



Genotype X Environment Interaction and Yield Performance of 43 Improved Cassava (*Manihot esculenta* Crantz) Genotypes at Three Agro-climatic Zones in Nigeria

M. G. Akinwale^{1&2}, B. O. Akinyele^{1*}, A. C. Odiyi¹ and A. G. O. Dixon²

¹Department of Crop, Soil and Pest Management, Federal University of Technology, Akure, Nigeria.

²International Institute of Tropical Agriculture (IITA), PMB 5320 Ibadan, Oyo State, Nigeria.

Research Article

Received 21st June 2011
Accepted 7th July 2011
Online Ready 18th July 2011

ABSTRACT

Aim: To determine the possible effects of environment and genotypic differences on root yield and other related traits.

Methodology: 43 improved cassava genotypes were evaluated for root yield, root number, root dry matter, cassava mosaic disease and Cassava bacterial disease. The experiments were conducted using a randomized complete-block design with four replications for two years in three representative agro-ecological zones (Mokwa, Ibadan and Onne) in Nigeria. The data collected were subjected to combined analyses of variance using the GLM procedure of Statistical Analysis System (SAS 9.2) to determine the magnitude of the main effects and interactions. GGEbiplot software (GGEbiplot, 2007) was applied for visual examination of the GEI pattern of the data.

Results: Genotype, Location and genotype by environment (GXE) interaction were highly significant for all the traits studied ($P < 0.001$), indicating genetic variability between genotypes by changing environments. The partitioning of GGE through GGE biplot analysis showed that PC1 and PC2 accounted for 61.3% and 28.8% of GGE sum of squares respectively for root yield, explaining a total of 90.1% variation.

Conclusion: Genotypes G4 and G15 were the highest yielding and stable genotypes. G2 and G7 were equally stable but with poor roots yield. G43, which had a mean yield similar to the grand mean, may be regarded as a desirable genotype. Mokwa and Ibadan were

*Corresponding author: Email: yele174@yahoo.co.uk;

found to be the most discriminative and the least representative environments for root yields while Onne environment was found to be the most representative and the least discriminative.

Keywords: Cassava; GXE interaction; GGE-biplot analysis; multilocational trial; genotype;

ABBREVIATIONS

G - Genotype; L - location; Y - year; GEI - Genotype x Environment Interaction; GXL - genotype by location; YL - year by location; PC - Principal Component;

1. INTRODUCTION

Cassava (*Manihot esculenta* Crantz) is a perennial crop, native to tropical America (Olsen and Schaal, 2001). After rice, sugar cane and maize, it ranks fourth as a source of energy in the tropical regions of the world (Akinwale et al., 2010) and is a major source of calories for roughly two out of every five Africans (Nweke et al., 2002). Cassava is Africa's food insurance because it gives stable yields, even in the face of more frequent droughts, low soil fertility, and low intensity management. It can remain in the soil until needed, spreading out the food supply over time, thereby helping families through annual scarcities when seasonal harvests run out and averting the tragic "boom and bust" cycle of oversupply followed by shortage (Dixon et al., 2003). Its production in Nigeria has grown at an annual rate of 4.6% from 1970 to 2006 (FAO 2008), and the crop is now cultivated commercially in large hectares in different parts of the country.

The success of cassava in Africa, as a food security crop, is largely because of its ability and capacity to yield well in drought-prone, marginal wastelands under poor management where other crops would fail. Despite cassava's ability to grow in marginal areas (Mkumbira et al., 2003), large differential genotypic responses occur under varying environmental conditions. This phenomenon is referred to as genotype x environment interactions (GEI), which is a routine occurrence in plant breeding programmes. Recent studies on genotype x environment interactions in some economic crops include the works of Akinyele and Osekita (2011), Sakin et al. (2011), Ngeve et al. (2005) and Kilic et al. (2009). Both the genotype and the environment determine the phenotype of an individual. The effects of these two factors, however, are not always additive because of the interaction between them. The large GEI variation usually impairs the accuracy of yield estimation and reduces the relationship between genotypic and phenotypic values (Ssemakula and Dixon, 2007). GEI, due to different responses of genotypes in diverse environments, makes choosing the superior genotypes difficult in plant breeding programmes. Traditionally, plant breeders tend to select genotypes that show stable performance as defined by minimal GEI effects across a number of locations and/or years. The term stability is sometimes used to characterize a genotype, which shows a relatively constant yield, independent of changing environmental conditions. On the basis of this idea, genotypes with a minimal variance for yield across different environments are considered stable. This study was, therefore, designed to evaluate the influence of genotype (G), environment (E), and G x E interaction on fresh root yield, root number, dry matter content (DM), cassava mosaic disease (CMD) and bacterial blight (CBB)

of 43 cassava genotypes across three major agro-ecological zones of Nigeria, namely Mokwa, Ibadan and Onne.

2. MATERIALS AND METHODS

The study was conducted for two cropping seasons (two years) at three locations in Nigeria. The locations are: Ibadan (Derived savanna), Mokwa (Southern guinea savanna), and Onne (Humid forest). Forty-three cassava genotypes (Table 1) at advanced stages of breeding were used. The experimental design was a randomized complete block design with four replications at each site under rain-fed conditions. Each plot consisted of 36 plants in six (6)-plant rows. The ridges were 1 m apart, 30 cm high and 6 m long. Spacing between plants was 1 m, giving a total plant population of 10 000 plants ha⁻¹. Weeding was done when necessary. Data were collected from the inner 24 plants within a plot. Severity ratings of CMD and CBB were taken at 6 MAP using a scale of 1 - 5 (1 = no symptoms; 5 = severe damage) according to IITA (1990). At harvest (12MAP), data were collected from the inner 24 plants within a plot for fresh root yield, number of roots per plot and dry matter percentage. Dry matter percentages of tuberous roots were determined from a random bulk sample of four plants selected from the inner rows. The roots were peeled and shredded after washing. One hundred grams of fresh root (cortex) was taken in the form of chips and dried at 70°C for 72 h in a forced air oven. The dried samples were then reweighed to obtain the dry weights, and the dry matter percentage was calculated as the ratio of the dry weight over the fresh weight and multiplied by 100.

2.1 Data Analysis

The data were subjected to combined analyses of variance using the GLM procedure of Statistical Analysis System (SAS) to determine the magnitude of the main effects and interactions. The GGE Biplot methodology, which is composed of two concepts, the Biplot concept (Gabriel, 1971) and the GGE concept (Yan et al., 2000), was applied for visual examination of the GEI pattern of data by using GGE-biplot software (GGEbiplot,2009). The GGE biplot shows the first 2 principal components (PC1 and PC2) derived from subjecting environment centered yield data (Yan et al., 2000).

3. RESULTS

The combined analysis of variance across environments (Table 1) showed highly significant ($P < 0.001$) mean squares (MS) for yield and yield related traits and also for disease tolerance for nearly all the sources of variation. Location (L), genotypes (G) and genotype by environment interaction (GEI) showed highly significant MS ($P < 0.001$) for all traits evaluated. The relative magnitude of the main effects and their interactions for root yield as a proportion of the total sum of squares showed that 5.5% of the total yield variation was attributed to location (L), 0.2% to year × location (YL), 29% to G, 22.4% to genotype × location (GL) interaction, and 10.9% to genotype × year (GY) interaction (Table 2). Across locations, the fresh storage root yield varied significantly among the 43 genotypes.

Table 1. Combined analysis of variance showing the reaction of the 43 cassava genotypes to disease, yield and its components in three locations

Source	DF	RTNO	RTWT(kg)	DM	CMDS	CBBS
Year	1	4907.01***	614.42***	123.71***	0.76*	19.35***
Location	2	149722***	1913.12***	3035.75***	72.19***	6.06***
Year X Location	2	2318.12**	85.08**	90.85**	1.39***	12.18***
Replicates/YL	18	1882.82***	311.53***	22.54*	0.37***	0.25*
Genotype	42	6470.91***	484.53***	111.83***	6.71***	2.72***
Genotype X Year	42	2822.62***	186.67***	6.39ns	0.07ns	0.17ns
Genotype X Location	84	2917.09***	191.01***	39.46***	2.39***	0.31***
Genotype X year X Location	84	2833.73***	199.33***	5.43ns	0.06ns	0.14*
Error	751	501.53	41.63	14.31	0.12	0.14
CV%		24.27	21.31	12.39	22.77	15.04
R²		70	68	78	88	67

*, ** and *** = Significant at $P < 0.05$, 0.01 and 0.001 ; ns = not significant

3.1 Fresh Root Yield

The root yield ranged from 21.36 to 39.22kg with a mean of 30.27kg. Genotype 91/02324 had the highest root weight of 39.23kg while, the lowest value of 21.36kg was recorded for genotype 99/6012. Twenty-three genotypes had root yields of more than above the genotype mean (30.27kg) while nineteen genotypes yielded less than the mean. Genotypes 91/02324, 95/0289, 97/4779 and TME 419 constituted the top group in terms of root yield (Table 3).

Table 2. The combined analysis of variance for mean fresh root yield (Kg) in 43 cassava genotypes in three locations in Nigeria in two cropping seasons

Source	DF	Sum of Square	Mean Square	Explained variation (%)
Year	1	614.42	614.42***	0.85
Location	2	3826.24	1913.12***	5.3
Year X Location	2	170.16	85.08**	0.2
Replicates/YL	18	5607.54	311.53***	7.8
Genotype	42	20835.02	484.53***	29
Genotype X Year	42	7840.14	186.67***	10.9
Genotype X Location	84	16044.84	191.01***	22.4
Genotype X year X Location	84	16743.72	199.33***	23.4
Error	751	31270.84	41.63	
CV%			21.31	
R²			68	

** and *** = Significant at $P < 0.01$ and 0.001

3.2 Total Number of Roots

The total number of roots varied significantly among the genotypes and ranged from 63 to 145 with an across-genotype mean of 92 storage roots. Genotype 97/4779 had the highest root number of 145 while the lowest root number of 63 was recorded for genotype 98/0510 (Table 3).

3.3 Root Dry Matter

Analysis of variance showed that dry-matter content varied significantly among the genotypes. It ranged from 24.82 to 36.45%, with a mean of 30.52%. Genotype TME 419 had the highest root dry matter of 36.45% with genotype 97/4779 recording the lowest value of 24.82 % (Table 3).

3.4 Reaction to Cassava Mosaic Disease and Cassava Bacterial Disease

The reaction of the genotypes to CMD across the three locations varied significantly ($P < 0.001$) (Table 1). The reaction ranged from 1 to 2.5, with a mean of 1.5. Genotypes 91/02324, 96/1089A, 96/1565, 96/1569, 96/1632, 97/2205, 97/4763, 97/4779, 98/0505,

99/2123, 99/3073 and M98/0068 did not express any CMD symptoms. 30572 and 99/6012 expressed the most severe symptoms of 2.5. Reaction to CBB was also significantly different among the genotypes. The scores vary from 2.0 to 3.6 with a mean of 2.5. The susceptible genotypes (severity score > 2.5) were 91/02324, 94/0026, 95/0166, 95/0379, 97/4779, 96/0523, 96/1569, 98/2226, 99/3073, 99/6012 and 94/M98/0028. However, no genotype was free from CBB symptoms (Table 3).

Table 3. Mean performance of the 43 cassava genotypes evaluated for root yields and its components in two cropping seasons across three locations

S/N	Genotype	CMDS	RTNO	RTWT	DM	CBBS
1	30572	2.58	89.10	28.34	30.51	2.22
2	4(2)1425	2.65	74.17	29.09	31.80	2.24
3	82/00058	2.43	81.07	27.43	28.10	2.26
4	91/02324	1.00	112.63	39.23	31.01	3.33
5	92/0057	1.58	66.50	28.41	32.63	2.38
6	92/0067	1.67	68.88	24.18	30.97	2.21
7	92/0325	2.25	66.83	22.94	34.30	2.17
8	92/0326	2.33	75.08	30.67	29.57	2.25
9	92B/00061	2.13	80.25	33.37	32.38	2.29
10	92B/00068	1.83	84.50	32.55	29.93	2.25
11	94/0026	1.92	83.21	25.40	27.93	2.67
12	94/0039	1.83	118.92	34.01	30.14	2.50
13	94/0561	2.42	84.67	25.74	27.95	2.58
14	95/0166	2.00	85.25	31.05	29.12	2.67
15	95/0289	1.92	101.67	39.18	30.82	2.29
16	95/0379	1.63	89.29	31.49	28.97	2.63
17	96/0523	1.13	110.33	31.92	28.15	2.79
18	96/0603	1.46	95.83	30.41	29.84	2.42
19	96/1089A	1.00	102.64	33.99	30.47	2.27
20	96/1565	1.00	91.79	28.43	30.15	2.30
21	96/1569	1.00	87.83	30.71	32.70	3.00
22	96/1632	1.00	94.17	34.26	34.84	2.17
23	96/1642	1.33	112.08	26.88	27.87	2.17
24	97/0162	1.21	89.67	30.37	32.11	2.58
25	97/0211	1.09	80.23	22.13	30.62	3.17
26	97/2205	1.00	100.25	31.45	33.97	2.17
27	97/3200	1.21	89.88	32.93	26.94	2.58
28	97/4763	1.00	128.88	33.39	32.54	2.46
29	97/4769	1.58	94.67	30.17	29.15	2.54
30	97/4779	1.00	145.67	39.13	24.82	2.79
31	98/0002	1.04	98.17	34.87	31.02	2.29
32	98/0505	1.00	96.08	33.83	32.87	2.21
33	98/0510	1.38	63.21	30.03	31.66	2.38

34	98/0581	1.04	97.67	34.39	31.52	2.33
35	98/2101	1.25	85.92	22.88	29.15	2.50
36	98/2226	1.38	108.25	27.66	28.68	3.04
37	99/2123	1.00	95.17	22.43	30.20	2.58
38	99/3073	1.00	94.04	31.59	31.24	2.83
39	99/6012	2.54	74.58	21.36	26.73	3.63
40	M98/0028	1.45	90.91	26.39	30.96	2.64
41	M98/0040	1.04	85.58	31.10	29.36	2.46
42	M98/0068	1.00	95.63	29.27	32.92	2.21
43	TME419	1.50	88.96	36.97	36.45	2.04
Means		1.50	92.00	30.27	30.52	2.50
Cv		22.77	24.27	21.31	12.39	15.04
R²		88	70	68	78	67

CMDS, cassava mosaic disease severity; *CBBS*, cassava bacterial blight severity; *RTNO*, root; number; *RTWT*, root weight; *DM*, dry matter.

The partitioning of GGE through GGE biplot analysis showed that PC1 and PC2 accounted for 61.3% and 28.8% of GGE sum of squares respectively for root yield, explaining a total of 90.1% variation (Figure 2). A GGE-biplot based on genotype-focused scaling (Figure 1) was depicted in order to detect the locations of the genotypes. Genotypes that had PC1 scores >0 were identified as higher yielding and those that had PC1 scores <0 were identified as lower yielding (Figure 1 and Table 2). PC1 scores >0 detected the genotypes of interest (i.e. adaptable or higher yielding), while PC1 scores <0 discriminated the non-adaptable ones. Unlike the PC1, PC2, which was related to genotypic stability or instability, divided the genotypes of interest into 2 groups based on their scores. Group 1 consisted of 17 stable genotypes (G4, G14, G16, G32, G34, G29, G27, G9, G8, G26, G19, G43, G31, G12, G38, G24 and G41) that were higher yielding, since near-zero PC2 scores showed genotypic stability. As for Group 2, it consisted of 7 unstable genotypes (G30, G21, G22, G17, G15, G28, and G10) that were higher yielding, as absolute larger PC2 scores were associated with genotypic instability.

The GGE biplot (Figure 2) depicts the cultivars that had the best performance in each environment. The convex-hull drawn from the biplot origin gave 7 sectors with G15, G25, G30, G33, G37 and G39 as the vertex cultivars. G30 was the vertex and the winning genotype in mokwa. G15 was the winner in the second mega-environment (Mokwa and Ibadan), meaning that these cultivars are the best in these environments. No environment fell into sectors with G25, G33, G37 and G39 as the vertices, indicating that these cultivars were not the best in any environment.

Figure 3 shows the average environment coordinate (AEC) view of the GGE biplot based on the genotype focused scaling, showing the mean yield and stability of 43 genotypes in 3 environments. The AEA (the single-arrowed line) points to higher average yield. The double-arrowed line is the AEC ordinate; it points to greater variability (smaller stability) in either direction. Genotypes G4 and G15 were the highest yielding and stable genotypes; and G2 and G7 were equally stable but with poor roots yield. G30, though high yielding, was highly unstable while G33 was low yielding and unstable.

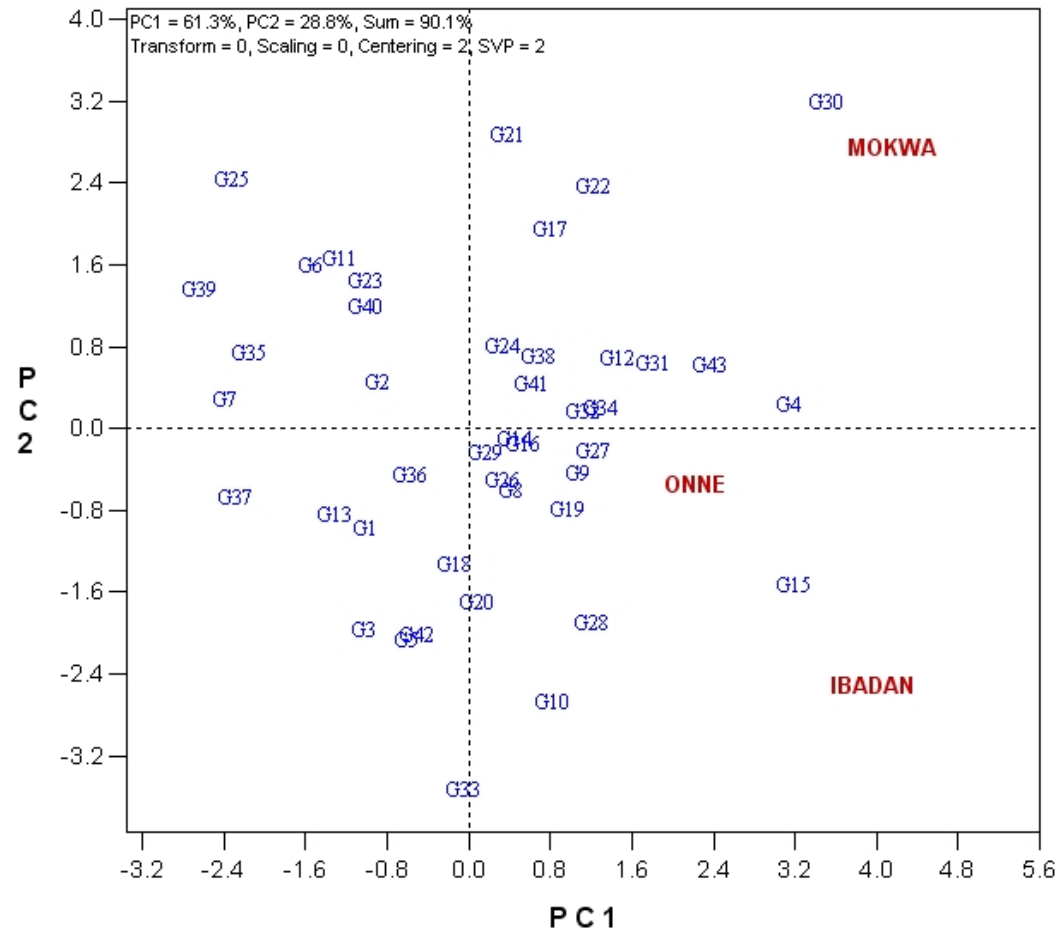


Fig 1. GGE biplot showing distribution of genotypes and environments.

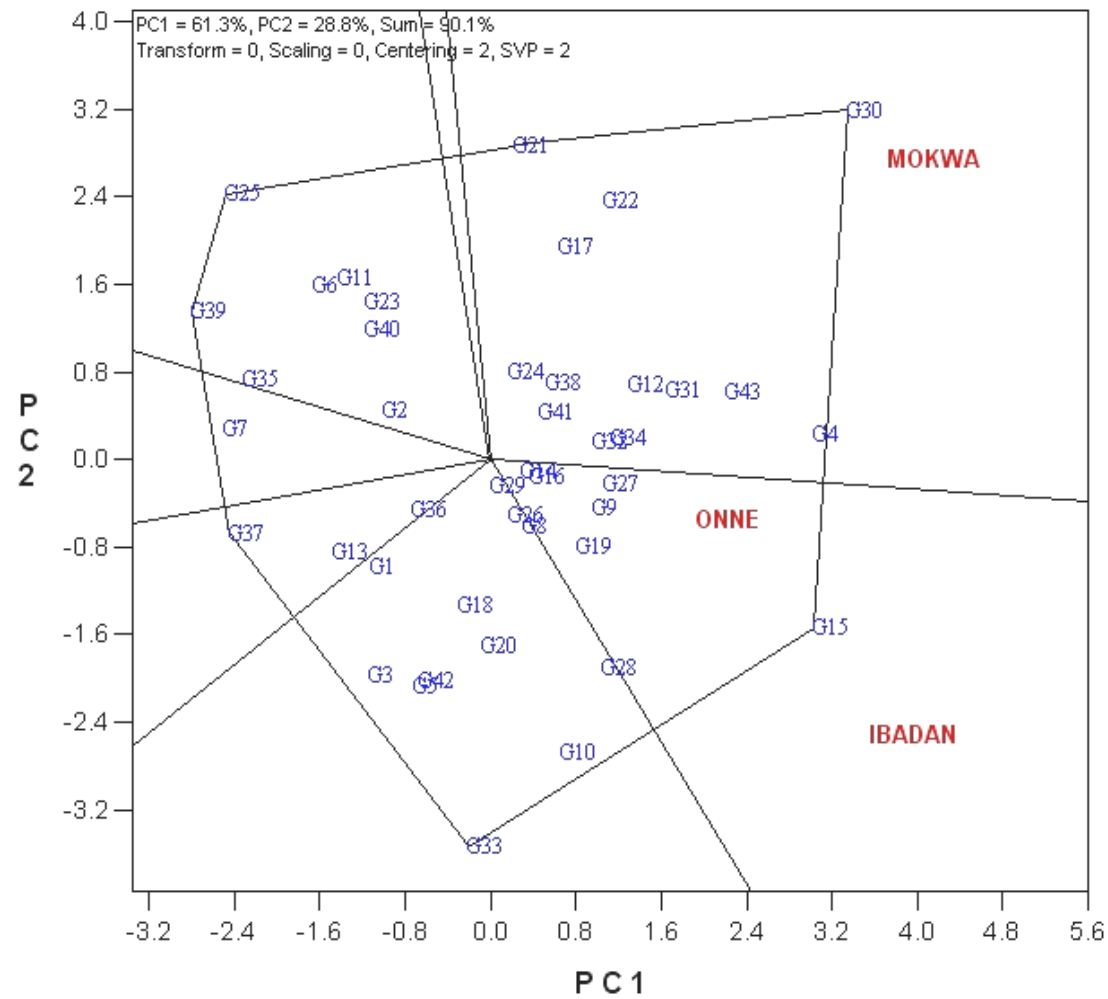


Fig. 2. GGE biplot for best genotypes in different environments

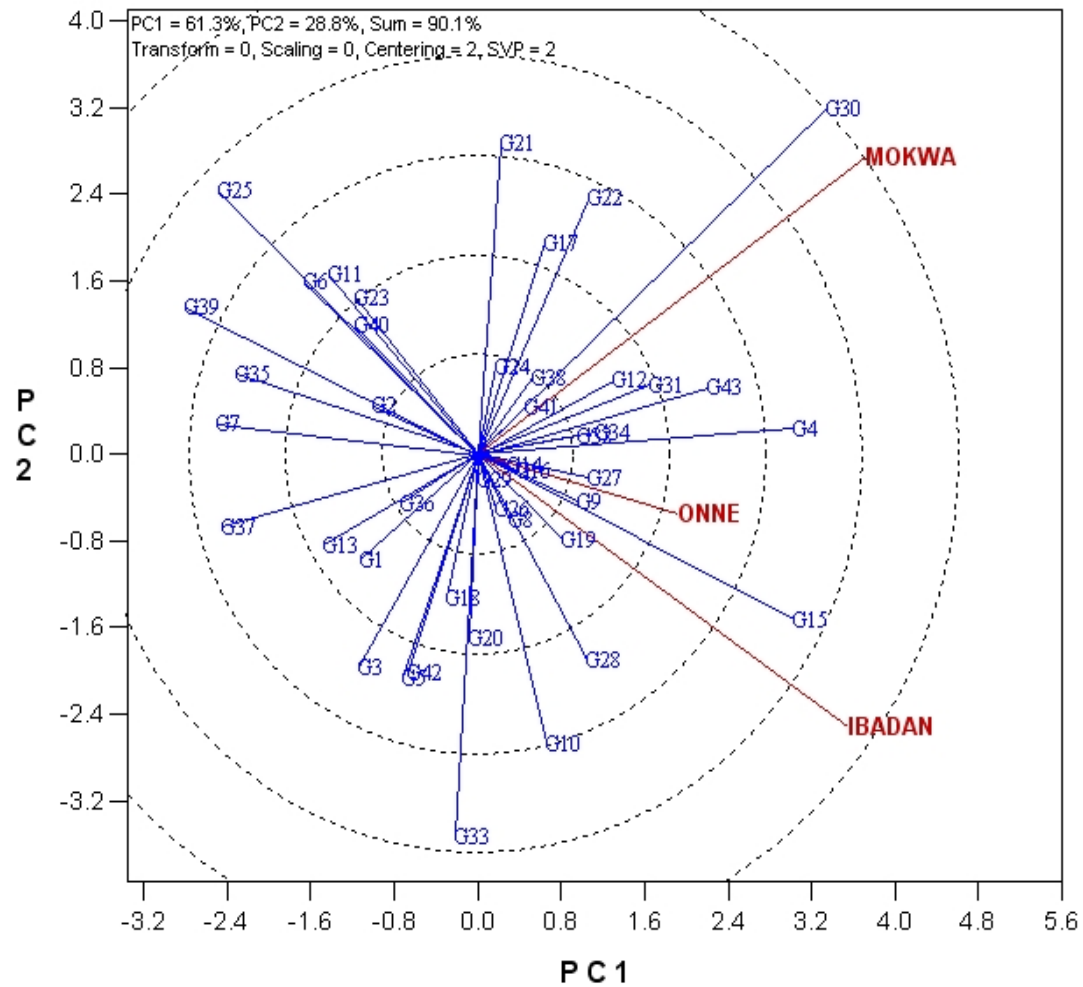


Fig. 3. The GGE biplot showing the performance of each genotype in each environment

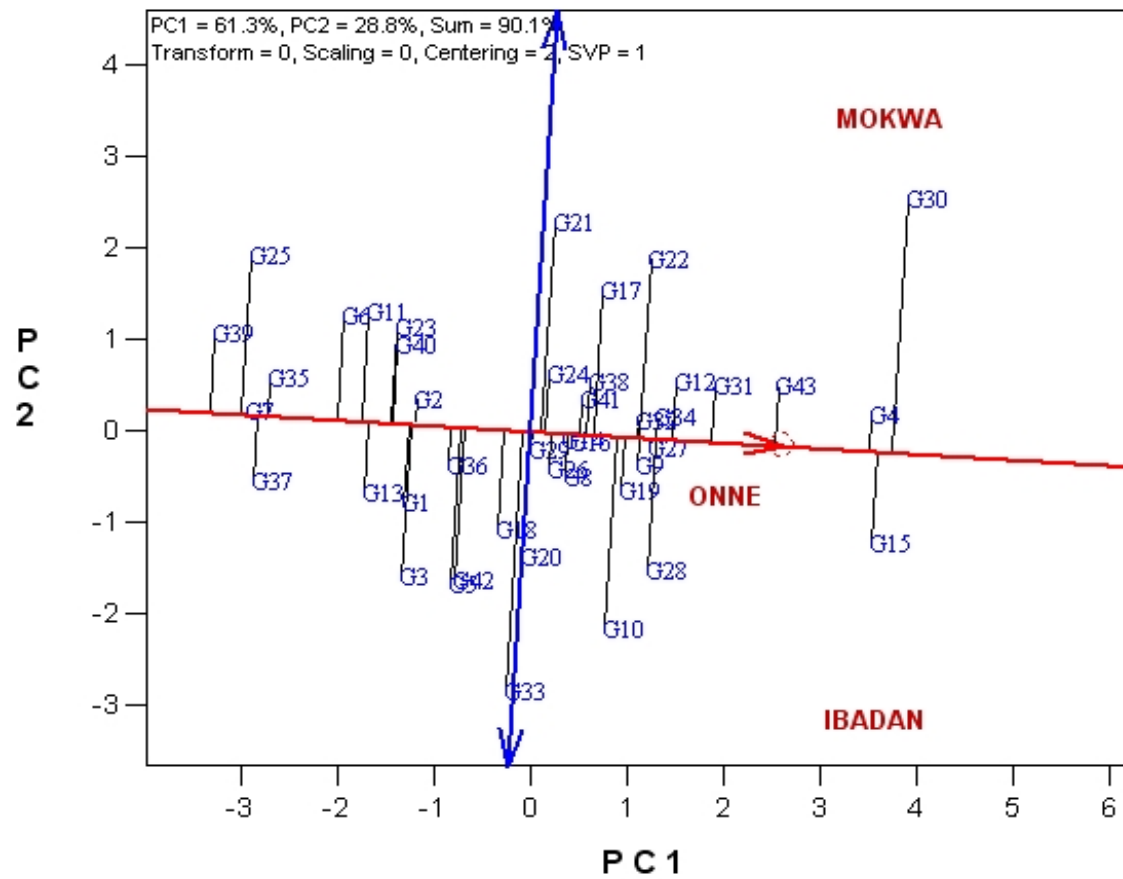


Fig. 4. The GGEbiplot showing mean performance and stability of 43 cassava genotypes

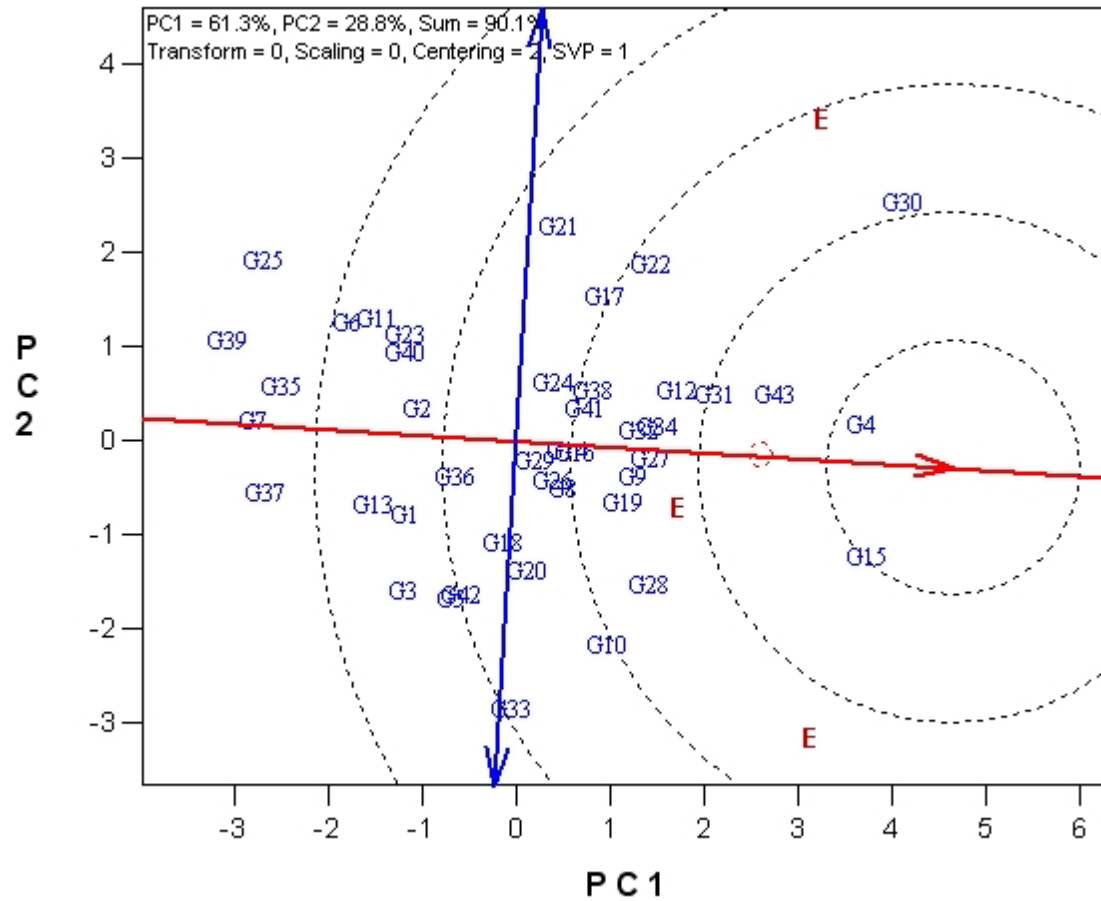


Fig. 5. The average-environment coordination (AEC) view to rank genotypes relative to an ideal genotype (the center of the concentric circles)

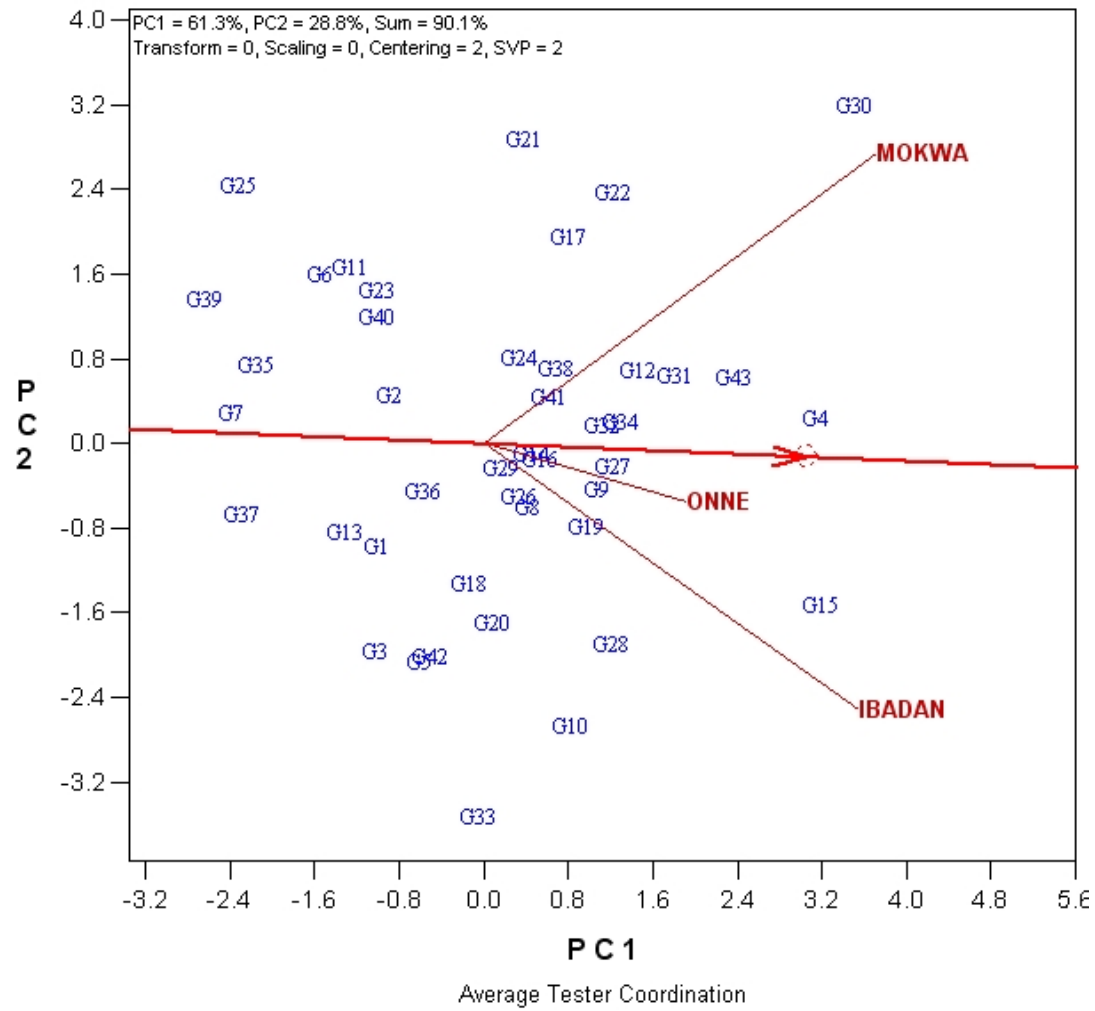


Fig. 6. GGEbiplot for representativeness and discriminating ability of environments

4. DISCUSSION

The combined analysis of variance across environments (Table 1) showed highly significant ($P < 0.001$) mean squares (MS) for yield, yield related traits, cassava mosaic disease and cassava bacterial disease. Effects from Genotype and location that showed highly significant MS reflected genotypic differences towards adaptation to different environments, suggest that genotypes may be selected for adaptation to specific environments. Aina et al. (2009) observed similar result when he evaluated eighteen cassava genotypes across four locations in Nigeria.

The high variability observed among cultivars as indicated by the range of their mean performance, indicates the presence of sufficient genetic variability for the traits studied. The significant interaction between genotype and environment (G×E) for all the traits indicates that there is the need for multilocational testing to identify good performers for specific locations. The significance of year effects also suggests the need to evaluate for more than one year for reliable inferences to be made on performance (Ssemakula and Dixon, 2007).

The GGEbiplot enabled visual comparison of the locations and genotypes studied and their interrelationships. The partitioning of GGE through GGEbiplot analysis showed that PC1 and PC2 accounted for 61.3% and 28.8% of GGE sum of squares respectively, explaining a total of 90.1% variation. This result revealed that there was a differential yield performance among cassava genotypes across testing environments which was due to the presence of GEI. This is in conformity with the findings of Egesi et al. (2007).

4.1 Suitability of Genotypes for Particular Environment Using the “Which-One-Where” Function of a GGEbiplot

Visualization of the which-won-where pattern of GGEbiplot is important for studying the possible existence of different mega-environments in Nigeria. The polygon view of a GGEbiplot explicitly displays the which-won-where pattern, and hence is a succinct summary of the GEI pattern (Figure 2). The polygon is formed by connecting the markers of the genotypes that are further away from the biplot origin such that all other genotypes are contained in the polygon (Yan et al., 2000, 2001). The 7 rays that divide the biplot into 7 sectors to which the three environments fall into 2 of them (Figure 2) showed that Mokwa environment fell into sector 1 and the vertex genotypes for this sector was G30, higher-yielding genotype. Similarly, 2 environments, Onne and Ibadan environments fell into sector 2 and the vertex genotype for this sector was G15, suggesting that the higher-yielding genotype for these 2 environments was G15. No environment fell into sectors with G25, G33, G37 and G39 as the vertices, indicating that these cultivars were not the best in any environment.

4.2 Choice of Genotypes

An ideal genotype should have the highest mean performance and be absolutely stable (i.e. perform the best in all environments). Such an ideal genotype is defined by having the greatest vector length of the high yielding genotypes and with zero GEI as represented by an arrow pointing to it (Figure 5). Although such an ideal genotype may not exist in reality, it can be used as a reference for genotype evaluation. A genotype is more desirable if it is located closer to the ideal genotype. The cosine of the angle between the vectors of two genotypes also measures their similarity or dissimilarity in response to their interaction with the

environments (Yan and Tinker, 2006). Using the ideal genotype as the center, concentric circles were drawn to help visualize the distance between each genotype and the ideal genotype. Figure 5 revealed that G4, which fell into the center of concentric circles, was the ideal genotype in terms of higher yielding ability and stability compared with the rest of the genotypes. In addition, G15, G43 and G31, located on the next concentric circle, may be regarded as desirable genotypes.

4.3 Mean Performance and Stability of Genotypes

Genotypes should be evaluated based on both mean performance and stability across environments (Yan and Rajcan, 2002). The single-arrowed line is the AEA which points to higher mean yield across environments (Figure 4) showed that G30 had the highest mean yield, followed by G15 and then, G4. G43 had a mean yield similar to the grand mean while G39 had the lowest mean yield. The double-arrowed line is the AEC ordinate; it points to greater variability (poorer stability) in either direction (Yan and Tinker 2006). Thus, Genotypes G4 and G15 were the highest yielding and stable genotypes while G2 and G7 were equally stable but with poor roots yield. G30, though high yielding, was highly unstable while G25 was low yielding and unstable.

4.4 Discriminating Ability and Representativeness of Test Environments

Discriminating power and representativeness view of the GGE- biplot are an important measure of testing environment (Dehghani et. al., 2006). In this study, the GGE biplot explained 90.1% of the G plus GE data (Figure 6) suggesting that the angles between the vectors of the environments are good indicators of correlation amongst the environments. For instance, the Mokwa environment was positively correlated to Onne and Ibadan. The cosine of angles between vectors of Mokwa, Onne and Ibadan were less than 90. This means that there were no negative correlations among test environments. Also in biplot analysis, the lines that connect the test environments to the biplot origin are called environment vectors. The length of the vectors approximates the standard deviation within the respective environments, which is a measure of the discriminating ability of the environments (Yan, 2005). Generally in this study, Mokwa environment had the longest vector and therefore the best (most discriminative) and the least representative environment while Onne location was the most representative and least discriminating environment. Onne environment which was averagely discriminating and most representative environment therefore can be used for genotypes with wide adaptation. The non-representative environments such as Mokwa and Ibadan are useful for selecting specifically adapted genotypes.

5. CONCLUSION

The biplots displayed pattern of variability of the genotypes, the locations, and their interactions. Interrelationships among agronomic characteristics allowed identification of optimal genotypes for the three locations. G4, G43 and G15 were the best genotypes based on mean performance and stability. Mokwa and Ibadan were the most discriminating and least representative locations while Onne environment was the most representative and the least discriminating environment. The high yielding genotypes with good agronomic attributes have potential to increase cassava productivity in Nigeria.

REFERENCES

- Aina, O.O., Dixon, A.G.O., Paul, I., Akinrinde, E.A. (2009). G×E interaction effects on yield and yield components of Cassava (landraces and improved) genotypes in the Savanna Regions of Nigeria. *Afr. J. Biotechnol.*, 8(19), 4933-4945.
- Akinwale, M.G., Akinyele, B.O., Dixon, A.G.O., Odiyi, A.C. (2010). Genetic variability among forty-three cassava genotypes in three agro-ecological zones of Nigeria. *J. Plant Breed. Crop Sci.*, 2(5), 104-109.
- Akinyele, B.O., Osekita, O.S. (2011). Genotype x Environment Interaction in NH47-4 Variety of Okra – *Abelmoschus esculentus* (Linn.) Moench. *Int. J. Gene. Mol. Biol.*, 3(4), 55-59.
- Dehghani, H., Ebadi, A., Yousefi, A. (2006). Biplot analysis of Genotype x Environment interaction for barley yield in Iran. *Agron. J.*, 98, 388-393.
- Dixon, A. G. O., Bandyopadhyay, R., Coyne, D., Ferguson, M., Ferris, S. B., Hanna, R., Hughes, J.d'A., Ingelbrecht, I., Legg, J., Mahungu, N., Manyong, V., Mowbray, D., Neuenschwander, P., Whyte, J., Hartmann, P., Ortiz, R. (2003). Cassava: From Poor Farmers' Crop to Pacesetter of African Rural Development. *Chron. Hortic.*, 43, 8–15.
- Egesi, C.N., Ilona' P., Ogbe, F.O., Akoroda, D.A. (2007). Genetic Variation and Genotype x Environment Interaction for Yield and Other Agronomic Traits in Cassava in Nigeria. *Soil Sci. J. Am.*, 99(4), 1137-1142.
- FAO. (2008). 9 Feb 2008; 2009 version verified 30 July 2009. FAO, Rome.
- Gabriel, K.R. (1971). The Biplot Graphic Display of Matrices with Application to Principal Component Analysis. *Biometrika*, 58, 453- 467.
- GGE-biplot (2009). GGE-biplot software version 5.2. The Complete Biplot Analysis System: GGEbiplot Pattern Explorer. Copy Right Weikai Yan, 2001-2009, USA.
- IITA. (1990). Cassava in Tropical Africa: A Reference Manual Int. Inst of Tropical Agriculture, Ibadan, Nigeria.
- Kilic, H., Sagir, A., Bayram, Y. (2009). Estimates of Genotype x Environment Interactions and Heritability of Black Point in Durum Wheat. *Not. Sci. Biol.*, 1(1), 92-96.
- Mkumbira, J., Mahungu, N. M., Gullberg, U.(2003). Grouping locations for Efficient Cassava Evaluation in Malawi. *Exp. Agric.*, 39, 167–179.
- Ngeve, J.M., Dixon, A.G.O., Nukenine, E.N. (2005). The Influence of Host Genotype x Environment Interactions on the Response of Cassava Anthracnose Disease in Diverse Agro-ecologies in Nigeria. *Afr. Crop Sci. J.*, 13(1), 1-11.
- Nweke, F., Spencer. D.S.C., Lynam, J.K. (2002). The Cassava Transformation, Africa's best kept secret. Michigan State University press, East Lansing, Michigan, USA. p. 273. Shaffi B, Mahler KA, Price WJ, Auld DL.
- Olsen, K.M., Schaal, B.A. (2001). DNA Sequence Data and Inferences on Cassava's Origin of Domestication. In *Genetics and Plant Domestication*. The Hague Mouton Publishers, Piperno, DR 1995. pp. 123-133.
- Sakin, M. A., Akincl, C., Duzdemir, O., Donmez, E. (2011). Assessment of Genotype x Environment Interaction on Yield and Yield Components of Durum Wheat Genotypes by Multivariate Analyses. *Afr. J. Biotechnol.*, 10(15), 2875-2885.
- Ssemakula, G., Dixon, A. (2007). Genotype X Environment Interaction, Stability and Agronomic Performance of Carotenoid-rich Cassava Clones *Sci. Res. Essay*, 2 (9), 390-399.
- Yan, W., Hunt, L.A., Sheng, Q., Szlavnic, Z. (2000). Cultivar Evaluation and Mega-environment Investigation based on the GGE Biplot. *Crop Sci.*, 40, 597–605.
- Yan, W., Cornelius, P. L., Crossa, J., Hunt, L.A. (2001). Two types of GGE Biplots for Analyzing Multi-environment Trial Data. *Crop Sci.*, 41, 656-663.

- Yan, W., Rajcan, I. (2002). Biplot Analysis of Test Sites and Trait Relations of Soybean in Ontario. *Crop Sci.*, 42, 11-20.
- Yan, W. (2005). Use of Biplot Analysis in Crop Breeding. Proceedings of the Eastern Wheat Workers and Southern Small Grain Workers Conference, May 9-12, 2005. Bowling Green, KY. pp. 7-30.
- Yan, W., Tinker, N.A. (2006). Biplot Analysis of Multi-environment Trial Data: Principles and Applications. *Can. J. Plant Sci.*, 86, 623-645.

© 2011 Akinwale et al.; This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/3.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.