



## Genotype x Environment Interaction Effects on Yield and Related Traits of Cassava (*Manihot esculenta* Cranz) in Nigeria

<sup>1</sup>Uba, E. and <sup>2</sup>Nwobi, F. N.

<sup>1</sup>National Root Crops Research Institute, Umudike, Abia State, Nigeria

<sup>2</sup>Imo State University, Owerri, Imo State, Nigeria

Corresponding Author's email: [ubaezenwany26@gmail.com](mailto:ubaezenwany26@gmail.com)

### Abstract

A significant genotype by environment interaction (GEI) presents challenges in the selection of superior genotypes. The objective of this study was to evaluate the stability of 12 improved cassava genotypes by examining their performance for yield and related traits in three environments. Accordingly, 12 cassava genotypes were evaluated to assess genetic variability for root yield and its components at three locations (Umudike, Otobi and Igbariam) in Nigeria during the 2018 – 2019 cropping season. This research was carried out to study the stability performance for cassava root yield and its components using a Randomized Complete Block Design. Genotype x Environment interaction was significant for all the traits studied, indicating considerable influence of the environment on the expression of the traits. The genotype by environment interaction effect was significant for all the traits studied.

**Keywords:** Cassava genotypes, Traits, Genetic Variability, Yield, Stability

### Introduction

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

The success of cassava in sub-Saharan Africa, as a food security crop, is mainly because of its ability to give good yields in marginal soils where other food crops would fail. Despite the ability of cassava to grow in marginal soils (Mkumbira *et al.*, 2003), large differences in genotypic responses occur under a wide-range of agro-environmental conditions. This phenomenon is referred to as genotype x environment interaction (GEI), which is a common occurrence in plant breeding programmes. Genotype x environment interaction (GEI) is the inconsistent performances of

genotypes in across environments (across locations and years). Previous work on GEI in some important crops include Akinyele and Osekita (2011), Sakin *et al.* (2011), Ngeve *et al.* (2005) and Kilic *et al.* (2009). The expression of a phenotype of an individual is determined by both the genotype and the environment. The effects of these two factors, however, are not always additive because of the combined effect of the genotype and the environment. The presence of the interaction between genotype and the environment (GEI) makes the varietal selection process difficult as it decreases the usefulness of genotypes by confounding their yield performance through reducing the relationship between genotype and phenotype (Farshadfar *et al.*, 2012).

A significant genotype x environment (GE) occurs due to changes in the magnitude of genotypes' differences in contrasting environments or from changes in the relative ranking of genotypes (Ssemakah and Dixon, 2007). Nonetheless, it is feasible to develop genotypes with low interaction between genotype and the environment through sub-division of diverse area into smaller, more similar sub-regions and by identifying and selecting genotypes that are stable across varying environments (Farshadfar *et al.*, 2011). GEI is considered as an opportunity as well as a challenge for plant breeders. Breeders face the GEI challenge by assessing genotypes

across environments to make sure that they select genotypes with stable and high performance for the trait(s) of interest. The term stability is often used to characterize genotypes which show relatively constant yield, independent of varying environmental conditions. In this regard, genotypes whose GEI is insignificant are said to be stable. The GEI analysis, therefore, becomes an essential tool used by plant breeders to assess the adaptation of genotypes and to identify and select parents for base populations.

A phenotype (P), is being known as the characteristic that is observed, depends on a combination of its genetic constitution, called the genotype (G), and the environment (E) and a component attributed to the interaction between genetic and ecological components (G×E). Since genes are expressed in an environment, the degree of expression of a heritable trait is impacted by its environment. This is usually expressed thus (Falconer and Mackay, 1996; Tumuhimbise, 2014);

$$P = G + E + GE \dots (1)$$

Where; P is Phenotype, G is Genotype, E is Environment, G x E is Genotype by environment interaction

The equation as stated below for phenotypic expression observed in the phenotype due to variation in the factors resulting in the genotype. The relationship can be described as:

$$VP = VG + VE + VGE \dots (2)$$

Where: VP is Phenotypic variation, VG is Genotypic variation, VE is Variation due to environment, VG x E is variation due to genotype by environment interaction

The knowledge of GEI can help to reduce the cost of extensive genotype evaluations by eliminating unnecessary testing sites and by fine tuning breeding programmes (Shafii *et al.*, 1992; Basford and Cooper, 1998). GEI relates to sustainable agriculture as it affects efficiency of breeding programmes and allocation of limited resources. According to Kang and Magari (1996), GEI is a major concern in plant breeding since it can reduce progress from selection and may make cultivar recommendation difficult as it is statistically impossible to interpret the main effects. Evaluating stability of performance and range of adaptation has become increasingly important for breeding programmes. Successful varieties must have good yield and other essential agronomic characters. Besides, their performance should be reliable across multiple environmental conditions. The basic factor responsible for the differences in stability between genotypes is a large occurrence of GEI. Environment refers to the combination of physical attributes of a location and the climatic and other attributes of a specific season (i.e. soil type, fertility, topography, relative humidity, temperature, rainfall, pest/disease challenge) that affect the plant growth in the growing season and a specific location. The interaction between the genotype and environment refers to the deviation in performance of any attributes of genotypes within the growing environments (Van *et al.*, 2016). The most important consequence of GEI is that the different traits under

consideration show a change in rank in different environments. Such changes of rank in the genotypes which is called crossover GEI (Kang, 2002) creates inconvenience in plant breeding. Analysis of GEI was used to estimate how much stability and adaptability of a variety if planted in the different environment (Masinde *et al.*, 2018).

## Materials and Methods

### Experimental Locations

Trials were conducted at three environments namely Igbariam, Otobi and Umudike representing the major cassava growing agro ecologies in Nigeria. Igbariam (forest-savanna transition) is located at 6.4°N and 6.93°E with annual rainfall of 1268.4 mm. Otobi (Derived Savanna) is located at 07°20'N and 08°41'E with annual rainfall of 1500mm. Umudike (Humid rainforest) is located at 05°29'N and 07° 33'E with annual rainfall of 2200mm. Planting was done in 2018/2019 cropping season during the onset of rains for each location.

### Planting Materials

Planting materials consist of twelve cassava genotypes. Eleven yellow-fleshed cassava genotypes from the Harvest plus cassava breeding program at National Root Crops Research Institute (NRCRI), Umudike, Nigeria and one white-fleshed cassava genotype from the germplasm collection of International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria were used in this study. Two of these cassava genotypes (TMS30572 and NR070220) were used as checks.

### Experimental Design

The experiments were carried out using randomized complete block design with three replicates. The genotypes were planted with a spacing of 1m x 1m, b rows planted with 6 plants per row and a plot size of 6m long and wide (6m x 6m) were used. No fertilizer was applied and central practices such as weeding, spraying of herbicides were undertaken to raise healthy crops. The model of the two factors experiment with n replications per cell is given as

$$Y_{ijk} + \mu + G_i + E_j + \gamma_{ij} + R_k + \epsilon_{ijk} \dots (3)$$

$$i=1, \dots, g, \quad j=1, \dots, e, \quad k=1, \dots, n$$

Where,

$G_i$  = effect of the  $i^{\text{th}}$  genotype

$E_j$  = effect of the  $j^{\text{th}}$  environment

$\gamma_{ij}$  = interaction effect of the  $i^{\text{th}}$  genotype and  $j^{\text{th}}$  environment

$R_k$  = kth replicate in the  $ij^{\text{th}}$  cell.

$\epsilon_{ijk}$  = is the error in observing  $k^{\text{th}}$  replication of the  $j^{\text{th}}$  environment and  $i^{\text{th}}$  genotype

$$\epsilon_{ijk} = \sim \text{iid } N(0, \sigma_{\epsilon}^2)$$

The hypotheses of interest are

$$H_0^1 : g_i = 0 \quad \forall_i$$

$H_1$ : the  $g_i$  are not all equal to 0.

$$H_0^2 : e_j = 0 \quad \forall_j$$

$H_2$ : the  $e_j$  are not all equal to 0

$$H_0^3 : \gamma_{ij} = 0 \quad \forall_{ij}$$

$H_3$ : the  $\gamma_{ij}$  are not all equal to 0.

$$H_0^4 : r_k = 0 \quad \forall_k$$

$H_4$ : the  $r_k$  are not all equal to 0

Where,  $\forall$  is define as for all

The relationship between different sum of squares of 3) is given as

Total sum of squares ( $SS_{total}$ ) = Sum of squares of factor E ( $SS_E$ ) + Sum of squares of factor G ( $SS_G$ ) + Sum of squares of interaction GxE ( $SS_{G \times E}$ ) + Sum of squares of errors ( $SS_{error}$ )

$$\text{i.e } SS_{total} = SS_E + SS_G + SS_{G \times E} + SS_{error}$$

## Results and Discussion

### Results

The dataset was obtained from a one-year field trial on cassava in 2018/2019 planting season. The experiments were conducted in a randomized complete block design with 2 factors: 12 genotype (G) levels in 3 locations (Environment, E) where each G ( $i = 1 \dots 12$ ) was replicated 9 times.

### By yield we mean the data on

- (i) Starch Content (%)
- (ii) Fresh Root Yield (t/ha)
- (iii) Dry Matter Content (DMC)
- (iv) Dry Root Yield (t/ha)

### Starch Content (%)

The combined ANOVA for starch across environments show highly significant ( $p < 0.001$ ) mean squares for genotype (G) and environment (E), and very significant ( $p < 0.01$ ) mean square for genotype x environment (GEI). The corresponding sum of square for environment, replication nested in environment, genotype, genotype by environment and the residuals are 1462.52, 28.48, 1293.33, 809.07 and 1008.25 respectively. The relative magnitude of the main effects and their interactions for starch content as a proportion of the total sum of squares showed that 40.7% of the total sum variation was attributed to environment (E), 36.28% to genotype and 22.5% to genotype x environment interaction (GEI) across environments, the starch content varied significantly among the 12 genotypes in Table 1.

### Fresh Root Yield (t/ha)

Table 2 presents the combined analysis of variance for fresh root yield across environments of 12 cassava genotypes. Fresh root yield show highly significant mean squares for all the sources of variance. Genotype (G), environment (E) and genotype by environment (GEI) showed highly significant differences ( $p < 0.001$ ). The relative magnitude of the main effects and their interactions for fresh root yield as a proportion of the total sum of squares showed that 29.92% of the total yield variation was attributed to environment (E), 51.8% to genotype (G) and 16.2% to genotype x environment interaction (GEI). Across environments, fresh root yield varied significantly among the 12 genotypes.

### Dry Matter Content (%)

The combined analysis of variance for root dry matter content showed highly significant differences ( $P < 0.01$ ) for genotypes (G), environments (E) and genotype by environment interaction (GEI). The relative magnitude of the main effects and their interactions for root dry matter content as a proportion of the total sum of squares showed that 41.7% of the total variation was attributed to environment (E), 36.10% to genotype (G) and 22.5% to genotype x environment interaction (GEI). Across environments, root dry matter content varied significantly among the genotypes (Table 3).

### Dry Root Yield (t/ha)

The combined analysis in Table 4 on variance for dry root yield showed highly significant differences ( $P < 0.01$ ) for genotypes (G), environment (E) and Genotype x Environment Interaction (GEI). The relative magnitude of the main effect and their interactions for dry root yield as a proportion of the total sum of squares showed that 51.24% of the total variation was attributed to environment (E), 30.84% to genotype (G) and 17.40% to genotype X Environment Interaction (GET).

Table 5 shows the overall summary of the agronomic attributes of the cassava genotypes across the environments. The dry matter content of the cassava genotypes ranged from 33.3 to 42.9%, whereas fresh root yield ranged from 3.6 to 33.3 t/ha. The mean agronomic attributes show significant differences among the cassava genotypes.

### Discussion

Cassava (*Manihot esculenta* Crantz) is an important food security crops as it can thrive in a wide range of agro-ecological zones. Due to its ability to perform well across diverse environmental conditions, large differential responses from the same genotypes occur when evaluated in contrasting environments. This phenomenon is known as genotype x environment interaction (GEI), which occurs frequently in plant breeding programmes. Breeders face the challenge caused by GEI by assessing genotypes across contrasting environments to make sure that they identify and select genotypes with high and stable performance. The main objective of this study was to evaluate the stability of 12 improved cassava genotypes by examining their performance for yield and related traits in three locations.

The performance of cassava genotypes is determined by the influence of genotype and environment main effects and their interactions (Egesi *et al.*, 2007; Aina *et al.*, 2007). The significance of the genotype and environment main effects for all traits indicated genotype differences towards adaptation to different environments. This implies that genotypes may be selected for adaptation to specific environments. Similar finding was observed by (Aina *et al.* (2009) when he evaluated eighteen cassava genotypes in four locations in Nigeria. The observed high variability among

genotypes as indicated by their varying mean performance implies the presence of sufficient genetic variability for the studied traits. Significant genotype by environment interaction (GEI) was observed for all the traits across the test environments as shown by some of the genotypes' crossover performances. This led to variations in average ranks of the genotypes over a wide range of environments. (Malosetti *et al.*, 2013). This indicates different adaptation by the different genotypes, suggesting the need for multi-location testing to identify good performers for specific environments. Phenotypic stability analysis is often used by plant breeders to identify and select genotypes with stable performance across environments.

### Conclusion

The genotype by environment interaction effect was significant for all the traits studied, suggesting the need to evaluate genotype over a range of environment before effective selection can be made. The study identified three genotypes as best performers for fresh root yield and dry matter content. These genotypes can be tested in multiple environments to determine their adaptability and possible recommendation for final release to farmers. For cassava root yield production, it is recommended to cultivate genotype NR150085 in environments where it performed best and genotypes NR150014, NR150008, NR150031 and NR150123 to be grown across all environments. Nonetheless, for root quality traits (dry matter and starch content) genotype NR150025 is recommended in environments where it performed well and genotypes NR150113 and NR150105 are recommended for all environments.

### References

Aina, O.O., Dixon, A.G.O., Ilona, P. and Akinrinde, E. (2009). G x E interaction effects on yield and yield components in the Savanna region of Nigeria. *African Journal of Biotechnology*, 8: 4933-4945.

Aina, O. O., Dixon, A. G. O. and Akinrinde, E. A. (2007). Additive main effects and multiplicative interaction (AMMI) analysis for yield of cassava in Nigeria. *Journal of Biological Sciences*, 7(5): 796-800.

Akinyele, B.O. and Osekita, O.S. (2011). Genotype x Environment interaction in NH47 – 4 variety of Okra – *Abelmoschus esculentus* (Linn.) Moench. *International Journal of Genetics and Molecular Biology*, 3(4): 55 – 59.

Basford, K. E. and Cooper, M. (1998). Genotype × environment interactions and some considerations of their implications for wheat breeding in Australia. *Australian Journal of Agricultural Research*, 49 ( 2 ) : 1 5 3 - 1 7 4 . <https://doi.org/10.1071/A97035>

Dixon, A. G. O., Bandyopadhyay, R., Coyne, D., Ferguson, M., Ferris, S. B., Hanna, R., Hughes, J.d'A., Ingelbrecht, I., Legg, J., Mahungu, N., Manyong, V., Mowbray, D., Neuenschwander, P., Whyte, J., Hartmann, P., Ortiz, R. (2003). Cassava: From Poor Farmers' Crop to Pacesetter of African Rural Development. *Chron. Hortic.*, 43: 8–15.

Egesi, C. N., Ilona, P., Ogbe, F. O., Akoroda, M. O. and Dixon, A. G. O. (2007). Genetic variation and genotype × environment interaction for yield and other agronomic traits in cassava in Nigeria. *Agronomy Journal*, 99(4):1137-1142.

Falconer, D.S. and Mackay, T.F.C. (1996). Introduction to Quantitative Genetics, Longman, New York, NY, USA.

FAO. (2008). 2009 version verified 30 July 2009. FAO, Rome.

Farshadfar, E., Mahmodi, N and Yaghotipoor, A. (2011). AMMI stability value and simultaneous estimation of yield and yield stability in bread wheat (*Triticum aestivum* L.). *Australian Journal of Crop Science*, 5(13):1837–1844.

Farshadfar, E., Rafiee, F. and Yghotipoor, A. (2012). Comparison of the Efficiency among Half Diallel Methods in the Genetic Analysis of Bread Wheat (*Triticum aestivum* L.) under Drought Stress Condition. *Ann. Biol. Res.*, 3 (3): 1607–1622.

Gabriel, K.R. (1971). The Biplot Graphic Display of Matrices with Application to Principal Component Analysis. *Biometrika*, 58: 453-467.

Kang, M.S. (2002). Quantitative genetics, genomics, and plant breeding. CABI Publishing, New York, USA

Kang, M.S. and Magari, R. (1996) New Developments in Selecting for Phenotypic Stability in Crop Breeding. In: Kang, M.S. and Gauch Junior, H.G., Eds., Genotype by Environment Interaction, Elsevier, New York, Pp. 11-14.

Kilic, H., Sagir, A. and Bayram, Y. (2009). Estimates of Genotype x Environment Interactions and Heritability of Black Point in Durum Wheat. *Not. Sci. Biol.*, 1(1): 92-96.

Malosetti, M., Ribaut, J. M. and van Eeuwijk, F. A. (2013). The statistical analysis of multi-environment data: modeling genotype-by-environment interaction and its genetic basis. *Frontiers in Physiology*, 4: 44 . <https://doi.org/10.3389/fphys.2013.00044>

Masinde, E. A., Mkamillo, G., Ogendo, J. O., Hillocks, R., Mulwa, R. M., Kimata, B. and Maruthi, M. N. (2018). Genotype by environment interactions in identifying cassava (*Manihot esculenta* Crantz) resistant to cassava brown streak disease. *Field Crops Research*, 215: 39-48.

Mkumbira, J., Mahungu, N. M., Gullberg, U. (2003). Grouping locations for Efficient Cassava Evaluation in Malawi. *Exp. Agric.*, 39: 167–179.

Ngeve, J.M., Dixon, A.G.O. and Nukenine, E.N. (2005). The Influence of Host Genotype x Environment Interactions on the Response of Cassava Anthracnose Disease in Diverse Agro-ecologies in Nigeria. *Afr. Crop Sci. J.*, 13(1): 1-11.

Olsen, K.M., Schaal, B.A. (2001). DNA Sequence Data and Inferences on Cassava's Origin of Domestication. In Genetics and Plant Domestication. The Hague Mouton Publishers, Piperno, DR 1995. Pp. 123-133.

Sakin, M., Akinci, C., Duzdemir, O. and Donmez, E. (2011). Assessment of genotype x environment

- interaction on yield and yield components of durum wheat genotypes by multivariate analyses. *African Journal of Biotechnology*, 10: 2875-2885.
- Shaffi, B., Mahler, K.A., Price, W.J. and Auld, D.L. (1992). Clone x Environment interaction effects on winter rape seed yield and oil content. *Crop Science*, 32: 922-927
- Ssemakula, G. and Dixon, A. (2007). Genotype x Environment Interaction, Stability and Agronomic Performance of Carotenoid-rich Cassava Clones. *Sci. Res. Essay*, 2 (9): 390-399.
- Tumuhimbise, R., Meli, R., Shanahan, P. and Kawuki, R. (2014). Genotype × environment interaction effects on early fresh storage root yield and related traits in cassava. *Crop Journal*, 2:329–337.
- Van Eeuwijk, F., Bustos-Korts, D. and Malosetti, M. (2016). What should students in plant breeding know about the statistical aspects of genotype × environment? *Crop Sci.* 56 (this issue).

**Table 1: Combined analysis of variance for starch**

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	%SS
ENV	2	1462.52	731.26	154.0822	6.966e-06 ***	40.7
REP(ENV)	6	28.48	4.75	0.3107	0.929254	
GEN	11	1293.33	117.58	7.6965	2.291e-08 ***	36.28
ENV:GEN	22	809.07	0.78	2.4073	0.003223 **	22.5
Residuals	66	1008.25	15.28			

**Table 2: Combined analysis of variance for fresh root yield**

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	% SS
ENV	2	4900.4	2450.20	42.4523	0.0002875 ***	29.92
REP(ENV)	6	346.3	57.72	1.0470	4033798	
GEN	11	8487.5	771.60	13.9973	2.21e-13 ***	51.82
ENV:GEN	22	2645.3	120.24	2.1813	0.0079376 **	16.15
Residuals	66	3638.2	55.12			

**Table 3: Combined analysis of variance for dry matter content**

	Df	Sum Sq	Pr(>F)	Mean Sq	F value	Pr(>F)	% SS
ENV	2	824.91		412.46	153.7746	7.007e-06 ***	41.7
REP(ENV)	6	16.09		2.68	0.3112	0.928966	
GEN	11	729.51		66.32	7.695	2.299e-08 ***	36.1
ENV:GEN	22	456.47		20.75	2.4075	0.003222 **	22.5
Residuals	66	568.81		8.62			

**Table 4: Combined analysis of variance for dry root yield**

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	%SS
ENV	2	1418.08	709.04	301.4757	9.565e-07 ***	51.24
REP(ENV)	6	14.11	2.35	0.3743	0.8928	
GEN	11	853.47	77.59	12.3494	3.189e-12 ***	30.84
ENV:GEN	22	481.65	21.89	3.4846	4.565e-05 ***	17.4
Residuals	66	414.66	6.28			

**Table 5: Mean of the agronomic characteristics of cassava genotypes across different locations.**

Genotypes	Starch	Fresh root yield	Dry matter content	Dry root yield
NR150025	32.8 <sup>a</sup>	26.9 <sup>ab</sup>	42.9 <sup>a</sup>	9.5 <sup>a</sup>
NR150113	28.6 <sup>ab</sup>	12.8 <sup>cd</sup>	39.7 <sup>ab</sup>	4.2 <sup>cd</sup>
NR150105	26.7 <sup>bc</sup>	17.9 <sup>bc</sup>	38.3 <sup>bc</sup>	4.7 <sup>bcd</sup>
NR150031	26.5 <sup>bcd</sup>	22.8 <sup>abc</sup>	38.1 <sup>bcd</sup>	6.8 <sup>abc</sup>
TMS30572	24.8 <sup>b<sup>cde</sup></sup>	27.7 <sup>ab</sup>	36.9 <sup>b<sup>cde</sup></sup>	8.3 <sup>ab</sup>
NR150014	24.4 <sup>b<sup>cde</sup></sup>	31.0 <sup>a</sup>	36.6 <sup>b<sup>cde</sup></sup>	9.4 <sup>a</sup>
NR150008	24.3 <sup>b<sup>cde</sup></sup>	33.3 <sup>a</sup>	36.5 <sup>b<sup>cde</sup></sup>	9.6 <sup>a</sup>
NR150060	23.1 <sup>b<sup>cde</sup></sup>	13.2 <sup>cd</sup>	35.6 <sup>b<sup>cde</sup></sup>	3.8 <sup>cd</sup>
NR150085	23.0 <sup>b<sup>cde</sup></sup>	27.7 <sup>ab</sup>	35.5 <sup>b<sup>cde</sup></sup>	8.9 <sup>a</sup>
NR150123	21.4 <sup>c<sup>de</sup></sup>	29.1 <sup>ab</sup>	34.3 <sup>c<sup>de</sup></sup>	8.2 <sup>ab</sup>
NR150040	20.5 <sup>d<sup>e</sup></sup>	3.6 <sup>d</sup>	33.7 <sup>d<sup>e</sup></sup>	0.8 <sup>d</sup>
NR070220	20.1 <sup>e</sup>	13.0 <sup>cd</sup>	33.3 <sup>e</sup>	3.6 <sup>cd</sup>