



Biplot analysis of phenotypic stability in upland cotton genotypes in Mato Grosso

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ABSTRACT. Seed cotton yield is a trait governed by multiple genes that cause changes in the performance of genotypes depending on the cultivation environment. Breeding programs examine the genotype x environment interaction (GE) using precise statistical methods, such as AMMI (additive main effects and multiplicative interaction) and GGE biplot (genotype main effects + genotype x environment interaction). The AMMI method combines the analysis of variance and principal components, to adjust the main effects (genotypes and environments) and the effects of GE interaction, respectively. The GGE biplot groups the genotype additive effect together with the multiplicative effect of the GE interaction, and submits both of these to the principal components analysis. The aim of this study was to investigate the association between the AMMI and GGE biplot methods and select cotton genotypes that simultaneously showed high productivity of seed cotton and stability in Mato Grosso environments. Trials were conducted with cotton cultivars in eight environments across Mato Grosso State in the 2008/2009 crop season. The experiment used a randomized block design with 16 genotypes and four replicates per genotype x environment combination. Data for seeds

cotton productivity were analyzed by AMMI and GGE biplot methods. Both methods were concordant in the discrimination of environments and genotypes for phenotypic stability. The genotypes BRS ARAÇÁ and LD 05 CV had high seed cotton productivity and phenotypic stability, and could be grown in all environments across Mato Grosso State.

Key words: AMMI; GGE biplot; GE interaction; *Gossypium hirsutum*

INTRODUCTION

Upland cotton (*Gossypium hirsutum* L.r. latifolium Hutch.) is an economically important crop in Brazil, which is the world's fifth largest seed cotton producer, with 3.9 million tons produced in the 2014/15 crop. Production is concentrated in the State of Mato Grosso primarily in the municipalities of Primavera do Leste and Sapezal (CONAB, 2015).

Suinaga et al. (2006) reported that the cultivars Delta Opal and BRS Cedro are the most common in the State of Mato Grosso, as they bring together high seed cotton productivity, fiber percentage, and phenotypic stability. However, other cultivars, such as Araça BRS, BRS Buriti, FMT 701, and NUOPAL are also widely cultivated as they have high yield potential (Galbieri et al., 2011).

The breeding program of EMBRAPA Cotton aims to develop more productive genotypes with higher-quality fibers. To achieve this, a large number of genotypes (G) is tested annually in different environments (E), before final recommendation and multiplication. In most cases, these environments vary substantially, and there are interactions between genotypes and environments (GE), that arise from differential genotypic responses to the environment. Understanding GE interactions affords an assessment of the real impact of selection and ensures greater reliability when recommending genotypes to maximize productivity and other agronomic traits of interest in a specific location or group of environments (Cruz et al., 2014).

Despite its importance, a simple GE interaction analysis does not provide complete and accurate information about the behavior of each genotype across varying environments. Therefore, it is necessary to analyze adaptability and phenotypic stability, to identify genotypes with predictable behavior that are responsive to environmental variation in specific or general conditions. Recent methods include the AMMI model (Gauch and Zobel, 1988), which is a statistical method for understanding the structure of interactions between genotypes and environments, and the GGE biplot model (Yan et al., 2000), which considers the sum of the main effect of the genotype and the genotype and environment interaction. Both analyses are based on biplot graphs and represent a data matrix.

The GGE biplot model is best suited to identifying mega-environments, selecting representative and discriminative environments, and appointing more adapted and stable genotypes to specific environments (Yan, 2011). In contrast, AMMI analysis can be used efficiently for identifying superior environmental conditions for the agricultural holding (selection of growing regions) and higher mean performance genotypes (Gauch et al., 2008).

To date, the GGE biplot method has been used to investigate GE interactions in several crops, but has not been applied to upland cotton in Brazil. Thus, the aim of this study is to investigate the association between AMMI and GGE biplot methods and select cotton genotypes that simultaneously contain high seed cotton yield and stability in environments of Mato Grosso State.

MATERIAL AND METHODS

Eight cotton cultivar competition experiments were conducted during the 2008/2009 crop season in Mato Grosso State. Soil and climate features of each environment are shown in Table 1. The experimental design was a randomized complete block with 16 genotypes (BRS ARAÇA, BRS BURITI, BRS 286, FMT 701, FM 993, FM 910, DELTA OPAL, IPR JATAI, LD CV 05, LD CV 02, BRS CEDRO, NUOPAL, CNPA MT 05 1245, CNPA MT 04 2080, CNPA MT 04 2088, and BRS 293) and four replicates of each genotype x environment combination. Each experimental unit consisted of four rows 5 m long, spaced 0.9 m apart, with a density of 9 plants/m. In each experimental unit, seed cotton yield was evaluated in two central rows, corrected to 13% moisture, and extrapolated to kg/ha.

Table 1. Edaphoclimatic features of the eight tested environments.

Environments	Abbreviation	Altitude (m)	Latitude	Longitude	Annual rainfall (mm)
Primavera do Leste	PVA	636	15°33'	54°17'	1713
Pedra Preta	PET	850	16°37'	54°28'	1558
Campo Verde	CV	736	15°32'	55°10'	1529
Lucas do Rio Verde	LRV	399	13°03'	55°55'	1970
Sapezal	SAP	387	12°59'	58°45'	2082
Campo Novo dos Parecis	CNP	564	13°40'	57°53'	1939
Nova Ubiratã	NUB	396	13°00'	55°15'	1990
Primavera do Leste II	PVA II	636	15°33'	54°17'	1713

Seed cotton yield data for each genotype were analyzed individually with ANOVA, with genotypes as fixed effects and the environments as random effects. The relationship between the largest and smallest MS of the residuals from the individual ANOVAs did not exceed the ratio 7:1, permitting a joint analysis of trials (Banzatto and Kronka, 2006). Data were then analyzed for adaptability and stability with the AMMI and GGE biplot methods.

For the AMMI biplot analysis, we considered genotypes and environments as fixed effects and the model was specified according to the equation:

$$Y_{ij} = \mu + g_i + a_j + \sum_{k=1}^n \lambda_k \gamma_{ik} \alpha_{jk} + \rho_{ij} + \bar{\varepsilon}_{ij} \quad (\text{Equation 1})$$

where in: Y_{ij} is the mean response of the i -th genotype ($i = 1, 2, \dots, G$ genotypes) in the j -th environment ($j = 1, 2, \dots, E$ environments); μ is the overall mean of the trials; g_i is the effect of the i -th genotype; a_j is the effect of the j -th environment; λ_k is the k -th singular value (scalar) of the original interaction matrix (denoted by GE); γ_{ik} is the element correspondent to the i -th genotype in the k -th column of the GE matrix singular vector; α_{jk} is the element correspondent to the j -th environment in the k -th line of the GE matrix singular vector; ρ_{ij} is the noise associated with the term $(ge)_{ij}$ of the classical interaction of genotype i with the environment j ; and $\bar{\varepsilon}_{ij}$ is the mean experimental error.

The GGE biplot model was specified according to the equation:

$$Y_{ij} - y_j = y_1 \varepsilon_{i1} \rho_{j1} + y_2 \varepsilon_{i2} \rho_{j2} + \varepsilon_{ij} \quad (\text{Equation 2})$$

where in: y_{ij} is the mean population yield of the population of order i in the environment of order j ; y_j is the overall mean of genotypes in the environment j ; $y_1 e_{i1} r_{j1}$ is the first principal component (PC1); $y_2 e_{i2} r_{j2}$ is the second principal component (PC2); y_1 and y_2 are the eigenvalues associated with IPCA1 and IPCA2, respectively; e_1 and e_2 are the values of PC1 and PC2, respectively, of the genotype of order i ; r_{j1} and r_{j2} are the values of PC1 and PC2, respectively, for the environment of order j ; and e_{ij} is the error associated with the model of the i -th genotype and j -th environment (Yan et al., 2000). Analyses used the Agricolae and GGEgui packages implemented in R software (R Development Core Team, 2015).

RESULTS AND DISCUSSION

In the joint analysis (Table 2), all effects were significant ($P \leq 0.05$), indicating contrasts between environments and differential genotypic responses to environmental effects. This was confirmed by the edaphoclimatic conditions of each environment (Table 1) that show differences in altitude, latitude, and longitude, and climatic effects, such as rainfall and temperature. Similar significant differences in the effects of G, E, and GE interaction were obtained by Silva Filho et al. (2008), Souza et al. (2006), and Suinaga et al. (2006) when evaluating cotton genotypes in multi-environment trials in Brazil. Significant GE interactions for seed cotton yield indicated that analyzes of adaptability and stability were appropriate as edaphoclimatic factors had the greatest influence on genotypes.

Table 2. Summary of joint ANOVA of seed cotton yield of 16 genotypes tested in eight environments.

Components of variation	Degrees of freedom	Mean square
Blocks/Environments	24	1,569,116.36
Genotypes (G)	15	2,247,856.24*
Environments (E)	7	76,415,198.24*
GE	105	659,283.76*
Error	360	346,994.25
Coefficient of variation (%)	-	12.58

*Significant at 1% probability by the F-test.

In the AMMI1 biplot (Figure 1A), stability was interpreted from the ordinate axis, with scores close to zero considered as stable genotypes and environments. Adaptability was interpreted from the abscises axis, where the means of genotypes and environments are plotted (Gauch and Zobel, 1988). The genotypes DELTA OPAL (G7), and BRS BURITI (G2) were the most unstable and contributed the most towards GE interaction (Figure 1). The genotypes BRS ARAÇÁ (G1), LD CV 05 (G9), and LD CV 02 (G10), had lower coordinates on the PC1 axis (were most stable), and therefore contributed the least towards GE interaction. BRS ARAÇÁ (G1) and LD CV 05 (G9) performed above the overall mean (Table 3), demonstrating adaptation to all environments and were therefore classified as generalists.

The environment Pedra Preta (PET) had higher mean yield (Table 3) and proved to be more unstable (higher score on the PC1 axis). Environments Campo Novo dos Parecis (CNP), Sapezal (SAP), and Nova Ubiratã (NUB) presented the lowest scores on the PC1 axis (Figure 1), and were thus considered the most stable. According to Oliveira et al. (2003), environmental stability is of great importance as it indicates the reliability of the order of genotypes in a specific test environment, compared to the ranking of means of tested environments.

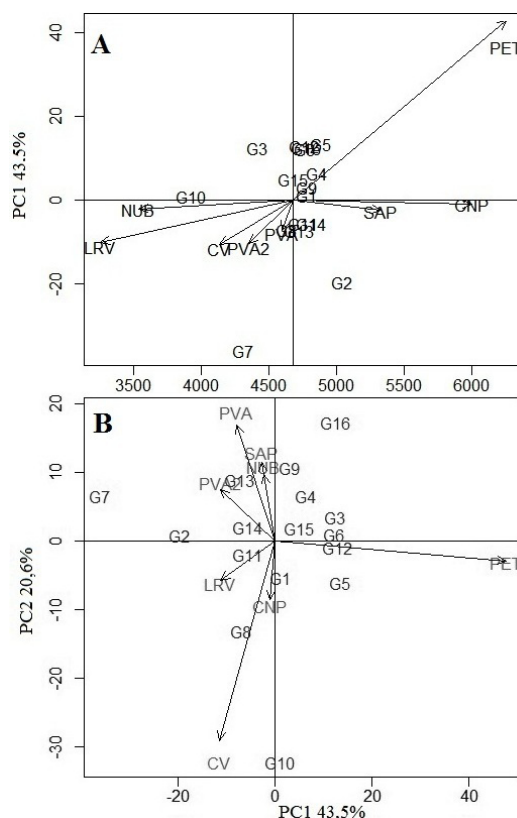


Figure 1. A. AMMI1 biplot of principal effects and GE interactions of seed cotton yield (kg/ha) and (B) AMMI2 biplot of the first principal component of the interaction (PC1) x second principal component of the interaction (PC2) of 16 genotypes, tested in eight environments (described in Table 1) across Mato Grosso.

Table 3. Mean seed yield (kg/ha) of 16 cotton genotypes in eight tested environments and overall mean of genotypes and environments¹.

Code	Genotype	PVA	PET	CV	LRV	SAP	CNP	NUB	PVA II	Mean
G1	BRS ARACA	4672	6505	4051	4086	5132	6248	3190	4414	4787
G2	BRS BURITI	4598	5636	4609	3937	6119	6313	4124	5012	5044
G3	BRS 286	4249	6541	3622	2854	5006	5677	3642	3763	4419
G4	FMT 701	4842	6688	4192	2995	5371	6023	4283	4484	4860
G5	FM 993	4400	7151	4341	3257	5682	6303	3241	4741	4889
G6	FM 910	4271	6953	3975	3338	5474	5930	3628	4594	4770
G7	DELTA OPAL	4827	4200	4072	3255	4888	5401	3409	4489	4318
G8	IPR JATAI	4435	5902	4811	3084	5344	5923	3387	4176	4633
G9	LD CV 05	4738	6475	3692	3501	5803	6082	3403	4562	4782
G10	LD CV 02	3180	5573	4379	2550	4083	5760	2725	3145	3924
G11	BRS CEDRO	4574	6060	4212	3712	5504	6093	3560	4348	4758
G12	NUOPAL	5164	7096	4361	3172	5024	5629	3287	4378	4764
G13	CNPA MT 05 1245	5098	5846	3826	2904	5396	6758	3312	4676	4727
G14	CNPA MT 04 2080	5026	6177	4482	3370	5502	5765	3614	4600	4817
G15	CNPA MT 04 2088	4686	6445	3999	3087	5192	6150	3697	4161	4677
G16	BRS 293	4797	6821	3575	3030	5747	5904	4177	4138	4774
Mean		4597	6254	4137	3258	5329	5997	3542	4355	4684

¹Environments described in Table 1.

AMMI2 biplot (Figure 1B) shows the stability of genotypes and environments, as well as specific GE interactions. The zone of stability corresponds to the central region of the biplot, at the intersection of zero scores on the first and second principal components axes. Genotypes and environments close to each other in any graph area represent specific adaptation of a genotype to the environment (Gauch and Zobel, 1988). Specific interactions were observed between LD CV 05 (G9) and Nova Uiratã (NUB) and Sapezal (SAP), CNPA MT 05 1245 (G13) and Primavera do Leste II (PVA2), BRS Araça and Campo Novo dos Parecis (CNP), and BRS Cedro and Lucas do Rio Verde (LRV).

Figure 2 shows a polygon connecting the genotypes BRS BURITI (G2), Delta Opal (G7), LD CV 02 (G10), BRS 286 (G3), and FM 993 (G5) that are furthest from the biplot point of origin. These genotypes have the highest vectors in their respective directions; the vector length and direction represents the extension of the genotypes response to the tested environments. All other genotypes are contained within the polygon and have smaller vectors, i.e., they are less sensitive to interaction with the environment in each sector (Yan and Rajcan, 2002). The vectors from the center of the biplot (0, 0) divide the graph into four sectors. Similar results were observed by Mattos et al. (2013), who observed six sectors of graph division when assessing the stem yield of sugarcane genotypes via the GGE biplot method.

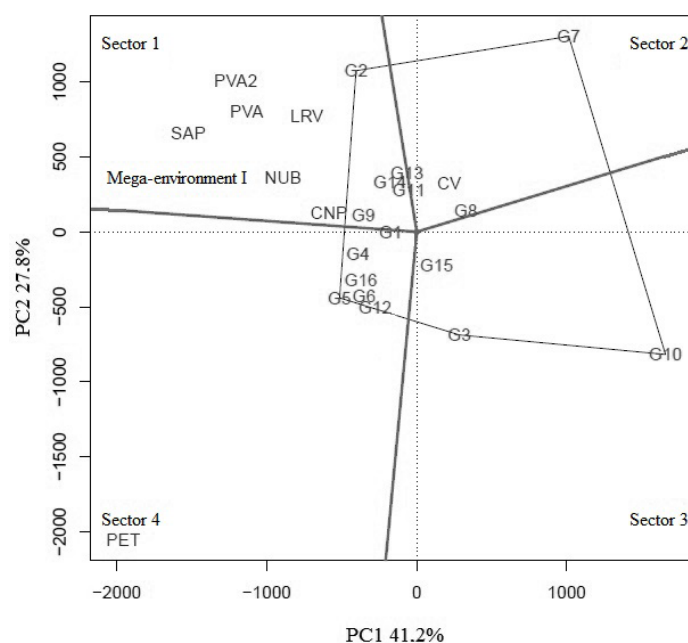


Figure 2. Sectors and mega-environments obtained from the GGE biplot model of seed cotton yield of 16 genotypes tested in eight environments (described in Table 1) across Mato Grosso.

Criteria for the formation of mega-environments are: significant differences between the genotypes in different environments; and variation, which is observed graphically, in one group must be significantly greater than in the other (Yan and Rajcan, 2002). The polygon from the GGE biplot (Figure 2) grouped the sites Campo Novo dos Parecis (CNP), Lucas do Rio

Verde (LRV), Primavera do Leste (PVA and PVA2), Nova Ubiratã (NUB), and Sapezal (SAP) in the mega-environment 1. The genotype BRS BURITI (G2) present at the vertex, achieved the highest means of seed cotton yield in the environments SAP and PVA2, and the highest mean among all of the genotypes (Table 3). When genotypes give rise to polygon vertices, but do not contain any clustered environments, they have low yield and are considered unsuited to the groups of tested environments (Karimizadeh et al., 2013). Thus, the genotypes BRS 286 (G3), LD CV 02 (G10), and CNPA MT 04 2088 (G15), located in Sector 3, are unsuitable for recommendation in these sites.

Seed cotton yield and stability of genotypes were assessed from the coordination of the middle environment (CAE) (Figure 3). Higher genotype projections on the CAE ordinate axis indicate more unstable genotypes, and a greater interaction with the environment (Yang et al., 2009). The genotypes BRS ARAÇÁ (G1) and LD CV 05 (G9) were notable for their phenotypic stability (Figure 3), showing high mean yield over all of the environments (Table 3). In contrast, the genotypes Delta Opal (G7) and BRS BURITI (G2) were the most unstable. Importantly, we note that the classification of genotypes based on phenotypic stability was similar from both methods used in this study, corroborating previous results (Balestre et al., 2009; Miranda et al. 2009; Camargo-Buitrago et al., 2011; Mattos et al., 2013; Sousa et al., 2015).

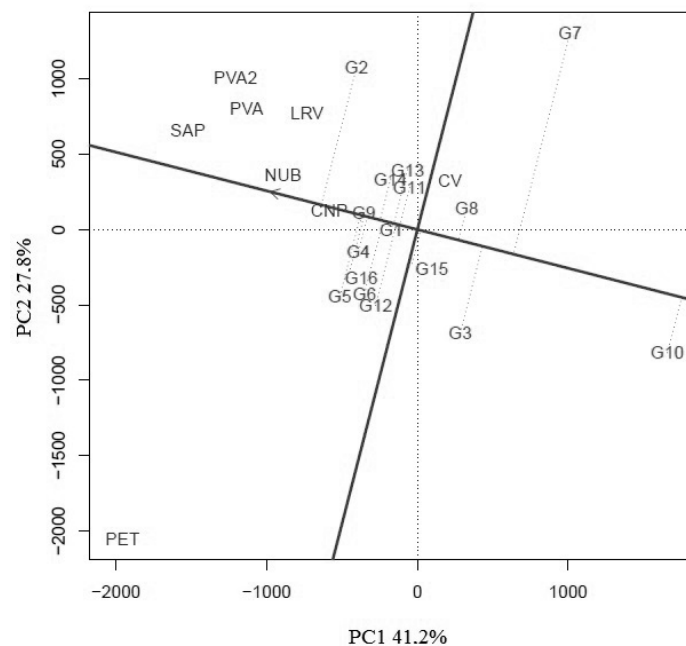


Figure 3. Mean *versus* stability assessed from the GGE biplot model of seed cotton yield of 16 genotypes tested in eight environments (described in Table 1) across Mato Grosso.

An ideal genotype should have a mean seed cotton yield that is consistently high over all environments of interest. This ideal genotype is graphically defined by the longest vector in PC1 and PC2 without projections, and represented by the arrow in the center of concentric circles (Yan and Rajcan, 2002). Although this genotype is more of a representative model, it is used as a reference for assessing genotypes. Thus, the genotypes LD CV 05 (G9) and FMT

0 9 1 31 36 50 5



Yang et al. (2009) concluded that an ideal environment should have a high PC1 score (greater power to discriminate genotypes from main genotype effects) and zero PC2 score (more representative of all the other environments). Similarly, the ideal environment is only a reference for selecting sites for multi-environment trials. Thus, the environment Sapezal (SAP) has, for the genotypes tested, the greatest ability to discriminate genotypes, and favor the selection of superior genotypes.

AMMI and GGE biplot methods were concordant in discriminating environments and genotypes for phenotypic stability. The genotypes BRS ARAÇÁ (G1) and LD CV 05 (G9) achieved high seed cotton yield and phenotypic stability in all environments across the State of Mato Grosso.

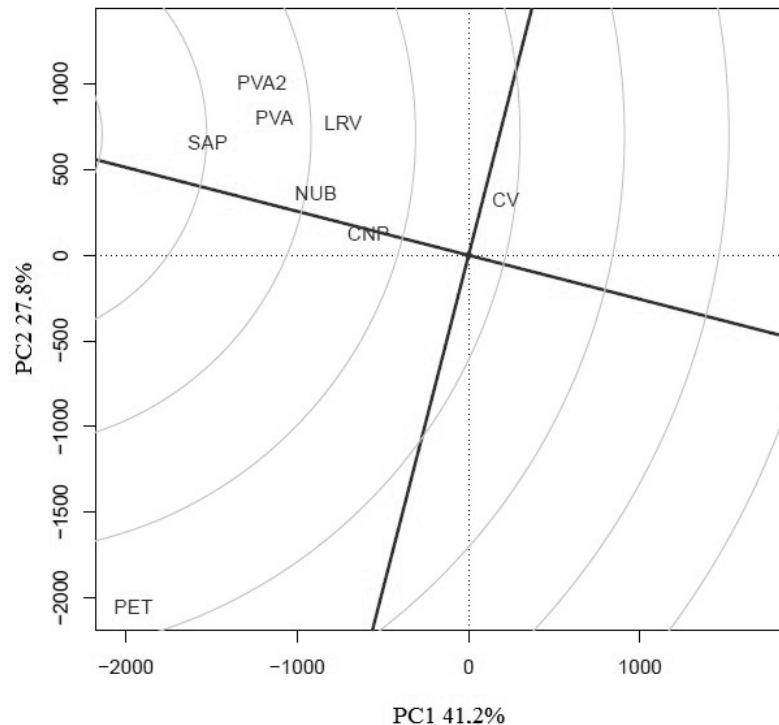


Figure 5. Relationship between the environments obtained from the GGE biplot model of seed cotton yield of 16 genotypes tested in eight environments (described in Table 1) across Mato Grosso.

Conflicts of interest

The authors declare no conflict of interest.

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