

Exploring Superiority of Different Cotton (*Gossypium hirsutum*. L) Genotypes Through the Application of Parametric Stability Models

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To cite this article:

Mare Marco, Chapepa Blessing, Mubvekeri Washington, Kutwayo Dumisani. Exploring Superiority of Different Cotton (*Gossypium hirsutum*. L) Genotypes Through the Application of Parametric Stability Models. *Journal of Plant Sciences*. Vol. 10, No. 4, 2022, pp. 130-138. doi: 10.11648/j.jps.20221004.11

Received: June 14, 2022; **Accepted:** June 29, 2022; **Published:** August 9, 2022

Abstract: Cotton (*Gossypium hirsutum*) is an important cash crop worldwide mainly grown for its unique natural fibre hence considered as an industrial and agricultural crop. Cotton Variety Development Programme in Zimbabwe has the mandate to develop cotton varieties which are superior in terms of the field and fibre attributes and such varieties increases cotton production and productivity. A Multi locational Yield Evaluation (MYE) study which aimed to select superior cotton genotypes through the use of different stability models was conducted in Zimbabwe at fifteen various locations from 2014/15 – 2020/21 season. Fifteen genotypes that are in the advanced stage of testing before final recommendation for possible release were evaluated. The trials was laid out in a Randomized Complete Block Design (RCBD) and replicated three times. Genstat 18th Edition was used to generate the Analysis of Variance (ANOVA), genotype stability and environments performance. Results from the accumulated Analysis of Variance (ANOVA) of seed cotton yield indicated highly significant differences ($P < 0.001$) due to genotypic, environmental, and GE interaction effects revealing more contribution (43.1%) of the total variation due to the environmental effects hence environments were variable and caused many fluctuations in seed cotton yield. Genotypic effects and GEI explained 0.9% and 8.7% respectively to the total variation whilst the seasons contributed about 19.7%. Matikwa and Chitekete recorded the highest total seed cotton of 3567kg ha^{-1} and 3534kg ha^{-1} respectively followed by Chizvirizvi that scored 2681kg ha^{-1} . Stability parameters, both multivariate and univariate were used in the study. Genotype and Genotype by Environment (GGE) biplot indicated that SZ-95-23 was an ideal, high-performing, and stable genotype and was the winner at ten test locations. Use of Wricke's Ecovalence and Finlay and Wilkinson's models also indicated that SZ-95-23 was the superior genotype possessing good yield performance, stability, and wide adaptability, recommended for commercial release and cultivation.

Keywords: Stability, Genotype by Environment Interaction (GEI), Total Seed Cotton Yield, Genotype and Genotype by Environment

1. Introduction

Upland Cotton (*Gossypium hirsutum*. L) also known as American Cotton is an important cash crop and the main source of unique natural fiber hence considered an industrial crop worldwide accounting for more than 95% production [17, 20]. The crop which has many uses is an important

source of feed, foodstuff, and oil, hence making it a unique and versatile crop for both home and industrial usage. In Zimbabwe, cotton is ranked second most important cash crop after tobacco, with an average annual production of 198357.3 metric tons and an average yield of 669kg ha^{-1} over the 20 years (Figure 1) whilst the industrial crop's global production in 2020 was 121.3 million bales [1, 20].

Cotton production and productivity in Zimbabwe have been fluctuating with a general decline in the trend due to some biotic and abiotic stresses which are linked to climate variability effects. These stresses include unpredictable rainfall patterns, perennial droughts, heat stresses, shortened rainy growing seasons, new emerging pests, weeds, and diseases among others. Some of the stresses coincide with the

crop's critical development stages such as initial crop development, flowering, and boll development hence causing serious cotton yield reduction. Such detrimental effects to cotton production invite the need for researchers to come up with climate-smart technologies, in which the development of superior and tolerant varieties is one of the important strategies.

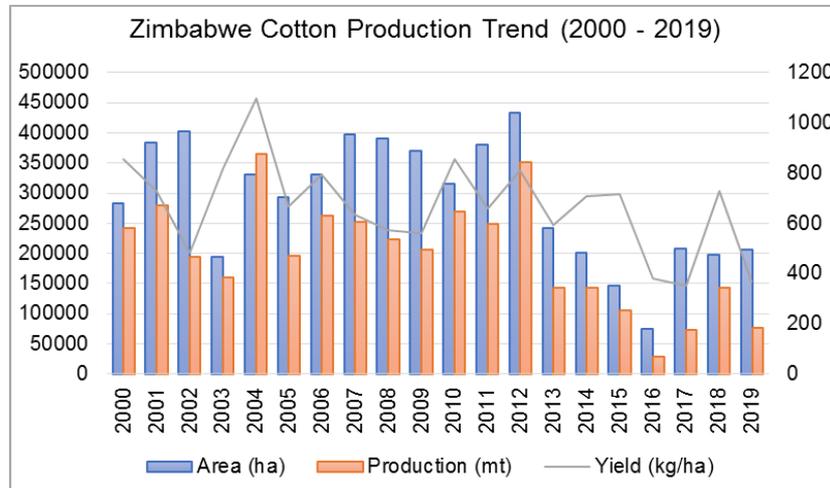


Figure 1. 20-year period (2000 - 2019) cotton production trend (Agricultural Marketing Authority, AMA 2020).

Crop development strategies that involve the determination and identification of key factors in genetic manipulation have been used by plant breeders leading to the development of superior genotypes thus improving crop production and productivity. The process of developing improved cotton cultivars requires uppermost consideration of the factors that are responsible for genotypic stability or Genotype by Environment Interaction (GEI) [15, 13]. When cotton genotypes are evaluated for superiority under diverse growing conditions they are affected by either the genotypic effects (G) or environmental effects (E) or by the interaction (GEI) of both effects in a multiplicative form which if present makes it difficult for plant breeders to select superior genotypes hence slowing down progress in breeding programs.

Yan also elucidated that in any field evaluation trial, the performance of a genotype is determined by the genotypic main effect (G), the environment main effect (E), and the interaction between the two ($G \times E$). GEI minimizes associations between phenotypes and genotypes hence complicating the testing and selection of superior genotypes [23]. According to Fahasat *et al.* (2015), the phenotype of an individual depends upon both the genetic make-up and environmental influences. Genotype \times environment interaction is considered as an important source of discrepancy in any crop, and different methods have been used to distinguish genotypes for their behavior in different environmental conditions [6].

Genotype superiority is based on high mean performance, stability, and adaptation across different test environments. This means the development of cotton genotypes that are stable and adapted to a wide range of diversified environments is the ultimate goal of any robust cotton

improvement program. The term “stability” is used to characterize a genotype that shows a consistent performance across tested environments for a trait of interest. Francis and Kannenberg defined a stable genotype as one that provides high yield and constant performance across locations [9]. The static mean of stability is defined by Becker and Leon; a stable genotype is the one possessing a constant performance irrespective of any changes in environmental conditions [2].

Many stability models for assessing the genotypic stability were developed and used in different crops and these include multivariate models thus the AMMI and GGE and univariate models thus Ecovalence (W^2i) suggested by Wricke, Joint regression analysis by Eberhart and Russel, Finlay Wilkinson static stability and superiority among others [4, 22, 8]. The main objective of the present study was to evaluate the performance of newly developed cotton genotypes for yield superiority over different environments using different stability models. This study used the GGE biplot for the multivariate stability model and univariate models Ecovalence (W^2i) suggested by Wricke (1962), Finlay Wilkinson static stability, superiority, and Stability coefficients for genotype by environment data.

2. Materials and Methods

2.1. Seasons and Experimental Sites

This study was carried out across five growing seasons 2014/15, 2015/16, 2016/17, 2019/20, and 2020/21 at fifteen (15) different locations which represented the Middleveld and Lowveld cotton growing zones in Zimbabwe (Table 2).

2.2. Genotypes and Experimental Layout

Included in this study were fifteen (15) cotton genotypes that comprised of ten (10) test genotypes and five (5) check varieties (commercially released varieties) (Table 1). The experimental layout used in the study was a Randomized Complete Block Design (RCBD) with three (3) replications. Each gross plot consisted of 6 rows which were 6m long with a spacing of 1m (Inter-row) and 0.30m (intra-row). Total seed cotton yield data was collected from a net plot which measured 16m².

2.3. Data Analysis

To determine the best genotype, and after observing the presence of genotype by environment interaction (GEI), one recent and commonly used multivariate model Genotype main effects and genotype by environment interaction (GGE) ((Yan *et al.* 2007)) and two univariate models Ecovalence (W²₁) suggested by Wricke (1962) and Finlay and Wilkinson (1963) static stability, superiority and Stability coefficients for genotype by environment data were used. Total Seed Cotton yield data, converted to standard hectare was subjected to an analysis of an Unbalanced Design using Genstat regression to generate an accumulated analysis of variance (ANOVA) and mean yield predictions using Genstat 18th Version. Environmental and genotypic means were also calculated and separated using the least significant differences (Fischer's unprotected LSD) at a 5% level of significance.

2.4. Agronomic and Cultural Practices

Trial agronomic management practices at all sites were performed according to the Cotton Handbook (1998). Basal fertilizer Compound L (5N:18P₂O₅:10K₂O:8S+0.1B) at planting and ammonium nitrate (34.5%N) as the top dressing at 8 weeks after crop emergence were applied. Integrated Weed Management (IWM) was practiced through the use of pre-and post-emergence herbicides and hand weeding. Pest management was carried out following the standard scouting and threshold level process.

Table 1. Information of genotypes used in the study.

Genotype	Status	Source
280-94-10	Experimental Line	Cotton Research Institute
645-98-11	Experimental Line	Cotton Research Institute
81-01-2	Experimental Line	Cotton Research Institute
81-02-2	Experimental Line	Cotton Research Institute
812-01-3	Experimental Line	Cotton Research Institute
830-01-7	Experimental Line	Cotton Research Institute
89-01-2	Experimental Line	Cotton Research Institute
CRI-MS-1	Commercial Variety	Cotton Research Institute
CRI-MS-2	Commercial Variety	Cotton Research Institute
LS9219	Commercial Variety	Cotton Research Institute
QM301	Commercial Variety	Cotton Research Institute
SN-96-5	Experimental Line	Cotton Research Institute
SS-95-6	Experimental Line	Cotton Research Institute
SZ-9314	Commercial Variety	Cotton Research Institute
SZ-95-23	Experimental Line	Cotton Research Institute

Table 2. Description of sites used in the multi-locational trials.

Location	Latitude	Longitude	Altitude (m)	Av. Annual Rainfall (mm)	Max Temp°C
Chitekete	17°25' South	28°56' East	914	450-500	45
Kadoma	18°19' South	29°53' East	1156	750-1000	38
Shamva	17°32' South	31°71' East	1149	675-700	38
Kuwirirana	21°15' South	30°48' East	1483	500-600	38
Matikwa	20°48' South	32°14' East	300	450-500	40
Panmure	17°16' South	31°47' East	881	700-800	35
Dande	16° 16' South	31°34' East	436	450-500	42
Masakadza	17°25' South	16°28' East	914	450-650	45
Tokwane	25° 47' South	31°15' East	1105	350-650	37
Save	21°29' South	32°51' East	466	450-500	41
Chibuwe	20°33' South	32°24' East	444	450-550	35
Umguza	20° 03' South	28°34' East	1374	450-500	34
Muzarabani	16° 23' South	31°00' East	432	600-800	42
Chisumbanje	20°47' South	32°13' East	448	450-500	40
Chizvirizvi	29°59' South	32°10' East	410	450-600	40

Source: Agritex planning branch: Zimbabwe natural regions and farming areas boundaries.

3. Results and Discussion

3.1. Analysis of Variance

The average estimated Total Seed Cotton yield, Lint yield, Gin-Out-Turn, Boll Weight and Plant Height for the fifteen genotypes, fifteen locations, and five years is shown in Table 3. Results from the accumulated Analysis of Variance (ANOVA) (Table 3) of seed cotton yield, Lint yield, Gin-Out-Turn, Boll Weight and Plant Height

indicated highly significant differences (P<0.001) due to genotypic, environmental, and GE interaction effects except for GOT% where its GEI was not significantly different (P=0.412).

3.2. Total Seed Cotton Yield (TSCY)

Genotype SZ-95-23 recorded the highest yield (2683kg^{ha}⁻¹) followed by 830-01-7, 89-01-2, 812-01-3 and 81-02-2 which recorded 2521kg^{ha}⁻¹, 2284kg^{ha}⁻¹, 2272kg^{ha}⁻¹ and 2127kg^{ha}⁻¹ respectively.

3.3. Lint Yield (LY)

A similar trend on the same candidates was true for Lint Yield where the highest was recorded for SZ-95-23 (1118kg ha^{-1}) followed by 830-01-7 (995.7kg ha^{-1}), 89-01-2 (925.8kg ha^{-1}), 812-01-3 (924.8kg ha^{-1}) and 81-02-2 (852.2kg ha^{-1}).

3.4. Gin-Out-Turn (GOT)

Highest ginning percentages were recorded for candidates 645-98-11, 81-01-2 and SZ-9314 above 42% followed by candidates SZ-95-23, CRIMS 2 and 280-94-10 which scored GOT that was above 41.5%.

3.5. Boll Weight (BW)

Large boll weights of above 5.9g were recorded for candidates 812-01-3, 645-98-11 and SZ-9314, whilst boll weights of above 5.8g were recorded for candidates 81-01-2, QM 301, CRIMS 1 and SZ-95-23. Important to note is that all the tested candidates recorded boll weights that were above 5.4g.

3.6. Plant Height (PH)

Three candidates recorded plant heights which were 125cm and below and these included 81-02-2 (122cm), 89-01-2 (123.3cm) and SZ-95-23 (125cm).

Table 3. Combined analysis of seed cotton yield and agronomic traits of fifteen cotton genotypes from 2014/15 to 2020/21 seasons.

GENOTYPE	TSCY (kg ha^{-1})	Rank	LY (kg ha^{-1})	GOT (%)	BW (g)	PH (cm)
SZ-95-23	2683 ⁱ	1	1118 ^g	41.69 ^{cde}	5.8 ^{cdef}	125 ^{abc}
830-01-7	2521 ^h	2	995.7 ^f	39.6 ^{7ab}	5.425 ^a	127.8 ^{abcd}
89-01-2	2284 ^{fg}	3	925.8 ^{ef}	40.57 ^{bc}	5.633 ^{abc}	123.3 ^{ab}
812-01-3	2272 ^f	4	924.8 ^{ef}	40.97 ^{bc}	5.946 ^{cdef}	125.3 ^{abcd}
81-02-2	2127 ^{ef}	5	852.2 ^{cde}	40.8 ^{bc}	5.636 ^{abcd}	122.2 ^a
LS9219	2084 ^{def}	6	801.7 ^{abcd}	38.06 ^a	5.474 ^{ab}	130.7 ^{bcd}
CRI-MS-1	1954 ^{cde}	7	808.8 ^{bcd}	41.49 ^{bcd}	5.821 ^{cdef}	126 ^{abcd}
QM301	1937 ^{bcd}	8	793.8 ^{abcd}	41.37 ^{bcd}	5.832 ^{cdef}	127.7 ^{abcd}
SZ-9314	1914 ^{bcd}	9	803.2 ^{bcd}	42.27 ^{ce}	5.917 ^f	128.8 ^{bd}
CRI-MS-2	1881 ^{abc}	10	771.2 ^{abc}	41.68 ^{cde}	5.611 ^{ab}	126.9 ^{abcd}
280-94-10	1878 ^{abc}	11	760.9 ^{ab}	41.52 ^{bcd}	5.739 ^{bcd}	125.7 ^{abcd}
645-98-11	1877 ^{abc}	12	787.7 ^{abcd}	42.33 ^{ce}	5.918 ^{df}	127.5 ^{abcd}
81-01-2	1844 ^{ab}	13	778.4 ^{abcd}	42.05 ^{cde}	5.886 ^{cdef}	126.2 ^{abcd}
SS-95-6	1798 ^a	14	748.5 ^a	41.02 ^{bcd}	5.787 ^{cdef}	127.9 ^{abcd}
SN-96-5	1796 ^a	15	745.1 ^a	41.11 ^{bcd}	5.741 ^{bcd}	125.9 ^{abcd}
Mean	2056		828.5	41.1	5.74	126.5
LSD (0.05)	160.5		75.5	1.6	0.24	5.1
P-Value (G)	<0.001		<0.001	<0.001	<0.001	0.026
P-Value (E)	<0.001		<0.001	<0.001	<0.001	<0.001
P-Value (GxE)	<0.001		<0.001	0.412	<0.001	<0.001
CV %	19.02		21.5	7.97	8.58	8.85

Means within a column with different letters are significantly different at $P < 0.05$, TSCY – Total seed cotton yield (kg ha^{-1}), BW – boll weight (g), GOT – ginning out turn (%), LY – lint yield (kg ha^{-1}), PH – plant height (cm).

3.7. Environments Performance

Matikwa and Chitekete recorded the highest total seed cotton yield of 3549kg ha^{-1} and 3482kg ha^{-1} respectively followed by Chizvirizvi who scored 2344kg ha^{-1} then Umguza and Dande scoring 2114kg ha^{-1} and 2070kg ha^{-1} respectively. Chisumbanje and CRI recorded the lowest yields that were less than 1000kg ha^{-1} .

Table 4. Site performance on Total seed cotton yield by fifteen cotton genotypes from 2014/15 to 2020/21 seasons.

Environment	Total Seed Cotton Yield Mean (kg ha^{-1})	Rank	Effect	s.e.
Matikwa	4164	1	2342	114.6
Chitekete	3528	2	1705	148.1
Chizvirizvi	2544	3	720.9	147.1
Umguza	2114	4	291	122.8
Dande	2070	5	247.6	101.5
Chibuwe	1780	6	-42.8	114.6
Masakadza	1758	7	-64.7	147.1
Tokwane	1482	8	-341.2	92.7
Panmure	1478	9	-344.6	224.6
Muzarabani	1257	10	-565.5	122.8
Save	1189	11	-633.8	136.7
Kuwirirana	1104	12	-718.9	203.2
Shamva	1028	13	-795	136.7
Chisumbanje	951	14	-871.5	208.3
CRI	895	15	-928	126.2

Environment	Total Seed Cotton Yield Mean (kg ha^{-1})	Rank	Effect	s.e.
Lsd (5%)	141.2			
Sed	72.63			

Note: Numbers under heading "Rank" give the position of each genotype, ranked according to the stability coefficient in the previous column (running downwards from 1 = best).

3.8. Genotype by Environment Interaction (GEI)

The presence of GEI complicates the selection process as GEI reduces the usefulness of genotypes by confounding their yield performance and minimizing the association between genotypic and phenotypic values [3] hence need to use other methodologies that can classify the genotypes according to their adaptability and stability, so the parametric (multivariate and univariate) stability models were used in this study [19].

High seed cotton yield variations for different genotypes at different locations were recorded hence revealing the need to further analyze and find the magnitude of effects by either environment, genotype, or interaction on performance variation. This will ease the decision to select cotton genotypes with high seed cotton yield and good stability. Figure 2 shows the presence of cross-over interaction for total seed cotton yield than indicated changes in ranks of genotypes across the fifteen environments (Genotype x environment interaction and yield stability analysis of sugarcane [5]).

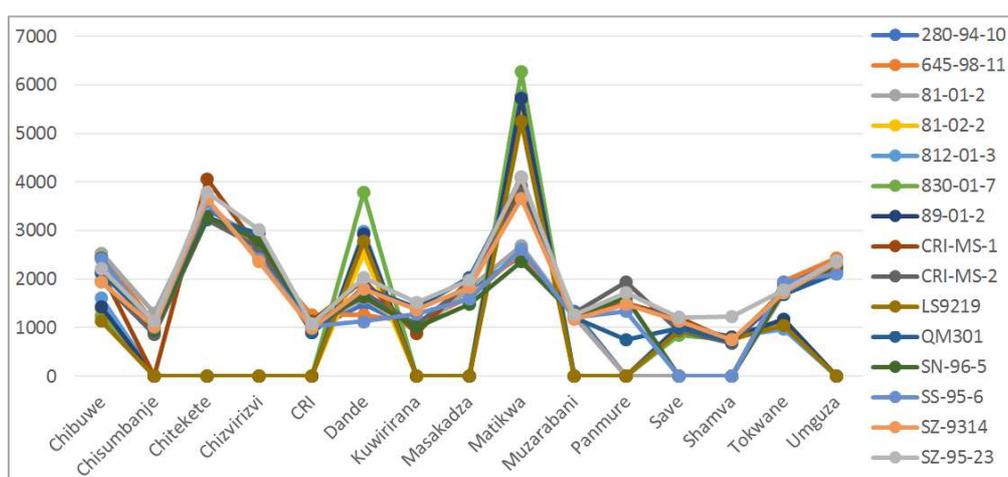


Figure 2. Total Seed Cotton yield performance of 15 genotypes tested across 15 locations showing cross-over interactions.

Cross-over interaction explains the rank and magnitude of performance of genotypes variations from location to location [12]. There was more contribution (43.1%) of the total variation due to the environmental effects hence exhibiting that environments were variable and caused many fluctuations in seed cotton yield (Table 5). This is in line with results obtained from a study that was done by Muhammad Riaz et al. (2019), where variation in seed cotton yield explained 72.4% environmental effect of the total variation [17]. Genotypic effects and GEI explained 0.9% and 8.7% respectively to the

total variation whilst the seasons contributed about 19.7%. The large influence of the environment on yield performance was also reported by Bantayehu, 2009 in a similar study where the author analyzed the correlation of stability parameters in malting barley [16]. Goa and Mohammed, 2013, also experienced the results in their study on GEI and Yield stability for field pea in Ethiopia, where the large sum of squares for environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield performance of field pea genotypes [10].

Table 5. Accumulated Analysis of Variance (ANOVA).

Source of Variations	d.f.	S.S.	M.S.	v.r.	Total variation explained %
Genotype (G)	14	15108749	1079196***	9.78	0.982166
Environment (E)	14	663157572	47368398***	429.24	43.10953
Year (Y)	4	303614231	75903558***	687.81	19.73689
GxE	137	133978551	977946***	8.86	8.709472
GxY	28	3392440	121159 ^{ns}	1.1	0.220531
ExY	12	342208002	28517333***	258.41	22.24573
GxExY	93	9451321	101627 ^{ns}	0.92	0.614397
Residual	607	66985656	110355		
Total	911	1.538E+09	1688593		

***, $P < 0.001$ – Highly significant, superscript (ns) – Not significant
DF = degree of freedom, SS = sum of square, MS = mean sum square.

3.9. Finlay-Wilkinson Stability Model, Wricke’s Ecovalence and Stability Coefficients and Genotype and Environmental Ranks

Finlay-Wilkinson stability ANOVA showed highly significant differences in environmental effects and sensitivities ($P < 0.001$) Table 6. The mean (μ_i), sensitivity and mean square deviation ($\text{var}(\epsilon)$) estimates were recorded in Table 5 where the information was used to rank the fifteen genotypes.

Table 6. Analysis of variance: Finlay and Wilkinson modified joint regression analysis.

Source	d.f.	s.s.	m.s.	v.r.
Genotypes	14	15112547.01	1079467.644 ^{ns}	1.17
Environments	14	663156828.1	47368344.86 ^{***}	51.2
Sensitivities	14	56107145.73	4007653.267 ^{***}	4.33
Residual	869	803932005.8	925123.1368	
Total	911	1538308527	1688593.333	

***, $P < 0.001$ – Highly significant, superscript (ns) – Not significant
 DF = degree of freedom, SS = sum of square, MS = mean sum square.

A low sensitivity value is equivalent to good stability. Genotypes with low sensitivity values were highly ranked

since their performance is less volatile to the environmental variations. Genotypes 645-98-11, SN-96-5, 280-94-10, SS-95-6, and 81-01-2 were ranked number 1, 2, 3, 4 and 5 respectively after recording low values of sensitivity (0.621, 0.621, 0.638, 0.658, and 0.684 respectively) however they were ranked poorly based on cultivar superiority thus 15th, 12th, 14th, 13th and 11th position and poorly as well on Wricke’s ecovalence where they were ranked on position 14, 13, 12, 11 and 8 respectively of the total of 15 tested genotypes. Test genotype SZ-95-23 (0.913) and checks SZ-9314 (0.931) and CRI-MS2 (0.937) recorded low sensitivity values of less than 1 hence regarded as fairly stable. Generally, low value means smaller deviations from the mean across environments and are thus more stable. So, based on the five stability parameter results, SZ-95-23 performed as the best and ideal variety as it maintained the good rank of between number 1 and number 6, followed by SZ-9314 (Check variety) which was generally ranked between number 1 and 7 across all the stability parameters used in the study. Check varieties CRI-MS1 and CRI-MS2 were also fairly ranked across the considered stability parameters as they were ranked between 3 to 10 and 2 to 9 respectively (Table 7).

Table 7. Stability by five parameters for 15 Cotton genotypes tested at 15 locations based on variance components models.

Trt Name	Wricke's Ecovalence	Rank	Cultivar superiority	Rank	Sensitivity	Rank	Variances of ranks	Rank	Mean - μ_i
280-94-10	3483036	12	891288	14	0.658	4	17.17	10	1753
645-98-11	3650788	14	895687	15	0.621	2	19.72	11	1755
81-01-2	2759842	8	795377	11	0.913	6	12.15	6	1737
81-02-2	2137153	6	342680	8	1.561	12	16	9	1842
812-01-3	2958286	10	228562	3	1.644	14	31.6	15	1986
830-01-7	6331390	15	206519	2	1.85	15	30	14	2105
89-01-2	2815158	9	236176	4	1.625	13	19.87	12	1970
CRI-MS-1	706051	4	284133	5	1.056	10	7.91	3	1853
CRI-MS-2	674030	3	357216	9	0.937	8	9.84	5	1734
LS9219	2256527	7	392160	10	1.487	11	25.07	13	1795
QM301	1139628	5	326543	6	1.01	9	8.54	4	1765
SN-96-5	3608680	13	845360	12	0.638	3	13.77	8	1708
SS-95-6	3315888	11	849906	13	0.684	5	13.42	7	1665
SZ-9314	375044	1	341185	7	0.931	7	7.12	2	1761
SZ-95-23	524322	2	191727	1	0.621	1	5.84	1	1914

Note: Numbers under heading “Rank” give the position of each genotype, ranked according to the stability coefficient in the previous column (running downwards from 1 = best).

Wricke’s ecovalence analysis was conducted and according to his model genotypes that have small equivalence have less volatility and hence are more stable [19]. Thus, a genotype with $W_i^2 = 0$ is considered stable so according to the results in Table 7 genotype SZ-9314, CRI-MS2, and SZ-95-23 were ranked first, second, and third respectively whilst genotypes 830-01-7, 645-98-11, and SN-96-5 were the most unstable candidates. Static Stability also showed that SZ-9314, SZ-95-23, and CRI-MS2 ranked first, second, and third respectively whilst on variances of ranks SZ-95-23 and SZ-9314 were ranked first and second respectively. The study displayed results similar to some work that was done by Goa and Mohammed on Genotype x environment interaction and yield stability in Field pea (*Pisum sativum* L.) tested over different locations in Southern Ethiopia where Wricke’s Ecovalence the

results revealed that most stable genotypes were G17, G2, G22, G5 and G7, and these genotypes were not the best ranked for mean yield, being 10th, 8th, 6th, 21st, and 23rd, respectively [10]. They also noted that the most unstable genotypes according to the ecovalence method were G18, G9, G12, G11, and G16 these cultivars were ranked 2nd, 8th, 19th, 7th, and 4th for mean yield respectively. Based on the information generated from the current study, test genotype SZ-95-23 has proved to be an ideal genotype based on seed cotton stability, good yield performance, and adaptability.

Finlay – Wilkinson stability model also estimated the effects of different locations based on the predicted means and Matikwa was ranked number 1 (4464kgha⁻¹), followed by Chitekete (3528kgha⁻¹) then Chizvirizvi (2544kgha⁻¹) and Umguza (2114kgha⁻¹).

3.10. GGE Stability Analysis by Biplots

The GGE technique was first proposed by Gabriel, 1971 and then developed by Kempton and Zobel et al. [11, 25] and then recently got widely used in examining the Genotype (G) and Genotype x Environment (GE) [7, 24]. After the results from combined analysis of variance showed a significant difference on GEI, visual assessment of environmental and genotypic effects through the use of GGE biplot (multivariate stability method) was done to enable selection of ideal, widely adaptable, and stable genotypes. The biplot showed the winning genotypes in specific environments, ideal and stable genotypes (Figure 3, Figure 4, and Figure 5) based on two principal components which explained a total of 94.07% (PC1-58.17% and PC2 - 35.89%).

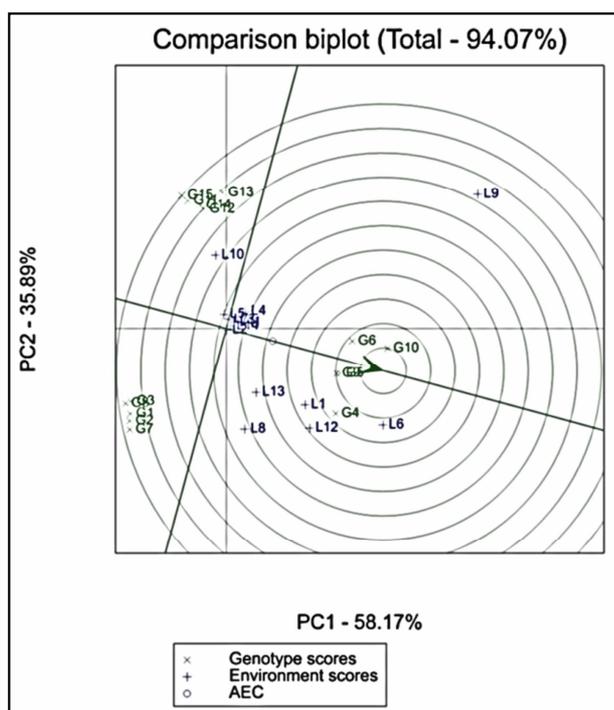


Figure 3. GGE biplot graph showing the scores of genotypes and environments (Genotype focused scaling), regarding ideal and good genotypes based on two Principal components.

Genotype names and Codes: 280-94-10 = G1; 645-98-11 = G2; 81-01-2 = G3; CRI-MS-1= G4; CRI-MS-2 = G5; QM301 = G6; SN-96-5 = G7; SS-95-6 = G8; SZ-9314 = G9; SZ-95-23 = G10; 81-02-2 = G11; 812-01-3 = G12; 89-01-2 = G13; 830-01-7 = G14; LS9219 = G15;

Location Names and Codes: Chibuwe = L1; Dande = L2; Kuwirirana = L3; Masakadza = L4; Matikwa = L5; Muzarabani = L6; Tokwane = L7; Umguza = L8; Chisumbanje = L9; Chitekete = L10; Chizvirizvi = L11; CRI = L12; Panmure = L13; Save = L14; Kuwirirana = L15.

3.10.1. Ideal Genotype

According to Yan and Kang, an ideal genotype has the highest mean yield and is stable (that ranks the highest in all environments) [24]. Such a genotype is defined by a long vector length of the high-yielding genotypes and with zero GE, as represented by the small circle (Inner concentric circle) with an arrow pointing to it [21, 23]. A genotype is more desirable if it is closer to the ideal genotype. Although such as ideal genotype

may not exist in reality, it can be used as a reference for genotype evaluation [18]. According to figure 3, SZ-95-23 (G10) which was positioned in the center of the concentric circle was the ideal genotype based on high yield ability and stability whilst SZ-9314 (G9) and CRI-MS2 (G5) were good or desirable genotypes (Similar results to work on sorghum stability analysis by Mare et al [14]. This is in agreement with the current study results gotten using Wricke's Ecovalence, Static Stability, Variance of ranks, and Finlay-Wilkinson's measure of sensitivity which indicated the three genotypes as the most stable ones.

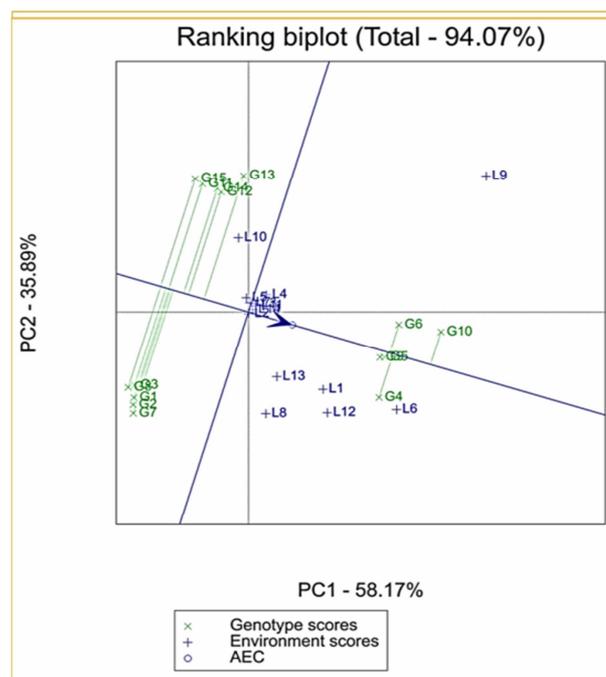


Figure 4. GGE biplot graph showing the ranking plot based on high mean performance and stability.

Genotype names and Codes: 280-94-10 = G1; 645-98-11 = G2; 81-01-2 = G3; CRI-MS-1= G4; CRI-MS-2 = G5; QM301 = G6; SN-96-5 = G7; SS-95-6 = G8; SZ-9314 = G9; SZ-95-23 = G10; 81-02-2 = G11; 812-01-3 = G12; 830-01-7 = G14; LS9219 = G15;

Location Names and Codes: Chibuwe = L1; Dande = L2; Kuwirirana = L3; Masakadza = L4; Matikwa = L5; Muzarabani = L6; Tokwane = L7; Umguza = L8; Chisumbanje = L9; Chitekete = L10; Chizvirizvi = L11; CRI = L12; Panmure = L13; Save = L14; Kuwirirana = L15.

3.10.2. High Yield Mean Performance and Genotype Stability

According to figure 4, lines perpendicular to the Average Environmental Axis (AEA) measure the stability of genotypes and when the perpendicular line is smaller and close to the Average Environmental Coordinate (AEC) such a genotype is regarded as stable. Accordingly, the biplot indicated that genotype SZ-95-23 (G10) was a stable genotype and recorded high mean performance as it was located on the furthest position in the direction of the AEA with short perpendicular axis followed by check genotypes SZ-9314 (G9) and CRI-MS2 (G5) which had the smallest perpendicular axis but not as better yielding as SZ-95-23 (G10). This is in agreement with the Finlay-Wilkinson stability models on ecovalence and stability coefficient parameters.

3.10.3. Winning Genotypes and Mega-environments

A set of lines drawn from the origin of the biplot and intersecting the sides of the polygon at some angles partitioning into sectors were shown in Figure 5. One or more environments were encircled together to form a mega-environment such that genotypes in those particular circles will be adaptable and well-performing in those environments. Figure 5 revealed 4 mega-environments that were overlapping an indication of much influence on the performance variation by the environments. Mega-environment 1 comprises Muzarabani (L6) and Chisumbanje (L9), then mega-environment 2 is comprised of L1 - Chibuwe, L8 - Umguza, L12 - CRI, and L13 - Panmure, and the third mega-environment comprised of L10 - Chitekete only whilst mega-environment 4 consisted of the remaining locations. Shown were the winning genotypes for particular sectors and these were positioned on the vertex of a polygon. G4 was the winner for the sector that comprised of locations L1 - Chibuwe, L8 - Umguza, L12 - CRI, and L13, whilst genotype SZ-95-23 (G10) was the winner for the sector which comprised ten locations; Dande (L2), Kuwirirana (L3), Masakadza (L4), Matikwa (L5), Muzarabani (L6), Tokwane (L7), Chisumbanje (L9), Chizvirizvi (L11), Save (L14) and Kuwirirana (L15). G13, G15, and G7 were winners in the other sectors.

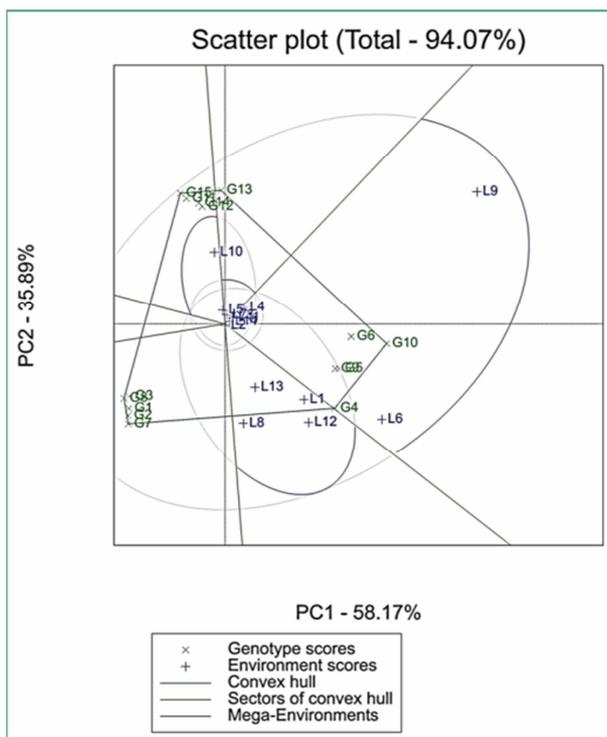


Figure 5. GGE biplot graph showing the winning genotypes for particular sectors (Mega-environments).

Genotype names and Codes: 280-94-10 = G1; 645-98-11 = G2; 81-01-2 = G3; CRI-MS-1 = G4; CRI-MS-2 = G5; QM301 = G6; SN-96-5 = G7; SS-95-6 = G8; SZ-9314 = G9; SZ-95-23 = G10; 81-02-2 = G11; 812-01-3 = G12; 830-01-7 = G14; LS9219 = G15;

Location Names and Codes: Chibuwe = L1; Dande = L2; Kuwirirana = L3; Masakadza = L4; Matikwa = L5; Muzarabani = L6; Tokwane = L7; Umguza = L8; Chisumbanje = L9; Chitekete = L10; Chizvirizvi = L11; CRI = L12; Panmure = L13; Save = L14; Kuwirirana = L15.

4. Conclusions

Investigating GEI is very important for identifying high-yielding, stable, and widely or specific adapted genotypes. The performance of different genotypes when tested under diverse environments is affected by either genotypic variation (G), environmental variation (E), or interaction (GEI). The current study aimed to determine the use of different parametric stability models and compare the magnitude of GE to enable breeders to select superior genotypes for production. This research used different models in the parametric category which include the multivariate and univariate parameters so that the best genotype possessing both high yielding performance and stability could be selected. The use of Finlay and Wilkinson and Wricke's stability models and GGE biplot analysis in this study enabled the selection of a superior genotype that is high yielding and stable. The study showed a positive relationship between the multivariate and univariate stability models and the two complement each other making it easy for the breeder to select superior genotypes.

The estimates of combined ANOVA of total seed cotton yield were highly significant for genotypes, environments and GxE multiplicative interaction. The environments had a higher contribution to the sum of squares an indication that the environments were variable and caused most of the fluctuations in seed cotton yield. The interaction on the sum of squares was 8.8 times greater than the genotypic effects. Results showed varied genotype yield performance at different locations (yield performance Top 5 included SZ 9523, SZ 9314, 830-01-7, 89-01-2, 812-01-3 and 81-02-2 which scored 2683kg/ha, 2521kg/ha, 2284kg/ha, 2272kg/ha and 2127kg/ha respectively). GGE Biplot indicated that SZ 9523 had high productivity, good adaptability and good stability and was the winning candidate for a ME that included Dande, Masakadza, Matikwa, Muzarabani, Tokwane, Chisumbanje, Chizvirizvi, Save and Kuwirirana.

The models revealed that genotype SZ-95-23 was the most stable and high performing genotype, and hence is recommended for wider cultivation in more than eleven out of the fifteen test locations which are cotton growing zones in Zimbabwe.

Declaration of Interest Statement

The authors declare that they have no competing interests.

Acknowledgements

First and foremost, special thanks go to Head of Ministry of Lands, Water, Agriculture, Fisheries and Rural Development (MLWAFRD), Head of the Department of Agricultural Research and Innovation Development (DARID), Head of Cotton Research Institute (CRI) for providing the financial support during the study period. We are also grateful for the participation and on-farm trial management by farmers in Masakadza, Chitekete, Umguza,

Kuwirirana, Shamva, Dande, Muzarabani, Matikwa, Chibuwe, Chizvirizvi and Tokwane through the assistance of Cotton Research Institute Research Facilitators. We also thank on-station technicians for trial management at Cotton Research Institute, Chisumbanje Experiment Station, Save Valley Experiment Station and Panmure Experiment Station. We further thank the Departmental Biometricians for their support and collaborative assistance on data cleaning and analysis. Lastly, we want to thank all members who gave indirect support during the study.

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