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An evaluation on cassava genotypes developed from bi-parental crosses involving cassava landraces

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Genetic enhancement of cassava aimed at increasing productivity through the provision of broad-based which improved germplasm and is also a major goal for cassava breeders. 10 genotypes (4 landraces and 6 developed lines) were evaluated at Fumesua, Ejura and Pokuase in 2 growing seasons in a randomized complete block design in 3 replicates to determine variability among genotypes for fresh root yield (FRY), root number (RTN), plant stands harvested (PSH), top weight (TW), harvest index (HI) and dry matter content (DMC) and their adaptation to different environments. Genotype main effect was significant ($P < 0.001$) for all the traits, GEI effect was significant ($P < 0.001$) for DMC, ($P < 0.01$) for TW and HI ($P < 0.05$). Environment main effect was significant ($P < 0.001$) for FRY, RTN and TW. The most stable and high yielding genotype for dry matter content was LA07/012. Genotypes AW07/001 and AW07/015 were adjudged as the most productive genotypes in terms of FRY, DMC, HI and stability. The high genotype and low environmental effects, and the relatively low interaction on DMC imply that evaluation and selection can be effectively done in fewer environments to select clones with high performance while FRY requires multiple environments to identify clones with broad and specific adaptation. The partitioning of GGE through GGE biplot analysis showed that PC1 and PC2 accounted for 84.1 and 9.2% of GGE sum of squares respectively for dry matter content, explaining a total of 93.3% variation. Fum-2, Eju-2 and Pok-2 were the most discriminating and least representative environments while Fum-1 and Ejua-1 environments were the most representative environments.

Key words: Cassava, additive main effects and multiplicative interactions (AMMI), genotype by environment interaction (GGE) biplot, dry matter content.

INTRODUCTION

Cassava is an important crop in Africa where it serves as a famine reserve crop, rural and urban food staple,

industrial raw material and livestock feed (Nweke et al., 2002). About 70 million people derive more than 500 cal/

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day from food based on its roots (Chavez et al., 2005). Breeding efforts are focusing on the improvement on storage root yield potential and storage root quality traits through development of many new cassava genotypes. One major way of realizing this objective is by harnessing valuable genetic resources including landraces that could constitute useful genetic materials for variety development. The maintenance and conservation of local germplasm is therefore, crucial in cassava improvement (Aina et al., 2009). A number of Africa's cassava landraces have been reported to possess useful agronomic and food quality characteristics that could be potentially utilized for further quality and productivity improvement (Raji, 2004). Despite this, the use of African genetic resources for cassava improvement has been very limited compared to breeding initiatives in Latin America and Asia where cassava genetic resources have been highly introgressed into elite gene pools.

Genetic resources have been widely explored globally in the improvement of crops. Landraces of white lupin have been identified as important source of alleles for shortening the vegetative period, reducing plant height, as well as improving yield components (Raza and Msgsrd, 2005). Rubio et al. (2004) observed wide variation among landraces for trait phenology, plant structure, and yield characters, indicating the possibility of improving yield components and increasing yield among locally adapted landraces of lupins. Evidence of drought tolerance has also been identified among landraces of chickpea (Kashiwagi et al., 2005). The findings of Brocke et al. (2003) also confirmed higher variations within landraces populations' of pearl millet than for other populations. Sharma et al. (2000) discovered that traditional landraces of durum wheat were low yielding but generally stable and suggested the need to enhance landraces cultivation with modern varieties to improve competitiveness in yield. Landraces were useful in the incorporation of diseases and pests resistant genes into *Musa* sp. in International Institute of Tropical Agriculture (IITA) (Herzberg et al., 2004). The improved new rice for Africa rice (NERICA) was as a result of crosses between the African landrace *Oryza glaberrima* and the Asian rice *Oryza sativa*, which produced combined positive characters of high grain yield and resistance to pests and diseases (Futakuchi et al., 2003). Selection rapidly advances crop breeding. However, the advancement in crop improvement will depend on the nature and the extent of heritable variations in the populations and the trait of interest (Sapey et al., 2015). Information on genetic variability can be positively explored to enhance genetic gains through the efficient selection of parents for breeding activities. Genetic dissection based on the efficient partitioning of the overall trait variability into its heritable and non-heritable components with the use of suitable genetic parameters such as genotypic coefficient of variation, heritability estimates, genetic advance and phenotypic

variances will be crucial in genetic improvement of productivity traits in cassava. Studies have revealed strong and significant genotype \times environment interaction ($G \times E$) effect for storage root yield in cassava (Kvitschal et al., 2007). The magnitude and dimension of environmental effect may vary from genotype to genotype, thus, necessitating the need to assess $G \times E$ interaction for genotypes under evaluation for selection (Okoye et al., 2008). In developing superior materials for commercial use, assessment and selection of cultivars with higher yield and stability is very important (Carneiro, 1998). Stable yields play a major role in developing countries, where small-scale farmers, particularly those cultivating in marginal areas, are working towards risk-minimization (Adugna and Labuschagne, 2002).

The objective of this study was to evaluate six cassava genotypes developed from bi-parental crosses involving cassava landraces to explore heterosis for fresh root yield and yield related characters as well as wider adaptation to environments.

MATERIALS AND METHODS

Ten cassava genotypes at advanced yield stage were used for the study (Table 1). The evaluation was conducted in two planting seasons (2012/2013 and 2013/2014) at Fumesua (forest ecozone), Pokuase (coastal savanna) and Ejura (transition ecozone). The soil characteristics for the trial sites were Fumesua (Asuasi series, a ferric Acrisol with sandy loam top soil over sandy clay), Pokuase (Adam series, sandy loam) and Ejura (Amantin series, chronoxisols with sandy loam top soil). The genotypes were grown under rain fed conditions in a randomized complete block design with 3 replicates. Neither pesticides nor fertilizers were applied, and planting was done using disease-free stakes planted in four rows per genotype at seven plants per row making a plot size of 28 m². Weeding was done as deemed necessary. Data were collected from the 10 plants in the two middle rows for every genotype. Cassava mosaic disease severity were done at one, three and six months after planting (MAP) using a scoring scale of 1 to 5 (1 = no symptoms; 5 = severe symptoms) (IITA, 1990). At harvest (12 MAP), data were collected on fresh storage root yield, storage root number and top weight. Dry matter content of tuberous roots was determined from a random bulk sample of four plants selected from the inner rows. The roots were peeled and shredded after washing. A sample of 100 g of fresh root 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 content was calculated as the ratio of the dry weight over the fresh weight expressed in percentage. Storage roots were uprooted by carefully removing the top soil, and the roots were then pulled out and counted as number of roots per plot. Harvest index was calculated as the ratio of the fresh storage root weight over total plant weight. The number of plant stands harvested per plot was counted as stands harvested.

Statistical analysis

Data were subjected to combined analysis of variance using GenStat 17.0. The AMMIs statistical model (MATMODEL 2.0 (Gauch, 1993) was used to analyze the yield data to obtain mean estimates. The E and $G \times E$ interaction biplot analysis for windows application 7.9 (Yan, 2012) was used to generate the E and $G \times E$

Table 1. Description of the planting materials for the study.

Genotype	Status	Source
AW07/015 (Agric × Wenchi alata)	F ₁	CRI
AW07/001(Agric × Wenchi alata)	F ₁	CRI
DD07/001(Debor × dabodabo)	F ₁	CRI
DL107/015 (Debor × Lagos)	F ₁	CRI
DL107/009 (Debor × Lagos)	F ₁	CRI
LA07/012 (Lagos × Agric)	F ₁	CRI
Agric	Landrace	farmer
Debor	Landrace	farmer
Lagos	Landrace	farmer
Wenchi Alata	Landrace	farmer

CRI, Crops Research Institute.

Table 2. Mean performance of 10 cassava genotypes across six environments (three locations in two years).

Genotypes	HI	RTN	FRY	STD	TW	DMC
AW07/015	0.52	51.28	26.31	7.50	23.23	30.61
Agric	0.47	51.83	24.56	8.28	28.48	30.34
AW07/001	0.57	49.83	29.27	8.28	21.86	30.99
DD07/001	0.40	33.28	16.42	7.39	22.54	30.54
Debor	0.47	57.39	24.59	9.39	29.19	31.39
DL107/015	0.30	34.83	13.97	6.39	29.41	24.57
DL107/009	0.47	51.28	20.39	6.39	22.16	27.44
LA07/012	0.41	29.72	9.27	5.80	12.51	35.74
Lagos	0.46	49.28	23.35	7.50	26.98	24.88
Wenchi alata	0.39	35.11	17.27	7.39	25.09	26.35
Grand mean	0.45	44.28	20.54	7.43	24.14	29.31
S.e.d	0.07	10.20	5.33	1.20	7.05	1.37
CV%	18.1	28.1	31.80	19.80	35.80	5.7

HI= harvest index, RTN= number of root, FRY= fresh storage root yield, STD= stands harvested and TW= top weight.

interaction biplot used to analyze the multi-environment trial (MET) data. The model used for the E and G × E interaction biplot analysis was the no-scaling and tester-centered model. Traits component and magnitude of variation responsiveness to selection was calculated based on Okwuagwu et al. (2008). Expected genetic advance of the mean for each trait was calculated according to Allard (1960).

RESULTS

Annual rainfall for the environments during the trial period was Fumesua (1605 mm), Pokuase (1250 mm) and Ejura (1350 mm). Mean performance of the 10 cassava genotypes (combined analysis) in three locations and two years are given as shown in Table 2. Fresh root yield (FRY) ranged from 9.27 to 29.27 t/ha with a mean of 20.54 t/ha. Dry matter content (DMC) ranged from 24.99 to 35.74% with a mean of 29.31%. F₁ genotype AW07/001 (29.27 t/ha and 0.57) had both the highest

FRY and harvest index (HI) respectively across location and over years; followed by AA07/015 (26.31 t/ha and 0.52) and LA07/012 (9.27 t/ha) recorded the lowest FRY but DL107/015 (0.30) had the lowest HI. The highest FRY and HI were recorded in Ejura -2012/2013 (34.27 t/ha, 51) and the lowest in Pokuase- 2012/2014 (7.43 t/ha, 0.38). AW07/001 and AW07/015 performed better than their parents and also the average of their parents in terms of FRY and HI. LA07/012 (f₁) recorded the highest DMC (32.74 %) with the least recorded by Lagos. There were highly significant positive correlations between HI and FRY, root number (RTN) and FRY, RTN and stands harvested (STD), FRY and STD, FRY and top weight (TW) and RTN and TW and DMC and HI (Table 3). Genotype (G), location (L), year (Y) and environment × year interaction showed high significant mean square (P <0.001) for FRY (Table 4). G × L × Y showed significant differences for the FRY. Genotype, Genotype × Location

Table 3. Phenotypic correlation coefficients for five traits measured on 10 cassava genotypes across six environments.

Trait	HI	RTN	FRY	STD	TW	DMC
HI	-					
RTN	0.21**	-				
FRY	0.53***	0.57***	-			
STD	-0.03 ^{ns}	0.63***	0.30***	-		
TW	-0.24**	0.58***	0.60***	0.35***	-	
DMC	0.25***	0.06 ^{ns}	0.02 ^{ns}	0.12 ^{ns}	-0.17*	-

*** Significant at $P < 0.001$, ** significant at $P < 0.01$, * significant at $P < 0.05$ and ns= non-significant.

Table 4. Combined analyses of 10 cassava genotypes evaluated for two years at three locations in Ghana for root yield, harvest index, stands harvested, top weight, dry matter content and root number.

Source	df	Mean square	% of total ss
Harvest index			
Genotype (G)	9	0.10***	30.24
Location (L)	2	0.02*	1.37
Year (Y)	1	0.55***	18.90
G × L	18	0.01*	7.22
G × Y	9	0.01 ^{ns}	3.78
L × Y	2	0.02*	1.37
G × L × Y	18	0.01**	8.59
Error	118		
Total	179		
Root number			
Genotype (G)	9	1777.7***	22.12
Location (L)	2	2442.3***	6.75
Year (Y)	1	140.4 ^{ns}	0.19
G × L	18	170.2 ^{ns}	4.24
G × Y	9	456.0**	5.67
L × Y	2	10608.6***	29.33
G × L × Y	18	241.2 ^{ns}	6.00
Error	118	156.0	
Total	179		
Stands harvested			
Genotype (G)	9	20.26***	23.13
Location (L)	2	8.22*	2.09
Year (Y)	1	30.99***	3.93
G × L	18	3.27 ^{ns}	7.46
G × Y	9	8.37***	9.56
L × Y	2	49.50***	12.56
G × L × Y	18	4.59**	10.46
Error	117	2.17	
Total	178		
Fresh root yield			
Genotype (G)	9	696.01***	23.66
Location (L)	2	1950.63***	14.73
Year (Y)	1	3508.60***	13.25

Table 4. Contd.

G × L	18	63.23 ^{ns}	4.30
G × Y	9	88.68*	3.01
L × Y	2	1966.87***	14.86
G × L × Y	18	103.44**	7.03
Error	118	42.68	
Total	179		
Top weight			
Genotype (G)	9	457.81***	13.98
Location (L)	2	2192.89***	14.89
Year (Y)	1	12.67 ^{ns}	0.04
G × L	18	176.73**	10.80
G × Y	9	56.38 ^{ns}	1.72
L × Y	2	3561.23***	24.17
G × L × Y	18	71.72 ^{ns}	4.38
Error	117	74.63	
Total	178		
Dry matter content			
Genotype	9	215.02***	72.01
Location	2	4.24 ^{ns}	0.31
Year	1	6.88 ^{ns}	0.26
G × L	18	7.87***	5.27
G × Y	9	22.46***	7.52
L × Y	2	7.63 ^{ns}	0.57
G × L × Y	18	1.87 ^{ns}	1.25
Error	118	2.81	12.36
Total	179		

*** significant at $P < 0.001$, ** significant at $P < 0.01$, * significant at $P < 0.05$ and ns= non-significant.

and Genotype × Year interactions showed highly significant differences for DMC. Interaction between genotype and environment was significant for harvest index but not for FRY.

The relative magnitude of the main effects and their interactions measured as a proportion of the total sum of squares showed that, G had more impact on DMC, HI, STD and FRY than other sources of variations. E × Y interaction had more impact on RTN and TW. The results show that, there were variable responses to the impact of environment on the five traits of the cassava genotypes studied. The environment was pronounced on all the traits but the magnitude was higher for FRY and TW compared to the other four traits. Partitioning of the sources of variation showed that G × L was the main contributor of Genotype × environment interaction (GEI) for harvest index indicating that the location contributed more to fluctuations in performance than years but not for DMC (Table 4).

The magnitude of phenotypic coefficient of variation

(PCV) was higher than their corresponding genotypic coefficient of variation (GCV) among all the traits studied (Table 5) but the differences were narrow for DMC, HI and FRY.

AMMI analysis

The analysis of variance of the AMMI for HI and DMC shows that the effects of G and E were significant ($P < 0.001$) and GEI was also significant but at $P < 0.01$ for HI. Genotype main effect and the interaction between Genotype and Environment were highly significant for DMC but the environment main effect was not. G accounted for 30.24 and 72.0% of total sum of squares for HI and DMC respectively, 21.65 and 1.1% were attributable to E effects for HI and DMC respectively, and GEI accounted for 19.59 and 12.6% as shown in Table 6. Two interaction principal component analysis axis (IPCA) were necessary to explain the interaction (GEI) but only

Table 5. Coefficients of variation, heritability and genetic advance for the traits.

Traits	Mean	GCV	PCV	h^2b	GAs
HI	0.45	17.56	18.00	93.94	34.83
RTN	44.38	25.51	27.53	85.68	48.60
FRY	20.54	32.96	33.93	94.44	66.02
STD	7.43	17.36	19.38	80.58	32.17
TW	24.14	19.76	23.32	71.70	34.45
DMC	29.31	12.25	12.96	89.00	23.78

GCV=genotypic coefficient of variation, PCV=phenotypic coefficient of variation GAs=genetic advance as percentage of the mean, h^2b =heritability in the broad sense, HI= Harvest index, RTN= number of root, FRY= Fresh storage root yield, STD= stands harvested, TW= Top weight and DMC= Dry matter content.

Table 6. Analysis of variance (AMMI) for harvest index and dry matter content of 10 cassava genotypes planted at three locations in Ghana for two years.

Source	df	Sum of square	Mean square	% of total ss
HI				
Total	179	2.91	0.02	
Trt	59	2.08	0.04***	71.48
Genotype	9	0.88	0.10***	30.24
Environments	5	0.63	0.13***	21.65
Block	12	0.11	0.01 ^{ns}	3.78
Interaction	45	0.57	0.01**	19.59
IPCA 1	13	0.30	0.02***	
IPCA 2	11	0.15	0.01*	
Residual	21	0.13	0.01 ^{ns}	
Error	108	0.72	0.01	
DMC				
Total	179	2683.3	15.01	
Trt	59	2343.2	39.71***	87.2
Genotype	9	1935.2	215.02***	72
Environments	5	30.5	6.11 ^{ns}	1.1
Block	12	55.9	4.65 ^{ns}	2.1
Interaction	45	337.4	8.39***	12.6
IPCA1	13	209.8	16.14***	
IPCA2	11	100.5	9.14***	
Residual	21	67.1	3.20 ^{ns}	
Error	108	288.2		

the first PCA was extremely important in explaining the interactions for HI. IPCA 1 explained 52.63% of variation in the interaction with 28.89% interaction degrees of freedom (df). The first two IPCA axes jointly accounted for 78.95% of the GEI sum of squares, leaving 21.05% of the variation in the interaction (within 46.67% of the interaction df) in the residual. The residual accounted for only 4.47% of the total sum of squares. For dry matter content, two interaction principal component analysis axis (IPCA) were necessary to explain the interaction (GEI) and both were extremely important in explaining the interactions. IPCA 1 explained 62.2% of variation in the

interaction with 28.89% interaction degrees of freedom (df). The first two IPCA axes jointly accounted for 92% of the GEI sum of squares. The residual accounted for only 2.5 % of the total sum of squares.

AMMI biplot analysis for DMC

The AMMI biplot analysis (Figure 1) for dry matter content shows the main effects in the x- axis and IPCA 1 in the y-axis. The total treatment sum of squares accounted for 83.51%, leaving 16.49% in the residual

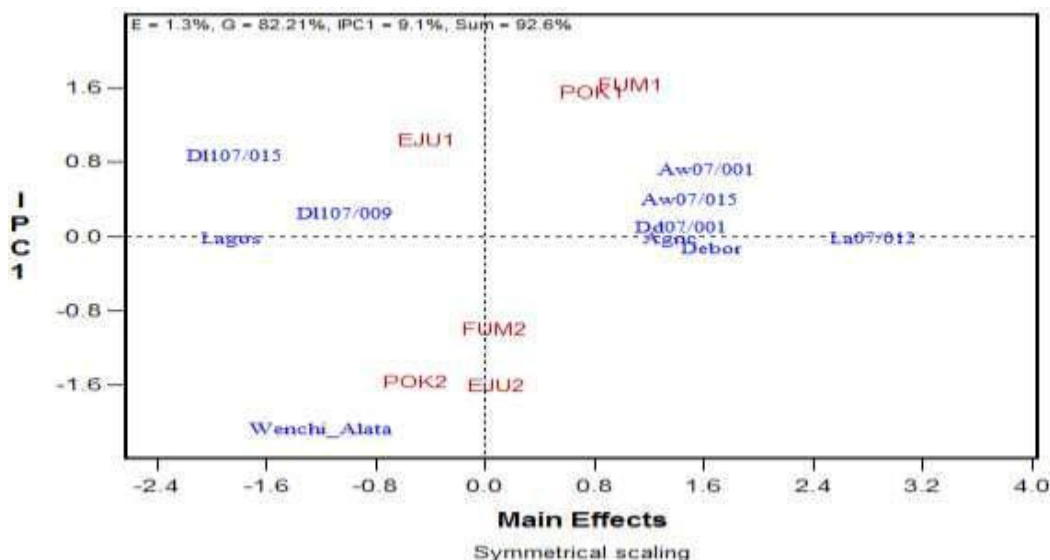


Figure 1. AMMI biplot for dry matter content of 10 cassava genotypes in 6 environments (Eju= Ejura, Fum= Fumesua and Pok= Pokuase) for two years.

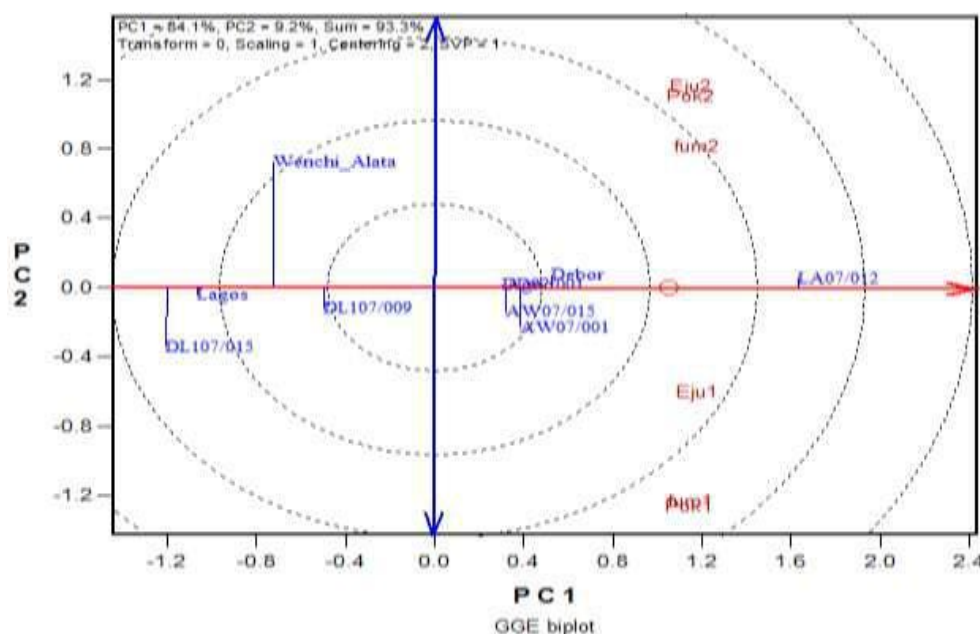


Figure 2. GGE biplot showing mean performance and stability of different cassava genotypes.

and revealed differential response of genotypes to the tested environments. Genotype LA07/012 was the least interactive with the environment (low IPCA 1 score) but had the highest dry matter content. Genotypes Lagos, Agric, LA07/012, DD07/001 and Debora were considered as stable genotypes being closer to the zero line from the Y- axis. DL107/015 had the highest positive interaction score (1.05) while Wench Alata (-2.51) had the highest negative score.

GGE biplot analysis

GGE biplot for average DMC and stability of genotypes

In Figure 2, the mean dry matter and stability performance of the cassava genotypes were shown. The genotypes were ranked along the average environment co-ordinate (AEC) x- axis with an arrow indicating the

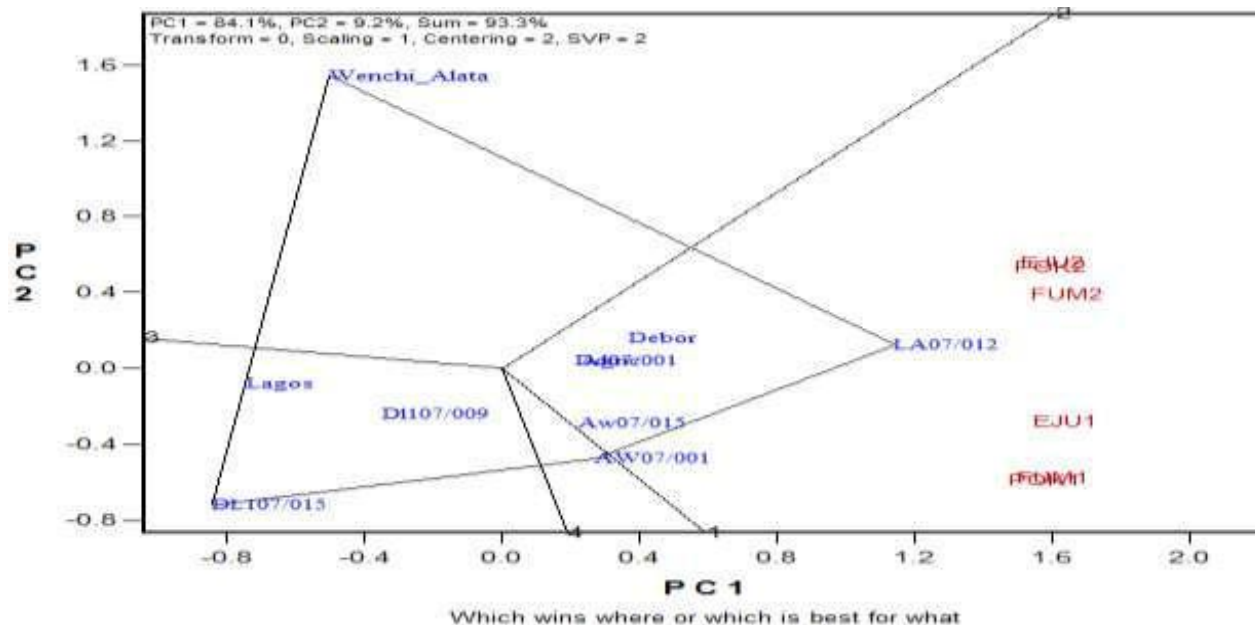


Figure 3. GGE biplot for best cultivars in different environments.

highest dry matter content. Thus, genotype LA07/012 which was closer to the AEC x-axis had the highest mean value while genotypes DL107/015 and Lagos had the lowest values because they were further away from the AEC x-axis. Wenchi Alata with the longest projection from the AEC x-axis was adjudged as an highly unstable genotype and also with DMC lower than the mean while genotypes DD07/001 and LA07/012 with small projection from the AEC x-axis were selected as being the most stable. AW07/001 (most productive genotype) recorded the highest fresh root yield (Table 2), quite stable and DMC higher than the mean. Although, LA07/012 recorded the highest DMC, the fresh root yield was the lowest as compare to the other genotypes.

The best performing genotype in each environment and mega- environments with GGE biplot for DMC

The GGE biplot (Figure 3) showed the genotypes that had the best performance in each environment. The model used to generate the biplot explained 84.1% in IPCA 1 and 9.2% in IPCA 2, both reflecting 93.3% of the DMC variation due to GGE. A convex -hull drawn on the genotypes from the origin of the biplot gave four sections with LA07/012, Wenchi Alata, DL107/015 and AW07/001 as the vertex genotypes. All the environments fell into the sector where LA07/012 was the vertex genotype. It suggests that the genotype is best in all the environments. The biplot grouped all the environments together, which is an indication of no existence of mega-environments.

GGE biplot for representativeness and discriminating ability of environments for DMC

In this study, the GGE biplot explained 93.3% of the G plus GE data (Figure 4) suggesting that the angles between the vectors of the environments might be good indicators of correlation amongst the environments.

DISCUSSION

Correlation analysis is an important tool for estimating the value and association of various characters in a crop (Edmeades et al., 1997). Correlation among traits plays a vital role in improving selection efficiency in plant breeding programs. In selection programs, yield and some yield components (Root number, number of stands harvested, top weight, dry matter content and harvest index) are some of the most economic traits usually targeted by plant breeders. The corroborative reports of significant positive correlation between fresh root yield and other yield components suggests that, any one of the traits could be used to select indirectly for fresh root yield. The relationship we observed between FRY and RTN in this study was as similarly reported by Peprah et al. (2013a), when studying genetic variability of three cassava traits in Ghana. This is in agreement with earlier findings by Parkes (2011) which efficiently selected root number indirectly for fresh root yield. The positive correlation could be explained by the fact that RTN normally has impact on the FRY. There was also significant negative correlation between HI and TW

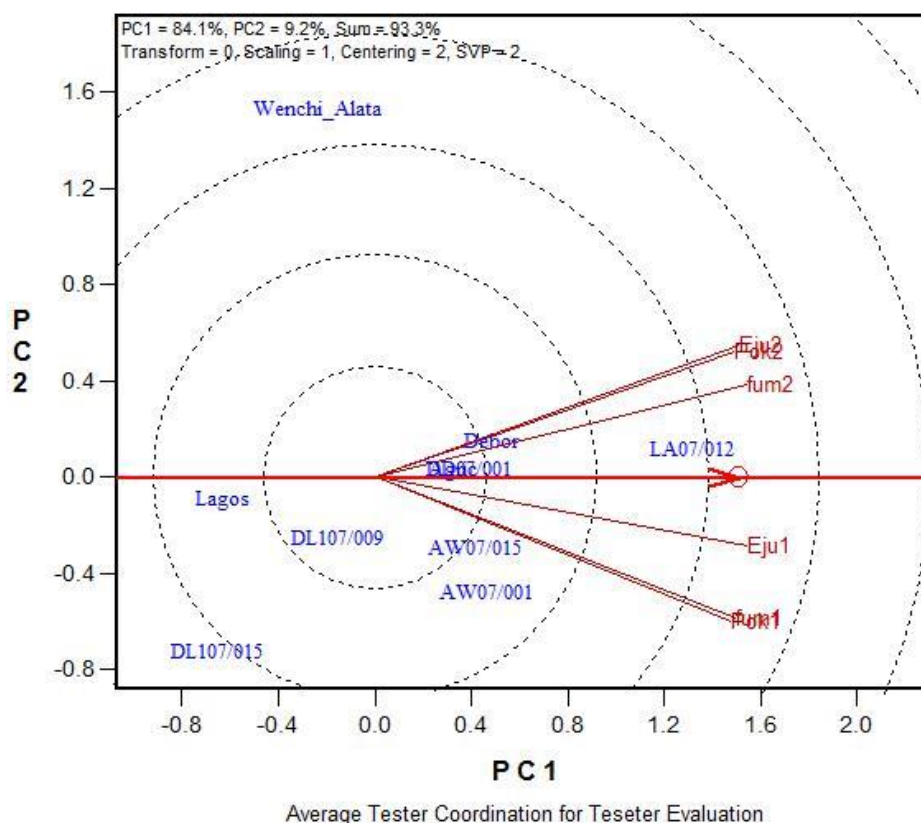


Figure 4. GGEbiplot for representativeness and discriminating ability of environments as average tester coordination for tester evaluation.

and it suggests that, selection of one trait may compromise the other trait.

The highly significant interaction between genotype and environment ($G \times E$) for DMC indicates that there is the need for multi locational testing to identify good performance for specific locations (Akinwale et al. 2011). As observed in the analysis, the non-significant GL interaction for FRY suggests that the genotypes might have similar responses across the locations in which they were evaluated and that all the genotypes can reliably be assessed under anyone of the locations used for this study in future or advance evaluation trials (Yan and Tinker, 2006). In other words, it might not be important to assess these genotypes simultaneously in the various locations used for the study in subsequent evaluations, thereby offering an opportunity to manage the limited resources available for the testing program (Tonk et al., 2011).

The high G and low E effects, and relatively low GEI for DMC, HI and FRY may necessitate evaluation over fewer environments to distinguish genotypes with high and stable performance. Peprah et al. (2013 b) also reported higher G and low E effects on DMC and FRY when working on cassava genotypes developed from landraces. This might be due to the same genotypes

(landrace) that were used to generate the hybrids in both studies and also the same locations used for the evaluation. This also suggest that improving landraces for important traits like fresh root yield and dry matter content in cassava is feasible because of the higher genotypic impact. The high significance of year effects on HI and FRY suggests the need to evaluate for more than one year for reliable inferences to be made on performance of the genotypes. The narrow differences for the three traits suggest limited environmental variation in the expression of these traits. This finding is in agreement with earlier reports by Aina (2007) and Akinwale et al. (2010). Broad sense heritability and genetic advance as percent of the mean for all the traits were high. It was suggested by Pradeepkumar et al. (2001) that, high heritability in broad sense does not always lead to better response to selection because it consists of non- additive genetic variance, therefore, genetic advance as a percentage of the mean is more of a useful response to selection combined with high heritability estimates. Selection of all the traits could be possible due to high broad sense heritability (Bhateria et al., 2006) and high genetic advance as a percentage of the mean. This may suggest that trait with significant positive correlation, high heritability estimates and

genetic advance like HI and FRY and DMC and RTN can be simultaneously improved. The large sum of squares for genotypic effects suggested that the genotypes were diverse with differences among the genotypic means for the two traits. This might be due to the diverse nature of the parental lines and probably due to where they were selected for the crosses. The highly significant ($P < 0.01$) GEI for HI and DMC suggest different performance of genotypes across environments. However, the impact of GEI was smaller than that of genotypic effects, indicating the presence of moderate variation among the genotypes over environments.

The residual mean squares for HI were not significant and even that for the IPCA 1 was twice the residual. This suggests that there were differences in performance among the 10 cassava genotypes across the six environments (3 locations and 2 years) due to the presence of high significant GEI effects (Agyeman et al., 2015). The residual mean squares were not significant and even that for the IPCA 1 was more than twice the residual. This result revealed that there was a differential performance in dry matter content among cassava genotypes across testing environments which was due to the presence of GEI. This is in conformity with the findings of Akinwale et al. (2011). This suggests that, there were differences in performance among the 10 cassava genotypes across the six environments (3 locations and 2 years) due to the presence of high significant GEI effects. The cosine of angles between vectors of all the environments were less than 90. This suggested that, there were no negative correlations among the test environments (Akinwale et al. 2011). The length of the environmental vectors (the lines that connect the test environments to the biplot origin) approximate the standard deviation within the respective environments, which is a measure of the discriminating ability of the environments (Yan, 2005). Fum-2, Eju-2 and Pok-2 environments with the longest projections from the biplot were found more discriminating of the genotypes and the least representative environments. Fum-1 and Ejua-1 were found to be more representative of other test environments due to their smaller angles with the AEAs. Eju- 1 was averagely discriminating and most representative environment therefore can be used for genotypes with wide adaptation. The non-representative environments such as Fum-2, Eju-2 and Pok-2 are useful for selecting specifically adapted genotypes. Dry matter content is an important cassava trait in Ghana. Processors and consumers placed more importance on the trait because of the way it's consumed, although, cassava is now becoming an industrial crop.

Conclusion

The study revealed that genotype AW07/001(progeny) outperformed the parents (Checks) indicating that it has

the potential to increase cassava productivity in Ghana and also might be easily adopted by farmers because it is a progeny from farmers cultivars. The study also revealed some positive correlations between some important agronomic traits (FRY and RTN, RTN and TW, HI and FRY, FRY and STD, DMC and HI) of cassava which can aid indirection in the selection for cassava breeding. 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. AW07/001 and AW07/015 were the best genotypes based on mean performance (FRY, DMC and HI) and stability. Eju-2, Fum-2 and Pok-2 were the most discriminating and least representative environments while Fum-1 and Eju-1 environments were the most representative environments.

Conflict of Interests

The authors have not declared any conflict of interests.

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