



Yield stability and adaptability of maize hybrids based on GGE biplot analysis characteristics

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ABSTRACT - The objective of this study was to evaluate stability and adaptability of the grain yield of commercial intervarietal maize hybrids by the GGE (Genotype and Genotype by Environment Interaction) biplot and AMMI (Additive Main Effects and Multiplicative Interaction) analyses. Two intervarietal hybrids (BIO 2 and BIO4) were evaluated together with single, double and three-way cross hybrids. The performance of the intervarietal hybrid BIO 4 was superior to all double and three-way cross hybrids and outmatched the single-cross hybrids by 43%. In terms of stability, BIO 2 was more stable than BIO4, which is desirable, but biological stability, which is not necessarily desirable, was also observed, since the yield was below the environmental mean. The graphical GGE biplot analysis was superior to the AMMI1 since a greater portion of the sum of squares of GE and G+GE was captured and the predictive accuracy was higher. On the other hand, the AMMI2 graph outperformed the GGE biplot in predictive accuracy and explanation of G + GE and GE, although the difference in accuracy was smaller than between GGE2 and AMMI1.

Key words: Intervarietal hybrids, AMMI, mega-environments.

INTRODUCTION

In Brazil, open-pollinated varieties (OPVs) of maize are still commonly used in family farming. This is a consequence of the high cost of hybrid seed, often making a purchase impossible for small farmers.

In view thereof, official institutions as well as private companies synthesize and/or breed new maize varieties to provide low-income farmers with productive, appropriate and stable varieties every year, at an affordable cost.

Among the alternatives to the OPVs are the intervarietal hybrids, derived from commercial single-cross hybrids in F₂ (Miranda Filho and Viégas 1987). The advantage of using intervarietal hybrids would be

the easy establishment, resulting in lower seed cost and greater adaptability, aside from the exploitation of heterosis, since only F₂ populations or populations in equilibrium of genotypic frequencies are recombined, to ensure the maintenance of heterosis.

The use of the F₂ generation of single to breed double-cross hybrids was recommended by Kiesselback, at the beginning of the 1930s (Souza Sobrinho et al. 2002). However, to date little research has been done to explore this technology. Some studies report that the yield performance of double F₂ hybrids can be as high as F₁ hybrids (Souza Sobrinho et al. 2002).

To recommend OPVs and/or hybrid cultivars, these genotypes must be evaluated in different environments

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to identify consistent and high-yielding genotypes. It is therefore essential to quantify the interaction of these genotypes with the environments in which they were assessed. The understanding of the causes of the genotype-by-environment (GE) interaction is extremely important because it can contribute to determine the breeding objectives, identify ideal test conditions and recommend regional cultivars with better adaptation (Yan et al. 2000).

Different methodologies have been developed and/or enhanced to evaluate adaptability and stability. These procedures are based on analysis of variance, linear regression or non-linear analysis, multivariate analysis, biplots and/or non-parametric statistics. Among the new statistical approaches proposed for the interpretation of GE interaction, based on the use of biplots, the AMMI (Additive Main Effects and Multiplicative Interaction) analysis stands out for the larger number of technical interpretations it provides (Duarte and Vencovsky 1999). AMMI interprets the effects of genotypes and environments as additive and the GE interaction as multiplicative, by principal component analysis. Yan et al. (2000) designated the AMMI biplot as "GE biplot".

More recently, a modification of the conventional AMMI analysis, proposed by Yan et al. (2000), called GGE biplot (Genotype and Genotype-Environment Interaction) has been used to study the GE interaction. The GGE analysis groups the genotype effect, which is an additive effect in the AMMI analysis, together with the GE interaction, multiplicative effect, and analyzes these effects by principal components. The main advantage of this technique over the AMMI analysis lies in the fact that the biplot always explains an intermediate proportion of the sum of squares of genotypes + genotypes by environments (G + GE), compared to the graphs AMMI1 and AMMI2 mega-environment, making the graphical representation of GGE more accurate than AMMI1 and more practical than AMMI2 mega-environment (Yan et al. 2007).

In the graphs AMMI1 and AMMI2 mega-environment (AMMI2 *), the genotype effect is embedded in the graphic analysis, that discriminates mainly AMMI2 * from the original biplot (AMMI2), in other words, these graphs become comparable with the GGE biplot in the definition of the mega-environments and determination of the which-won-where pattern (Yan

et al. 2007, Gauch et al. 2008). The incorporation of the genotype effects may be considered a useful strategy in the selection of superior genotypes to facilitate the selection of stable and productive plants, as well as paving the way for the recommendation of genotypes for environment groups.

The main issue raised by Gauch et al. (2008) concerning the GGE biplot analysis was that the advantages of the GGE biplot over the AMMI1 mega-environment must be questioned when the graphic analysis is charged with noise. They also claimed that, when this is not the case or in the absence of noise i.e. when the GGE biplot captures only G and GE patterns, this graphs still tends to retain a lower portion of G and GE than the AMMI2 mega-environment (Gauch et al. 2008). This statement was however questioned by Yan et al. (2007), mainly because AMMI2 * can not be considered a true biplot because it is based on artifacts (use of table-predicted means) to include genotype effects in the biplot.

The objective of this study was to evaluate the stability and adaptability of two intervarietal hybrids, in comparison with commercial hybrid cultivars (single, double and three way cross hybrids of lines) using the GGE biplot and AMMI methodology.

MATERIAL AND METHODS

The grain yield of 36 maize hybrids was evaluated, two of which were intervarietal, 22 single, three double and 10 triple-cross hybrids, for a total of 36 treatments.

The intervarietal hybrids were synthesized based on the best hybrid combinations identified by Balestre et al. (2008). According to on the results of these authors, the F₂ generations of four single-cross hybrids were established by self-pollination and later intercrossed to synthesize the intervarietal hybrids BIO 2 and BIO 4.

Hybrids BIO 2 and BIO 4 were compared with the single, double and triple-cross hybrids. These hybrids were evaluated at 19 locations, treated here as environments, across the state of Minas Gerais (Table 1).

A complete randomized block design with three replications was used. The plots consisted of two 4 m rows where 450 kg ha⁻¹ of NPK fertilizer (8-28-16) was applied at sowing and 100 kg ha⁻¹ nitrogen as sidedressing.

Table 1. Means of grain yield (t ha⁻¹), codes of the GGE biplot graphic analysis and principal components (PC 1 and PC 2) used in the construction of the biplot analysis based on the evaluation of 36 maize genotypes, in 19 environments of the state of Minas Gerais

Code	Environments	State	Yield	PCA 1	PCA 2
S1	Água Comprida	MG	9,8166	0.62552	1.0707
S2	Boa Esperança	MG	7,317	0.99378	-0.0470
S3	Campo Florido	MG	9,153	1.27645	0.1157
S4	Capinópolis	MG	6,826	0.64756	0.1397
S5	Conquista	MG	10,546	0.99192	0.2214
S6	Indianópolis	MG	6,310	1.05537	-1.4336
S7	Lavras - UFLA	MG	10,468	1.46578	0.3673
S8	Oratórios - EPAMIG	MG	10,587	0.91143	0.7676
S9	Paracatu	MG	6,602	1.22875	1.2805
S10	Patos de Minas - Biomatrix	MG	9,639	1.1950	-1.4393
S11	Patos de Minas - EPAMIG	MG	9,377	0.8543	-0.0599
S12	Patos de Minas-Faz. Recanto	MG	7,582	1.2819	0.0079
S13	Porto Firme	MG	11,292	1.0137	0.8313
S14	Rio Paranaíba	MG	9,143	2.0702	-0.0655
S15	S. Sebast. do Paraíso-EPAMIG	MG	12,252	1.8723	-0.5452
S16	Sete Lagoas - EMBRAPA	MG	8,104	1.2229	0.5457
S17	Três Pontas - EPAMIG	MG	7,793	1.3102	0.1622
S18	Uberaba	MG	8,672	1.1059	-0.0532
S19	Uberlândia	MG	4,133	0.5609	0.3815

The combined analysis was performed according to Ramalho et al. (2000) and the means served as basis for the AMMI analysis, considering the following model:

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

where: Y_{ij} is the mean response of genotype i in environment j ; μ is the overall mean; G_i is the genotype effect; E_j is the environmental effect; GE_{ij} is the multiplicative component (GE interaction effect)

modeled by $\sum_{k=1}^n \lambda_k \gamma_{ik} \alpha_{jk} + \rho_{ij} + \varepsilon_{ij}$, where λ_k is the k^{th} singular of the matrix of original interactions (GE); γ_{ik} is the element corresponding to the i^{th} genotype on the k^{th} singular vector of the GE matrix column; α_{jk} is the element corresponding to the j^{th} environment on k^{th} singular vector of the GE matrix row; ρ_{ij} is the noise associated with expression $(ga)_{ij}$ not explained by the principal components; and ε_{ij} is the associated error.

To verify how far the GGE biplot method is able to explain the genotype (G) and interaction (GE) effects, compared with AMMI1 and mega-environment AMMI2, the GGE biplot analysis was performed considering the simplified model for two principal components:

$$Y_{ij} - y_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

where: Y_{ij} is the mean yield of cultivar i in environment j ; y_j is the mean of environment j ; $\lambda_1 \xi_{i1} \eta_{j1}$ is the first principal component (PC1); $\lambda_2 \xi_{i2} \eta_{j2}$ is the second principal component (PC 2); λ_1 and λ_2 are the eigenvalues associated with the components PCA1 and PCA 2; ξ_{i1} and ξ_{i2} are scores of the axes PC 1 and PC 2 for genotype effects; η_{j1} and η_{j2} are the scores of the axes PCA 1 and PCA 2 for environment effects; and ε_{ij} is the error associated with the model.

All analysis and biplot constructions were performed using the computer package SAS with IML (Interactive Matrix Language) and SAS GRAPH (SAS Institute 2000).

The efficiency in retaining most of the sum of squares of the effects of GE as well as G + GE of the graphs AMMI1, AMMI2 * and GGE biplot was compared.

For this purpose the sum of squares of G of GE contained in the PC 1 and PC 2 of the GGE biplot was partitioned as suggested by Gauch et al. (2008), by the following expression:

$$SSG = trace(a_1 b_1' K K b_1 a_1') + trace(a_2 b_2' K K b_2 a_2')$$

$$SSGE = trace(a_1 b_1' P P b_1 a_1') + trace(a_2 b_2' P P b_2 a_2')$$

where: SSG and SSGE are the sums of squares of G and GE contained in the first two principal components of

GGE2; a_1 , a_2 and b_1 , b_2 are the first two scores for G and E respectively; K is the matrix of phenotypic means distributed along the k^{th} column; and $P = I - K$, where I is the identity matrix contained in the singular value decomposition (SVD) of $G + GE$.

The graphic accuracy of the identification methods of mega-environments and winner genotypes was tested by the cross-validation procedure proposed by Gabriel (2002). For this purpose the statistics PRESS and PRECORR were used that measure the discrepancy between the observed and predicted value and the predictive correlation (Dias and Krzanowsky 2003).

RESULTS AND DISCUSSION

The summary of the combined analysis of variance (Table 2) showed that all sources of variations were significant by the F test. These results demonstrate the existence of environmental heterogeneity and also indicate significant differences between the genotypes, since their responses were not coincident in the test environments.

It was observed that the intervarietal hybrid BIO 4 performed better than all double and three-way cross hybrids and outperformed 43% of the single-cross hybrids (Table 3). On the other hand, the performance of hybrid BIO 2 was not satisfactory, compared to the other double and triple-cross hybrids.

In a similar study with double F_1 hybrids and their respective double intervarietal hybrids (F_2 hybrids), Souza Sobrinho et al. (2002) observed no significant yield difference among the hybrids, with regard to their origin (F_1 and F_2). However, Velasques (1969) and Marinque and Nevado (1970), cited by Sánchez (1988), observed a small difference (5%) between the response of double-cross hybrids and F_1 and F_2 .

The adaptability and stability of hybrid grain yield was analyzed (Figure 1). In the GGE biplot analysis, the first principal component (PC 1) indicates the genotype

adaptability, i.e., adaptability is highly correlated with yield (Yan et al. 2000). In this sense, it was observed that the single-cross hybrid 36 was the most adapted to the network of evaluation sites, followed by single-cross hybrid 29. The second principal component (PC 2) indicates the phenotypic stability, i.e., the genotypes with PC 2 closest to zero would be the most stable genotypes (Yan et al. 2000), ranking the hybrids in decreasing order of stability: 34, 22, 31, 24, and 17. In this case, the single-cross hybrids 24, 36 and 13 were identified as ideal genotypes for recommendation, because the yields of these genotypes were high (and high positive PC 1) and the stability good (PC 2 near zero).

According to Allard and Bradshaw (1964), the heterogeneity is lower in single hybrids than in double-cross hybrids, so the population homeostasis of the latter is higher. Comparing the ideal with the most stable genotypes, it was observed that single hybrids can be bred that are as stable as double and triple-cross hybrids. An example is the single-cross hybrid 24, which ranked fourth in stability index, i.e., it can be considered a highly stable genotype. Similar results were observed by other authors (Carvalho et al. 2005, Machado et al. 2008). Moreover, the performance of the most stable double and three-way cross hybrids, as well as all others with this genetic structure, was below the environmental mean (low PC 1). A characteristic of the performance of these hybrids was biological stability, in other words, more stable genotypes with normally low yields. According to Cruz and Carneiro (2003) this is not advantageous for breeding programs aiming at stable and productive hybrids.

These results indicate that intervarietal hybrids do not fit in the group of ideal genotypes, in other words, the yield of hybrid BIO 4 was good (high PC 1 score), but not very stable (high PC 2 score), whereas the performance of genotype BIO 2 was characteristic of hybrids with biological stability (low PC 1 and PC 2 scores), which limits the recommendation of this genotype. This result demonstrates that the GGE biplot technique is efficient to identify productive and stable genotypes in a single analysis. However, although these intervarietal hybrids were discarded as ideal genotypes for recommendation in the tested environments, their performance is comparable to that of the double and triple-cross hybrids. In this case, hybrid BIO 4 would be the ideal genotype, since it was the only one with a performance above the

Table 2. Summary of the combined analysis of variance for the trait grain yield in the evaluation of 36 maize genotypes in 19 environments of the state of Minas Gerais

Source of variation	df	SS	MS
Locations	18	7693.57	427.421**
Genotypes	35	2036.61	58.189**
Genotypes x Environments	630	1521.36	2.415**

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

environmental mean and more stable than some single-cross hybrids; that is, the yield of BIO 4 was higher than of the 23 hybrids evaluated in this study.

The GGE method, besides the genotype analysis, also allows the analysis of environments. Accordingly, the PC 1 axis indicates the environments with greater capacity for discrimination of genotypes, and the PC 2 axis, the most representative environments of the group (Yan et al. 2000). The conclusion can be drawn that S14

(Rio Paranaíba), São Sebastião do Paraíso and Paracatu, are environments that discriminated the genotypes more clearly (higher PC 1). On the other hand, the most representative environments of the set were Patos de Minas (Fazenda Recanto), followed by Boa Esperança and Uberaba (Figure 1). The environments with the highest means were São Sebastião do Paraíso and Porto Firme, with 12,252 t ha⁻¹ and 11,292 t ha⁻¹, respectively.

Table 3. Mean grain yield (kg ha⁻¹) and principal component analysis of the GGE biplot in the evaluation of 36 maize genotypes in 19 environments of the state of Minas Gerais

Code	Genotype	Genetic structure	Prod.	PCA 1	PCA 2
36	DOW 2B707	SH	10464 a	1.499	-0.193
29	BM 709	SH	10452 a	1.474	-0.417
11	PLEX 6410	SH	10282 a	1.352	-0.346
24	RB 9108	SH	10220 a	1.376	-0.024
14	PLEX 1103	SH	10118 a	1.283	-0.366
13	30F35	SH	9808 a	0.946	0.107
15	HS7262	SH	9743 a	0.877	0.962
26	AS1567	SH	9605 a	0.790	1.630
19	HS7338	SH	9582 a	0.781	-0.184
21	BM 502	SH	9491 a	0.636	0.395
27	DOW 2B587	SH	9472 a	0.628	-0.330
9	IMPACTO	SH	9193 a	0.387	-0.366
5	BIO 4	HI	9070 a	0.335	-0.811
33	AS1577	SH	9010 a	0.231	0.084
6	AS1592	SH	8816 b	0.162	0.570
28	BX 1382	SH	8807 b	0.107	0.967
10	XB 6012	SH	8752 b	0.045	0.353
35	DKB455	TH	8710 b	-0.037	-0.203
16	RB 9308	DH	8661 b	-0.067	-0.633
8	CMS2C17EC	TH	8539 b	-0.086	-0.645
22	PZ242	TH	8432 b	-0.292	-0.011
4	AS1540	SH	8429 b	-0.320	0.293
3	CMS2C18EC	TH	8387 b	-0.210	-0.294
18	AGN20A06	TH	8237 b	-0.417	-0.449
30	XGN 7361	SH	8178 b	-0.476	-0.471
2	XGN 7266	TH	8071 b	-0.550	-0.762
25	XGN 6110	SH	8057 b	-0.570	0.067
7	XGN 6311	SH	7966 b	-0.662	0.086
23	BIO 2	HI	7958 b	-0.679	0.159
32	XB 7110	TH	7802 b	-0.812	0.409
34	XBX 63511	TH	7752 b	-0.869	-0.002
20	XBX 72632	TH	7504 b	-1.106	0.481
12	XB 7116	TH	7446 b	-1.092	0.248
1	XGN 7320	SH	7378 b	-1.160	-0.318
17	PZ 677	DH	6892 b	-1.597	0.034
31	XB 8010	DH	6528 b	-1.903	-0.019
Means			8717		

The measures followed by the same letter do not differ from each other at 5% probability (Scotti-Knott)

SH- Single-cross hybrid; DH- double hybrid; TH- three-way cross hybrid; HI- intervarietal hybrid; OPV- Open-pollinated variety

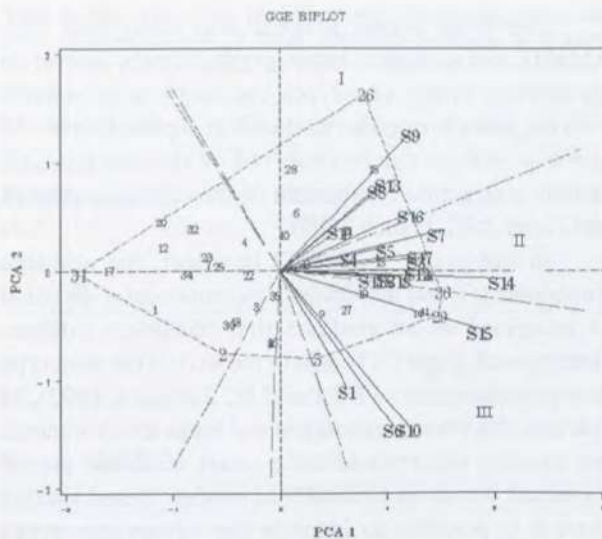


Figure 1. GGE biplot of 36 maize genotypes evaluated at 19 locations in the state of Minas Gerais. The codes I, II and III correspond to the mega-environments at the 19 identified sites

The formation of three mega-environments, that is, environments defined by winner genotypes, is shown in Figure 1. These genotypes are located on the borders of the polygons, and the mega-environments are separated by lines perpendicular to the polygon. The genotypes 26, 36 and 29 determine the mega-environments I, II and III, respectively; i.e., the genotypes are recommended for environments included within each mega-environment. In mega-environment III the environments of Patos de Minas (Biomatrix) and Indianapolis were quite distinct from the others (high PC 2 values). This indicates that these environments contributed most to the GE interaction, and were therefore recommended for studies of stability and adaptability, even within megaenvironment III.

In a more detailed trial analysis, environments with the same GE response pattern can be discarded. For example, in future evaluations it would make no sense to use the environments Oratório and Porto Firme of mega-environment I simultaneously, because the genotype response and GE interaction in these environments were similar. This resulted in practically identical positions in the graph (Figure 1). The same is true for the environments Patos de Minas (Biomatrix) and Indianapolis in mega-environment III, and for six environments in mega-environment II (S2, S3, S11, S12, S17 and S18). This result demonstrates the ease of environmental analysis by the GGE biplot method since

environments with the same pattern of genotype response and similar pattern of GE interaction are eliminated.

The grain yield of hybrid BIO 4 was good, but stability not satisfactory (Figure 1). However, the GGE biplot can identify the best environments for this genotype (Figure 2). In this case, we can infer that the best environments for this genotype recommendation would be Patos de Minas (Biomatrix), Indianópolis, São Sebastião do Paraíso, and Água Comprida. Moreover, the stability of hybrid BIO 2 was good (the 10th best index) and it was more stable than BIO 4; nevertheless, the performance was below the environmental mean, and the mean grain yield was lower than of six of the most stable genotypes, exceeding only the genotypes 17, 31 and 34 (Figure 1). This result shows that the yield of genotype BIO 2, although stable, was not satisfactory (Figure 1).

The GGE biplot analysis indicates in which environments genotypes of interest perform best. In this case, a line is drawn between the two genotypes to be compared and by a line perpendicular to the first, which passes through the origin of the graph, this comparison is possible. Genotype 36, for example, outperformed hybrid BIO 4 in all test environments (Figure 3).

In recent years, several studies have been conducted comparing GGE biplot and AMMI (Yan et al. 2007, Gauch et al. 2008). The GGE biplot method has proved superior to AMMI analysis in several aspects and has therefore been used in a number of studies of genotype stability and adaptability and to group environments (Ma et al. 2004, Voltas et al. 2004). Among these aspects, we can cite the higher proportion of the sum of squares of G + GE retained in the graphic analysis of the GGE biplot method compared to AMMI (Ebdon and Gauch 2002, Yan et al. 2007, Gauch et al. 2008), resulting, in most cases, in a greater graphic accuracy of identification of mega-environments and winner genotypes. Moreover, according to Yan et al. (2007) the graphic analysis of the GGE biplot is more practical than of megaenvironment AMMI 2, in other words, there is no need to use artifacts to include G + GE to identify megaenvironments and winner genotypes.

The recovery of the sum of squares of genotypes (G) and genotype by environment (GE) contained in the methods AMMI1, AMMI2* and GGE2 is represented in Table 4. The GGE biplot method explained much of the

sum of squares G + GE in the first two principal components. Apart from this result, the GGE biplot analysis outperformed the model AMMI 1, by retaining more of the sum of squares of GE and G + GE, which exceeded 13.74% in the explanation of GE, and 5.78% in the explanation of G + GE. The same result was obtained in several other studies (Yan et al. 2000, Ma et al. 2004, Samonte et al. 2005, Yan et al. 2007, Gauch et al. 2008).

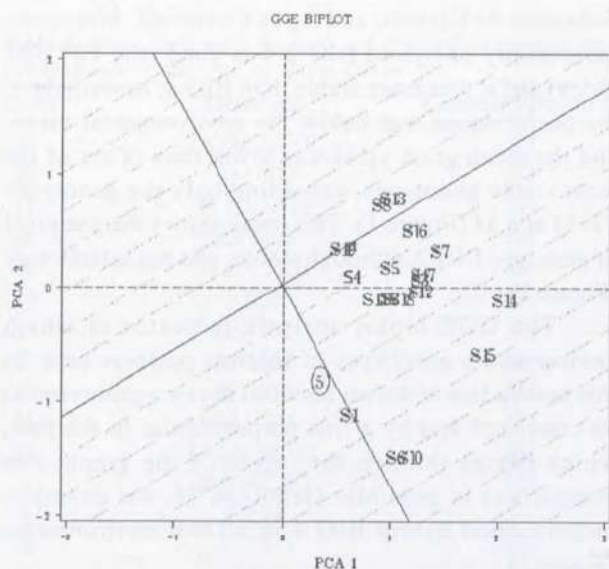


Figure 2. Biplot of the best environments for hybrid BIO 4, considering the 19 locations in the state of Minas Gerais

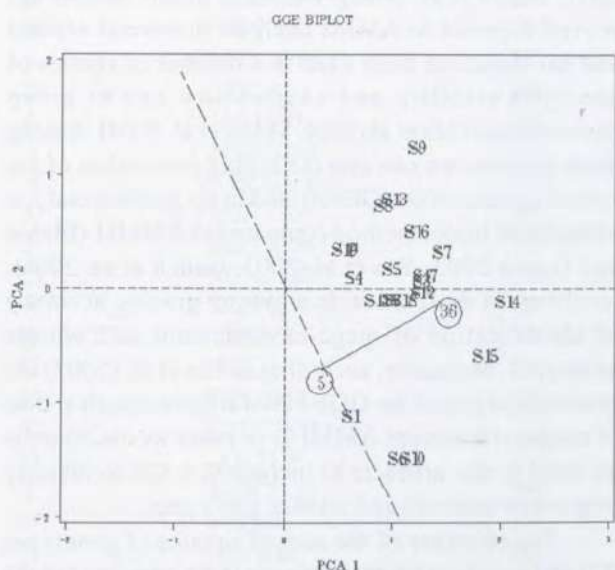


Figure 3. Biplot of a comparison of the performance of the genotypes 5 (BIO 4) and 36 (DOW 2B707), at 19 locations in the state of Minas Gerais

The GGE biplot graphic was compared with AMMI1 because this latter graph is very useful in identifying winner genotypes and mega-environments with the same properties as the GGE biplot, that is, the genotype effects can be observed on the abscissa axis and the interaction component on the ordinates (Gauch and Zobel 2002, Gauch 2006).

In the graph * AMMI2 however, the additive component (G) and multiplicative component (GE) could be imagined as an analysis that considers a three-dimensional graph (3D), where the axis of the genotype runs perpendicular to PC 1 and PC 2 (Gauch 1992). In practice, the winner genotypes and mega-environments are usually determined by a chart with the means corrected based on the AMMI2 model. Based on this chart it is possible to identify the winner genotypes and overlie these genotypes in the mega-environment AMMI 2 biplot, i.e., it is possible to incorporate the additive genotype effect in the AMMI biplot without the need of an additional axis (Gauch et al. 2008).

In this case, the graph mega-environments AMMI 2 captured both GE and G. However, the graphical analysis depends on an artifact (use of a table) which, according to Yan et al. (2007), makes the graphic AMMI2 * a conclusive analysis rather, than a direct product of the biplot.

The GGE biplot analysis explained almost the same proportion of GE and G + GE compared with the model megaenvironment AMMI2 (Table 4). According to Gauch et al. (2008), the retention of G + GE in the graphic analysis follows the rule: AMMI1 <GGE2 <AMMI2. However, in this study, the GGE biplot method retained almost the same proportion of GE and G + GE as AMMI 2 in a simple and direct graphical analysis without the use of artifacts such as tables.

The main question raised by Gauch (2006) addressed the fact that the greatest explanation of G + GE by the GGE biplot compared with AMMI1 * did not always result in the greatest graphical accuracy. This is because if GGE2 contains noise, the graphical accuracy of AMMI1, despite retaining lower G + GE, will be greater. On the other hand, if the more accurate model is GG3, G GG4 and so on, or/and AMMI3, AMMI4 and so on, the graph GGE will be less accurate than AMMI2 * because it will contain a lower proportion of G + GE and consequently capture a lower pattern of G + GE (see Ockham's razor or principle of parsimony). So, according to Gauch et al. (2008), the biplot GGE2 will only be superior to the AMMI plot * if the flat peak of "Ockham's Hill" is around AMMI1 and AMMI2.

Table 4. Recovery of the sum of squares of genotypes (SS_G) and GE interaction (SS_{GE}), methods AMMI1, AMMI2 and GGE2 based on grain yield (kg ha^{-1}) of 36 maize genotypes evaluated in 19 environments of the state of Minas Gerais. In the first principal component (PC1) of the AMMI1 graph, the additive effects of G and E were used; it was therefore assumed that this PC retained 100% of the additive effects

Model and axis	Genotype (SS_G)	% SS_G	Interaction (SS_{GE})	% SS_{GE}	PRESSm	PRECORR
AMMI 1					0.7718	0.9279
Principal	2036.61	100	0.0	0		
PC1	0	0	261.378	17.18		
Sum	2036.61	100	261.378	17.18		
%G+GE	64.58					
AMMI 2					0.7187	0.9322
PC1	0.0	0	261.378	17.18		
PC2	0.0	0	250.295	16.45		
Sum	0.0	0	511.673	33.63		
Means AMMI 2*	2036.61					
%G+GE	71.62					
GGE2					0.7394	0.9301
PC1	2036.11	99.8	216.93	14.26		
PC2	0.00174	0.01	253.41	16.66		
Sum	2036.13	99.9	470.34	30.92		
%G+GE	70.36					

* Graph of megaenvironment AMMI 2 captures 100% of the genotype effects by the use of charts, so no additional axes are needed (Gauch et al. 2008)

In this study, the results of cross validation confirmed that the GGE2 biplot was superior to AMMI1, since the prediction sum square (PRESSm) was lower and the correlation of prediction higher, confirming the greater graphical accuracy as also indicated by the higher proportion of G + GE (Table 4). On the other hand, the prediction error was greater and the correlation lower when compared with AMMI2*, which had also been expected by the sum of squares of GE or G + GE retained in the graphics.

Although the advantage in accuracy of GGE2 over AMMI1 was greater than of AMMI2* over GGE2, it should be noted that the graph AMMI2* was superior and also chosen as best model by cross validation. The question may arise whether this difference in accuracy of AMMI2* to GGE compensate for the graphical facilities of the GGE biplot method, since as pointed out above the original AMMI2 informs only about GE, whereas AMMI2*, based on the inclusion of genotype effects, contributes to identify mega-environments and winner genotypes, but requires the use of predicted means to incorporate the G effect in the graph.

Another interesting result, although not shown, is that the GGE1 model was more predictive than AMMI1*, i.e., although it explains a lower proportion of GE

and G + GE it reached a PRESSm of 0.7515 and PRECORR of 0.929, which may indicate that the decomposition of the G + GE effects together can increase the graphical accuracy. On the other hand, since the best model was the GGE2 and the difference in GE explained by the method was close to the method AMMI2 one could expect that this method would be more accurate, which was not the case. The gain in accuracy of GGE2 compared to AMMI1 was however greater than the gain of AMMI2 compared to GGE2, as also observed by Dias and Krzanowsky (2003).

Based on the results presented in this study, it was concluded that the intervarietal hybrids BIO 4 and BIO 2 were not identified as ideal genotypes by the GGE biplot analysis, although the GGE biplot analysis classifies these genotypes as productive or stable, respectively.

It was possible to identify single-cross hybrids as stable as double hybrids, but it was not possible to identify double and three-way cross hybrid that outperformed the overall mean.

The GGE biplot analysis was superior to the graph AMMI1 mega-environment for being more efficient in explaining the sum of squares of GE and G + GE, as confirmed by its greater predictive accuracy.

The proportion of G + GE in the graph AMMI2 mega-environment was greater and the predictive accuracy higher than in GGE2, but the fact that artifacts are needed to incorporate the genotype effect in the graph AMMI2 may not compensate for its advantage in accuracy, considering the relative accuracy of the GGE2 over AMMI1.

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Estabilidade e adaptabilidade produtiva de híbridos de milho utilizando a análise GGE biplot

RESUMO - O objetivo deste trabalho foi avaliar a estabilidade e adaptabilidade da produtividade de grãos de híbridos intervarietais de milho, em relação a cultivares híbridas comerciais utilizando-se a metodologia GGE biplot e AMMI. Foram avaliados dois híbridos intervarietais (BIO 2 e BIO4), juntamente com híbridos simples, duplos e triplos. O híbrido intervarietal BIO 4 apresentou melhor desempenho que todos os híbridos triplos, duplos e foi superior a 43% dos híbridos simples. Quanto à estabilidade, o híbrido BIO 2 foi mais estável que o híbrido BIO4, porém, apresentou estabilidade biológica, pois obteve produtividade abaixo da média ambiental. O método gráfico GGE biplot foi superior ao gráfico AMMI1, pois captou maior porção do soma de quadrados de GE e G+GE e obteve maior acurácia preditiva. Por outro lado, o gráfico AMMI2 foi superior ao GGE biplot em acurácia preditiva e explicação de G+GE e GE, porém diferença de acurácia foi menor quando comparada à acurácia do GGE2 em relação ao AMMI1.

Palavras-chave: Híbridos intervarietais, AMMI, mega-ambientes.

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