Crop Breeding and Applied Biotechnology 9: 299-307, 2009
Brazilian Society of Plant Breeding. Printed in Brazil

Comparing Biplot Multivariate Analyses with Eberhart and Russell' method for genotype x environment interaction

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Received 03 November 2008

Accepted 15 August 2009

ABSTRACT - *The aim of this study was to compare the multivariate methods GGE (Genotype main effects and Genotype x Environment interaction) and AMMI (Additive Main effects and Multiplicative Interaction) with the method of Eberhart and Russell for interpreting genotype x environment interaction. The AMMI and GGE analysis explained around 50% of the sum of squares of the genotype x environment interaction, whereas the method of Eberhart and Russell explained only 9.1 and 15.8% each year. The cultivars classified as minor contribution to the genotype x environment interaction by methods of AMMI and GGE were also the same classification method of Eberhart and Russell. The AMMI and the GGE biplot analyses are more efficient than the Eberhart and Russell. The GGE biplot explains a higher proportion of the sum of squares of the GxE interaction and is more informative with regards to environments and cultivar performance than the AMMI analysis.*

Key words: Genotype x environment interaction, breeding, GGE, *Zea mays*.

INTRODUCTION

The genotype x environment interaction is important for plant breeding because it affects the genetic gain and recommendation and selection of cultivars with wide adaptability (Deitos et al. 2006, Souza et al. 2009). On the other hand, different genotypes have different performance in each region that can be capitalized to maximize productivity (Souza et al. 2008). Eberhart and Russell (1966) developed a methodology for identifying cultivars with greater adaptability and stability that has been widely used in the identification of genotypes for this purpose (Miranda et al. 1998, Grunvald et al. 2008). However, other methods for identifying cultivars with adaptability and stability have been developed and many multivariate techniques are available such as GGE (Genotype main effects and Genotype x Environment interaction) and AMMI (Additive Main effects and Multiplicative Interaction) with new information for cultivars, environmental stratification and cultivar x environment interaction (Miranda et al. 2009).

Yan et al. (2007) compared the GGE biplot analysis and AMMI analysis with three aspects of genotype-by-environment data (GED) analysis, namely mega-environment analysis, genotype evaluation, and test-environment evaluation. Yan et al. (2007) concluded that both GGE biplot analysis and AMMI analysis combine rather than separate G and GE in mega-environment analysis and genotype evaluation. The authors maintain

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that the GGE biplot is superior to the AMMI1 graph in mega-environment analysis and genotype evaluation because it better explains G+GE and has the inner-product property of the biplot. Moreover, the discriminating power vs. representativeness view of the GGE biplot is effective in evaluating test environments, which is not possible with AMMI analysis. Model diagnosis for each dataset is useful, but the accuracy gained from model diagnosis should not be overstated.

The GGE biplot analyses are used in many cultivars x environments interaction studies. The grain yield stability of 13 Chinese maize hybrids tested across 10 environments was evaluated via the GGE biplot analysis, and identified non representative and/or non discriminating locations (Fan et al. 2007). The GGE biplot analysis ranked hybrids with above-average yield across years and for stability of performance. The GGE biplots revealed that cv. Hai He had the highest yield in seven and cv. LD10 exhibited the highest yield in 10 environments. Three common locations were found among the time periods studied.

The best environments for selective productive sugarcane (*Saccharum* spp.) cultivars in Florida for organic and sand soils were identified (Glaz and Kand 2008). The results revealed the desirability of replacing an organic-soil location with a sand-soil location in the final testing stage of this sugarcane breeding and selection program. They concluded that the ability to identify productive cultivars on organic soils by the Florida sugarcane selection program would be least compromised by replacing either Osceola or Knight with a sand-soil location.

Thus, the objective of this work was to compare the AMMI and GGE multivariate methods with Eberhart and Russell method for the interpretation of genotype x environment interaction.

MATERIAL AND METHODS

The data used were obtained from the Maize Cultivar Evaluation National Network carried out by the Maize National Assay in the agricultural years of 1998/1999 and 1999/2000, using early maturation cultivars in Minas Gerais municipalities, Brazil.

Forty-two cultivars were evaluated in the 1998/1999 harvests, with assays installed in ten locations. In 1999/2000, forty-nine genotypes were evaluated in nine locations.

The experimental designs used were the 7 x 6 rectangular lattice (1998/1999 harvests) and the 7 x 7 square lattice (1999/2000 harvests). All assays were composed of two replications, each plot comprising two 5-meter rows, 0.9 meters apart, representing a final stand of approximately 55 thousand plants per hectare.

SAS statistical software version 8 was used for the individual and combined analyses (SAS 1999). Lattice analyses were carry out using intrablock information.

AMMI (Additive Main Effects and Multiplicative Interaction) analysis combines, in a single model, additive components for the main effects of genotypes and environment as well as multiplicative components for interaction effects (Duarte and Vencovsky 1999). Therefore, the mean response of a genotype i, in an environment p, is:

$$Y_{ij} = \mu + G_i + E_j + \sum_{K=1}^{n} \lambda_k \gamma_{ik} \alpha_{jk} + \rho_{ij} + \varepsilon_{ij}$$

with GE_{ij} represented by $\sum_{K=1}^{n} \lambda_k \gamma_{ik} \alpha_{jk} + \rho_{ij}$.

Under the restrictions $\sum_i G_i = \sum_j E_j = \sum_i (GE)_{ij} = \sum_j (GE)_{ij} = 0$, in addition to the general mean (μ), and the mean experimental error ε_{ij}, the remaining terms of the model are a result of the so- called Decomposition by Singular Values (DSV) of the interaction matrix $GE_{(gxe)} = [GE_{ij}]$. The interaction matrix is obtained as a residual of the adjustment of the main effects, through variance analysis, applied to the mean matrix $Y_{(gxe)} = [Y_{ij}]$. Thus, λ_k is the k-th singular value of GE (scalar), and $\lambda_{k(gx1)}$ and $\alpha_{k(1xa)}$ are the respective singular values (column vector and line vector) associated with λ_k (Good 1969, Mandel 1971, Piepho 1995). Hence, γ_{ik} and α_{jk} are the elements related to genotype i and to environment j for vectors $\lambda_{k(gx1)}$ and $\alpha_{k(1xa)}$, respectively. The k index (k = 1, 2 … m, where m = min), is the rank of taken until n in the sum (n < m). This index determines an approximation of the least squares for the matrix by the n first-terms of DSV (Good 1969, Gabriel 1978), leaving the additional residual denoted by ρ_{ij}. For n = m there is no longer approximation, but rather the exact decomposition of the matrix implied in a null ρ_{ij}.

Yan et al. (2000) proposed the GGE (Genotype and Genotype-by-Environment Interaction) biplot analysis for the graphical interpretation of genotype x environment interactions, based on the SREG (Sites Regression) model, suggested by Cornelius et al. (1996),

and Crossa and Cornelius (1997)

$$Y_{ij} = \bar{y}_{.j} + \sum_{k=1}^{n} \lambda_k \xi_{ik} \eta_{jk} + \varepsilon_{ij}$$

GGE biplot analysis is based on the simplified model with two principal components (Yan et al. 2000):

$$Y_{ij} - \bar{y}_{.j} = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

In which

Y_{ij} is the productivity mean of cultivar i in environment j; $\bar{y}_{.j}$ is the general mean of the cultivars in environment j; $\lambda_1 \xi_{i1} \eta_{j1}$ is the first principal component (PCA1); $\lambda_2 \xi_{i2} \eta_{j2}$ is the second principal component (PCA2); λ_1 and λ_2 are the eigenvalues associated with PCA1 and PCA2, respectively; ξ_{i1} and ξ_{i2} are the values of the first and second principal components, respectively, for cultivar i; η_{j1} and η_{j2} are the values of the first and second principal components, respectively, for environment j; and ε_{ij} is the error ij associated with the model.

The graphic axes of this analysis are the first two principal components (eigenvalues) of the multivariate analysis and represent most of the variance data, assuming the environment as fixed, i.e., variance in productivity is due exclusively to the effects of G and G x E. Thus, this analysis identifies which cultivars are superior in the various environments.

The GGE biplot is generated by placing ξ_{i1} and ξ_{i2} and η_{i1} and η_{i2} in such a way that each cultivar or each environment is represented by a single point on the biplot.

The interpretations performed in terms of the vectorial relations 1) genotype x genotype, 2) environment x environment, and 3) genotype x environment, as presented for AMMI analysis, are equally valid for GGE biplot analysis.

The linear regression method was proposed by Eberhart and Russell (1966) and software Genes was used for analyses (Cruz 2006)

The analysis carried out used an algorithm developed for the GGE model by Vargas and Crossa (2000) as well as SAS (1999) to generate a GGE biplot.

RESULTS AND DISCUSSION

In all the combined analyses, significant cultivar, environment, and cultivar x environment effects were detected, indicating that some maize cultivars exhibit different productivity in at least one of the environments evaluated for two years (Table 1). The methodology of Eberhart and Russell (1966) captured 9.18% of SS_{GxE} by regression analysis (Genotype x Linear Environment SS/ Genotype x Environment interaction SS) in 1998/1999.

For the 1998/1999 harvest, the sum of square G x E, SS_{GxE}, object of the DVC decomposition, represented 16% of the SS_{TOTAL} (SS of G + SS of E + SS of G x E). The first principal axis (PCA1) captured 30.5% of the SS_{GxE}, the second 20.2% and, the third 15.5%. Using the F test, seven of nine interaction axes were significant at 5% probability, which led to the selection of the AMMI 7 model. However, AMMI 7 is more complex to interpret due to its difficult graphic visualization. Observation of only the first two axes ensures better graphical visualization in the AMMI 2 model; this model captures 50.7% of the SS_{GxE}, much greater than the 9.18% captured by the Eberhart and Russell methodology (Table 1).

Table 1. Summary of analysis of variance combined with decomposition of the sum of squares of environments according to the methodology of Eberhart and Russell (1966) for early cycle maize commercial hybrids (National Assay of 1998/1999 and 1999/2000 harvests)

Source of variation	1998/1999 harvest		1999/2000 harvest	
	df	SS	df	SS
Environment (E)	9	1971612927**	8	1662432504**
Genotype (G) adjusted	41	170795951**	48	315499557**
G x E interaction	369	415535498**	384	599917000**
E/genotype	378	2387148425	392	2262349505
Linear E	1	1971612927	1	1662432504
G x Linear E	41	38150313	48	94956561
Combined deviation	336	377385184	343	504960439
Residue	290	131187122	324	238163144
Total	839	-	881	-

** significant at 5 and 1% probability by the F test

In 1998/1999, by Eberhart e Russell' method, most of cultivars showed wide adaptability (b = 1) and only few cultivars showed specific adaptability to favorable environments (b>1; BRS 3060, P30F33, DINA 657, XB 7011 and, XL 550) and unfavorable environments (b<1; CX 9610, NB 6077, C 701, CD 3121, Z 8392 and, R&G01E). The environments classified as favorable were CO, P1, SL and ID and as unfavorable were CA, J, U1, U2, IH and P2. The stability cultivars were CX 9610, CX 9856, P30F45, HT 7105-3, AG 8014, P 3071, C 701, C 747, G 186 C, AG 5016, Z 8420, AG 5011, P 3042, MTL 9877, XB 8010 and, SHS 4040.

AMMI biplot for the 1998/1999 harvest (Figure 1) shows that the environment marker closer to the origin, with scores close to zero, is the Janaúba (J) environment, followed at a considerable distance by Patos de Minas 1 (P1). With regard to the genotype, P 30F45 (5) was closer to zero, followed by SHS 4040 (33), CX 9856 (4), R&G 01E (42), AG 8014 (8), Z 8420 (18) and, AG 5016 (16). The environments and genotypes closer to the origin contributed very little to G x E interaction. Janaúba (J), close to the origin, and the genotypes close to this environment, such as Z 8420 (18) and P 30F45 (5), possess a more reliable classification, determined primarily by the genotypic effects characterizing the reduced G x E interaction. All cultivars identified as stable by the AMMI biplot also were by the Eberhart and Russell (1966) methodology. However, the environment classification was very different between the methods because Janaúba and Patos de Minas 1 showed higher environment indexes and opposite directions.

The Patos de Minas 1 (P1) and Uberlândia 2 (U2) environments and the genotypes Z 8466 (26), P 30F33 (21), XB 7011 (34), Z 8420 (18), C 747 (12) and AG 5011 (19) contributed the least to the interaction captured by the PCA 2 axis. The PCA 1 must be determined by the differences between environment pairs (U1)/(IH) and (P2)/(U2). However, U1 and IH are similar, as are P2 and U2. PCA 2 apparently resulted mainly from the differences between the environments (U1) and (IH) (Figure 1). By Eberhart and Russell's method, the environments U1, IH, P2 and U2 were considerately unfavorable, but by the AMMI method, the environment captured 20.2% of environment x genotype interaction.

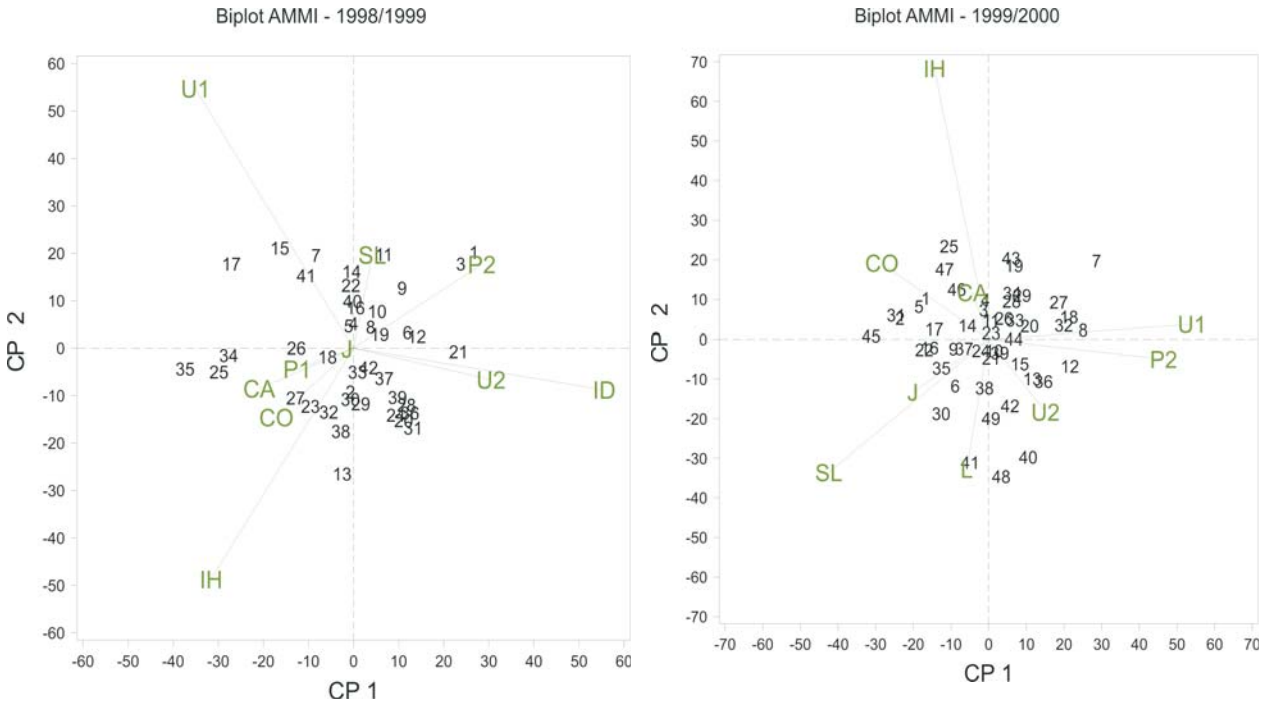

Figure 1. AMMI analysis biplot based on grain yield of early cycle maize comercial hybrids, relative to the National Assay of 1998/1999 and 1999/2000 harvests in Minas Gerais, Brazil

The methodology of Eberhart and Russell (1966) captured 15.8% by regression analysis in 1999/2000. The G x E sum of square, SS_{GxE}, object of the DVC decomposition, accounted for 23% of the SS_{TOTAL} ($SS_G + SS_E + SS_{G\,x\,E}$). The first principal axis captured 24.4% of the SS_{GxE}, the second 20.9% and, the third 17.3%.

Based on the F test, six of the eight interaction axes were significant (5% probability), leading to the selection of the AMMI 6 model. Similar to the analysis of the 1998/1999 harvest, the AMMI 2 model was chosen, aiming at a graphical visualization of the first two axes that also captured 45.37% of the SS_{GxE}. Again, similar to the analysis of the 1998/1999 harvests, the AMMI 2 model captured a higher proportion of SS_{GxE} in relation to the Eberhart and Russell (1966) methodology.

By Eberhart and Russell's method, in 1999/2000, the cultivars with specific adaptability in a favorable environment were XB7012, SH50EX556, P30207, P3041, AG6690 and HT971011; and unfavorable environments were CDX99T05, NB7228, NB5318, DINA500, COE9743 and MTC817C.

The favorable environments were J, IH, L e SL and unfavorable were U2, U1, CO, P2 e CA. The Capinópolis (CA) environment showed the lowest absolute value of the environmental index and U2 and SL, the extreme values of the environment index, but in opposite directions.

According to the graphic shown in Figure 1, Capinópolis (CA) was the environment closest to the origin that still contributed to the G x E interaction, results that agree with Eberhart and Russell' method. The cultivars with the greatest proximity were PL 6403 (23), followed, in increasing order, by 98 HT 19 A (10), Z 8460 (24), DKB747 (39), DINA 1000 (11), PL 6440 (21), and SHS 4040 (21). These genotypes have more reliable classifications, basically determined by the genotypic effects, with reduced G x E interaction. All these genotypes were considered stable by the Eberhart and Russell' method, the only ones that were not stable were CDX 97501, NB7228, DINA 1000, CO 34, Z 8490, AX 4646, MTL 833N, BRS 3150 and, HT 7105-3.

The Inhaúma (IH) and Lavras (L) environments and the HT 7105-3 (48) and HT 2628-9 (29) genotypes contributed the least to the interaction captured by the PCA 1 axis. For the PCA 2, the Uberlândia 1 (U1) and Patos de Minas 2 (P2) environments axis, the HT 97 1011 (45) genotype contributed the least to the G x E interaction. Moreover, IH and SL / L environments were the most divergent and possibly the cause of 20.92% of the variance explained by the PCA 2. However, these environments were considered positive by Eberhart and Russell's method.

Analysis of variance for the GGE method, attributing degrees of freedom to the interaction components PCA_k according to the Gollob (1968) system, shows by the F test that eight out of ten interaction axes are significant in the 1998/1999 harvest. This would compel a selection of the eight axis model, making interpretation of the results unreliable, due to the difficulty of analyzing a high number of possible axis combinations. The first two principal components were chosen according to recommendations of the original method. The first main axis, PCA 1, captured 35.6% of the ($SS_G + SS_{GxE}$); the second, 18.3%, totaling 53.9% for the two first principal components. The third principal component captured 14.3%.

The environments were grouped into eight sectors (separated by dotted lines) in the 1998/1999 harvest (Figure 2). The first sector was composed of the Coimbra (CO), Patos de Minas 1 (P1), Janaúba (J), Sete Lagoas (SL), Uberlândia 2 (U2), Patos de Minas 2 (P2) and Indianápolis (ID) environments, with genotype P 30F33 (21) as an outlier for this mega-environment. The second sector was composed of the Uberlândia 1 (U1) and Inhaúma (IH) environments, with genotype XL 357 (25) as an outlier. Capinópolis (CA) can also be included in the XL 357 (25) genotype group, although it is located in another sector, constituting another mega-environment. Since the remaining sectors had delimiting genotypes close to one another yet far from the origin, they did not delineate environments, due to a similarity in productivity levels. This classification does not present any similarity with the environment classification other than the one obtained with the Eberhart and Russell method.

In the 1998/1999 harvest, the cultivars located at the extremities of the polygons were (Figure 2): P 30F33 (21), P 3041 (22), BRS 3060-A (1) (positive PCA 1 scores); AGROMEN 2E2 (31), HATA 3052 (39), XB 7011 (34), XL 355 (35), XL 357 (25) (negative PCA 1 scores). In addition, this classification does not present any similarity with the results obtained by the Eberhart and Russell method (1966).

The modeling of the technique yielded positive PCA 1 scores for all the environments, as seen in the 1998/1999 harvest. This suggests that the scores of the PCA 1 genotypes in the GGE biplot represent proportional productivity differences across the various environments and occurred due to a simple G x E interaction (in which genotype superiority is maintained throughout the various environments), as opposed to representing a fraction of the complex G x E interaction (Crossa and Cornelius 1997).

PCA 2, in contrast, demonstrated the most important sources of variation that contribute to a complex G x E interaction. The environments may have positive or negative values. Thus, the complex G x E interaction among optimal genotypes leads to differentiation in mega-environments.

Considering that mega-environments are delimited by various optimal genotypes (Gauch and Zobel 1996), Figure 2 suggests the existence of two mega-environments for the 1998/1999 crop of early maize in the Minas Gerais state, designated as niches of P 3041 (22) and XL 357 (25).

The analysis of variance was used to determine the combined sources of variation affecting the 1999/2000 crop with regards to the sum of squares for the environment (E), genotype (G), and G x E interaction. Environment (E) was shown to be the most important source of variation with regards to productivity (65%). G x E interaction accounted for 23%, higher than genotype (G), which accounted for 12%. The superiority of G x E interaction in relation to genotype (G) suggests the existence of different mega-environments. Through the F test, six out of nine interaction axes were significant at 5% probability, which would compel the selection of the six-axis model. The first two principal components were chosen, as originally recommended by the method.

The first principal axis, PCA 1, captured 37.6% of the ($SS_G + SS_{GxE}$); the second captured 14.6%, totaling 52.2% for the first two principal components.

In Figure 2, the most responsive genotypes, located in the extremities of the polygons formed and delimiting the sectors, were: 98 HS 16B (36), AG 6690 (37), AX 4646 (31), NB 5318 (8) (positive PCA 1 scores); CO 34 (18), PL 6443 (22), PL 6440 (21), HT 97 1011 (45) (negative PCA 1 scores); AX 4646 (31) (PCA 1 score of zero). Eight sectors were formed; the first one, delimiting a mega-environment, comprised of the following environments: Janaúba (J), Capinópolis (CA), Lavras (L), Patos de Minas 2 (P2), Uberlândia 2 (U2), and Uberlândia 1 (U1), with the genotype 98 HS 16B (36) as an outlier.

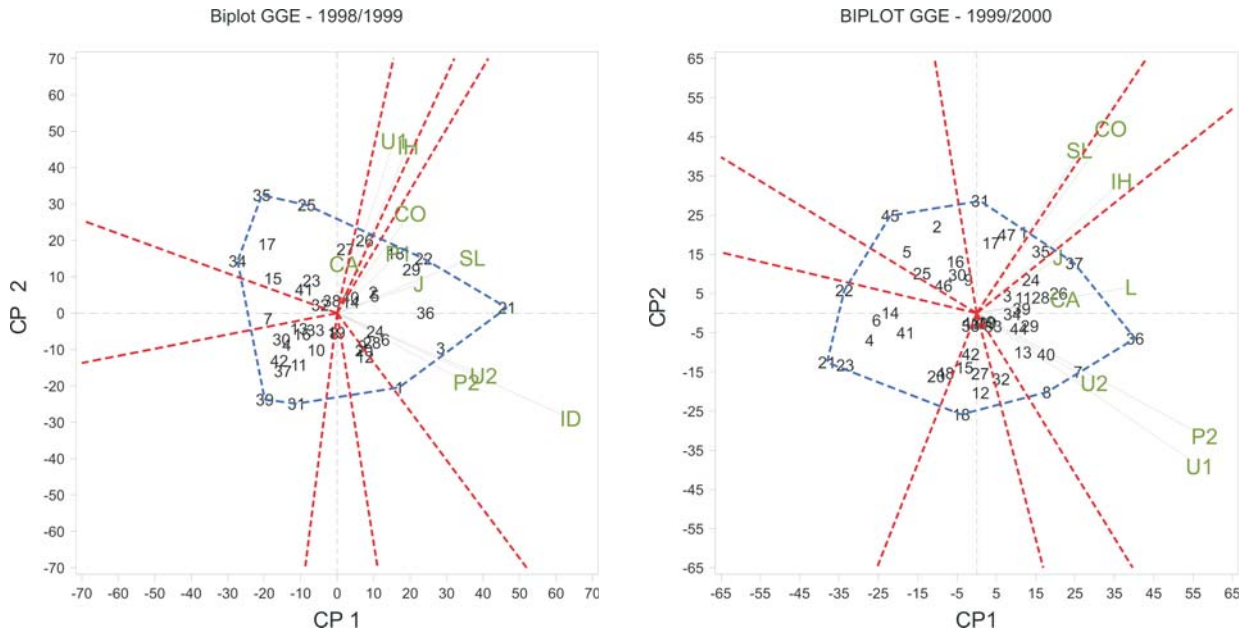

Figure 2. GGE (Genotype and Genotype-Environment interaction) biplot, based on grain yield of early cycle maize commercial hybrids, relative to the National Assay of 1998/1999 and 1999/2000 harvests in Minas Gerais, Brazil

The second sector, also a mega-environment, contains the Coimbra (CO) and Inhaúma (IH) environments, with genotype AG 6690 (37) as an outlier. The third sector contains only the Sete Lagoas (SL) environment, but is very close to the perpendicular separation between genotypes AG 6690 (37) and AX 4646 (31), closer to the latter. Thus, the AG 6690 (37) and AX 4646 (31) genotypes have similar productivity in the Sete Lagoas (SL) environment.

All the environments possessed positive scores for PCA 1. Figure 2 suggests the existence of two mega-environments for the 1999/2000 crop of early maize in the state of Minas Gerais, highlighting 98 HS 16B (36) and AG 6690 (37).

Eight sectors were formed in the 1998/1999 and 1999/2000 harvests, comprising only two distinct mega-environments, often studied for data analysis of other harvests. This shows that despite the high number of experiments used to evaluate cultivars in Minas Gerais, these experiments represent a uniform input and management level, which reduces the edaphoclimatic variation. This variation, unpredictable over the forthcoming years, can thus be simulated by means of different planting times, drought stresses, temperatures, disease pressures, plant populations, and input levels. Hence, evaluating fewer years may be more appropriate than evaluating many years with little unpredictable variation.

Inhaúma tended to be the best representative of a mega-environment, because it repeatedly appeared as a distinct group in the 1998/1999 and 1999/2000 harvests, although it was grouped in different environments. As for the other mega-environment, it is not possible to define the best representative environment, as all the cultivars generally behaved in a similar manner across environments.

GGE biplot analysis validity can be inferred through applying AMMI. In a review by Gauch and Zobel (1996), it was concluded that in 70% of the cases AMMI 1 (with a multiplicative term) is the best model; for the remaining cases, AMMI 2 is the best.

For both AMMI and GGE biplot, the bi-dimensional biplot based on GGE 2 always uses an intermediate number of degrees of freedom and explains an intermediate magnitude of the G + G x E sum of squares for AMMI 1 and AMMI 2. Thus, the GGE biplot will always be closer to the optimal model.

In the 1998/1999 harvest, the GGE biplot analysis explained 53.4% of the G x E sum of squares, as opposed to 50.8% explained by the AMMI analysis. In the 1999/2000 harvest, the GGE biplot analysis explained 52.3% and the AMMI analysis explained 45.4%. These results show the superiority of the GGE method, since in both harvests the GGE biplot analysis explained most of the G x E sum of square, as well as including the genotype effect. The Eberhart and Russell method explained only 9.1% and 15.8% and showed its limitations. In our results the AMMI2 mega-environment display did not incorporated more of the genotype main effect and did not capture more of the genotype × environment (GE) interaction than GGE2 but, displayed the which-won-where pattern more accurately for our datasets. The GE interaction was not captured well by one principal component so, the AMMI1 didn't display the genotype nominal yields described winning genotypes and we could not draw conclusions on the adaptive responses more simply and clearly than the GGE2 biplot.

Gauch Junior et al. (2008) reviewed many articles between AMMI and GGE and concluded that it required clarification after controversial statements and contrasting conclusions appeared between these methods. The AMMI2 mega-environment display incorporates more of the genotype main effect and captures more of the genotype × environment (GE) interaction than GGE2, thereby displaying the which-won-where pattern more accurately for complex datasets. When the GE interaction is captured well by one principal component, the AMMI1 display of genotype nominal yields describes winning genotypes and adaptive responses more simply and clearly than the GGE2 biplot. For genotype evaluation within a single mega-environment, a simple scatterplot of mean and stability is more straightforward than the mean vs. stability view of a GGE2 biplot. Diagnosing the most predictively accurate member of a model family is vital for either AMMI or GGE, both for gaining accuracy and delineating mega-environments.

CONCLUSIONS

The AMMI and the GGE biplot analyses are more efficient than the Eberhart and Russell analysis.

The GGE biplot analysis explains a higher proportion of the sum of squares of the GxE interaction and is more informative with regard to environments and cultivar performance than the AMMI analysis.

In the 1998/1999 and 1999/2000 harvests, only two distinct mega-environments were formed, demonstrating the need for genotype evaluation of other harvests and further experiments performed under contrasting environmental conditions.

Comparação das análises multivariadas Biplot com o método de Eberhart e Russell na interação genótipo x ambiente

RESUMO - *O objetivo desse estudo foi comparar os métodos multivariados GGE (Genotype main effects and Genotype x Environment interaction) and AMMI (Additive Main effects and Multiplicative Interaction) com o método de Eberhart e Russell para a interpretação da interação genótipo x ambiente. As análises AMMI e GGE explicaram por volta de 50% da soma de quadrados da interação genótipo x ambiente, enquanto o método de Eberhart e Russell explicou somente 9,1 e 15,8% em cada ano. Os cultivares classificados com menor contribuição para a interação genótipo x ambiente pelos métodos AMMI e GGE também o foram pelo método de Eberhart e Russel. As análises AMMI e GGE são mais eficientes do que a análise de Eberhart e Russel. A análise GGE explica maior proporção da soma de quadrados da interação genótipo x ambiente e é mais informativa para o desempenho de cultivares e ambientes do que a análise AMMI.*

Palavras-chave: Interação genótipo x ambiente, melhoramento, GGE, *Zea mays*.

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