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Genetic Variability in Cassava as it Influences Storage Root Yield in Nigeria

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Abstract: Genetic variability in shoot and root characteristics among 20 broad-based cassava genotypes was studied in four agroecological zones in Nigeria to determine its effects on root yield. Seventeen agronomic parameters were evaluated on a plot size of 40 m², at spacing of 1×1 m in a Randomized Complete Block Design (RCBD) in four replicates. Analysis of variance (ANOVA) showed significant differences ($p < 0.001$) among genotypes within and across locations for most parameters. Significant genotype by environment (G×E) interaction effects was also observed. Estimates of genetic variances for phenotypic and genotypic coefficients of variation were higher for root characters than for shoot characters. PCV ranged from 4.3 to 36.5%; GCV ranged from 3.2 to 22.6%. Broad sense heritability (H^2) estimates were high for root characters, ranging from 75 to 88.6%, but low for shoot characters, ranging between 10.6 and 38%. Consequently, considerable scope exists for the improvement of economic traits, such as storage root yield. Shoot traits have little control on storage root yield while root traits with high genetic influence had major control on storage root yield. Number of roots, root size and Harvest Index are major yield determinants to be considered when selecting for root yield in cassava.

Key words: Cassava, storage root yield, coefficient of variation, heritability and genetic influence

INTRODUCTION

Cassava (*Manihot esculenta* Crantz) is the most important staple crop in the humid tropics serving as food for more than 250 million people in tropical Africa and 800 million people worldwide (FAO, 2004). Cassava is a reliable source of energy and can also be bred for enhanced nutritional quality such as micronutrients and proteins (CIAT, 2004). Cassava has moved from being a subsistence crop to a fully commercial crop, due to its income generating capacity and enormous potentials for industry, animal feed and human consumption. It has a comparative advantage over many other crops and can produce outstanding yields under harsh environmental conditions where other crops would fail (Nweke *et al.*, 1994).

Yield improvement, a major thrust in crop improvement programmes, can be achieved by exploiting the genetic variability within a germplasm and the wide variability that exists among cassava genotypes for shoot and root characteristics can be utilized for improving storage root yield. The expression of yield depends on the functioning and interaction of many physiological components that vary among genotypes, thus making it difficult to improve yield directly. Progress in breeding for yield characters depends largely on the nature and

magnitude of genetic variability. Genetic variation in a population, however, depends on the number and genetic diversity of parents used to form the population.

Selection for morphological characters will become useful when the performance of that character is correlated with the primary character hence, phenotypic correlation among characters provides a preliminary indication of the association between such characters. Number of storage roots, storage root size and Harvest Index showed high correlated responses with storage root yield (Ntawuruhunga *et al.*, 2001). Earlier reports, however, indicated that root yield was significantly correlated to both shoot and root characters (Mahungu, 1983).

Recent studies on the genetic variability among cassava genotypes showed remarkable intravarietal variation (Asante and Offei, 2003; Zaldivar *et al.*, 2004). This study was conducted to determine how genetic variation in shoot and root characteristics of cassava genotypes influences storage root yield in four agroecological zones of Nigeria.

MATERIALS AND METHODS

Twenty broad-based cassava genotypes were evaluated at four agroecological zones in Nigeria; Ibadan

Table 1: Climatic and soil characteristics of experimental sites in Nigeria

Climatic factors	Ibadan	Mokwa	Zaria	Mallamadori
Latitude	7° 26'N	9° 29'N	11° 11'N	11° 78'N
Longitude	3° 54'E	5° 04'E	7° 38'E	9° 34'E
Altitude (masl)	243	152	610	472
Radiation (Mj/m ² /day)	17.25	17.41	18.33	20.38
Mean annual temp. (°C)				
Minimum	22.70-23.25	18.78-23.45	14.27-25.04	13.35-24.86
Maximum	27.75-34.54	28.75-35.78	29.13-36.62	29.03-38.98
Mean annual rainfall (mm)	1259.57	1117.96	941.23	744.38
Agroecological zones	Forest savanna transition	Southern Guinea savanna	Northern Guinea savanna	Sudan savanna
Length of growing period (days)	211-270	181-201	151-180	<150
Soil type	Ferric Luvisol	Ferric Luvisol	Orthic Luvisol	Eutric Regosol

Masl-meters above sea level, Source: Ibadan: Geo-Spatial Lab (IITA), Ibadan, Oyo State; Mokwa: NCRI, substation, Mokwa, Niger State; Zaria: ABU Teaching and Research farm, Zaria, Kaduna State; Mallamadori: IITA experimental plot, Mallamadori, Jigawa State

(forest savanna transition), Mokwa (southern Guinea savanna) Zaria (northern Guinea savanna) and Mallamadori (Sudan savanna) for two cropping seasons (1999/2000 and 2000/2001) in a randomized complete block design with four replicates. The climatic and soil characteristics vary for each of the agroecological zones (Table 1).

Plants were established under rainfed conditions using healthy stakes 25 cm long at a spacing of 1×1 m in 40 m² plots of 4 rows of 10 plants per row. Weeding was done manually when necessary and neither fertilizer nor pesticides was applied. Morphological characterization data were collected at 3, 6 and 9 Months After Planting (MAP), for plant height, stem girth, number of nodes, height to first branching, leaf size and leaf retention. Yield data were collected at harvest, 12 MAP on parameters such as fresh root weight (kg), fresh shoot weight (kg), total number of roots, root size categorized based on storage root weight and size into small sized roots (size 3), medium sized roots (size 5) and large sized roots (size 7). Harvest Index (HI) and root dry matter percentage (RTDM) were also determined.

STATISTICAL ANALYSIS

All data generated were analyzed using the Statistical Analytical System (SAS), version, (1996). Analysis of variance (ANOVA) was carried out on plot mean basis using the Generalized Linear Model (GLM) procedures for randomized complete block design. Estimates of variance components were obtained by equating the observed mean squares from ANOVA with their Expected Mean Squares (EMS). Phenotypic variances for varied combination of years and locations are calculated as derived from the formulae by Obilana and Fakorede (1981). Broad sense heritability, phenotypic (PCV) and genotypic (GCV) coefficients of variation were computed using the formula by Singh and Chaudhary (1985). Principal component analysis (PCA) was done using the PROC PRINCOMP procedures of SAS (1996). Linear

regression among traits was determined with PROC REG procedures of SAS.

Variance component estimation: Variances were estimated from EMS as follows:

- $\sigma^2_g = (Msg + Msgly - Msgl - Msgy) / rly$
- $\sigma^2_{gl} = (Msgl - Msgly) / ry$
- $\sigma^2_{gy} = (Msgy - Msgly) / rl$
- $\sigma^2_{gly} = (Msgly - Mse) / r$
- $\sigma^2_e = Mse$
- $\sigma^2_g =$ genotypic variance
- $\sigma^2_{gl} =$ variance due to genotype and location
- $\sigma^2_{gly} =$ variance due to genotype, location and year
- $\sigma^2_e =$ error variance,
- $r =$ replicate,
- $Ms =$ Mean Squares

Phenotypic variance (σ^2_{ph}) across locations was calculated as follows:

$$\sigma^2_{ph} = \frac{\sigma^2_e}{rly} + \frac{\sigma^2_{gly}}{ly} + \frac{\sigma^2_{gy}}{y} + \frac{\sigma^2_{gl}}{l} + \sigma^2_g$$

- $r =$ number of replicates,
- $l =$ number of locations,
- $y =$ number of years (Obilana and Fakorede, 1981)

Phenotypic coefficients of variation

$$PCV = \frac{\sqrt{\sigma^2_p}}{x} \times 100$$

Genotypic coefficients of variation

$$GCV = \frac{\sqrt{\sigma^2_g}}{x} \times 100$$

Broad sense heritability (H_2)

RESULTS

$$H^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

where:

H² = Broad sense heritability

σ²p = Phenotypic variance

σ²g = Genotypic variance

x = mean of the population

(Singh and Chaudhary, 1985).

The analysis of variance across locations (Table 2) revealed highly significant differences (p<0.001 among genotypes for most parameters evaluated. The percentage coefficient of variation (CV%) ranged from 17.2 (stem girth) to 86.0 (size 7 roots). Plant height followed by leaf size had the widest ranges in mean values while shoot weight and stem girth had the smallest

Table 2: Phenotypic variability among twenty cassava genotypes for seventeen characters

Character	Mean±SE	Range	CV (%)	Mean squares		
				B/w clones df= 19	loc×clone df = 57	Error df=430
Plant height	114.71±1.50	55.33-290.11	32.80	3490.56***	1934.4***	235.21
No. of stems	2.44±0.04	1.00-9.00	44.30	3.95***	2.74***	0.53
Stem with leaves	38.06±0.75	4.33-210.22	49.40	798.77***	245.4***	157.47
Stem girth	1.79±0.01	0.92-3.31	17.20	0.33***	0.11***	0.04
No. of nodes	28.78±0.18	18.00-47.00	16.01	50.12***	45.37**	21.67
Leaf size	100.79±1.73	24.57-262.31	42.90	2067.62***	1170.45***	530.95
First branch ht.	56.26±1.22	0.00-179.00	53.50	1979.40***	2754.1***	198.11
Stands at harvest	14.86±0.29	0.00-20.00	48.10	69.65***	45.5***	23.52
No. of roots	4.81±0.10	0.33-30.00	53.10	20.52***	8.62***	2.79
Size 3 roots	2.97±0.07	0.00-18.00	60.20	12.35***	4.26***	1.66
Size 5 roots	1.52±0.05	0.00-8.00	76.20	2.30***	1.28***	0.36
Size 7 roots	0.33±0.02	0.36-4.00	86.00	0.18***	0.12***	0.09
Yield/ plant (kg)	1.42±0.04	0.05-4.60	66.50	1.86***	1.06***	0.18
Yield (t ha ⁻¹)	11.9±0.40	0.00-45.00	83.40	184.94***	88.54***	12.35
Shoot weight (kg)	1.54±0.03	0.26-2.00	50.90	10.09***	6.66***	57.62
Harvest Index (HI)	0.50±0.01	0.05-0.93	28.70	0.07***	0.04***	0.01
Root dry matter (%)	29.59±0.28	10.65-45.20	23.60	152.94***	26.54***	17.60

, * significant level at P< 0.01 and 0.001. Stem with leaves = length of stem with leaves, First branch ht = height to first branching, Stands at harvest= number of stands harvested, Size 3= small sized roots, Size 5= medium sized roots, Size 7= large sized roots

Table 3: Mean squares from combined analysis of variance for 20 genotypes for shoot and root characters

Source of variation	df	Plant height (cm)	Stem girth (cm)	Leaf size (cm)	Canopy volume (m ³)	No. of stands harvested	No. of storage roots	Root yield (t ha ⁻¹)	Size 3 roots (small)	Size 5 roots (medium)	Size 7 roots (large)	Root dry matter (%)
Year	1	53578.9***	2.0***	102434.0***	0.3***	327.5***	74.2***	1791.4***	3.4***	89.5***	7.3***	487.9***
Loc	3	174777.6***	4.7***	182244.8***	121.8***	4107.0***	463.1***	12291.0***	71.7**	117.3***	8.9***	4488.3***
Loc x year	3	4717.6***	0.9***	16001.1***	5.6ns	555.4***	86.5***	1406.3***	141.3***	9.0***	2.8**	225.3***
Rep (Loc x year)	24	1394.5***	0.1***	1465.7***	3.1***	47.2***	5.4***	48.0***	3.5***	0.8***	0.1ns	55.0***
Clone	19	3490.5***	0.3***	2067.6***	4.4***	69.6***	20.5***	185.3***	12.3***	2.3**	0.1***	157.3***
Loc x Clone	57	631.2***	0.1***	1170.3***	2.0***	45.8***	6.0***	67.1***	2.5**	1.1***	0.1*	26.3***
Clone x year	19	714.9***	0.1***	1070.6***	1.1*	47.2***	2.2ns	26.7***	0.8ns	0.9***	0.1ns	20.2ns
Loc x Clone x year	57	409.0***	0.1***	1011.2***	1.2***	20.8ns	3.1ns	26.1***	1.9ns	0.6***	0.1*	14.3ns
Error	442	235.21	0.04	530.95	0.64	23.25	2.79	12.31	1.66	0.36	0.09	17.11

*, **, *** significant level at P< 0.05, 0.01 and 0.001 respectively, ns= not significant

Table 4: Estimates of genetic variances, phenotypic (PCV) and genotypic (GCV) coefficient of variation and broad sense heritability for 17 characters

Character	δ ² g	δ ² gl	δ ² gy	δ ² gly	δ ² e	δ ² Ph	PCV	GCV	H ²
Plant height	79.80	27.77	19.12	43.45	235.21	109.08	9.10	7.79	73.15
No. of stems	0.07	0.04	0.05	0.05	0.53	0.12	14.40	10.48	52.92
Stem lth. with leaves	12.26	12.81	4.32	19.33	157.47	24.96	13.13	9.20	49.12
Stem girth	0.00	0.01	0.00	0.01	0.04	0.01	5.63	3.33	34.96
No. of nodes	0.85	0.74	-0.51	0.63	21.67	1.53	4.27	3.17	55.25
Leaf size	26.18	19.89	3.71	120.07	530.95	64.61	7.98	5.08	40.52
First branching ht.	18.47	20.91	42.17	170.66	198.11	61.86	13.98	7.64	29.86
Stands at harvest	0.23	1.88	1.02	1.84	23.52	2.18	9.93	3.24	10.66
Number of roots	0.48	0.36	-0.06	0.08	2.79	0.64	16.65	14.42	75.00
Size 3 roots	0.34	0.07	-0.07	0.08	1.66	0.39	20.92	19.69	88.61
Size 5 roots	0.03	0.06	0.02	0.08	0.36	0.07	17.63	10.69	36.76
Size 7 roots	0.00	0.00	0.00	0.01	0.09	0.01	22.43	13.32	35.29
Yield (kg plt)	0.03	0.06	0.00	0.04	0.18	0.06	16.98	12.88	57.49
Yield (t ha ⁻¹)	3.66	5.13	0.04	3.44	12.35	5.78	20.20	16.08	63.34
Shoot wt (kg)	0.12	0.30	-0.69	10.70	57.62	0.32	36.46	22.57	38.30
Harvest Index (HI)	0.00	0.00	0.00	0.00	0.01	0.00	9.15	6.94	57.57
Root dry matter (%)	3.82	1.62	0.27	1.01	17.60	4.78	7.39	6.60	79.83

*, **, *** significant level at p<0.05, 0.01 and 0.001, Stands at harvest = number of stands harvested, Size 3 = small sized roots, Size 5 = medium sized roots, Size 7 = large sized roots

Table 5: Eigenvalues for the first four principal components and eigenvectors for 15 characters

Character	Prin1	Prin2	Prin3	Prin4
No. of stems	0.132	-0.022	-0.104	-0.422
Plant height	-0.111	0.419	0.090	0.030
Stem length with leaves	-0.127	0.263	0.330	0.140
Stem girth	-0.134	0.351	-0.201	0.083
No. of nodes	0.041	-0.238	0.070	0.014
Leaf size	0.146	-0.040	-0.366	-0.059
Storage root yield (t ha ⁻¹)	0.350	0.009	-0.015	0.266
Stands harvested	0.233	0.196	0.082	-0.263
No. of roots	0.354	0.151	-0.027	0.074
Size 3 roots	0.327	0.160	-0.048	-0.014
Size 5 roots	0.308	0.142	0.050	0.238
Size 7 roots	0.123	-0.186	-0.012	0.271
Shoot weight	0.211	0.250	-0.338	-0.148
Harvest Index (HI)	0.280	-0.082	0.218	0.348
Dry matter	0.042	-0.062	0.456	-0.160
Proportion (%)	27.7	18.6	11.0	9.0

ranges. There was highly significant ($p < 0.001$) mean squares (MS) among genotypes for most traits within and across locations (Table 3). Estimates of genetic variances, PCV and GCV and broad sense heritability (H^2) for various traits across the four agroecological zones (Table 4) showed wide variability among genotypes for genetic parameters. PCV, GCV and H^2 values were higher for root characters than for shoot characters, PCV ranged from 4.27% (number of nodes) to 36.5% (shoot weight) and GCV ranged from 3.2% (number of nodes) to 32.4% (shoot weight). H^2 ranged from 10.6% (number of stands harvested) to 88.6% (size 3 roots) and was high ($>70\%$) for plant height (73.2%), number of roots (75.0%), root dry matter (79.8%) and small sized roots (88.6%). Moderate H^2 (50-69%) obtained for Harvest Index, root yield, stem

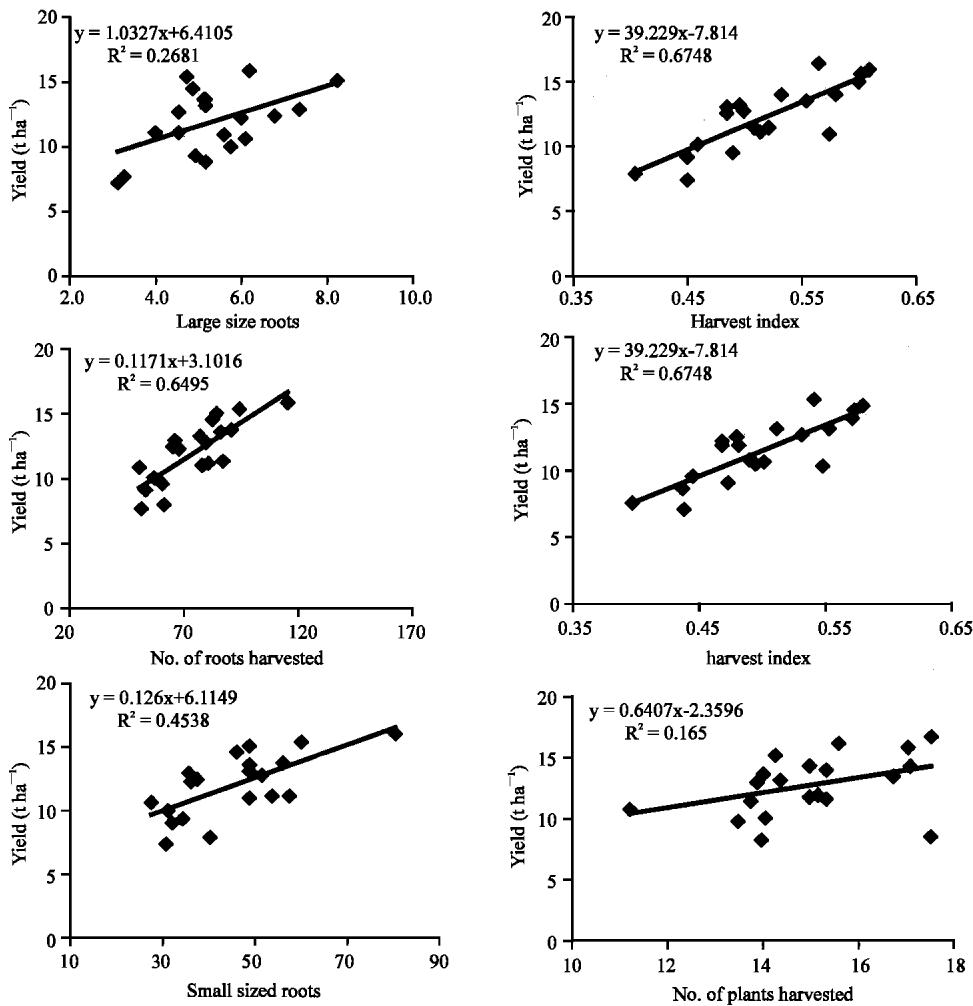


Fig. 1: Relationship between root yield and other yield traits for 20 genotypes

number and number of nodes; heritability estimates were low (<50%) for stem with leaves, stem girth, leaf size, first branching height and number of stands at harvest. Results of the PCA (Table 5) showed that eigenvalues of the first four Principal Components (PC) accounted for a total variation of 67.8%, with all the PCs having eigenvalues greater than 1. PC 1 alone accounted for 35.1% of the total variance which was mostly controlled by root parameters. PC 2 accounted for a smaller fraction of total variance (13.2%) and was largely controlled by shoot parameters. PC 3 accounted for 11% of total variance and was largely due to the influence of both shoot and root characters, PC 4 accounted for the least variation (9.0%), which was largely due to root characteristics. The coefficient of determination (R^2) for linear regression ranged from 0.17 for number of plants harvested to 0.70 for medium sized roots (Fig. 1).

DISCUSSION

The highly significant MS that were observed among genotypes within and across locations, as well as the significant genotype by environmental interaction ($G \times E$) indicated significant variability in the performance of genotypes across the different agroecological zones due to differential response of the genotypes to diverse edaphic, climatic and biotic conditions in each agroecology. The range of the CV% indicated low to very high variation among the genotypes. Root characters that showed high CV% suggest wide variability for such characters which could be utilized in improving storage root yield in cassava. The widest range observed for plant height in this study was in line with the findings of Naskar *et al.* (1989). A high estimate of H^2 was also observed for plant height, indicating high genetic variability for this trait. Plant height, however, does not show any correlated response with root yield, indicating that the high genetic variance that was observed for plant height has little or no direct linkage with root yield. The study of Makame (1995), however, showed that plant height had the narrowest variation out of all the variables that were evaluated.

Higher PCV values than GCV values indicated the considerable role of the environment on the expression of these characters. Similar observations were made by Kamalam *et al.* (1978) and Birader *et al.* (1978). Number of nodes and stem girth had the lowest PCV and GCV while shoot weight, large sized roots and small sized roots had the highest, indicating the possibility of improving these characters through selection in a breeding programme. The degree of success in selection however, depends on

the magnitude of heritable variations determined through heritability and also on genetic advance (Panse, 1957). Estimated H^2 that ranged from low to very high suggested that characters with low heritability have high environmental influence while those with high heritability have high genetic influence. Most of the shoot characters, with the exception of plant height, with low to moderate H^2 , therefore showed a high level of environmental influence and hence cannot be improved upon through breeding efforts. Most of the root characters with moderate to H^2 indicated that these characters, with high genetic influence, can be improved upon and direct selection for these traits based on their phenotypic performance can be successfully achieved through breeding. PC 1, which accounts for the highest proportion of the total variance, is largely controlled by root parameters. PC2 is largely controlled by shoot parameters; PC3 is controlled by both root and shoot parameters. The larger proportion of the observed variability was being controlled largely by root parameters. The high direct effect observed for root number and root size from path analysis indicates that they both play a major role in determining yield. Hence, selection should be concentrated on producing large sized storage roots as well as on increasing the number of roots produced, because a preponderance of small-sized roots will result in a negative effect on yield. Environmental factors that could result in a reduction in number and size of storage roots should be investigated and eliminated through any possible means. The preponderance of small-sized roots will have an adverse effect on final yield as an increase in the number of roots is not accompanied with a proportional increase in final weight. Increasing production of shoot growth over root growth may also result in a negative effect on final storage root yield. Remarkable intravarietal variation observed among cassava genotypes that were evaluated in this study fell in line with the findings of Asante and Offei (2003) and Zaldivar *et al.* (2004).

CONCLUSIONS

Assessment of variability is therefore a prerequisite for crop improvement to judge the potential of the population as a base for genetic improvement. Significant variability has been observed among cassava cultivars and selection of desirable characters will lead to progress in plant genetic improvement. Root number and size with high heritability contributed significantly to yield in cassava and could be used as important selection criteria in the enhancement of genetic improvement of cassava.

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