

ENVIRONMENTAL STRATIFICATION IN THE BRAZILIAN CERRADO ON THE YIELD AND FIBER QUALITY OF COTTON GENOTYPES

ESTRATIFICAÇÃO AMBIENTAL NO CERRADO BRASILEIRO SOBRE O RENDIMENTO E A QUALIDADE DA FIBRA DOS GENÓTIPOS DE ALGODÃO

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ABSTRACT. Environmental stratification studies are important for the plant breeding, since they allow to adequately plan the experimental network. The objective of this work was to identify similar environments for cotton cultivation in the Brazilian Cerrado regarding yield and fiber quality. Nineteen field studies were carried out in a randomized complete block design with twelve genotypes and four replicates. Agronomic (cotton seed yield and fiber percentage) and technological traits (length, micronaire, fiber strength) were evaluated. These results indicate that there are six environments (PVA3, MON, SHE1, SIN, PPA e TRIN) in which the cotton trials should be installed as a matter of priority owing to the phenotypic response pattern obtained for the evaluated traits. The remaining 13 environments are similar to each other for all traits and can be summarized in strategic locations depending on the ease of installation of the trials.

KEYWORDS: *Gossypium hirsutum*. Genotypes x environments interaction. Fiber quality.

INTRODUCTION

The development and release of cotton cultivars in Brazil follows growers demands for competitive fiber yield, and fulfill industrial textile requirements in the Cerrado environment, the largest cotton growing area in Brazil (MORELLO et al., 2010, MORELLO et al., 2012; MORELLO et al., 2015). Before cultivar recommendation, multiple assays are performed to evaluate genotypes in different environments. The differential behavior of a genotype for a given trait as a function of environmental variation is defined as genotype x environment (GxE) interaction. Thus, investigating the GxE interaction is essential for accurate recommendation of the best genotypes for a given region.

For this, the breeders perform several trials in the final stages of breeding programs. Regarding this, Embrapa Algodão divided its experimental network into two large regions from Brazil: Cerrado and Semi-Arid, where most cotton cultivation is concentrated in the Cerrado, according data from Conab (2017). This biome occupies about 22% of the Brazilian territory and has peculiar edaphoclimatic characteristics along its extension in terms of rainfall, temperature, relative air humidity, as well as different types of soil.

Recently, in this biome has been highlighted an important growing modality denominated off-

season cotton, characterized by the sowing of the cotton after the harvest of a previous growing in rainfed system (FREIRE, 2015). This practice has been carried out by farmers in the Mid-West region after the soybean harvest, sown in early October. This fact also contributes to the GxE interaction observed among the sites located in the Cerrado, since the climatic conditions of the off-season are different from those found in the traditional growing season.

In this sense, valuable information for breeding programs concerns environmental stratification. It is important to identify similarity in the pattern of response of genotypes throughout the experimental network. Lin (1982) proposed an algorithm to estimate the sum of squares of the GxE interaction and to cluster environments whose interaction is not significant. In addition to facilitating the recommendation of the best genotypes, this procedure makes it possible to evaluate the representativeness of the network and allows the breeder to make decisions regarding the disposal of environments, aiming at minimizing the cost with the trials.

Another way of identifying environments is through the phenotypic correlation between environments. Environments whose genotypes have similar performance have high magnitude correlations. The representation of these estimates can be made through the correlation network. This

analysis has already been used efficiently to characterize complex systems in many areas, such as biology (URSEM et al., 2008; DILEO et al., 2011; PEARCE et al., 2015), public health (SABA et al., 2014) and food science (Monforte et al. 2015). However, there are no studies using the correlation network for environmental stratification in plant breeding.

Silva Filho et al. (2017) evaluated the environmental stratification of cotton genotypes for cotton seed yield. However, environmental stratification studies of traits related to fiber quality do not yet exist. Therefore, the objective of this study was to identify similar environments for cotton growing in the Brazilian Cerrado regarding yield and quality fiber.

MATERIAL AND METHODS

Nineteen trials of cotton cultivars were conducted in the 2013/2014 and 2014/2015 harvests (years). The environments were constituted by the combinations between locations and years, according to edaphoclimatic characteristics (Table 1) and graphic representation of locations. The cultivars used as standards were: (TMG 41 WS, TMG 43 WS, IMA CV 690, IMA 5675 B2RF, IMA 08 WS, NUOPAL, DP 555 BGRR, DELTA OPAL, BRS 286, BRS 335, BRS 368 RF and BRS 369 RF). The cultivars were not the same in all years and locations. The selection was based on the criterion of participation in the largest number of experiments, to reduce the imbalance of the analysis of variance.

Table 1. Locations and geographic coordinates as altitude (ALT), latitude (LAT), longitude (LONG), rain fall (RF), average annual temperature (TEMP) in the 2013/2014 and 2014/2015 harvests.

Location/State	Initials ¹	Harvest	Alt. (m)	Lat. (S)	Long. (W)	RF. (mm)	Temp. (°C)	Climate ²
Trindade/MG	TRI	2013/2014	927	21°06'	44°10'	1467	23.2	Aw
Santa Helena do Goias/GO	SHE1 SHE2	2013/2014 2014/2015	562	17°48'	50°35'	1539	24.3	Aw
Pedra Preta/MT	PPA1 PPA2	2013/2014 2014/2015	248	16°37'	54°28'	489	25,1	Bsh
Primavera do leste/MT	PVA1 PVA2 PVA3 PVA4	2013/2014 2013/2014 2014/2015 2014/2015	465	15°33'	54°17'	1784	22,0	Aw
Campo Verde/MT	CV1 CV2	2013/2014 2014/2015	736	15°32'	55°10'	1902	26.3	Af
Sinop/MT	SIN	2013/2014	345	11°51'	55°30'	1818	25.0	Aw
Luiz Eduardo Magalhães/BA	LEM	2013/2014	769	12°5'	45°47'	1511	24.2	Aw
São Desidério/BA	SDES	2013/2014	497	12°21'	44°58'	1289	24.7	Aw
Montividiu/GO	MON	2013/2014	821	17°26'	51°10'	1512	23.0	Aw
Magalhães de Almeida/MA	MAG	2013/2014	36	03°23'	42°12'	1430	27.2	Aw
Teresina/PI	TER	2013/2014	72	05°05'	42°48'	1349	27.6	Aw
Chapadão do Sul/MS	CHA	2014/2015	810	18°47'	52°37'	1600	22.7	Aw
Sorriso/MT	SOR	2014/2015	365	12°32'	55°42'	1883	25.0	Aw

¹: abbreviations of locations. ²: Köppen classification.

The experimental design used in each trial was a randomized complete block with 12 treatments and four replicates. Experimental unit consisted of four rows of 5 m in length, spaced at 0.90 m between rows with a density of 9 m⁻¹ plants. In each experimental unit, cotton seed yield was evaluated in the two central lines, being corrected for 13% moisture and extrapolated to kg ha⁻¹ by covariance method.

The joint analysis of variance considered effect of genotypes (G) as fixed and effects of environments (E) and genotypes x environments (G x E) as random. The environments were stratified by Lin (1982) traditional method and the clusters were constituted by genotypes whose mean squares values of the G x E interaction were not significant. The F test estimated the probability of forming groups using the Genes software (CRUZ, 2013).

The graphical expression was performed by the functional relationship between the estimates of the correlation coefficients between the environments using the correlations network, performed by Rbio software (BHERING, 2017), in which the proximity between nodes (traces) is proportional to the total correlation value between these (FRUCHTERMAN; REINGOLD, 1991) using package “qgraph”. The thickness of the edges was controlled by applying the cut-off value equal 0.60, wherein only $|r_{ij}| \geq 0.60$ have their edges highlighted. Thus, positive correlations were highlighted in green, while negatives in red.

RESULTS AND DISCUSSION

The effect of genotypes was significant for all traits evaluated (Table 2), except cotton seed yield (YIELD). This is explained by the environment effects magnitude and GxE interaction, which consumed the variability among the genotypes for this trait (CRUZ et al., 2012). For the effects of environment and G x E interaction the traits were significant. Therefore, the data presented here has credibility for the study on environmental stratification in agronomic and technological traits of cotton.

Table 2. Summary of the joint analysis of variance for the agronomic traits cotton seed yield (YIELD) and fiber percentage (FP) and technological variables micronaire (MIC), fiber length (FL) and fiber strength (FS) evaluated in 12 early cotton genotypes in 19 trials in Brazilian Cerrado in the 2013/2014 e 2014/2015 harvest.

Variation sources	DF	YIELD	FP	MIC	FL	FS
Block/Environment	54	582221.44	4.32	0.13	0.73	2.91
Genotype (G)	11	1310128.57 ^{ns}	136.68**	1.86**	23.79**	79.78**
Environment (E)	18	61511492.56**	104.32**	5.00**	35.18**	88.02**
GxE	198	874829.53**	7.84**	0.13**	1.06**	3.76**
Error	627	333939.13	2.51	0.06	0.58	2.33**
CV (%)		13.88	3.77	5.77	2.55	5.04

** : Trait/source combinations marked with asterisk are significantly different ($P < 0.01$); ^{ns}: not significance; by the F test. DF: degrees of freedom. CV: coefficient of variation.

The presence of significant GxE interaction can be attributed to predictable factors such as: soil management, pest and disease, additional irrigation, basis fertilizer and other; and unpredictable: rainfall, temperature, air humidity and radiation throughout the crop cycle, among others. Similar results were verified by other authors when studying the G x E interaction in cotton in localities in Brazil (SOUZA et al., 2006; SUINAGA et al., 2006; SILVA FILHO et al., 2008; FARIAS et al., 2016).

The coefficient of variation estimates obtained in the joint ANOVA show good experimental accuracy according to the Pimentel-Gomes (2015) and are inferior to other works related to the competition cotton genotypes (BLANCHE; MYERS 2006; BAXEVANOS et al., 2008; NG et al., 2013; NAI-YIN et al., 2013; FARIAS et al., 2016).

By forming groups of localities with non-significant interaction due to the YIELD (Table 3), the environments MAG, TER, SIN, CV1, LEM, PVA2, SOR, CHA, CV2 and PPA2 demonstrated similarity among themselves. MON and PVA3 presented different behavior in relation to the other environments. Considering that each localities and year characterize a different environment, it can be

assumed that YIELD was affected by changes in the environment. In addition, there are fluctuations in altitude, latitude and longitude in the main cotton producing regions of Brazil. These peculiar features of the country reinforce the importance of environmental stratification studies for the main agricultural crops, such as cotton.

These results indicate that it is important to evaluate the YIELD in MON and PVA3, these environments have edaphoclimatic characteristics that provided different behavior of the genotypes. The clustering of the other clustered environments demonstrates the possibility of reducing the Cerrado experimental network, allowing the Embrapa breeding program to optimize its financial resources.

For FP, localities that did not demonstrate similarity were SHE1, SIN, MON and PVA3; the others formed a group with non-significant GxE interaction. The PPA1 environment had no similarity pattern with no other environment for the MIC trait. Similar fact occurred for FL, where PVA3 was the only environment that did not cluster with the other environments. For the FS trait, TRIN, SIN and PVA3 environments were isolated and showed no similarity.

Table 3. Clustering of cotton cultivar for cotton seed yield (YIELD) and fiber percentage (FP) and technological variables micronaire (MIC), fiber length (FL) and fiber strength (FS) based on the non-significant G x E interaction, according to Lin (1982), in 19 environments and 12 genotypes.

Trait	Similar Environments	¹ F _{cal}	F _{tab}	Non-similar environments
YIELD	MAG, TER, SIN, CV1, LEM, PVA2 SOR, CHA, CV2 and PPA2	1.18	1.27	PVA3 and MON
FP	MAG, CHA, PVA1, PVA2, PVA4, LEM, SDES, CV1, CV2, PPA1, PPA2, TRIN, SHE2, SOR and TER	0.91	1.21	SHE1, SIN, MON and PVA3
MIC	SDES, CHA, TRIN, LEM, SHE1, SHE2, PPA2, PVA1, PVA2, PVA4, CV1 and CV2	1.19	1.24	PPA1
FL	CV1, CV2, SHE1, TRIN, PPA1, PPA2, SDES, SIN, LEM, SHE2, SOR, PVA1, PVA2, PVA4, CHA and MAG	1.18	1.21	PVA3
FS	CV1, CV2, PPA1, PPA2, CHA, SHE2, SHE1, PVA1, PVA4, MAG, TER, SDES, PVA2, SOR and MON	1.14	1.21	TRIN, SIN and PVA3

¹F_{cal}: calculated F value; F_{tab}: tabulated F value at 5% probability.

In the correlation network analysis, the environments were represented by nodes, which are connected by traces. Each end contains a thickness that indicates the correlation magnitude (weak, moderate or strong). Figure 1A demonstrates the phenotypic correlations network for the YIELD. It is possible to

observe that the correlations were positive and of high magnitude (>0.70) only for the SHE2, SHE1, SDE and PPA1 environments; and moderate in SHE1, TRI and TER, MAG. These results demonstrate that identifying redundant localities for this trait is harder.

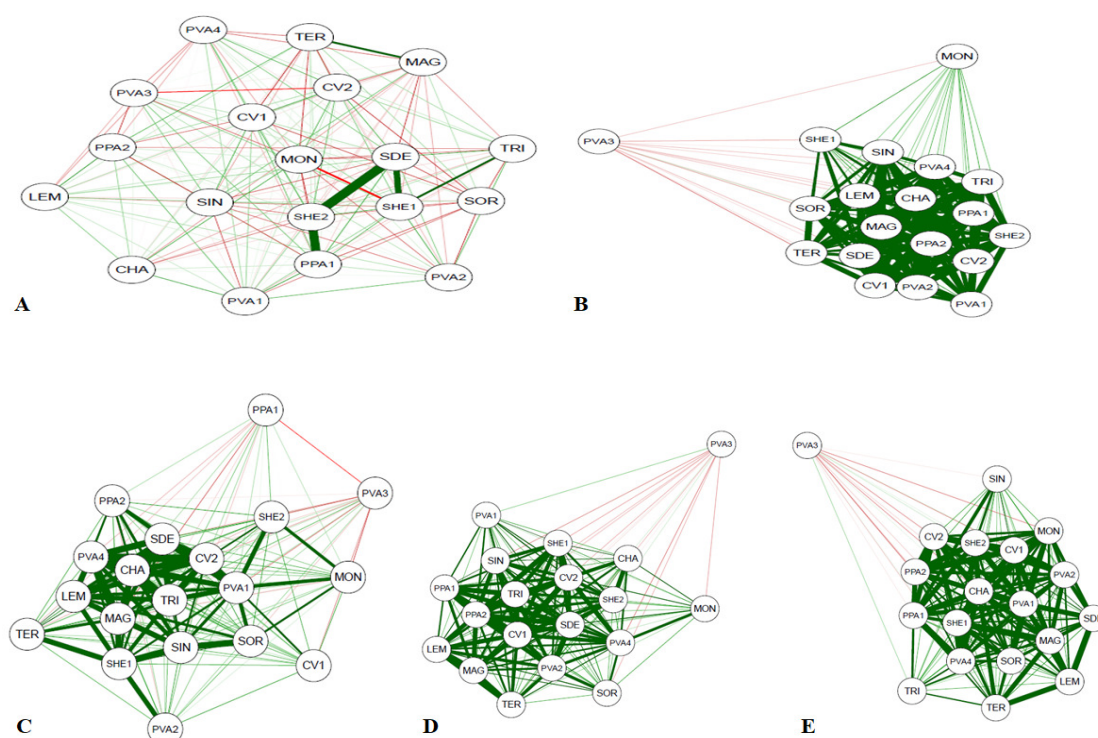


Figure 1. Phenotypic correlations network among the environments (Table 1) for cotton seed yield (A) and fiber percentage (B) and technological variables micronaire (C), fiber length (D) and fiber strength (E). Positive correlations are highlighted in green and negative in red, where the thickness of the traces indicates the strength of the correlation.

For FP (Figure 1B), all environments, except PVA3 and MON, showed a positive strong magnitude correlation (>0.70). The PVA3 environment presented negative correlation and MON positive correlation, both of weak magnitude. For MIC, the PVA3 environment also showed negative correlation of weak magnitude (Figure 1C), as well as PPA1. Corroborating with the other traits, for FL and FS, the PVA3 environment also confirmed negative and positive correlation of weak magnitude (Figure 1D and 1E).

It is important to note that PVA3 showed differences in four of the five analyzed variables. This result points out the need for the genotypes to be evaluated in this environment in future research. Similarly, the MON, SHE1, SIN, PPA and TRIN environments did not present similarity pattern with the other environments in at least one of the evaluated traits. These results indicate that there are six environments (PVA3, MON, SHE1, SIN, PPA and TRIN) in which cotton trials should be prioritized because of the phenotypic response pattern obtained for the traits evaluated. The

remaining 13 environments are similar to each other for all trait and can be summarized in strategic locations depending on the ease of installation of the trials.

However, it is important to emphasize that owing to exclusion, it is advisable to have information on a larger number of crops, agroclimatic characteristics of the environments with similar altitudes, latitude and climate, coinciding with the established agroclimatic zoning for the cotton crop.

CONCLUSIONS

There are six environments (PVA3, MON, SHE1, SIN, PPA1, PPA2 e TRIN) in which the cotton trials should be installed as a matter of priority owing to the phenotypic response pattern obtained for the evaluated traits.

The remaining 13 environments are similar to each other for all traits and can be summarized in strategic locations depending on the ease of installation of the trials.

RESUMO: Os estudos de estratificação ambiental são importantes para a criação de plantas, uma vez que permitem planejar adequadamente a rede experimental. O objetivo deste trabalho foi identificar ambientes similares para cultivo de algodão no Cerrado brasileiro quanto a produtividade e qualidade da fibra. Dezenove experimentos foram realizados em um delineamento de blocos ao acaso com doze genótipos e quatro repetições. Foram avaliados caracteres agrônômicos (produtividade de algodão em caroço e porcentagem de fibra) e tecnológicas (comprimento, micronaire, resistência de fibras). Os resultados indicam que existem seis ambientes (PVA3, MON, SHE1, SIN, PPA e TRIN) em que os ensaios de algodão devem ser instalados como prioritários devido ao padrão de resposta fenotípica obtido para os traços avaliados. Os 13 ambientes restantes são semelhantes entre si para todos os caracteres e podem ser resumidos em locais estratégicos, de acordo com a facilidade de instalação dos ensaios.

PALAVRAS-CHAVE: *Gossypium hirsutum*. Interação genótipos x ambientes. Qualidade da fibra.

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