

# Yield Performance and Stability-Based Comparative Evaluation of Different Cotton (*Gossypium hirsutum* L.) Genotypes Under Diverse Environments of Zimbabwe

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**Abstract:** Cotton (*Gossypium hirsutum* L.) is an important cash and natural fibre crop grown worldwide. The present study was performed to assess and identify superior cotton genotypes with high mean and stable performance across different environments. The experimental gross plot sizes used in the experiment comprised of six rows which are one meter apart and six meters long (6m x 6m = 36m<sup>2</sup>). Data was collected from a net plot which measured 4m x 4m (16m<sup>2</sup>). The combined analysis of variance (ANOVA) using Genstat 18<sup>th</sup> version was generated and manifested significant differences for tested genotypes (G), locations (L), years (Y), genotype × year (GY), and genotype × location (GL) and GxLxY interactions revealing higher influence by environmental factors on yield ( $P < 0.001$ ). High TSC means were recorded for SZ-9523, 81-01-1 and SN-96-5, where the three candidates obtained 3045.62kg/ha-1, 2721.56kg/ha-1 and 2705kg/ha-1 respectively. AMMI ANOVA showed that two IPCAs (IPCA1 and IPCA2) out of four were highly significant ( $P \leq 0.001$ ), and they accounted for 60.4% and 31.9 respectively (92.3% of the GEI). GGE Showed that SZ-9523 recorded high yield means and was also very stable. Generally, both biplots revealed that SZ-9523, 81-01-2 and SN-96-5 were high mean performers across all sites, whilst SZ-9523 was the most stable, and ideal genotype. These candidates are recommended for commercial release in Zimbabwe as well as for use as for use as parents in future breeding programmes.

**Keywords:** Cotton, MANOVA, AMMI, GGE, Stability, Genotype

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## 1. Introduction

Cotton is one of the most essential and valuable cash crops and a source of natural fibre in the world. The contribution of cotton to the total fibre used world-wide is about 35% [12]. Upland Cotton (*Gossypium hirsutum* L.) is predicted to be the largest cultivated species accounting for more than 90% of the world cotton production areas, which is a justified reflection of widespread high adaptability and high yield production characteristics. The versatile crop which is also known as “The White Gold” in Zimbabwe plays an important role in elevating the country’s economy as it contributes significantly to the country’s foreign currency. Adverse climate change effects, biotic stresses and poor general crop production and management have been the chief driving forces of decline in cotton production and productivity in

Zimbabwe [7, 13].

As a result, there is a dire need to address the challenges by providing timely solutions which are practically sound in the face of climate variations. The improvement of cotton genetics is a continuous phenomenon and one of the key facets of sustainable cotton production and productivity. Based on the fact that Zimbabwe is comprised of diverse environments distinguished by rainfall, temperature, and soil types among others, multi-locational evaluation of cotton genotypes is a key approach that enhances the identification, selection and recommendation of high performing-stable varieties.

Multi-environmental testing (METs) of cotton trials is a very important process in variety development programmes bearing the aim to identify genotypes with consistent performance across a wide range of diverse environments [1].

Such genotypes should possess a high mean yield with minimal fluctuation in performance across the testing environments. The cultivar performance is generally affected by three factors, which include the Environment  $\times$  main effect, Genotype (G) main effect and interaction of the two (GEI) [16]. The presence of GEI makes it difficult to identify and select a variety hence the need to further apply some statistical analysis that decomposes the GEI. Such methods further break down the contribution by genotype and by environment in the interaction, whereby for such purpose high performing and stable varieties across the test environments will be identified. Any breeding programme seeks to identify a genotype that possesses high mean performance, good stability and wide adaptation to a range of diversified environments [10]. The methods are divided into Parametric and Non-parametric stability statistics and the former is further divided into multivariate and univariate stability statistics or models. Under multivariate, models such as the Genotype and Genotype by Environment (GGE) [15] and Additive Main Effects and Multiplicative Interaction (AMMI) model [8] are used. Therefore, the study sought to identify superior cotton genotypes with high mean and stable performance across different environments using the multivariate stability models; AMMI and GGE.

## 2. Materials and Methods

### 2.1. Experimental Description

Ten experimental genotypes that comprised seven test-candidates and three checks (Table 1) were evaluated at five different locations (Table 2) across five seasons, including 2018, 2019, 2020, 2021 and 2022. Randomized Complete Block Design (RCBD) laid in three replications was used.

**Table 1.** Information of sites used in the experimental 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
CRIMS 1	Commercial Variety	Cotton Research Institute
CRIMS 2	Commercial Variety	Cotton Research Institute
QM301	Commercial Variety	Quton Seed Company
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 experimental study sites.

Location	Latitude	Longitude	Altitude (m)	Av. Annual Rainfall (mm)
Chitekete	17°25' South	28° 56' East	914	450-500
Kadoma	18°19' South	29° 53' East	1156	750-1000
Tokwane	25° 47' South	31° 15' East	1105	350-650
Umguza	20° 03' South	28°34' East	1374	450-500
Chisumbanje	20°47' South	32°13' East	448	450-500

### 2.2. Experimental Procedures and Cultural Practices

The experimental gross plot sizes used in the experiment comprised of six rows which are one meter apart and six meters long (6m x 6m x 1m = 36m<sup>2</sup>). Data was collected from a net plot which measured 4m x 4m x 1m (16m<sup>2</sup>). Data recorded included Average Total Seed Cotton Yield (TSC) recorded in kg ha<sup>-1</sup>. Planting was done on opened rows which are 3-5cm deep depending on the soil type. 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. Trial agronomic management practices at all the experimental sites were executed according to the Cotton Handbook (1998). 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.

### 2.3. Statistical Analysis

The recorded data was subjected to a Multivariate Analysis of Variance (MANOVA) using Genstat Statistical Package 18<sup>th</sup> Version to determine the effect of Locations, Genotypes

(G), Years (Y), and the presence and magnitude of G $\times$ E, G $\times$ L and G $\times$ L $\times$ Y interactions. After realizing the presence of GEI, two Multivariate Stability Models namely AMMI and GGE were used to assess the magnitude of the interaction and predict the stability of all test candidates the pooled ANOVA and computation of Interaction Principal Components in the case of AMMI and Bi-plot analysis by both models.

## 3. Results and Discussion

### 3.1. Combined Analysis of Variance (ANOVA)

The combined analysis of variance (ANOVA) manifested significant variations for tested genotypes (G), locations (L), years (Y), genotype  $\times$  year (GY), and genotype  $\times$  location (GL) and G $\times$ L $\times$ Y interactions revealing the influence of five environmental factors (L and Y) on yield (Table 3). The variation on Total Seed Cotton Yield as a result of the first and second order interactions justifies the need to assess the magnitude of the interaction to enable easy identification of high performing, stable and adaptable genotypes. This is in agreement with other researchers [3, 17], where significant variations in the performance of cotton genotypes was due to the genotypes, locations and season.

**Table 3.** Summary of Mean Squares (M. S.) from Analysis of Variance over genotypes (G), locations (L), years (Y), and their first and second order interactions.

Degrees of freedom	Source of Variation	Mean Squares (M. S.)				
		Total Seed Cotton Yield	Lint Yield	Gin Out Turn	Plant Height	Boll Weight
2	Rep/ Location	355034	93980	19.554***	1028.4	0.2738
9	Genotype (G)	5749580***	1030648***	10.325	2373.9***	0.9818***
4	Locations (L)	12872466***	2696977***	82.809***	3165.6***	16.0867***
4	Year	18890777***	2339585***	291.333***	864.0	10.6615***
16	Genotype x Location (GxL)	1662368***	317922***	11.146	3658.1***	0.3223
36	Genotype x Year (GxY)	915577***	180757***	12.298***	2343.6***	0.6810***
16	Location x Year (LxY)	5040204***	1140146***	129.970**	2343.6***	11.0958***
144	Genotype x Location x Year (GxLxY)	906678***	171800***	10.573**	1437.2***	0.4593***
	Residual	272301	56573	8.268	539.3	0.2644

### 3.2. Genotypic Mean Performance

#### Total Seed Cotton Yield (TSC kg ha<sup>-1</sup>)

Highly significant differences ( $P < 0.001$ ) were observed due to the genotypic, environmental, and seasonal effects and all the interactions as shown in Table 4. The overall mean performance for the ten genotypes was 2479.28 kg ha<sup>-1</sup>. High TSC means were recorded for SZ-9523, 81-01-1 and SN-96-5, the three candidates obtained 3045.62 kg ha<sup>-1</sup>, 2721.56 kg ha<sup>-1</sup> and 2705 kg ha<sup>-1</sup>, respectively. The mean yields were statistically different from all the check varieties which performed below the overall mean. Genotypic mean performance was significantly different at all test locations

with Chisumbanje recording the highest mean of 2873.24 kg ha<sup>-1</sup>, followed by Chitekete which recorded 2710.13 kg ha<sup>-1</sup> whilst CRI recorded the least mean of 2215.39 kg ha<sup>-1</sup> (Table 4). Seasonal average performances were also recorded where seasons 2021 and 2020 recorded the highest means of 2891.14 kg ha<sup>-1</sup> and 2893 kg ha<sup>-1</sup> respectively. The least mean performance of 2098.45 kg ha<sup>-1</sup> was recorded for season 2018. SZ-9523 recorded high yields at Chisumbanje, Chitekete and Umguza whilst SN-96-5 was the highest-yielding genotype at CRI and Tokwane. The trend of the results was similar to those obtained by Mohammed et al., 2022 [3].

**Table 4.** Total Seed Cotton (TSC – kg ha<sup>-1</sup>) for Medium Staple cotton genotypes.

GENOTYPE	ENVIRONMENTS					
	CHISUMBANJE	CHITEKETE	CRI	TOKWANE	UMGUZA	ACROSS ENV. MEAN
280-94-10	2358.24 <sup>a</sup>	2494.44 <sup>abc</sup>	1906.44 <sup>ab</sup>	2002.87 <sup>ab</sup>	2029.35 <sup>ab</sup>	2158.27 <sup>a</sup>
645-98-11	2539.27 <sup>a</sup>	2584.44 <sup>cd</sup>	2708.81 <sup>e</sup>	2221.02 <sup>bc</sup>	2238.14 <sup>abc</sup>	2458.34 <sup>a</sup>
81-01-2	3397.11 <sup>cd</sup>	3012.97 <sup>e</sup>	2441.48 <sup>cde</sup>	2324.24 <sup>bc</sup>	2433.12 <sup>bcd</sup>	2721.56 <sup>d</sup>
CRIMS 1	3514.27 <sup>d</sup>	2615.27 <sup>cd</sup>	2263.56 <sup>bcd</sup>	2011.34 <sup>ab</sup>	2040.31 <sup>ab</sup>	2488.73 <sup>c</sup>
CRIMS 2	3155.24 <sup>bc</sup>	2512.02 <sup>bc</sup>	1983.08 <sup>abc</sup>	1823.97 <sup>a</sup>	1952.47 <sup>a</sup>	2285.36 <sup>ab</sup>
QM301	3092.16 <sup>b</sup>	2179.64 <sup>a</sup>	2284.05 <sup>bcd</sup>	2252.28 <sup>bc</sup>	1916.42 <sup>a</sup>	2344.91 <sup>bc</sup>
SN-96-5	2436.96 <sup>a</sup>	2878.06 <sup>de</sup>	2613.99 <sup>de</sup>	2892.32 <sup>d</sup>	2704.56 <sup>d</sup>	2705.09 <sup>d</sup>
SS-95-6	2289.89 <sup>a</sup>	2878.06 <sup>de</sup>	2185.58 <sup>abcd</sup>	2163.29 <sup>abc</sup>	2489.34 <sup>cd</sup>	2415.98 <sup>bc</sup>
SZ-9314	2372.76 <sup>a</sup>	2237.54 <sup>ab</sup>	1727.9 <sup>a</sup>	2417.17 <sup>c</sup>	2090.03 <sup>abc</sup>	2169.00 <sup>a</sup>
SZ-95-23	3577.18 <sup>d</sup>	3634.31 <sup>f</sup>	2038.98 <sup>abc</sup>	2860.56	3117.23 <sup>e</sup>	3045.62 <sup>e</sup>
AVERAGE	2873.24	2710.13	2215.39	2296.82	2300.84	2479.28
CV %	12.3	16.6	19.9	22.7	30.8	21.0
LSD (5%)	256.607	325.085	491.826	377.704		167.831
SED	129.34	163.815	247.838	190.378	559.352	85.214

GENOTYPE	SEASONS MEANS					
	2018	2019	2020	2021	2022	AVERAGE
280-94-10	1800.33	1934.24	2738.22	2545.18	1773.37	1773.37
645-98-11	2134.38	2032.47	2835.88	2867.87	2421.09	2421.09
81-01-2	2369.36	2446.96	2891.14	3094.69	2805.68	2805.68
CRIMS 1	1822.87	1808.47	3132.63	3153.98	2525.7	2525.7
CRIMS 2	1617.73	1776.29	2564.9	3082.76	2385.1	2385.1
QM301	1769.09	1797.64	2701.36	3047.87	2408.59	2408.59
SN-96-5	2414.74	2600.27	2839.08	2891.88	2779.48	2779.48
SS-95-6	2436.05	2332.62	2413.91	2329.18	2568.12	2568.12
SZ-9314	1730.4	1850.18	2519.82	2735.29	2009.31	2009.31
SZ-95-23	2889.58	3016.42	3074.69	3182.71	3064.69	3064.69
AVERAGE	2098.45	2159.56	2771.16	2893.14	2474.11	2479.28

### 3.3. AMMI Model

The AMMI analysis of variance revealed four Interaction Principal Components (IPCA) (Table 5), thus one less than the experimental sites used in the study. Two IPCAs, IPCA 1 and IPCA 2 out of four were highly significant ( $P \leq 0.001$ ), and they accounted for 60.4% and 31.9% of the GxE interactions respectively thus 92.3% of the GEI. IPCA 3 and IPCA 4 accounted for only 12.06% and 0.09% respectively. The large sum of squares for genotypes over the environment signaled that the variation on yield performance was largely influenced

by the genotypic performance. The percentage contributions, showed that the GEI contributed more [1], followed by the genotypes and then the environment (9.7%, 8.4%, and 8.5% respectively). These findings opposed the results obtained by Esayas et al. 2019 [6] where the author reported that large sum of squares and a significant effect for environments demonstrated that the experiments were carried out under divergent climatic conditions resulting in differences for environmental means causing variation in sugar yield.

**Table 5.** Analysis of variance for the AMMI model of ten genotypes across five environments.

SOURCE	D. F.	S. S.	M. S.	IPCA Contribution to GxE Interactions	Contribution to TSS
Total	749	619432444	827013		
Genotypes	9	51746220	5749580***		8.4%
Environments	4	51489864	12872466***		8.3%
Interactions	36	59845231	1662368***		9.7%
IPCA 1	12	33823978	2818665***	56.52%	
IPCA 2	10	18750757	1875076***	31.33%	
IPCA 3	8	7218261	902283	12.06%	
IPCA 4	6	52236	8706	0.09%	
Error	690	452835873	656284		

\*\*\*Significant at  $<0.001$  probability level. DF = degree of freedom; SS = sum of square; MS = mean square; TSS=Total Sum of Squares; IPCA = Interaction Principal Component Axis.

#### 3.3.1. AMMI Model for Environment and Genotype Means and Scores

AMMI calculated the genotype means and environment means and scores and ranked them according to their performance (Table 6). SZ-9523 was ranked first as it recorded an average yield of 3046kg $ha^{-1}$  coupled with a low IPCAg1 (-1.9357) indicating that it was the most stable genotype, followed by 81-01-2 and SN-96-5 that recorded

2722kg $ha^{-1}$  and 2705kg $ha^{-1}$  respectively but revealed higher IPCAg1 values indicating that they were unstable. These results are in agreement with Esayas et al. 2019 where they assessed GEI by AMMI model in a sugarcane experiment [6]. Pertaining environmental means and scores, Chisumbanje was ranked first followed by Chitekete that recorded mean yields of 2873kg $ha^{-1}$  and 2710kg $ha^{-1}$  respectively. CRI ranked last, by recording the least mean performance of 2215kg $ha^{-1}$ .

**Table 6.** Average yield (kg/ha) for the ten genotypes and five environments, the magnitude (absolute value) of the IPCAs scores from AMMI model.

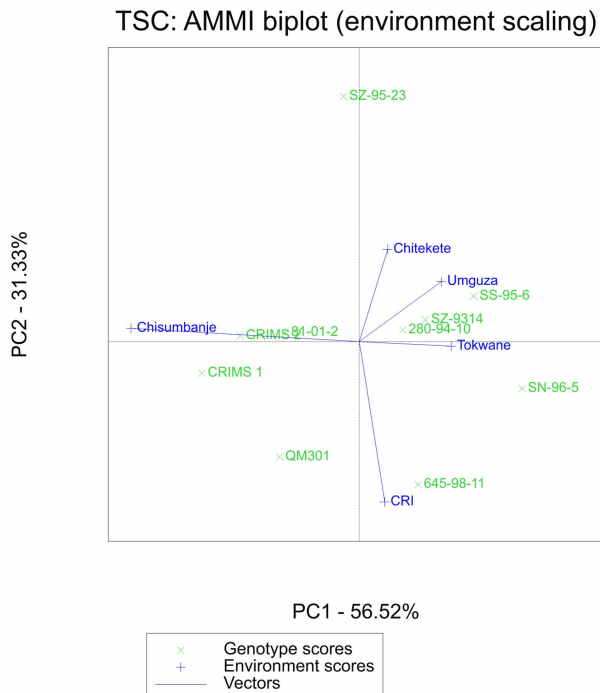
Genotype means and scores				
Genotype	Number	Mean (kg $ha^{-1}$ )	IPCAg1	IPCAg2
SZ-95-23	1	3046	-1.9357	25.91433
81-01-2	2	2722	-9.03976	0.95841
SN-96-5	3	2705	19.92362	-5.03515
CRIMS 1	4	2489	-19.2426	-3.42317
645-98-11	5	2458	7.19498	-15.1311
SS-95-6	6	2416	14.01414	4.78288
QM301	7	2345	-9.74269	-12.2262
CRIMS 2	8	2285	-14.5715	0.62745
SZ-9314	9	2169	8.0721	2.30292
280-94-10	10	2158	5.32736	1.22963
Environment means and scores				
Environment	Number	Mean (kg $ha^{-1}$ )	IPCAe1	IPCAe2
Chisumbanje	1	2873	-33.7237	2.27359
Chitekete	2	2710	4.20637	15.76244
Umguzi	5	2301	12.14664	10.27275
Tokwane	4	2297	13.59696	-0.77137
CRI	3	2215	3.77377	-27.5374

#### 3.3.2. AMMI Bi-Plot of IPCA Scores

Genotypes closer to the origin are insensitive to the

interaction and regarded as widely adapted. This is true for genotypes like 280-94-10 and SZ-9314 but these candidates experienced lower mean performance. Genotypes such as

SZ-9523, 645-98-11 and SN-96-5 are located a distant from the origin hence are sensitive to the environmental interaction and are specifically adapted. The bi-plot also showed the relationship between test locations where Chitekete, Umguza and Tokwane had a positive correlation whilst Umguza and Chitekete were negatively correlated to Chisumbanje and CRI. On the other hand, the three sites that had positive correlation showed short vectors thus closer to the origin and that meant they had a weak interactive force, whilst Chisumbanje and CRI had long vectors which indicated that they had strong interactive forces.



**Figure 1.** AMMI bi-plot of IPCA scores showing the magnitude of GEI between the genotypes and environments and correlations between environments.

### 3.4. GGE Bi-Plot Analysis

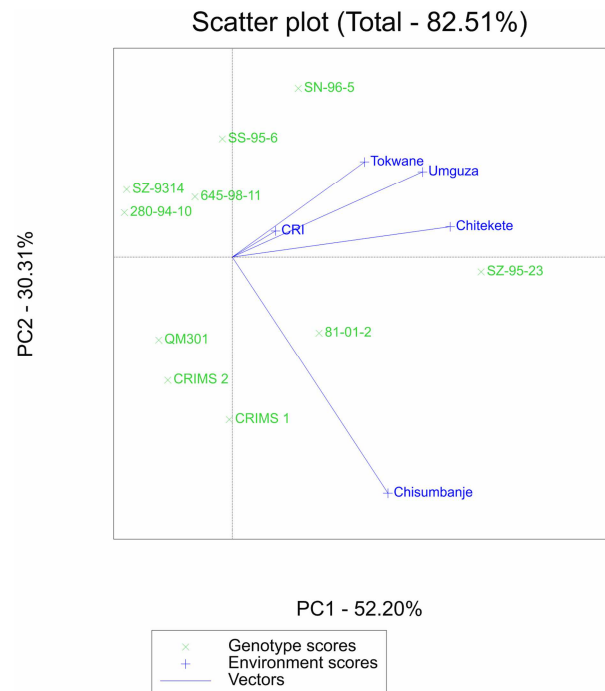
#### Mean Performance and Stability

GGE bi-plot has the strength to graphically display Gx E interaction in a two-way system [5, 15].

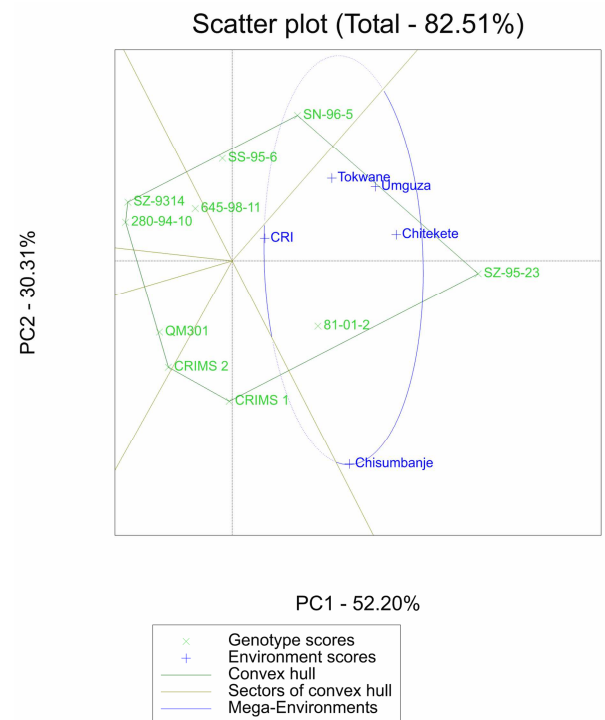
The bi-plot carries same objective with the AMMI model bi-plot (Figure 1) to establish the interrelationship among environments. The angle between environment vectors suggests whether there is correlation or not if so, is it negative or positive correlation (Figure 2). All environments were positively correlated except for Tokwane and Chisumbanje as well as CRI and Chisumbanje where these were separated by right angle apart. Similar results by a sugarcane researcher were reported by Mattos et al. 2013 [9] where negative correlations were identified.

Regarding the identification of winning candidates in particular sectors and establishing Mega-Environments (Figure 3), the bi-plot showed that there was one ME, and winning candidates are identified as those sitting at the vertex of the polygon, and these were SZ-9523, SN-96-5 and checks

CRIMS 1, CRIMS 2 and SZ-9314. The one ME reflects that the environments responded similarly to the effects caused to the genotypes' performance. However, candidate SZ-9523 was the winning candidate for the sector that bears the ME. This is in agreement with what Darai et al. 2017 deduced from a study on stability analysis where the genotype identified won in all test locations [2, 11].



**Figure 2.** GGE bi-plot - Scatter plot showing interrelationships among environments and genotypes.



**Figure 3.** GGE Bi-plot - Showing winning candidates (Which-Won-Where WWW) and Mega Environments (MEs).

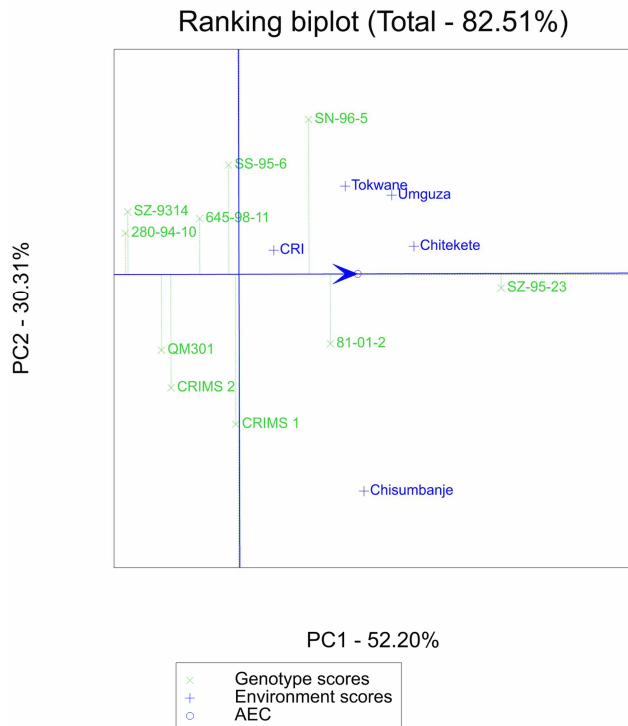


Figure 4. GGE Bi-plot - Identifying stable and high-performing genotype.

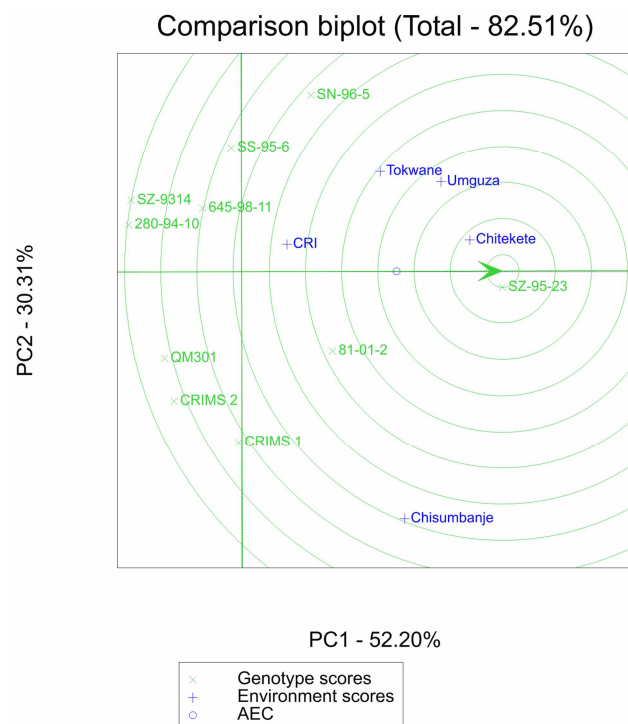


Figure 5. GGE Biplot - Identification of ideal and good genotypes.

The Bi-plot also depicted the most stable and high-performing genotype (Figure 4), where candidate SZ-9523 was the highest-performing genotype considered based on its position along and arrow-ward of the Average Environment Axis (AEA) and Average Environment Coordinate (AEC). Added to that, SZ-9523 was also very stable as revealed by the shortest perpendicular line to the

AEA. Candidate 81-01-2 also highly performed and showed relative stability. The findings of this study confirmed similar to what Sholihin, 2021 observed in an experiment for interpreting GxE Interaction on Cassava promising genotypes for environment and stability analysis [14].

Another important aspect brought forward by GGE bi-plot is to identify an ideal genotype (high yielding and stable) and this should be located in the inner concentric ring or circle, whereby any genotype near the ideal genotype is a good candidate (Figure 5). This is a similar application on environments. Candidate genotype SZ-9523 was identified as the ideal genotype as it was located on the inner concentric ring. Near the ideal genotype was candidate 81-01-2. Using the same principle, Chitekete was the ideal environment thus it generated more information about varied performance among test genotypes. These findings were in agreement with a study on GGE stability analysis on maize [4, 5].

## 4. Conclusion

Based on the results from the Multi-Environmental-Trials carried out for five years, different approaches that included Combined Analysis of Variance, mean performance across different environments and seasons, AMMI stability model and GGE model, significant differences were revealed. The differential behavior of the test genotypes was revealed across the diverse test locations. The results were consistent and in agreement with other research done where the genotypic effects contributed much to the yield variations obtained amongst the genotypes. AMMI and GGE biplots revealed that SZ-9523, 81-01-2, and SN-96-5 were high mean performers across all sites, whilst SZ-9523 was the most stable, and ideal genotype. SZ-9523 was also the winning candidate for a sector that accommodated all the test environments, that formed one mega environment.

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## Conflict of Interests

The authors declare that they have no competing interests.

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