Research Article

Genotype × Environment Interaction of Mosaic Disease, Root Yields and Total Carotene Concentration of Yellow-Fleshed Cassava in Nigeria

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Twenty-one yellow-fleshed cassava genotypes were evaluated over two years in five major cassava growing agroecological zones in Nigeria. The trials were established in a randomized complete block design with four replications to assess genotype performance and Genotype × Environment interaction for cassava mosaic disease (CMD), fresh and dry root yield (FYLD; DYLD), root dry matter content (DMC), and total carotene concentration (TCC). Combined analysis of variance showed significant differences ($P < 0.001$) among genotypes (G), environment (E), and Genotype × Environment interaction (GE) for all the traits tested. For reaction to CMD, the best genotypes showing stable resistance were TMS 07/0539 and TMS 07/0628. For root yield, the best genotypes were TMS 01/1368 and TMS 07/0553. Genotype TMS 07/0593 was the best for DMC and TCC across the 10 environments. Variation among genotypes accounted for most of the Total Sum of Squares for CMD (72.1%) and TCC (34.4%). Environmental variation accounted for most of the Total Sum of Squares for FYLD (42.8%), DYLD (39.6%), and DMC (29.2%). This study revealed that TMS 07/0593 has the highest and most stable TCC, DMC with the lowest CMD severity score and appeared to be the best genotype.

1. Introduction

Vitamin A deficiency (VAD) is a global problem of public health significance in under-privileged communities of the world [1]. Xerophthalmia is the most readily recognized and the most widely employed criterion for discussing whether VAD poses a significant public health problem in any particular community [2]. Vitamin A deficiency in the early stage leads to night blindness and Xerophthalmia, which may ultimately progress to blindness [3]. A nationwide food consumption and nutrition survey conducted in Nigeria revealed that 29.5% of children under 5 years of age were vitamin A deficient (serum retinol <0.70 μmol/L) [4]. Cassava (*Manihot esculenta* Crantz) is an important food security crop and a major source of calories for about two of every five Africans [5]. Although the starchy root is the primary product, fresh leaves are also used for animal and/or human consumption [6]. In 2008, Nigeria was the leading cassava producing country in sub-Saharan Africa, producing 44.6 million tons on 3.8 million ha [7]. In Nigeria, more than 70% of cassava production is processed at the village level into *gari,* the principal source of calories for 70–80 million Nigerians. Cassava varieties often demonstrate specific adaptation due to their high sensitivity to the genotype-by-environment interaction (G × E) that occurs in both short-term and long-term crop performance trials [8] and is a major concern in plant breeding because it reduces progress from selection. This makes cultivar recommendation difficult because the choice of superior cultivars changes with locations [9].

β-carotene is the most potent and widespread form of pro-vitamin A [10] and is the predominant carotenoid in cassava, occurring as a mixture of 13-*cis*-β-carotene; *trans*-β-carotene and 9-*cis*-β-carotene forms [11]. Because the

cis-isomers are known to have lower vitamin A activity and are present in insignificant levels compared with the *trans*-form, the quantitative method should determine the *trans* and the *cis*-isomers individually. However, this makes the analysis more expensive and complicated. An earlier study in cassava [12] revealed in (0.1–3 mg kg^{-1} Fresh Weight) of β-carotene and (0.05–0.6 mg kg^{-1} FW) of lutein. Other carotenoids present in cassava roots but in very small amount included α- γ- and ζ-carotene and β-cryptoxanthin [12]. In Brazil, one the cassava clone (UnB 500) which has been grown by indigenous farmers and available at the University of Brasilia gene bank showed a high lycopene content. Lycopene was shown to be the major carotenoid, although α-carotene and *cis*-lycopene were also found [13]. In the same study, another clone (UnB 400) analyzed for carotenoids showed *trans*-β-carotene reached 27.40 μg/g. *Trans*-β-carotene acts as an antioxidant that helps to prevent heart attacks and cancer, lowers cataract risks and muscular disorders, and enhances the immune system [14]. β-carotene is also required for growth, reproduction, vision and the maintenance of the integrity of epithelial tissue. Structurally, vitamin A (retinol) is essentially one-half of the β-carotene molecule. The average daily requirement recommended by the World Health Organization is 2.4–3.5 mg for adults. The typical white-fleshed cassava genotypes largely used in Nigeria contain only small amounts of β-carotene [15]; however, yellow-fleshed cassava contains up to about 100 times as much [16]. Studies have been conducted on retention of β-carotene from cassava roots that had been boiled, oven-dried, sun-dried, shadow-dried, or used for gari preparation. Oven-drying, shadow drying and boiling retained the highest levels of β-carotene (71.9%; 59.2% and 55.7% resp.) and gari the lowest (about 34.1%) [17]. Increasing the consumption of yellow-fleshed cassava roots and their processed food products can provide a significant proportion of the required dietary vitamin A intake. It is therefore important to breed and promote the cassava varieties enriched with high levels of β-carotene to combat the widespread vitamin A deficiency in Nigeria.

2. Materials and Methods

This study was conducted at the advanced multilocation yield trial breeding stage (called uniform yield trial) with 21 yellow-fleshed cassava genotypes including two checks. The trial was run for two cropping seasons (2009-2010 and 2010-2011) at five locations representing the major cassava growing agroecological zones in Nigeria. The checks, TMS 01/1368 and TMS 01/1371, were improved yellow-fleshed genotypes that were officially released in Nigeria in December 2011. The trial locations were Ibadan (7°38′N, 3°89′E; forest-savanna transition, 227 masl, annual rainfall 1312 mm, annual average temperatures 20.3–33.8°C; soil type Ferric Luvisols); Ikenne (6°86′N, 3°71′E; humid forest, 44 masl, annual rainfall 1515 mm, annual average temperatures 22.3–33.4°C; soil type Dystric Nitosols); Ubiaja (6°65′N, 6°38′E, subhumid forest, 287 masl, annual rainfall 1186 mm, annual average temperatures 19.9–32.6°C; soil

type Dystric Nitosols); Mokwa (9°28′N, 5°05′E, southern Guinea savanna, 132 masl, annual rainfall 1149 mm, annual average temperatures 18.1–37.3°C; soil type Dystric Nitosols); and Zaria (11°16′N, 7°63′E; northern Guinea savanna, 687 masl, annual rainfall 1076 mm, annual average temperatures 13.9–35.5°C; soil type Ferric Luvisols). The five locations combined with the two cropping seasons constituted the 10 evaluation environments. The environments are coded in the graphics as follows: Ibadan 2009-2010 (E_1), 2010-2011 (E_2); Ikenne 2009-2010 (E_3), 2010-2011 (E_4); Ubiaja 2009-2010 (E_5), 2010-2011 (E_6); Mokwa 2009-2010 (E_7), 2010-2011 (E_8); and Zaria 2009-2010 (E_9) and 2010-2011 (E_{10}). The graphic representations of the genotypes were G_1 to G_{21}. The cassava genotypes were grown for two 12-month cropping seasons under rainfed conditions in a randomized complete block design with four replications. Each plot was 6 m by 6 m consisting of 36 plants spaced 1 m apart in 6 rows on 30 cm ridges spaced 1 m apart. No fertilizer was applied. Weeds were controlled as necessary. Harvesting in all locations was at approximately 12 months after planting (MAP). A border of 1 m was left and only the inner plants (maximum of 16 per plot) were harvested. The severity of cassava mosaic disease (CMD) was scored using the scale 1 to 5 system described by IITA [18] (1 = no symptom and 5 = severe symptoms). An average CMD severity was calculated based on ratings taken at 1, 3, and 6 MAP. Root fresh yield/ha was calculated based on the weight of roots of inner plants harvested/plot. The root dry matter content (DMC) was determined for each genotype from a random sample of three roots/plot from only two replications. To determine the dry matter percentage, a 100 g sample (taken after the three roots had been washed and shredded) was oven-dried at 70°C for 48 hr. The percentage of DMC was calculated as the ratio of the dry weight multiplied by 100 over the fresh weight as indicated below:

$$\text{DMC} = \frac{\text{Sample dry weight} \times 100}{\text{Sample fresh weight}}. \tag{1}$$

The dry root yield (DYLD) is the product of the fresh root yield (FYLD) multiplied by the percentage of the DMC:

$$\text{DYLD} = \text{FYLD} \times \text{DMC}. \tag{2}$$

For laboratory determinations of total carotene concentration (TCC), five medium sized roots were collected from the harvested roots in two replications. Three of the five roots were washed dried, peeled, and again washed and dried. Each peeled root was cut longitudinally in half and the halves were again cut longitudinally into quarters. Two opposite quarters of the three roots were pooled for total carotene quantification. The six quarters were cut in small pieces of about 1 cm^3 and mixed together. After many subdivisions, a sample of approximately 10–15 g of small pieces of root was taken as a uniform and representative sample and ground in refrigerated acetone solvent using a mortar and pestle. During sample preparation, special care was taken to avoid directly exposing the storage roots to sunlight and the lights in the laboratory were protected with UV filters. Samples were covered with aluminum foil when not under processing.

All the total carotene analyses were completed within 24 hr after each harvest, using the spectrophotometer method described in the HarvestPlus handbook for Carotenoid Analysis [19] as follows. Twenty ml of petroleum ether (PE) with low boiling point of 35–60°C (used as solvent in extraction or partition) is put in a 500 mL separatory funnel with Teflon stop-cock and add the acetone extract. Distilled water was slowly added (~300 mL), flowing along the walls of the funnel to avoid formation of an emulsion. After adding the distilled water, two separated phases were identified. The two phases were allowed to separate and the lower aqueous-acetone phase discarded. This washing with distilled water was done 3 to 4 times to remove residual acetone. In the last washing, the totality of the lower phase was completely discarded. The PE phase was then collected in a volumetric flask through a small funnel containing anhydrous sodium sulphate to remove the residual water. The separatory funnel was washed with PE and the washing in the volumetric flask by passing through the funnel and the sodium sulphate. For spectrophotometer reading and calculation, it is important to make up to volume with PE and take the absorbance at 450 nm. It may be necessary to concentrate or dilute the carotenoids solution so that the absorbance should be between 0.2 and 0.8. The total carotenoids concentration is calculated using the following formula:

$$\text{TCC } (\mu g/g) = \frac{A \times \text{volume (mL)} \times 10^4}{A_{1\,cm}^{1\%} \times \text{sample weight (g)}}, \quad (3)$$

where A = absorbance, volume = total volume of extract, and $A_{1\,cm}^{1\%}$ = absorption coefficient of β-carotene in PE (2592).

Data collected were statistically analyzed using analysis of variance and GGE biplot. "GGE biplot" is a data visualization tool that is based on principal component analysis (PCA) of environment-centered or standardized G × E data because these biplots display both genotype main effects (G) and genotype by environment interactions (GE), which are the two sources of variation that are relevant to variety evaluation [20]. G × E data analysis includes three major aspects: (i) megaenvironment analysis (ii) test environment evaluation, and (iii) genotype evaluation [21, 22]. A GGE biplot is constructed by plotting the first principal component (PC1) scores of the genotypes and the environments against their respective PC2 scores resulted from the singular value decomposition (SVD) of environment-centered or standardized G × E data. The "which-won-where view" of the GGE biplot [23] is an effective tool in megaenvironment analysis. It consists of a polygon and a set of perpendicular lines to the sides of the polygon. The polygon is drawn on genotypes located farthest away from the biplot origin in various directions such that all genotypes are contained in it. The perpendicular lines are drawn from the biplot origin to divide the biplot into sectors. If all environments fall into a single sector, it means that a single genotype had the highest yield (performance) in all environments. If the environments fall into different sectors, it means that different genotypes won in different sectors.

3. Results and Discussion

Mean performance of the 21 yellow-fleshed cassava genotypes across the 10 environments are presented (Table 1). The lowest CMD score 1.0 was recorded for TMS 07/0539 (G_{10}) and TMS 07/0628 (G_{14}). The mean CMD was 2.0. The highest means for FYLD and DYLD were recorded by the check TMS 01/1368 and the overall averages across the environments were 10.6 tha^{-1} (FYLD) and 2.3 tha^{-1} (DYLD). The mean of DMC was 21.0% with the highest value recorded by the genotype TMS 07/0593 (G_{13}). The mean TCC was 7.8 μg g^{-1} and the genotype TMS 07/0593 had the highest average of 11.7 μg g^{-1}.

The combined analysis of variance tables showed for all traits that G, E, and GE were significant ($P < 0.001$).

3.1. Cassava Mosaic Disease.
The average severity score of CMD of the 21 genotypes across the 10 environments was higher than the scoring results reported in similar studies conducted from 2004 to 2006 in Nigeria [24]. The combined analysis of variance of CMD scores of the 21 yellow-fleshed genotypes evaluated during 2 years in five locations showed significant differences ($P < 0.001$) among G, E, and GE. Genotypes TMS 07/0539 (G_{10}) and TMS 07/0628 (G_{14}) did not show any visible symptoms of CMD (score = 1.0) in any of the 10 environments and were grouped together with G_3, G_4, G_7, G_9, G_{13}, and G_{16} which, on average, scored 1.1 (Table 1). On the contrary, genotypes G_1, G_5; G_6 G_8, G_{11}, G_{12}, G_{15}, and G_{17} showed severe CMD symptoms and had the highest severity scores across the 10 environments.

The combined analysis of variance of CMD revealed that G contributed 72.1% of the total sum of squares; E contributed 7.4% and GE 8.7% as per Table 2.

In the GGE biplot analysis, the PC1 (91.2%) and PC2 (2.7%) together explained 93.9% of the total variability attributed to G and GE. A polygon view of the GGE biplot (Figure 1) showed which genotypes performed better or worse for CMD in which environments. The vertex genotypes for CMD severity were G_2, G_4, G_{13}, G_5, G_6, and G_{17}. Two megaenvironments were defined. The first megaenvironment included E_2, E_3, E_5, and E_6 with the winning niche occupied by genotypes G_5 and G_6. The second megaenvironment fell in the sector of genotype G_{17} and comprised environments E_1, E_4, E_7, E_8, E_9, and E_{10}.

3.2. Fresh Storage Root Yield Per Hectare.
Analysis of variance of the FYLD showed significant differences ($P < 0.001$) among G, E, and GE. The significant GE for FYLD indicated fluctuations in genotypic responses to different environments. FYLD is a trait that typically demonstrates high GE effects [25, 26]. This was observed in the present study and emphasizes the importance of the multi-environment evaluations of newly developed varieties. The average yields of 7.0 to 17.9 tha^{-1} of this study were lower than 11.5 to 25.1 tha^{-1} observed in a similar study in Benin [27].

The combined analysis of variance for FYLD (Table 3) indicated that G accounted for 12.1% of the total sum of squares for FYLD; E contributed for 42.8% and 17.1%

Table 1: Average CMD severity score, fresh root yield (tha^{-1}), root dry matter content (%), root dry yield (tha^{-1}), and total carotene concentration ($\mu g\,g^{-1}$) of 21 yellow-fleshed cassava genotypes in 10 environments.

Genotype		CMD	FYLD (tha^{-1})	DMC (%)	DYLD (tha^{-1})	TCC ($\mu g\,g^{-1}$)
TMS 01/1368[1]	G_1	2.7^{ab}	17.9^a	22.7^{abc}	4.1^a	8^{bc}
TMS 01/1371[1]	G_2	1.7^d	12.6^{abc}	20.9^{abcd}	2.8^{ab}	6.9^c
TMS 06/0889	G_3	1.1^e	7.8^{cd}	16.1^d	1.2^c	7.0^c
TMS 06/1635	G_4	1.1^e	10.1^{bc}	22.1^{abc}	2.4^b	8.8^{bc}
TMS 07/0481	G_5	2.9^{ab}	11.2^{bc}	22.3^{abc}	2.7^{ab}	6.4^c
TMS 07/0498	G_6	3.2^a	8.5^{cd}	22.1^{abc}	1.9^{bc}	6.3^c
TMS 07/0520	G_7	1.1^e	12.5^{abc}	18.0^{cd}	2.4^b	7.6^{bc}
TMS 07/0525	G_8	2.8^{ab}	10.5^{bc}	20.6^{abcd}	2.1^{bc}	6.7^c
TMS 07/0534	G_9	1.1^e	8.9^{cd}	24.0^a	2.9^{ab}	7.0^c
TMS 07/0539	G_{10}	1.0^e	11.8^{abc}	20.1^{abcd}	2.4^b	8.7^{bc}
TMS 07/0553	G_{11}	2.9^{ab}	15.5^{ab}	20.3^{abcd}	3.3^{ab}	7.6^{bc}
TMS 07/0576	G_{12}	3.1^a	8.9^{cd}	19.9^{abcd}	1.6^c	7.9^{bc}
TMS 07/0593	G_{13}	1.1^e	10.6^{bc}	24.3^a	2.8^{ab}	11.7^a
TMS 07/0628	G_{14}	1.0^e	8.2^{cd}	20.1^{abcd}	1.8^{bc}	7.1^c
TMS 07/0632	G_{15}	3.3^a	10.6^{bc}	17.9^{cd}	1.8^{bc}	6.8^c
TMS 07/0749	G_{16}	1.1^e	12.2^{abc}	23.4^{ab}	2.8^{ab}	7.7^b
TMS 07/0824	G_{17}	3.3^a	10.3^{bc}	19.5^{abcd}	1.9^{bc}	8.8^b
TMS 07/0874	G_{18}	1.6^d	7.0^{cd}	20.5^{abcd}	1.7^c	6.7^c
TMS 07/0952	G_{19}	1.9^{cd}	3.5^d	18.7^{bcd}	0.8^c	9.2^b
TMS 07/0962	G_{20}	2.4^{bc}	9.6^{bcd}	19.4^{abcd}	1.8^{bc}	6.5^c
TMS 07/0999	G_{21}	2.4^{bc}	7.8^{cd}	19.7^{abcd}	1.9^{bc}	7.9^{bc}
Mean		2.0	10.6	21.0	2.3	7.8
SE		0.4	4.5	3.5	1.1	1.3
CV%		20.2	42.1	16.8	47.9	17.3

[1]: genotypes used as checks.
Means with the same letter in a column are not significantly different at 95% level.

Table 2: Combined analysis of variance table of genotype, environment, and genotype by environment contributions to the sum of squares of CMD severity of 21 yellow-fleshed genotypes in 10 environments.

Cassava mosaic disease (CMD)					
Source	DF	SS	MS	F	P	% Total SS
Total	776	867.1				
Genotype	20	625.6	31.3	187.1	<0.001	72.1
Environment	9	63.7	7.1	42.4	<0.001	7.4
GE	170	75.8	0.4	2.7	<0.001	8.7
BLK (ENV)	30	10.5	0.3	2.1		
Error	547	91.5	0.2			

Table 3: Combined analysis of variance table of genotype, environment, and genotype by environment contributions to the sum of squares of fresh root yield of 21 yellow-fleshed genotypes in 10 environments.

Fresh Root Yield (FYLD)					
Source	DF	SS	MS	F	P	% Total SS
Total	756	47344.3				
Genotype	20	5750.1	287.5	14.3	<0.001	12.1
Environment	9	20274.6	2252.7	111.9	<0.001	42.8
GE	169	8116.4	48	2.4	<0.001	17.1
BLK (ENV)	30	2569.7	85.7	4.2		
Error	528	10633.5	20.1			

was attributed to GE. In the GGE biplot analysis, PC1 and PC2 explained together 80.5% of the total variation and graphically summarized genotype performance in relation to the environments evaluated in the study. A polygon view of the GGE biplot (Figure 2) shows which genotypes performed best or worst in which environments for FYLD. The vertex genotypes were G_1, G_{11}, G_{19}, and G_6. The other genotypes were located within the polygon and were found less responsive. The megaenvironment made up of E_3, E_4, E_5, E_6, E_7, E_8, E_9, and E_{10} fell in the niche where genotype

TMS 01/1368 (G_1) used as check was the best performer. The second megaenvironment, E_1 and E_2, fell in the sector where genotype G_{11} was the best.

3.3. Root Dry Matter Content. The combined analysis of variance for root DMC of the 21 yellow-fleshed cassava genotypes showed significant differences ($P < 0.001$) among G, E, and GE. The mean root DMC ranged from 16.1 to 24.3% with an average of 21.0%. These results are lower than those reported in earlier studies of yellow-fleshed genotypes
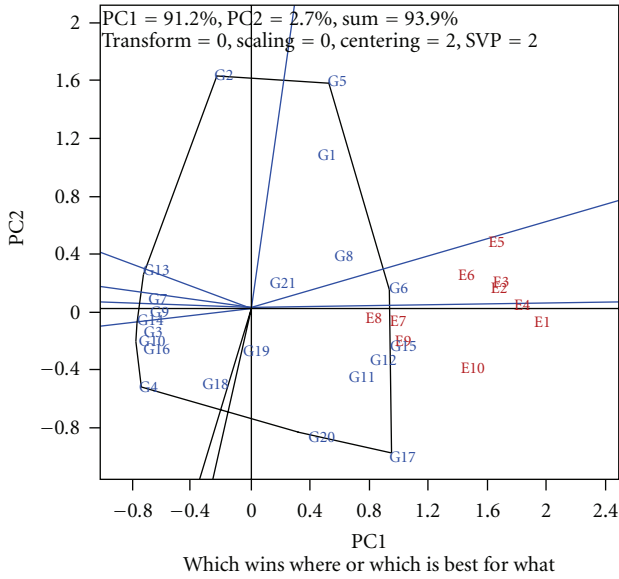
FIGURE 1: Megaenvironment defined by different winning yellow-fleshed cassava genotypes tested in 10 environments for the average severity score of CMD.
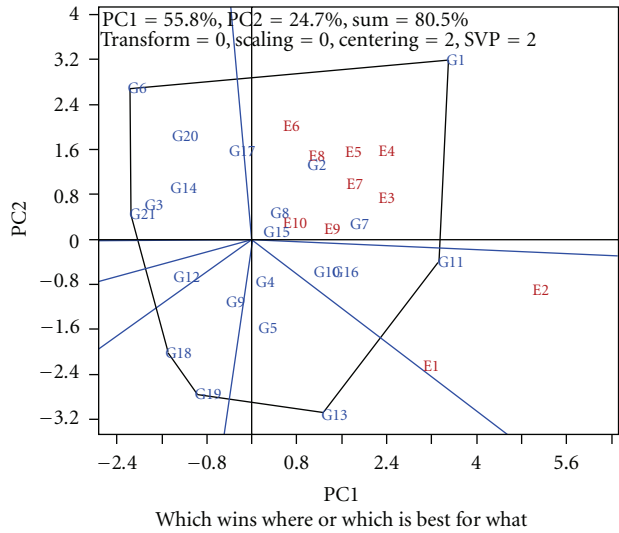

FIGURE 2: Megaenvironments defined by different winning yellow-fleshed cassava genotypes tested in 10 environments for the average FYLD (tha^{-1}).

TABLE 4: Combined analysis of variance table of genotype, environment, and genotype by environment contributions to the sum of squares of dry matter content of 21 yellow-fleshed genotypes in 10 environments.

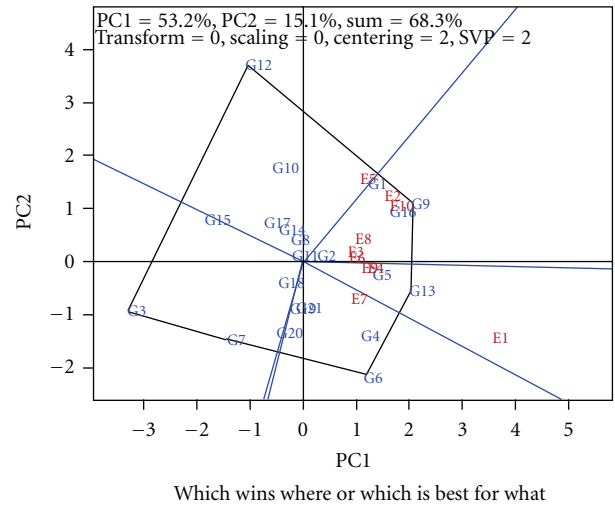| Source	DF	SS	MS	F	P	% Total SS
			Dry Matter Content (DMC)			
Total	574	13648.1				
Genotype	20	2269.4	113.5	9.1	<0.001	16.6
Environment	9	3986.8	443	35.4	<0.001	29.2
GE	167	2532.8	15.2	1.2	<0.001	18.6
BLK (ENV)	20	376.8	18.8	1.5		
Error	358	4482.4	12.5			

FIGURE 3: Megaenvironments defined by different winning yellow-fleshed cassava genotypes tested in 10 environments for the average root DMC (%).

made of E_2, E_3, E_6, E_8, and E_{10}. The second fell in the sector with genotype G_{13} made of environments E_1, E_4, E_7, and E_9, and the third was led by genotype G_{12} and made of environment E_5.

3.4. Root Dry Yield (DYLD). Combined analysis of variance of DYLD revealed significant differences ($P < 0.001$) for G, E, and GE. The average DYLD of the 21 genotypes across the 10 environments ranged from 0.8 to 4.1 tha^{-1}. The highest average DYLD (4.1 tha^{-1}) was recorded by the check TMS 01/1368 (G_1). The overall average DYLD was 2.3 tha^{-1}. These results were lower than those reported in [24] on 25 yellow-fleshed genotypes in Nigeria.

The combined analysis of variance (Table 5) for DYLD indicated that 13.6% of the variation of the total sum of squares was contributed by G, 39.6% by E and 23.0% was due to GE.

In GGE biplot analysis PC1 and PC2 explained together 77.3% of the total variation. Figure 4 summarizes the relative performance of each genotype and shows which genotypes performed best or worst in which environments for DYLD. The vertex genotypes were G_1, G_3, and G_9. One of the

in Nigeria [28]. The highest DMC of 24.3% was obtained for the genotype TMS 07/0593 (G_{13}) followed by G_9 (24.0%) and G_{16} (23.4%). G accounted for 23.8% to the total sum of squares variation for DMC, 42.3% of the total sum of squares were attributed to E, and 19.1% to GE (Table 4).

For the GGE biplot analysis, PC1 and PC2 together explained 68.3% of the total variation (Figure 3). The polygon view of the GGE biplot of DMC showed which genotypes performed best or worst in which environment. The vertex genotypes for DMC were G_3, G_6, G_{13}, G_9, and G_{12}. According to the biplot, three megaenvironments were defined. The first was the winning niche of genotype G_9

TABLE 5: Combined analysis of variance table of genotype, environment, and genotype by environment contributions to the sum of squares of root dry yield of 21 yellow-fleshed genotypes in 10 environments.

	Root dry yield (DYLD)					
Source	DF	SS	MS	F	P	% Total SS
Total	571	2085				
Genotype	20	283.1	14.1	11.6	<0.001	13.6
Environment	9	826.6	91.8	74.9	<0.001	39.6
GE	166	479.7	2.9	2.3	<0.001	23.0
BLK (ENV)	20	59.3	3	2.4		
Error	356	436.3	1.2			

TABLE 6: Combined analysis of variance table of genotype, environment, and genotype by environment contributions to the sum of squares of total carotene concentration of 21 yellow-fleshed genotypes in 10 environments.

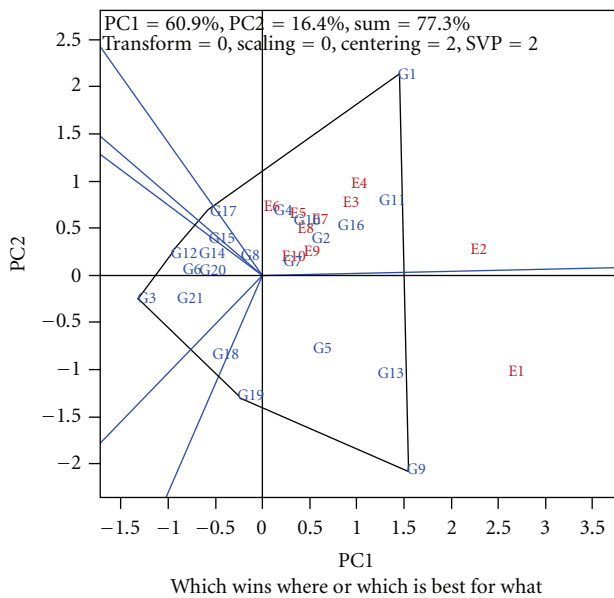|	Total carotene concentration (TCC)					
Source	DF	SS	MS	F	P	% Total SS
Total	542	2186				
Genotype	20	752.3	37.6	20.8	<0.001	34.4
Environment	9	247.5	27.5	15.2	<0.001	11.3
GE	167	559.6	3.4	1.8	<0.001	25.6
BLK (ENV)	18	32.1	1.8	1		
Error	328	594.4	1.8			

FIGURE 4: Megaenvironments defined by different winning yellow-fleshed cassava genotypes tested in 10 environments for the average DYLD (tha^{-1}).

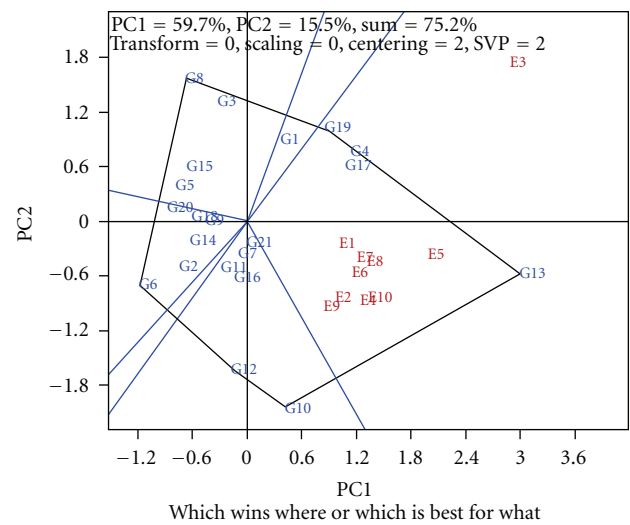FIGURE 5: Mega-environment defined by different winning yellow-fleshed cassava genotypes tested in 10 environments for average TCC ($\mu g\,g^{-1}$).

genotypes used as check, TMS 01/1368 (G_1), was the vertex genotype of a megaenvironment made up of 9 out of 10 environments (E_2 to E_{10}). The remaining environment (E_1) was the niche of genotype TMS 07/0534 (G_9).

3.5. Total Carotene Concentration in Fresh Storage Root (TCC). The combined statistical analysis of TCC recorded for the 21 yellow-fleshed cassava genotypes showed significant differences among G, E, and GE. The average TCC recorded ranged from 6.3 to 11.7 $\mu g\,g^{-1}$ fresh weight. These TCC values were higher than the range of 1.4 to 7.7 $\mu g\,g^{-1}$ obtained in a similar study conducted in Ghana [29]. The overall average of TCC of this study (7.8 $\mu g\,g^{-1}$) was also higher than the 4.8 $\mu g\,g^{-1}$ reported in 2007 for 25 yellow-fleshed genotypes in Nigeria [30].

The best genotype for TCC was TMS 07/0593 (G_{13}) (Table 1). For TCC, G contributed 34.4% to the variation of the total sum of squares, E contributed 11.3%, and GE contributed 25.6% as per Table 6.

In the GGE biplot analysis of TCC, the PC1 and PC2 together explained 75.2% of the total variation. The polygon view of the GGE biplot of TCC (Figure 5) showed which genotypes performed best or worst in which environments. The vertex genotypes for TCC were G_{13}, G_{10}, G_6, and G_8. The genotype TMS 07/0593 (G_{13}) that had the highest average TCC was the best in each of the 10 environments.

4. Conclusion

The combined analyses of datasets of the five traits (CMD, FYLD, DMC, DYLD, and TCC) of the 21 genotypes in 10 environments showed significant differences ($P < 0.001$) among G, E, and GE. With respect to each trait studied, genotypes showed differences in performance in specific environment. Considering FYLD and DYLD, the two checks TMS 01/1368 and TMS 01/1371, together with TMS 07/0553 and TMS 07/0749 have the highest performance for FYLD and DYLD. For reaction to CMD, eight genotypes (TMS 07/0539, TMS 07/0628, TMS 06/0889, TMS 06/1635, TMS 07/0520, TMS 07/0534, TMS 07/0593, and TMS 07/0749)

showed very few or no symptoms in the 10 environments. For percentage DMC, 17 genotypes were grouped in the first category led by TMS 07/0593 and TMS 07/0534 with the highest DMC. The highest TCC was recorded by the genotype TMS 07/0593. From the results of this study, TMS 07/0593 showed outstanding performance for TCC and good performance for most other traits. It appeared to be the best genotype for food technologists and nutritionists to use for feeding trials to combat vitamin A deficiency. It will be a very good source for breeders to improve carotene concentration and resistance to CMD in yellow-fleshed cassava varieties.

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