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Domingos Garbuglio, Deoclécio; Furtado Ferreira, Daniel; de Araújo, Pedro Mário; Gerage, Antonio Carlos; Sentaro Shioga, Pedro
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Comparison of multivariate methods for studying the G×E interaction

Comparação de métodos multivariados para estudo da interação G×A

Deoclécio Domingos Garbuglio[1*]; Daniel Furtado Ferreira[2];
Pedro Mário de Araújo[1]; Antonio Carlos Gerage[1]; Pedro Sentaro Shioga[1]

Abstract

The objective of this work was to evaluate three statistical multivariate methods for analyzing adaptability and environmental stratification simultaneously, using data from maize cultivars indicated for planting in the State of Paraná-Brazil. Under the FGGE and GGE methods, the genotypic effect adjusts the G×E interactions across environments, resulting in a high percentage of explanation associated with a smaller number of axes. Environmental stratification via the FGGE and GGE methods showed similar responses, while the AMMI method did not ensure grouping of environments. The adaptability analysis revealed low divergence patterns of the responses obtained through the three methods. Genotypes P30F35, P30F53, P30R50, P30K64 and AS 1570 showed high yields associated with general adaptability. The FGGE method allowed differences in yield responses in specific regions and the impact in locations belonging to the same environmental group (through r_E) to be associated with the level of the simple portion of the G×E interaction.

Key words: Multivariate analysis, factor analysis, genotypic effect, maize

Resumo

O objetivo deste trabalho foi avaliar três métodos estatísticos multivariados, para análise de adaptabilidade e estratificação ambiental simultaneamente, utilizando dados de cultivares de milho indicadas para cultivo no estado do Paraná. Nos métodos GGE e FGGE, o efeito genotípico atuou como um coeficiente de ajuste das interações G×A ao longo dos ambientes, implicando em altos porcentuais de explicação, associados a um menor número de eixos. A estratificação ambiental pelos métodos GGE e FGGE apresentou respostas similares, enquanto pelo método AMMI não houve garantia de agrupamento de ambientes. As análises de adaptabilidade apresentaram poucas divergências de resposta, pelos três métodos. Os genótipos P30F35, P30F53, P30R50, P30K64 e AS 1570 apresentaram altas produtividades associadas à adaptabilidade geral. O método FGGE permitiu associar as diferenças de respostas de produtividade entre determinados conjuntos de ambientes e o impacto em localidades pertencentes ao mesmo conjunto ambiental (através de r_A), com o auxílio do nível de porção simples atuante da interação G×A.

Palavras-chave: Análise multivariada, análise de fatores, efeito genotípico, milho

[1] Pesquisadores, Instituto Agronômico do Paraná, IAPAR, Londrina, PR, Brasil. E-mail: ddgarbuglio@iapar.br; pmaraujo@iapar.br; milhoger@iapar.br; shioga@iapar.br.
[2] Prof., Universidade Federal de Lavras, UFLA, Lavras, MG, Brasil. E-mail: danielff@dex.ufla.br
[*] Author for correspondence

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Introduction

Final trials among cultivars are conducted annually throughout the world in a wide range of environments for various breeding companies and seed producers, both private and public. The key point is to identify superior cultivars in terms of productivity, combined with a wide adaptability and high stability of this production in the face of environmental fluctuations, which are increasingly common in new agricultural scenarios.

It is also important to understand the behavior of these cultivars in certain agricultural regions of interest and to determine whether these regions can be subdivided into different mega-environments (YAN et al., 2000) or sub-regions that are more uniform, excluding any significant GE interactions. Alternatively, in some situations, the goal may be to exclude a significant interaction with the predominance of a simple part, i.e., not interfering with the recommendation of cultivars.

There are several methods aimed at evaluating G×E interactions, and the choice of method will depend on the experimental data, especially the number of environments available, the required accuracy and the type of information desired. In recent years, multivariate techniques have gained importance in this type of study, due to the widespread use of computers and modern statistical packages that allow calculations involving complex matrix algebra and linear models to be performed in seconds.

One such method, referred to as AMMI, considers additive models for the main effects (genotypes and environments) and multiplicative models for the G×E interaction effects (CROSSA et al., 1990). Thus, the average response of a genotype (*i*) in an environment (*j*) is given by the following equation:

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^{n} \lambda_k \gamma_k \alpha_k + \rho_j + \varepsilon_j ,$$

with $(ge)_{ij}$ being modeled by $\sum_{k=1}^{n} \lambda_k \gamma_{ik} \alpha_{jk} + \rho_{ij} + \varepsilon_{ij}$. Under identifiability restrictions, in addition to the general mean (μ) and the average experimental error (ε_{ij}), the remaining terms of the model result from the called singular value decomposition (SVD) of the matrix of interactions: $GE_{(gxe)}=[(g\hat{e})_{ij}]$ (DUARTE; VENCOVSKY, 1999).

Another multiplicative method that is gaining popularity is referred to as the SREG – GGE Biplot. The multiplicative model SREG (CROSSA; CORNELIUS, 1997) is similar to the AMMI model in relation to the modeling of G×E interactions, with the difference that the main effects of genotypes are considered along with the effect of G×E interactions, which in AMMI, are estimated as additive effects (YAN et al., 2000). Thus, the biplot originated through this method contains genotypic effects added to G×E interaction effects and is therefore referred to as a GGE biplot, differing from the AMMI method, in which the biplot is based on the SVD of G×E matrix interactions and can be termed a GE Biplot.

The factor analysis technique is similar to the principal components technique, in the sense that both are proposed to study the structure of covariance or correlations in populations (FERREIRA, 2008). However, a full explanation of covariances or correlations in a principal components analysis is performed using all latent variables, whereas in a factor analysis, it is possible to explain all covariances or correlations using only a few unobservable or latent variables, which are referred to as factors (FERREIRA, 2008).

The originally proposed technique considered a matrix of phenotypic means as the input, which can lead to erroneous inferences, due either to the adaptability of cultivars, as in the process of environmental stratification, or to the noise present in the G×E interaction. This principle also implies a large number of factors, depending on the nature of the variables to be considered in grouping.

The proposal derived from the factor analysis, referred to as FGGE by Garbuglio and Ferreira (2015), considers a matrix containing the genotypic

effects added to the G×E interaction effects as the input, thereby seeking to improve the efficiency of the process of factoring, aimed at environmental stratification and the analysis of adaptability through a reduction of the noise present in the G×E interaction.

The aim of this study was to compare three multivariate statistical methods for the analysis of adaptability and environmental stratification simultaneously using data from maize cultivars that are suitable for cultivation in the State of Paraná, Brazil.

Materials and Methods

In this study, data from fifteen maize cultivars suitable for cultivation in the state of Paraná were used. These cultivars included nine single-cross hybrids (AS 1570, AS 1575, DOW 2A525, DOW 2B710, AG 8021, P30F35, P30F53, P30K64 and P30R50), four three-way hybrids (BM 1120, DKB 566 and SHS 5070) and two two-way hybrids (IPR 119 and SHS 4050). The data used in the analyses were related to variable grain yields (corrected to 14% moisture and converted to $kg.ha^{-1}$) and were obtained from experiments conducted in a randomized block design, with three replications per environment. The experimental plots consisted of two rows, 5 m in length, with 80 cm between the rows, retaining 25 plants per row after thinning. The environment was considered to be the combination of the crop season and location. Thus, from the combination of the five study locations (Londrina, Campo Mourão, Wenceslau Braz, Ponta Grossa and Pato Branco) and two crops (2005/2006 and 2006/2007), ten environments were obtained (E1, E2,..., E10).

After individual and joint analyses of variance, multivariate analyses were performed, with an emphasis on adaptability and environmental stratification, using the SREG GGE-Biplot (YAN et al., 2000), AMMI (ZOBEL et al., 1988) and FGGE (GARBUGLIO; FERREIRA, 2015) methods.

The multiplicative SREG (sites regression) model is similar to the model used in the AMMI method, an noted previously. The mean of one genotype (i) in an environment (j) is commonly described by a linear model: $Y_{ij} = \mu + g_i + e_j + \phi_j$, wherein μ is the overall average; g_i is the additive effect of genotypes; a_j is the additive effect of the environment; and f_{ij} is the interaction effect between genotype i and environment j. The exclusion of g_i and/or a_j, or the group $\mu + g_i + e_j$ allows the variance explained by the excluded terms to be absorbed into f_{ij}; in other words, using only the component f_{ij} in SVD, without exclusions, results in the AMMI model.

In the GGE-biplot, the SREG model is employed, which his obtained after removal of the component g_i and submitting f_{ij} to DVS (YAN et al., 2000). Hence,

$$\phi_{ij} = Y_j - \mu - e_j = \sum_{n=1}^{r} \xi_{in}^{*} \eta_{jn}^{*} ,$$

where $\xi_{in}^{*} = \lambda_n^{0.5} \xi_{in}$ and $\eta_{jn}^{*} = \lambda_n^{0.5} \eta_{jn}$ are used to obtain symmetrical scale scores between genotypes and the environment to construct the biplot. Within the model, λ_n is the singular value of CP_n (principal component "n"), where the squared value corresponds to the sum of squares explained by CP_n, and ξ_{in} and η_{jn} are the scores of the i-th genotype and j-th environment for PC_n.

The FGGE model obtained from a matrix containing gi effects added to the $ge_{(ij)}$ effects, which are estimated factors that, when combined linearly, explain each variable, was used here. The factorial model (FGGE) is given by the following equations:

$$x_1 = \ell_{11} F_1 + \ell_{12} F_2 + \ldots + \ell_{1m} F_m + \varepsilon_1$$

$$x_2 = \ell_{21} F_1 + \ell_{22} F_2 + \ldots + \ell_{2m} F_m + \varepsilon_2$$

$$x_h = \ell_{h1}F_1 + \ell_{h2}F_2 + ... + \ell_{hm}F_m + \varepsilon_h$$

$$\text{or } x_j = \sum_{k=1}^{m} \ell_{jk}F_k + \varepsilon_j$$

for m<h, where ℓ_{jk} is the factor loading for the j-th variable associated with the k-th vector; F_k is the k_{th} common factor; and ε_j is the specific factor associated with the j-th variable, where h = p for genotypes and h = q for environments. In the application of factor analysis in studies addressing adaptability and environmental stratification, it should be noted that $X_1, X_2 ... X_h$ represents a single variable, such as the yield, but evaluated in each *j* environment in which the genotypes were assessed, or for *i* genotypes related to environment *j*. Thus, the effects of the genotypes added to the genotype x environment effects were used as variables. In this case, the genotypes or environments, relative to the values of this sum, represented the variable h.

For environmental stratification, grouping of environments was conducted based on the information about the magnitude of the final factor loadings obtained after rotations. Factor loadings with an absolute value greater than or equal to 0.70 indicated environments with high correlations, which were grouped within the same factor. Final factor loadings with low values (≤ 0.50) indicated that the associated environment should not belong to the group. Factor loadings with intermediate values did not guarantee any grouping definition.

The adaptability analysis based on factor analysis was performed graphically using the scores in relation to the factors. Quadrants II and IV included those genotypes showing specific adaptability to the region determined by the factor. Quadrants I contained the genotypes with broad adaptability, and quadrant III comprised the poor genotypes, which showed low performance and were capable of discharge or were not suitable for cultivation.

In situations where only two factors were sufficient to explain more than 80% of the total variation, determining only two sub-regions, the adaptability analysis was based on information from a single graph. However, values above 70% were sufficient to explain the identified variation, as indicated by other authors using different multivariate techniques (GARBUGLIO et al., 2007; RAMOS et al., 2009; YAN et al., 2000; ZOBEL et al., 1988). Nevertheless, there are no studies demonstrating what occurs in grouping environments, due to the reduction of the percentage of variation to determine the final number of factors. Thus, for the grouping of environments, it was considered that the final number of factors would be equal to the number of eigenvalues corresponding to at least 80% of the variation, while for the adaptability analysis, the factors were used to represent 70% of the variation.

Results and Discussion

AMMI method

The G×E interaction was significant at a 1% probability (Table 1), in other words, genotypes showed different responses across the evaluated environments, which can hamper the recommendation of cultivars for the region covered by this study.

Table 1. Mean squares obtained via analysis of variance, with unfolding of the G×E interaction through the original AMMI method.

SV	DF	[(a)]MS	F_G	DF	[(a)]$MS_{AMMIres}$	F_R
Genotype	14	2846.7	**			
Environment	9	6253.6	**			
G × E	126	179.85	**			
IPCA-1	22	114.28	**	104	48.46	**
IPCA-2	20	86.13	**	84	39.49	**
IPCA-3	18	59.08	**	66	34.14	
IPCA-4	16	52.01	*	50	28.42	
IPCA-5	14	43.27		36	22.65	
IPCA-6	12	28.5		24	19.73	
IPCA-7	10	25.28		14	15.76	
IPCA-8	8	24.46		6	4.16	
IPCA-9	6	4.16		0	0	

[(a)]: MS x 10^4

AMMI analysis is expected to capture most of the structural pattern of $SS_{G\times E}$ in the first components. In agreement with the AMMI model, the original G×E interaction could be decomposed into nine components (matrix rank G×A), among which the first four components were highly significant ($p<0,01$). According to the Gollob rule, which would lead to the choice of model AMMI4, alluding to the fact that it would require four main axes to significantly explain the interaction. In this case, it would be possible to construct six graphs involving 4PCs, combined in a 2-by-2 manner. While the selection of axes is a liberal criterion (PIEPHO, 1995), an alternative would be to apply the F_R test to the AMMI residuals, which Piepho (1995) defends as one of the more robust methods. Based on this criterion, the AMMI model is selected from the IPCA in which the AMMI residue becomes nonsignificant. In this case, the model employed was AMMI3, which explained 70.2% of the variation in the G×E interaction (Table 2). However, there is no consensus regarding the minimum ratio of the sum of squares of G×E that must be accumulated by the first principal component for the construction of a biplot.

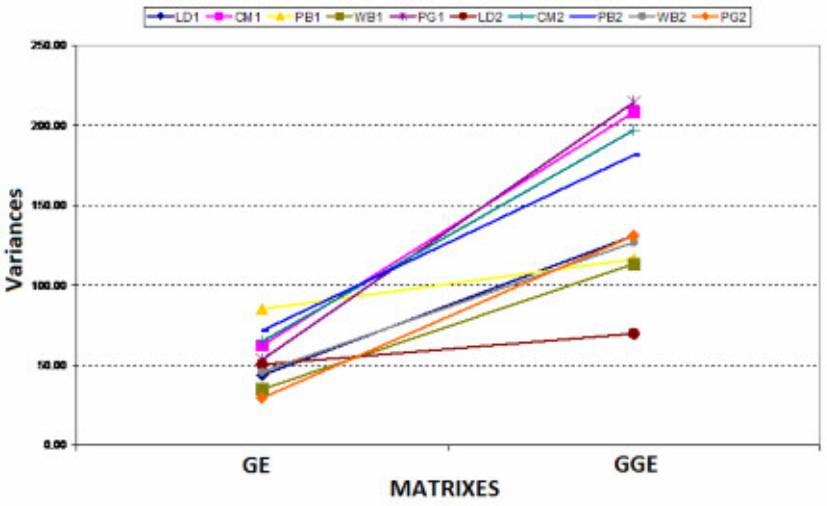
Table 2. Percentages of cumulative explanation for different methods employed the multivariate analysis.

Axes	% Cumulative Explanation		
	AMMI	GGE Biplot	FGGE
1	33.3	67.3	64.9
2	56.1	79.3	77.7
3	70.2	85.9	84.6
4	81.2	90.4	89.6
5	89.2	93.6	93.6
6	93.7	96.2	96.1
7	97.1	97.8	97.7
8	99.7	99.0	99.0
9	100.0	99.9	99.9

Carbonell et al. (2004) mentioned that it is convenient to perform a prior visual analysis. According to Duarte and Vencovsky (1999), the biplots can be presented because the first axis accumulates ratios between 27.1% and 71%. In the present study, one biplot was constructed using averages and scores for the first component, which absorbed 33.3% of the variance, and a second biplot was generated involving the scores of the first and second components, which absorbed 56.1% of the variation.

For the SREG-GGE and FGGE models, it was found that the first two components absorbed 79.3% and 77.7% of the variation, respectively (Table 2), and when another component was included, they explained 85.9% and 84.6% of the variation, respectively. These high percentages of explanation, associated with a small number of axes, may be due to the genotypic effect acting as an adjustment of the coefficient of the G×E interactions across environments. Thus, for estimation of eigenvalues through the main components, the variances of each variable (in this case, the environments) and the covariance between variables are maximized (Figure 1). However, this does not occur proportionally, considering that the genotypic effect is constant among environments and variable within environments, which may have resulted in an increased efficiency of the uptake of variation for both genotypes and environments studied simultaneously.

Figure 1. Estimated variances for the yields (kg.ha^{-1}) within environments using GE and GGE matrixes. Data from fifteen maize hybrids evaluated in five locations in the state of Paraná (LD – Londrina; CM – Campo Mourão; PG – Ponta Grossa; WB – Wenceslau Braz; PB – Pato Branco) in two crop seasons (1 – 2006/2007 and 2 – 2005/2006).

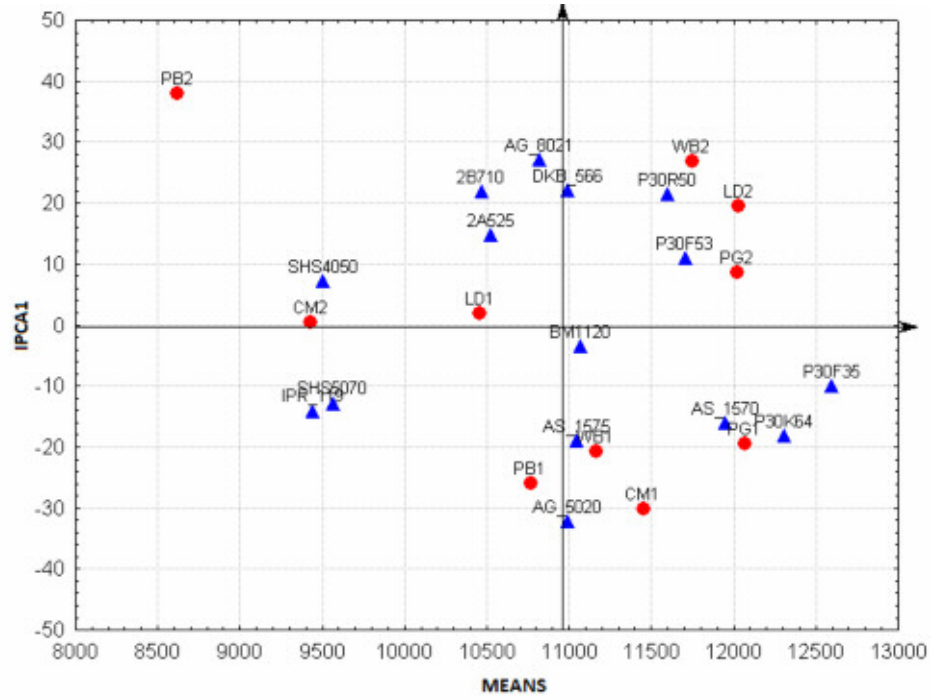


One approach that is frequently used under the AMMI method is the construction of biplots involving averages × IPCA1, referred to as AMMI1 (CARBONELL et al., 2004; MAIA et al., 2006; OLIVEIRA et al., 2003). In this case, an approach that is complementary to the characteristics of adaptability and phenotypic stability, such as the average yields of genotypes, is essential for the recommendation of a new cultivar.

Among the fifteen hybrids evaluated Through AMMI1 (Figure 2), nine showed averages above the overall average (10973 kg.ha^{-1}). The hybrids that presented relatively low interactions with certain environments, whose ratings were basically determined by genotypic effects, were P30K64, AS 1570, P30F53, P30R50 and AS 1575, in descending yield. P30F35 presented the highest average yield (12598 kg.ha^{-1}), though it did not show even weak

effects of specific interactions with any of the environments tested. The environments presenting higher yields (PG1, PG2 and LD2) did not stand out in terms of stability, as they are far from the origin. Environments CM2 and LD1 displayed lower average yields (9426 kg.ha^{-1} and 10457 kg.ha^{-1}) compared to other environments, but showed high stability considering the first IPCA, which can facilitate the selection of genotypes in these environments.

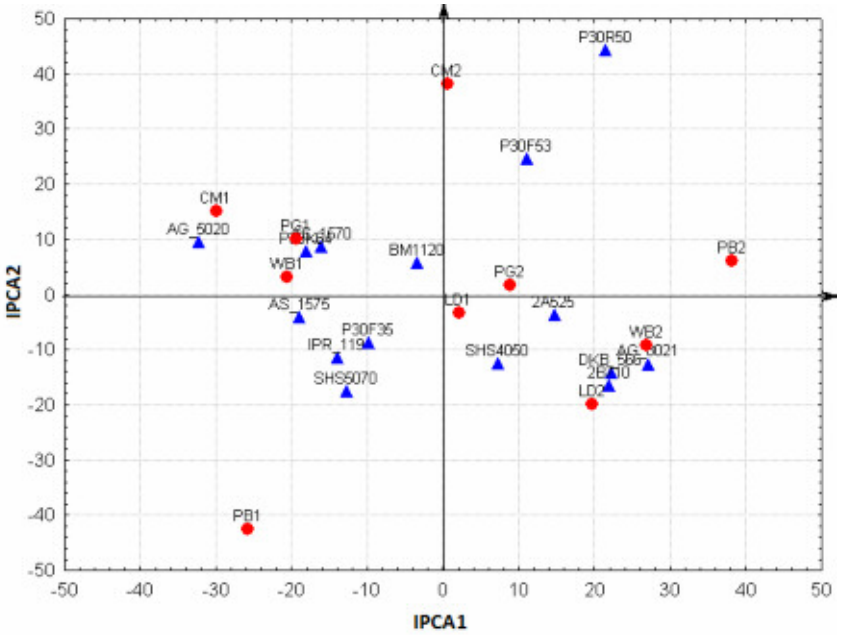
Figure 2. AMMI biplot for yield data (kg.ha^{-1}) from fifteen maize hybrids in five locations in the state of Paraná (LD –- Londrina; CM – Campo Mourão; PG – Ponta Grossa; WB – Wenceslau Braz; PB – Pato Branco) in two crop seasons (1 – 2006/2007 and 2 – 2005/2006).



Adaptive relationships may be found easily in a AMMI2 biplot (Figure 3), observing the signs of the scores for each pair of genotypes and environments (MAIA et al., 2006). Thus, genotypes and environments showing scores with the same sign (-,- or +,+) should interact positively, while opposite signs (-,+ or +,-) indicate negative interactions (DUARTE; VENCOVSKY, 1999).

The only genotype that showed a low contribution to the cross-interaction was BM 1120, which presented a yield that was slightly above the overall average (11072 kg.ha^{-1}). The other genotypes exhibited high magnitudes of the effect of the G×E interaction. A group formed by genotypes P30K64 and AS1570 showed positive interactions with environments PG1 and WB1 and an average stability, as did hybrids 2B710 and DKB566 with the LD2 environment and genotype AG 8021 with WB2. However, based on the 2005/2006 crop season, the high water stress that impacted the maize-producing areas should be considered, meaning that recommendations should be made cautiously, giving greater weight to stability, rather than the average yield potential of these hybrids This statement is also valid for the recommendation of genotypes characterized as unstable, such as P30F53 and P30R50, which show a high yield potential.

Figure 3. AMMI2 biplot for data on grain yields (kg ha^{-1}) fifteen maize hybrids in five locations in the state of Paraná (LD –- Londrina; CM – Campo Mourão; PG – Ponta Grossa; WB – Wenceslau Braz; PB – Pato Branco) in two crop seasons (1 – 2006/2007 and 2 – 2005/2006).



A group formed by genotypes AS 1575, P30F35, IPR 119, SHS 5070, SHS 4050 and 2A525 showed a stable general average. Environments LD1 and PG2 were more stable, being close to the origin of the axes. However, genotypes IPR 119, SHS 4050 and 5070 SHS may not be suitable for cultivation in the study group because of their low yield. CM2, although it lies far from the origin of IPCA2, was characterized as showing medium stability, being positioned at the origin of IPCA1, which displays the greatest amount of variation captured and is associated with a high standard G×E interaction. Among the environments presenting the most increased G×E interactions, CM1, PB1 and PB2 stand out.

One of the problems of the AMMI method is restricting the level of stability of a given genotype to its yield range. Therefore, a genotype with a low yield potential that is maintained even under improving environmental conditions is characterized as stable, as is the case for genotype SHS 5070. However, genotypes showing high yields, up to 12000 kg ha^{-1}, may be characterized as unstable if their yield presents a 10% decrease, as observed for the P30F35 genotype.

Carbonell et al. (2004) analyzed the stabilities of different bean cultivars through the AMMI and maximum deviation of yield, or MDY, methods (LINN; BINNS, 1988 cited by CARNEIRO, 1998) and found that the MDY method invariably identified cultivars as being more stable and more productive, whereas these findings were not always verified by AMMI method. The reason given by the authors for this discrepancy is that the MDY method identifies the most stable cultivars as those showing less deviation from the highest mean yield in each studied environment. Thus, the procedure is largely related to a recent definition of adaptation presented by Cecarelli (1996), where cultivars / lines that are considered to be adapted show the highest economic yields.

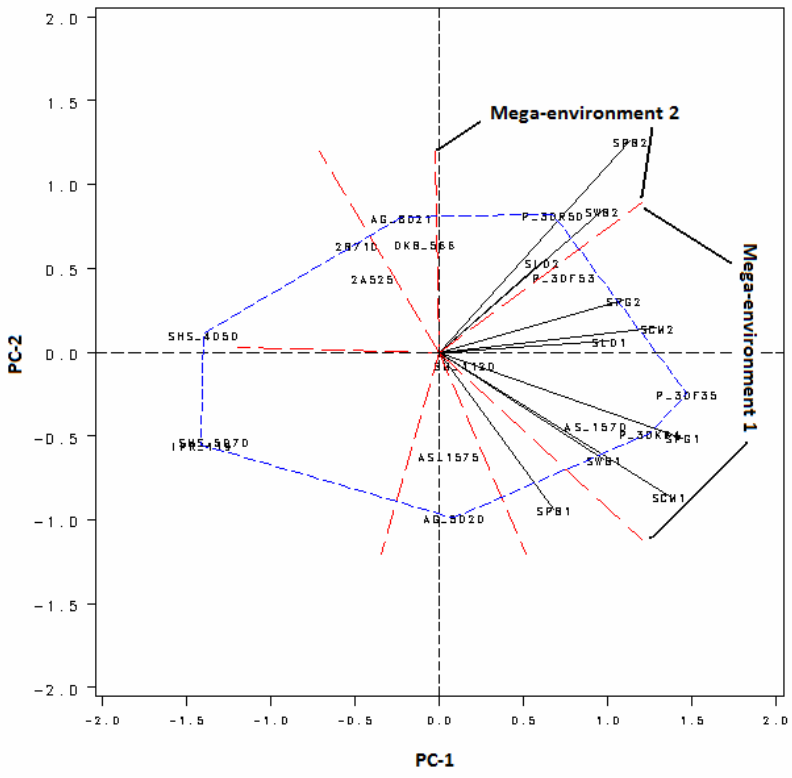
SREG-GGE Biplot Method

Under the GGE-biplot method, the yield of a genotype (*i*) in a given environment (*j*) will be approximately the product of the scores of PC1 for genotype *i* and PC1 for environment *j* plus the product of the score of PC2 for genotype *i* versus the score of PC2 for environment *i*. Geometrically, this will be the length of the vector environment (the absolute distance from the origin to the marker genotype), multiplied by the length of the vector genotype (the absolute distance of the marker from the origin) and by the cosine of the angle between them (KROONENBERG, 1995).

According to Yan et al. (2000), this property allows the following information to be displayed: i) the similarity and dissimilarity between the environment and the different responses of the induced genotypes; ii) the similarity and dissimilarity between genotypes and environmental responses; and iii) the positive or negative nature and magnitude of the interaction between any genotype and any environment.

In Figure 4, genotypes located at the vertices of the generated polygon present the greatest distance from the origin of all genotypes within the sector delimited as the most responsive. Characteristics such as being the best or worst genotypes in some or all locations can be used to identify potential mega environments. The genotypes within the polygon were less responsive to the environments located within the sectors.

Figure 4. Graphical plot from the SREG GGE-Biplot analysis for fifteen maize hybrids evaluated in five locations in the state of Paraná (LD –- Londrina; CM – Campo Mourão; PG – Ponta Grossa; WB – Wenceslau Braz; PB – Pato Branco) in two crop seasons (1 – 2006/2007 and 2 – 2005/2006).



The genotypes located at the vertices were P30K64, P30F35, P30R50 and AG 5020 (positive PC1 scores) as well as AG 8021, SHS 4050 and IPR 119 (negative PC1). By connecting the markers situated at the extremes of these genotypes, a polygon is formed. Perpendicular lines drawn for each side of the polygon, starting from the origin, divide the environments into two major sectors, which may show one or more winning genotypes at the vertices. The first sector contains the largest set of environments, inclining PG2, CM2, LD1, PG1, WB1, CM1 and PB1, and showing the P30K64 P30F35 genotypes as winners. The second sector, formed by the PB2 WB2 and LD2 environments, all of which refer to the 2005/2006 crop, was identified as presenting P30R50 as the winning genotype.

In general, the GGE biplot method separated the set of environments according to the crop season, indicating the existence of two mega-environments. This result was expected because the number of tested research locations represented the agricultural area of maize production in the state of Paraná in two distinct seasons, despite high levels of GE interaction. The allocation of CM2 and PG2 with other locations in 2006/2007 may be related to conditions such as the rainfall areas located within these experimental sites during the 2005/2006 season (GERAGE et al., 2006), reflecting good yield results. Another favorable factor for CM2 was the early planting carried out at that locality.

When the simple Pearson correlation coefficient was calculated between the scores of PC1 and the effects of the genotypes (the average yield in all environments), the obtained value was 0.99 (data not shown), which was significant ($p < 0,01$). This nearly perfect correlation between the PC1 scores and mean was also observed by Souza (2004) and confirmed the suggestion made by Yan et al. (2001) that when G is 40% of the sum of squares or is higher than G×E, the correlation between the G and PC1 shows high values ($r > 0.90$). In this study, 33.5% of SS_{total} was due to genotypic effects, which contributed 18.7% of the G×E interaction, as shown in the previous chapter. Through analyzing the estimates of the quadratic components, it is clear that the proportions are equivalent (28,66% for $\hat{\phi}_G$ and 13,19% for $\hat{\phi}_{G\times A}$).

However, when a low correlation occurs, it may be due to a high magnitude of the complex G×E interaction, particularly when data for several years are analyzed together, generally accompanied by similar amounts of the sum of squares being explained by PC1 and PC2 (YAN; HUNT, 2001). Therefore, genotypes with higher scores for PC1 show higher average yields and are the best genotypes identified in environments that also display high scores for PC1. This finding emphasizes the assertion made by Yan and Hunt (2001) that the genotype effect (also referred to as the main effect of the genotype) is ultimately a result of the G×E interaction itself.

The modeling technique leads all environments to exhibit scores with the same sign for PC1. Thus, according Crossa and Cornelius (1997), these scores represent the proportional differences in yield in various environments due to the simple G×E interaction, non-presenting any complex components. In turn, PC2 summarizes the sources of variation that lead to complex interactions. Environments and genotypes can indistinctly obtain positive and negative values, Thus, the complex component among the best genotypes leads to differentiation of mega-environments.

It was noted that the location of Pato Branco showed higher levels of complex G×E interactions in both seasons, which was also observed by the AMMI method.

In the GGE biplot, the genotypes are evaluated in terms of adaptability, based on rough estimates given by the scores of PC1, and stability, according to the scores of PC2. Thus, productive, stable genotypes should exhibit higher scores for PC1, but scores that are close to zero for PC2. These genotypes are more easily identified in environments with high scores for PC1 and scores near zero for PC2.

The genotypes that showed the closest correspondence to this concept were P30F35 and P30K64. The results obtained through the AMMI method indicated average adaptability or specific adaptability to a small set of environments for these genotypes. One cause of this difference may be associated with the low explanatory power of the first two IPCAs, particularly IPCA 1, which contains a higher percentage of patterns associated with the variation captured in the shaft.

Genotype BM 1120, despite showing high stability, achieved only an average yield, as demonstrated through the AMMI method. In the continuing search for new productive and stable genotypes in environments that facilitate identification, it was found that Londrina (2006/2007) and Campo Mourão (2005/2006) are adequate, due to possessing markedly high scores for PC1 and low scores for CP2. Through the AMMI method, the stability of these locations was demonstrated, despite their low average yields. However, it should be noted that the 2006/2007 crop season shows a better definition of positioning, due to better weather conditions during this period. Therefore, the best choice would be Londrina.

In mega-environment 1, beyond the winning cultivars, AS1570 and P30F53 stood out. Cultivars allocated to this sector may present more generalized planting indications, as seven of the ten tested environments constitute this mega-environment. P30R50 showed specific adaptability to other locations in the 2005/2006 crop season, which were grouped into mega-environment 2, as revealed by the AMMI method in part. However, under AMMI2, this genotype would be regarded as unstable, diverging from the GGE method. The other genotypes located at the vertices, such as SHS 4050 and IPR 119, together with SHS 5070, showed low yields and, because they were distant from the marker environments, reflected low adaptability in all ten tested environments.

This result was also found through the AMMI method, but only for genotypes IPR 119 and 5070 SHS. The other sectors, due to presenting delimiting genotypes that were near each other, including those that were distant from the origin, showed no environments located in the sectors they formed. This was attributed to the similar yields in all environments. Thus, the perpendicular intersection between them could be ignored in the analysis, or not plotted.

Under the GGE method, the genotype effect is considered to be multiplicative in terms of the G×E interaction, and assuming that the scores of PC1 for locations/environments tend to exhibit the same sign, PC1 represents the simple G×E interaction (YAN et al., 2000). Because to the scores of PC1 for genotypes are highly correlated with the effects of the genotypes (means), for practical purposes, the scores can override the effects of the genotypes. However, it should be noted that conceptually, these parameters are very different.

As shown previously, the genotypic effect is constant in any environment. However, the yield predictions obtained from PC1 using the GGE method for a given genotype were not constant. These predictions varied over the environments in direct proportion to the PC1 scores for locations/environments. Yan et al. (2000) believe that this proportionality in the yield response of genotypes may be more logical and biologically plausible than the concept of additive main effects. However, the only property that supports this concept is that the locations/environments that facilitate the identification of genotypes with large main effects are also simultaneously displayed.

Yan et al. (2000) emphasized that another important property of GGE analysis is the differentiation between the proportional or disproportional responses of cultivars and their implications in simple and complex GE interactions. An understanding of these interactions can be obtained by correlating the genotypic scores of PC1 (simple interaction) and PC2 (complex interaction), or through environmental covariance (SOUZA, 2004). The AMMI method, despite being

represented by a biplot, requires good knowledge of advanced statistics on the part of the breeder so that they can extract all possible interpretations for the investigated genotypes, environments and their interactions, while differentiation of the proportional and disproportional responses of genotypes/cultivars is not permitted.

The two-dimensional biplot based on SREG2, beyond more direct visual responses, always uses the same number of degrees of freedom and explains an intermediate magnitude of the sum of squares for G+G×E between AMMI1 and AMMI2. Thus, the GGE biplot will always be close to one of the models, though it may present a higher percentage of explanation in the first several axes. Souza (2004) applied a simplified method suggested by Gauch and Zobel (1996) to estimate "patterns" and "noise" in the evaluation of maize cultivars in Minas Gerais-Brazil and verified that SREG2 was the best model for the 1998/1999 crop season in relation to AMMI2 because it explained the largest proportion of the sum of squares of the G×E interaction. These authors also found that in the 1998/1999 crop season, the GGE method explained 53.4% of $SS_{G\times E}$, compared to 50.8% in the AMMI analysis, while in the 1999/2000 crop season, GGE explained 52.3%, and AMMI explained 45.4%.

FGGE Method

Through the FGGE method, the environments were grouped into three factors (Table 3). Due to the high proportion of complex components, it was not possible to reduce the number of environments tested, but a macro-region of maize cultivation was identified in the state of Paraná. This grouping was due to the predominance of weather effects on the crops, such as stress from a lack of water during critical stages in crop development.

Pato Branco (2005/2006) was again isolated in factor 3, due to the high proportion of complex part, possibly due to the high water stress that occurred in this season, impacting the pre-flowering and grain-filling stages. At this location during the 2006/2007 crop season, the weather conditions were not as favorable, but allowed a good crop development to occur (SHIOGA et al., 2007). Through the GGE method, the separation of these two environments from others within their mega-environments was clear, in terms of both the distance from the origin and CP1.

Under the FGGE method, factor 1 generally clustered the environments of the 2006/2007 crop season, while the second factor grouped the environments of 2005/2006. For factor 2, the locations of Londrina and Ponta Grossa displayed factor loadings of 0.6746 and 0.6780, respectively, which are close to 0.7, potentially confirming them under factor 2, through there is no guarantee of their groupings. Through the GGE method, although LD2 was allocated to the second mega-environment, it was close to perpendicular, where in relation to WB2, it showed an $r = 0.75$ ($p < 0.01$) and SP% of 50.2%, compared to the values of 0.62 ($p < 0.05$) and 42.9% obtained for PG2, which may be influenced by its position, as CP1 is closely related to the SP% of the G×E interaction. Using the AMMI1 and AMMI2 methods, it is possible to check the levels of environmental stability, due to their distances from IPCA1 (for AMMI1) and origin (for AMMI2). However, the establishment of groups of similar environments is subjective, particularly in apparent cases of specific adaptability, as exemplified in P30F53 in PG2 and P30R50 in LD2 and WB2 via AMMI1, which cannot be confirmed when there is an increase in the information captured by the second axis (AMMI2). Duarte and Vencovsky (1999) observed similar responses using bean yield data obtained in five environments.

Table 3. Environmental stratification through factor analysis using 15 genotypes and 10 environments in the state of Paraná during the 2005/2006 and 2006/2007 crop seasons.

Environments	Agricultural year	Factor loadings after rotation			Commonalities
		Factor 1	Factor 2	Factor 3	
Londrina	2005/2006	0.4668	0.6746	0.1712	0.89
Campo Mourão	2005/2006	0.2513	**0.8042**	0.4000	0.82
Pato Branco	2005/2006	0.1347	0.2695	**0.9352**	0.85
Wenceslau Braz	2005/2006	0.1883	**0.8751**	0.3294	0.91
Ponta Grossa	2005/2006	0.4057	0.6780	0.4809	0.98
Londrina	2006/2007	**0.8396**	0.1587	0.2049	0.92
Campo Mourão	2006/2007	0.4563	**0.8052**	-0.0493	0.84
Pato Branco	2006/2007	**0.8729**	0.3286	-0.0050	0.80
Wenceslau Braz	2006/2007	**0.8474**	0.3216	0.1330	0.94
Ponta Grossa	2006/2007	**0.7115**	0.4819	0.2866	0.93

Eigenvalue	Accumulated Percent	Eigenvalue	Accumulated Percent
6.49	64.9%	0.24	96.1%
1.27	77.7%	0.16	97.7%
0.70	84.6%	0.12	99.0%
0.50	89.6%	0.09	99.9%
0.40	93.6%	0.01	100.0%

The GGE and FGGE methods allow direct inferences and are strongly related to the simple (PC1) and complex portions (PC2) of the G×E interaction, in the case of the GGE method, and to covariance and correlation, in the case of FGGE method. Hence, we sought consider the grouping of environments only using these two methodologies, restricting the AMMI method to the evaluation of genotypes.

Through GGE and FGGE analysis, it was possible to separate two large sets of environments in the state of Paraná. However, in both sets, the G×E interaction predominated due to the effect of crop seasons, as observed previously. In forming these sets, the differences in the positioning of certain locations, in reference to different factors or mega-environments, are due to the basis of the applied methodology. Under the GGE method, these differences are attributed to the SP%, whereas under the FGGE method, the effects that predominate are the SP% plus the correlation among environments.

Therefore, the association between r_E and SP% effects under the FGGE method allows the environments contained within each factor to represent mega-environments for the indication of crops within the same crop season. Still, based on the r_E effect, it can be inferred that possible increases or decreases in yield that occur under production in certain niches (analyzed by pairs of environments) are taken into consideration in the formation of groups of environments.

Graphical analysis of adaptability through the FGGE method (Figure 5) indicated that P30F35, P30F53, P30R50, P30K64 and AS 1570 show wide adaptability to the set of grouped environments in factors 1 and 2. Regarding the AMMI1, low magnitudes of the effects of the interactions of P30F53, P30R50, P30K64 and AS 1570 with the environments were found as well as high yields. P30F35 was not included because it presented high magnitudes of the effects of the interactions with all of the tested environments, despite its higher mean yield. In this case, genotype AS 1575 was included,

due to presenting a small effect of the specific interaction with environment WB1. However, due to combining general stability with a high mean yield, the best genotype to be included would be 1120, instead of BM AS 1575, as confirmed by the GGE and FGGE methods.

According to the GGE method, genotypes P30F35 and P30K64 were winners in mega-environment 1, which comprised seven of the ten environments tested. This polygon included P30F53, AS 1570 and BM1120, while, in the mega-environment 2, genotype P30R50 was the winner.

The three methods confirmed most of the same genotypes as showing wide adaptability, with some differences being found in the investigation of specific adaptabilities related to particular groups of environments formed by the GGE and FGGE methods. Under GGE, genotype P30R50 was indicated to show adaptability to three locations in the 2005/2006 crop season (Wenceslau Braz, Pato Branco and Londrina). However, considering the yield, this genotype was allocated to the 2nd, 3rd and 7th positions in these environments (Table 4). In other locations in the same crop season and the 2006/2007 season, Pato Branco presented low yields for this genotype, while in other localities, it displayed among the six highest yields in most cases. This may contribute to confirming the adaptability observed by the FGGE method.

Figure 5. Graphical analysis of the adaptability of fifteen maize cultivars from the scores obtained, considering the seven factors contained in the environments under good edaphoclimatic (Factor 1) and bad edaphoclimatic conditions (Factor 2).

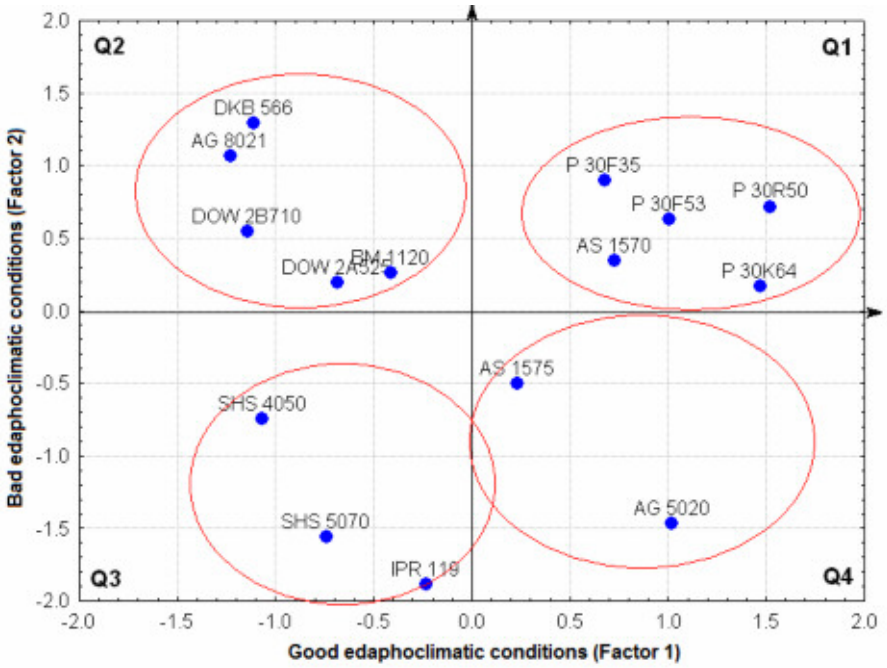


Table 4. Estimates of the average yield (kg.ha^{-1}) between and within ten environments and ranking (rk) of fifteen maize cultivars in the state of Paraná.

	[a] 1	rk	[a] 2	rk	[a] 3	rk	[a] 4	rk	[a] 5	rk		
P 30F35	12624	4	10542	3	9826	4	13945	1	13235	2		
P 30K64	12566	5	10295	5	9761	5	12403	5	13112	3		
AS 1570	12934	2	10525	4	8840	8	11658	10	14125	1		
P 30F53	12304	8	11087	2	10032	2	12307	6	12830	5		
P 30R50	12377	7	12080	1	9962	3	12912	2	12383	6		
BM 1120	11996	9	9721	7	8663	9	11946	7	12880	4		
AS 1575	12423	6	9288	9	7992	11	11578	11	11197	12		
DKB 566	13458	1	9457	8	8573	10	12589	3	12270	7		
AG 5020	11016	13	10204	6	7784	12	10515	12	11555	11		
AG 8021	12754	3	9214	10	10069	1	11845	8	11834	9		
2A525	11471	12	8315	11	9192	7	11665	9	12076	8		
2B710	11532	11	7395	15	9215	6	12422	4	11613	10		
SHS 5070	10971	14	7987	12	6511	14	9947	15	10046	15		
SHS 4050	11551	10	7706	13	7048	13	10019	14	10957	13		
IPR 119	10476	15	7578	14	5791	15	10402	13	10149	14		
	[a] 6	rk	[a] 7	r_k	[a] 8	r_k	[a] 9	rk	[a] 10	r_k	[b] Média Geral	rk
P 30F35	12512	2	12595	3	13117	1	12740	2	14844	1	12598 a	1
P 30K64	12538	1	14472	1	11906	2	12928	1	13095	4	12307 a	2
AS 1570	10798	5	12981	2	11622	4	12316	3	13728	2	11953 a	3
P 30F53	11666	3	11938	7	10199	10	11681	6	13024	5	11707 a	4
P 30R50	11213	4	11972	6	8871	15	11950	5	12299	8	11602 a	5
BM 1120	8904	15	11920	8	10995	6	10468	11	13224	3	11072 b	6
AS 1575	9859	9	12366	5	11293	5	12019	4	12432	7	11045 b	7
DKB 566	10685	6	10583	10	10727	8	10428	12	11175	11	10995 b	8
AG 5020	10519	8	12592	4	11674	3	11417	7	12601	6	10988 b	9
AG 8021	9788	10	10154	12	10946	7	10513	10	11084	12	10820 b	10
2A525	9573	11	10183	11	10066	12	10587	9	12121	9	10525 c	11
2B710	10657	7	10772	9	10120	11	9749	14	11203	10	10468 c	12
SHS 5070	9229	14	9867	14	10686	9	10186	13	10207	14	9564 c	13
SHS 4050	9437	13	9943	13	9504	14	9619	15	9272	15	9506 c	14
IPR 119	9471	12	9395	15	9715	13	10819	8	10652	13	9445 c	15

[a]: coding environments tested during the 2005/2006 season: 1: Londrina; 2: Campo Mourão; 3: Pato Branco; 4: Wenceslau Braz; 5: Ponta Grossa and the 2006/2007 crop season. 6: Londrina; 7: Campo Mourão; 8: Pato Branco; 9: Wenceslau Braz; 10: Ponta Grossa.
[b]: Grouping of means by the Scott-Knott test at 1% probability.

Regarding specific adaptability, the three methods showed good agreement. However, the GGE and AMMI methods, a visual analysis based on general information of yield, it is necessary for a correct guidance of cultivars.

Under these methods, particularly AMMI2, genotypes DKB 566, 2B710 and AG 8021 remained close, while 2A525 was slightly farther away. The AMMI method detected a weak interaction of these genotypes with LD2 and WB2. Using the GGE method, these same genotypes were found to be near the delineation polygon and perpendiculars, which means that they can be directed at the discretion of the breeder for the grouped environments in mega-environment 2. However, the percentage of the complex portion should be considered because it is

near PC2. Through the FGGE method, the grouping of the genotypes in environments related to the 2005/2006 crop season allocated to factor 2 (WB2 and CM2 in this case) was confirmed.

Genotypes AS 1575 and AG 5020 can be considered to show specific adaptability to mega-environment 1 or factor 1 under the GGE and FGGE methods. Through the AMMI1 graph, it was verified that these genotypes are close to WB1, CM1 and PB1, while through AMMI2, CM1 and WB1 remained near, moving away from PB1 and approaching PG1. As mentioned previously, the AMMI method presents some differences in the obtained responses as new axes are incorporated in the analysis. However, it is possible to observed the adaptation of these genotypes associated with the locations during the 2006/2007 crop season, confirming the responses obtained through other methods.

Using the three tested methodologies, SHS 4050, SHS 5070 and IPR 119 were the genotypes that showed the least satisfactory performances in terms of yield and adaptability within the set of genotypes and environments studied.

Conclusions

Under the GGE and FGGE methods, the genotypic effect acted as an adjustment coefficient for GE interactions across environments, resulting in a high percentage of explanation, associated with a smaller number of axes.

Environmental stratification through the GGE and FGGE methods showed similar responses, while under the AMMI method, there was no guarantee of grouping environments..

Adaptability analyses revealed few differences in the responses to the three methods.

Genotypes P30F35, P30F53, P30R50, P30K64 and AS 1570 showed high yields associated with general adaptability.

The FGGE method allowed the differences in yield responses in certain regions and the impact on locations belonging to the same set of environments (through r_E) to be associated with the level of the simple active portion of the GE interaction.

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