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Estimates of Genetic Parameter Contributing to Early Bulkiness of Yellow Root Cassava (*Manihot esculenta* Crantz) Genotypes in Niger State, North Central Nigeria

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Abstract:- Genetic variability among different genotypes for root yield component characteristics was studied in Guinea Savannah Agroecological zones of Niger state to determine its effect on early root bulkiness. Sixteen parameters were evaluated in 420m^2 at spacing of 1mx1m in a randomized complete block design in three replicates. Cassava genotypes were evaluated at 3 and 6 MAP (Month After Planting) to evaluate root bulkiness. REML/BLUP showed significant difference among genotypes for different harvesting periods for Harvest Index and fresh storage root yield (FSRY). Estimates of genetic variance for phenotypic (PCV) and genotypic coefficient of variation (GCV) were very close. PCV estimates were higher than GCV and varied from 39% to 13% for root weight and root size respectively. Broad sense heritability estimates were high for FSRY and ranged from 81% to 8% among root yield components. GCV estimates was higher for harvest index (34%) and least for number harvested (6.15%). Heritability was highest for fresh storage root yield (81%) and least for shoot weight (0%), Environmental coefficient of variation was least for harvest index (HI) with 0.36 and shoot weight had the highest coefficient of variation and the least being for harvest index. Genotype IKN120036 performed best among the genotypes with 3.61tha^{-1} and had the highest genetic gains in terms of selection criterion FSRY. FSRY and HI had higher heritability and were strongly correlated (R= 0.61). Root number was not significant(P>0.05; R=-0.24) and negatively correlated with FSRY.

Keywords:- *Genetic Variability, Root Bulkiness, Heritability.*

I. INTRODUCTION

Cassava (*Manihot esculenta* Crantz) is a perennial shrub originated in the neotropics. Its most important product is the starchy roots used as a source of caloric energy by millions of people, particularly in Sub-Saharan Africa (Stapleton 2012; Norton 2014). Cassava is the fourth most important basic food after rice, wheat, and maize worldwide, but is the second most important food staple in terms of calories consumed in sub-Saharan Africa (Cacamisi, 2010; Tarawali *et al.*, 2012).

The crop is called Africa's food insurance because it offers reliable yields even in the face of drought, low soil fertility, low intensity management and because of its resilience to face the effects of climate change (Burns *et al.*,2010). Late bulking cassava stay long on the farm predisposing it to bush fires and animal invasion particularly during dry season especially in the northern part of the country. Late bulking cultivars occupy land for extended periods of time and consequently the land cannot be effectively utilized for other crops and it is the single most important factor responsible for rejection and abandonment of cassava cultivars in African countries (Okechukwu & Dixon,2009; Kamau *et al.*, 2011). Farmers usually cultivates local varieties with low yields and high yielding and early-bulking varieties could only guarantee higher yields when harvested at 12 months (Nweke, 2004). As cassava has no specific maturation period; therefore, harvest can take place as soon as reasonable root yield has been formed. Farmers

preferred early bulking genotypes to late bulking genotypes because studies have revealed that late bulking is a contributory factor responsible for rejection of cassava genotypes in sub Saharan Africa due to demographic and market pressures (Nweke *et al.*,1994). One of the ways to prevent animal invasions destroying farmlands in Nigeria and especially in north central Nigeria is to introduce to farmers cultivars that can be harvested early as a result of early root bulkiness.

II. MATERIALS AND METHODS

A. Experimental Material

Ten parental genotypes namely IKN120036, IKN120016, IBA070593, IBA130896 and IBA141092, TMEB419, IBA090525, IBA090581, IBA130818, IBA980581 sourced from IITA germplasm was used for this study. The genotypes are yellow fleshed-root cassava genotypes which are still under improvement.

B. Experimental Site

The study was conducted at the International Institute of Tropical Agriculture (IITA) Trial Fields, ABU farms, Mokwa, Niger state. (Southern Guinea Savannah Zone with Global Positioning System (GPS) co-ordinates of 06.32812ºN, 005.63599ºE and altitude of 212.7m) from 2018 to 2019.

C. Treatments and Experimental Design

The treatments were genotypes (IKN120036, IKN120016, IBA070593, IBA130896, IBA141092 TMEB419, IBA090525, IBA090581, IBA130818, IBA980581) and harvesting periods (3rd and 6th Months After Planting MAP) arranged in a randomized complete block design with three replications. Treatment plots per block consist of six ridges of 4m length and 1m apart. The net plots contain 16 plant stands with $24m^2$ treatment plot size while the total treatment plot per replicate was $120m^2$ and gross replicated area was $420m^2$. The parental genotypes were planted at a spacing of 1x0.8m in 3 replicates in July, 2018 and were evaluated in October and January.

D. Cultural Practices

➢ *Land Preparation and Planting*

The land was mechanically prepared with tractor and cassava stakes was planted on ridges. The ridges in each treatment plots per block is 1m apart and of 4m length and Cassava cuttings with same nodes number was cut at 2.5cm length and planted on all the ridges making the planting distance of 0.8m inter row and 1m intra row spacing with 36 plant population. Planting was done at a planting distance of 1m x 0.8m and at an orientation of angle 45º and data was taken from each of the blocks on the net plot area only. The 36 cuttings/stakes of each genotypes were planted on each of the ridged field per treatment plot which measured 6mx4m. The net plot is $24m^2$ with 16 plant stands while the experimental size area is 30mx14m ($0.0420m^2$) which contain 540 plants stands. The field was kept free of weeds by regular hand using hoe weeding as from three (3) months after planting (MAP). Harvesting was manually done by using hand to pull out cassava from the soil at 3rd and 6th months After Planting (MAP) so as to evaluate the genotypes for early bulkiness traits.

E. Data Collection

Data were collected per plot basis. Each plot contained six rows of five plants per row. Data were taken from the net plot at 3 and 6 MAP and were summed up for each trait observed per plot.

➢ *Data Collection on Growth and Yield Parameter*

- **Number of harvested plants:** This was taken by counting the number of Cassava plants that were harvested.
- **Root Number:** This was taken by counting the number of roots per plants.
- **Root size**: This was taken based on the groupings according to the girth, length and weight of the stems into 3 marketable sizes; small, medium and big with score of 3, 5 and 7 respectively (Fukuda *et al.*,2010).
- **Root weight:** This was taken using spring balance and expressed in kilogram.
- **Storage Root Diameter:** This was taken with the aid of a measuring tape around the girth of the root.
- **Fresh Storage Root Yield (FSRY)**: This was obtained by multiplying weight of known number (n) of bulked root weight by 10,000 and dividing it by the known number of bulked roots multiplied by 1,000 and express in tha^{-1}.
- **Dry Matter Content (DMC)**The dry matter percentage in tubers was determined by drying 20 g of fresh tuber slices/cubes or chopped pieces in an oven at 50 °C till a constant weight was obtained. From the weight of dried sample, percentage of dry matter will be calculated.
- **Dry Storage Root Yield (DSRY):** This was obtained by multiplying the percentage of DMC by FSRY and dividing by 100, and express in tha^{-1}.
- **Shoot weight:** This was obtained by weighing the stalks using spring balance (kilogramme).
- **Harvest Index:** This was obtained by dividing the weight of the roots by the sum of weight of roots and the above ground mass as described by Kawano, (1980).

III. DATA ANALYSIS

The data collected was subjected to statistical analysis using SAS version 9.4 (SAS Institute Inc. 2014). A two-stage analysis was considered (i) genotype was made random in order to estimate variance parameters and heritability and (ii) genotype was fitted as fixed term in second approach such as to obtain unshrunken predicted means. The statistical model used to estimate genetic variance components in this study were based on a linear mixed model. The mixed procedure

model is based on restricted maximum likelihood (REML) and described as follows:

$y = \mathbf{X}\beta + \mathbf{Z}b\ \varepsilon$

where y is a vector of observations from plots for each cassava variety

β and b are the fixed and random effect vectors respectively, e denotes the random error vector, and X is the incidence matrix of the fixed effects for the variety; Z the incidence matrix of random effects corresponding to replication; and ε, the random residual variance when the genotype and replication was considered fixed and random respectively and vice-versa. The effect of MAP was evaluated using combined analyses where genotype effect was considered as fixed while MAP is random and genotype effect was made random while MAP was fixed.

$b \sim N(0, G)$
$\varepsilon \sim N(0, R)$
$\mathrm{Cov}[b, \varepsilon] = 0$
$V = ZGZ' + R$

$$E = \begin{matrix} Y \\ R \\ \varepsilon \end{matrix} = \begin{matrix} XG \\ 0 \\ 0 \end{matrix}; \mathrm{Var}\begin{matrix} R \\ \varepsilon \end{matrix} = \begin{bmatrix} I\sigma 2R & 0 \\ 0 & I\sigma 2\varepsilon \end{bmatrix}$$

The random effects are assumed to be distributed as μ~ MVN (0; G) and ε~MNV (0; R) where MVN (U; V) means multivariate normal distribution with mean μ and variance-co-variance matrix V (Piepho *et al*., 2008).

➢ *Broad sense Heritability Estimates*

Broad sense heritability (h^2) of the all traits were calculated according to the formula as described by Allard (1960) as follow: $h^2bs = [(\sigma^2 G) / (\sigma^2 P)] \times 100$, where: h^2bs = heritability in broad sense; $\sigma^2 G$ = Genotypic variance; $\sigma^2 P$ = Phenotypic variance.

➢ *Genetic Advance Estimates*

Estimation of genetic advance Genetic advance (GA) was determined as described by Johnson *et al*., (1955): GA = K (σ_p) h^2, where: K = the selection differential (K = 2.06 at 5% selection intensity); σ_p = the phenotypic standard deviation of the character; h^2 = broad sense heritability. The genetic advance as percentage of the mean (GAM) was calculated as described by Johnson *et al*., (1955) as follow: GAM (%) =GA/ X * 100, where: GAM = genetic advance as percentage of the mean, GA = genetic advance, and x = grand mean of a character.

➢ *Genotypic Coefficient of Variation*

Genotypic coefficient of variation was calculated as the square of genetic variance component expressed as a percentage of mean as follows:

(σ^2 G x 100)/X where X is the phenotypic mean, and σ^2 G is the genotypic variance (Asante & Dixon, 2002).

➢ *Phenotypic Coefficient of Variation*

Phenotypic coefficient of variation was calculated as the square of phenotypic variance component expressed as a percentage of mean as follows:

(σ^2 P x 100)/X where X is the phenotypic mean and σ^2 P is the phenotypic variance (Asante & Dixon, 2002).

IV. RESULTS

	soil depths
soil parameters	0-30cm
Textural Class	Sandy loam
PH	7.10
Phosphorous(g/kg)	11.47
Carbon(g/kg)	8.56
Nitrogen(g/kg)	0.74

Table 1:- Physicochemical properties of trial field

Effects of genotypes and harvest time on FSRY

Genotype	3 MAP FSRY	6 MAP FSRY
IBA070593(c)	2.16	2.17
IBA090525	2.00	1.89
IBA090581	2.59	2.32
IBA130818	0.98	0.89
IBA130896	2.16	2.17
IBA141092	2.63	2.65
IBA980581(c)	2.29	2.28
IKN120016	1.31	1.32
IKN120036	3.61	3.47
TME419(c)	1.72	1.71

Table 2:- Mean performance of 10 yellow cassava genotypes for FSRY at 3 and 6 MAP.

Effects of genotypes and harvest time on DSRY

GENOTYPE	3 MAP DSRY	6MAP DSRY
IBA070593(c)	0.67	0.75
IBA090525	0.71	0.72
IBA090581	0.67	0.76
IBA130818	0.24	0.26
IBA130896	0.82	0.84
IBA141092	0.71	0.77
IBA980581(c)	0.86	0.87
IKN120016	0.51	0.53
IKN120036	0.99	1.06
TME419(c)	0.69	0.73

Table 3:- Mean performance of 10 yellow cassava genotypes for DSRY at 3 and 6 MAP.

Effects of genotypes and harvest time on HI

Genotype	3 MAP HI	6 MAP HI
IBA070593(c)	0.34	0.38
IBA090525	0.52	0.49
IBA090581	0.44	0.45
IBA130818	0.11	0.12
IBA130896	0.31	0.33
IBA141092	0.56	0.6
IBA980581(c)	0.36	0.38
IKN120016	0.23	0.27
IKN120036	0.54	0.53
TME419(c)	0.34	0.38

Table 4:- Mean performance of 10 yellow cassava genotypes for Harvest Index at 3 and 6 MAP.

Identifying high yielding and early storage root bulking genotypes at 3 and 6 MAP in terms of HI.

Genotype	3 MAP		6 MAP	
	HI	Rank	HI	Rank
IBA070593(c)	0.30	6	0.38	5
IBA090525	0.50	3	0.49	3
IBA090581	0.40	4	0.45	4
IBA130818	0.10	10	0.12	10
IBA130896	0.30	8	0.33	8
IBA141092	0.60	1	0.60	1
IBA980581(c)	0.40	5	0.38	5
IKN120016	0.20	9	0.27	9
IKN120036	0.50	2	0.53	2
TME419(c)	0.30	6	0.38	5

Table 5:- Rank of 10 genotypes in 3 and 6 MAP using mean performance.

Identifying high yielding and early storage root bulking genotypes at 3 and 6 MAP in terms of FSRY.

GENOTYPE	EBI%	3MAP	6MAP
		FSRY	FSRY
IBA070593(c)	120.00	6.00	5.00
IBA090525	100.00	7.00	7.00
IBA090581	100.00	3.00	3.00
IBA130818	100.00	10.00	10.00
IBA130896	83.00	5.00	6.00
IBA141092	100.00	2.00	2.00
IBA980581(c)	100.00	4.00	4.00
IKN120016	100.00	9.00	9.00
IKN120036	100.00	1.00	1.00
TME419(c)	100.00	8.00	8.00

Table 6:- Early Bulking percentage of 10 yellow cassava genotypes based on FSRY at 3 and 6 MAP

Performance of 10 genotypes in 3 and 6 MAP

GENOTYPE	DMC	DSRY	FSRY	HI	INNCOL	NOHAV	RTNO	RTWT	SC	STWT	VIGOR	CMDS	PLPCOL
IBA070593(c)	31.36	0.67	2.16	0.34	1.00	1.00	9.67	1.13	16.37	9.67	3.00	3.00	0.00
IBA090525	36.20	0.71	2.00	0.52	1.00	1.33	10.33	1.95	23.40	11.00	1.80	6.33	0.00
IBA090581	28.15	0.67	2.59	0.44	1.00	1.33	10.33	2.52	14.26	11.00	3.26	5.67	0.00
IBA130818	24.64	0.24	0.98	0.11	1.00	1.67	7.00	0.72	10.05	8.33	5.29	5.00	0.00
IBA130896	28.35	0.82	2.16	0.31	1.00	1.67	11.00	2.30	25.51	10.33	4.88	5.00	0.00
IBA141092	26.98	0.71	2.63	0.56	1.67	1.33	10.67	3.09	12.86	11.00	4.84	3.67	0.00
IBA980581(c)	37.61	0.86	2.29	0.36	1.00	2.00	12.33	2.82	24.80	13.00	4.84	5.67	0.00
IKN120016	38.60	0.51	1.31	0.23	1.00	1.33	10.67	1.35	26.21	8.00	4.69	4.33	0.00
IKN120036	28.25	0.99	3.61	0.54	1.00	1.00	7.00	2.70	12.86	12.00	2.05	4.33	0.00
TME419(c)	40.11	0.69	1.72	0.34	1.00	1.33	10.67	1.65	27.62	10.00	3.38	6.33	0.00
GrandMean	33.02	0.69	2.14	0.38	1.07	1.40	9.97	2.02	19.39	10.43	3.81	4.93	0.00
SE	3.88	0.15	0.46	0.07	0.11	0.28	2.80	0.58	4.35	1.22	1.45	0.76	0.00
CV	16.62	23.25	21.03	23.95	13.98	28.17	39.74	39.40	31.75	11.94	53.86	21.79	0.00

Table 7:- Mean performance of traits at 3 and 6 MAP

	FSRY	**3 MAP**	**6MAP**
Yield component	**Correlation Coeff. (R)**	**P-Value**	
Root Size	0.41	0.0060**	0.0066**
Shoot weight	-0.11	ns	ns
Root Number	-0.24	ns	ns
Harvest Index	0.61	0.0018**	<0.0001***
Storage Root Diameter	0.26	0.0219*	ns
Root Weight	0.57	ns	0.0017**
Dry Matter Content	-0.3	ns	ns

Table 8:- Pearson correlation coefficient of some selected yield component trait.

*, **, *** Significant at 0.05, 0.01 and 0.001 probability levels, respectively

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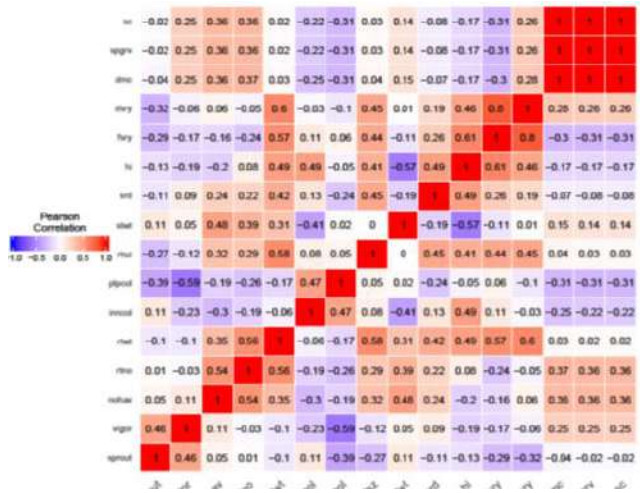

Fig 1

V. RESULT & DISCUSSION

➢ *Effects of genotypes and harvest time on fresh storage root yield, dry storage root yield and Harvest Index*

Fresh storage root yield was highly significant (P<0.01) at 3 MAP and at 6 MAP. Genotype IKN120036 was the highest in terms of FSRY at 3 months after planting (MAP) followed by IBA141092 while genotype IBA130818 had the lowest FSRY at the same month as shown in table 1. At 6 MAP, genotype IKN120036 still maintained having the highest yield at 3 MAP followed by IBA141092 while genotype IBA130818 still had the lowest FSRY.

Dry storage root yield was significant (p<0.05) at 3 MAP and was highly significant at 6 MAP (P<0.01). Genotype IKN120036 had the highest DSRY with 0.99t/ha followed by IBA98/0581 which had 0.81t/ha at 3 MAP while IBA130818 had the lowest. At 6 MAP, genotype IKN120036 maintained the highest DSRY with 1.86t/ha followed by IBA980581 with 0.87t/ha while IBA130818 still maintained the lowest DSRY (Table 2).

Harvest Index was significant (P<0.01) at 3 MAP and very highly significant at (P<0.001) 6 MAP. Genotype IBA141092 had the highest HI of 0.56 followed by IKN120036 with 0.54 at 3 MAP and IBA130818 had the least of 0.11. At 6 MAP, genotype IBA141092 had the highest harvest index with 0.60 followed by genotype 120036 while genotype IBA130818 had the least harvest index of 0.12 (Table 3)

There was significant difference among the yield component traits among genotypes studied (Table 8) at 3 and 6 MAP. This shows that genotype variability among the genotypes is responsible. There was however no significant difference for root weight at 3 MAP but there was significant difference at 3 MAP for storage root diameter but the same traits were not significant at 6 MAP among the genotypes. A non-significant (P>0.05) genotypic treatment effects were observed for dry storage root yield, fresh storage root yield, Harvest Index, root size, storage root diameter and root weight.

One of the targets of cassava breeding program is cassava root yield which is a complex trait and which depends on different factors which directly or indirectly affects root yield (Tewodros *et al.*,2013). Late bulking cultivars forms reasonable roots by occupying land for a longer periods of time and therefore rendering the lands to be ineffectively utilized for other crops (Okechukwu & Dixon,2009; Kamau *et al.*, 2011). Cattle invasion is another reason farmer ultimately need to use early bulking genotypes so that it could be harvested before the period nomads move around with their cattle as it is common in the north central region of the country. Guinea savannah zone is characterized by short rainfalls periods and long dry periods with bush fires and cattle invasions (Adu-Gyamfi *et al.*,2016). It is therefore essential to identify cassava cultivars that can produce reasonable early storage root yield. Farmers preferred early bulking genotypes to late bulking genotypes (Nweke *et al.*,1994).

Cassava root yield component in terms of fresh storage root yield (FSRY) was significant and shows that the traits is controlled more by genetic variability than the environment (Table 2) and this is also confirmed by study conducted by Adu-Gyamfi (2016) where they noticed significant difference in the root formation at 4, 5, and 6 months after planting (MAP). High and early storage root bulkiness among genotypes has been linked to genotypic variability (Okogbenin and Fregene, 2008, Joseph Adjebeng, 2016). Root bulkiness is related to early bulkiness which varies on cultivar (Wholey and Cock,1974).

The study shows that genotype IKN120036 performed best among the genotypes studied and above the checks (TME 419, IBA980581 and IBA070593) at 3 and 6 MAP in terms of fresh storage root yield (Table 3) this is confirmed by a study by Adjebeng-Danquah (2016) who indicated that genotypes that partitioned dry matter production into storage root earlier than others were able to bulk 60% of their final storage root yield by 6 MAP and are characterized by high source to sink abilities which translated into early bulkiness(Adu-Gyamfi *et al.*,2016).

Genotype IKN120036 was shown to have matured earlier than the rest of the genotypes and this could be detected as from 3 MAP when compare with other genotypes under study. Measurement of relative growth rate after 30 days' best display differences among genotypes (Kumar *et a*l., 2012). It shows that the genotype was able to allocate higher source to sink capacity as reported by George *et al* (1998) whose study revealed that cultivars with higher root yields were able to allocate higher proportion of dry matter to storage roots. Genotype IKN120036 possesses superior root characteristics to other genotypes studied. In study conducted by Michael

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Adu *et al* (2018), they found that high performing genotypes are characterized by high relative root growth rate. It has also been found that early maturing cultivars rapidly initiated storage root development thereby reaching their maximum yield within a short growing period (Adjebeng-Danquah *et al*, 2016).

- *Relationship between FSRY and other root yield component*

Improvement of cassava root yield can be achieved based on the performance of root yield components (Adu-Gyamfi *et* al, 2016). Harvest Index was significant at 3 MAP ($P<0.01$) and highly significant at 6 MAP ($P<0.001$). Pearson correlation coefficient showed that Harvest Index ($R=0.61$) and Root size ($R=0.41$) strongly correlates with fresh storage root yield at both 3 and 6 MAP (Table 4,8,9).

According to Adu-Gyamfi *et al* (2016) which stated that fresh storage root yield is determined by root size and harvest index in their study, same results was also achieved from this study where root size and harvest index positively correlated with fresh storage root yield component.

Root number and dry matter content (Table 4) at 3 and 6 MAP revealed that their association with fresh storage root yield is not genotypic but has more of environmental influence. This study further revealed that there is a negative correlation between root number and dry matter content with fresh storage root yield which has similar result to what was obtained by Adu-Gyamfi (2016) where non-significant correlation between root number and dry matter content with fresh storage root yield was recorded.

Root number is determined by fresh storage root yield as reported by Adu-Gyamfi *et* al (2016). Root number according to Ntawurungha *et* al., (1998) can be influenced by environment although it is heritable. To further test this traits association with fresh storage root yield in order to ascertain their real performance of the genotype, the genotypes should be study in more different environments.

Root size ($R=0.41$) was highly significant at both 3MAP ($P<0.01$) and 6 MAP ($P<0.01$) (Table 4). This shows that the traits are an indication of a genotypic effect and are not due to the environment. This means that wherever these genotypes are planted, the traits will manifest itself with little or no environmental effect. This therefore makes selection of the best performing genotypes based on these traits possible.

Storage root diameter (Table 8) was significantly different ($P<0.05$) at 3 MAP and positively correlated with fresh storage root yield ($R=0.61$) which was similar to result obtained by Tewodros *et* al., (2013) where they recorded a significant genotypic and phenotypic correlation between storage root diameter and fresh storage root yield. This is an indication of genotypic effect over the environmental effect.

However, at 6 MAP, storage root diameter became non-significant ($P>0.05$) and this revealed the impact of environment influence during the sixth month after planting. This result is similar to result obtained from the study conducted by Adu-Gyamfi *et* al., (2016) where they reported that storage root diameter does not correlates significantly with fresh storage root yield. The rate of storage of root bulking in cassava varies over a long period due to prevailing environmental conditions (Ekanayake *et al*.,1998). These further reveals that genotypic manifestation could be affected by prevailing environmental influence.

Root weight correlates ($R=0.57$) with fresh storage root yield. Root weight as a yield component also affects fresh storage root component (Adu-Gyamfi *et al*.,2016). Root weight was not significant at 3 MAP which revealed the effects of environmental influence rather than genotypic but was however highly significant at 6 MAP which shows the impact of genotypic effects. These further reveals that traits can be affected by environments.

Harvest index (HI) for the best genotype IBA141092 and IKN120036 of 56% and 54% is an indication of high root production since HI shows higher level of heritability in the study and selection for HI also indirectly select for fresh storage root yield traits (Table 5).

HI and shoot weight (stwt) negatively correlated which implies that high value for HI may also be an effect of low shoot growth and this means that selection for one trait is indirectly selecting the other. This was also reported by Rodrigo de Souza *et al.,* (2016) where they reported that high value for HI may be an effect of low shoot growth (Figure 1).

- *Root Bulkiness*

Storage root expansion begin to form from cassava fibrous root system from 2 – 3 months after planting. Tuber bulkiness is as a result of secondary thickening due to storage root formation and development (Cock *et al*., 1979). Early bulking cassava genotypes is an important farmers' preferred trait and this is usually so because threat of drought, bushfires and invasion by animals could be averted (Adjebeng-Danquah *et al.,*2016).

Root bulking begins about 3 months after planting (Table 3) and this could be observed from genotype IKN 120036 but rapid starch deposition does not occur before 6MAP (Izumi,1999, Priscilla, *et al*., 2015). Tuber bulking starts from 2 MAP but it was observed from 3 MAP (Tsay *et al.*, 1988; Priscilla *et al*., 2015). And has been reported to be stable after 3 MAP (Izumi,1999) and this was also observed in this study (Table 6). It has also been reported that root bulking increased with time and it differed among cultivars and varies over a long period due to changes in environmental conditions (Ekanayake *et al.*,1998)

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Late bulking genotypes develop sufficient above ground mass before storage root bulking (El shakawy, 2004; Alves, 2002) while early bulking genotypes begins storage root development and shoot simultaneously and usually due to genetic variability among genotypes (Okogbenin *et al.*, 2008). Earliness in root yield is related to rapid bulking and it varies according to genotypes. Early bulkiness genotype has high source and sink capacities which translates into total biomass for the early bulking group (Okogbenin *et al.*, 2008 and Adu-Gyamfi *et al.*,2016).

Slow bulking or late bulking genotypes develops sufficient above ground mass before it starts storage root bulking. Early bulking genotypes on the other hand begins storage root development and shoot at the same time (El shakawy, 2004; Alves, 2002).

Difference in bulking rate among different genotypes and bulking periods are the major determinant for high or low yielding cassava. Early maturing genotypes bulks at early stage (Suja *et al*., 2010)

Character			Range		3 MAP		6 MAP	
	Mean	CV	Min	Max	Genotype	Error	Genotype	Error
					df=9	df=20	df=9	df=220
FSRY	2.14	21.03	0.98	3.61	2.14**	1.70	2.09**	1.68
HI	0.38	23.95	0.11	0.56	0.38**	0.36	0.39***	0.37
NOHAV	1.4	28.17	1.00	2.00	1.4^{ns}	1.39	1.93**	1.90
RTNO	9.97	39.74	7.00	12.33	9.97^{ns}	9.97	13.77^{ns}	11.86
RTWT	2.02	39.4	0.72	3.09	2.02^{ns}	1.71	2.82**	1.90
STWT	3.81	53.86	1.80	5.29	3.81^{ns}	3.81	4.48^{ns}	3.40

Table 9:- Range, mean, coefficient of variation of traits evaluated at 3 and 6 MAP.

*, **, *** Significant at 0.05, 0.01 and 0.001 probability levels, respectively

TRAITS	σ^2p	σ^2G	σ^2E	% PCV	%GCV	Heritability	GA	GAM
DMC	33.02	16.38	16.64	17.39	12.26	0.50	22.96	69.53
DSRY	0.69	0.03	0.66	29.68	24.71	0.69	0.18	26.08
FSRY	2.14	0.44	1.70	34.27	30.88	0.81	1.12	52.34
HI	0.38	0.02	0.36	38.00	34.02	0.80	0.07	18.42
INNCOL	0.00	0.00	0.00	19.76	17.12	0.75	0.17	15.89
PLPCOL	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NOHAV	1.40	0.01	1.39	21.88	6.15	0.08	0.05	3.57
RTNO	9.97	0.00	9.97	25.68	0.00	0.00	0.00	0.00
RTSZ	3.13	0.13	3.00	13.46	11.65	0.75	0.57	18.21
RTWT	2.02	0.31	1.71	39.15	27.50	0.49	0.83	41.08
SC	19.39	24.20	-4.81	34.59	25.36	0.54	21.30	109.85
SPRT	0.79	0.04	0.75	28.33	24.60	0.75	0.14	17.72
SRD	10.43	1.57	8.86	14.68	12.01	0.67	5.44	52.16
STWT	3.81	0.00	3.81	36.87	0.00	0.00	0.00	0.00
VIG	4.93	0.65	4.28	22.48	16.37	1.85	1.85	37.53

Table 10:- Genetic parameter estimates of traits evaluated

Genotype	P	u+g	G%
IKN120036	3.61	4.05	6.02
IBA141092	2.63	3.07	4.38
IBA090581	2.59	3.03	4.32

Table 11:- Genetic gains of top three genotypes.

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➢ *Genetic Variability*

Understanding variability in crop genotypes is the key for a successful plant breeding program as this plays an important role in selection of desirable genotypes (Idahosa *et al*., 2010; Ndukaub *et al*., 2015). The genetic parameters of 10 cassava genotypes planted in early season of 2018 and evaluated at two different harvesting periods (3 and 6 months after planting MAP) are displayed in table (Table 10).

Genetic variations for cassava root yield components has been identified in different studies in Africa (Aina *et al*., 2007, Ojulong *et al*., 2008, Tumuhimbise *et al*., 2015). The coefficient of variation compares the relative amount of variability between crop plant traits (Sharma,1988). The highest coefficient of variation was recorded for shoot weight followed by root number, root weight, number harvested, harvest index in that order and the least being root size. It shows that the shoot weight having the highest coefficient of variation had the higher amount of exploitable genetic variability among the traits of the genotypes studied. It also showed that this trait can be selected compare to others (Eid 2009, Ndakauba *et al*., 2015). The root size having the least coefficient of variation shows that the traits has a low exploitable genetic variability and as a result has less potential for favorable advance for selection when compared to other traits (Chikezie *et al*., 2015).

This study revealed that shoot weight (Stwt) had zero heritability and genotypic coefficient of variation (GCV) which implies that its phenotypic expression is not due to its genetic component but as result of the environmental influence (Table 10). A greater difference between phenotypic coefficient of variation (PCV) and GCV is an indication of greater degree of environmental control (Chikezie *et al*., 2016). Conversely, in similar study conducted by Rodrigo de Souza *et al* (2016), they reported high genotypic coefficient of variation and low heritability for shoot weight. It will be therefore suggested that the traits be studied in multi environmental trial such as to accurately detect if the manifestation of the traits is as a result of genotype or environment. This then revealed that the highest coefficient of variation value exhibited by the traits was influenced the environment. Low heritability may be an effect of high environmental coefficient of variation which shows on low value of genetic gains (Rodrigo de Souza *et al*., 2016).

Coefficient of variation for fresh storage root yield was 21.03% and this affect selection as a result of genetic variability. This was similar to the coefficient of variation obtained for fresh storage root yield in study conducted by Neto *et al* (2013) when 10 cassava genotypes were evaluated.

Significant difference was observed in harvest index (HI) at different harvesting periods of 3 and 6 months after planting (MAP) among genotypes (Table 4). This shows effect of genetic variation and possibility of genetic gains. This was similar to result obtained by Rodrigo de Souza *et al* (2016) where significant difference was observed in HI. HI had the highest genotypic coefficient of variation (GCV) of 34% among the traits with phenotypic coefficient of variation (PCV) of higher value of 38%. The GCV values ranges from 34% to 6.5% while PCV values ranges from 39% to 13% for traits studied. High PCV indicate the existence of greater scope for selection for the traits under consideration (Khan et al, 2009) and GCV shows a measure of genetic variation existing in different traits. The HI thus indicate the presence of exploitable genetic variability which could assist in selection of the particular traits (Yadav et al,2009). The environmental coefficient of variation ranges from 16.62% to 0.36% for dry matter content and HI respectively. And this further revealed that the environment had little or no influence on the traits which implies selection for the trait in any environment.

Estimates of PCV were higher than those of GCV but were close, this implies that genotype contributed more than the environment in the expression of these characters and selection based on these phenotypic values is attainable.

There is narrow scope of selection for root size (rtsz) due to their low variability as a result of moderate PCV of 13%. On the other hand, high PCV of 39 % for root weight indicates the existence of greater scope for selection for the traits (Khan et al, 2009).

Fresh storage root yield (fsry) had the highest heritability values of 81%. Heritability among traits ranges from 81% to 0% for fsry and stwt (Shoot weight) respectively. High heritability is an indication of less environmental influence in the observed variation (Eid, 2009).

➢ *Heritability Estimates*

The ability to express a particular trait as a result of genetic component and phenotypic reliability in predicting its breeding value is provided by estimates of heritability (Ndakauba *et al.*, 2015). Heritability values for traits studied ranges from 81% to 0% for fsry and stwt respectively. Traits fsry having the highest heritability value of 81% shows that there is considerable genetic variation in the traits to warrant selection for the best genotypes. Thus, such traits can be given more attention for the purpose of improvement (Chikezie *et al*., 2016). Heritability alone does not provide effective means of selection, genetic advance for the traits should be considered (Ullah *et al*., 2012).

In this study, high heritability was observed with high genetic advance over mean for fresh storage root yield and dry storage root yield which is an implication of genotypic effect rather than environmental influence which implies that the genotypes will maintain their performance in any environment.

For traits such as the harvest index and root size which had higher heritability with low genetic advance over means is an indication of environmental influence and this shows that

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the genotype will perform well in this environment and improvement could be made for the traits in this particular environment. The high heritability observed might be due to the favourable influence of the environmental impact rather than genotype.

High heritability and high genetic advance over mean for a given trait is an indication of the traits being governed by additive gene action and thereby provides effective means for their selection (Chikezie *et al*., 2016; Tazeen *et al*.,2009).

Heritability and genetic gain for Root number (Rtno) is zero with 9.97% and 0% for PCV and GCV respectively. There was no significance difference (P>0.005) among the genotypes for the traits (Table 11). This is an indication that the Rtno is influenced by the environments and not due to genotype. It shows that the traits have non heritable component of phenotypic variance. However, Bareto & Resende (2010) identified lower values of heritability (0.18%) and GCV (19.3%) for root number with genetic gains varying from 26.4% to 32.85 with selection of best five genotypes. Also, Oliveria et al (2015) identified medium heritability of 0.51% and moderate GCV of 33.6% for root number and genetic gains which varied from 16.1% to 33.8% for the 10 best genotypes.

The zero genetic gains were probably due to no significant difference among the genotypes for root number traits which implies that there is no genetic variation among the genotypes. As reported by Rodrigo de Souza *et al* (2016) that lower genetic gains for root number was as a result of an effect of lower genetic variation among genotypes for root number. The low environmental coefficient of variation (ECV) of 9.97% this was similar to what was reported by Rodrigo de Souza et al (2016) where they observed ECV value for Rtno to be to be below 30%.

Root weight has moderate heritability value of 49% has possibility for improvement. Cassava root traits with moderate heritability values can be improved base on their phenotypic performances (Aina *et al*., 2007).

HI shows high level of heritability (80%) as also confirmed by Kawano et al (1989) which implies less environmental influence on the traits. Aina *et al*., (2007) also found higher values of heritability of 57% in their studies. Similar result was obtained by Ojulong *et al*., (2008) when they obtained moderate heritability for HI traits from the analyses 979 genotypes from International Institute of Tropical Agriculture in their studies.

A lowest value of environmental coefficient of variation was observed for HI which shows high genetic control of the traits. This result was similar to what was obtained by Rodrigo de Souza et al (2016) where they reported low value of coefficient of environmental variation for HI.

Fsry showed high level of heritability and was highly significant at P<0.01 which shows the influence of genotype on the control of the traits. Rodrigo de Souza et al (2016) reported low heritability for fsry and was not significant.

Genotypes differs in better values between Rtno and fsry traits in this study and this was also reported by Rodrigo de Souza (2016) where they observed that Genotypes with better values for Rtno differs from genotype with better values for fsry (Table 8).

VI. CONCLUSION

Fresh storage root yield(fsry) and Harvest Index (HI) can be considered as a good criterion for selection regarding root yield since fsry and HI showed a high heritability and both were highly significant at P<0.01 with less environmental influence. Varying root size traits manifestation for each of the genotypes was as a result of environmental influence which means that the environment has effect on the genotyic performance.

Root number and fresh storage root yield traits can be improved by direct crossing among selected genotypes. Crossing have been successfully used in genetic breeding programs of cassava (Ceballos *et al*., 2004).

- *Genetic Gain of 3 Best Genotypes*

Genetic gains varied from 6 to 4% considering the selection of the three best genotypes when compared with the general mean of the population (Table 11)

RECOMMENDATION

Genotype IKN120036 had the highest FSRY value of 3.61t/ha at both 3 and 6 MAP, therefore made genotype IKN120036 the best genotype of all genotype. Genotype IKN120036 had the highest genetic gains in terms of FSRY. However, to confirm that the genotype had the best gene expression for the trait FSRY used as a selection criterion, the trial should be repeated over a long period of time length such as to confirm the accuracy and the reliability of the genetic gain base on the trait.

LIMITATION

For adaptation and stability of the genotypes across different location other than Niger state, phenotypic evaluation trials and analyses will have to be conducted in multiple environments.

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