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FACTOR ANALYSIS AND GGE BIPLOT FOR ENVIRONMENTAL AND GENOTYPIC EVALUATION IN SUNFLOWER TRIALS

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Abstract - The definition of mega-environments is of critical relevance for a more accurate cultivar recommendation. This study aimed to verify the potentialities of the GGE biplot and factor analysis for environmental evaluation, to investigate possible mega-environment, and to evaluate the adaptability and stability of sunflower genotypes. A factor analysis and GGE biplot were used for evaluating the individual effects of genotypes, environments, interactions and mega-environment discrimination based on the data from 16 sunflower genotypes evaluated in 14 environments. The factor analysis was able to identify mega-environment inconsistency and, consequently, excluded a mega-environment for recommendation. The genotype BRS 387 showed wide adaptability and high stability in the mega-environment to which it belonged, indicative of its efficiency for the region to which it is being tested. Although the GGE biplot has many interpretation possibilities, extra care is needed when making decisions because important phenomena may be left unidentified in this analysis.

Keywords: Mega-environment, genotype by environment interaction, stability, adaptability

Introduction

The sunflower is one of the main oil crops in the world (Jocic et al., 2015). The main objectives of sunflower breeding include the development of cultivars with high oil and grain yield and high phenotypic stability (Nobre et al., 2012). For an appropriate identification of superior genotypes, cultivar evaluation in multi-environment trials is indispensable. In Brazil, sunflower genotypes developed in different breeding programs have been evaluated by Sunflower Trials Network of Brazil, coordinated by Embrapa.

Investigating genotype behavior in different environments based on adaptability and stability or by environmental stratification may facilitate the genotype recommendation (Grunvald et al., 2014). Numerous techniques have been proposed to recommend genotypes, including those based on analysis of variance (Plaisted and Peterson, 1959), linear regression (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Cruz et al., 1989), and non-parametric methods (Lin and Binns, 1988).

Methods based on analysis of variance conceptualize stability as invariance (Becker and Léon, 1988). However, Cruz et al. (2014) argue that this concept does not fit with the breeding purposes, since cultivars of smaller variances are, in general, less productive. Although some regression-based methods consider stability as invariance (Finlay and Wilkinson, 1963), others like Eberhart and Russell (1966) add to this concept the idea of predictability of behavior. However, in all cases, the calculated environmental index is not independent of the data, which can cause distortions in the results (Becker and Léon, 1988). In addition, some

methods are rather subjective such as the non-parametric methods, in which the comparison between genotypes is not associated with significance tests.

Currently, approaches such as factor analysis (FA), the additive main effects and multiplicative interaction (AMMI), and the genotype main effect plus genotype by environment interaction biplot method (GGE biplot) are preferred because they integrate environment analysis with environmental stratification (Nai-yin et al., 2014) for mega-environment (ME) formation.

Additive main effects and multiplicative interaction method combines, in a single model, additive components for the main effects of genotypes and environments as well as multiplicative components for the interaction effects. This methodology allows for interaction visualization through a biplot graph (Hadi and Sa'diyah, 2016). However, according to Yan et al. (2007), the fact that the biplot axes are at different scales and that the effects of genotypes and interactions are separated may result in distortions in the method.

To overcome these limitations, Yan et al. (2000) proposed the GGE biplot, which simultaneously considers the effects of genotypes and interactions and then subjects them to a principal component analysis. This analysis allows for the identification of MEs, the selection of stable genotypes, widely or specifically adapted, and the selection of representative and discriminative environments. The GGE biplot has been extensively reported in the literature to evaluate genotype and environment performances (Samonte et al., 2005; Yan et al., 2007; Gauch et al., 2008; Kendal et al., 2016).

Factor analysis, allows for minimization of the number of environments evaluated in orthogonal factors among each other and conserves the maximum information (Cruz et al., 2014). In this analysis, the performance in each environment is decomposed into a set of common factors and a specific factor. Subsequently, each common factor can be expressed as a linear combination of genotype performance in all the environments. Environments clustered in one specific factor have a high correlation among themselves and are poorly correlated with other factors. In addition, the scores obtained in the factors are plotted and, therefore, allow for graphical adaptability visualization in relation to factors (Murakami and Cruz, 2004) that come to represent the ME.

Yang et al. (2009) and Dziuban and Shirkey (1974) emphasize that the use of GGE biplot and factor analysis should consider some basic aspects so that the interpretations are realistic. The quality of the biplot analysis depends on the percentage of variation of the data that is absorbed in the first two principal componentes, and the partition of the singular values, which will define which interpretations can be extracted from each biplot (Yan and Tinker, 2006). Factor Analysis should consider values of communality to define a mega-environment. Factor analysis has already been used successfully for environmental evaluation in wheat (Peterson, 1992; Peterson and Pfeiffer, 1989), maize (Garbuglio and Ferreira, 2015) and common bean (Peixouto et al., 2016).

Although using multivariate techniques provides a more accurate cultivar recommendation, the joint use of these techniques in evaluating the performance of sunflower germplasm is still limited. Therefore, the objective of this work was to verify the potentialities of the GGE biplot and factor analysis for environmental evaluation, to investigate possible mega-environment, and to evaluate the adaptability and stability of sunflower genotypes of the Sunflower Trials Network in Brazil.

Material and methods

Experimental data

Sixteen sunflower genotypes from different breeding programs (Dow AgroSciences, Embrapa Soja, Heliagro do Brasil, and Advanta) (Table 1) were evaluated in 14 environments (two years and 10 municipalities) belonging to the Sunflower Trials Network of Brazil (Table 2), coordinated by Embrapa. The experiments were installed in randomized complete blocks with four replicates. The plots consisted of four rows of six meters in length, with a useful area corresponding to the two central rows, eliminating 50 cm at the ends of the lines. Seeds were sowed by hand at a depth of 0.04 m, placing three seeds per hole. Sixteen days after the emergence the plants were thinned, leaving one plant per hole. Basic fertilization was carried out with application of 10 kg ha^{-1} of N, 70 kg ha^{-1} of P_2O_5, 60 kg ha^{-1} of K_2O, and 2 kg ha^{-1} of B. After 30 days of emergence, the cover fertilization was carried out with 60 kg ha^{-1} of N and 1 kg ha^{-1} of B. The capitula were hand harvested when the crop reached phenological maturity. The grains were weighted (kg ha^{-1}) and the values were adjusted to 11% moisture content, after determination of the humidity level.

Statistical analysis

Firstly, univariate analysis of variance were performed for grain yield (GY) and after detecting that the relationship between the largest and smallest residual mean squares did not exceed the ratio 7:1 (Pimentel-Gomes, 2009), the joint analysis of variance was performed, in which the genotype effect was considered fixed and the block/environment, environment, and the GE interaction was considered random, according to Equation 1:

$$Y_{ijk} = \mu + B/E_{jk} + G_i + E_j + GE_{ij} + e_{ijk} \quad \text{(Eq 1)}$$

In which Y_{ijk} is the genotype value of the k^{th} block, evaluated in the i^{th} genotype and j^{th} environment, μ is the overall average, B/E_{jk} is the effect of the block k within the environment j, G_i is the effect of the i genotype, E_j is the effect of the j^{th} environment, with $E_j \sim N(0; \sigma^2)$, GE_{ij} is the effect of the interaction of genotype i with the environment j, with $GE_{ij} \sim N(0; \sigma^2)$, e_{ijk} is the experimental error associated with observation Y_{ijk}, with $e_{ijk} \sim N(0; \sigma^2)$.

After identifying a significant GE interaction, the data were subjected to the factor analysis (Murakami and Cruz, 2004) and GGE biplot (Yan et al., 2000). The factor analysis was performed according to the model expressed in Equation 2:

$$x_j = \sum_{k=1}^{m} \ell_{kj} F_k + \varepsilon_j \qquad \text{(Eq. 2)}$$

In which x_j is the mean of the grain yield in the j^{th} environment, with j = 1, 2, …, v (variables), l_{kj} is the factor loading for the j^{th} variable associated to the k^{th}factor, in which k = 1, 2, …, m (common factors); F_k is the k^{th} common factor and, ε_j is the specific factor associated to the j^{th} variable. The definition of ME or factor number was given by the number of principal components that explained at least 80% of the total variation of genotypes in the environments or, similarly, by a communality average value that exceeded the minimum of 0.80 (Cruz et al., 2014). The final factor loadings, obtained after applying a varimax rotation method, were clustered according to their magnitudes. Within a given factor, the environments with factor loadings greater than or equal to 0.70 indicated a similarity pattern and the formation of an ME, while loadings between 0.50 and 0.70 indicated the uncertainty of adding the environment to the ME, and loadings less than 0.50 indicated the exclusion of the environment associated with the formed ME (Cruz et al., 2014). An adaptability assessment was graphically performed, according to Murakami and Cruz (2004). Considering that the factor loadings were positive and that there is interest in enhancing the variable value, it was possible to identify genotypes with wide adaptability to the pairs of MEs, which were located in the first quadrant of the scatter plot. Genotypes specifically adapted to the region determined by the factor (or specific ME), which were located in the second and fourth quadrants, and poorly adapted genotypes, which were located in the third quadrant.

The GGE biplot analysis was carried out according to the model expressed in Equation 3:

$$Y_{ij} - \mu - \beta_j - \lambda_1 \xi_{i1} \eta_{1j} + \lambda_2 \xi_{i2} \eta_{2j} + \varepsilon_{ij} \qquad \text{(Eq. 3)}$$

In which Y_{ij} is the average yield of genotype i in environment j; μ is the overall average; β_j is the main effect in environment j; λ_1 and λ_2 are the singular values (SV) for the first and second principal components (PC), respectively; ξ_{i1} and ξ_{i2} are eigenvectors of genotype i for PC1 and PC2, respectively; η_{j1} and η_{j2} are eigenvectors of environment j for PC1 and PC2, respectively; and ε_{ij} is the residual of the model associated with the genotype i in environment j.

The data were centered on the environment (column-metric preserving) to visualize the environmental relationships. Thus, similarity (covariance) between the two environments was given by both the length and the cosine of the angle between them (Mare et al., 2017; Yan and Tinker, 2006). Environment discriminant ability was determined by the length of the environmental vector, which was proportional to the standard deviation, and the environment representativeness was given by a relation between the distance of each environment in relation to an average environment (Yan et al., 2000).

Mega-environment identification was performed by visualizing the which-won-where graph. The outermost genotypes were connected by vertices that formed a polygon that contained all other genotypes inside it. A set of perpendicular lines was drawn from the origin biplot subdividing it into sectors to facilitate visualization (Mare et al., 2017). For genotypic evaluation, the data were centered on the genotype (row-metric preserving). Genotype stability and average performance throughout the environments belonging to the same ME were evaluated by examining the abscissa and ordinate axes of the mean environment (Yan and Tinker, 2006).

The adequacy of GGE biplot analysis was measured by the criterion proposed by Gauch and Zobel (1996), which is based on the percentage of total variation of G + GE that is absorbed by biplots. By this criterion, the expected noise of sum of squares (SS) is estimated by the degrees of freedom multiplied by the error of mean of squares (MS) of each variation source, the expected pattern SS is given by the total SS for the source minus its expected error, and the expected pattern SS vs. total SS ratio is calculated for each source. Expected pattern values greater than 80% are considered suitable for biplot analysis (Yan and Tinker, 2006). All the analyses were performed by the software Genes (Cruz, 2016).

Results and discussion

The analysis of variance showed significant differences for genotype, environment, and GE interaction effects ($p < 0.01$) (Table 3). Among the sources of variation that affected grain yield, environment accounted for approximately 82% of the total phenotypic variation (G + E + GE interaction), while genotypes and interactions contributed 6.32% and 11.47%, respectively. Similar results were reported by Tonk et al. (2011), Abate et al. (2015) and Pan-pan et al. (2016), which confirms the importance of environmental studies for cultivar selection (Mortazavian et al., 2014).

It was verified in the factor analysis that five eigenvalues explained approximately 84% of the total variation (that corresponds to the communality average of the common factors) regarding the genotype performance for grain yield in the environments (Table 5). Initially, five different MEs were defined. Communalities presented acceptable values, with the exception of the experiment carried out in Planaltina 2013, in which the variance due to the common factors reached 0.5797 (Table 5) and, therefore, did not allow for inferences about environmental strata or genotypic adaptability (Cruz et al., 2014). However, in the previous year in this same municipality, the communality value was high, suggesting that external

factors influenced the assay of 2013.

Factor loading values indicated that the ME determined by Factor 1 was constituted by the experiments carried out in 2012 and 2013 in Vilhena and by the experiment carried out in Muzambinho in 2013. Although the municipalities described are located in different regions, both experienced adequate rainfall during the evaluated periods and are located at altitudes varying from 615 to 944 meters (Table 2). The second ME was formed by the environments of Nova Porteirinha 2012 and Campo Verde 2013, while the third ME was formed by Chapadão do Sul 2013. The fifth ME was formed solely by the experiment carried out in Jaíba 2013. The environments Planaltina 2013, Manduri 2013 and Uberlândia 2012 presented factor loadings less than 0.70 for all factors and, therefore, were not included in a specific ME. The fourth ME, constituted by the trials carried out in 2012 in the municipalities of Palmas and Planaltina, added locations with a negative performance correlation. For recommendation purposes, this ME was ignored because GE interaction impacted the performance of some genotypes.

Mega-environment formation was independent of altitude, since contrasting environments formed an ME. In addition to indicating the sunflower plasticity (Bezerra et al., 2014). In relation to the water regime, additional irrigation applied in some places made it difficult to evaluate the importance of this trait for the environment stratification. Therefore, the mega-environments pointed out in the analysis should be better investigated in order to confirm its subdivision.

Genotypic adaptability in the ME one, two, three and five indicated a lack of adaptability of the BRS 324 and BRS 315 genotypes (Figure 1) in most of the MEs, since these were located mainly in the third quadrant. The hybrid BRS 387 was classified as widely adapted since it was located mainly in the first quadrant.In the dispersions involving ME5 (which presented a negative factor loading), there was a change in the quadrant interpretations and, therefore, genotypes of wide adaptability were located in the third quadrant; those that were poorly adapted were located in the second quadrat and those specifically adapted were located in quadrants one and three. Of the three times that HLE 20 hybrid appeared in the second quadrant, two of these times were in dispersions that involved ME5, a fact that allowed us to classify it as poorly adapted to this ME. The variety Embrapa 122 (T) showed specifically adaptability based on information from half of the dispersion charts. This variety appeared at least twice in ME3 and was therefore considered specifically adapted to this ME. When not classified as specifically adapted to this ME, it corresponded to the genotype class of wide adaptability in ME1 and ME2 and to the poorly adapted class in ME5 (Figure 1).

Some studies involving GE interactions based on a graphical analysis tend to use only two axes for the purpose of Cartesian dispersion. However, when a technique is capable of identifying and mapping an unfixed number of axes or factors, the one that is more accurate tends to be the genotypic recommendation, since the researcher will be able to observe the classification pattern repeatability and make decisions based on a more robust criterion. In situations in which only two axes are adopted as sufficient to absorb large portions of genotype and environment variation, decisions are made based on a simplified genotype behavior pattern, which may reduce the recommendation reliability (Cruz et al., 2014).

The first two PC accounted for 84% of the variation of G + GE in the biplots, which means that GGE biplot should account for approximately 84% of the total G + GE, value considered adequate to perform the analysis, according to Gauch and Zobel (1996). It was possible to observe that, except for the environment pairs Planaltina in 2012 and Vilhena A in 2013, and Planaltina in 2012 and 2013, all the others were positively correlated (Figure 2 a). The experimental conditions that occurred in Planaltina in the evaluation years may have caused this result since it was the same location, and a high correlation was expected between them. As there were no environments in which the correlation was highly negative, it was possible to infer that the complex interaction among environments was of a low magnitude.

Three MEs were identified by the GGE biplot analysis (Figure 2 b). A curious fact is that the two trials carried out in the municipality of Planaltina constituted two different mega-environments. In the trial of Planaltina in 2012, the genotype that presented the best performance was the hybrid HLE 20. However, in Planaltina in 2013, the genotype with the best performance in it was the hybrid HLE 23. The other environments constituted the third ME, highlighting the hybrid BRS G39. As shown in Figure 2 a, the only environmental pair that presented some complex interaction (negative correlation between environments) was Planaltina in 2012 and 2013. Although the interaction was of low magnitude, this was sufficient to demonstrate the classification inconsistency. In practice, this result showed that tests performed in Planaltina were not valid to characterize the genotypes evaluated in this work. Therefore, we excluded MEs 2 and 3 from any interpretation.

Considering the ME 1, it was possible to evaluate the representativeness by means of the environmental angle in relation to the average-environment axis (AEA), and the informativeness, through the lengths of the environmental vectors. The local represented by Vilhena B was the most representative of all sites evaluated in the two years, followed by Vilhena A (Figure 2 d), since they presented the smaller angles in relation to the AEA. In addition, these environments were informative, that is, were able to better discriminate genotypes. According to Yan and Tinker (2006), discriminatory and representative

environments are ideal for selecting genotypes adapted to the whole ME. Therefore, these environments are the ideal to characterize genotypes for ME 1.

As the stability concept by the GGE biplot is invariance, it is fundamental to evaluate not only the stability but also the average of the genotypes (Yan and Tinker, 2006). The hybrid BRS G39 presented the highest average in comparison with the others, since it was the first in the direction of the AEA arrow, followed by hybrids Dow M734 (T) and BRS 387, while the hybrid BRS 324 presented the worst performance since it remained at the opposite end of the direction of the highest mean (Figure 2 c). Genotype vectors, represented by dotted lines parallel to the vertical axis that pass through the biplot origin, highlighted the hybrid HLE 20 as the most stable. This same hybrid presented a great average for ME1, which identified it as a superior genotype. In contrast, the BRS G39 hybrid was one of the least stable and presented the highest mean. Therefore, it may not be the most recommended since it is unstable.

The factor analysis and GGE biplot results were discordant in the definition of ME. The exact definition of ME is only possible from repeated data over years. Therefore, the possible ME found in this study should be investigated for more years until the definition of ME, since the identification of the patterns that characterize ME is directly proportional to the number of environments evaluated. Yan et al. (2011) state that, in addition to classification in mega-environments, a tested site should be discriminative so that it can contrast differences among genotypes, and repeatable so that genotypes perform better over the years. Bhartiya et al. (2017), using GGE biplot to study GE interaction in soybean, identified discriminative and representative locations to be used in multi-location trials.

Considering the information from both analyzes, it was possible to notice that the environments of Vilhena A and B (in the years of 2012 and 2013) have always remained in the same ME, which reinforces the information of the representativeness and informativeness of these locals for the ME. Besides that, it was possible to observe that the efficiency of the factor analysis in capturing information was greater than in the GGE biplot since the five MEs absorbed a greater variance percentage than the two biplot axes. The factor analysis allowed for the easy identification of the Planaltina problem in 2013, in which only the inspection of its communality defined its exclusion from all the MEs, a fact that was confirmed by GGE biplot analysis when it was identified that Planaltina in 2013 was grouped separately from its pair (Planaltina 2012). Therefore, the genotypic recommendation for Planaltina requires a careful evaluation of the mean and genotypic stability as reported by Yan and Tinker (2006).

The genotypic adaptability interpretation was also possible in both analyzes. In the factor analysis, from the information from several dispersions, it was possible to identify the genotypes specifically adaptability to certain MEs, the widely adapted genotypes, and the poorly adapted genotypes. In the GGE biplot, this identification was made based on a graph and was dependent on the environment representativeness and informativeness; thus, it was only possible to identify genotypes of wide adaptability. Based on the information from both analyzes, it was possible to highlight BRS 387 and Embrapa 122 (T) genotypes as widely adapted for ME1. On the other hand, the genotypes BRS 324 and BRS 315 should be discarded since they showed low adaptability and low averages in the ME to which they belong (Figure 2 d).

Table 1. Identification, name and classification of sunflower genotypes evaluated out-of-season in 2012 and 2013 by the Sunflower Trials Network of Brazil.

Identification	Genotype	Classification	Identification	Genotype	Classification
1	Dow M734 (T)	Hybrid	9	BRS G34	Hybrid
2	HELIO 358 (T)	Hybrid	10	BRS 315	Variety
3	Embrapa 122 (T)	Variety	11	BRS G38	Hybrid
4	MG 341	Hybrid	12	BRS G39	Hybrid
5	HLE 20	Hybrid	13	BRS 323	Hybrid
6	HLE 22	Hybrid	14	BRS 324	Variety
7	HLE 23	Hybrid	15	V 90631	Hybrid
8	BRS 387	Hybrid	16	BRS G36	Hybrid

Table 2. Description of the environments used for evaluation of the sunflower genotypes between 2012 and 2013.

Id.	Municipalities	State †	Year	Latitude	Longitude	Altitude	Rainfall	Irrigation
1	Nova Porteirinha	MG	2012	15º48'09" S	43º18'02" W	436 m	33.9 mm	368 mm
2	Planaltina	DF	2012	15º35'30" S	47º42'30" W	1007 m	314.6 mm	0.0 mm
3	Palmas	TO	2012	10º12'46" S	48º21'37" W	230 m	585.0 mm	0.0 mm
4	Uberlândia	MG	2012	18º57'16" S	48º10'46" W	920 m	337.5 mm	0.0 mm
5	Vilhena A	RO	2012	12°44'26" S	60°08'45" W	615 m	1060 mm	0.0 mm
6	Vilhena B	RO	2012	12°44'26" S	60°08'45" W	615 m	1060 mm	0.0 mm
7	Planaltina	DF	2013	15º35'30" S	47º42'30" W	1007 m	310.6 mm	0.0 mm
8	Chapadão do Sul	MS	2013	18º47'39" S	52º37'22" W	810 m	496 mm	0.0 mm
9	Campo Verde	MT	2013	15°45'12" S	55°22'44" W	740 m	391.4 mm	0.0 mm
10	Jaíba	MG	2013	15°20' 18" S	43°40' 28" W	436 m	0.0 mm	307 mm
11	Manduri	SP	2013	23°00'12" S	49°19'19" W	589 m	888.9 mm	0.0 mm
12	Muzambinho	MG	2013	21°22'14" S	46°31'34" W	944 m	585.2 mm	0.0 mm
13	Vilhena A	RO	2013	12°44'26" S	60°08'45" W	615 m	662.0 mm	0.0 mm
14	Vilhena B	RO	2013	12°44'26" S	60°08'45" W	615 m	662.0 mm	0.0 mm

† Minas Gerais: MG, Distrito Federal: DF, Tocantins: TO, Rondônia: RO, Mato Grosso do Sul: MS, Mato Grosso: MT, São Paulo: SP; Id.: Identification.

Table 3. Joint analysis of variance, expected error of sum of squares (SS), expected pattern of sum of squares, and expected pattern ratio for each variation source combination for the grain yield data (t ha^{-1}) evaluated in 16 sunflower genotypes cultivated in 14 environments by the Sunflower Trials Network of Brazil.

Sources of variation	Num. d.f.	Den. d.f.	Sum of Squares	Mean Squares	p-value	Expected error SS	Expected pattern SS	Expected pattern (%)
Block/E	42	300	-	-		-	-	-
Environment (E)	13	42	502.572	38.659	0.0000**	2.0462	500.526	99.59%
Genotype (G)	15	97	38.6168	2.5744	0.0064**	2.3610	36.2558	93.88%
GE interaction	97	300	70.1297	0.7229	0.0000**	15.268	54.8613	78.22%
Error	300	-	47.2217	0.1574		-	-	-
G + GE	112	-	108.746	-		17.629	91.1172	84.06%
Mean							2.013	
CV (%)							19.70	

** Significant according to a F-test at the 0.01 probability level; Num. d.f.: Numerator degrees of freedom; Den. d.f.: Denominator degrees of freedom; SS: Sum of squares; CV: coefficient of variation.

Table 4. Establishment of mega-environments according to communality and final factor loadings of the factor analysis.

Id.†	Environments	Communality	Final factor loadings				
			Factor 1	Factor 2	Factor 3	Factor 4	Factor 5
1	Nova Porteirinha 2012	0.6776	0.0721	**0.7883**	-0.1434	0.1250	-0.1213
2	Planaltina 2012	0.8205	0.2165	0.3538	0.1377	**0.7919**	-0.0488
3	Palmas 2012	0.7839	0.3251	0.3424	0.0148	**-0.7339**	-0.1486
4	Uberlândia 2012	0.7362	0.2611	**0.6924**	0.4312	-0.0522	-0.0050
5	Vilhena A 2012	0.9715	**0.9040**	0.1774	0.1026	-0.3274	0.0719
6	Vilhena B 2012	0.9248	**0.9136**	0.2925	0.0474	0.0479	-0.0018
7	Planaltina 2013	0.5797	0.3682	0.0157	0.4348	-0.4097	-0.2949
8	Chapadão do Sul 2013	0.8042	0.1074	0.1043	**0.8699**	0.1054	-0.1181
9	Campo Verde 2013	0.8863	0.4982	**0.7705**	0.1908	-0.0884	0.0140
10	Jaíba 2013	0.9515	-0.0992	0.0434	0.1564	-0.0790	**-0.9535**
11	Manduri 2013	0.9245	0.5969	**0.6945**	0.2500	-0.0752	0.1334
12	Muzambinho 2013	0.8826	**0.7704**	0.3682	-0.1656	0.1096	-0.3377
13	Vilhena A 2013	0.9782	**0.9398**	0.1697	0.1918	-0.1609	0.0592
14	Vilhena B 2013	0.8801	**0.8606**	0.1712	0.2881	0.1200	0.1128
Eigenvalues			6.6572	1.6697	1.4610	1.1053	0.9080
Eigenvalues percentage			47.551	11.926	10.436	7.8955	6.4860
Communality average			47.551	59.478	69.914	77.810	84.296

† Id.: Identification. Numbers in bold show in which factor the environment has the biggest loading.

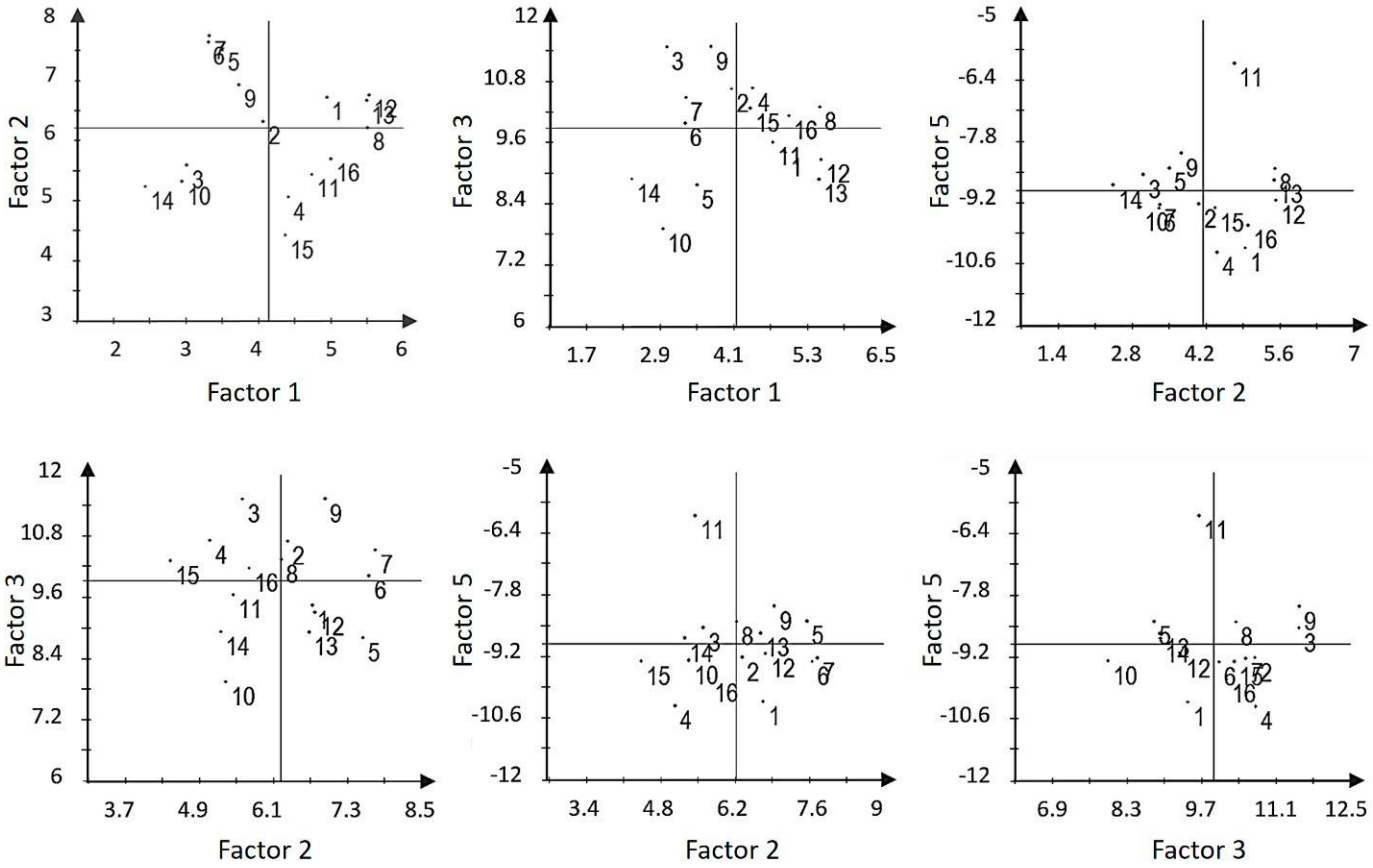

Figure 1. Genotype dispersion in relation to representative axes of environmental strata in the factor analysis. Factors 1, 2, 3 and 5 represent the mega-environments ME1, ME2, ME3, and ME5, respectively. The identification for the genotypes is described in Table 1.

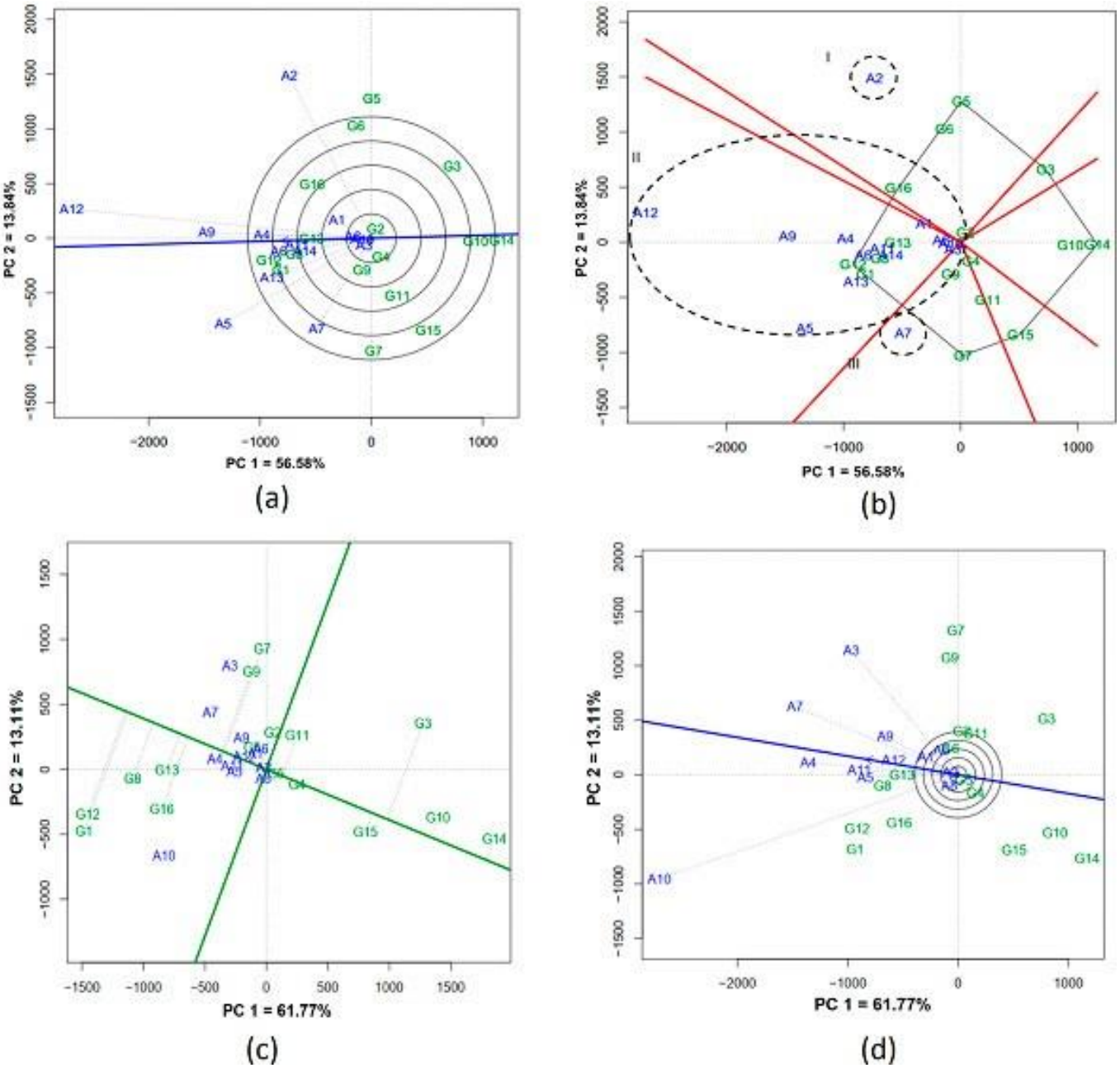

Figure 2. GGE biplots. (a) Similarity, discrimination and representativeness among the test environments. Non-parallel dotted lines represent the environment vectors, and the solid line represents the average-environment axis (AEA). (b) Which-won-where view. (c) Means versus stability. The arrow on the AEA indicates the direction of the highest grain yield average. The identifications for the genotypes and environments represented in (a), (b) and (c) are described in Tables 1 and 2. (d) GGE biplot for mega-environment one. Blue dotted lines represent the different environments. A1 refers to Nova Porteirinha 2012; A2: Palmas 2012; A3: Uberlândia 2012; A4: Vilhena A 2012; A5: Vilhena B 2012; A6: Chapadão do Sul 2013; A7: Campo Verde 2013; A8: Jaíba 2013; A9: Manduri 2013; A10: Muzambinho 2013; A11: Vilhena A 2013; A12: Vilhena B 2013. This biplot is based on environment-centered. The straight line, which passes the biplot origin, represents the AEA of the mega-environment.

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