environment, what is defined by the center of concentric circles (Figure 4) and works more as a representative model than a maize ideotype. In this sense, genotypes located near the ideotype are more desirable for selection (Yan & Tinker, 2006). The genotype G1 was allocated in the third concentric circle, that is closer to the ideal in terms of yield and phenotypic stability.

In addition, the GGE-Biplot method also takes into account the existing relationship among the test environments (Figure 5). For Oliveira *et al*. (2019), evaluating maize genotypes an ideal test environment should effectively discriminate genotypes and represent the environments.

Environmental differences are indicated by vectors originating at the center of the biplot (Figure 5). E5 and E8

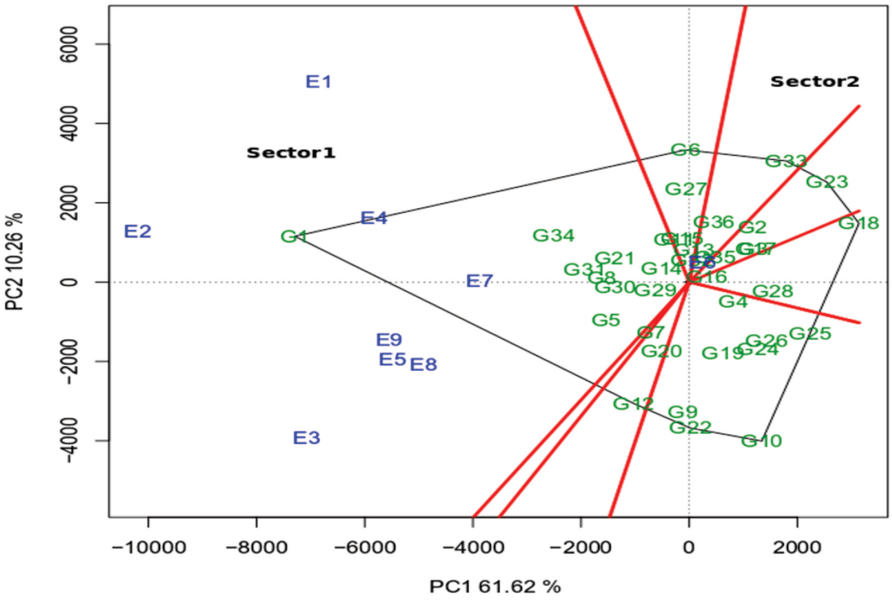

Figure 2: GGE Biplot graph: which-won-where for grain yield (kg ha^{-1}) of 36 maize genotypes grown in nine environments of central Brazil in the 2012/2013 season.

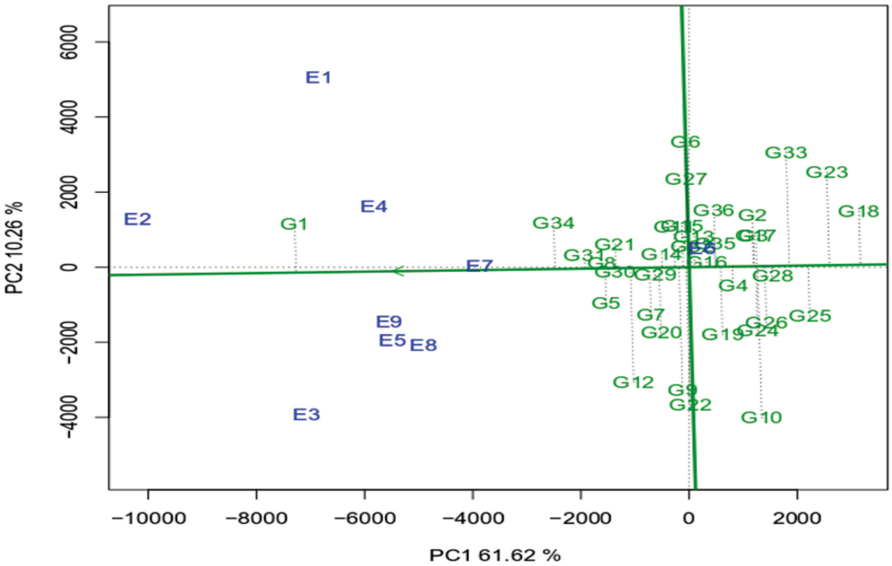

Figure 3: GGE-Biplot graph: mean x stability for grain yield (kg ha^{-1}) of 36 maize genotypes grown in nine environments of central Brazil in the 2012/2013 season, and their respective production stabilities.

were similar between each other because they had the lowest acute angle among environments. However, similar environments suggest data redundancy in breeding programs, increasing the cost of developing new genotypes and impairing representation of more contrasting environments (Felipe *et al*., 2010).

These results suggest the predominance of a simple GxE interaction, genetic variability among genotypes, and correlation among environments. The prevailing interaction in the evaluated dataset could not be identified through the methods of Lin & Binns (1988) with decomposition, and AMMI-Biplot. This led to the selection of the GGE-Biplot method as more advantageous.

The criterion MHPRVG*MG was able to connect yield, stability, and adaptability simultaneously (Figure 6). This method shows the overall adaptability of genotypes and related genotype productivity with genotype stability and adaptability. In this sense, G18 was the most unstable genotype in relation to the tested environments.

Additionally, the analysis by mixed models allowed classification of the environments into favorable and unfavorable based on the mean yield of genotypes in each site. E1, E3, E5, E6, and E8 were classified as favorable environments due to their grain yield superiority (6,853.14 kg ha"1). Conversely, E2, E4, E7, and E9 were considered unfavorable for showing yield values below the overall mean.

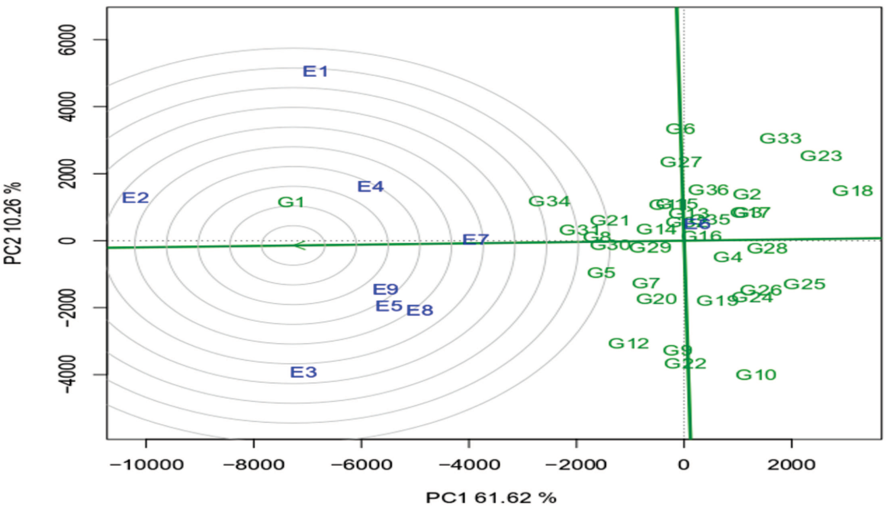

Figure 4: GGE-Biplot graph: projection of an ideal genotype for grain yield (kg ha"1) among 36 maize genotypes grown in nine environments of central Brazil in the 2012/2013 season.

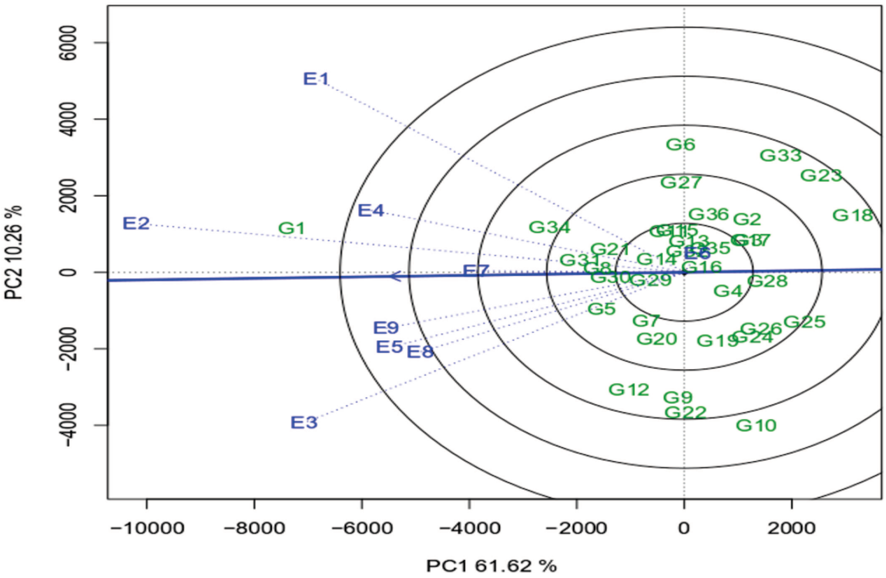

Figure 5: GGE-Biplot graph: discriminative x representative environments for grain yield (kg ha"1) of 36 maize genotypes grown in nine environments of central Brazil in the 2012/2013 season.

In the graph between favorable and unfavorable environments, G1 was classified as a genotype of broad adaptability and high stability, with the highest average (Figure 7). G34 and G31 showed adaptation to unfavorable environments, while G8 and G5 to favorable environments. Lastly, the remaining genotypes presented low stability and adaptability, as they did not perform well in any of the tested environments.

As observed by Rodovalho *et al* (2015), the results of MHPRVG method were similar to those of Lin & Binns (1988) with decomposition. However, it is worth highlighting that the former analyzes genotypic rather than phenotypic features, as the non-parametric one. Besides informing the type of interaction, allowing graphical analysis, and providing results in the same unit of the variable, and all of it in a single estimate, the MHPRVG is more pratical and can be used together with other adaptability and stability methods, presenting complementary information.

The methods Lin & Binns (1988) with decomposition, GGE-Biplot, and MHPRVG were unanimous in selecting genotype G8 for favorable environments. AMMI-Biplot categorized it as specifically adapted to E3, which was neither a favorable nor an unfavorable environment by this method. Conversely, the models Lin & Binns (1988) with decomposition, and MHPRVG considered E3 as a favorable environment. In brief, G8 can be recommended for favorable environments.

Both AMMI-Biplot and GGE-Biplot methods agreed in classifying G5 as a moderately stable genotype; yet, Lin & Binns (1988) with decomposition, and MHPRVG classified it as stable and recommended for favorable environments. The GGE-Biplot method captured half of the total variation and the AMMI explained even less; therefore, the results should be interpreted cautiously. Given this, Yan (2011) encouraged the association of such methods with mixed models to better understand the results obtained. Based on mixed models, the MHPRVG method provides results that must be interpreted at a genetic level, already penalized or capitalized by adaptability and stability estimates (Rodovalho *et al*., 2015).

The genotypes G1, G34, G31, G8, and G5 were similarly classified by the methods MHPRVG and Lin & Binns (1988) with decomposition. In this case, only one change was verified in the ordering of the first five selected genotypes. It is known that these methods penalize genotypes with unfavorable performance in all environments when compared to the general mean of the evaluated environments (Rodovalho *et al*., 2015).

Cargnelutti Filho & Guadagnin (2018) observed that genotypes indicated by the method Lin & Binns (1988) with decomposition are usually associated with high yield and low predictability. In this study, this association could be verified for G1, which was considered unstable according AMMI-Biplot. GGE-Biplot classified this genotype as moderately stable and the closest to the ideal since it is a simple hybrid. This difference may occur because the AMMI-Biplot method separates genotype and environment effects from GxE interaction, while the GGE-Biplot select plants based on genotype and GxE interaction simultaneously. Yan (2011) observed that these last two effects should be considered simultaneously for selecting superior genotypes because breeders seek to understand genotype performance associated with GxE interaction.

All the methods were in accordance in terms of classification of G10, G18, and G34 as unstable genotypes. Nevertheless, they did not reach an agreement regarding the most adapted, stable, and productive genotypes. The genotype that was closest to this relationship was G1 by the methods Lin & Binns (1988) with decomposition, GGE-Biplot, and MHPRVG.

No relationship was verified between the GGE-Biplot method and the others, and it can be used as an auxiliary tool for genotype selection. In addition, only the GGE-Biplot, AMMI-Biplot, and MHPRVG methods showed the predominance of a simple interaction for the evaluated dataset. GGE-Biplot is a remarkably informative method since it allows analyzing together the performances of environments, genotypes, and GxE interaction.

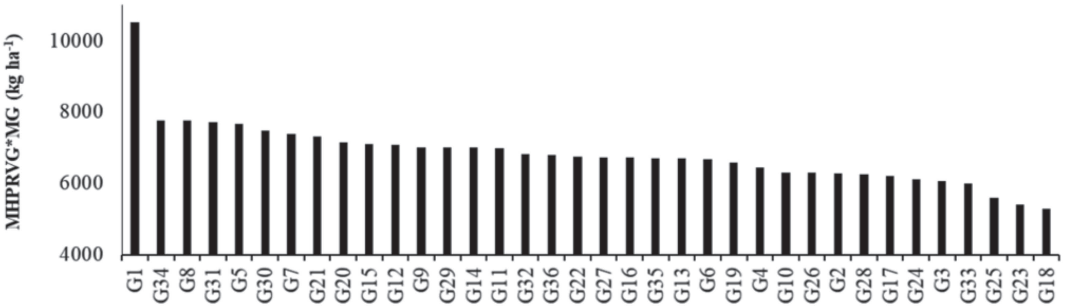

Figure 6: Means of MHPRVG*MG for grain yield (kg ha^{-1}) of 36 maize genotypes grown in nine environments of central Brazil in the 2012/2013 season.

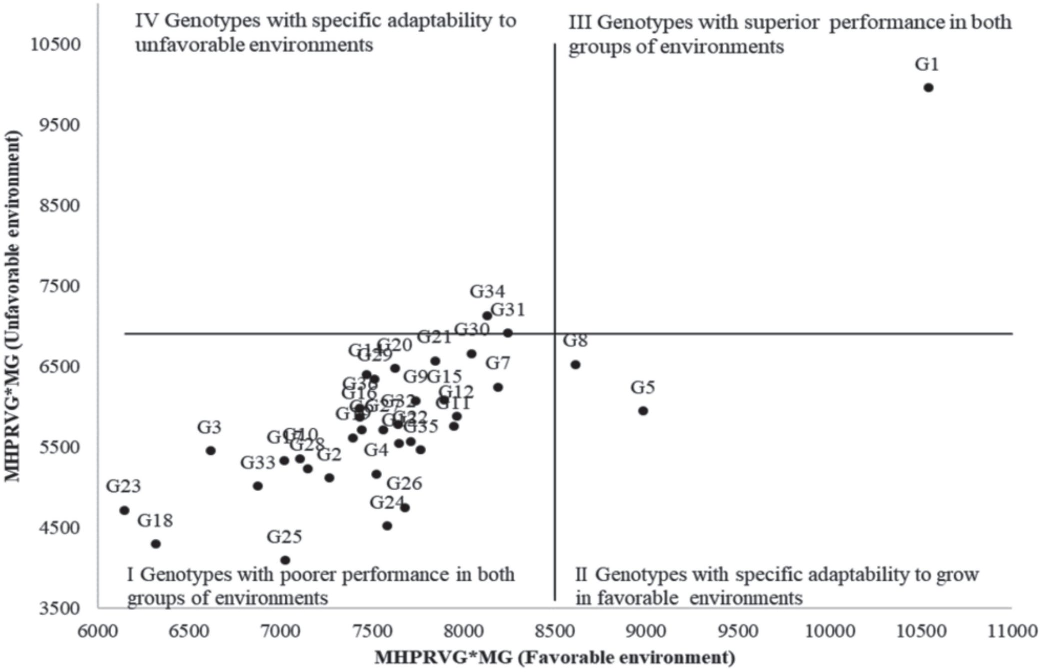

Figure 7: Scatterplot between favorable and unfavorable environments using MHPRVG*MG for grain yield (kg ha^{-1}) of 36 maize genotypes grown in nine environments of central Brazil in the 2012/2013 season.

CONCLUSIONS

AMMI method presented superior quality than GGE Biplot, especially regarding the pattern of GxE interaction.

The method Lin & Binns (1988) with decomposition presented similarity with MHPRVG, but these one is most practice, accurate and informative than Lin & Binns.

Stability and adaptability were not always associated with higher yield; thus, the methods MHPRVG and GGE-Biplot should be used together to select the most promising genotypes.

The genotypes G5 and G8 were recommended for cultivation in central Brazil due to their great adaptability and stability combined with increased yield.

REFERENCES

Abate M (2020) Genotype by environment interaction and yield stability analysis of open pollinated maize varieties using AMMI model in Afar Regional State, Ethiopia. Journal of Plant Breeding and Crop Science, 12:08-15.

Bocianowski J, Nowosad K & Tomkowiak (2019) Genotype – environment interaction for

seed yield of maize hybrids and lines using the AMMI model. Maydica, 64:01-08.

Borem A, Miranda GV & Fritsche-Neto R (2017) Melhoramento de plantas. 7ª ed. Viçosa, Editora UFV. 523p.

Cargnelutti Filho A & Guadagnin JP (2018) Number of experiments for adaptability and stability analysis in maize by Lin and Binns method. Ciência Rural, 48:01-08.

Carneiro PCS (1998) Novas metodologias de análise da adaptabilidade e estabilidade de comportamento. Tese de Doutorado. Universidade Federal de Viçosa, Viçosa. 155p.

Cornelius PL, Seyedsadr M & Crossa J (1992) Using the shifted multiplicative model to search for “separability” in crop cultivar trials. Theoretical and Applied Genetics, 84:161-172.

Cruz CD (2013) GENES - A software package for analysis in experimental statistics and quantitative genetics. Acta Scientiarum Agronomy, 35:271-276.

Cruz CD, Regazzi AJ & Carneiro PCS (2012) Modelos biométricos aplicados ao melhoramento genético. 4ª ed. Viçosa, Editora UFV. 514p.

Faria SV, Luz LS, Rodrigues MC, Carneiro PCS & Delima RO (2017) Adaptability and stability in commercial maize hybrids in the southeast of the State of Minas Gerais, Brazil. Revista Ciência Agronômica, 48:347-357.

Felipe CRP, Duarte JB & Cmarano LF (2010) Estratificação ambiental para avaliação e recomendação de variedades de milho no estado de Goiás. Pesquisa Agropecuária Tropical, 40:186-199.

Gollob HF (1968) A statistical model which combines features of factor analytic and analysis of variance techniques. Psychometrika, 33:73-115.

Hongyu K, García-Peña M, Araújo LB & Dias CTS (2014) Statistical analysis of yield trials by AMMI analysis of genotype × environment interaction. Biometrical Letters, 51:89-102.

Hongyu K, Silva FL, Oliveira ACS, Sarti DA, Araújo LB & Dias CTS (2015) Comparação entre os modelos AMMI e GGE biplot para os dados de ensaios multi-ambientais. Revista Brasileira de Biometria, 33:139-155.

INMET - Instituto Nacional de Meteorologia (2017) BDMEP - Banco de Dados Meteorológicos para Ensino e Pesquisa. Available at: <http://www.inmet.gov.br/projetos/rede/pesquisa/>. Accessed on November 17th, 2017.

Lin CS & Binns MRA (1988) Superiority measure of cultivar performance for cultivar x location data. Canadian Journal of Plant Science, 68:193-198.

Machado NG, Lotufo-Neto N & Hongyu K (2019) Statistical analysis for genotype stability and adaptability in maize yield based on environment and genotype interaction models. Ciência e Natura, 41:01-09.

Mendes FF, Guimarães LJM, Souza JC, Guimarães PEO, Pacheco CAP, Machado JRA, Meirelles WF, Silva AR & Parentoni SN (2012) Adaptability and stability of maize varieties using mixed model methodology. Crop Breeding and Applied Biotechnology, 12:111-117.

Oliveira IJ, Atroch AL, Dias MC, Guimarães LJ & Guimarães PEG (2017) Selection of corn cultivars for yield, stability, and adaptability in the state of Amazonas, Brazil. Pesquisa Agropecuária Brasileira, 52:455-463.

Oliveira RL, Pinho RGV, Balestre M & Ferreira DV (2010) Evaluation of maize hybrids and environmental stratification by the methods AMMI and GGE biplot stratification by the methods AMMI and GGE biplot. Crop Breeding and Applied Biotechnology, 10:247-253.

Oliveira TRA, Carvalho HWL, Oliveira GHF, Costa EFN, Gravina GA, Santos RF & Carvalho Filho JLS (2019) Hybrid maize selection through GGE biplot analysis. Bragantia, 78:166-174.

Oliveira IJ, Fontes JRA & Morais RR (2020) Agronomic performance of eight corn genotypes in two sowing periods. Revista Agro@mbiente, 14:01-16.

Purchase JL, Hatting H & Vandeventer CS (2000) Genotype × environment interaction of winter wheat (Triticum aestivum L.) in South Africa: Stability analysis of yield performance. South African Journal of Plant and Soil, 17:101-107.

R Development Core Team (2018) R: A language and environment for statistical computing. Vienna, R Foundation for Statistical Computing. 2673p.

Resende MDV (2016) Software Selegen-REML/BLUP: a useful tool for plant breeding. Crop Breeding and Applied Biotechnology, 16:330-339.

Resende MDV & Duarte JB (2007) Precisão e controle de qualidade em experimentos de avaliação de cultivares. Pesquisa Agropecuária Tropical, 37:182-194.

Rezende WS, Beyene Y, Mugo S, Ndou E, Gowda M, Sserumaga JP, Asea G, Ngolinda I, Jumbo M, Oikeh SO, Olsen M, Borem A, Cruz CD & Prasanna BM (2020) Performance and yield stability of maize hybrids instress-prone environments in eastern Africa. The Crop Journal, 8:107-118.

Rezende WS, Cruz CD, Borem A & Rosado RDS (2021) Half a century of studying adaptability and stability in maize and soybean in Brazil. Scientia Agricola, 78:01-09.

Rodovalho MA, Coan MMD, Scapim CA, Pinto RJB & Contreras-Soto RI (2015) Comparison of HMRPGV, Lin and Binn’s, and Annichiarico’s methods for maize hybrid selection for high and stable yield. Maydica, 60:M10.

Santos DC, Pereira CH, Nunes JAR & Lepre AL (2019) Adaptability and stability of maize hybrids in unreplicated multienvironment trials. Revista Ciência Agronômica, 50:83-89.

Yan W (2011) GGE Biplot vs AMMI graphs for genotype-by-environment data analysis. Journal of the India Society of Agricultural Statistics, 65:181-193.

Yan W & Tinker NA (2006) Biplot analysis of multi-environment trial data: Principles and applications. Canadian Journal of Plant Science, 86:623-645.

Zobel RW, Madison JW & Gauch HG (1988) Statistical analysis of a yield trial. Agronomy Journal, 80:388-393.