Multi-Locational Evaluation of Medium-Staple Cotton Genotypes for Seed-Cotton Yield under the Middleveld Agro-Ecological Zone of Zimbabwe.

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Abstract

Background The Zimbabwe national cotton breeding programme has the mandate to develop superior cotton (Gossypium Hirsutum) varieties with good field performance and high fibre properties. Cotton productivity in Zimbabwe has remained very low, with national average seed cotton yield record of 650 kg/ha (AMA Report, 2019) compared to the potential 2000 kg/ha. Though this is a result of many biotic and abiotic factors, field experiments laid in a Randomized Complete Block Design were conducted on ten genotypes (seven test genotypes and three check varieties) from 2012 to 2019 across 13 diverse locations in Zimbabwe to evaluate cotton yield performance, stability and adaptability by Analysis of Variance (ANOVA) and Genotype and Genotype by Environment Interaction (GGE) Biplot methods.

Results The Analysis of Variance indicated significant (P < .001) effects of Genotype (G), Environment (E) and their Interaction (GE). The highest percentage of variation was explained by E/G/GE (60.34%) while G/E + GE together explained the rest of the variation (< 40%). Joint effects of G and GE were partitioned using the GGE biplot analysis explaining total of 59.08% (PC1 = 36.96% and PC2 = 22.12%) of the GGE sum of squares. The biplot analysis revealed that candidates 917-05-7, TN96-05-9, 912-05-1 and GN 96 (b)-05-8 were the ideal and stable genotypes. The candidate variety 917-05-7 significantly (P < .001) showed superior yield performance over checks CRI-MS1 and CRI-MS2 recording 5% and 5.5% yield increase respectively. Candidate 917-05-7 recorded a higher earliness index (78.11%) over checks CRI-MS1 and CRI-MS2 (77 and 76% respectively) thus indicating potential attributes for good cotton production with more pick-able bolls earlier than the current commercial varieties.

Conclusion Candidate 917-05-7 has been identified as the ideal genotype in terms of high yielding potential, and stability hence recommended for commercial release and use as breeding parent for future breeding programs.

Background

Cotton (Gossypium Hirsutum) is predominantly a smallholder crop and represents a crucial source of income for millions of farmers and their families in more than 20 countries across all regions of Sub-Saharan Africa (Travella, 2017). Despite its economic potential, cotton variety development in Zimbabwe has been very low leaving farmers to continuously cultivate obsolete varieties. Currently cotton production in Zimbabwe is very low, with national average seed cotton yield of 650 kg/ha (Fig. 1)

The cotton genotype selection and recommendations by breeders has been slowed down due to the effects of genotype by environment interaction (GEI). This complicates the identification of superior cotton genotypes, thus making selection and recommendation of new genotypes for different environments difficult and expensive. Some multi-locational field experiments from 2012 to 2019 growing season were conducted aiming to evaluate relative response of cotton genotypes across different environments and identify varieties with good adaptation and stability (Baaﬁ and Safo-Kantanka, 2008) through use of GGE biplot analysis. Multilocalional Yield Trials (MYT) are important to evaluate the
relationship between genotypes and environments for selected traits by use of a genotype by genotype by environment (GGE) biplot that allows visual assessment of genotype by environment interaction (GEI) pattern (Yan et al., 2000; Yan and Hunt, 2001). GGE is the most recent approach proposed by Yan et al. (2000), and has shown extensive usefulness and a more comprehensive tool in quantitative genetics and plant breeding (Yan et al., 2001; Yan and Rajcan, 2002). This tool for analysis of GEI is increasingly being used in GEI studies in plant breeding research (Butran et al., 2004). The objectives of this study were (i) to identify the genotype and environmental components that are associated with the GxE interaction across the diverse environments, looking at percentage source of variation and joint effects of G and GE as partitioned by Principal Components (PC) in the total sum of squares, (ii) to identify the ideal genotype(s) based on high yielding potential and stability across test-locations, (iii) to identify mega, representative and ideal environment for testing genotypes and (iv) to identify which variety won where of the given test-locations.

**Materials And Methods**

**Study Sites**

The multi-locational experiments were conducted for six seasons (2011/12, 2013/14, 2015/16, 2016/17, 2017/18 and 2018/19 growing seasons) at four On-station sites (CRI, Panmure, Chisumbanje Exp, and Save Valley Exp) and eight Off-station sites (Matikwa, Shamva, Kuwirirana, Muzarabani, Wozhele, CC Mollen, Umguza & Chitekete). The sites represent the high cotton production zones, thus the Middleveld, and Lowveld. The sites are generally characterized with low average annual rainfall (< 800 mm) and high temperatures (> 36°C). General description of the sites encompassing longitude, altitude etc., is given in Table 3.
Table 3
Description of sites used in the multi-locational trials

| Location     | Code | Latitude       | Longitude       | Altitude | Av. Annual Rainfall | Max Temp°C |
|--------------|------|----------------|-----------------|----------|---------------------|------------|
| Chitekete    | E1   | 17° 25' South  | 28° 56' East    | 914      | 450–500             | 45         |
| Kadoma       | E2   | 18° 19' South  | 29° 53' East    | 1156     | 750–1000            | 38         |
| Wozhele      | E3   | 19° 31' South  | 30° 14' East    | 1345     | 650–790             | 37         |
| Kuwirirana   | E4   | 21° 15' South  | 30° 48' East    | 1483     | 500–600             | 38         |
| Matikwa      | E5   | 20° 48' South  | 32° 14' East    | 300      | 450–500             | 40         |
| Shamva       | E6   | 17° 32' South  | 31° 71' East    | 1149     | 675–700             | 38         |
| Muzarabani   | E7   | 16° 23' South  | 31° 00' East    | 432      | 600–800             | 42         |
| Panmure      | E8   | 17° 16' South  | 31° 47' East    | 881      | 700–800             | 35         |
| CC Mollen    | E9   | 18° 30' South  | 29° 13' East    | 1120     | 700–850             | 38         |
| Save Valley  | E10  | 21° 29' South  | 32° 51' East    | 466      | 450–500             | 41         |
| Chisumbanje  | E11  | 20° 47' South  | 32° 13' East    | 448      | 450–500             | 40         |
| Umguza       | E12  | 20° 03' South  | 28° 34' East    | 1374     | 450–500             | 34         |

Source: Agritex planning branch, (2019): Zimbabwe natural regions and farming areas boundaries

Experimental Description

The experiment included ten genotypes thus seven test genotypes (TN 96-05-9, 912-05-1, S0-99-9, GN 96 (b)-05-8, 917-05-7, 932-05-3 and 938-05-3) and three check varieties (SZ9314, CRI-MS1 and CRI-MS2 (Table 4). All the test-genotypes were developed by Cotton Research Institute using the Pedigree Breeding Method. The experiments were laid in a Randomized Complete Block Design replicated three times and each treatment was represented by plots measuring 32.4 m².
Table 4
Description of Cotton genotypes used in the multi-locational trials

| Genotype Name | Code | Type & breeding status | Origin                          |
|---------------|------|------------------------|---------------------------------|
| TN 96-05-9    | G1   | Experimental Line      | Cotton Research Institute       |
| 912-05-1      | G2   | Experimental Line      | Cotton Research Institute       |
| S0-99-9       | G3   | Experimental Line      | Cotton Research Institute       |
| GN 96 (b)-05-8| G4   | Experimental Line      | Cotton Research Institute       |
| 917-05-7      | G5   | Experimental Line      | Cotton Research Institute       |
| 932-05-3      | G6   | Experimental Line      | Cotton Research Institute       |
| 938-05-3      | G7   | Experimental Line      | Cotton Research Institute       |
| SZ9314        | G8   | Commercial Check Variety| Cotton Research Institute       |
| CRI-MS1       | G9   | Commercial Check Variety| Cotton Research Institute       |
| CRI-MS2       | G10  | Commercial Check Variety| Cotton Research Institute       |

Trial/Crop Management

Uniform crop management was done at all the sites and across all the various projects in the programs. Compound L (N: P: K: S = 5:18:10:8: (0.25B)) was banded at a rate of 250 kg per hectare to the planting furrows manually. Ammonium nitrate (34.5% N) was applied at a rate of 150 kg per hectare to the crop at the ninth week after crop emergence. The crop was thinned to one plant per station at 1 m inter-row by 0.3 m within row to achieve a desired plant population of about 33 333 plants per hectare. Weeding using herbicides and hand hoeing was done to remove any weeds from the trials when necessary. Weeding at all sites was averagely done three times for the whole season. The following cotton pests were controlled using the general recommended cotton pest scouting and control protocol developed at CRI in 1993 by the Cotton Research Institute entomology section (Annual Report, 1993). The pest controlled were: aphids (*Aphis gosypii*), red boll worms (*Diaparposis castanea*) and Heliothis bollworm (*Helicorvepa amirgera*). Pests were kept at below the economic thresholds levels following weekly scouting.

Field Data Collection And Analysis

Crop performance data from emergence to post-harvest (seed cotton yield, lint yield, seed weights, boll weights, seed weights, lint ratios, earliness index) was collected from all experiments. The genotype and genotype by environment (GGE) model was used to understand and structure interactions between genotypes and the environment. The model was used to identify mega, representative and ideal environment for testing genotypes. The Principal Component Analysis (PCA) was used to explain
patterns in the Genotype x Environment interaction. It was also used to identify superior genotypes and estimate adaptability and stability of the genotypes across the sites in different years. GenStat 14th edition for windows was the statistical software for the partitioning of the variance components (general combined analysis of variance (ANOVA). Where significance difference was noted, treatments means were separated using the Fischer’s (1930) Least Significant Difference at $P \leq 0.05$ (Williams and Abdi, 2010).

**Results**

An across seasons and environments, general combined analysis of variance (ANOVA) was conducted and the results indicated that variance on the measured yield and yield-related traits was due to the presence of genotype by environment interaction (GEI) ($P < 0.001$) except for boll weights. The highest percentage of variation was explained by $E/G/GE$ (60.34%) while $G/E + GE$ together explained the rest of the variation (< 40%) (Table 1). Joint effects of G and GE were partitioned using the GGE biplot analysis explaining total of 59.08% (PC1 = 36.96% and PC2 = 22.12%) of the GGE sum of squares (Table 1). The effect of GxE interaction on the parameters invited the need for further analysis using the GGE biplot analysis to be able to identify genotypes which are stable and adaptable. Overall seed cotton yield mean for the candidates was 1663 kg/ha, whilst candidate recorded 1755 kg/ha (Table 2) which was 5% and 5.5% yield gain over checks CRI-MS1 and CRI-MS2 respectively (Fig. 2).

| Source of variation          | d.f. | s.s.      | m.s.   | v.r.  | Fpr.     | Exp% ss |
|------------------------------|------|-----------|--------|-------|----------|---------|
| Genotype (G)                 | 9    | 5618628   | 624292 | 4.93  | < .001   | 14.06   |
| Environment (E)              | 11   | 227076442 | 20643313 | 163.18 | < .001   | 25.6    |
| Genotype x Environment (GEI) | 99   | 15502745  | 156593 | 1.24  | 0.005    | 60.34   |
| Residual                     | 234  | 29433635  | 42169  |       |          |         |
| Total                        | 353  | 277631450 | 786491 |       |          |         |

** DF = Degrees of freedom; SS = sums of square; MS = means square.**

Table 1

Summary of the general analysis of variance for grain yield (kg/ha) showing the level of significance for the genotype, environment and GEI of advanced cotton genotypes.
Table 2
Overall Field performance of the genotype 917-05-7 against three commercial check cultivars during the 7 seasons (2012–2019)

| Genotype name | Seed cotton yield (kg ha$^{-1}$) | Boll weight (g) | Earliness Index (%) | Gin out Tum (%) | Lint Yield (kg ha$^{-1}$) | 100 seed weight (g) |
|---------------|----------------------------------|----------------|---------------------|----------------|---------------------------|--------------------|
| 917-05-7      | 1755$^{d}$                       | 6.4            | 78.11               | 41.83          | 743.9                     | 10.88              |
| CRI-MS-1      | 1677$^{bcd}$                     | 6.3            | 77.04               | 42.12          | 717.9                     | 11.40              |
| CRI-MS-2      | 1659$^{bcd}$                     | 6.3            | 76.13               | 41.54          | 709.1                     | 10.96              |
| SZ9314        | 1737$^{cd}$                      | 6.3            | 78.58               | 41.92          | 744.7                     | 11.06              |
| Grand Mean    | 1663                             | 6.4            | 77.4                | 41.8           | 709.8                     | 11.12              |
| F-Pro (G)     | ***                              | ***            | **                  | ns            | ns                        | ***                |
| F-pr (G x E)  | **                               | ns             | ***                 | ***           | ***                       | ***                |
| Av. SED       | 60.34                            | 0.1163         | 1.278               | 1.249          | 27.6                      | 0.081              |
| CV %          | 21.2                             | 10.91          | 9.98                | 17.78         | 21.26                     | 4.31               |

-Sig - Significance level, LSD Least Significant Differences, CV% Coefficient of Variation, SE Standard Error of Differences, *** significantly different at < 0.001, ** - significantly different at < 0.01, * - significantly different at < 0.05, NS – Not significantly different.

NB: The Grand mean, F-pr, LSD and CV% values displayed above are for the whole trial (all the genotypes).

Genotype Stability Analysis (GEI) for total seed cotton yield for cotton genotypes across seasons and environments

Which-won-where And Mega-environments (me)

The GGE scatter plot (Fig. 3) showed dissected pentagon into sectors with winning genotypes located at the vertex of the polygon. The biplot revealed that candidate 917-05-7 (G5) and TN96-05-9 were the winning genotypes in six environments (Chisumbanje Exp, Umguza, Muzarabani, Matikwa, Panmure and Save Valley) which fell under that sector/ mega-environment 1. The biplot revealed the existence of three Mega-environments (ME), with ME1 comprised of Chisumbanje Exp, Umguza, Muzarabani, Matikwa, Panmure and Save Valley, ME2 comprised of Chitekete, CC Mollen and CRI where CRI-MS1 was the winner whilst ME3 consisted of Wozhele, Kuwirirana and Shamva where SZ9314 was the winner.
Genotype Ranking Based On Mean Performance And Stability

Genotype by genotype-by-environment (GGE) interactions biplot analysis revealed that candidate 917-05-7 was high yielding and stable thus located on the far right and a short projected perpendicular line to the environmental axis whilst candidate TN96-05-9 was more stable and above average in terms of yield performance (Fig. 4). Candidate 912-05-1 was moderately yielding thus above average and very stable. So candidates 917-05-7, TN96-05-9 and 912-05-1 are selected as good varieties which are high yielding and stable compared to the check varieties CRI-MS1 and SZ9314 which were around average yield performance and highly unstable.

Ideal Genotype And Environment

The GGE analysis positioned the candidate genotype 917-05-7 in first concentric ring (Fig. 5), identifying it as the ideal genotype. This also reveals that the genotype is high yielding and moderately stable compared to check varieties which positioned in the 11th concentric ring thus low yielding and unstable. Some good varieties closer to the ideal genotypes were shown, and these included TN96-05-9, 912-05-1 and GN 96 (b)-05-8. The biplot displayed Umguza as the most ideal environment (Fig. 5) identified by its location in the second concentric circle. However, Umguza showed poor discriminating ability as compared to Save Valley which had the best discriminating ability thus gave more information about the performance of tested genotypes. This indicates that the GEI greatly influenced the effect of Umguza site to the performance of the test-genotypes. Good environments such as Matikwa, Save Valley and Chisumbanje Experiment were displayed.

Discussion And Conclusions

The general analysis of variance recorded candidate genotype 917-05-7 as the highest yielding (1755 kg/ha) over the check varieties (< 1680 kg/ha) across seasons and environments by recording > 5% yield advantage more than the commercial check varieties. The GGE biplot analysis was successful in giving more information about the test genotypes and test environments which could not be synthesized by analysis of variance (ANOVA) only. Biplot analysis revealed good varieties based not only on high yielding but stability, which is very important when yield experiments are done in many different environments. Candidate variety 917-05-7 was the ideal variety based on high mean yield performance and stability, and candidate variety TN96-05-9 was a good variety which was moderately yielding and very stable. Other candidate genotypes such as 912-05-1 and GN 96 (b)-05-8 were presented as good varieties with high and moderate stability respectively. The biplot analysis gave more information about the relationship between environments and genotypes, whereby high mean performing environments with high discriminating ability were revealed, the identified sites were Umguza and Save Valley respectively. Umguza recorded high mean yield but was not well discriminating whilst Save Valley was moderately high yielding and high discriminating compared to the other environments. Good environments such as
Matikwa, Save Valley and Chisumbanje Experiment were displayed in the biplot graphs. Three mega environments (ME) were shown through the GGE biplot analysis, and candidate varieties 917-05-7 and TN96-05-9 were the winning genotypes for ME1 which consisted of six environments out of twelve. The information revealed on mega-environments was relevant to the general information about the experimental sites where all the Lowveld institutes fell in one ME. This means no much differences were realized in terms of their effect on the variety performances and the sites are similar. This study was relevant in context of making good progress in selecting the best ideal and stable varieties under multi-locational variety trials. The study with reference to Zimbabwe's national cotton variety development programme, enabled the breeder to efficiently select and recommend superior genotypes for further evaluations and subsequent release (Yan et al., 2001; Yan and Rajcan, 2002). The use of GGE biplot analysis in the study showed extensive expediency in quantitative genetics and plant breeding hence the researcher implies this as a more comprehensive and relevant tool in multilocational research trials. Henceforth, the study results have identified genotypes 917-05-7, TN96-05-9, 912-05-1 and GN 96 (b)-05-8 as the superior candidates for commercial use as varieties and as parents for future hybridization programmes.

**Abbreviations**

CRI Cotton Research Institute

AMA Agricultural Marketing Authority of Zimbabwe

GGE Genotype and Genotype by Environment

PCA Principal Component Analysis

ME Mega Environment

ANOVA Analysis of Variance

GEI Genetic by environmental interaction

RCBD Randomized complete block design

E Environment

G Genotype

DF Degrees of Freedom

SS Sums of Square

MS Means Square
Declarations

Ethics approval and consent to participate
Not Applicable

Consent for publication
Not Applicable

Availability of data and materials
The data (Analyzed) was generated through some institutional programmes and it is contained in this paper and access to the raw data is not publicly available

Competing interests
The authors declare that they do not have competing interests

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Authors’ contributions
MM collected, analyzed and interpreted the data, as well as writing the research paper

BC assisted in the collection of data and analysis

WM assisted in editing of the research paper, and guided in data analysis

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Figures

Figure 1

Cotton production trend (average yield, production and area under production) for the period 2008 -2018 (Source: AMA 2019).

Figure 2

Overall seed cotton yield performance of 917-05-7 and percentage increase over check varieties over five seasons.
Figure 3

Best performing genotypes (Which-won-where) and mega-environments
Figure 4

Ranking biplot showing the high yielding and stable test genotypes
Figure 5

Comparison biplot showing the ideal genotype and ideal environment