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Article

Performance and Stability of Improved Cassava (*Manihot esculenta* Crantz) Clones in Demand Creation Trials in Nigeria

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Abstract: Cassava fresh root yield and dry matter content constitute major determinants of demand by end-users. Increased demand for the seeds of improved varieties will facilitate the development of a sustainable seed system. However, for wide acceptability, there is a need to continuously evaluate candidate varieties for stability across different agroecological zones. Participatory Demand Creation Trials (DCTs) were established to evaluate cassava varieties with farmers and processors utilizing the best agronomic practices. The multi-year DCTs were conducted in 20 environments (7 locations) during the 2016–2017, 2017–2018, 2018–2019, and 2019/2020 cropping seasons with two replications. The plot sizes were 320 m^2 with a spacing of 1 m × 0.8 m. The traits evaluated were Plant Vigor (PV), root number, fresh yield, dry yield, Dry Matter Content (DMC), and bundle estimation. The traits were subjected to a GGE biplot in R software to identify high-yielding and stable genotypes. Results obtained from the 20 environments showed that genotype (G), environment (E), and GXE interaction effects were significant ($p < 0.01$) for all the traits but PV. The heritability ranged from 56% (PV) to 96% (DMC). The average fresh yield t/ha ranged from 25.5 (IBA30572) to 35.4 (IBA980505). The DMC ranged from CR36/5 (36.1%) to IBA010040 (30.7%). The dry yield ranged from 8.8% (IBA30572) to 11.4 (IBA980505). Estimated bundles ranged from 13.5 (CR36-5) to 15.7 (IBA950289). Three varieties, IBA961632, TMEB419, and CR36/5, were identified as the most promising high dry matter content varieties for cassava processors and farmers in Nigeria, and genotype IBA961632 was the most stable. The study revealed greater genotypic effects than from the environment and high genetic advances.

Keywords: sustainable seed system; demand creation; GGE biplot and stability

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1. Introduction

The growing world population demands continuous food production to meet human food and nutritional needs. The need to combat hunger is clearly reflected in the Sustainable Development Goals (SDGs) of the UN, whose target is to eradicate hunger by 2030 [1]. Achieving food and nutritional security is closely linked to the increased production and availability of crops that are key food sources for the populace. In sub-Saharan Africa (SSA), roots and tubers contribute a substantial amount of the required calories; they are highly nutritional, cheap, and, therefore, form an essential constituent of human diets in the region [2]. Cassava is well adapted to most agro-ecologies in SSA, and it thrives and produces reasonable yields where most crops fail, thereby fitting as a food security crop and an important source of dietary energy [3]. Cassava forms an essential part of the diet of more than half a billion people and provides a livelihood for millions of farmers, processors, and traders worldwide [1]. The FAO [1] food outlook report put global production of cassava at 202.6 million tonnes on 18.5 million hectares, with Nigeria as the largest producer, accounting for 57 million tonnes from a cultivated area of 3.8 million hectares.

Cassava's tolerance to erratic weather conditions, long-term storability on the farm, and ability to produce a substantial yield in soils where other crops would fail are some factors that make it unique [4]. Sub-Saharan Africa is the world's largest cassava-growing region; however, this is due to the consistent expansion of land area committed to planting cassava and not per hectare productivity [2]. In addition, the current cassava yield is only 12.3 t ha^{-1}, whereas the potential yield is 28.0 t ha^{-1} [5], and the yield of improved varieties at research stations ranges from 13–40 t ha^{-1} [6]. As Nigeria increases its participation in the global cassava market due to growth in the processing of the crop into secondary industrial products, such as starch, flour, ethanol, animal feed, glucose syrup, etc., the need to identify varieties well suited for the diverse product purposes becomes eminent. However, a huge percentage of its production still lies internally in the hands of small-scale farmers [7]. In Nigeria, 56 improved varieties have been officially released, out of which less than ten are popular among farmers and other users [8]. These cassava varieties are used across different products, which does not maximize the quality traits they possess. Cassava root farmers have benefitted little in the sale of roots to industries and processors because they do not have the required varieties. Processors, when buying roots, look out for traits such as starch and flour in addition to fresh root yield based on feedback from the demand creation trials.

The demand for cassava is on the rise, particularly with more industries utilizing roots as raw materials. Increasing cassava yields, therefore, becomes pertinent so that industrial usage does not affect its availability as a food source. However, smallholder farmers who have relied greatly on landraces that are susceptible to pests and diseases and, consequently, low yielding mostly grow cassava. The development of high-yielding and superior genotypes, therefore, becomes imperative. Identification and release of such genotypes are, however, notoriously reliant on Genotype x environment interaction (GEI). GEI refers to variation in the response of genotypes to varied environmental (season, location, years, crop management practices, etc.) conditions such that genotypes with a desirable performance under one growing condition may be poor in another environment [9]. However, understanding GEI patterns from GEI analyses has contributed tremendously to cultivar development. For instance, GEI has necessitated multi-environment trials (METS) from which breeders have identified genotypes that are adapted to a particular environment and those superior across several growing regions [10]. Test environments have also been categorized and representative sites identified, thereby eliminating unnecessary test locations and reducing the cost of cultivar evaluation [11]. The direct implication of a significant GEI is the need to select genotypes based on consistent positive performance over a wide range of environments. The selection of high-yielding but unstable genotypes in a breeding program or commercial farm will lead to devastating results. Stability refers to performance with respective changing environmental factors over time within a given location. [11]

Plant breeders have thus developed several statistical techniques, including the Genotype + Genotype × environment (GGE) biplot by Yan et al. [11] and Yield Stability Index (YSi), to aid decisions on the superiority or desirability of genotypes and exploit the potentials of GEI. The efficiency of the GGE biplot has been compared with other techniques for cassava in making reliable decisions [12,13]. The GGE biplot is the most recent and sophisticated among the proposed techniques [14], while YSi is superior among methods that integrate yield with a stability rating [15,16]. The performance of crops depends on the genotypes and prevailing conditions, including the environment in which plants are grown and genotype-by-genotype interaction [17–19]. Genotypes and environmental factors (plant population, fertilizer rate, pest control, etc.) can be controlled. However, other factors of the environment, such as rainfall, day length, soil properties, and solar radiation, are fixed, difficult to change, and termed uncontrollable factors [18,20]. Information from this work will be crucial to efforts aimed at increasing the cassava yield in farmers' fields to meet local and international demands. This brings about the importance of the product profiling of cassava. Demand Creation Trials are a decision-making tool developed by the IITA Cassava breeding program in collaboration with Sahel Agriculture Consulting under the BASICS project. Processors identified by Sahel Agriculture Consulting are engaged to conduct the Demand Creation Trial and make product decisions, like selecting the preferred variety for their production and making production plans. The objective of establishing the Demand Creation Trial is to obtain feedback from processors and farmers to facilitate market creation and quality-assured stem delivery of improved varieties; this informs the development of product profiles that align with the needs of end-users. Demand Creation Trials have proven to be a useful decision tool for breeders, seed producers, large-scale growers, processors, and farmers. These are currently serving as an important source of evidence-based information for breeders. Hence, this study.

2. Materials and Methods

***Genotypes*:** The genotypes, *viz.*, CR36-5, IBA010040, IBA30572, IBA950289, 101 IBA961632, IBA980505, IBA980581, and TMEB419, were obtained from the Cassava Breeding Unit of the International Institute of Tropical Agriculture (IITA) Ibadan, Nigeria. Genotypes under testing were improved and officially released white-fleshed cassava varieties in Nigeria. The check TMEB419 was commercially cultivated, which is white rooted, found to be CMD resistant, and preferred.

***Test locations*:** The multi-year field trials were conducted in 20 cassava processor environments in Nigeria during the 2016–2017, 2017–2018, 2018–2019, and 2019/2020 cropping seasons. The test locations and their respective coordinates included AgoOwu (N07 11.774, E004 11.004), CrestAgro (N07 51.716, E006 30.052), Eagleson (N07 46.748, E003 37.757), Funnab (N07 14.241, E003 26.151), Abuja (N09 16.504, E007 34. 175), Ikenne (N06 61.238, E003 51.788), Psaltry (N07 46.649, E003 24.395), and Shao (N08 40.439, E004 32.029) and represented the major cassava growing agro-ecologies in the country. Nigeria has a tropical climate with variable rainy and dry seasons depending on the location.

Study environments in Nigeria and their codes: This multi-year study was carried out over four seasons. The environment codes used for this study included: AgoOwu17 (E1), AgoOwu18 (E2), AgoOwu20 (E3), CrestAgro 18 (E5), CrestAgro 19 (E6), Eagleson18 (E7), Eagleson19 (E8), Funnab19 (E9), Funnab20 (E10), Abuja20 (E11), Ikenne18 (E12), Ikenne19 (E13), Ikenne20 (E14), Psaltry18 (E15), Psaltry19 (E16), Psaltry20 (E17), Shao18 (E18), Shao19 (E19), and Shao20 (E20).

Environment climatic conditions: Nigeria is characterized by three distinct climate zones, a tropical monsoon climate in the South, a tropical savannah climate for most of the central regions, and a Sahelian hot and semi-arid climate in the North. This leads to a gradient of declining precipitation amounts from South to North. Nigeria has an estimated average annual rainfall of 2000 mm, which varies for both the coastal areas and inland regions. The trials environment and their climatic features are as follows: Ikenne and Funnab (humid forest zone), Eagleson, AgoOwu and Psaltry (forest savannah transition), Shao (southern guinea savannah), and Abuja (derived savannah).

***Trial description and experimental design*:** The experiment was established using a randomized complete block design with 2 replications at each location. The test genotypes were planted in a plot of 20 rows with 20 stands on each row using a planting spacing of 1 m × 0.8 m. All measurements were based on the inner 18 rows, discarding the first and the last stands on each ridge to give a total of 324 plants per net plot. This study was conducted under rainfed conditions, and no fertilizers were applied. Trials were independently managed by farmers/processors. Recommended weed management routines for cassava were adopted. Harvesting in all locations was performed 12 months after planting (MAP).

Measurements of traits:

***Biotic stress*:** The severity of cassava mosaic disease (CMD) and cassava bacterial blight disease (CBB) was scored using the 1 to 5 scale system described by IITA (1 = no symptoms and 5 = severe symptoms). The average CMD and CBB severity was then calculated based on ratings taken at 1 and 6 MAP.

Agronomic traits: At 12 MAP, the trials were harvested, and measurements were taken on the number of harvested plants, marketable and non-marketable root number, number with root rot, marketable and non-marketable root weight, number of bundles, bundle weight, and shoot weight. Marketable roots are commercial roots that have large sized of storage roots, while non-marketable roots are non-commercial roots that have small sized of storage roots. Bundle is a term used to describe the quantity of cassava stems, and information on the bundle weight is used to determine the shelf life of stems. The roots were sampled from each plot across the replications and processed for estimation of dry matter content (DMC) following the oven drying method described by Norbert et al. [21]. Fresh root yield (FYLD), t/ha, and dry matter content (DMC) per plot were further used to derive the dry yield (DYLD) in tonnes per hectare using the expression: DYLD = FYLD/100 × DMC.

Data analysis**:** All agronomic and post-harvest data collected were analyzed using R software version 4.0.3 with the following main R packages: Agricolae (Analysis of variance), GGEbiplot version 7.10 (GGbiplot) [22,23], Coorplot (correlation) [24–26], and StatgensSTA (estimate of variance component and heritability).

3. Results

The mean agronomic performance of 8 cassava varieties was evaluated during the 2016–2017, 2017–2018, 2018–2019, and 2019–2020 rainy seasons across 20 locations in Nigeria (Table 1). The fresh yield value in tonnes per hectare ranged from 25.5 (IBA30572) to 35.4 (IBA980505). CR36/5 had the highest dry matter content (36.1%), and IBA010040 had the lowest (30.7%). The mean dry yield was 10.4%, with 6 varieties outperforming the overall mean. The mean estimated bundle value per plot of 320 m^2 ranged from 13 to 16. The mean root number (RTNO) per hectare was 1312.59, with a range of 1039.41 (IBA30572) to 1579.05 (CR36/5). Three improved genotypes had higher root numbers than the mean, while all 6 genotypes had higher root numbers than the widely cultivated TMEB419. The mean plant height was 228.57 cm, with a range of 203.36 cm (IBA961632) to 234.83 cm (CR36/5).

Table 1. Estimate of genetic parameters and heritability of eight improved cassava clones.

Trait	Mean	δ^2p	δ^2g	δ^2e	CV	H^2
Fresh yield (t/ha)	30.1	54.7	13.3	33.1	19.1	84
Dry yield (%)	10.4	6.3	1	4.1	19.4	76
Dry matter (%)	34	14	6.9	3.5	5.4	96
Bundle estimate	14.6	36.9	1.2	5.6	16.2	74
Root number	1312.6	168,488.4	45,570.2	77,589.7	22.2	88
Plant height (cm)	228.5	1825.2	307.4	512	9.9	90
Vigor	6	0	0.1	0.5	12.2	56

Where δ^2p = phenotypic variance, δ^2g = genotypic variance, δ^2e = error variance, CV = coefficient of variation, and H^2 = Broad sense heritability.

The mean fresh root yield performance across locations was 29.99 t ha^{-1}. IITA-TMS-IBA980505 (56.83 t ha^{-1}) gave the highest at Ago owu in 2017 (Table 2). The lowest performer across locations was TME419 (12.04 t ha^1) in 2020 at Funnab. The marketable root number mean value ranged from 538.74 (CR36/5 at Ago owu in 2017) to 2355.40, observed in 2018 at Ago owu for IBA980505. The mean performance of the commercial stem in a bundle per plot was 14.36. The lowest produced was 3.58 for IBA961632 in 2020 at the Psaltry field, whilst the highest mean value was 34.03 at Ago owu for TME419, followed by IBA980581 (32.97) in 2018 at the same location. The mean percentage dry matter value was 34.83%. These values ranged from 22.78% for IBA010040 in 2018 at Ikenne to 44.10 (IBA961632) in 2018 at Shao farms. It was observed that the Ago owu environment produced the highest dry yield value in tonnes per hectare in 2018, with a mean value of 15.41 t/ha for CR36/5, followed by TME419 (14.43).

Table 2. Mean agronomic performance of eight cassava genotypes evaluated across locations for the *2016–2017*, *2017–2018*, *2018–2019*, and *2019/2020* cropping seasons.

Genotype	Plant Vigor	Plant Height (cm)	Root Number	Fresh Yield (t/ha)	Dry Yield (%)	Bundle Estimate	Dry Matter (%)
CR36-5	5.86	234.83	1579.05	30.22	10.82	13.48	36.08
IBA010040	5.92	223.74	1244.38	33.03	10.39	14.53	30.74
IBA30572	5.61	231.39	1039.41	25.51	8.82	13.85	32.92
IBA950289	6.31	234.05	1371.09	31.74	10.36	15.69	32.11
IBA961632	6.22	203.36	1311.41	28.85	10.78	13.55	37.27
IBA980505	5.91	213.57	1512.49	35.39	11.38	14.69	31.91
IBA980581	6.34	228.59	1381.88	27.10	9.43	15.42	33.89
TMEB419	6.07	258.57	1061.01	28.95	10.84	15.40	37.33
Grand Mean	6.03	228.51	1312.59	30.10	10.35	14.58	34.03
LSD	0.75	21.80	213.61	3.92	1.24	1.43	1.85
CV	12.20	9.90	21.22	19.12	19.56	16.17	5.47

The estimate of heritability ranged from 56% for plant vigor to 96% for dry matter; the content of Table 3 shows the combined analysis of variance for the traits studied. Combined ANOVA provided clear evidence of the presence of GEI in all traits studied ($p < 0.001$). A similar trend was observed for the genotype main effect. The main environmental effects were significant for plant height, total root number, fresh root yield, and dry matter content only. In addition, it was observed that the genotype by environment interaction accounted for the highest proportion of the total sums of squares for all the studied traits.

Table 3. Combined analysis of variance and contributions to the mean sum of squares of the studied traits of eight clones tested in nine environments (2016–2020).

Source of Variation	DF	Plant Vigor	Plant Height (cm)	Root Number	Fresh Yield (t/ha)	Dry Yield (%)	Bundle Estimate	Dry Matter (%)
GEN	7	0.01 *	1123.2 *	9084.2 *	46.7 *	5.2 *	5.0 *	20.3 *
LOCATION(REP)	8	0.03	244.5 *	41,292.7 *	20.5 *	2.1 *	0.72	0.4
YEAR	3	1.2 *	3192.2 *	1,978,160.3 *	528.4 *	80.2 *	313.6 *	23.3 *
GEN × LOCATION	41	0.01	37.2 *	4130.9 *	2.7 *	0.2 *	0.4 *	0.30 *
GEN × YEAR	13	0.1 *	83.6 *	11,812.7	4.8 *	0.4	0.7	0.3
LOCATION × YEAR	10	0.3 *	617.1 *	77,639.8 *	34.3 *	3.8 *	21.6 *	2.7 *
GEN × LOCATION × YEAR	39	0.01	20.4	3197.7	0.9	0.1	0.2 *	0.1
Mean		6.38	232.58	1288.03	29.99	10.33	14.36	34.83
CV		10.81	10.42	23.86	19.93	20.4	16.74	5.96
RSQUARE		0.78	0.91	0.88	0.87	0.86	0.95	0.92
MSE		0.69	24.25	307.34	5.97	2.1	2.4	2.07

* Indicates a significant level at $p < 0.01$. FYLD = Fresh root yield in tonnes per hectare; Dry matter content; Dry root yield in tonnes per hectare; REP = replication; GEN = genotype; LOC = location.

Pearson correlation coefficients were computed to assess the interrelationships among some selected traits, including plant height, vigor, fresh yield, dry yield, dry matter, root number, and bundle estimate (Table 4). Results indicated that 13 positive correlations existed among the studied traits and ranged from a low value of 0.04 (fresh yield and dry matter) to 0.78 (fresh yield and dry yield). The dry matter content and plant vigor had a strong positive association of 0.73. Weak associations were observed among traits in this study, and these values ranged from −0.08 to −0.24 for plant height and vigor and plant height and dry yield, respectively.

Table 4. Pearson correlation among selected traits of eight improved cassava clones.

Trait	FYLD	DYLD	DMC	Bundle	RTNO	PH	Vigor
Fresh yield (t/ha)	1	0.78	0.04	0.12	0.69	0.03	−0.05
Dry yield (%)		1	0.58	0.12	0.55	−0.24	0.31
Dry matter (%)			1	−0.04	−0.08	−0.63	0.73
Bundle estimate				1	0.26	0.64	−0.44
Root number					1	0.3	−0.31
Plant height (cm)						1	−0.96
Vigor							1

Where FYLD = Fresh yield, DYLD = Dry yield, DMC = Dry matter content, PH = Plant height, RTNO = Root number.

Stability Analysis

The GGE biplot showed that the first and second principal components accounted for 68.1% and 10.0%, respectively, of the Genotype + Genotype × Environment (GGE) variation for dry yield, with both accounting for 78.1%. Following the 'which wins where' rule, a total of nine sectors resulted in the biplot with genotypes (Figure 1). Environment *viz.* (E4, E11, E15, E8, and E17) fell into the sector where genotypes IBA961632 and TMEB419 were the vertex clones. This means that IBA961632 and TMEB419 were the best clones in this environment. The two other environments, namely, E12 and E2, fell into the sector in which genotype CR36/5 was the vertex clone. This clone outyielded all other clones by producing the maximum dry yield in these two environments. No environment fell into sectors where the genotypes *viz.*, IBA010040, IBA980581, and IBA30572 were placed on the vertices. This demonstrated that these clones did not perform well in any of the environments. In other words, these genotypes were identified as poor-performing clones in some or all of the environments. Moreover, genotypes *viz.*, IBA980505, and IBA950289 were located near the origin and were found to be less responsive to the environment compared to those located on the vertices far away from the origin.

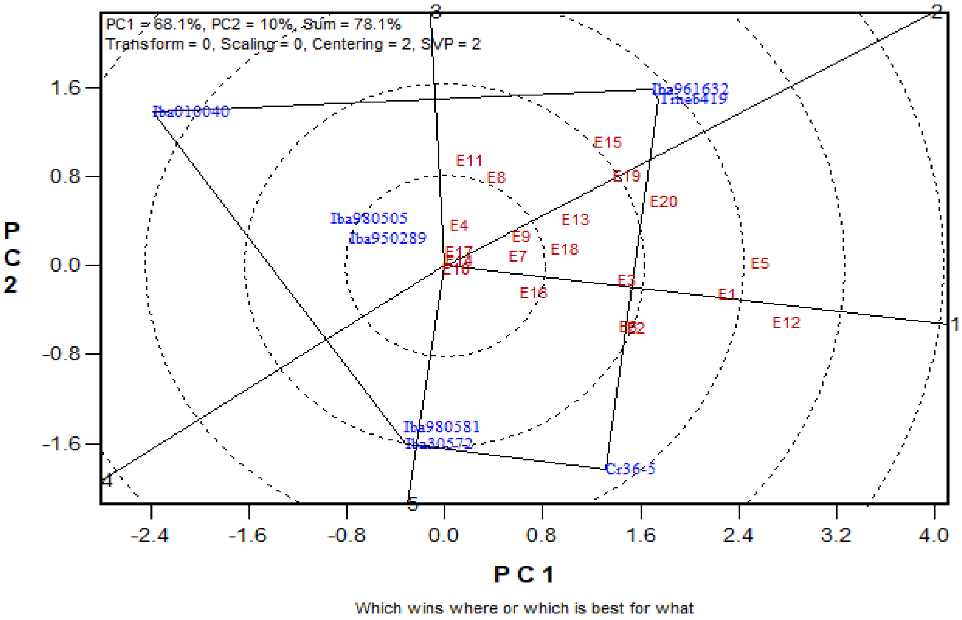

Figure 1. Polygonal view of the GGE biplot based on environmental scaling for the 'which-wins-where' pattern of genotypes and environments.

Average dry yield and stability of the clones: Average dry yield and stability in the performance of the different clones are shown in Figure 2. The genotype TMEB419 produced the highest average dry yield, followed by genotype IBA961632, being placed far away from the origin in a positive direction. However, genotype IBA010040 followed by IBA950505 were identified as low-yielding genotypes in terms of dry yield being placed in the negative direction. Similarly, stability and suitability are estimated through the projection of the corresponding cultivar along the ATC Y-axis. The stability of a cultivar is described by the absolute length of the projection. A lower value is desirable—revealed stability. Thus, genotypes IBA191632 and TMEB419 were identified as the most stable, followed by CR36/5, whereas genotype IBA010040 was found as the least stable clone.

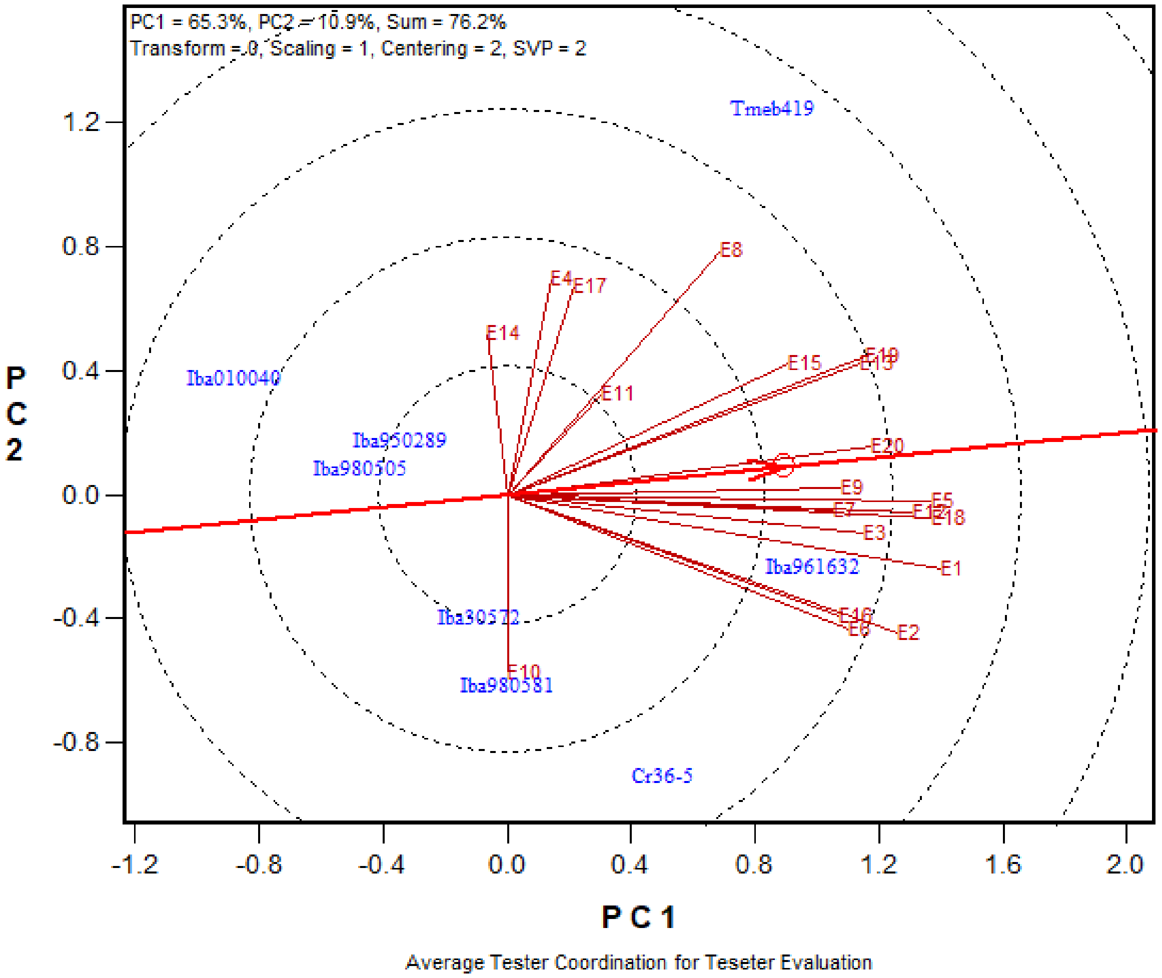

Figure 2. The average tester coordination for tester evaluation.

The representative and discriminating ability of environments: In the present study, less vector length was observed in environment E10 (Figure 3), thus demonstrating that genotype variation was high in this environment for the dry yield. Moreover, the angle between the vectors of this environment was high as compared to the vectors of the other environments, which clarified that the relationship between E10 and other environments was a relatively long vector length. Most of these environments showed a close angle among their vectors and, thus, depicted a close relationship with one another.

The GGE biplot, for the evaluation of the mega environments among the twenty environments regarding dry matter content and stability performance, indicated that all the tested environments were clustered as two mega environments (Figure 4) in this study. Eagleson 19 (E8) was found in a mega environment. However, a total number of seven environments were clustered in a mega environment, indicating that these environments shared the same type of winning varieties. These environments included Funnab20 (E10), Shao19 (E19), Ikenne18 (E12), Funnab19 (E9), Psaltry18 (E15), AgoOwo19 (E3), CrestAgro19 (E6), Ikenne19 (E13), and Psaltry19 (E16).

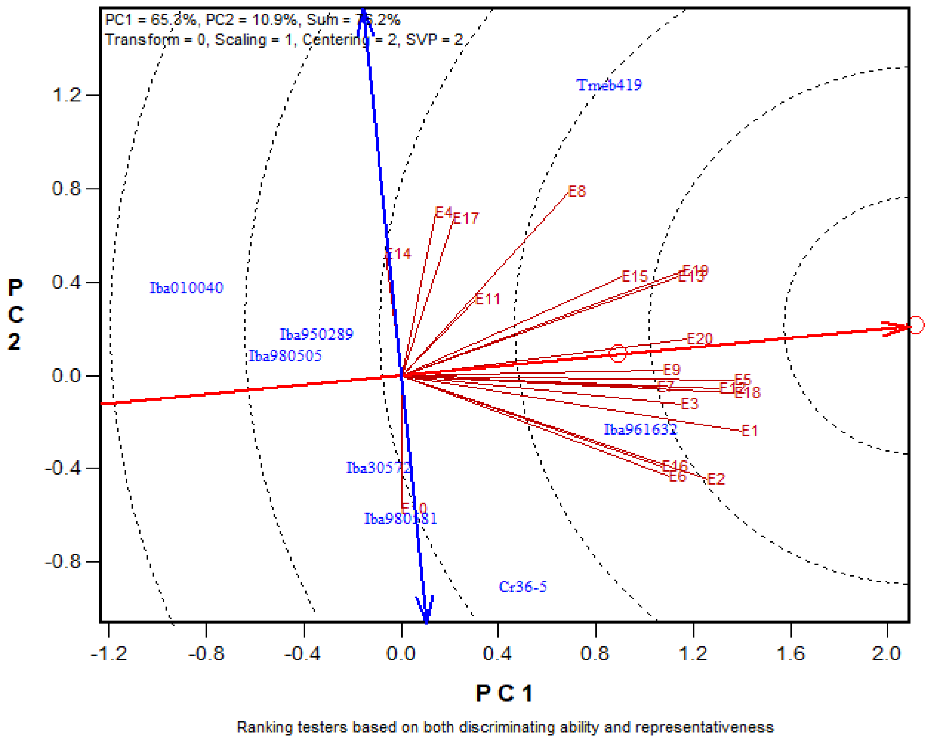

Figure 3. GGE biplot for the evaluation of the relationships among the twenty environments.

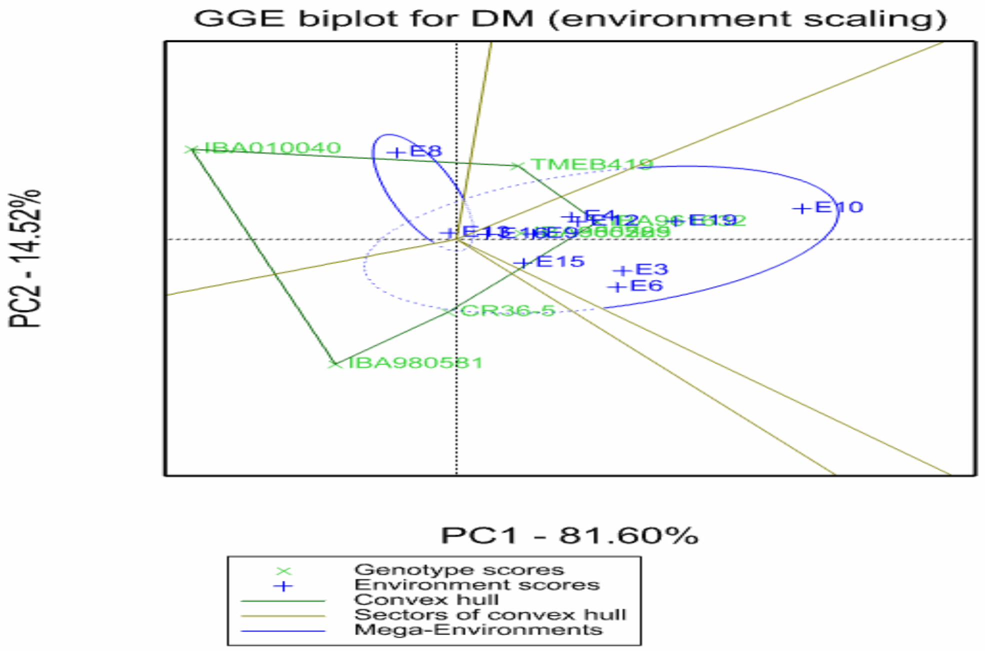

Figure 4. GGE biplot for the evaluation of the mega environments among the twenty environments.

4. Discussion

The objective of our study was to determine stable and high-yielding IITA-improved cassava genotypes in independent commercial cassava processors' fields in order to accelerate acceptance of improved varieties by processors, thereby creating demand for stems of these varieties to increase productivity, translating to higher income. There was a highly significant GEI effect for all studied traits. This implies that there was a high difference in the response of the genotypes across the test locations, which could be due to the variations in climatic and edaphic features of each location. Highly significant variations observed for most of the traits tested among genotypes across all locations indicate the existence of variability among the tested genotypes. The high heritability observed for fresh root yield and dry matter concentration was in accordance with the reports of Aina et al. [13], Norbert e al. [21], and Akinwale et al. [27]. This is a result of several years of intense selection for the economic traits imposed on the population from which they were derived. The observed larger impact of the genotype's main effect over the environment's effect on the performance of the traits studied agrees with the reports of Akinwale et al. [27] and Peprah et al. [28]. However, it was in contrast with the report of Norbert et al. [21], who reported that the environment's main effect had more impact than the genotype's effect. The GE effects were found to be generally higher than the E and G effects in cassava; this was in agreement with the trends that have been reported by researchers, as cited earlier.

Three improved genotypes that included IBA961632, TMEB419, and CR36/6 outperformed the other clones for dry yield, translating to high starch production for processors and farmers in Nigeria. This implies that the improved genotypes have the potential to increase the production and productivity of cassava in test regions and locations with similar agroclimatic conditions. The mean dry matter content observed in our study was comparable to results obtained by several authors [12,21,27], which calls for the need to further increase the genetic gain in dry matter content as the productivity of cassava is highly dependent on it. High dry matter content is required to improve upon a processor's main products, such as high-quality cassava flour, starch, and granulated and paste products, such as gari and fufu, which was the basis for this study.

The GGE biplot analysis provided excellent visual information on the performance and stability of the evaluated improved cassava varieties. An excellent genotype should combine high mean fresh root yield, dry matter, and high stability within its mega environment [29]. Hence, IBA961632 was identified as the best-performing and most stable genotype from this study, followed by TMEB419 and CR36/5. This means that they are high yielding and more stable, and, hence, desirable for testing and promotion to improve the production and productivity of cassava and provide more security and income generation for farmers in the face of consistent weather fluctuations. However, genotypes IBA010040, followed by IBA950505, were identified as low-yielding genotypes in terms of dry yield, being placed in the negative direction. This is In agreement with Kauh [20]. Similarly, stability and suitability are estimated through the projection of the corresponding cultivar along the ATC Y-axis. The stability of a cultivar is described by the absolute length of the projection. A lower value is desirable—revealed stability. Thus, genotypes IBA191632 and TMEB419 were identified as the most stable, followed by CR36/5, whereas genotype IBA010040 was found as the least stable clone.

In the present study, less vector length was observed in environment E10 (Figure 3), thus demonstrating that genotype variation was high in this environment. Moreover, the angle between the vectors of this environment was high compared with the vectors of the other environments, which clarified that the relationship between E10 and the other environments was a relatively long vector length. Most of these environments showed a close angle among their vectors and, thus, depicted a close relationship with one another. For various agronomic traits in *G. hirsutum* L., significant genotype and environment main effects and G × E interaction effects were reported by Gul et al. [18]. Such commonalities have been reported in numerous studies conducted on *G. arboreum* L., such as Iqbal et al. [30].

Our study identified Funnab 20 (E10) to have a good discriminating ability and representativeness. Although, some environments had good representativeness because they had the shortest vector length and were slightly apart from other environments, meaning that they had a poor discriminative ability, which was further evident by the non-significant interaction effects in this study. However, our results on the aforementioned environments were in contrast with Akinwale et al. [27], who reported that Mokwa in northern Nigeria had good discriminating ability. This discrepancy could be attributable to a year or within-location effect. The highly correlated environments in this study imply that these environments gave the same information about the improved genotypes. Therefore, it would be interesting to conduct further studies to confirm the mega environments and ascertain if the GEI effect is repeatable across years, such that redundant environments may be identified and removed to minimize the cost of multilocation testing by plant breeders.

5. Conclusions

GGE biplot analysis provided an excellent graphical representation of GEI effects. Three varieties were identified, IBA961632, TMEB419, and CR36/5, as the most promising high dry yield varieties for cassava processors and farmers in Nigeria, and genotype IBA961632 was the most stable. The high variability that existed among the tested cassava clones for fresh yield and related traits calls for further analysis to uncover redundancy among these environments; this offers the possibility of regional and specific environment breeding for a greater impact of research.

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