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Performance of nine cassava (*Manihot esculanta* Crantz) clones across three environments

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The study was carried out to quantify the genotype × environment interaction (G × E) and to estimate the phenotypic stability by genotype genotype × environment (GGE) biplot of nine cassava clones comprising 5 hybrids, 3 parent checks and 1 improved variety. The study was planted across three different environments; Fumesua, Pokuase and Ejura representing forest, coastal savanna and forest transition zones, respectively. Genotype main effect was significant (P < 0.001) for fresh root yield and dry matter content, G × E interaction effect was significant (P < 0.001) for fresh root yield only and environment main effect was significant (P < 0.01) for only fresh root yield. The most stable clone for fresh root yield with above average performance was La02/026 (hybrid). The high genotype and low environment effects, and the relatively low interaction on dry matter content imply that evaluation and selection can be effectively done in fewer environments to select clones with high performance for the trait whiles fresh root yield requires multiple environments to identify clones with broad and specific adaptation.

Key words: Genotype genotype × environment (GGE) biplot, stability, fresh foot yield, dry matter content, cassava.

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/day from food based on its roots (Chavez et al., 2005). Cassava, however, shows a strong and significant genotype × environment interaction (G × E) effect (Fukuda, 1996; Kvitschal et al., 2007), due to its diverse difficult cropping condition, thus makes selection difficult. Breeding cassava for superior cultivars should be performed taking G × E effect in consideration. A detailed assessment of magnitude and significance of G × E is important to ensure greater precision in the selection and release of high yielding and stable clones (Kvitschal et al., 2009). The assessment and selection of cultivars with high yield and stability is very important in any genetic breeding program, to indicate superior materials for commercial use (Carneiro, 1998). Stable yields play a major role in developing countries, where small-scale farmers, particularly those living in marginal areas, are working towards risk-minization (Adugna and Labuschagne, 2002).

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

Clone	Source
DI102/007 (Debor × Lagos)	CRI
DI102/006 (Debor × Lagos)	CRI
DI102/005 (Debor × Lagos)	CRI
La02/007 (Lagos × Agric)	CRI
La02/026 (Lagos × Agric)	CRI
Dokuduade	Improved variety
Agric	Landrace
Debor	Landrace
Lagos	Landrace

CRI, Crops Research Institute.

Breeders face the GEI challenge by evaluating genotypes in several environments to ensure that they select genotypes with high and stable performance (Ssemakula and Dixon, 2007). In yield trials, standard statistical methods that have been applied include analysis of variance (ANOVA), principal component analysis (PCA), linear regression (LR), additive main effects and multiplicative interaction (AMMI) and genotype genotype × environment (GGE) biplot. A combined ANOVA can quantify interactions and describe the main effects; however, it is not informative for explaining G×E. The genotype and G × E biplot define an ideal genotype, based on both mean performance and stability across environments. The GGE biplot explains more G+GE than AMMI (Aina et al., 2009) and therefore is considered a better presentation of the GGE dada. In the AMMI biplot, each genotype is represented by a linear line defined by the genotype's mean yield and its interaction principal components axis (IPCA) score on the y-axis and mean yield on the x- axis. Both axes in GGE biplot are results of least square solutions, whereas, only the IPCA1 is the result of least squares in AMMI. The GGE biplot therefore exemplified data from multi-environment trials (MET) indicating the accurate positioning of both cultivars and environments on a single biplot (Aina et al., 2009). The objective of the study was to study the G × E and to assess the fresh yield performance of nine cassava clones.

MATERIALS AND METHODS

Nine cassava genotypes (Table 1) at preliminary yield stages were used for the study. The environments were Fumesua, Pokuase and Ejura which represent forest, coastal savanna and forest transition zones, respectively. The soils 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, chronic lixisol with sandy loam top soil). Annual rainfall for the environments during the trial period was Fumesua (1605 mm), Pokuase (1250 mm) and Ejura (1350 mm). Plantings were done at different dates for the three environments. The materials were grown under rainfed 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 on 6 row plots of 5 plants / row with a plot size of 30 m^2. Weeding was done as deemed necessary. Data were collected from the 20 inner plants within a plot. Severity ratings of cassava mosaic disease were taken at 1, 3 and 6 months after planting (MAP) using a scale of 1 to 5 (1 = no symptoms; 5 = severe symptoms) according to International Institute of Tropical Agriculture, IITA (1990). At harvest (12 MAP), data were collected from the 20 inner plants within a plot for fresh root yield 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. 100 grammes 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 weighs, and the dry matter percentage was calculated as the ratio of the dry weight over the fresh weight and multiplied by 100.

Data collected were first analyzed separately, then combined over environments using GenStat 9.2. The AMMIs statistical model (MATMODEL 2.0 (Gauch, 1993) was used to analyze the yield data to obtain mean estimates. The E and G × E Interaction biplot analysis for windows application (version 6.3 Yan, 2001) was used to generate the E and G x E interaction biplot used to analyze the MET data. The model used for the E and G × E interaction biplot analysis was the no-scaling and tester-centered model.

RESULTS AND DISCUSSION

Genotype, environment and genotype by environment interaction showed high significant mean square ($p < 0.01$) for fresh root yield (Table 4), indicating genetic variability between genotypes by changing environments. Effects from genotype and environment that showed highly significant mean square reflected genotypic differences towards adaptive to different environments, thus, the highly significant G × E effects for fresh root yield suggest that clones may be selected for adaptation to specific environment (Aina et al., 2009). It also suggests that, there is the need for multi-environmental testing to identify good performers for specific environments (Akinwale et al., 2011; Maroya et al., 2012).

Fumesua recorded the highest grand mean for dry matter content and fresh root yield. Also Fumesua recorded the lowest score for cassava mosaic disease severity (Table 2). The root yield ranged from 26.4 to 49.7 t/ha with a mean of 37.8 t/ha. Agric had the highest root yield of 49.7 t/ha, while the lowest value of 26.4 t/ha was recorded for DI102/005. Four of the clones had root yields of more than above the mean (37.8 t/ha), while five clones yielded less than the mean (Table 3). ANOVA showed that dry matter content varied significantly among the genotypes (Table 4). It ranged from 25.6 to 34.3%, with a mean of 30.5%. The reaction of the clones to cassava mosaic disease across the three environments varied significantly ($P < 0.001$). The reaction ranged from 1.0 to 2.4 with a mean of 1.4 (Table 3).

G × E accounted for 34.46% of the total sum of squares for root yield, while environment accounted for 7.11% and

Table 2. Performance of nine cassava clones planted across three environments in Ghana.

Clone	Environments								
	Fumesua			Pokuase			Ejura		
	CMDS	Yield (t/ha)	DMC (%)	CMDS	Yield (t/ha)	DMC (%)	CMDS	Yield (t/ha)	DMC (%)
Agric	1.3	60.0	30.0	1.6	34.4	30.0	1.3	34.7	30.0
Debor	2.5	57.9	31.7	2.0	12.8	35.6	2.8	29.4	35.6
Lagos	1.0	50.0	26.8	1.5	45.5	25.4	1.0	34.7	25.4
La02/007	1.9	37.5	32.2	2.7	31.4	32.7	1.5	22.0	30.6
La02/026	1.9	49.6	31.5	2.5	42.7	31.8	2.7	41.0	31.2
Dl102/005	1.2	17.2	33.0	1.3	28.4	31.2	1.1	33.7	31.2
Dl102/006	1.1	23.3	30.0	1.0	18.2	23.6	1.0	54.3	23.6
Dl102/007	1.1	55.6	31.0	1.0	31.1	30.6	1.3	42.1	30.6
Dokuduade	1.0	40.2	32.1	1.0	33.3	33.5	1.0	39.0	33.5
Grandmean	1.4	43.5	30.9	1.6	33.1	30.5	1.5	36.8	30.3
Sed	0.4	8.9	1.7	0.3	8.4	1.5	0.2	10.7	1.6
CV%	30.7	25.1	6.9	19.1	31.1	5.9	13.7	35.5	6.3
P(< 0.05)	0.009	0.001	0.007	<0.001	0.004	<0.001	<0.001	0.24	<0.001

CMDS = Cassava mosaic disease severity; YIELD = Fresh tuber yield; DMC (%) = Dry matter content.

Table 3. Mean performance of nine cassava clones evaluated across three environments (Combined data).

Clone	Yield (t/ha)	DMC (%)	CMDS
Agric	49.7	30.0	1.4
Debor	33.4	34.3	2.4
Lagos	43.4	25.9	1.2
La02/007	30.3	31.8	2.0
La02/026	44.5	31.7	2.3
Dl102/005	26.4	31.8	1.2
Dl102/006	32.0	25.6	1.0
Dl102/007	42.9	30.7	1.1
Dokuduade	37.5	33.0	1.0
Grandmean	37.8	30.5	1.5
Sed	9.4	1.7	0.3
CV (%)	30.5	6.7	21.8

CMDS = Cassava mosaic disease severity; YIELD = Fresh tuber yield and DMC (%) = Dry matter content; CV = Coefficient of variation, Sed = Standard error of differences of means.

Table 4. Means squares of fresh root yield and dry matter content.

Source	Df	Root Yield	DMC	CMDS
Genotype	8	544.10***	79.66***	2.94***
Environment	2	746.60**	2.66^{ns}	0.20^{ns}
G × E	16	452.00***	7.43^{ns}	0.29**

*, ** and *** = Significant at P<0.05, 0.01 and 0.001%, respectively; ns = not significant.

genotype 20.75%. Similarly, genotype, environment and G × E sources of variation also accounted for 64.46, 0.54 and 12.02% of the total sum of squares, respectively, on dry matter content. Also, G, E and G × E accounted for 68.49, 1.19 and 16.69% on cassava mosaic disease (Table 5). The high genotype and low environment

Table 5. Combined ANOVA of the two traits of nine cassava clones in three environments.

Source	Df	FRY		DMC		CMDS	
		SS	Total ss (%)	SS	Total ss(%)	SS	Total ss (%)
Genotype (G)	8	4356.7	20.75	637.26	64.46	23.56	68.49
Environment (E)	2	1493.2	7.11	5.32	0.54	0.41	1.19
G × E	16	7235.7	34.46	118.87	12.02	5.74	16.69

SS = sum of squares; FRY = fresh root yield; DMC = Dry matter content; CMDS = Cassava mosaic disease severity.

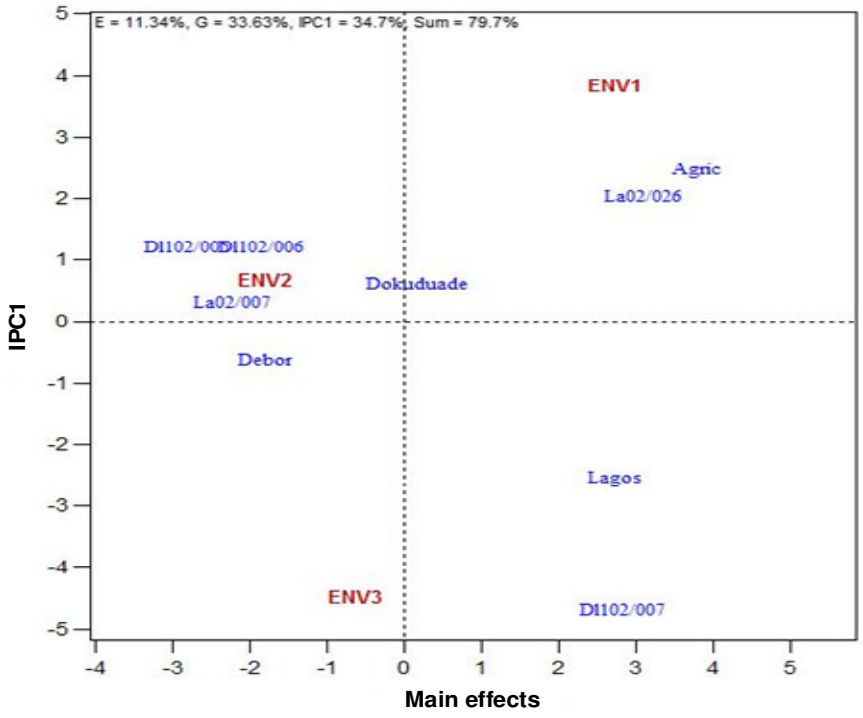

Figure 1. GGE Biplot showing distribution of clones and environments for fresh root yield. ENV1 = Fumesua, ENV 2 = Pokuase and ENV 3 = Ejura.

effects and relatively low G × E interaction for dry matter content suggest that this trait is not drastically influenced by the environment and, therefore, that fewer environments may be needed to distinguish clones with high and stable performance. This also suggests good prospects for the improvement of the clones for dry matter content (Ssemakula and Dixon, 2007) since simple phenotypic recurrent selection will be needed. Ssemakula and Dixon (2007), and Benesi et al. (2004) also reported higher genotype than environment effects on dry matter in cassava. The high genotype effects on cassava mosaic disease has also been reported by Maroya et al. (2012) when working on G × E interaction of mosaic disease, root yields and total carotene concentration of yellow- fleshed cassava in Nigeria. However, the surprising higher genotype impact on fresh root yield than environment observed in this study needs to be confirmed by further studies since yield is a polygenic trait (Manrique and Hermann, 2000). This result was contrary to work done by Ssemakula and Dixon (2007). This could be due to the differences in the genetic background of genotypes being evaluated and environmental conditions for the two studies.

The GGE biplot for AMMI (Figure 1) explained by the two axes showed that environment explained 11.34%, genotype 33.63% and the IPCA1 34.7%, reflecting 79.7% of the fresh root yield variation due to AMMI. The biplot showed, as expected, that Agric and La02/026 are high yielding clones. La02/007 was found to be specifically adapted to Environment 2 (Pokuase). Clones should be evaluated based on both mean performance and stability across environments (Yan and Rajcan, 2002). On the biplot, the single-arrowed line is the average environment coordinates abscissa which points to higher mean fresh root yield across environments (Figure 2). The double arrowed line is the average environment coordination

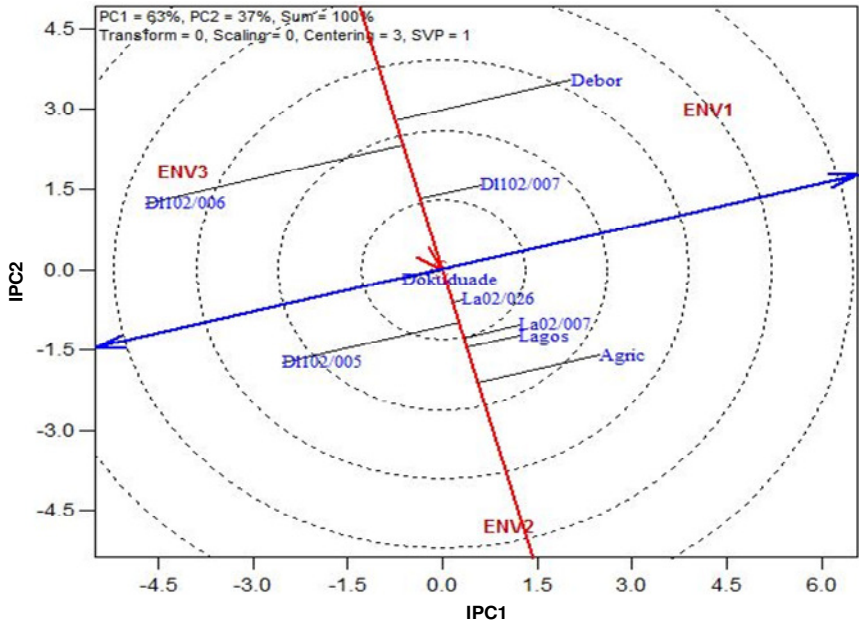

Figure 2. GGE biplot for average root yield and stability of different cassava clones. ENV1 = Fumesua, ENV 2 = Pokuase and ENV 3 = Ejura.

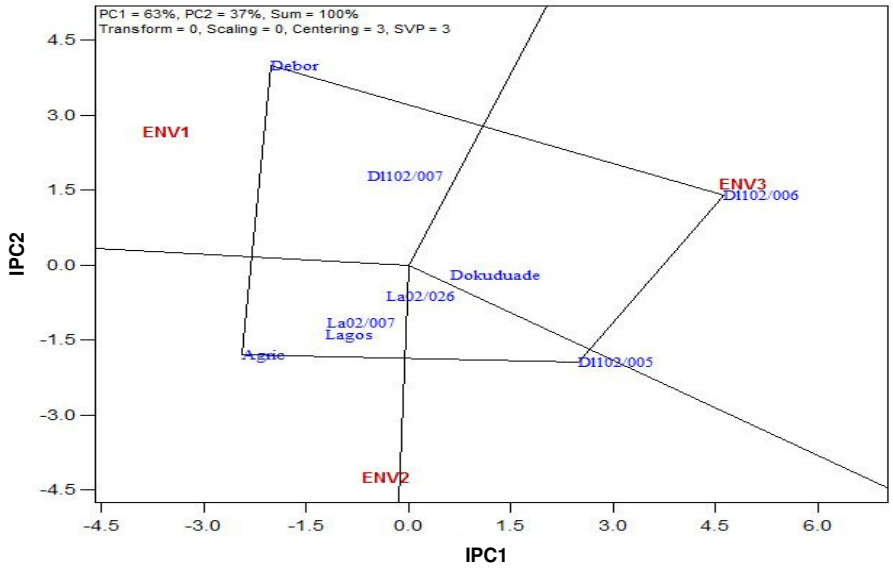

Figure 3. Mega-environment defined by different winning cassava clones for fresh root yield. ENV1 = Fumesua, ENV 2 = Pokuase and ENV 3 = Ejura.

ordinate and it points to greater variability in either direction (Yan and Tinker, 2006). Agric had the highest mean yield, followed by Lagos and then La02/007. Dokuduade had a mean yield similar to the grand mean, while Debor had the lowest mean yield. Lagos and La02/007 were the highest yielding and stable clones, while DI102/007 was equally stable but with poor root yield. Agric, though high yielding but was unstable, while DI102/006 was low yielding and unstable.

A G × E biplot was used to identify wining clones and mega-environments (Figure 3). The biplot explained 63 and 37% of GGE sum of squares, respectively, explaining a total of 100% variation. On the biplot, some vertex clones, which are the most responsive ones, can be visually identified. These are either the best or the poorest clones at some or all environments (Yan et al., 2001). The vertex clones were Debor, Agric, DI102/005 and DI102/006. Environment 3 (Ejura) fell into Sector 1 and

the vertex clone for the sector was DI102/006.

Environment 1 (Fumesua) fell into Sector 2 in whichDebor was the vertex clone. Environment 2 (Pokuase) fell into Sector 3 where Agric was the winning niche. No environment fell into Sector 4 with DI102/005 as the vertex clone, indicating that this clone was not the best in any environment but the poorest in some or the entire environments. The GGE biplot in Figure 3 also showed that all the environments were different and can be used in evaluating cassava clones in Ghana. Further analysis for G × E was not done for dry matter content and cassava mosaic disease because it was not significant.

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