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Phenotypic adaptability and stability of herbaceous cotton genotypes in the Semiarid region of the Northeast of Brazil

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ABSTRACT: Cotton (*Gossypium hirsutum* L.) crop areas in the Northeast region of Brazil present high edaphoclimatic variability, which contributes to a strong genotype versus environment interaction (G × E). This situation requires the use of adaptability and stability methodologies to study G × E interaction before the selection and recommendation of cultivars. Among these methodologies, the genotype + G × E (GGE) biplot analysis has been currently used and highly recommended. Thus, the objective of this study was to evaluate the G × E of cotton genotypes through GGE biplot analysis, focusing on the identification of adapted and stable genotypes for the Semiarid region of the Northeast of Brazil. Four crop value and use tests were conducted in the municipalities of Apodi, state of Rio Grande do Norte, and Barbalha, state of Ceará, Brazil, in 2016 and 2017. A randomized block experimental design, with 17 treatments and four repetitions, was used. The treatments consisted of 17 cotton genotypes. The variables evaluated were: cotton seed and fiber yields. According to the analysis, the genotypes CNPA BA 2011-4436, CNPA BA 2011-1197, and CNPA BA 2010-1174 were stable and presented high adaptability to the evaluated region.

Key words: *Gossypium hirsutum* L., breeding, genotype versus environment interaction, GGE biplot analysis, yield

Adaptabilidade e estabilidade fenotípica de linhagens de algodoeiro herbáceo para as condições do semiárido nordestino

RESUMO: A cultura do algodoeiro (*Gossypium hirsutum* L.) na região do Nordeste brasileiro é submetida a alta variabilidade edafoclimática, o que contribui para a ocorrência de forte interação genótipo versus ambiente (G x A). Nessa situação, faz-se necessário o uso de metodologias de adaptabilidade e estabilidade para o estudo da interação G x A antes da seleção e recomendação de cultivares. Dentre estas, a análise genótipo + G x E (GGE) biplot se destaca como uma das mais recomendadas e usadas atualmente. O objetivo deste estudo foi avaliar a interação genótipo versus ambiente (G × A) de linhagens finais de algodoeiro por meio da metodologia GGE biplot, visando identificar genótipos adaptados e estáveis para as condições do semiárido nordestino. Foram conduzidos quatro ensaios de valor de cultivo e uso nas cidades de Apodi, RN, e Barbalha, CE, Brasil, nos anos de 2016 e 2017. O delineamento experimental foi de blocos casualizados, com 17 tratamentos e quatro repetições. Os tratamentos foram constituídos de 17 genótipos de algodoeiro. As variáveis avaliadas foram: produtividade de algodão em caroço e produtividade de fibra. A análise identificou as linhagens CNPA BA 2011-4436, CNPA BA 2011-1197 e CNPA BA 2010-1174 como estáveis e com ampla adaptabilidade para a região avaliada.

Palavras-chave: *Gossypium hirsutum* L., melhoramento, interação genótipo versus ambiente, produtividade e análise GGE Biplot

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INTRODUCTION

Herbaceous cotton (*Gossypium hirsutum* L.), also known as upland cotton among cotton fiber producers, has high global importance, since approximately 60 countries in tropical and subtropical regions consume and produce cotton, generating employment and income (Dhivya et al., 2014).

Brazil is one of the main cotton fiber producers and exporters in the world. Most cotton produced in Brazil is from the states of Bahia and Mato Grosso; these two states had mean cotton fiber yields of 1,800 and 1,662 kg ha^{-1} in the 2018/2019 crop season, respectively, making the country to reach a mean yield of 1,717 kg ha^{-1} (CONAB, 2020)

The development of breeding programs that select cultivars adapted to the conditions of the Semiarid region of the Northeast of Brazil is essential for maintaining cotton yield and increasing the competitive capacity of producers in this region (Farias et al., 1997). Herbaceous cotton has tolerance to droughts, which is important for semiarid regions. This crop is essential for the regional development and generation of jobs in the Brazilian Semiarid region, it results in different products that can be used for different purposes within different sectors; they can be marketed as fiber (textile industry), cotton seed (biodiesel production, kitchen oil), and bran (animal feed) (Zonta et al., 2016).

Detailed studies about adaptability and stability of cultivars considering environmental variations and characters of economic importance are needed for the safe recommendation of genotypes for this region (Silva & Duarte, 2006). Thus, the study of genotype versus environment interaction (G × E) are required before the selection and recommendation of cultivars. It is based on phenotypic stability and adaptability tests, and assists on the selection of the best genotypes (Ramalho et al., 2012; Carvalho et al., 2017).

GGE biplot analysis is a multivariate method that stands out among the methodologies that adequately explain the main effects of genotypes and environments and their interaction (Yan et al., 2000). This methodology was used in several studies on cotton crops (Farias et al., 2016; Silva Filho et al., 2017; Ali et al., 2017; Xu et al., 2017; Riaz et al., 2018; Sadabadi et al., 2018; Teodoro et al., 2018).

Thus, the objective of this study was to evaluate the G × E of cotton genotypes in the Semiarid region of the Northeast of Brazil, through GGE biplot analysis.

MATERIAL AND METHODS

The experiments conducted in the present study were part of the cotton crop value and use tests of the Cotton Breeding Program of the Brazilian Agricultural Research Corporation (Embrapa Algodão) for the conditions of the Semiarid region of the Northeast of Brazil. The experiments were conducted in 2016 and 2017 in the municipalities of Apodi, state of Rio Grande do Norte, and Barbalha, state of Ceará, Brazil.

The municipality of Apodi is located at 5° 37’ 19” S and 37° 49’ 6” W and presents altitudes ranging from 128 to 132 m; it is in the Chapada do Apodi microregion, Oeste Potiguar mesoregion, state of Rio Grande do Norte, Brazil, at 342 km distant from the state capital, Natal (IBGE, 2017). The mean annual air temperature in Apodi vary from 21 to 37 °C; the mean annual rainfall depth vary from 600 to 700 mm, with a rainy season starting in autumn. The climate of the region is BSwh, tropical semiarid, according to the Köppen classification (Zonta et al., 2016).

The experiment was conducted at the experimental station of the Agricultural Research Corporation of the State of Rio Grande do Norte (EMPARN). The soil of the experimental area was classified as a Typic Dystrudept of sandy-clay texture (49% sand, 45% clay, and 6% silt). The soil textural and physical attributes were analyzed at the Laboratory of Irrigation and Salinity of the Agricultural Engineering Academic Unit of the Federal University of Campina Grande (LIS-UAEA-UFCG), using soil samples from the 0-40 cm layer.

The municipality of Barbalha is located at 7° 18’ 18” S and 39° 18’ 7” W, with mean altitude of 414 m, in the Cariri Cearense region, in the state of Ceará, Brazil. The climate of the region is Aw, equatorial humid with dry winter, according to the Köppen classification, presenting mean annual rainfall depth of 1,047.9 mm (83.3% from January to April), mean annual air temperature of 24.1 °C, and air relative humidity of 63% (IBGE, 2017). The soil of the experimental area was classified as a Typic Udorthent, of clay-loam texture; its textural and physical attributes were analyzed in the same laboratory (LIS-UAEA-UFCG), using samples from the 0-40 cm layer.

Soil fertilizing was applied to the two experimental areas, according to technical recommendation to the crop, based on the soil fertility analysis (Table 1).

The experiments were conducted in a randomized block design with 17 treatments (genotypes) and four repetitions. The genotypes and respective breeders are listed in Table 2. The experimental plots consisted of two 5-m plant rows spaced 1.0 m apart (total area of 10 m^2).

All plots were equally irrigated with 3-day intervals to ensure the full establishment of plants; the irrigation water depth was determined by the crop evapotranspiration. The irrigation ended when the crop presented 60% opened bracts. Other cultural practices were carried out from planting to harvest, according to the production system recommended by the Embrapa Algodão.

A sprinkler irrigation system was used for each location, with flow of 1.49 m^3 h^{-1}, based on previous tests conducted by Bezerra et al. (2010). The experimental plot consisted of two 5-m plant rows spaced 0.90 m apart. The plants were spaced 0.14 m apart in the rows, totaling 70 plants per plot.

Table 1. Chemical attributes of the soil 0-0.40 m layer in the experimental areas. Apodi, RN, and Barbalha, CE, Brazil

Location	pH	P	Na^+	K^+	Ca^{2+}	Mg^{2+}	H + Al	CEC	OM
	H_2O	mg kg^{-3}		(cmol$_c$ dm^{-3})					(g kg^{-1})
Apodi RN	6.2	10.7	0.4	1.6	34.8	10.0	23.1	69.9	16.4
Barbalha CE	6.5	24.7	3.4	4.7	163.4	57.0	0.0	228.5	22.9

CEC - cation exchange capacity; OM - Organic matter

Table 2. Genotypes used in the cotton crop value and use tests

Treatments	Genotype	Breeder
G1	FM 993	BAYER
G2	BRS 286	EMBRAPA
G3	BRS 336	EMBRAPA
G4	CNPA BA 2011-102	EMBRAPA
G5	CNPA BA 2011-4436	EMBRAPA
G6	CNPA BA 2011-1197	EMBRAPA
G7	CNPA BA 2011-1149	EMBRAPA
G8	CNPA BA 2010-1174	EMBRAPA
G9	CNPA BA 2011-4964 FL	EMBRAPA
G10	CNPA BA 2011-4970 FL	EMBRAPA
G11	CNPA MT 2009-152	EMBRAPA
G12	CNPA GO 2010-152	EMBRAPA
G13	CNPA GO 2010-139	EMBRAPA
G14	CNPA NE 2012-2008	EMBRAPA
G15	CNPA NE 2012-2050	EMBRAPA
G16	CNPA NE 2012-143 FL	EMBRAPA
G17	CNPA NE 2012-5-1-1 COL	EMBRAPA

The variables evaluated were cotton seed yield (CSY, kg ha^{-1}) and cotton fiber yield (CFY, kg ha^{-1}). The data were obtained and statistical analyses were carried out using the Genes 1990.2018.49 program (Cruz, 2013), and the Agricolae and GGEGui packages were installed in the R program (R Development Core Team, 2014) to plot the graphs with the first and second principal components (PC1 and PC2) of the GGE biplot analysis.

The joint analysis of variance was carried out according to Ramalho et al. (2012), considering the effects of the genotypes as fixed and the effects of the locations as random efects, using Eq. 1:

$$Y_{ij} = m + \left(\frac{b}{a}\right)_{ka} + g_i + a_j + (ga)_{ij} + e_{ij} \qquad (1)$$

where:

m - overall mean;

$(b/a)_{ka}$ - effect of the block k within the location a (k = 1, 2, 3, 4);

g_i - effect of the genotype i (i = 1, 2, ..., 17);

a_j - random effect of the location a (a = 1 a 4);

$(ga)_{ij}$ - effect of the interaction between the genotype i and the location a; and,

e_{ij} - experimental error.

The CSY and CFY data were used for the adaptability and stability analyses, considering each year-location combination as an environment. Thus, the performance of the cotton genotypes was evaluated in four environments: Apodi 2016 (E-1), Barbalha 2016 (E-2), Apodi 2017 (E-3), and Barbalha 2017 (E-4). The adaptability and stability of the genotypes were evaluated through GGE biplot analysis using Eq. 2 (Yan et al., 2000):

$$Y_{ij} - y_i = y_1\varepsilon_{i1}\rho_{j1} + y_2\varepsilon_{i2}\rho_{j2} + \varepsilon_{ij} \qquad (2)$$

where:

Yij - mean yield of the population i in the environment j;

y_j - overall mean of genotypes in the environment j;

$y_1\varepsilon_{i1}\rho_{j1}$ - first principal component (PC1);

$y_2\varepsilon_{i2}\rho_{j2}$ - second principal component (PC2);

y_1 and y_2 - values associated with the IPCA1 and IPCA2, respectively;

ε_1 and ε_2 - values of PC1 and PC2, respectively, of the genotype i;

ρ_{j1} and ρ_{j2} - values of PC1 and PC2, respectively, of the environment j; and,

ε_{ij} - error associated with the model of the ith genotype and jth environment.

The correlation between the highest and lowest residual mean square of the individual analysis of variance was evaluated before the joint analysis of the data. The value found did not exceed the ratio 7:1, thus, the residual variances were homogeneous and allowed for the joint analysis of the experiments (Pimentel-Gomes, 2000).

RESULTS AND DISCUSSION

The results of the joint analysis of variance are shown in Table 3. The analysis showed that the genotypes and the G × E had significant effects ($p \leq 0.01$) on the characters evaluated. The significantly different results of the genotypes in the different environments indicated the need for a detailed study of G × E, and enabled the application of studies on the adaptability and stability of the genotypes.

The coefficients of variation in the joint analysis were 16.18% for cotton seed yield (CSY) and 16.72% for cotton fiber yield (CFY), which are medium variances, below 20%, according to Pimentel-Gomes (2000).

These variables are quantitative and, thus, very affected by the environment. Therefore, variances of 10 to 20% are expected. Similar variances were found for these variables in experiments evaluating cotton crops, conducted by Farias et al. (2016) and Carvalho et al. (2016).

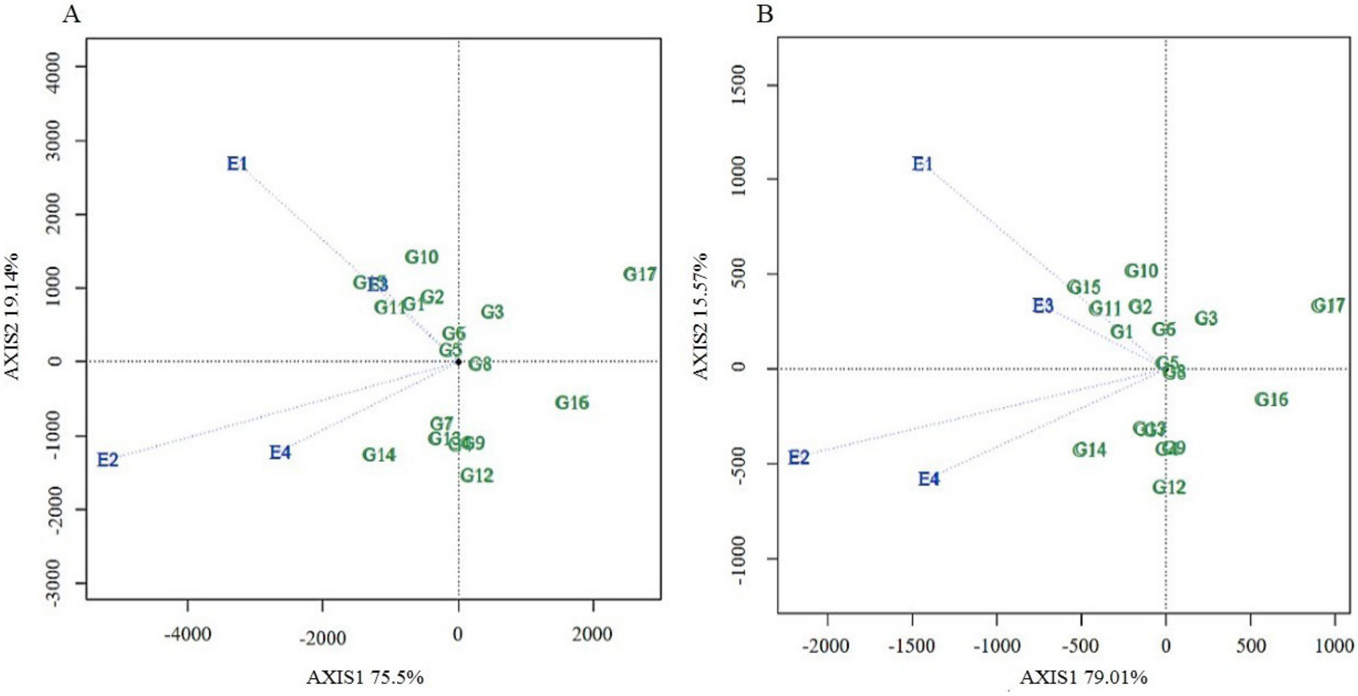
The GGE biplot analysis was used to graphically represent the 17 genotypes (G1 to G17) and 4 environments (E1 to E4) evaluated, as shown in Figures 1A and B.

Figure 1A shows that 75.5% of the variance was explained by PC1, and 19.14% by PC2. The graph of the GGE biplot analysis explained 94.64% and 94.58% of the total variance of G × E for CSY and CFY, respectively (Figure 1B). These results are higher than the minimum percentage of explanation (70%) recommended by Yan et al. (2000), and higher than those found in other studies using GGE biplot analysis for cotton crops (Ng et al., 2013; Farias et al., 2016; Ali et al., 2017; Teodoro et al., 2018).

Table 3. Joint analysis of variance for cotton seed yield (CSY) and cotton fiber yield (CFY)

Source of variation	Mean square		
	Degrees of freedom	CSY	CFY
Block/E	12	9733377.47	2789712.76
Genotype (G)	16	152564441.06**	33100293.14**
Environment (E)	3	159613376.63**	25045613.93**
G × E	48	89749753.26**	13744051.39**
Residual	192	163420329.72	28420939.73
Mean (kg ha^{-1})		5698.76	2299.70
Coefficient of variation (%)		16.18	16.72

** - Significant at $p \leq 0.01$ by the F test

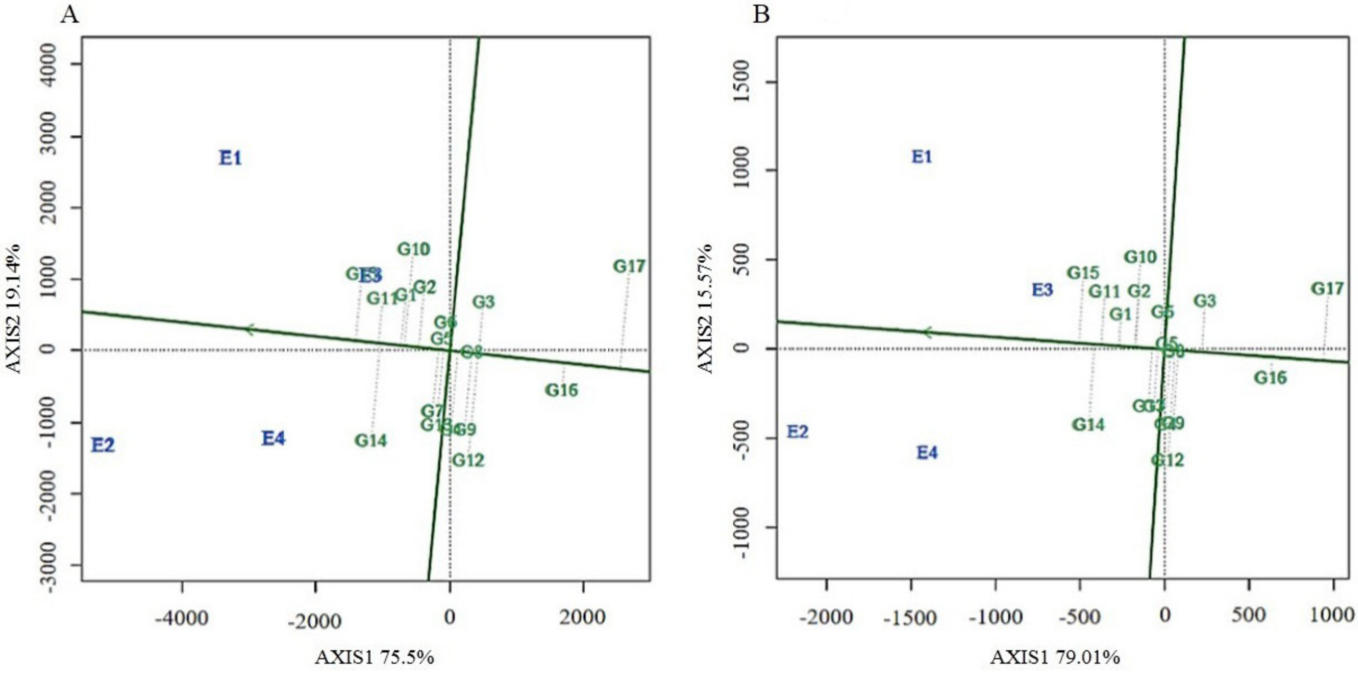


Environments: E1 - Apodi 2016, E2 - Barbalha 2016, E3 - Apodi 2017, E4 - Barbalha 2017. Genotypes: G1 - FM-993; G2 - BRS-286; G3 - BRS-336; G4 - CNPA-BA-2011-102; G5 - CNPA-BA-2011-4436; G6 - CNPA-BA-2011-1197; G7 - CNPA-BA-2011-1149; G8 - CNPA-BA-2010-1174; G9 - CNPA-BA-2011-4964-FL; G10 - CNPA-BA-2011-4970-FL; G11 - CNPA-MT-2009-152; G12 - CNPA-GO-2010-152; G13 - CNPA-GO-2010-139; G14 - CNPA-NE-2012-2008; G15 - CNPA-NE-2012-2050; G16 - CNPA-NE-2012-143-FL; G17 - CNPA-NE-2012-5-1-1-COL

Figure 1. Genotype + genotype × environment (GGE biplot analysis) for cotton seed yield (CSY, kg ha^{-1}) (A) and cotton fiber yield (CFY, kg ha^{-1}) (B) of 17 cotton genotypes in four environments

According to Hongyu et al. (2015), the straight line from the biplot central point to the environment or genotype name is called environment vector or genotype vector, and shows the specific G × E of these vectors (performance of each genotype in each environment). The environment E2 (Barbalha 2016) significantly contributed to the interaction (more distant from the center of the graph), followed by the environment E1 (Apodi 2016) and E4 (Barbalha, 2017), whereas environment E3 (Apodi, 2017) had the lowest contribution.

The genotype distribution from the central point of the graph was relatively homogeneous (Figures 1A and B). According to Riaz et al. (2018), the stability zone corresponds to the central



Environments: E1 - Apodi 2016, E2 - Barbalha 2016, E3 - Apodi 2017, E4 - Barbalha 2017. Genotypes: G1 - FM-993; G2 - BRS-286; G3 - BRS-336; G4 - CNPA-BA-2011-102; G5 - CNPA-BA-2011-4436; G6 - CNPA-BA-2011-1197; G7 - CNPA-BA-2011-1149; G8 - CNPA-BA-2010-1174; G9 - CNPA-BA-2011-4964-FL; G10 - CNPA-BA-2011-4970-FL; G11 - CNPA-MT-2009-152; G12 - CNPA-GO-2010-152; G13 - CNPA-GO-2010-139; G14 - CNPA-NE-2012-2008; G15 - CNPA-NE-2012-2050; G16 - CNPA-NE-2012-143-FL; G17 - CNPA-NE-2012-5-1-1-COL

Figure 2. Genotype + genotype × environment (GGE biplot analysis; mean × stability) for cotton seed yield (CSY; kg ha^{-1}) (A) and cotton fiber yield (CFY; kg ha^{-1}) (B) of 17 cotton genotypes in four environments

region of the biplot, in the intersection of zero in PC1 and PC2. Thus, the CSY and CFY of the genotypes G5 (CNPA BA 2011-4436), G6 (CNPA BA 2011-1197), and G8 (CNPA BA 2010-1174) were stable; and those of the genotypes G16 (CNPA NE 2012-143 FL) and G17 (CNPA NE 2012-5-1-1 COL) were unstable, presenting the highest distances from the center of the graph.

According to Gauch & Zobel (1996), the proximity of genotypes to an environment in any area of the graph denotes the specific adaptability of the genotype to that environment. The genotypes G15 (CNPA NE 2012-2050), G11 (CNPA MT 2009-152), G1 (FM 993), and G10 (CNPA BA 2011-4970 FL) were close to the environment E3 (Apodi 2017) (Figures 1A and B). The formation of this group denotes that these genotypes were the most adapted to that environment.

The production yield and stability of each genotype are shown in Figures 2A and B. According to Yan (2011), the GGE biplot (mean × stability) is an efficient tool to evaluate genotypes in both aspects. The straight line with an arrow passing through the biplot central point indicates the direction of the genotypes with higher performances (Hongyu et al., 2015).

Therefore, the genotypes in the left to right direction of the graph had the highest yields (CSY and CFY); these genotypes were: G15 (CNPA-NE-2012-2050), G11 (CNPA-MT-2009-152), G14 (CNPA-NE-2012-2008), G1 (FM-993), G10 (CNPA-BA-2011-4970-FL), G2 (BRS-286), G7 (CNPA-BA-2011-4436), G5 (CNPA-BA-2011-4436), G6 (CNPA-BA-2011-1197), and G8 (CNPA-BA-2010-1174) (Figures 2A and B). The least three (G5, G6, and G8), despite the average production performance, were the genotypes that presented the best stability and adaptability to the environments, since they were closest to the central axis of the graph, as shown in Figures 1A and B. The genotypes G16 and G17, located more distant from the center and at the right of the graph, had the lowest yields, considering the whole set of tests.

Conclusions

1. The cotton seed yield and cotton fiber yield of the genotypes within the four environments evaluated were different, denoting the existence of genotype-environment interaction (G × E). E2 (Barbalha, 2016) was the environment that most contributed to the interaction, and E3 (Apodi, 2017) presented the lowest contribution.

2. CNPA-BA-2011-4436, CNPA-BA-2011-1197, and CNPA-BA-2010-1174 were the most promising genotypes, presenting high production potential, adaptability, and stability. Therefore, these genotypes are recommended for approval and launch of cultivars focused on environments in the Semiarid region of the Northeast of Brazil.

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