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.
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. The experiments were conducted at seven locations in Zambia. Thirty (30) genotypes were planted randomly on 2-row plots in all environments and identified the ideal test environment capable of discriminating yield differences among genotypes.

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
| 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  | C1116    | CDT    | Indeterminate|
| G5 | Rocket x CA336   | C2612    | CDT    | Indeterminate|
| G6 | Cameroon A x Zim II | C1107 | CDT | Indeterminate |
| G7 | MF20Kg x VH4 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      | 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    | Determine   |
| G25| MV 513 x MV515   | C567     | Mahyco | Determine   |
| G26| MV513 x MV 517   | C571     | Mahyco | Determine   |
| G27| MV513 x           | C569     | Mahyco | Determine   |
| G28| (G319-16xcza87)x(BIII-F3xG319-16)| CDT II | CD | Determine |
| G29| CA336             | CDT V    | CDT    | Determine   |
| G30| Chureza           | CDT      | 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 533kg/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
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].

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); Msekera, 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.

![Comparison biplot (Total - 91.45%)](image)

**PC1 - 83.81%**

**PC2 - 7.64%**

**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.*

| 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 | 911042.88 | 72.60   |       |
| IPCA(2)         | 32  | 6356038 | 198626.20 | 14.89   |       |
| Residuals       | 108 | 5333129 | 49380.82 | 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    | 0.044   |
| 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| 8.81    | -2.02   |
| G9 | C 2602   | 80  | 111 | 357 | 626 | 32  | 320 | 135 | 9.87| 6.79    | 1.47    |
| G10| C 2619   | 34  | 119 | 353 | 572 | 48  | 195 | 68  | 153| 6.89    | 3.65    |
| G11| C 2618   | 22  | 132 | 407 | 639 | 198 | 34  | 89  | 209| 9.03    | 9.03    |
| G12| C 1110   | 202 | 775 | 654 | 565 | 64  | 206 | 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 | 1392| 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   | 138 | 731 | 1012| 1164| 215 | 816 | 243 | 678| 0.35    | 1.93    |
| G24| C1211    | 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- Liiempe, Mag- Magoye, Mas- Masumbwa, Mis- Msimufu, Mse- Msekeru; 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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