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Agronomic performance of 42 genomic selected genotypes across three Agroecological zones in Nigeria

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Abstract

Forty-two (42) genomic selected cassava genotypes were planted, drawn from the germplasm of the National Root Crops Research Institute, Umudike (NRCRI), and evaluated in an advanced yield trial (AYT). Umudike is located in the rainforest, Otobi is in the derived savanna, and Kano is in the semi-arid area. Three replicates of 20 plants per plot with an inter- and intra-plot spacing of 1 x 8m are used in a randomised complete block design (RCBD). The goal is to determine the impact of genotype x environment on the performance of the cassava genotypes by choosing those that perform well throughout the zones for future improvement. Minjibir displayed the lowest total rainfall and relative humidity, measuring 536.22 and 63.10, respectively, while Umudike had the highest total rainfall and mean relative humidity, measuring 2075.90mm and 88.00, respectively. Otobi followed with a total rainfall and mean relative humidity of 82.00. On the other hand, Minjibir recorded the greatest mean temperature (40.33) and total solar radiation (106.15), followed by Otobi (78.30 and 35.30), and Umudike (50.10 and 29.30) with the lowest values All agronomic characteristics (apart from plant architecture) showed extremely high significant differences (p<0.001). Plant vigour, height, cbb, cgm, and cmd all displayed very high genotypic significant differences, with mean square values of 2.55, 0.52, 0.49, 2836.40, and 0.24, respectively, although plant architecture exhibited no significance. Genotype x Environment showed significant differences (p<0.001) across the agronomic traits. Genotype x Location interactions showed very highly significant difference (p<0.001) with means square of root number= 130.57, shoot weight= 49.59, DMC= 27.33, and fry= 120.33; on the other hand, root weight was significantly different (p<0.05) with means square of 34.78. Combining a simple correlation analysis of the major cassava evaluated across locations revealed that DMC correlated negatively with fry = r-0.43, plant architecture = r-0.34, plant height = r-0.33, cmd = r-0.09, and cgm = r-0.06, and very positively with starch (r=0.99 at p<0.001). Additionally, a substantial association between root number and sprout (r0.77) and root weight (r0.87) was found in this study at p<0.001. The following traits showed a p<0.01 connection with root number: shoot weight = r0.57, fry = r0.47, and dry = r0.49 (Table 4). The analysis's result showed a strong link (p<0.001) between dry and fry (r=0.96). At the same time, vigor had a negative correlation (p<0.01) with the following variables (plant height = r0.65, shoot weight = r0.61) and a negative correlation (p<0.001) with DMC = -0.36 and starch = r-0.36. Keywords: Genomic selection, agronomic performance, agroecological zones

Introduction

Millions of people, primarily in Africa, Asia, and Latin America, rely on cassava (Manihot esculenta Crantz), which is the world's second-most important source of starch, behind maize (Ceballos et al., 2015). In developing nations, family farming has a high correlation with the production of cassava (Halsey et al., 2008). Due to its numerous uses in the food, pharmaceutical, cosmetic, and fabric industries, as well as in the manufacturing of paper and biofuels, among other industries, it has enormous commercial potential (Oliveira et al., 2012) (Saengchan et al., 2015). Due to the country's economic hardships, hunger, and rising market prices for food and other goods, Nigeria must assess the cassava produced bv biotechnology in each of its three agroecological zones. This makes this investigation necessary. The goal is to determine the impact of genotype x environment on the performance of the cassava genotypes by choosing those that perform well throughout the zones for future improvement. Umudike in Abia, Otobi in Benue, and Minjibir station in Kano State were the sites of the trial. Kano lies in the semi-arid area, Umudike is in the rain forest, and Otobi is in the derived savanna. At an altitude of 252 meters above sea level, Umudike is situated at longitude 6° 44' East and latitude 5° 29' North. Conversely, Otobi is located at longitude 8° 40' East, latitude 7° 55' North, and an elevation of 131 meters above sea level, but Minjibir is placed at longitude 8°.39' East, latitude 12° 10.10' North, and an elevation of 449 meters above sea level." In three of Nigeria's agro-ecological zones, 42 genetically diverse cassava genotypes were planted, drawn from the germplasm of the National Root Crops Research Institute, Umudike (NRCRI). Umudike is located in the rain forest, Otobi in the derived savanna, and Kano in the semiarid area. Three replicates of twenty plants per plot with an inter- and intra-plot spacing of 1 x 8m are used in a randomized complete block design (RCBD). At three, six, and nine months after planting (MAP), manual weeding was done. At three MAP, fertilizer (NPK 15:15:15) was sprayed at the recommended rate of 600 kg/ha.

Materials and Methods

Data on the main cassava pests and diseasescassava green mite (CGM), cassava mosaic disease (CMD), cassava bacterial blight (CBB), and cassava anthracnose disease (CAD) were gathered three, six, and nine months after planting. For aboveground symptoms, a severity scale of 1 to 5 (Gondwe et al., 2003) will be used: 1- no foliar symptom (no yellow patch of the leaves); 2-mild foliar symptom (little yellow patch of the leaves); 3- pronounced foliar chlorotic symptoms (pronounced yellow patch of the leaves); 4- severe foliar chlorotic symptoms (pronounced yellow patch and shrinking of few leaves); and 5- very severe foliar symptoms (pronounced yellow patch and shrinking of almost the whole leaves, potentially causing plant death). Agronomic characteristics include shoot weight, drv matter content, fresh root yield, dry yield, length of roots per clone, plant height (cm), plant architecture, vigor, fresh root weight, and height at first branching (cm). In vear after planting, the CET will be harvested.

Harvest Index (HI): Harvestable yield to total yield is expressed as this ratio. Harvesting will involve uprooting three plants per genotype and meticulously removing each plant's harvestable roots. The biomass (stems, branches, and leaves) above ground and the weight of the roots will be measured independently for each genotype. The weight of the roots that could be harvested was divided by the total biomass (both above and below ground) calculate HI;

$$HI = \frac{WR}{WR + WAB} \quad \dots$$

Where WR = root weight and WAB = above ground biomass

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Following the report of Chavez *et al.* (2005), the dry matter content (DMC) and root starch content (RSC) will be evaluated using the specific gravity methodology (Kawano *et al.*, 1987). From each genotype's pool of roots, a sample weighing between two and five kilograms was taken, and it was thoroughly cleaned to remove any dirt or other debris. A spring balance was used to weigh the samples in air (WA) kg after they were placed in a punctured gunny bag. The same samples, with the roots submerged in water, were weighed in water (WW) kg. The following

formulas were used to estimate the dry matter and root starch contents:

$$DMC = \frac{WA}{WA - WW} x \ 158.3 - 142 \ \dots 2$$

RSC = $\frac{WA}{WA - WW} x \ 112.1 - 106.4 \dots 3$

Where, DMC = t Dry matter content, RSC = t Root starch content, WA = t Weight in air, WW = t Weight in water, 158.3= constant, 142 = t constant, 112.1 constant, and t 106.4 constant.

Number of roots (NR): The number of roots per plot was counted from three plants of each genotype from the net plots and divided by three. Harvested roots from net plot was counted and averaged, recorded.

Plant Height (PH): The plant height will be determined on the stem from the ground level, using a measuring stick calibrated in centimeters. The measurements were taken 12 months after planting.

Plant Height at First Branching (PHFB): Plant height at first branching was determined on the stem from the ground level to the point where the plant first forked using a measuring rule calibrated in centimeters.

Plant Vigor (PV): The plant vigor was assessed visually using a scale of 3, 5 and 7 (3 = not healthy, 5=moderately healthy, 7=healthy) at 6 months after planting (Next Generation Cassava Project Ontology, 2012).

Fresh Root Yield (FRY): fresh root yield was determined with root weight in kg divided by number of plants in the net plot multiplied by 10 as reported by Chavez *et al* (2005).

 $FRY = \frac{Root weight}{Net Plot} x 10 \dots 4$

DRY: Dry root yield (DRY) was determined with the fresh root yield (FRY) multiplied by dry matter (DMC) content divided by 100 as reported by Chavez *et al* (2005).

 $DRY = \frac{FRY \times DMC}{100} \dots 5$

Data Analysis

Using the Ime4 package that implemented the R program, the gathered were subjected to analysis of variance (Bates *et al.*, 2015). The R analytical package (Arnhold, 2013) for R software (R Core Development Team) was used to analyze correlations for the statistic model Yij= μ + τ i+ β j+Eij, where μ stands for general mean, τ i for treatment effect, β j for block effect, and eij for residual effect. Using R

analytical program, the genetic by environment will be ascertained.

Results and Discussion

Total rainfall and solar radiation, mean temperature, and average relative humidity in 2019 during the period of this work across locations

The environmental conditions of the three agroecological zones where this experiment was conducted varied significantly. Minjibir displayed the lowest total rainfall and relative humidity, measuring 536.22 and 63.10, respectively, while Umudike had the highest total rainfall and mean relative humidity, measuring 2075.90mm and 88.00, respectively. Otobi followed with a total rainfall and mean relative humidity of 82.00. On the other hand, Minjibir recorded the greatest mean temperature (40.33) and total solar radiation (106.15), followed by Otobi (78.30 and 35.30), and Umudike (50.10 and 29.30) with the lowest values (Table 1). Umudike is located in a rain forest, Otobi in a derived savanna, and Minjibir in semi-arid regions, according to the differences that were noticed. All agronomic characteristics (apart from plant architecture) showed extremely high significant differences (p<0.001) (Table 2). Plant vigour, height, cbb, cgm, and cmd all displayed very high genotypic significant differences, with mean square values of 2.55, 0.52, 0.49, 2836.40, and 0.24, respectively, although plant architecture exhibited no significance. The findings of this analysis suggested that differences existed among the locations for the chosen genotypes. Of the agronomic traits tested, locations showed very high significant differences (p<0.001), with the exception of plant architecture, which showed significant differences (p<0.01) with mean square values of cbb = 27.13, cgm = 43.79, cmd = 4.37, plant height = 11750.10, plant vigour = 64.19, and plant architecture = 2.54 (Table 2). This finding indicated that the sites where the studies were conducted varied (Table 1). The results demonstrated both that gene and environment contributed to the phenotypic

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performance of the examined cassava genotypes. Genotype x environment showed very high significant differences (p<0.001) across the agronomic traits.

Table 3 showed the combination of analysis of variance on yield and yield-related traits of 42 cassava genotypes across locations. Results showed that there were verv highly significant difference (p<0.001) for yield and yield related traits (Table 3). Genotypes showed high variability on the following traits at p<0.001 with mean square values, root number= 335.22, root weight= 76.45, shoot weight=72.21, dry matter content= 29.59 and harvest index= 0.045 while fresh root yield were significant at p<0.01 with mean square value of 156.80 and dry root yield showed no significant different (Table 3). This result showed that the performance of evaluated genotypes on yield and yield related traits across locations were due to variations among the genotypes, in the same trend locations showed very highly significant difference on mean square values P<0.001 on the traits evaluated apart from dry yield with no significant difference (Table 3). This implies that locations contributed to the performance the genotypes across the locations. Genotype x Location interactions showed very highly significant difference (p<0.001) with means square of root number= 130.57, shoot weight= 49.59, DMC= 27.33 and fry= 120.33, in the other hand root weight were significantly difference (p<0.05) with means square of 34.78 (Table 3). This indicated that the performance of root number, shoot weight, DMC and Fry were influenced by both genotypes and locations.

Combining a simple correlation analysis of the major cassava evaluated across locations revealed that DMC correlated negatively with fry = r-0.43, plant architecture = r -0.34, plant height = r-0.33, cmd = r-0.09, and cgm = r-0.06 and very positively with starch (r=0.99 at p<0.001) (Table 4). Additionally, a substantial association between root number and sprout (r0.77) and root weight (r0.87) was found in this study at p<0.001. The following traits showed a p<0.01 connection with root number: shoot weight = r0.57, fry = r0.47, and dry = r0.49 (Table 4). According to Table 4, the analysis's result showed a strong link (p<0.001) between dry and fry vigor (r=0.96), while had а negative correlation (p<0.01) with the following variables (plant height = r0.65, shoot weight = r0.61) and a negative correlation (p<0.001) with DMC = -0.36 and starch = r-0.36). These findings suggested that higher root dry matter content corresponds with higher starch content, which in turn suggests higher shoot weight, dry matter content, and fry and dryness. They also demonstrated that the gene regulating root number contributes to these increases, meaning that higher root number corresponds to higher fry and dryness. According to this conclusion, there was a negative link between vigor and DMC and starch, meaning that when a plant grows more vigorously, it uses up more starch and DMC. The discovered negative link between the DMC and fry suggested that genotypes with low DMC should be chosen in order to facilitate progress, rather than solely focusing on fry.

Conclusion

One of the greatest methods for cassava breeders to ease cassava breeding is the breeding pipeline; biotechnological instrument, this genomic selection, is used to choose the genotypes of NRCRI. The results showed that there were ten genotypes that fared well in all areas, indicating that cassava could be produced in the same semiarid region of Nigeria. This would significantly lessen the country's hunger and food scarcity. In order to choose cassava whose performance is highly genetic and minimally influenced by the environment, the plant breeders should use biotechnological tools. This will help drastically reduce hunger in Nigeria.

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 Table 1: Total rainfall and solar radiation, mean temperature and average relative humidity in 2019

 during the period of this work across locations

Environments	Total Rainfall	Mean Temperature	Total Solar Radiation	Mean Relative		
	(mm)	(°C)	(MJ/m2)	Humidity (%)		
Umudike	2075.90	29.30	50.10	88.00		
Otobi	1114.97	35.30	78.30	82.00		
Minjibri	536.22	40.33	106.15	63.10		

 Table 2: Combined analysis of the variance of agronomical traits of 42 cassava genotypes across locations

Source	Df	cbb	cgm	cmd	plt_ht	vigour	arch	
Rep	1	0.26	0.28	0.09	6.70	0.261	1.21	
Geno (G)	40	0.24***	0.52***	0.49***	2836.40***	2.55***	0.56na	
Loc (L)	2	27.13***	43.79***	4.37***	11750.10***	64.19***	2.54**	
GxL	60	0.14***	0.39***	0.11***	720.10***	1.91***	1.27***	
Error	77	0.13	0.21	0.049	679.90	1.22	0.61	

Table 3: Combined analysis of variance on yield and yield-related traits of 42 cassava	genotypes across
locations	

Source	Df	Rt_no	Rt_wt	Sht_wt	Dmc	Dry	Fry	Hi
Rep	1	27.76	0.56	22.64	27.85	0.32	78.80	0.013
Geno (G)	40	335.22***	76.45***	72.21***	29.59***	13.36na	156.80**	0.045***
Loc (L)	2	317.53**	128.81***	204.51***	2194.50***	9.55na	810.14***	0.067***
GxL	60	130.57***	34.78*	49.28***	27.33***	11.82na	120.33***	0.016na
Error	77	74.02	23.54	23.20	8.27	10.01	92.42	0.012

	DMC	Rt no	arch	cbb	cgm	cmd	dry	fry	hi	plt ht	rt wt	sht wt	sprout	starch	vigour
vigour	-0.36	0.35	0.08	0.36	0.41	-0.29	0.10	0.18	-0.29	0.65	0.39	0.61	0.43	-0.36	
starch	0.99	-0.28	-0.35	-0.32	-0.10	-0.09	-0.24	-0.43	-0.07	-0.31	-0.33	-0.17	-0.14		
sprout	-0.11	0.77	-0.07	0.55	0.48	-0.26	0.15	0.14	0.14	-0.01	0.71	0.48			
sht_wt	-0.15	0.57	-0.06	0.21	0.54	-0.10	0.23	0.20	-0.54	0.36	0.57				
rt_wt	-0.33	0.87	-0.12	0.41	0.49	-0.24	0.62	0.61	0.27	0.01					
plt_ht	-0.31	0.07	0.05	0.09	0.17	-0.10	-0.05	0.03	-0.43						
hi	-0.09	0.14	-0.06	0.11	-0.16	-0.04	0.38	0.39							
fry	-0.43	0.47	0.10	0.19	0.26	-0.04	0.96								
dry	-0.24	0.49	0.01	0.13	0.30	-0.06									
cmd	-0.09	-0.21	0.28	-0.02	-0.14										
cgm	-0.06	0.55	0.02	0.37											
cbb	-0.33	0.43	0.21												
arch	-0.34	-0.06													
Rt_no	-0.26														

Table 4: Combined correlation analysis of 42 cassava genotypes evaluated across locations