



Genotype by Environment Interaction of Cotton Genotypes for Seed Cotton Yield in Zambia

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Authors' contributions

This work was carried out in collaboration among all authors. Author MLS undertook the research, performed the statistical analysis, interpreted the data and wrote the manuscript. Authors DML and LT guided the execution of research, data interpretation process and proof read the manuscript. All authors read and approved the final manuscript.

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ABSTRACT

Cotton (*Gossypium hirsutum* L.) is an important cash crop in Zambia. The national seed cotton yield (SCY) per hectare ranges from 200-500 kg/ ha as compared to the potential of up to 2500 kg/ ha. Understanding the specific performance of several genotypes across different environments is an option, which may maximize specific genotypic performance. In addition, the performance of specific environments if known concerning specific and mean genotypic performance may guide the breeding approaches to these environments. This study therefore investigated the presence of SCY mega-production environments in Zambia and delineated the environments and identified the ideal test environment capable of discriminating yield differences among genotypes. Thirty (30) genotypes, were planted following a 6 x 5 lattice design with three replications in seven environments of Zambia. Additive main effects and multiplicative interaction (AMMI) model and genotype plus genotype by environment (GGE) biplot were used to explore the genotype by genotypic environmental interaction (GEI). Three mega environments (M1, M2 and M3) were identified. Genotype G27, G26 and G28 were the best performing genotypes in M1, M2 and M3 with overall mean SCY of 1416, 1320 and 960 kg/ ha respectively. Among the locations, Masumba

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was identified as an ideal test environment with mean SCY of 1249 kg/ ha. Therefore, testing seed cotton genotypic yield and selecting desirable genotypes in Masumba may be sufficient for evaluation.

Keywords: Seed cotton yield; mega environment; AMMI; GGE biplot; ideal environment.

1. INTRODUCTION

Cotton is the most important fibre (lint) crop used in the manufacture of a large proportion of clothing and garments [1]. Seed cotton when ginned, produces about 40% lint, 57% cotton seed, and 3% waste [2]. Cotton is a major source of foreign exchange in Africa and is a source of income for smallholder farmers and their families. The world's largest conventional producer of cotton is India, with an annual production of approximately 5.6 million tonnes [3]. Burkina Faso and Mali are by far the biggest cotton producers in Sub-Saharan Africa with mean yields of 1374 and 1017 kg/ha of SCY respectively [4].

The average SCY in Zambia are low, averaging 200-500 kg/ha compared to optimum yield of up to 2500 kg/ha under research and good management [5]. Identifying desirable high yielding genotypes is key in improving SCY. Previous authors have suggested the use of molecular marker- assisted selection in selecting for desirable genotypes, as they are independent of the environmental effect [6,7]. However, in this study we tend to explore the phenotypic performance (P) taking into consideration genetic make-up (G), various environments (E) subjected to, and the genotype x environmental interaction (GEI). Bearing in mind, the differential response of genotypes across environments (GE) tends to limit response to selection and subsequently progress in a crop improvement programme [8].

It is therefore necessary, to determine the pattern of genotypic response to environment and quantify the environmental performance with regard to crop productivity. Furthermore,

knowledge on specific environmental performance and GEI may guide the breeding approaches to apply to these environments with a view of maximizing production. In this multi-environmental trial, additive main effects and multiplicative interactions (AMMI) and genotype main effects plus genotype-by-environment interaction (GGE) was employed to i) investigate the presence of SCY mega production environments in Zambia and ii) delineate the environments and identify the ideal test environment capable of discriminating yield differences among genotypes.

2. MATERIALS AND METHODS

2.1 Experimental Sites and Description of Experiment

The experiment was conducted at seven locations (Table 1) representing major cotton-growing regions in Zambia. Thirty (30) genotypes (Table 2) were evaluated in 2018/2019 cropping season.

The experiments were laid following a 6 x 5 alpha lattice design in seven environments. Rows were 4 m long and spaced 90 cm apart; inter plant spacing was 30 cm. All genotypes were planted randomly on 2-row plots in all seven environments in the 2018/2019 cropping season. Fertilizers were applied as follows; basal dressing [NPK(NP₂O₅)] at 200 kg per hectare at 4th leaf stage and top fertilizer urea(CH₄N₂O) at 150 kg/hectare at flowering stage. Weeding and pest management was carried out according to scouting recommendations as by Bbebe et al. [9]. Harvesting of seed cotton in all environments was done as by Raiz et al. [10].

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

Location	Coordinates	ALT(m)	Soil Type	Soil pH	TRF(mm)	MAT (°C)
Liempe	15°22'S, 28°26'E	1171	Sandy loam	5.21	862	23.7
Magoye	15°59'S, 27°37'E	1018	Sandy clay loam	5.63	512.9	23.3
Gwembe	16°29'S, 27°35'E	534	Sandy Clay	6.21	345.9	28.2
Msekera	13°38', 32°34' E	1032	Sandy loam	5.73	1106	24.3
Masumba	13°22'S, 31°56'E	546	Loamy sand	5.97	770	28.1
Mutanda	12°25'S, 26°12'E	1300	Sandy loam	6.1	1305	23.2
Misamfu	10°17'S, 31°22' E	1536	Sandy clay loam	4.43	1399.4	22.6

ALT- Altitude, TRF- Total Rain Fall, MAT- Mean Annual Temperature

Table 2. Germplasm used in the multi-environmental trial during the 2018/ 19 cropping season

GC	Genotype pedigree	Genotype	Source	Growth habit
G1	BC4 x CDT II	C1104	CDT	Indeterminate
G2	BC4 x CDT V	C1105	CDT	Indeterminate
G3	CDT-09 x BP 52	C1112	CDT	Indeterminate
G4	CDT II x Turk A	C1109	CDT	Indeterminate
G5	Rocket x CA336	C2612	CDT	Indeterminate
G6	Cameroon A x Zim II	C1107	CDT	Indeterminate
G7	MF20kG x VH8 4620	C2614	CDT	Indeterminate
G8	BC1 x C2511	C1103	CDT	Indeterminate
G9	CA347 x F135	C2602	CDT	Indeterminate
G10	C457 x CA336	C2619	CDT	Indeterminate
G11	Rocket x G319-18	C2618	CDT	Indeterminate
G12	CDT II x Turk B	C1110	CDT	Indeterminate
G13	CDT II x BP 52	C1111	CDT	Indeterminate
G14	BC4 x ISC 4	C1101	CDT	Indeterminate
G15	Ihmad 742 x Chureza	C1116	CDT	Indeterminate
G16	CA223 x CDT V	C1114	CDT	Indeterminate
G17	CA223 x CDT II-09	C1113	CDT	Indeterminate
G18	Stam29ABG1818 x CDT II-09	C1106	CDT	Indeterminate
G19	Cameroon A x Zim III	C1108	CDT	Indeterminate
G20	Turk B x BP52	C1119	CDT	Indeterminate
G21	CDT II-06 x Cameroun A	C1115	CDT	Indeterminate
G22	Turk B x Cameroun A	C1120	CDT	Indeterminate
G23	BC 3 x ISC 6	C1102	CDT	Indeterminate
G24	Cameroun A x BP 52	C1121	CDT	Determinate
G25	MV 513 x MV515	C 567	Mahyco	Determinate
G26	MV513 x MV 517	C571	Mahyco	Determinate
G27	MV513 x	C 569	Mahyco	Determinate
G28	(G319-16xcza87)x(BIII-F3xG319-16)	CDT II	CDT	Determinate
G29	CA336	CDT V	CDT	Determinate
G30	C1188 x L299)	Chureza	CDT	Indeterminate

GC- Genotypic code, CDT- Cotton Development Trust

2.2 Data Analysis

Inspection of the plot of residuals (data not shown) revealed no violation of ANOVA preconditions, allowing subsequent analysis of the data without any transformation. Analysis of variance for SCY was combined across locations, assuming a fixed model. AMMI and GGE biplots were computed and constructed using GenStat 13th Edition [11]. AMMI analysis was based on the model by Gauch et al. [12] and GGE biplot was based on the model for two principal components according to Yan and Kang [13].

3. RESULTS

3.1 Genotypic and Environmental Performance Based on AMMI

The combined AMMI analysis of variance for 30 genotypes tested across seven environments indicated highly significant differences ($P < 0.001$) for environments (E), genotypes (G), and genotype by environment interaction (GEI) (Table 3). The environments and genotypes however contributed significantly higher to the mean SCY variations and accounted for 42.61% and 22.55% of the treatment SS, respectively. The interaction between genotypes and the environment (GEI) accounted for approximately 22.87% of the treatment sum of squares (SS).

Furthermore, AMMI analysis revealed that the first and second IPCA axis were significantly higher ($P < 0.001$) than the residuals. The interaction (GEI) was further divided into two interaction principal component analysis [IPCA(1) and IPCA(2)] scores. Both interaction PCAs were highly significant ($P < 0.001$). The first and second IPCAs captured 72.60% and 14.89% respectively of the interaction sum of squares (SS).

The two IPCA axes jointly accounted for 87.49% of the interaction SS, leaving 12.50% of the variation due to GEI in the residuals.

The mean SCY across the seven environments was 533 kg/ ha. Further analysis revealed across environments showed that G27 and G26 were the highest yielding with mean values of 1416 and 1320 kg/ ha respectively (Table 4). With reference to IPCA(2), they were however unstable relative to other genotypes across environments. Genotype G2, though with a low mean value performance (440 kg/ ha) across environments had the most stable performance

with an IPCA(1) and IPCA(2) scores of 3.33 and 0.004 respectively. Masumba exhibited the highest mean (1248.8 kg/ ha) environmental performance across all genotypes.

3.2 Genotype and Genotype by Environments (GGE) Biplot Analysis

Based on the seven locations used in this study, three mega environments with different "winning" genotypes were identified using a scatter plot with polygon bisectors (Fig. 1). The mega-environments are further enclosed in blue circles that fall in rays as M1, M2, and M3. Two environments Masumba and Mutanda fell in one mega environment (M1). G27 was found to be the best performing genotype in M1 as it was at the corner of the convex hull polygon in this segment (Fig. 1).

The other mega environment (M2) contained four environments (Liempe, Msekera, Misamfu, and Gwembe) and the best genotype was genotype G26 as it was observed at the corner of the polygon near this mega environment. The remaining environment, Magoye, was contained in a smaller segment on its own as a mega environment (M3), with G28 as the best performing genotype.

3.2.1 Discriminating and representative ability of test environments

Masumba was the most discriminating and representative of the seven environments, as evidenced by the longer environment vector and a smaller angle between location vector and the average environmental coordinate (AEC) (Fig. 2). Because of having both qualities, Masumba was identified as the ideal environment. On the other hand, Magoye, Gwembe, Mutanda and Misamfu were found to be less discriminating. Msekera and Liempe were more discriminating but lesser representative than Masumba.

4. DISCUSSION

4.1 Seed Cotton Yield and Environmental Performance

Selecting cotton genotypes with high genetic potential for specific environments is a viable and cheaper approach to increasing production and productivity in SCY. This study revealed G27 and G26 as the best performing genotypes with mean values across environments of 1416 Kg/ ha and

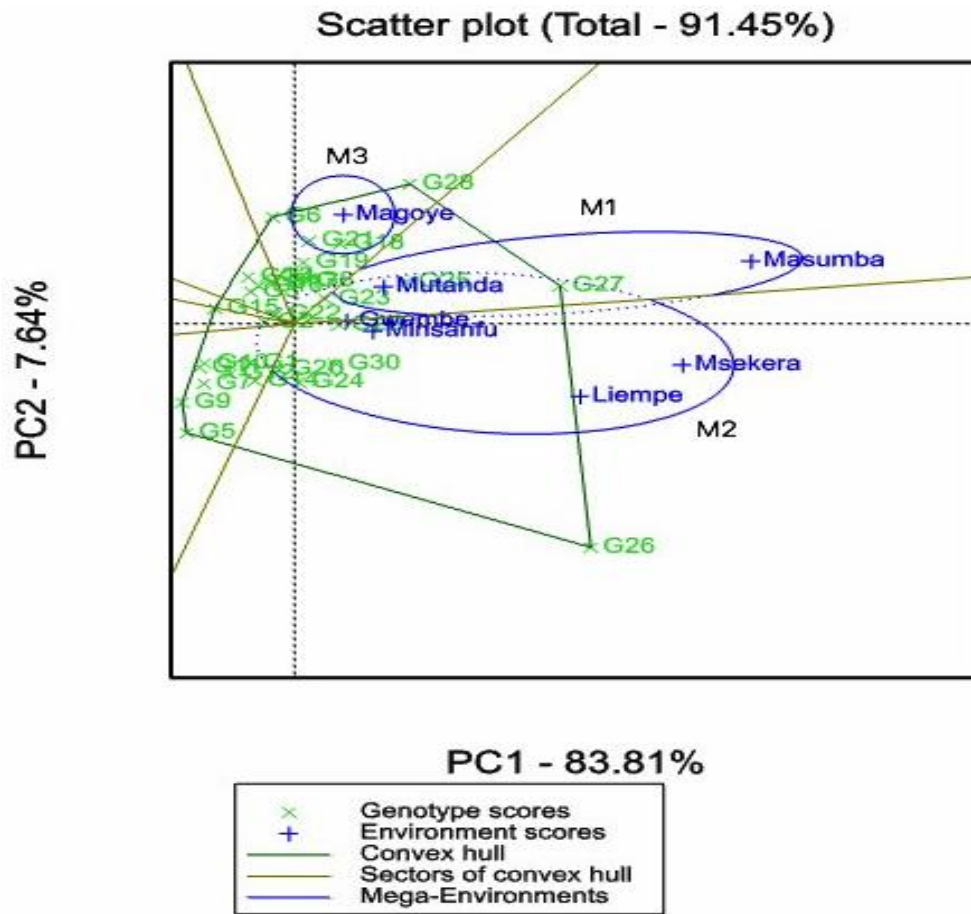


Fig. 1. Biplot exhibiting mega environment classification

M1-First Mega environment, M2-Second mega environment and M3-Third mega environment, Genotype-Green cross symbol, Environments- Blue plus symbol, Mega environments- Blue circles

1320 kg/ ha respectively. However, these two genotypes were not stable across environments. The high yielding stable genotype is expected to possess a high IPCA(1) but with a much lower (closer zero) IPCA(2) score (Table 4) [14]. Only genotype G2 though lower-yielding was however stable across environments, with IPCA(2) score of 0.004. Though this genotype may not be recommended as being desirable, it may find its usefulness in molecular mapping studies. Such a genotype (G2) can be crossed with a relatively high yielding genotype (such as G27) to create a mapping population to utilise in QTL associated tagging for seed cotton yield [7,15]. Based on AMMI evaluation of environment performance, Masumba was the best performing environment followed by Magoye with average seed cotton yield of 1249 kg/ha and 731 kg/ha respectively. The high performance of this area could be attributed to a roundup favourable environment in the area i.e temperature, rainfall amount, type of

soil etc (Table 1). On the other hand, despite Misamfu receiving abundant rainfall (1399 mm), the performance of cotton was relatively poor. This could be attributed to high acidic soils (pH 4), prevalent in this area. Low pH makes essential elements such as phosphorus and nitrogen unavailable to the plants hence stunting the plant growth and tap root growth of cotton [16].

When GEI ($P < 0.05$) is significant, it suggests that there is a possibility of having different mega environments [17]. A mega environment is a location or group of locations that share different winning genotype or groups of genotypes [18,19]. In this study, three mega environments were identified. Masumba and Mutanda formed one mega-environment (M1); Msekeru, Liempe, Gwembe, and Misamfu formed another mega environment (M2) and Magoye (M3). Genotypes G27, G26, and G28

were the best performing genotypes for mega environments M1, M2, and M3 respectively. The biplot results (Fig. 1) on winning genotypic performance in mega environments compare similarly to genotypic environmental mean performance generated by AMMI analysis (Table 4). This shows the reliability of the specific

performance of each winning genotype in the specific mega environment. A similar study [20], obtained three mega-environments on the performance of lint percentage, implying that understanding mega-environment is essential when embarking on an extensive cotton-breeding program.

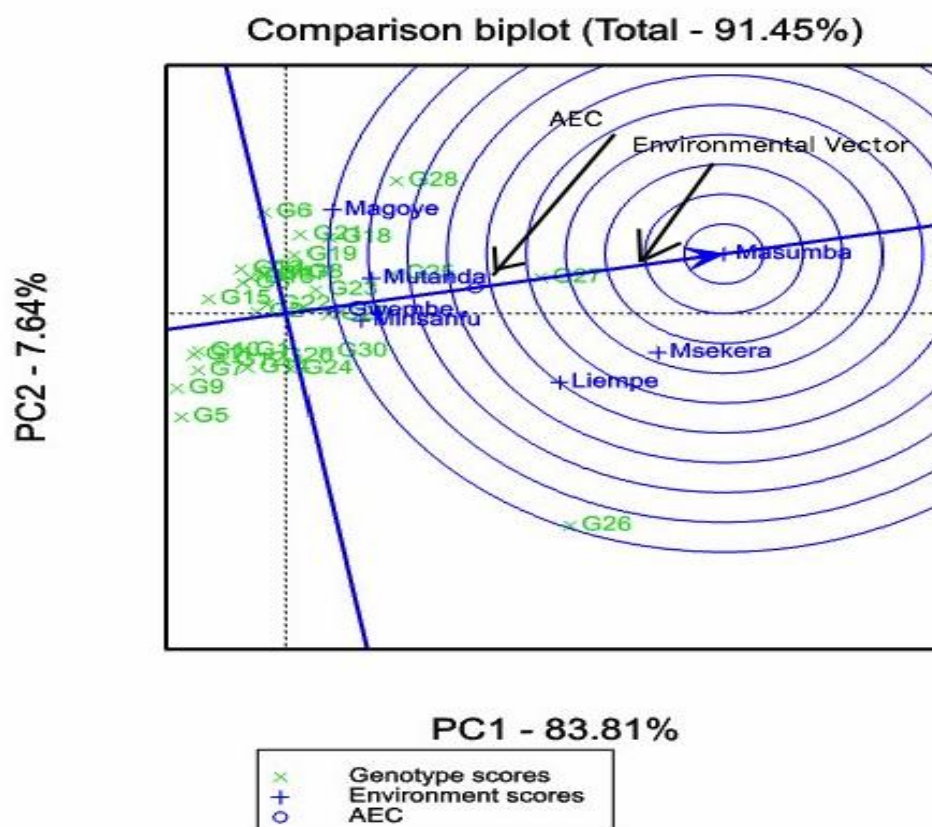


Fig. 2. Biplot exhibiting discrimination and representativeness of environments
 Genotype- Green cross symbol, Environments- Blue plus symbol, AEC-Average environmental coordinate.
 Environmental vector- distance from the environment to the cross junction where the two dotted lines meet

Table 3. Analysis of variance based on the AMMI model for seed cotton yield (SCY) across seven environments analysed during the 2018/19 growing season

Source	DF	SS	MS	E %	E GEI
Total	629	253640476	403244		
Genotypes	29	42058334	1450287.38***	22.55	
Environment	6	79467546	13244591***	42.61	
rep/environment	14	16459086	1175649		
Rep/Block	84	23256240	276860		
GEI	174	42664626	245199***	22.87	
IPCA(1)	34	30975457	911042.882***		72.60
IPCA(2)	32	6356038	198626.206***		14.89
Residuals	108	5333129	49380.82794		12.50
Error	406	33976516	83686		

*** Significant at 0.001 probability level. DF-Degrees of freedom, SS-Sum of squares, MS-Mean Square, IPCA=Interaction Principal Component Axis, GEI=Genotype by environment interaction. E- Explained

Table 4. Mean seed cotton yield (SCY) (kg/ha) and IPCA scores of 30 genotypes tested across seven environments

GC	Genotype	Gwe	Lie	Mag	Mas	Mis	Mse	Mut	GM	IPCA[1]	IPCA[2]
G1	C1104	29	317	590.	983	83	569	173	345	2.17	2.50
G2	C1105	123	252	619	948	212	533	251	440	3.33	0.004
G3	C1112	196	172	735	937	142	362	110	399	5.26	-3.04
G4	C 1109	203	304	809	910	154	527	465	464	4.06	-4.72
G5	C2612	16	143	76	538	112	84	33	117	7.31	7.59
G6	C1107	202	278	1040	1299	163	378	224	495	4.44	-10.67
G7	C2614	63	82	99	723	109	51	14	175	5.84	2.22
G8	C1103	149	717	873.	1209	266	616	422	608	1.52	-2.02
G9	C 2602	80	111	226	358	32	320	106	135	9.87	6.79
G10	C 2619	34	119	353	572	44	68	153.	195	6.89	1.47
G11	C 2618	22	132	407	639	198	34	89	209	9.03	3.65
G12	C1110	202	775	654	565	64	206	232	377	9.72	9.03
G13	C 1111	70	251	687	1248	201	152	378	404	6.19	-4.83
G14	C1101	141	499	517	961	155	418	136	396	3.51	6.04
G15	C1116	65	168	830	563	203	116	244	314	10.77	0.65
G16	C1114	30	381	795	882	133	379	354	441	5.24	-2.40
G17	C 1113	125	216	586	1283	244	303	429	480	2.97	-4.96
G18	C 1106	134	678	1213	1411	249	885	430	724	-1.74	-4.72
G19	C 1108	106	486	1197	1256	273	827	466	650	4.33	-0.14
G20	C1119	200	888	682	975	238	389	433	546	5.05	8.22
G21	C 1115	112	316	913	1589	202	477	277	569	-2.16	10.40
G22	C 1120	126	426	791	1060	99	431	341	497	3.47	1.12
G23	C 1102	128	731	1012	1164	215	816	243	678	0.35	1.93
G24	C1121	232	672	364	1323	298	478	263	516	-2.75	2.87
G25	C567	225	407	884	2394	286	1194	302	832	-15.36	-9.51
G26	C571	332	2159	748	2802	534	2982	553	1416	-36.40	22.74
G27	C569	362	1109	811	3584	393	2312	834	1320	32.645	-11.02
G28	CDT II(C)	220	540	1394	2530	266	1230	792	960	-8.80	-13.20
G29	CDT V(C)	78	270	997	1441	139	1209	354	637	-6.51	-0.82
G30	Chureza	147	508	1011	1316	105	1163	497	666	-4.24	5.61
Means		138.	470.3	731	1249	194	635	318	533		
SE		51.5	317.9	222.5	271.7	84.1	216.6	116.3	77.1		

GC- Genotype code, Gwe- Gwembe, Lie- Liempe, Mag- Magoye, Mas- Masumba, Mis- Misamfu, MSe- Msekera; Mut- Mutanda, GM- Genotypic mean across environments, SE-Standard error of mean

4.2 Discriminating and Representative Environments

In this study, the ideal environment, Masumba being the most discriminative and representative can be used for sufficient testing of genotypes for SCY. This helps in an event where evaluating across environments is limiting due to lack of resources. Therefore, in Zambia testing Cotton genotypes for SCY may sufficiently be done in Masumba. On the other hand, Msekera and Liempe being discriminative and less representative cannot be used in selecting superior genotypes but can be used in culling unstable ones [14,19]. The other environments (Magoye, Matanda, Misamfu, Gwembe) offer little information on differences in genotypic performance.

5. CONCLUSION

The genotypes G27 and G26 were found to have the highest mean SCY across environments exhibiting means of 1416 and 1320 kg/ ha respectively. The environments were also successfully delineated. The mega environments obtained in this study were M1 consisting of Masumba and Mutanda, M2 consisting of Msekera, Liempe, Misamfu and Gwembe, and M3 consisting of Magoye. Genotype G27, G26, and G28 were the best performing genotypes in M1, M2, and M3 respectively. Among these environments, Masumba was both discriminating and representative therefore, it was considered to be the ideal environment for testing cotton genotypes. Thus, it reduces on trial costs and enhances early generation selection. Furthermore, in future, stability analysis needs to be done for adaptation.

DISCLAIMER

The materials used for this research are commonly and predominantly used products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the materials because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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