Genotype by Environment Interaction on Yield Components and Stability Analysis of Elite Cassava Genotypes

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Newly developed varieties can only contribute to increased productivity if high producing varieties are released in production niches they are adapted to. In order to enhance adoption of new improved cassava varieties in western Kenya, a study was conducted to evaluate the effects of genotype by environment interaction (GEI) on agronomic and farmer preferred traits of cassava and to assess yield stability of 16 cassava genotypes. The study was conducted in randomized complete block design with three replications across five different environments of western Kenya. AMMI analysis of variance identified highly significant (P= 0.001) GEI effects for plant height, height at first branching, and fresh root yield. Generally, GEI effects accounted for 14.98%, 24.64% and 28.3% variability in PH, HB, and FRY respectively. GGE biplot analysis shows that MM06/0138, MM96/9308, MM97/0293, MM98/3567, MM06/0074, MM96/4271 were high yielding and stable genotypes. AMMI stability value revealed that genotype MM06/0143 combined high stability for plant height, height at first branching, number of storage roots and fresh root yield. Genotypes MM06/0138, MM98/3567, MM96/9308, MM97/0293, and MM06/0074 outperformed the check in storage roots yield exhibited high yields in farmer preferred traits and were classified as stable genotypes. Therefore, recommended for release to farmers.

Key Words: Elite cassava, Farmer preferred traits, Genotype X Environment interaction, AMMI analysis, GGE-biplot analysis

INTRODUCTION

Cassava (Manihot esculenta Crantz) is an important staple grown for its starchy tuberous roots. Its roots and leaves are suitable for human consumption as well as animal feed. The tuberous roots are an important source of carbohydrates while the leaves are cheap valuable source of proteins, minerals and vitamins A, B and C (Montagnac et al., 2009). The storage roots are also used as industrial raw materials like starch extractions for various industrial uses, breweries, pharmaceutical, and biofuel among other uses (Nweke, 2004; Jackson et al., 2014). Cassava is the second most important food crop after maize in Western and coastal regions of Kenya (Njeru & Munga, 2003). However, production level in Kenya is 11 t/ha, below the potential of 90 t/ha, which is attributed to low yield of popular varieties, poor access to quality planting material, lack of well adapted varieties, pests and diseases (Mwango’mbe, et al., 2013). Cassava mosaic disease (CMD) and cassava brown streak disease (CBSD) are the leading yield limiting biotic constraints for cassava production causing an estimated loss of more than US$ 14 million per annum in CMD (Alabi, et al., 2015). Cassava genetic improvement has been difficult due to the biology of the crop (Ceballos et al., 2004).

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Use of improved varieties is the current leading tool for solving viral disease challenges in cassava (Alabi, et al., 2015), hence continuous deployments of elite resistant cultivars are necessary as CMDs are known to evolve producing virulent strains while different strains of CBSD are being reported in Kenya (Mware, 2009). However, low adoption of the new improved varieties has been reported in western Kenya (Odendo et al., 2010; Woyengo & Omari, 2014).

In the last three decades, cassava breeding has majorly concentrated on increasing yields and resistance to pest and disease (Ceballos et al., 2004). However, there has been lack of focus on farmer preferred traits by breeding programmes which has been observed to be the major course of low adoption of improved varieties despite the high yield and resistance to common pests and diseases (Woyengo, 2011). Moreover, some of the improved varieties fail to perform well in target production niches due to lack of detailed stability studies of these traits. It’s therefore a prerequisite that cassava varieties should not only be released on the basis of average yield and reaction to diseases pests but also on the presence of farmer preferred traits and stability. The work of Achepong et al. (2013), identified longevity and disease resistance as two major attributes of cassava that influence adoption of improved varieties in Ghana. Njukwe et al. (2013) observed regional differences for farmer preference in cassava attributes and cassava genotypes in Cameroon, for instance farmers in Ebolowa and Bertoua preferred leafy, sweet roots and early branching varieties while those in Bamenda and Ngoundere preferred tall, drought tolerant and in some cases flowering varieties. In Kenya the work of Were (2011), identified farmer preferred traits that encourage adoption of improved cassava genotypes by order of preference as high root yield, tall plants and lower height of first branching. However, no study has been reported on influence of environment on farmer preferred traits and stability of new improved cassava genotypes.

Genotype stability and adaptability are ultimate resources for achieving food security which is an allusive goal for Kenya and Sub-Saharan Africa at large (Muzari et al., 2012). Lobell (2009) stated that agricultural adaptability should be a priority in meeting food security presently and in future in the face of severe climate change. This is achieved by development of stable varieties of crops. Stability of performance of quantitative traits is influenced by genotype, environment and genotype by environment interaction (GEI) effects. GEI is important in plant breeding because it complicates demonstration of a superiority of a variety. An effective method which has been used to reduce GEI is stratification of environment such that the sub-region in which the breeder is developing improved varieties are somehow similar (specific adaptation). However, this is not mineable to breeding since even with the refinement of this technique the interaction of genotypes within a location in a sub-region and with environments encountered at the same location in different years frequently remains too large (Crossa 1990). Moreover, Woyengo and Omari, (2014) clearly pointed out that it is not feasible to breed for specific adaptation with current erratic climatic conditions and effect of climatic change hence breeding for stable varieties remains as the only viable option. Many statistical procedures have been advocated for the basis of analysis of GEI and stability of genotypes. Studies show that stability of performance are expected to become more relevant issues as greater emphasis is placed on sustainability of agricultural systems (Kang et al., 2012). The objective of this study therefore, was to evaluate GEI effects on agronomic and farmer preferred traits of cassava and to assess yield stability of 16 cassava genotypes across five environments of western Kenya.

MATERIALS AND METHODS

The study was conducted across five environments (Kakamega, Sang’alo, Alupe, Kibos and Migori), which represent major cassava growing zones of western Kenya, between 2014 and 2015. The experimental material consisted of 15 elite cassava clones (G1=MH95/0183 G3=MM06/0013, G4=MM06/0046, G5=MM06/0074, G6=MM06/0082, G7=MM06/0083, G8=MM06/0131 G9=MM06/0138, G10=MM06/0139, G11=MM06/0143, G12=MM96/2480, G13=MM96/4271, G14=MM96/9308, G15= MM97/0293, G16=MM98/3567) in advanced stage of yield trials performance and one local check (G2=migyera). Improved clones’ seeds were developed and introduced from International Institute of Tropical Agriculture (IITA). The clones were derived from half-sib progenies of elite varieties. They have been tested by Kenya agricultural livestock and research organization (KALRO) Kakamega for resistance to CMD and CBSD. The experiment was laid in randomised complete block design with three replications and established under rain fed conditions. No fertilizer nor pesticide were applied. Each experimental plot had six rows and 30 plants spaced of 1m by 1m between plants and rows.

Data Collection

Data was collected on agronomic traits (Dry matter content and starch content) and traits preferred by farmers in western Kenya as identified by Woyengo, (2011) which include plant height, height at first branching, number of storage roots per plant and fresh root yield. Data was collected at twelve months after the date of planting and at harvesting. Data were recorded on plant and plot basis. Five plants per plot were sampled from the inner rows. Data were recorded on plant height (PH), height at first branching (HB), number of storage roots per plant (NSR) and fresh root yield converted to tonnes per hectare (FRY). Data on dry matter content (DMC) and starch content was collected according to the methodology described by Fukuda et al., (2010) converted to DM% and Starch % as follows:
Table 1: Agro-ecological description of experimental sites

<table>
<thead>
<tr>
<th>Site</th>
<th>Longitude</th>
<th>Latitude</th>
<th>Elevation (m.a.c.l)</th>
<th>Rainfall (mm)</th>
<th>Temperature (Range °C)</th>
<th>Soil texture</th>
</tr>
</thead>
<tbody>
<tr>
<td>Kakamega</td>
<td>34°47'E</td>
<td>00°17'N</td>
<td>1554m</td>
<td>1191</td>
<td>(18.5-21.0)</td>
<td>Red friable Nitosols</td>
</tr>
<tr>
<td>Sang’alo</td>
<td>34°6'E</td>
<td>00°5'N</td>
<td>1421m</td>
<td>1628</td>
<td>(20.9- 22.0)</td>
<td>orthic ferralsols</td>
</tr>
<tr>
<td>Alupe</td>
<td>34°5'E</td>
<td>00°29'N</td>
<td>1173m</td>
<td>1627</td>
<td>(21.0-22.2)</td>
<td>clay-loam Acrisols</td>
</tr>
<tr>
<td>Kibos</td>
<td>34°48'E</td>
<td>00°04'N</td>
<td>1690m</td>
<td>1912</td>
<td>(15.3-30.0)</td>
<td>Black clay vertisols</td>
</tr>
<tr>
<td>Migori</td>
<td>34°31°E</td>
<td>00°59'S</td>
<td>1423m</td>
<td>1396</td>
<td>(20.4-21.7)</td>
<td>Mollic Nitosols</td>
</tr>
</tbody>
</table>

Root sample weighing 3-5kg was prepared, the weight of the sample was measured in air (Wa) using a digital weighing balance. The same sample was also measured in water (Ww). Specific gravity(x) was computed at:

Ww/ (Wa-Ww)

%DMC was computed using the formula DMC = (158.3x-142)/100

%starch was computed using the formula starch = (112.1x-106.4)/100

Statistical Analysis

Genotypic stability for each clone was computed using GenStat software, 14th edition. The additive main effects and multiplicative interactions (AMMI) statistical model suggested by Gauch and Zobel (1996) was used to analyze yield data to obtain (AMMI) analysis of variance and (AMMI) mean estimates as follows as follows:

\[ Y_{ger} = \mu + \alpha_g + \beta_e + \sum \lambda_i y_{gj} \delta_{en} + \rho_{ge} + E_{ger} \]

Where: \( Y_{ger} \) = yield of genotype \( g \) in environment \( e \) for replicate \( r \), \( \mu \) = grand mean, \( \alpha_g \) = genotype mean deviation (genotype means minus grand mean), \( \beta_e \) = environment mean deviation, \( n \) = number of principal component analysis (PCA) axes retained in the model, \( \lambda_i \) = singular value for PCA axis \( n \), \( y_{gj} \) = genotype eigenvector values for PCA axis \( n \), \( \delta_{en} \) = environment eigenvector values for PCA axis \( n \), \( \rho_{ge} \) = residuals, \( E_{ger} \) = error term.

The AMMI stability value (ASV) proposed by Purchase et al. (2000) was used to quantify and rank genotypes according to the yield stability. The ASV has been defined as the distance from the coordinate point to the origin in a two-dimensional scatterplot of first interaction principal component axis (IPCA1) scores against the second interaction principal component axis (IPCA2) (Farshadfar et al., 2012). Since IPCA1 accounts for most of the GEI variation, the IPCA1 scores are weighted by the ratio of IPCA1SS (from AMMI ANOVA) to IPCA2 SS in the ASV formula as follows:

\[ ASV = \sqrt{\frac{SSIPCA1}{SSIPCA2} (IPCA1 score)^2 + (IPCA2 score)^2} \]

The lower the ASV, the more stable a genotype is.

Another important point was further explained by Yan et al. (2007) that genotype and genotype-by-environment effects must be considered simultaneously to make a meaningful decision in selection. Significant genotype by environment interaction was also analyzed by GGE biplot which was also useful in ranking genotypes based on their average performance and stability for farmer preferred traits in cassava. The model for the GGE biplot based on singular value decomposition (SVD) of first two principal components is:

\[ Y_{ij} - \mu - \beta_j = \lambda_1 \xi_1 \eta_1 + \lambda_2 \xi_2 \eta_2 + e_{ij} \]

Where: \( Y_{ij} \) = measured mean of genotype \( i \) in environment \( j \), \( \mu \) = grand mean, \( \beta_j \) = main effects of environment \( j \), \( \lambda_1 \) and \( \lambda_2 \) = are the singular values (SV) for the first and second principle components (PCA 1 and PCA 2) respectively. \( \xi_1 \) and \( \xi_2 \) = are eigenvectors of genotype \( i \) for PCA 1 and PCA 2 respectively; \( \eta_1 \) and \( \eta_2 \) = eigenvectors for environment \( j \) for PCA 1 and PCA 2, respectively. \( e_{ij} \) = residual associated with genotype \( i \) in environment \( j \).

RESULTS AND DISCUSSION

The results from AMMI analysis of variance (Table 2) reveal that environment gives the most effect (64.81 %) of variability on plant height. Moreover, environmental variation contributed to more than 47% of the total variability in fresh root yield. Aina et al. (2007) in Nigeria reported 88.9% of environment sum of squares (SS) when evaluating for root yield stability in cassava. The large sum of squares for environments indicated that the environments were diverse, with differences among the environmental means causing more than a third of the variation in plant height, height at first branching and number of storage roots. This might be probably due to the differences in environmental conditions which has been known to have impact on cassava yield (De Vries et al., 2010). Besides, highly significant GEI interaction (Ps < 0.001) was observed for PH, HB, and FRY. These results are in agreement with the findings of Adjeibeng-Danquah et al. (2017) who observed highly significant GEI for these trait. These suggests that genotypes responded differently to environments which necessitates the investigations of the nature of different response of the genotypes to environments. GEI effects contributed with 14.98%, 24.64% and 28.3% for plant height, height at first
branching and fresh root respectively, meaning more than 24% variability observed in height at first branching and fresh root yield is due to GEI effects. In spite of this, the magnitude of the genotype sum of squares for plant height and height at first was branching was larger than that of GEI (20.2% and 50.9%) respectively which indicates presence of moderate control of genotype effects over genotype by environment interaction effects for these traits.

On the other hand, there was non-significant GEI effects for number of storage roots, dry matter content and starch. The phenomenon was also the same as reported by Peprah et al. (2013) who observed non-significant GEI for dry matter content. This finding also agrees with those of Aina et al. (2007) who reported non-significant GEI effects for number of storage roots and dry matter content. Similarly, Benesi et al. (2004) reported non-significant GEI for starch.

An obvious deduction from non-significant GEI effects on number of storage roots, dry matter content and starch is that, genotypes might have similar responses across the locations in which they were evaluated and that they can consistently be evaluated under any of the locations used for this study in impending performance trials. This view is in conformity with the view of Peprah et al. (2013) who found non-significant GEI effects for dry matter content and reported that fewer environments may be needed to distinguish clones with high and stable performance for this trait. In other words, evaluating genotypes for these traits concurrently in the various locations used for these studies in consequent evaluation trials might not be important. Thereby, offering an opportunity to manage inadequate means available for testing programme (Tonk et al., 2011).

Complementary to previous results, ASV was computed for the traits so as to quantify and rank genotypes according to their stability Table 3 shows the ranking of the 16 genotypes according to AMMI stability value. Genotypes varied in ranking for stability across the studied traits. However, some genotypes combined satisfactory results for stability in various traits. For instance, genotype MM06/0143 is very stable as it ranked 2 in number of storage roots, dry matter content and fresh root yield (FRY)
storage roots and fresh root yield. MM98/3567 combines stability for plant height and fresh root yield while MM97/0293 combines stability for plant height, number of storage roots and fresh root yield. Genotypes MM06/0046, MM06/0083, MM06/0143, and MM06/0074 were stable genotypes for plant height, height at first branching, number of storage roots per plant and fresh root yield respectively. These suggest the possibility of identifying clones exhibiting stable performance in both agronomic and farmer preferred traits.

GGE Biplot analysis

According to Yan et al. (2007) genotype-by-environment interaction effects must be considered simultaneously to make a meaningful decision in selection. These requires biplot analysis that considers genotype and GEI simultaneously. Additionally, genotypes should be evaluated based on combined performance of the mean across environments with their stability which also necessitates the use of a biplot analysis.

Analysis of GGE biplot further elucidated the yield performance and stability of genotypes across the study sites for fresh root yield and number of storage roots. Analysis of yield stability of genotypes was evaluated using GGE biplot by an average environment coordination (AEC) method on fresh root yield and number of storage roots. In this method, the average principle components are used in all environments, as depicted in Figures 1 and 2. The AEC ordinate separate genotype with below average means from those with above average means. A line is then drawn through this average environment axis and serves as the abscissa of the AEC.

The arrow points to a greater genotype main effects, the AEC ordinate and either direction away from the biplot origin indicates greater GEI effects and reduced stability. Hence, the stability of a variety or environment was determined by the length of the vector from genotype marker to the average environment coordinate (AEC) abscissa. The vector which was closer to the AEC abscissa was considered to have less interaction effects and hence regarded as stable. A clone located at the origin is not influenced by environment in any way hence it would rank the same in all the environments and therefore considered as the most stable.

In Figure 1 the mean number of storage root per plant and stability performance of cassava genotypes was depicted. The genotypes were ranked along the average environment co-ordinate (AEC) x-axis with an arrow indicating the highest mean. Thus, results revealed that G16 (MM98/3567) which was closer to the AEC had the highest number of storage roots while G4 (MM06/0046) was the lowest yielding genotype because they were further away from the AEC axis. However, the lengths of vectors from genotype marker to the AEC abscissa concentrated around zero for most of the clones suggesting that the candidate clones were stable for this trait (number of fresh root yield). Though clones G2 (migyera), G11 (MM06/0143) and G4 (MM06/0046) revealed some displacement on the Y-axis from the origin, it’s clear that the PC scores for these clones in this Y’-axis is less than one (near zero) for the three clones hence it was adjudged that all the candidate clones were stable for this trait.

![Figure 1: Mean performance and stability of 16 cassava genotypes (G1 – G16) at five environments (K: Kakamega, S: Sangalo, A: Alupe, B: Kibos, M: Migori) for number of storage roots.](Image)

Ranking of genotypes along (AEC) for fresh root yield revealed that candidate clones varied greatly in yield performance and stability across the study sites. Generally, G16 (MM98/3567) was the highest yielding genotype because it was located closer to the (AEC) while G4 (MM06/0046) was the lowest yielding genotypes because it was located further away from (AEC). G9 (MM06/0138), G14 (MM96/9308), G15 (MM97/0293), G16 (MM98/3567) and G5 (MM06/0074) are high yielding and stable depicted by shortest projection of genotype vectors from the AEC axis and having less than 0.2 values along the Y-axis. G12 (MM96/2480), G10 (MM06/0139) and G3 (MM06/0013) were also closer to zero-line value on the Y-axis, had positive values above zero on X-axis and hence were considered as high yielding with average stability. G13 (MM96/4271) was stable but below average in yield. G1 (MH95/0183), G8 (MM06/0131), G6 (MM06/0082) and G4 (MM96/9308) are low yielding and unstable depicted by longest projections of genotypes vectors from AEC axis (Figure 2).
Figure 2: Mean performance and stability of 16 cassava genotypes (G1-G16) at five environments (K: Kakamega, S: Sangalo, A: Alupe, B: Kibos, M: Migori) for fresh root yield.

The polygon view of the GGE biplot explicitly displays the "which won where pattern" and hence is a concise summary of the GEI pattern (Figures 3 and 4). The polygon is formed by connecting the markers of the genotypes that are further away from the biplot origin such that all the genotypes are contained in the polygon (Yan et al., 2007; Akinwale, 2011). Convex-hull are drawn from the biplot origin which divides the biplot into sectors that demarcate mega-environment the vertex genotypes in a sector of environment are considered the most stable for that environment. In Figure 3, the "which won where" pattern of the GGE biplot on number of storage roots grouped all the environments in one sector. Moreover, the genotypes clustered around the origin of the biplot revealing that the genotypes had the same response across the environments. Generally, the GGE biplot on number of storage roots accounted for 95.74% of the total GEI variation due to GEI effects on number of storage roots with PC1 and PC2 accounting for 87.52% and 8.22%, respectively.

In Figure 4, the "which won where" pattern of the GGE biplot on fresh root yield explained 77.15% of the total variation due to GEI effects, PC1 accounted for 51.7% while PC2 accounted for 25.45%. The biplot revealed the best genotypes across environments and identified the best clones with respect to site. The seven rays that divide the biplot into seven sectors to which five environments fall into two of them showed that (Alupe, Sangalo and Kibos) environments fall into sector one and the vertex genotypes for this sector was G16 (MM98/3567). Similarly, two environments (Kakamega and Migori) fell into sector two and the vertex genotypes for this sector was G9 (MM06/0131). No environment fell into sectors with G10 (MM06/0131), G4 (MM06/0046), G2 (migyera) and G8 (MM06/0131) as vertices indicating that these cultivars were unstable in all the environments. Genotypes G5 (MM06/0074) and G13 (MM96/4271) were located at the origin of the biplot revealing that they were highly stable clones across the sites.
Another important feature of GGE biplot analysis is its ability to evaluate test environments for effective selection of superior genotypes (Yan et al., 2007). In Figure 5 the discriminatory power of the environments was detected by the length of the vector from the origin of the GGE biplot to the coordinate of the location. The length of the vectors approximates the standard deviation within respective environments which is a measure of the discriminating ability of the environments (Yan, 2005). The longer the vector, the more discriminatory power. Migori environments was the most discriminating but the least representative environment having the long vector length from biplot origin with large absolute PC2 scores and large PC1 scores. Contrarily, Kakamega environment was the least discriminative and the most representative environment based on short vector length from the origin and having large absolute PC2 scores and small PC1 scores. However, Kibos environment was considered as ideal environment for selection of superior clones based on its discriminating ability and representativeness. Noerwijati et al. (2013) identified Kediri environments as ideal for selection of superior cassava genotypes based on the discriminating and representative view of the GGE biplot having small absolute PC2 scores and large PC1 scores. Likewise, Agyeman et al. (2015) identified (PK08) as the ideal environment having a small angle (representativeness) to the average environment axis and a long vector length from the biplot (discriminating ability) in a cassava study using GGE biplot analysis. Generally, if financial limitations allow only few test environments Kibos should be the first choice. Migori environments cannot be used in selecting superior genotypes, but it is useful in ‘culling’ unstable genotypes.

CONCLUSION

Genotype by environment interaction was significant for fresh root yield, plant height, and height at first branching indicating the need of assessing genotypes for stability and adaptability before effective selection can be done. Six genotypes (MM98/3567, MM06/0138, MM96/9308, MM97/0293, MM06/007, and MM96/4271) were classified as stable and outperformed the check cultivar in fresh root yield across five environments of western Kenya. On the other hand, number of storage roots, dry matter content and starch are not influenced by GEI, this implies that evaluation of genotypes for these traits can effectively be done in a single location and variety selection can effectively be done based on the mean performance of genotypes.

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CONFLICT OF INTEREST

There is no conflict of interest for this paper.
REFERENCES


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