Usefulness of the HMRPGV method for simultaneous selection of upland cotton genotypes with greater fiber length and high yield stability

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ABSTRACT. The harmonic mean of the relative performance of genotypic predicted value (HMRPGV) method has been used to measure the genotypic stability and adaptability of various crops. However, its use in cotton is still restricted. This study aimed to use mixed models to select cotton genotypes that simultaneously result in longer fiber length, higher fiber yield, and phenotypic stability in both of these traits. Eight trials with 16 cotton genotypes were conducted in the 2008/2009 harvest in Mato Grosso State. The experimental design was randomized complete blocks with four replicates of each of the 16 genotypes. In each trial, we evaluated fiber yield and fiber length. The genetic parameters were estimated using the restricted maximum likelihood/best linear

unbiased predictor method. Joint selection considering, simultaneously, fiber length, fiber yield, stability, and adaptability is possible with the HMRPGV method. Our results suggested that genotypes CNPA MT 04 2080 and BRS CEDRO may be grown in environments similar to those tested here and may be predicted to result in greater fiber length, fiber yield, adaptability, and phenotypic stability. These genotypes may constitute a promising population base in breeding programs aimed at increasing these trait values.

Key words: *Gossypium hirsutum*; Genotype x environment interaction; REML/BLUP

INTRODUCTION

Upland cotton (*Gossypium hirsutum* L. r. *latifolium* Hutch.) is one of the main economically important crops in Brazil (Farias et al., 2016). In Brazil, which is the world's fifth largest cotton seed producers with 4.4 million tons produced during the 2013/2014 harvest, the production is concentrated to the Midwest region. In this region, 66% is produced in the Mato Grosso State, the largest national producer. In the Northeast, the Bahia State stands out as the largest producer of this crop (Conab, 2015).

Genotype x environment (GE) interactions are one of the greatest challenges in plant breeding, both in the selection procedures and in the recommendation of cultivars. This is because plant breeders typically look for stable genotypes with improved performance in relation to a particular trait (Ramalho et al., 2012; Cruz et al., 2014). Studies on GE interactions for agronomic traits in cotton are scarce in Brazil (Souza et al., 2006; Suinaga et al., 2006; Silva Filho et al., 2008; Carvalho et al., 2015b). In general, these studies have revealed the presence of GE interactions for fiber length and fiber yield. These studies have succeeded in maximization of genotype performance in different environments, thus significantly exploiting the GE interaction.

Selecting cotton genotypes that provide longer fiber lengths as well as high fiber yield is the main goal of genetic-breeding programs. To this end, it is necessary to use methods of adaptability and phenotypic stability that enable the identification of genotypes with predictable behavior in these traits and that are responsive to both specific and general environmental conditions. Thus, selection methods that incorporate adaptability and phenotypic stability in a single parameter can be advantageous, compared to methods involving only production as a selection criterion (Resende, 2007).

Restricted maximum likelihood/best linear unbiased predictor (REML/BLUP) analysis allows for consideration of correlated errors within sites as well as stability and adaptability in superior genotype selection. Thus, in the genetic values this analysis provides, instability has already been accounted for and the values may be applied to any number of environments. In addition, this method generates results in the unit or scale of the assessed trait that can be directly interpreted as genetic values, which is something other methods do not allow for. Thus, selection by harmonic mean of the relative performance of genotypic predicted values (HMRPGV) implies selection, simultaneously, for productivity or fiber length and stability. In terms of adaptability, this refers to the relative performance of the genotypic values in the environment. In this case, the predicted genotypic values are expressed as a proportion of the

overall average for each site and, subsequently, an average value of this ratio for all sites is obtained. Simultaneous selection for productivity or fiber length, adaptability, and phenotypic stability in the context of mixed models can be performed using the HMRPGV method (Silva et al., 2011; Rosado et al., 2012).

This methodology has been used for interpreting the genotypic stability and adaptability of crops such as the common bean (Carbonell et al., 2007), sugarcane (Bastos et al., 2007), cashew (Maia et al., 2009), eucalyptus (Rosado et al., 2012), rice (Regitano Neto et al., 2013), and cowpea (Torres et al., 2015, 2016). However, its application in cotton is still scarce and restricted to a single study by Moiana et al. (2014). In the present study, we aimed to use mixed models to select cotton genotypes that simultaneously have longer fiber lengths, high fiber yield, and phenotypic stability in these traits.

MATERIAL AND METHODS

Eight trials with cotton genotypes were conducted in the 2008/2009 harvest; the environmental edaphoclimatic characteristics are shown in Table 1. The experimental design was randomized complete blocks 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 replications. The experimental unit consisted of four 5.0-m long rows, with 0.90 m spacing between rows, and a density of nine plants/m. At harvest, cotton fiber yield (kg/ha) and fiber length (mm) were evaluated, following the method described by Carvalho et al. (2015a).

Table 1. Edaphoclimatic features of the eigth environments evaluated in Mato Grosso State.

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

To evaluate the GE interaction effect on fiber length and yield, we used the REML/BLUP statistical model:

$$Y = Xb + Zg + Wc + e \qquad \text{(Equation 1)}$$

where Y, b, g, c, and e correspond to the data vector, the effect of blocks within different environments (fixed), genotype effects (random), effects of GE (random), and random errors, respectively. X, Z, and W are the incidence matrices for b, g, and c, respectively. The genetic parameters were estimated using the REML/BLUP method.

Joint selection considering, simultaneously, fiber length, fiber yield, stability, and adaptability is given by the HMRPGV method, as follows:

$$HMRPGV_i = \frac{n}{\sum\limits_{j-l}^{n} \dfrac{1}{Vg_{ij}}} \qquad \text{(Equation 2)}$$

where n is number of environments (N = 8) in which the genotype was assessed, Vg_{ij} is the value of the genotype i in environment j, expressed as a proportion of the mean in that environment (Resende, 2007). This analysis was performed using model 54 in the Selegen software (Resende, 2007).

RESULTS AND DISCUSSION

The coefficient of experimental variation (CV_e) was 12.86% for fiber yield and 2.42% for fiber length (Table 2). These values are lower than those observed in other studies on cotton crop (Souza et al., 2006; Suinaga et al., 2006; Hoogerheide et al., 2007; Silva Filho et al., 2008; Moiana et al., 2014; Carvalho et al., 2015a). According to Cruz et al. (2014), for continuously distributed phenotypic traits, CV_e values lower than 20% reflect excellent experimental accuracy. In contrast, the coefficient of genetic variation (CV_g) quantifies the magnitude of genetic variation for selection and, therefore, higher values are desirable. The CV_g values obtained here were 6.71% for fiber yield and 1.41% for fiber length, which indicates that the median fraction of the genetic variance was extracted from the total phenotypic variation. The joint evaluation of CV_g and CV_e is reflected in the $\hat{r}_{g\hat{g}}$ statistics (Resende and Duarte, 2007). The accuracy of >90% obtained for both traits indicates good experimental quality, and hence, accurate selection of superior genotypes for both traits.

Table 2. Estimates of variance components (individual REML) for fiber yield and fiber length of 16 cotton genotypes evaluated in seven environments in the Mato Grosso State.

Parameter	Fiber yield (kg/ha)	Fiber length (mm)
$\hat{\sigma}^2_g$	17,995.48	0.19
$\hat{\sigma}^2_c$	15,072.09	0.06
$\hat{\sigma}^2_e$	66,086.92	0.55
$\hat{\sigma}^2_f$	99,154.50	0.80
$\hat{h}^2_g$	0.18	0.24
$\hat{h}^2_{mg}$	0.82	0.89
$\hat{r}_{g\hat{g}}$	0.91	0.94
c^2	0.15	0.07
$\hat{r}_{gloc}$	0.54	0.77
CV_g (%)	6.71	1.41
CV_e (%)	12.86	2.42
M	1999.66	30.82

Estimates of genotypic variance (σ^2_g); genotype x environment interaction variance (σ^2_c); residual variance between plots (σ^2_e); individual phenotypic variance (σ^2_f); individual heritability coefficient in the broad sense ($\hat{h}^2_g$); heritability coefficient of the genotype average ($\hat{h}^2_{mg}$); accuracy in the selection of genotypes ($\hat{r}_{g\hat{g}}$); coefficient of determination of genotype x environment interaction effects (c^2); genotypic correlation through the environments ($\hat{r}_{gloc}$); coefficient of genetic variation (CV_g); coefficient of experimental variation (CV_e); overall mean (M).

Heritability of the genotype mean ($\hat{h}^2_{mg}$) is estimated when using block averages as evaluation and/or selection criterion (Resende, 2007). Given the values obtained for both traits (>0.80), the selection of cotton genotypes based on the predicted genotypic values can be performed with relative ease. The variance of the genotypic effects (σ^2_g) obtained was >0.80 for both traits. This suggests that selection of cotton genotypes based on the predicted genotypic values may be performed with relative ease. The σ^2_g was similar than the variance in the GE interaction effect (σ^2_c), the latter constituting 15.20 and 7.50% of the total phenotypic variability for fiber yield and length, respectively. These results suggest that for both traits, the interaction is of the simple type, i.e., the genotypes respond differently to the environment, but there are no changes in the rankings.

Due to the greater or lesser adaptability/genetic individual stability, the σ^2_c can inflate the phenotypic expression of a trait (Bastos et al., 2007). This measure quantifies the fraction of the total variation that is due to the GE interaction. Small estimates of σ^2_c indicate that the GE interaction has little influence on the phenotypic value (Maia et al., 2009). In this context, a genotype with greater fiber length or fiber yield in a certain environment tends to maintain similar levels in other environments as well. This genotype responds favorably to environmental variability (through a correlation between the genotypic values among enviroments), and also shows considerable predictability in the face of environmental variation. In our case, the σ^2_c estimates can be considered low for both traits, which favored the obtained moderate phenotypic correlation ($\hat{r}_{gloc} > 0.50$) between the environments.

The phenotypic value corresponds to the values obtained in field evaluations, which are influenced by the genotypic, environmental, and the GE interaction effects. In the latter, the sum of genotypic variance (the residual variance between plots (σ^2_e) and the σ^2_c) results in the individual phenotypic variance (σ^2_f). In our study, the σ^2_e represented the majority of σ^2_f for both traits, suggesting a need to improve the experimental precision in experiments with cotton.

The five genotypes that stood out as providing the highest fibers yield, adaptability, and phenotypic stability were CNPA MT 04 2080, FM 993, BRS BURITI, FM 910, and BRS CEDRO (Table 3). On the other hand, genotypes BRS 293, CNPA MT 04 2088, CNPA MT 04

Table 3. Harmonic means of the relative performance of predicted genotypic values (HMRPGV) for fiber yield (kg/ha) and fiber length (mm) of 16 cotton genotypes as predicted by a BLUP analysis.

Genotype	Fiber yield	Fiber length
BRS ARAÇA	1960.60	30.19
BRS BURITI	**2118.15**	30.19
BRS 286	1875.51	30.32
FMT 701	2078.99	30.59
FM 993	**2119.97**	30.60
FM 910	**2093.27**	30.60
DELTA OPAL	1830.32	30.64
IPR JATAI	1934.07	30.67
LD CV 05	2045.22	30.79
LD CV 02	1598.70	30.88
BRS CEDRO	**2089.93**	**31.18**
NUOPAL	1945.44	31.14
CNPA MT 05 1245	1992.73	**31.16**
CNPA MT 04 2080	**2133.14**	**31.30**
CNPA MT 04 2088	2051.03	**31.43**
BRS 293	2078.29	**31.56**

Highlighted in bold are the five genotypes that yielded the highest fiber yields and fiber lengths, respectively.

2080, CNPA MT 05 1245, and BRS CEDRO provided the highest fiber length, adaptability, and phenotypic stability. Thus, using the values obtained from the HMRPGV method, it is possible to select genotypes CNPA MT 04 2080 and BRS CEDRO as those that provide greater yield in terms of both fiber length and fiber yield, as well as high adaptability and phenotypic stability for these traits (Table 3). Hence, these genotypes may be used in environments similar to those used in this study (simple GE interaction type), because the mixed-model method penalizes the predicted genotypic values (Maia et al., 2009).

Identification of upland cotton genotypes that meet high productivity in terms of fiber yield and fiber length are the major goals of the breeding programs in Brazil. Based on our results, new strategies to improve this crop could be applied using genotypes CNPA MT 04 2080 and BRS CEDRO. These strategies may include obtaining segregated and/or experimental hybrid populations.

Conflicts of interest

The authors declare no conflict of interest.

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