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Happy World Cotton Day

Cotton is one of the most common fabrics in our wardrobes, it is comfortable, hypoallergenic, breathable and durable. But cotton represents so much more than just a commodity. The natural fabric is a life-changing product worldwide that sustains 32 million growers “almost half of them women” and benefits over 100 million families across 80 countries in 5 continents. This means that, behind any cotton clothing, following back its trade chain, there is a personal story.

In August 2021, the General Assembly of the United Nations recognized the unique benefits of cotton by proclaiming 7 October of as World Cotton day !!

CONTENT

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Stability and Adaptability of Cotton (*Gossypium hirsutum* L.) Genotypes Based on AMMI Analysis

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Introduction

Cotton is an important commodity in the world economy and it is grown as crop in more than 100 countries (ITC, 2007). The world uses more cotton than any other fiber and over 150 countries are involved in exports or imports of cotton (Carvalho et al., 2015). In Mozambique, cotton is important and involves 300,000 small-scale farmers in its production as a cash crop and is the most important agricultural export crop in the country, contributing close to 17 percent of total agricultural exports and almost 2 percent of total exports (Dias, 2012; IAM, 2015). The cotton sector in Mozambique is generally characterized by low yields (500 kg.ha^{-1}) compared to the world average yield (800 kg.ha^{-1}) and to the neighboring countries such as Malawi (800 kg.ha^{-1}), Tanzania (750 kg.ha^{-1}) and Zambia (800 kg.ha^{-1}) (Dias, 2012; Mekuria, 2012). One of the reasons is the low yielding and less adaptable varieties (Maleia et al., 2010). The cotton research program in the country has been developing and introducing new different germplasm/ genotypes, in order to find the suitable varieties to the local edaphoclimatic conditions (Maleia et al., 2010). However, recommendation of varieties has been a challenge, as it depends largely on the variety adaptability to the soil and climatic conditions of the region. The crop is grown under unpredictable weather patterns which cause a need for the identification of stable genotypes having specific adaptation to specific environments (Pretorius et al., 2015). This factor has given the great variations on the performance of the same variety in different locals of production (Maleia et al, 2010; Pretorius et al., 2015). So, before recommending, any variety should be assessed for adaptability and stability (Cruz and Carneiro, 2006). Among the various statistical procedures developed for this kind of study, AMMI (Additive Main effects and Multiplicative Interaction) has been frequently used by researchers. The AMMI has shown efficient in stability analyses (Ebdon and Gauch,

2002; Miranda et al., 2009; Riaz et al., 2013; Abuali et al., 2014; Bose et al., 2014, Akter et al., 2014; Agyeman, et al., 2015). The Additive Main effects and Multiplicative Interaction (AMMI) is a tool to study GE interaction pattern and so to estimate the adaptability of different varieties on multi-environment trials. Since, GE interaction is naturally multivariate; the AMMI offers an appropriate statistical analysis of yield trials that have a G x E interaction (Anandan et al., 2009; Sabaghpour et al., 2012). The AMMI model, which combines ANOVA with principal components analysis (PCA) extracts genotype and environment main effects and uses the PCA to explain patterns in the GxE interaction, which provides a multiplicative model and is used to analyze the interaction effect from the additive ANOVA model (Zobel et al., 1988; Sabaghpour et al., 2012). This model also allows conclusions regarding phenotypic stability, genotypic behavior of the cultivars, and the degree of genetic divergence between cultivars and the environments that optimize performance (Miranda et al., 2009). This study aimed to assess the G x E pattern and to evaluate the stability and adaptability for seed cotton yield of new cotton germplasm in Mozambique based on AMMI analysis.

Materials and Methods

Genotypes, location and seasons

The seven genotypes, namely BA2018, BA320, BA919, Flash and BA525, originally from Turkey, FK37, from Burkina Fasso and QM301, from Zimbabwe were seen to have a high potential in the countries, where they were developed (Table 3). This was to determine their agronomic potential for varying environmental conditions prevailing in the cotton-growing regions in Mozambique, compared to the local and most cultivated ones, as check genotypes/varieties (Chureza, Albar SZ9314, CA324 and ISA 205). The seven genotypes (Table 3) were evaluated comparing with four actual used cultivars, during 3 seasons (2011/12; 2012/13; 2013/14) in Namialo (14S58' 00 and 39E51' 00) district of Meconta, province of Nampula; 2 seasons (2012/13; 2013/14) in Namara (13S 22' 58 and 38E25' 13) district of Balama, province of Cabo Delgado and 1 season (2013/14) in Nhamatanda (19S15' 15 and 34E14' 31), district of Nhamatanda, province of Sofala, providing 6 different environments through the combination between locals and seasons.

The cotton production in Mozambique is most concentrated in the agro-ecological regions 6, 7 and 8. Agro-ecological region 6 (R6) represents the semi-arid region of the Zambezi Valley and South Tete, this region consists of a vast dry area. In contrast, agro-ecological region 7 (R7) is a region of medium altitude in the Zambezia, Nampula, Tete, Niassa and Cabo Delgado provinces, the soil texture is variable and consistent with the topography. In almost all this region, there is great potential for cotton production that has been practiced for several decades. Agro-ecological region 8 (R8) represents the coast of the Zambezia, Nampula, and Cabo Delgado provinces and the soils of this region are generally sandy but heavy in the lower zones. Low soil fertility is one of the great limiting factors in this zone. Namialo village, located in between the R7 and R8 agro-ecological

regions, is classified by an Aw type climate, dry sub-humid, according to Koppen (Koppen, 1948) classification, with an average annual rainfall of 800 to 1000 mm and potential evapotranspiration from 100 to 1,400 mm, and in some areas of this region have higher temperatures above 25 °C and other moderately warm (between 20 and 25 °C). The soil texture is variable generally weighed having low fertility. In most of the region there is a great potential for cotton production, which has been practiced for several decades (MAE, 2005a). Namara, located in the R7 agroeclological region, presents an Aw, tropical climate, with an average precipitation between 800 and 1200 mm and potential evapotranspiration varying between 1300 and 1500, the average annual temperature varies between 20 and 25 °C. The soils are classified as rhodic ferralsols with medium to weighed texture, deep and well drained (MAE, 2005b). The Nhamatanda, located in the R4 agroecological region, presents both Aw, rainy tropical savanna climate and Cw, tropical humid and temperate climate, with an average annual rainfall of 846 and potential evapotranspiration of 1559 mm. The average temperature is around 25 °C. The soils are deep, well drained, with good fertility and nutrient retention capacity (MAE, 2005c).

Experimental design

The treatments (Table 3) were set up in a randomized complete block design, with four replications. The plots were consisted of five rows of 5.0 m length, where the two lateral rows were considered as side borders and the three central as the useful ones, where the data was collected, in a spacing of 0.70 m between the rows and 0.20 cm between the plants. Sowing was carried out manually, putting 4-10 seeds per hole of about 4 cm of depth. The first thinning took place 15 days after the emergency, leaving two plants per hole and the second thinning was carried out leaving one plant per hole at 21 days after the emergency.

Management and evaluation of variables

Weeds were controlled manually using a hoe, whenever deemed necessary. Spraying was carried out once with acetamiprid insecticide (222 $g.lt^{-1}$) for the first control of pests in a dosage of 50 $ml.ha^{-1}$, followed by five applications of Lambda-cihalothrin (60 $g\ L^{-1}$) every two weeks from the fourth week after the emergency, in a dosage of 250 $ml.ha^{-1}$. Insecticides were applied with a micro-ulva (ULV). The variable evaluated was the seed cotton yield ($Kg.ha^{-1}$).

Statistical analysis

Before the analysis of variance (ANOVA), the data was submitted to tests of homogeneity of variances and normality (Bartlet, 1937; Shapiro-Wilk, 1965) to ensure the feasibility of ANOVA (Ramalho et al., 2000). For the Individual ANOVA, every combination of local and season/year was regarded as an environment. Before conducting the combined ANOVA, the assessment of homogeneity of the residual variances of the environments was conducted, using the Hartley's Fmax test (Hartley, 1950), at 5% of probability, to ensure the feasibility of combine analysis of variance (Cruz and Regazzi, 2001). The combine ANOVA was conducted after the residual variances of all the environments were regarded as homogeneous ($p > 0.05$), considering the effect of genotypes as fixed,

and the effect of the environments and blocks as random (Cruz and Regazzi, 2001). When a significant genotypes x environments (GxE) interaction was revealed, stability and adaptability analysis based on the AMMI (Additive Main Effects and Multiplicative Interaction) model was applied, where the original GxE interaction was decomposed into the Principal Component analysis (Zobel et al., 1988; Gauch, 1988; Gauch, 1992; Cornelius et al., 1996). All analyses were conducted under the GENES (Cruz, 2006a; Cruz, 2006b) and SAS (SAS, 2008) statistical softwares.

Results and Discussion

Tests for normality and homogeneity of variances

Shapiro-Wilk's normality of the error (1995) and Bartlett's homogeneous variance of errors (1937) for the seed cotton yield allowed preceding the individual ANOVA in each of six environments. Then, the assessment of the Hartley's Fmax test (1950) indicated homogeneous error variances among the evaluated environments that allowed conduction of combined ANOVA. It shows that the assumption of homogeneous variance and normality of the error was proved; so the ANOVA could be validated. According to Ghasemi and Zahediasl (2012), statistical errors are common in scientific literature, so the assumption of homogeneous variance and normality of the error need to be checked before, for many statistical procedures, namely parametric tests such as analysis of variance (ANOVA), because their validity depends on it. The use of statistical tools in any research work is very important. However, many researchers often fail to pay attention to the important concepts prior to any parametric tests. So, prior to the application of any inferential or parametric test two characteristics of data sets must be considered, normal distribution and uniformity of variances (Granato et al., 2014).

Analysis of variance

The combined ANOVA revealed a significant difference among genotypes, environments and a significant GxE interaction (Table 1), which indicates that the environment had an impact over the differentiated performance of the genotypes and the broad range of diversity among them (Anandan et al., 2009). In this study, we also found that the GxE interaction accounted for less variation than the main effect of genotype and environment, showing that the environment had a greater effect on seed cotton yield than either genotype or GE interaction alone. This is in corroboration with Maleia et al. (2010), Pretorius et al. (2015) and Farias et al. (2016), evaluating cotton genotypes in different environments. In addition, it shows that some varieties had better performance in one environment and low performance in others, which provided a change of their performance standard under the environmental variation revealed by the significant of GxE interaction (Table 1). This is often observed when a complexed (multigenic) trait such as seed cotton yield or a trait governed by multiple genes that cause changes in the performance of genotypes over different environments being studied. Similar significant effects of genotype and GxE interaction were observed by Maleia et al. (2010), Riaz et al. (2013), Moiana et al. (2014), Pretorius et al. (2015), Carvalho et al. (2015) and Faria et al. (2016), evaluating

cotton genotypes in multi-environmental trials in Mozambique, Pakistan, South Africa and Brazil.

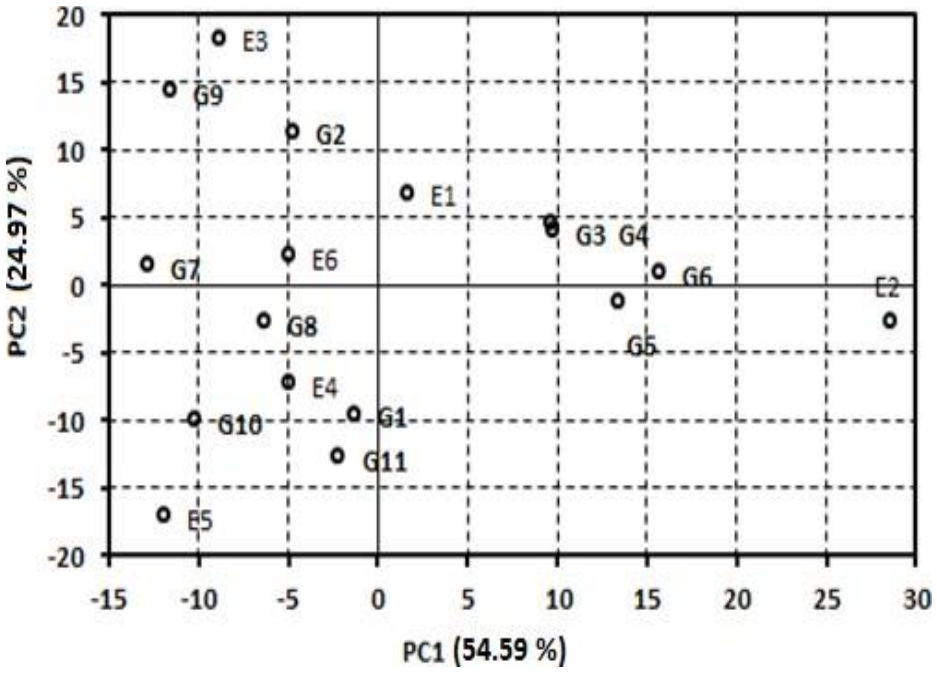
AMMI analysis

The GxE interaction composed of 5 principal components (Table 2), among which the first two (PC1 and PC2) were highly significant ($p < 0.01$) and explained about 80% of the detected interaction (54.59% and 24.97% for PC1 and PC2, respectively). This makes the stability and adaptability study based on the AMMI method more concise (Gauch, 1992). The Genotypes G3 (BA 919) and G4 (Flash) were grouped together on the biplot of PC1 against PC2. It shows that they differed only on the main effect but not in interaction effect, while G5 (BA 525) and G9 (Albar SZ9314) differed only on the interaction effect but not on the main effect (Fig.1). These differences among genotypes over interaction and main effects might have been due to the environment diversity. The AMMI graphic (Fig.1) emphasizes that there were a yearto year variation, indicating the importance of seasonal climatic variation in the same local, as the environments were scattered without any grouping on different quadrants (Anandan et al., 2009). The biplot graphic (Fig.1) also revealed that there are 4 mega-environments: two main ones, represented by 2 environments (E3; E6, in the 2nd quadrant and E4; E5, in the 3rd quadrant) while the 2 minor ones were represented by 1 environment (E1, in the 1st quadrant and E2, in the 2nd quadrant). Classifying genotype in mega- environment can minimize the GxE interaction by identifying the group of environments, in which the interaction is not significant for the group of genotypes under evaluation. In fact, in multi-environmental trials the number of environment should be high, whenever possible, in order to group similar environments. Cotton is a rain fed crop in Mozambique, as it is in many other cotton growing countries in sub-Saharan Africa. Its yield is closely related to climate, in particular to rainfall variability. Seed cotton yields drop during drought seasons or when the rainfall distribution is abnormal during the growing period. The environmental conditions of cotton growing regions are highly diversified and it leads to cultivar environmental variability. Gul et al. (2014) studied the genotype by environment interaction and association of yield variables in cotton and found that the seed cotton yield is highly affected by environment complex than genotype itself. So, identification of genotypes with high adaptability and stability to the different growing conditions is an option to deal with this fact (Cruz and Carneiro, 2006). The genotypes showed a dissimilar genetic performance once they were positioned in opposing quadrants as can be observed for BA919 (G3), Flash (G4), FK37 (G6) and BA2018 (G1), Churedza (G8), CA324 (G10), ISA 205 (G11); (G5) andBA320 (G2), QM 301 (G7), Albar SZ9314 (G9). These results suggest that the 3 new varieties (BA919, Flash, FK37) performed better and differently compared to the most of the check varieties (Churedza, CA324, ISA 205) used in this study. The pair of environments comprising Namialo 2014 (E3)/ Nhamatanda 2014 (E6) and Balama 2014 (E5)/ Balama 2013 (E4) was similar and suitable for BA320 (G2),

QM 301 (G7), Albar SZ9314 (G9) and BA2018 (G1), Churedza (G8), CA324 (G10) and ISA 205 (G11), respectively as are grouped into the same quadrant (Fig. 1). The environment Namialo 2012 (E1), suitable for the BA919 (G3), Flash (G4), FK37 (G6) and the environment Namialo 2013 (E2) for BA525 (G5) showed to be different to any others (Fig.1). The most stable genotypes, with less contribution for the G×E interaction captured by the axis PC1 and PC2, were G1 (BA 2018), G2 (BA 320) compared to the already used varieties.

Table 1. Summary of combine ANOVA of seed cotton yield (Kg.ha^{-1}).

Source of Variation	DF	Mean Square
Blocks/Environment	18	556173.61
Environments (E)	5	15711132.87*
Genotypes (G)	10	426619.22**
G x E	50	173685.03*
Residue (Error)	180	196699.03
Total	263	
Overall Average		1530.61
CV (%)		28.98



**** Significant at 1% of probability, *Significant at 5 % of probability.**

Fig 1. Graphics biplot of PC1 against PC2 and seed cotton yield of 11 genotypes (G1 to G11) in 6 environments (E1 to E6). G1: genotype BA2018; G2: genotype BA320; G3: genotype BA919; G4: genotype Flash; G5: genotype BA525; G6: genotype FK37; G7: genotype QM 301; G8: genotype Chureza; G9: genotype Albar SZ9314; G10: genotype CA324; G11: genotype ISA205. E1: Namialo, 2012 season; E2: Local: Namialo, 2013 season; E3: Local: Namialo, 2014 season; E4: Balama, 2013 season; E5: Balama, 2014 season; E6: Nhamatanda, 2014 season.

Table 2. Composition of GxE interaction into principal components.

Source of variation			DF	SS	MS
Interaction (G x E)			50	8684251.59	173685.03*
Principal Components	%	Accumulated %			
PC1	54.59	54.59	14	4740798.49	338628.46**
PC2	24.97	79.56	12	2168687.05	180723.92**
PC3	10.99	90.55	10	953994.47	95399.45
PC4	5.99	96.54	8	520413.37	65051.67
PC5	3.46	100.00	6	300358.21	50059.70
Residue (Error)	-	-	180	35405824.66	196699.03

** Significant at 1% of probability, * Significant at 5 % of probability

Table 3. The name and characterization of culivars.

Treatment	Genotype/ cultivar	Origin (type)	Tolerance to sucking insects (*Empoasca fasciallis* and *aphis gossypii*)	GOT (%)	Crop cycle (Days)
1	BA2018	Turkey (OPV)	Poor	> 43	120 -140
2	BA320	Turkey (OPV)	Poor	> 43	120 -140
3	BA919	Turkey (OPV)	Poor	> 43	120 -140
4	Flash	Turkey (OPV)	Poor	> 43	120 -140
5	BA525	Turkey (OPV)	Poor	> 43	120 -140
6	FK37	Burkina Fasso (OPV)	Fair	40-42	130 - 150
7	QM 301	Zimbabwe (OPV)	Fair	> 41	130 -150
8	Chureza	Zambia (OPV)	Fair	40 - 41	130 - 150
9	Albar SZ 9314	Zimbabwe (OPV)	Fair	> 41	> 150
10	CA 324	Ivory Cost (OPV)	Fair	40-42	130 - 150
11	ISA 205	Cameron (OPV)	Fair	39	130 - 150

Source: IAM, 2015

Churedza (G8) and ISA 205 (G11). This illustrates that these are the ones that revealed a lower variable response standard due to the environmental (local and year) variation. Therefore, the most stable genotypes showed low seed cotton yield (Fig. 1). Among the new genotypes, FK 37 (G6) and BA 919 (G3), followed by Flash (G4) showed above average seed cotton yield, indicating that was the most adaptable. The seed cotton yield performance of genotype G4 was not significantly differed to G10 (CA 324). The results show that the most stable genotypes across to the different environments were not the most adaptable. The limitations of farming inputs in development countries increase the need for the stable genotypes. Therefore, genotypes with good performance and stability should be recommended (Sabaghpour et al., 2012). For instance, from the tested genotypes, FK 37, BA 919 and Flash should be recommended, where the availability of farming input is ensured, while BA 2018 and BA 320 could be recommended for the places that availability of inputs is not secured. Riaz et al. (2003) and Pretorius et al. (2015) also identified stable and best performing cultivars when using AMMI analysis for stability, adaptability of cotton genotypes for yield improvement in Pakistan and to analyze cultivar by environmental interaction in cotton under irrigation in South Africa, respectively

Conclusion

The AMMI was useful to study the GxE interaction and to assess the stability and adaptability on the multi- environmental trial. The results illustrated that the genotypes and environments showed dissimilarity once they were positioned in opposing quadrants and the most stable genotypes across the different environments were not the most adaptable. The genotypes FK 37, BA 919 and Flash were the most adaptable to the Mozambican cotton growing environment, while BA 2018 and BA 320 were the most stable across the variation of environment.

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Delineation of Cotton Genotypes Based on Agronomic Traits

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ABSTRACT

Cotton is an important cash crop in the world and is mainly grown for its fibre. In Zambia, the existing cotton varieties have low seed cotton yield (SCY) ranging between 300 to 600 kg/ ha, compared to the potential of up to 3500 kg/ha. Its production is affected by both biotic and abiotic stresses. One critical factor to genetic improvement is the creation or identification of genetic variability among the germplasm. The objective of this study was therefore to i) identify traits which best discriminate the cotton genotypes and ii) cluster cotton genotypes into distinctive grouping. Thirty (30) genotypes were planted in an incomplete block design replicated three times, in seven sites. Several agronomic traits were recorded and mean performance noted. Data analysis using principle components revealed that the parameters Number of bolls and SCY with loading scores of 0.52 and 0.51 respectively, were the best at discriminating genotypic performance. In this study, the most dissimilar paired parental genotypes were identified as MG27 (from cluster group A) and MG5 (From cluster group C) with a similarity value 29.7 %. This parental cross is expected to create maximum genetic variability among offspring's, creating a wider spread of choice in selecting for desirable genotypes for release or being used as parents in other crosses.

Keywords: Cluster analysis, Similarity, Multi-variate, Genetic variability

1.0 Introduction

Cotton (*Gossypium hirsutum*) is grown in many parts of the world especially the

tropics and temperate regions mainly for its fibre (Egbuta et al. 2017). India is the largest cotton producer in the world with an annual production of approximately 6.4 million tonnes (ICAC, 2019). Cotton is a source of seedcake for animal feed, oil and also a reliable source of income (FAO, 2018). In Zambia, the cotton varieties are preferred for their heat and disease tolerance, but have very low seed cotton yield (SCY) of between 300 to 600 kg/ha as compared to the potential of 2000kg to 3500 kg/ha (CDT, 2015). Its production is affected by many factors both biotic, mostly pests and abiotic conditions such as rainfall, soil fertility and to some extent genetic degeneration.

Critical to genetic improvement is the creation or identification of genetic variability among the germplasm (Dhivya et al., 2013). Characterization of cotton germplasm is a vital tool in the selection of potential parents for development of subsequent desirable hybrids and selection of superior progenies arising from genotypic cross advancement (Murtaza et al., 2005). In this regard, the delineation of germplasm into different genetic groupings allows for genotypes which perform similarly to be grouped together into clusters, to allow the choice of potential parents. Molecular marker and phenotypic trait analysis, known as multi-variate analysis have been employed in characterization and clustering genotypes into distinct groups (Tembo and Munyinda, 2015; Asha et al., 2013). Use of molecular marker analysis are preferable being that they are independent of the environment and hence considered as a more efficient approach (Mbwando et al., 2016). However, where molecular markers are unavailable or inaccessible, use of multi-variate trait analysis for phenotypic characterization and delineation of germplasm is an option. It should be noted that the accuracy of obtaining reliable cluster grouping is to a larger extent dependent on the efficiency of phenotypic scoring. Thus, the use of mean score trait values across environments offers more reliable mean data for multivariate analysis especially for quantitative traits.

Apart from clustering genotypes, multi-variate analysis has been used in identifying traits that best discriminate the genotypes within the same species. Knowing such traits is important in breeding as it helps the breeder to minimise costs where funds are limiting by choosing fewer and appropriate traits as an aid to genotypic selection. In Zambia, the Cotton Development Trust (CDT) has developed and released a number of varieties and also in possession of introduced genotypes (Simasiku et al., 2020). Though their performance across several environments has been established (Simasiku et al., 2020), their genetic similarity and cluster grouping is still unknown. Therefore, the objectives of this study were to i) identify traits which best discriminate the cotton genotypes and ii) cluster cotton genotypes into distinctive grouping.

2.0 Materials and Methods

2.1 Experimental layout and site

This study was undertaken in seven sites of Zambia namely: Magoye, Masumba, Liempe, Mutanda, Minsanfu, Msekera and Gwembe (Table 1). Thirty (30) genotypes (Table 2) were planted in an incomplete block design and replicated three times in all the seven sites as by Simasiku et al., 2020.

Plants were established in two-row plots at a spacing of 90cm by 30cm in 4-metre long rows. All recommended management and agronomic practices were followed.

Table 1. Experimental sites used in the trial during the 2018/ 19 cropping season

Location	Coordinates	Altitude (m)	Soil Type
Liempe	15º22'S, 28º26'E	1171	Sandy loam
Magoye	15º59'S, 27º37'E	1018	Sandy clay loam
Gwembe	16°29'S, 27°35'E	534	Sandy Clay
Msekera	13°38', 32°34' E	1032	Sandy loam
Masumba	13º22'S, 31º 56'E	546	Loamy sand
Mutanda	12º25'S, 26º12'E	1300	Sandy loam
Misamfu	10°17'S, 31°22' E	1536	Sandy clay loam

Table 2. Germplasm used in the multivariate cluster analysis during the 2018/19 cropping season

Genotype Code	Genotypic Pedigree	GN	CGH
M G1	BC4 x CDT II	C1104	Indeterminate
MG2	BC4 x CDT V	C1105	indeterminate
MG3	CDT-09 x BP 52	C1112	indeterminate
MG4	CDT II x Turk A	C1109	indeterminate
MG5	Rocket x CA336	C2612	indeterminate
MG6	Cameroon A x Zim II	C1107	indeterminate
MG7	MF20kG x VH8 4620	C2614	indeterminate
MG8	BC1 x C2511	C1103	indeterminate
MG9	CA347 x F135	C2602	indeterminate
MG10	C457 x CA336	C2619	indeterminate
MG11	Rocket x G319-18	C2618	indeterminate
MG12	CDT II x Turk B	C1110	indeterminate
MG13	CDT II x BP 52	C1111	indeterminate

Genotype Code	Genotypic Pedigree	GN	CGH
MG14	BC4 x ISC 4	C1101	indeterminate
MG15	Ihmad 742 x Chureza	C1116	indeterminate
MG16	CA223 x CDT V	C1114	indeterminate
MG17	CA223 x CDT II-09	C1113	indeterminate
MG18	Stam29ABG1818 x CDT II-09	C1106	indeterminate
MG19	Cameroon A x Zim III	C1108	indeterminate
MG20	Turk B x BP52	C1119	indeterminate
MG21	CDT II-06 x Cameroun A	C1115	indeterminate
MG22	Turk B x Cameroun A	C1120	indeterminate
MG23	BC 3 x ISC 6	C1102	indeterminate
MG24	Cameroun A x BP 52	C1121	Determinate
MG25*	MV 513 x MV515	C 567	Determinate
MG26*	MV513 x MV 517	C571	Determinate
MG27*	MV513 xMV516	C 569	Determinate
MG28	(G319-16xcza87)x(BIII-F3xG319-16)	CDT II	Determinate
G29	CA336	CDT V	Determinate
MG30	C1188 x L299)	Chureza	indeterminate

Genotype Pedigree- GP, GC- Genotype Code; CGH- Characteristic Growth Habit, *CDT- Cotton Development Trust.* *- Genotypes MG 25, MG26 and MG 27 are F1 hybrids obtained from Mahyco, while the rest are lines obtained from CDT

2.2 Data Collection and Analysis

Data for all measured parameters was collected for all the seven sites and mean values for each parameter across sites was recorded. Collection of the SCY was done at 50 % boll opening and at harvest using a digital weighing scale. Counting of the number of open bolls was carried out at harvest. Plant height was measured when the plants were approximately 130 days after germinating, using a tape meter. The ginning out-turn (GOT) was evaluated after harvest using a laboratory ginning machine. The GOT was computed as a ratio of the amount of lint over the total seed cotton weight and expressed as a percentage. Seed index, which is the weight of 100 cotton seeds per genotype was also measured. Multi-variate analysis, utilizing the means of all measured parameters were undertaken using principal

component analysis (PCA) to determine the most discriminating parameter and to schematically apportion the genotypes in distinct groups. The dendrogram and similarity matrix was finally constructed using cluster analysis. All data analysis was performed using GenStat statistical software 18th edition (Payne et al., 2010).

3.0 RESULTS

3.1 Mean Parameter Measurements across Locations

The mean performance of SCY, GOT, Plant height, seed index and number of bolls were recorded (Table 3). The standard error of the mean was computed as 45.6 kg/ ha, 0.3 %, 2.1 cm, 0.1 g and 9.4 bolls respectively. The standard error values indicate that several genotypic mean performances for all measured parameters fell above or below the grand genotypic (population) mean.

Table 3. Mean performance of measured parameters across locations

Genotype	SCY (Kg/ha)	GOT %	Height (cm)	Seedx (g)	Nbolls
MG1	345.21	42.38	62.63	10.76	79.19
MG10	195.30	40.40	41.79	10.24	50.76
MG11	208.60	40.66	41.86	10.48	29.38
MG12	386.60	41.59	72.54	10.75	80.25
MG13	404.43	41.93	51.77	9.76	72.10
MG14	396.04	43.29	65.46	10.67	96.24
MG15	313.69	42.94	68.70	10.38	80.48
MG16	440.87	43.02	65.54	10.86	102.71
MG17	479.56	43.06	67.77	10.29	83.62
MG18	724.07	44.30	70.42	11.00	128.00
MG19	648.88	42.90	73.50	10.38	129.19
MG2	439.88	42.20	62.26	10.90	94.14
MG20	546.23	42.88	64.31	10.10	114.33
MG21	568.72	42.71	70.83	10.29	118.48
MG22	497.16	42.43	66.68	10.57	127.38
MG23	678.17	42.90	69.22	11.14	112.38
MG24	516.14	41.26	69.44	10.86	136.95

Genotype	SCY (Kg/ha)	GOT %	Height (cm)	Seedx (g)	Nbolls
MG25	831.61	39.83	68.82	11.00	155.33
MG26	342.13	40.01	38.67	10.67	20.00
MG27	1320.17	40.34	76.28	12.10	269.71
MG28	960.38	44.02	79.55	11.10	184.33
MG29	637.50	42.85	70.60	10.90	134.24
MG3	399.21	43.17	60.10	10.00	94.33
MG30	665.67	42.71	77.92	10.67	157.33
MG4	463.82	42.37	65.04	9.86	82.19
MG5	116.60	39.40	43.51	9.95	19.05
MG6	494.58	42.27	63.16	10.00	83.71
MG7	175.13	39.84	48.74	10.33	31.86
MG8	633.33	42.92	68.61	11.00	106.20
MG9	134.59	38.66	44.54	10.38	38.38
Means	498.8	42.0	63.0	10.6	100.4
SE	45.6	0.3	2.1	0.1	9.4

GOT= Ginning out turn, SCY=Seed cotton yield, Height= Plant height, Seedx=Seed index, Nbolls=Number of bolls, SE=Standard error of the mean

3.2 Multi-variate evaluation of genotypes

3.2.1 Evaluation of Principle Components and measured parameters

Analysis on eigen values (Figure 1) showed that two principle components (PC),1 and 2 contributed most to variations in genotypic responses. This was represented as root 1 and 2 with eigen values of 3.5 and 1 respectively. PC1 and PC2 contributed 68.5 % and 21.5 % respectively giving a total of 90 % of percentage variation explained (Table 4).

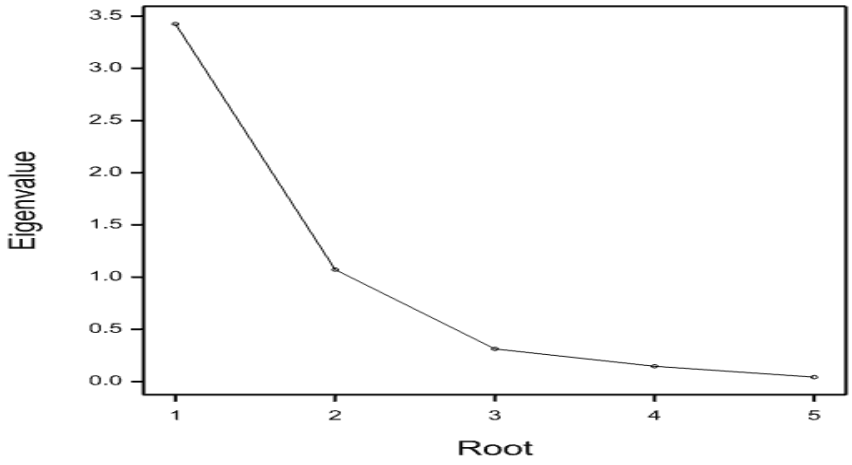

Figure 1. Screen plot eigen values and roots (Principle components). Root (PC) 1 and 2 represented with eigenvalue 3.5 and 2 respectively.

The parameters, number of bolls and SCY exhibited higher contribution (greater than 0.5) in differentiating genotypic responses with a loading score of 0.52 and 0.51 respectively. Arising from the fact that PC 1 had a much higher contribution of the percentage variation explained (68.5 %). This was followed up by GOT and seed index arising from PC2 with a loading score of 0.77 and 0.53 respectively. The other three Principle components (PC 3 to 5) had very low percentage variation (approximately 10 %) to be considered as a reasonable contribution.

Table 4. Latent loadings of the measured parameters corresponding for computed principle components 1 to 5

Parameters	1 (68.5%)	2 (21.5 %)	3 (6.3%)	4 (2.9%)	5(0.9%)
Ginning out turn	0.29	0.77	0.42	0.37	0.12
Number of bolls	0.52	-0.13	-0.38	0.06	0.75
Plant height	0.49	0.29	-0.11	-0.76	-0.28
Seed index	0.40	-0.53	0.75	-0.07	0.02
Seed cotton yield	0.51	-0.18	-0.32	0.52	-58

In brackets percentage variation explained by each principal component

3.2.2 Genotypic grouping

The scatter plot (Figure 2) revealed that the genotypes clustered into five distinct sets of which MG27 and MG 25 and MG 28 were

singletons. Group C consisted of, MG5, MG7, MG9, MG10, MG26 and D the largest group, consisted of MG1, MG2, MG3, MG4, MG6, MG12, MG13, MG17, MG18, MG19, MG20, MG21, MG22, MG23, MG24, MG29, MG30. Further analysis, using cluster revealed that these groups were generated at similarity level of 97.5 % (Figure 3).

Detailed analysis using the similarity matrix (Figure 4) showed that genotypic pair MG27 and MG5 were most dissimilar genotypes with a similarity score of 29.7 %. These were followed by genotypic pair MG27 and MG9 which had a similarity score of 38.9 %. On the other hand, the least dissimilar pair were MG14 and MG16 with a similarity matrix score of 99.8 %. These were followed by genotypic pair MG1 and MG2 which had a high similarity score of 99.7 %.

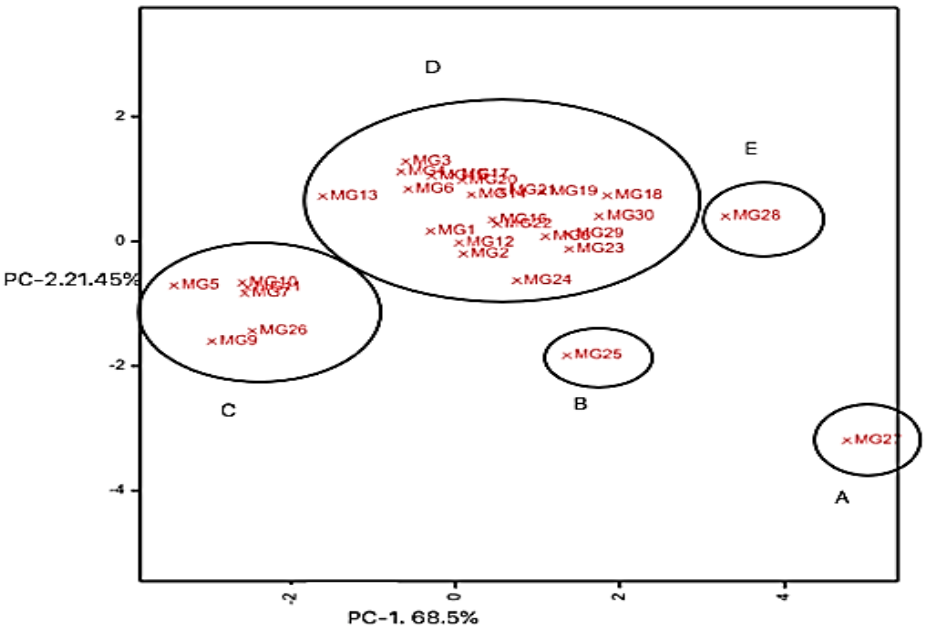

Figure 2. Scatter plot for Principal Component analysis with a total percentage variation explained of 90 %. Two cluster groups C and D and singletons A, B and C were generated giving a total of five

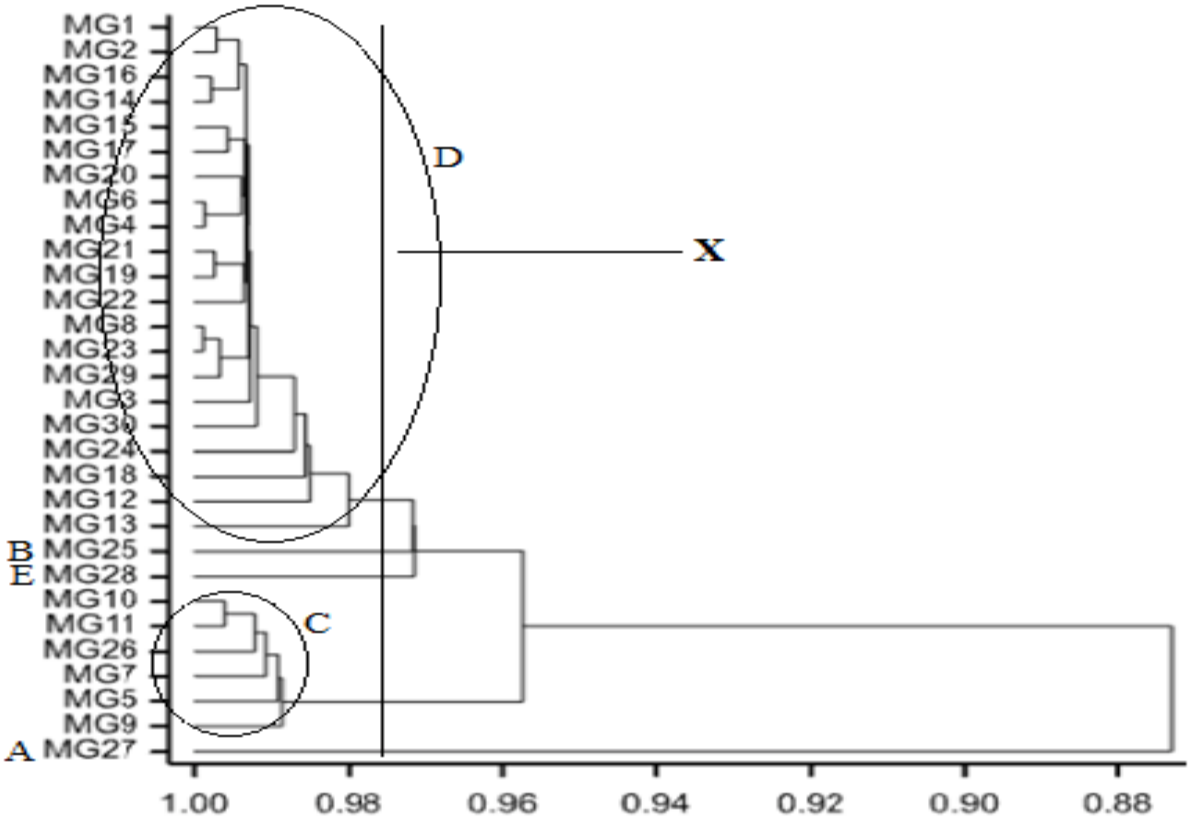

Figure 3. Dendrogram showing genotypic groupings as generated by cluster analysis. X-Line at 97.5 % cluster sets. This line crosses five lines depicting the tail end of each set. Two cluster groups C and D and singletons A, B and C were generated

	MG1	MG10	MG11	MG12	MG13	MG14	MG15	MG16	MG17	MG18	MG19	MG2	MG20	MG21	MG22	MG23	MG24	MG25	MG26	MG27	MG28	MG29	MG3	MG4	MG5	MG6	MG7	MG8	MG9
MG1	----																												
MG10	90.8	----																											
MG11	91.6	99.6	----																										
MG12	98.4	86.0	86.6	----																									
MG13	94.7	95.7	94.8	91.2	----																								
MG14	99.2	86.1	86.9	97.5	93.4	----																							
MG15	98.8	86.7	87.1	98.1	94.4	99.3	----																						
MG16	99.3	85.8	86.8	97.9	92.3	**99.8**	98.7	----																					
MG17	98.3	86.0	86.2	97.5	95.0	99.2	99.6	98.6	----																				
MG18	94.0	72.7	74.1	92.8	84.3	96.9	94.4	97.3	95.6	----																			
MG19	95.8	79.2	79.0	96.7	90.5	97.6	97.4	97.6	98.5	97.2	----																		
MG2	**99.7**	89.9	90.8	98.3	93.7	98.9	97.9	99.4	97.7	94.9	96.2	----																	
MG20	97.2	87.0	86.4	95.9	96.3	98.3	98.4	97.6	99.3	94.8	98.5	97.0																	
MG21	97.1	83.1	82.8	97.5	93.2	98.3	98.5	98.1	99.3	96.2	99.7	97.1	99.3	----															
MG22	98.6	86.5	86.4	98.2	93.7	99.0	98.5	99.2	98.8	96.2	98.9	98.9	98.9	99.3	----														
MG23	96.9	79.6	81.0	96.7	87.2	97.7	95.7	98.7	96.5	98.6	97.5	98.0	95.4	97.1	98.1	----													
MG24	97.2	85.2	85.1	98.5	90.1	96.3	95.8	97.4	95.8	93.5	97.0	98.2	95.7	97.3	98.7	97.4	----												
MG25	90.1	79.9	79.5	93.1	83.4	88.2	87.0	90.4	88.2	87.0	91.7	92.6	89.2	91.5	93.2	93.1	97.2	----											
MG26	88.5	98.5	99.2	83.5	91.7	82.7	82.3	83.2	81.9	70.3	74.8	88.2	82.3	78.7	82.9	78.5	82.8	79.6	----										
MG27	64.0	40.4	40.7	68.7	47.2	64.2	58.9	68.9	61.7	74.0	72.5	69.8	63.6	69.0	71.8	78.4	78.7	87.3	42.5	----									
MG28	85.7	58.2	59.0	87.3	73.2	89.7	86.8	91.0	88.9	97.1	94.6	87.9	88.8	92.1	91.4	95.2	90.3	87.0	55.3	83.6	----								
MG29	96.9	79.7	80.4	97.1	88.4	98.1	96.6	98.8	97.3	98.5	98.9	97.8	96.9	98.4	99.0	99.6	98.2	93.5	77.2	78.2	95.8	----							
MG3	97.3	89.8	89.4	94.4	97.8	98.0	98.4	96.9	98.9	92.4	96.0	96.3	99.3	97.6	97.5	93.0	93.2	84.6	84.8	54.2	83.7	94.3	----						
MG30	93.7	73.7	73.6	95.9	85.2	95.7	95.1	96.3	95.9	97.0	99.2	94.7	95.8	98.3	97.7	97.6	97.2	93.0	69.5	79.0	96.8	99.0	92.2	----					
MG4	96.7	89.2	88.5	95.9	97.7	96.9	98.3	95.9	98.9	90.9	96.8	95.8	99.2	98.3	97.4	92.6	94.3	87.4	84.3	56.2	83.4	94.2	99.1	----					
MG5	85.8	98.6	97.8	82.3	93.0	79.8	82.1	79.3	81.0	63.3	73.1	84.3	81.7	77.8	80.7	72.0	80.1	75.2	96.9	**29.7**	47.7	72.4	84.8	85.9	----				
MG6	97.5	90.5	90.0	96.4	98.0	97.5	98.4	96.7	99.0	91.8	97.0	96.9	99.4	98.4	98.0	93.8	95.3	89.0	86.4	59.0	84.2	95.0	99.2	99.9	86.9	----			
MG7	91.9	99.1	98.9	89.3	94.7	86.7	88.1	86.7	87.0	73.1	80.6	90.9	87.0	84.4	87.4	81.1	87.5	82.7	97.9	43.3	59.6	81.1	89.1	90.0	98.9	91.1	----		
MG8	97.8	81.6	82.8	97.4	89.3	98.6	97.0	99.3	97.6	98.5	98.1	98.6	96.6	97.9	98.7	99.9	97.7	92.7	80.0	75.7	94.4	99.7	94.6	94.3	74.5	95.3	83.0	----	
MG9	85.7	97.8	97.3	83.3	89.9	78.9	80.5	79.3	79.0	63.2	72.4	85.1	79.6	76.7	80.7	73.4	82.4	79.6	97.4	**38.9**	49.2	73.4	81.8	83.2	98.8	84.7	98.9	75.3	----

Figure 4. Similarity matrix scores exhibiting levels of similarities between genotypes. Highlighted and in bold show genotypic pairs with the highest and lowest level of similarity between genotypes

4.0 Discussion

4.1. Evaluation of the parameters that best discriminates the genotypic responses

The discrimination of parameters (traits) is an important aspect to a breeder because it makes him/ her aware of what traits are most important in screening of the candidate genotypes (Egenids et al., 2011). Generally screening of germplasm may be costly and identification of important traits may help the breeder to narrow down to a few parameters or traits as an aid to selection. In this study principle component (PC) 1 which explains 68.5 % of the percentage variation was associated with Number of bolls and SCY, with a latent loading score 0.52 and 0.51 respectively (Table 4). Implying that where resources are limiting, genotypic selection can only be employed based on number of bolls and SCY. On the other hand, Principle Component 2 was explained by GOT and seed Index with latent loadings score of 0.77 and 0.53 respectively. However, PC 2 only contributed 21.5 % compared to 68.5 % for PC1 of the percentage variation. Therefore, parameters

associated with PC1, Number of bolls and SCY can be sufficient to utilise in selection for genotypic performance of cotton.

4.2. Genotypic Clustering

Comprehending the genetic relationships among germplasm is particularly useful in breeding programs. Such information can be used in planning crosses, assigning heterotic groups, and in precise identification with respect to plant varieties (Sigh and Gupta, 2019). Principle component and cluster analysis has been used as vital analytical multivariate tools. In this study a two-dimensional PCA scatter grouping and cluster analysis (at 97.5% similarity) generated two cluster groups and three singletons (Figure 2 and 3). The reliability of the generated cluster groups from the two-dimensional PCA scatter is likely to be associated with total percentage variation explained (Chiseche et al., 2020). The higher the combined total phenotypic percentage variation of the two PC scores, the more reliable the two-dimensional scatter plot is expected to be. In this study a combined PC1 and PC2 gave an approximate higher value of 90 %. The fact that the cluster pattern obtained in a PCA analysis (Figure 2) was replicated in cluster analysis (Figure 3) entails that the results were reliable.

In this study five cluster sets, A, B, C, D, E were generated at a similarity index of 97.5 % as earlier mentioned. Clustering at such a level is expected among genotypes within the same species. The clustering of the genotypes at a higher level could be due to selection over time, which may ultimately have led to concentration of the elite lines within a similar gene pool (Esbroeck et al.,1998). Lower percentage similarity level clustering is common among different species or genera and is a common feature occurrence in evolution studies (Gori et al., 2016). From this study we can deduce that selection of parents to utilise in generating hybrids or in creating of a variability of offsprings for further breeding, should come from two distinct sets. It was suggested that effective generation of diverse offspring to select from and creation of a molecular mapping population should employ a careful selection of two diverse genotypes, especially for traits which are quantitatively inherited (Tembo et al., 2014; Acquaah, 2007). Chapepa et al., 2020 used the same approach to identify 3 clusters of morphological traits for verticillium wilt disease variation in Cotton in Zimbabwe. In this study the least similar paired parental genotypes were identified as MG27 (from cluster set A) and MG5 (From cluster set C) with a similarity value of 29.7 % (Figure 4). This parental combination is expected to create maximum genetic variability among offspring for further selection. It is expected that the F1 product (MG27 X MG5), when advanced, could create maximum genetic variability among offspring generating a wider spread of choice in selecting for desirable genotypes for release or being used as parents in other crosses

Similarity matrix has also been used in marker assisted genetic diversity among upland cotton by a number of authors (Zhang et al., 2005; Chaudhary et al .,2010; Ali et al., 2011). Genotypic pair MG1 and MG2 had a high level of similarity score of 99.7 % probably because they both have the same genotypic background sharing the same ancestral parent, BC4 (Table 2) whose genes may have dominated the other unshared parent CDII and CD IV. These

genotypes nevertheless, can act as ample sources of germplasm in a breeding program in situations where one genotype is unavailable. For instance, MG1 can be a proxy or a replacement MG2.

6.0 Conclusion

In this study, the parameters Number of Bolls and SCY were identified as the best at discriminating genotypic performance responses. In this study, the cotton genotypes clustered into five distinct sets. The most dissimilar paired parental genotypes were identified as MG27 (from cluster group A) and MG5 (From cluster group C) with a similarity value 29.7 % (Figure 4). This parental combination is expected to create maximum genetic variability among offspring, generating a wider spread of choice in selecting for desirable genotypes for release or being used as parents in other crosses.

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Disclosure Statement

The authors declare that they have no conflict of interest

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Implications of Genotype by Environment Interactions on Heritability Estimate and Variance Components of Cotton (*Gossypium hirsutum* L.)

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Abstract:

Genetic variation in cotton is crucial when traits are heritable and elucidation of the underlying genetic components of these helps in selecting elite genotypes. A research work was done to determine broad-sense heritability of traits through variance components in different cotton genotypes. The trials were laid out in randomized complete design with three replications. Ten cotton genotypes were used in the study. The results revealed highly significant differences among genotypes on all the characteristics. The experimental lines 917–05-7 had the highest yield (1919 kg/ha), the biggest bolls (6.33 g), produced more lint (853.9 kg/ha), and had taller plants (123.9 cm). Significant genotype by environmental interactions were detected which caused low heritability values, low error variance, and low genotype by environment variances, which allowed easier selection of genotypes. Further partitioning of the genotype by environment effects revealed the most stable and highly performing genotypes and these were 907–05-9 and TN96-05-9 which were concluded to be the best performing cotton lines.

Keywords: Genotype by environment interaction; variance components; co-efficient of genotypic variance; coefficient of phenotypic variance; broad-sense heritability; seed cotton yield

1. Introduction

Cotton (*Gossypium hirsutum* L.) has been widely cultivated for its fibre world over with little grown for seed (Maheshwari & Kovalchuk, 2016). The global production of cotton was 121.30 million bales (218 kg each) in 2019/20 season (USDA, 2021). The fibre is used as a raw material for the textile industry and the cotton seed is a vital source of edible oil and livestock feed. The demand of the crop has been on the increase especially with the expansion of the textile

industry which has resulted in cotton consumption outstripping supply and hence the need to increase its production (Naeem et al., 2014; USDA, 2021). Development of a good variety is an important factor for yield improvement in any crop and in cotton utilizing different genetic manipulation and breeding approaches have made cotton production a success even in marginal regions. The information on pre-existing genetic variation of different polygenic characters and the development of new variation based on the known genetic constitution is useful in improving and maintaining higher crop production standard (Naeem et al., 2014).

Expression of traits in cotton is often affected by the interactions between the genes and environment. The information of character associations between the traits and within the traits themselves is important for selection of the proper breeding material (Iqbal et al., 2006). Some of these characteristics are affected by the genotypic and environmental differences (Camas & Esendal, 2006). An estimate of the heritability is a requirement in order to determine the effectiveness of the breeding program (Arslan, 2007). The benefit of the genetic differences will not be realised in the succeeding progenies resulting in no genetic gain. Genetic variation in cotton of yield and other contributing components is crucial when it is heritable and elucidation of the underlying genetic components helps in selecting elite genotypes (Sahar et al., 2021). According to Rehman et al. (2020), heritability values ranges from medium to high for seed cotton yield and fibre traits.

The genetic variation can be elucidated by the use of variance components, which are important in estimating the contribution of each random effect to the variance of the dependent variable thereby estimating genetic gain (Mackay, 2016). In the absence of genotypic information in crop improvement, variance-component estimation can be used to estimate heritability of quantitative traits using trait values (Abney et al., 2000). Precise estimation of variance components coupled with accurate selection in cotton breeding is important and can be achieved through use of optimal estimations which will lead to the maximization of genetic gain from selections (Furlani et al., 2005). Yield component traits are strongly influenced by dominant effects of genes, while additive-environment interaction effects have certain contribution (Shahzad et al., 2019). The principal aim of the study was to determine the influence of genotype by environment interaction on heritability and estimates of variance components for plant height, number of sympodial branches, seed weight, ginning outturn (GOT), boll weight, lint yield and seed cotton yield so as to make informed decisions in selecting the best performing cotton lines under diverse conditions. In addition, the magnitude of genotype by environment interaction of the traits was also studied.

2. Materials and methods

2.1. Experimental location, germplasm, and management

The study was conducted at various testing locations around Zimbabwe from 2017/18 to 2020/21 seasons. These sites used in the study and their general description were as listed below in Table 1:

Experimental lines at advanced variety evaluation stage and commercial check

varieties were used in the experiment and these were as listed in Table 2:

The agronomic management practices at all sites were done according to the Cotton handbook (CGA, 1998).

Table 1. Description of sites used in the study

Location	Latitude	Longitude	Altitude (m)	Average rainfall (mm)	Maximum Temp (°C)
CRI -Kadoma	18°20′S	29°54′E	1156	750–1000	38
Chibuwe	20°33′S	32°24′E	444	450–550	38
Kuwirirana	21°15′S	30°48′E	1483	500–600	38
Chitekete	17°25′S	16°28′E	914	450–500	42
Masakadza	17°25′S	16°28′E	914	400–650	38
Matikwa	20°48′S	32°14′E	300	400–500	40
Muzarabani	17°48′S	31°05′E	432	600–800	42
Dande	16°33′S	30°58′E	600	600–800	36
Chisumbanje	20°48′S	32°14′E	448	450–500	40
Panmure	17°16′S	31°47′E	881	700–800	35
Save Valley	21°29′S	32°51′E	466	450–500	41

Source*: Agritex Planning Branch (2019); Zimbabwe natural regions and farming areas boundaries*

Table 2. List of cotton lines used in the experiment

Treatment	Status	Source
912–05-1	Breeding line	Cotton Research Institute
917–05-7	Breeding line	Cotton Research Institute
932–05-3	Breeding line	Cotton Research Institute
938–05-3	Breeding line	Cotton Research Institute
CRI MS 1	Commercial variety	Cotton Research Institute
CRI MS 2	Commercial variety	Cotton Research Institute
GN96(b)-05-8	Breeding line	Cotton Research Institute
SO-99-9	Breeding line	Cotton Research Institute
SZ9314	Commercial variety	Cotton Research Institute
TN96-05-9	Breeding line	Cotton Research Institute

A standard uniform seeding rate of 20 kg/ha was used across all the trials with a seeding depth of 20 mm. Fertilizer nutrient application involved the use of Compound L

(5 N:18P_2O_5:10K_2O:8S + 0.1B) as the basal fertilizer and ammonium nitrate (34.5%N) as the top dressing at 8 weeks after crop emergence. Weed management was done using Cotogard WG as the pre- emergence herbicide and Fusion (Fluazifop-P-butyl, Fenoxaprop-P-ethyl) as the post-emergence herbicide coupled with hand weeding where necessary. Pest management was carried out following the threshold method as indicated in the handbook.

3. Experimental design and data description

At each location, trials were established in a randomized complete block design with 10 genotypes as the treatments and replicated three times. The individual gross plot sizes which were used in the experiment were 36 m^2 with net plots of 16 m^2. Data collection was done on plant height, seed weight, ginning outturn (GOT), boll weight, lint yield, and seed cotton yield. Plant height was measured on 10 plants out of 56 plants in each individual net plot from the ground level to the tip of the plant and averaged to get the plant height for each variety. The number of bolls and sympodial branches of these 10 plants were also counted and averaged. One hundred boll samples were collected from each net plot and ginned with table saw gins to separate fibre and seeds. The seeds were counted and 100 seeds were weighed to get the 100 seed weight index. The ginning outturn (GOT) was calculated by dividing the weight of fibre with the total seed cotton and multiplied by 100 to get the GOT percentage. Lint yield was calculated per hectare using the fibre weight obtained in the net plots as well as the total seed cotton.

4. Data analysis and statistical methods

Analysis of variance was carried out on the collected data using GenStat 18th version statistical package (Geodhart & Thissen, 2016). Means that exhibited statistical differences were separated using least significant differences (Fischer's protected LSD) test at 5% level of significance. The heritability values (H^2) and variance components were calculated according to the equations suggested by Comstock and Moll (1963). Heritability is expressed by $H^2 = V_g/V_p$, where H is the heritability estimate, V_g the variation in genotype, and V_p the variation in phenotype.

5. Results and discussion

5.1. Genotype mean performance

The analysis of variance showed significant differences among genotypes on all the characteristics as shown in Table 3. According to Dhivya et al. (2014), this indicated considerable genetic diversity among the genotypes. The magnitude of variability available in the cotton genotypes for different characteristics is important for selecting the best candidate line. The experimental line 917–05-7 had the highest yield of 1919 kg/ha which was comparable to TN96-05-9 (1758 kg/ha) and the commercial check varieties CRI MS 1 (1752 kg/ha) and SZ9314 (1856 kg/ha).

Table 3. Combined analysis of seed cotton yield and agronomic traits of 10 cotton genotypes from 2017/18 to 2020/21 seasons (GenStat 18$_{th}$ version was used)

Genotype	SCY	BW	GOT	LY	SWI	FG	PH
912–05-1	1570a	5.97abc	41.98b	724.9a	10.44ab	5.99b	114.4a
917–05-7	1919c	6.33c	40.75b	853.9c	10.54bc	6.01b	123.9d
932–05-3	1654ab	6.24bc	41.66b	744.8a	10.99e	6.13b	119.5bc
938–05-3	1601ab	5.98abc	40.97b	720.4a	10.81cde	6.10b	119.9bcd
CRI MS 1	1752bc	5.93ab	41.88b	784.2abc	10.98de	6.10b	117.8ab
CRI MS 2	1560a	5.64a	34.49a	711.4a	10.22a	5.64a	122.2 cd
GN96(b)-05-8	1652ab	6.32c	42.05b	739.6a	10.47ab	6.15b	120.2bcd
SO-99-9	1555a	5.83a	40.89b	708.2a	10.47ab	6.02b	121.0bcd
SZ9314	1856c	5.90ab	41.98b	832.1bc	10.71bcd	5.98b	120.2bcd
TN96-05-9	1758bc	5.89ab	41.22b	767.8ab	10.82cde	5.99b	119.5bc
LSD	175.5	0.39	3.75	79.98	0.28	0.173	4.28

Means within a column with different letters are significantly different at P < 0.05, SCY—seed cotton yield (kg ha^{-1}), BW—boll weight (g), GOT—ginning out turn (%), LY—lint yield (kg ha^{-1}), SWI—100 seed weight index (g), FG—fuzz grade, PH—plant height (cm)

The same genotype produced the biggest bolls (6.33 g) which were statistically similar to GN96(b)-05-8 (6.32 g). 917– 05-7 also produced more lint (853.9 kg/ha) which was comparable to the commercial check varieties CRI MS 1 (784.2 kg/ha) and SZ9314 (832.1 kg/ha). GOT% was comparable for all the genotypes except for CRI MS 2 which recorded a low value of 34.49%. Large seeds were obtained in the experimental line 932–05-3 which had 100-seed weight index of 10.99 g which was comparable to 938–05-3 (10.81 g) and CRI MS 1 (10.98 g). The commercial check variety CRI MS 2 had little fuzz linters (5.64) that remained on the seed after ginning compared to the rest of the genotypes. Tall plants were observed in the experimental line 917–05-7 which produced plants that 123.9 cm tall whilst 912–05-1 produced the shortest plants (114.4 cm). These results were also observed by Mukoyi et al. (2018), who detected genetic variation among tested genotypes with experimental lines performing better than the commercial lines. Similarly, Raheel et al. (2017), obtained similar results on field performance of cotton under irrigated conditions which were used as selection basis for high performing cotton lines.

6. Combined analysis of variance across years by locations and variance components

The homogeneity of variance tests indicated homogeneous error variance for all traits in each of the location by year environments and according to Campbell and Jones (2005), this allowed for a combined across environment analysis (Table 4). The analysis of variance (ANOVA) across environments indicated significant variation among genotypes for the traits tested and significant interaction for the overall genotype by environment (GE) for seed cotton yield, lint yield, seed weight index and fuzz grade which justified genotype and genotype by environment (GGE) analysis. This method was observed to be efficient for selecting stable and productive genotypes by Milioli et al. (2018). This greatly influenced the heritability and variance of components of the traits that were studied in this experiment. The results pertaining to variance of components which estimated the contributions of different experimental factors made to the overall variability, as expressed by their variance based on the mean squares according to Mather and Jinks (1971) are also shown in Table 3. These were genotypic variance, genotypic by environment variance, phenotypic variance, genotypic coefficient of variation, phenotypic coefficient of variation and heritability in broad sense.

Seed cotton yield recorded the highest value for genotypic variance (8146.04) and phenotypic variance (12,728.18) followed by lint yield which had a genotypic variance of 879.97 and phenotypic variance of 2218.44. Fuzz grade exhibited the lowest genotypic variance (0.0027) and phenotypic variance (0.0096). Selection of suitable cotton varieties is hindered by the existence of the large error and GE variance components which are caused by large genotype by environment interactions. In this study, low error and GE variances compared to genetic variances were observed which made selection of genotypes easier (Abbas et al. 2008). This situation was also observed on several studies in cotton (Maleia et al., 2010; Meredith et al., 2012). The co-efficient of genotypic variance (GCV) and phenotypic variance (PCV) were calculated for all the traits that were studied and the GCV ranged from 0.86% (fuzz grade) to 4.98% (lint yield). PCV ranged from 1.34% (plant height) to 7.74% (lint yield). In the study, there was a close similarity between all the traits except for fuzz grade between the GCV and PCV, indicating less environmental influence on these characters. In all the genotypes under study PCV was higher than the GCV for all characters showing the extent environment plays on the expression of all these traits. Similar observations in cotton was reported by Dheva and Potdukhe (2002) where moderate PCV and GCV estimates that were almost close to each other were noticed for plant height, number of sympodia per plant, number of bolls per plant, lint index and seed index.

Heritability was low to moderately high for all the traits except for GOT%, seed weight index, boll weight, seed cotton yield, and plant height, which had values of 0.53,0.57, 0.63, 0.64 and 0.77, respectively. This indicated that these traits were heritable and were mainly controlled by genetic factors with little environmental influence. Lint yield had 0.41 and fuzz grade 0.28 indicating

that they were greatly affected by the environment. According to Wray and Visscher (2008), heritability is a tool used to estimate the degree of variation in a phenotypic trait in a population that is attributed to genetic variation among the individuals in that population. A heritability value of 1 indicates no environment effect on variation and a value of 0 mean that all variation in the population comes from differences in the environments experienced by the individuals. In this study, variations in these traits were greatly attributed to environment variations.

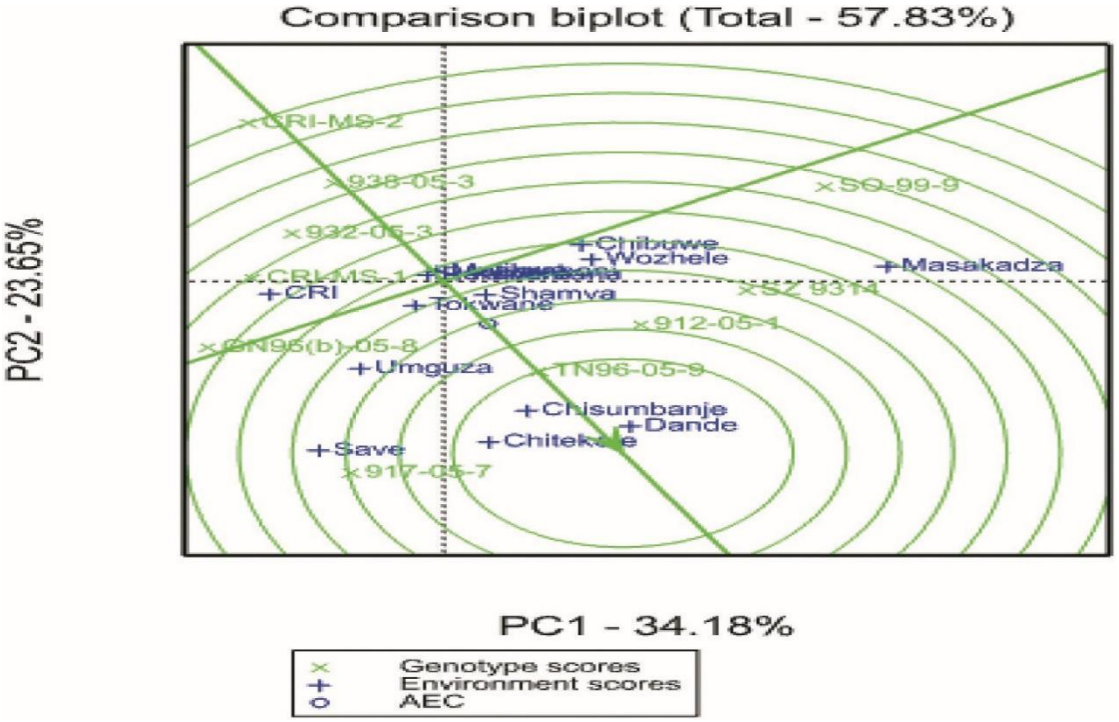

Figure 1. Comparison biplot showing the ideal genotype for different cotton genotypes.

7. Genotype by environment interaction analysis

7.1. Ideal genotype

The genotype comparison biplots based on seed cotton yield and lint yield produced a similar pattern of genotype ranking, based on mean yield and stability of these two traits (Figure 1). This is done to identify the ideal genotype. According to Yan (2002), this genotype has both high mean yield performance with the lowest interaction with the environment. The test genotypes that include TN96-05-9, 917–05-7, SO-99-9, and 912–05-1 with the commercial check variety SZ9314 were above the average environment coordinate; while the rest were below the line (Figure 1). However, the comparison biplots showed that genotypes TN96-05-9, was closer to the average environment coordinate; followed by 912–05-1 and then 917–05-7 for both seed cotton and lint yield. These were genotypes that had high means and good stability as they were closer to the centre of the concentric

circles, which represents the ideal genotype.-

8. Genotype ranking based on mean performance and stability

A number of genotypes were above the average environment coordinate ordinate, which included SO-99-9, 917–05-7, SZ9314, and TN96-05-9, which indicated high performance based on seed cotton yield as shown in Figure 2. The high-ranking experimental genotypes which had shorter perpendicular projected lines was TN96-05-9 followed by 912–01-5 followed by 917–05-7.

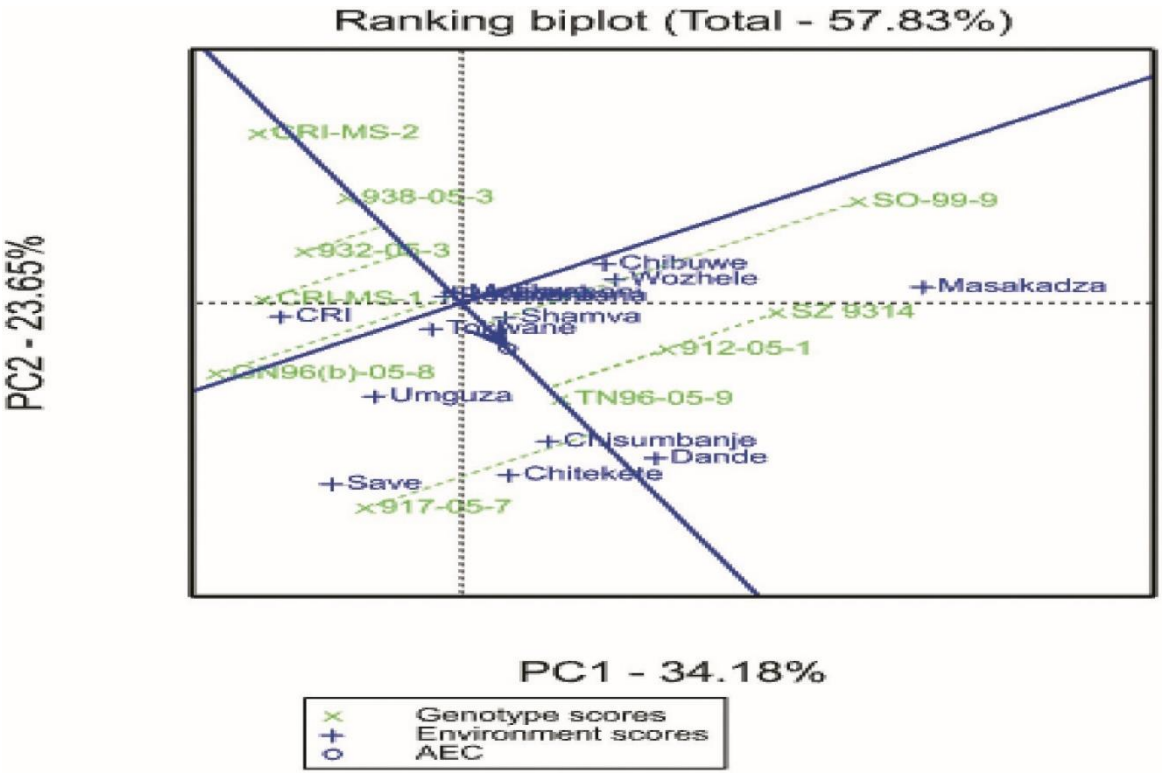

Figure 2. Genotype ranking of different cotton genotypes

9. Which-Won-Where

The which-won-where pattern revealed different genotypes that won in different environments (Figure 3). The environments fell into five different sectors with different winning genotypes suggesting large crossover of GE interaction. Five mega environments were therefore derived by compartmentalizing the target environments. The genotypes that were on the vertices of the polygon included 917–05-7, GN96(b)-05-8, SO-99-9 and the commercial varieties CRI MS 2 and SZ9314. The genotype 917–05-7 won in the sector that was represented by Save, Umguza, Chisumbanje, Chitekete, Dande, and Tokwane whilst GN96(b)-05-8 won in the sector with CRI, Umguza, and Tokwane. The genotype SO-99-9 won in the sector with Chibuwe, Matikwa, and Wozhele. The huge GE crossover posed challenges in

recommending varieties for wider adaptation because of several mega environments that were produced. Crossover type GE interaction has been suggested to cause difficulties in variety selection (Bernardo, 2002; Yan et al., 2000; Yan & Kang, 2002). Where a single mega-environment exists, a single breeding program focusing on the entire mega environment is recommended (Mukoyi et al., 2018).

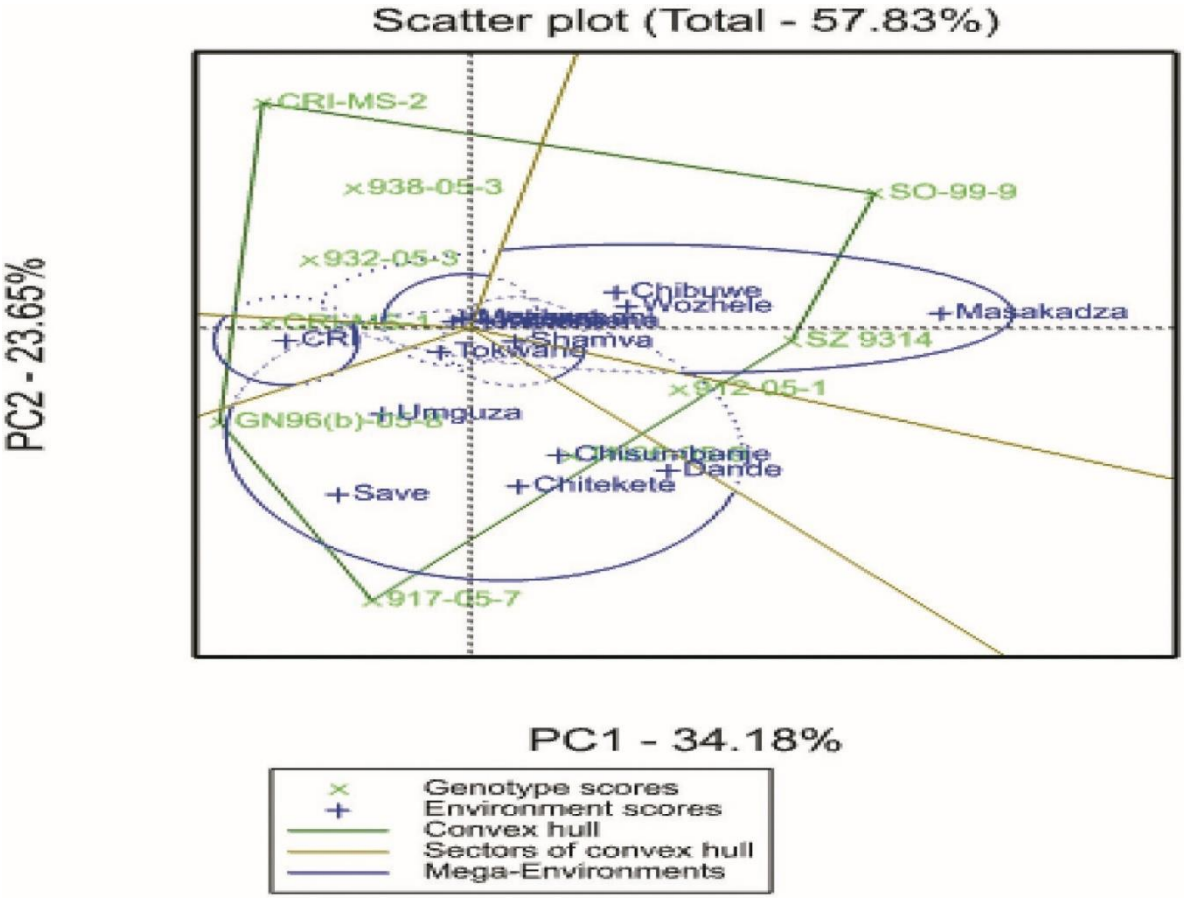

Figure 3. Best performing genotypes and mega environments for different cotton genotype

10. Conclusion

In this study, it was concluded that genotype by environment greatly impacted on heritability as environmental effects influenced most of the variation in the cotton genotypes. The variance components were also affected by the genotype by environment interaction as low error and genetic by environment variances were observed which made selection of the best cotton genotypes easier. The magnitude of the genotype by environment was partitioned to identify the cotton genotypes, which have high performance and yield stability. These best performing genotypes

that were identified in this study across the testing sites based on all the traits under study were TN96- 05-9 and 917–05-7. These genotypes had good boll size, GOT%, lint yield, plant height, and seed cotton yield which made them suitable for production in the most of the cotton growing regions of Zimbabwe

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