Grain Yield Stability in Three-way Cross Hybrid Maize Varieties using AMMI and GGE Biplot Analysis

1Sayo Sesay*, 2Alpha Bellah Jalloh, 3Vandi Aliu Sama

1,2,3Crop Improvement Programme, Rokupr Agricultural Research Center, Rokupr - Sierra Leone Agricultural Research Institute, PMB 1313, Tower Hill, Freetown, Sierra Leone.

A study to evaluate three-way cross hybrid maize varieties for wide adaptability and stability was conducted in eight environments in Sierra Leone using AMMI and GGE biplot analysis. There were significant genotype and environment main effects, and genotype x environment interactions (GEI) effects. Differences due to environments accounted for 70.1% of the total treatments sum of squares while genotypes and genotype x environment interaction accounted for 9.9% and 20.0%, respectively. The first four interaction principal component axes (IPCA) were also highly significant and accounted for 38.7%, 25.2%, 14.3% and 8.6%, respectively of the total genotype x environment interaction variation. The polygon view of the GGE biplot revealed that hybrid G14 produced the highest grain yield in environments E1, E5 and E7 whereas G24 was adaptive in environments E6, E8, E3, E4 and E2. Hybrids G24, G9, G17 and G6 also produced high grain yields and were relatively stable. Both AMMI and GGE biplot effectively partitioned treatments sum of squares and were more appropriate in explaining genotype x environment interaction. The models also identified G24 as the most desirable hybrid in terms of high grain yield and stability across environments. Therefore, this hybrid is recommended for commercial release.

Keywords: Genotype x environment interaction, grain yield, three-way cross hybrid, biplot analysis.

INTRODUCTION

The need to provide farmers and seed growers with new widely adapted maize varieties that will help boost their production and livelihoods has been the concern and effort of the maize breeding unit in Sierra Leone. In Sierra Leone, maize is the second most important cereal crop grown after rice, which is the country’s staple. The crop has a wide scope of adaptability and can grow in almost all agro-ecologies in the country. It is cherished by Sierra Leoneans and is grown in homesteads in the uplands during the raining season and inland valley swamps in the dry season (MAFFS, 2005). It has a very high commercial value when compared with other food crops grown in the country and is both a food and economic crop, contributing to poverty alleviation. Locally, maize is prepared into corn meal for human consumption, or eaten boiled or roasted (MAFFS, 2005). It is an excellent feed for poultry and livestock. Maize is also an excellent raw material for confectioneries, oil, starch and other useful products (Olawuyi et al., 2010; Randjelovic et al., 2011; Bello et al., 2013; Orhun, 2013). Despite all these benefits derived from maize, its potentials have not been fully realized in Sierra Leone. Yields are still very low, estimated to be 2tha⁻¹ in 2015 (USDA, 2015) and no new varieties with superior adaptability have been released for several years.

*Corresponding Author: Sayo Sesay, Crop Improvement Programme, Rokupr Agricultural Research Center, Rokupr - Sierra Leone Agricultural Research Institute, PMB 1313, Tower Hill, Freetown, Sierra Leone. Email: osaiosesay@yahoo.com. Tel: +23278084923
Production is erratic and there are numerous constraints to maize production and productivity- these include the deterioration of well-known maize varieties (Western Yellow, DMR-Yellow and TZR-ESR-yellow) under cultivation due to varietal mixtures, pests and diseases and other abiotic factors. There is the need to provide farmers and seed growers with new widely adapted maize varieties that will help boost their production and livelihoods. This implies the development and/or introduction of new maize genotypes with superior performance and wide adaptability.

Although different methodologies and procedures have been proposed for the interpretation of genotype x environment interaction and the evaluation of the adaptability and stability of genotypes, the AMMI (Additive Main Effects and Multiplicative Interaction) and GGE (Genotype main effects and Genotype x Environment interaction) biplot analyses stand out for the larger number of technical interpretations they provide (Duarte and Vencovský, 1999; Yan et al., 2000). Both AMMI and GGE Biplot analyses combine rather than separate G and GxE in mega-environment analysis and genotype evaluation (Yan et al., 2007). Both models interpret the effects of genotypes and environments as additive and the GxE interaction as multiplicative, by principal component analysis. However, several comparison studies between the AMMI and GGE biplot analyses have been conducted to evaluate genotypes, environments and genotype x environment interactions. Whereas some studies showed comparative advantages of the GGE biplot over the AMMI (Yan et al., 2007), others found equal advantages or little differences between the two models and conclude that they should complement each other in genotypes and environments evaluation. For instance, Mitrovic et al. (2012) found no large difference between the AMMI and GGE biplot analyses in the evaluation of experimental maize hybrids in different climatic conditions and that both methods can be used equally successfully. Miranda et al. (2012) concluded that utilizing both AMMI and GGE biplot simultaneously provides an innovative approach to the interpretation of genotype x environment interactions. Nassir (2013) further suggests that the combination of the two models would be necessary to take advantage of the respective areas of strength of each analysis to better serve the purpose of recommending genotypes for a location.

To take advantage of the respective strengths of AMMI and GGE biplot analyses for better decision makings in recommending genotypes in specific locations, the objective of this study was to evaluate three-way cross hybrid maize varieties for wide adaptability and stability of performance in eight environments in Sierra Leone.

**MATERIALS AND METHODS**

**Experimental Sites, Treatments and Design**

Trials were conducted in four different locations in the third and fourth week of June in the wet cropping seasons of 2012 and 2013, comprising of eight environments. Each of the test locations represented one District and were selected based on their large maize production and markets (Table 1).

The test genotypes were 23 three-way cross drought tolerant hybrid maize varieties and one check, Western Yellow. The hybrids were sourced from the International Institute of Tropical Agriculture, IITA, Ibadan, Nigeria (Table 2). At each environment, the land was well ploughed and harrowed and trial plots were laid out in a randomized complete block design with three replications. Each plot consisted of two rows (1.5m wide x 5m long), with 75cm between and 50cm within rows and two plants per hill were maintained. NPK 15:15:15 and urea fertilizers were applied at the rate of 120kg N/ha, 60kg P₂O₅/ha and 60kg K₂O/ha. The nitrogen fertilizer was applied in two splits - two and six weeks after planting. Weeding was done three times with a hoe and other standard crop management practices were applied. Grain yield (15% moisture content) was recorded in kilograms at harvest and later converted into tonnes per hectare.

**Statistical Analysis**

Grain yield data combined across the eight environments were subjected to AMMI analysis of variance to determine genotype and environment main effects, and genotype x environment interactions effects. The mean yields of genotypes in each environment and across environments and their first interaction principal component axis (IPCA) values were also analysed. The AMMI and GGE biplot models were used to identify genotype stability, which

<table>
<thead>
<tr>
<th>Region/Area</th>
<th>District</th>
<th>Location</th>
<th>Latitude</th>
<th>Longitude</th>
<th>Altitude (m)</th>
<th>Average annual temperature (°C)</th>
<th>Average annual rainfall (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>South</td>
<td>Bo</td>
<td>Bandajuma</td>
<td>7°57'0&quot;N</td>
<td>11°40'0&quot;W</td>
<td>98</td>
<td>26.2</td>
<td>2706</td>
</tr>
<tr>
<td>Western Area</td>
<td>Western Area Rural</td>
<td>Newton</td>
<td>8°20'6.6&quot;N</td>
<td>13°029.9&quot;W</td>
<td>36</td>
<td>26</td>
<td>3392</td>
</tr>
<tr>
<td>North</td>
<td>Kambia</td>
<td>Samu</td>
<td>9°55.9&quot;N</td>
<td>12°44'28.1&quot;W</td>
<td>65</td>
<td>26.8</td>
<td>2988</td>
</tr>
<tr>
<td>East</td>
<td>Kenema</td>
<td>Serabu</td>
<td>7°51'17.04&quot;N</td>
<td>11°17'13.56&quot;W</td>
<td>134</td>
<td>26.6</td>
<td>2853</td>
</tr>
</tbody>
</table>

genotype(s) performed best in which environment (s), and rank the genotypes based on high grain yield and stability. GenStat 12.1 (GenStat 2009) and Plant Breeding Tools version 1.4 (PBTools, 2014) Softwares were used to carry out the analyses.

RESULTS AND DISCUSSION

Analysis of Variance

The AMMI analysis of variance for grain yields of the 23 three-way cross hybrids grown in eight environments are presented in Table 3. The variance component due to treatments was highly significant and accounted for 96.3% of the total variation. This large percentage indicated that the AMMI model effectively partitioned treatments. The effects of genotypes, environments and genotype by environment interaction were significant. Differences due to environments accounted for 70.1% of the total treatments sum of squares while genotypes and genotype by environment interaction accounted for 9.9% and 20.0%, respectively. The largest portion accounted for by environments indicated the significant influence of environments on grain yield in the study areas. Similar results where the environment had the highest effect than other factors had been reported by several researchers in various crops (Naghash et al., 2013; Kılıç, 2014; Kendal and Dogan., 2015; Edugbo et al., 2015; Oyekunle et al., 2017). Assessment of genotypes in many locations and years could increase the reliability of plant breeding programs, but many location trials were more important than many years trials in the same location in determining performance of tested genotypes in terms of investigated traits (Ezzat et al., 2010; Sayar et al., 2013). This enhances the importance of our study conducted in many locations in two years, which were different from one another in terms of environmental conditions. Mosa et al. (2011) and Khalil et al. (2011) found significant GxE interaction for grain yield in maize genotypes. The first, second, third and fourth interaction principal component axes (IPCA) were also highly significant and accounted for 38.7%, 25.2%, 14.3% and 8.6%, respectively of the total genotype by environment interaction variation. The first IPCA mean square was almost six times and the second IPCA mean square was only four times larger than the residual mean square. The magnitude of the genotype by environment interaction sum of squares was about two

<table>
<thead>
<tr>
<th>Genotypes</th>
<th>Code</th>
<th>Pedigree</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>Western Yellow (Local check)</td>
<td>G1</td>
<td>Western Yellow (Local check)</td>
<td></td>
</tr>
<tr>
<td>M0826-1</td>
<td>G2</td>
<td>9071/1368xHix4269-1x1368-7-2-B’4/P43SRC9FS100-1-1-8-#1-B1-13-B1-B’4</td>
<td>1A20600B</td>
</tr>
<tr>
<td>M0826-2</td>
<td>G3</td>
<td>9071/1368xHix4269-1x1368-7-2-B’4/Obantapa-33-5-B’4</td>
<td>1A20602B</td>
</tr>
<tr>
<td>M0826-3</td>
<td>G4</td>
<td>9071/1368xHix4269-1x1368-7-2-B’4/(TZM501xKU1414x501)-1-4-3-1-B-BB</td>
<td>1A20604B</td>
</tr>
<tr>
<td>M0826-4</td>
<td>G5</td>
<td>9071/1368xHix4269-1368-7-2-B’4/161</td>
<td>1A20606B</td>
</tr>
</tbody>
</table>

Table 2: List of genotypes and their pedigrees used in the study
times larger than that for genotype and 12.5 times larger than the error mean square. This indicates that partitioning of the interaction sum of squares by AMMI was very effective (Makinde et al., 2013) and there were sizeable differences in responses of the genotypes across environments (Karimizadeh et al., 2013). According to Yan and Kang (2003), this suggests the possible presence of different mega-environments with different winner genotypes. This observation is in line with that of Adomou et al. (1997), Makinde and Ariyo (2011) and Edugbo et al. (2015).

**Mean Performance of Genotypes**

Table 4 presents genotype and environment means as well as their first IPCA values. Average grain yield ranged from 2.1 t/ha for the hybrid SC621 to 3.4 t/ha for SC719, 50% of the hybrids yielded above the grand mean. The highest grain yield (4.4 t/ha in 2012 and 3.7 t/ha in 2013) were obtained at Newton followed by Samu in 2013. Conversely, the lowest grain yield were recorded at Bandajuma in 2013 (1.7 t/ha) and Samu in 2012 (2.0 t/ha); 50% of the environments produced grain yields above the average. When a genotype and an environment have the same sign, their interaction is positive; if different, their interaction is negative (Taiiku et al., 2013). Therefore, hybrids M0826-4, M1124-15, M1124-16, M1124-18, M1124-23, M1124-24, M1124-26, M1126-28, M1124-29, M1124-31, Oba 98 and Oba Super1 had a positive interaction with the environments Samu in 2012 and 2013, Bandajuma, and Serabu in 2012 while the remaining hybrids had a negative interaction with the environments.
Grain Yield Stability in Three-way Cross Hybrid Maize Varieties using AMMI and GGE Biplot Analysis

Newton in 2012 and 2013, Bandajuma and Serabu in 2013 - 50% of the hybrids had a positive interaction with 50% of the environments. Likewise, 50% of the hybrids interacted negatively with half of the environments. The hybrids M0826-4 and M1124-23 (with PC1 scores of zero), and Oba Super 7 and SC719 (with PC1 scores nearly zero) can be fitted well by an additive model. Hybrid SC719 gave the highest grain yields at Newton and Samu in 2012 and 2013, respectively and showed consistent performance in the other environments, except location Serabu in 2012.

AMMI Analysis

Figure 1 presents the AMMI biplot with the genotype and environment main effects for grain yield on the X-axis and PC1 scores on the Y-axis. The vertical line at the middle represents the grand mean of the grain yield, while the horizontal line at the middle is the PC1 value of zero (Tolessa, 2015). The biplot revealed that genotypes G4, G5, G6, G7, G8, G9, G11, G12, G14, G17, G19 and G24 are high yielding since they were placed on the right hand side of the biplot. Similarly, the highest grain yield was produced in environments E3, E4, E6 and E8. On the other hand, the rest of the genotypes and environments were considered to be low yielding and were placed on the left hand side of the biplot. Genotypes or environments which appear almost on the perpendicular line to the grand mean line have similar means, while those that occur on a horizontal line to the zero PC1 line have similar interaction patterns (Badu-Apraku et al., 2003). Thus, genotypes G2, G13, G15, G20; G3, G18, G22, G23; G4, G5, G12; G6, G7, G14, G17 and G19 had similar mean effects while G5, G10, G19 and G24 showed the same interaction effects. None of the environments had similar means and interaction patterns, indicating that the environments were extremely different. The AMMI biplot further reveals that environment E1 and hybrids G18, G10, G15, G2, G13, G20, G5, G19, G24, G17, G9 and G6 were the least interactive while the highest genotype x environment interaction was shown by hybrids G12, G7, G16 and G14 in environment E6, and by hybrid G8 in environments E3, E4 and E8. However, stability should be accompanied with high yielding performance, thus genotypes G5, G19, and G24 were the most stable genotypes with high grain yields. However, G24 was considered to be the most desirable genotype because of its highest grain yield and absolute stability. Genotypes G9, G17 and G6 also produced better grain yields and were relatively stable.

GGE-biplot Analysis

Figure 2 shows the polygon view of which three-way cross hybrids were the best in which environment(s). The two principal component axes (PC1 and PC2) accounted for 63.8% of the total variation in grain yield, of which PC1
explained 45.7% and PC2 explained 18.1%. This result is in line with the finding of Oyekunle et al. (2017) who observed that the two PC axes accounted for 59.8% of the total variation, with PC1 and PC2 explained 44.7% and 15.1%, respectively of total variation for grain yield in early maturing hybrids.

The biplot is divided into four sectors, which placed genotypes into all the four sectors and test environments into two sectors. Yan et al. (2000) pointed out that the vertex hybrids in each sector represented the highest-yielding hybrid in the location that fell within that particular sector. Therefore, genotype G14 which is a vertex genotype in the first sector had the highest grain yield in environments E1, E5 and E7, while G24 which is the vertex genotype in the second sector produced the highest grain yield in environments E6 and E8. Genotype G24 also produced consistently higher grain yields in environments E3, E4 and E2. Genotypes G21 and G1 which are the vertex genotypes in the third and fourth sectors, respectively had the least grain yields in one or all of the environments.

The ranking of the 24 genotypes based on their mean grain yield and stability of performance and relative to an ideal genotype across eight environments is presented in Figure 3. The single arrowed line on the graph is the Average Environment Axis (AEA) abscissa which points to a higher genotype mean performance whereas the double-arrowed line that passes through the biplot origin and is orthogonal to the AEA abscissa is the AEA ordinate. Regardless of direction, it shows greater GEI effect and greater instability (Yan and Kang, 2003). The stability and instability of genotypes are associated with the vector line of the AEA abscissa on the biplot graph (Yan, 2001). A genotype with shorter vector from the AEC abscissa is considered more stable while genotypes with longer vector are unstable (Kaya et al., 2006; Yan, 2001). Thus, hybrids G14, G16, G7, G11, G20, G23, G22, G3, G8 and G19 with longer vector lines away from the AEA line are considered more stable while genotypes with longer vector lines away from the AEA line are considered to be unstable, while G1, G17, G18, G10, G5, G9, G4, G6, G2 and G12 with shorter vector lines are regarded as being stable. Hybrid G14 was the most unstable hybrid since it had the longest vector line away from the AEA line whereas G5 with the shortest vector line was considered to be the most stable hybrid. The stability of hybrids is meaningful only when considered simultaneously with high grain yield performance (Yan and Tinker, 2006). Therefore, hybrids G5, G6, G9, G12 and G17 had high grain yield performance and relative stability. Hybrids G1,
G10 and G18 were very stable but were among the low yielding hybrids and cannot, therefore, be recommended for commercial release. Hybrid G24 was considered to be the most desirable hybrid because it gave the highest grain yield and had absolute stability and is, therefore, recommended for commercial release. This hybrid is found near the ideal genotype represented by the small circle with an arrow pointing to it (Yan and Kang 2003).

CONCLUSIONS

There were significant differences between genotypes and environments and significant genotype x environment interactions. The polygon view of the GGE biplot identified the hybrid G14 as the most adaptive in environments E1, E5, and E7 whereas hybrid G24 was adaptive in environments E6, E8, E3, E4 and E2. Genotypes G24, G9, G17 and G6 produced high grain yields and were relatively stable. Both the AMMI and GGE biplot effectively partitioned treatments sum of squares and were more appropriate in explaining genotype x environment interaction. The models also identified hybrid G24 as the most desirable hybrid. This hybrid is therefore recommended for release for commercial production.

CONFLICT OF INTERESTS

There is no conflict of interest for this paper.

ACKNOWLEDGEMENTS

The authors are grateful to the Alliance for a Green Revolution in Africa (AGRA) for financial support and the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria for providing planting materials and technical support.
REFERENCES


MAFFS (Ministry of Agriculture Forestry and Food Security), “Crop Production Guidelines for Sierra Leone”, National Agricultural Research Coordinating Council (NARCC), Institute of Agricultural Research (IAR), Rice Research Station (RRS) and Njala University (NU), 10 July, 2005, pp. 17-18.


PBTools, version 1.4. 2014. Biometrics and Breeding Informatics, PBGB Division, International Rice Research Institute, Los Baños, Laguna.


**Accepted 29 September 2017**


**Copyright:** © 2017 Sesay et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are cited.