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Assessment of Genetic Parameters for Important Agronomic Traits in Sweet Potato (*Ipomoea batatas* (L.) Lam) Germplasm in Two Agro-ecological Regions of Nigeria

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

For an effective and efficient crop breeding program, collection of good genotypes that provides good agronomic background for the new variety to be developed must be available, and such genotypes must contain significant genetic variability for effective crop development. In order to determine the agronomic worth of a collection of sweetpotato genotypes so as to identify the superior ones under different agro-ecologies, and also to determine the extent of variability that exists among the genotypes, fifty-two genotypes were evaluated at Umudike (rainforest belt) and forty-eight at Otobi (humid guinea savannah) during the raining season using recommended protocols. While agronomic data were taken at 4 months after planting (MAP), sweetpotato virus disease (SPVD) incidence and severity scores were taken at 2 MAP. Results showed that significant ($p<0.001$) variation exists among the genotypes for all the traits except weight of unmarketable roots in both locations. Genotype PYT/12/074 had the highest root yield of 29.33 t/ha

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at the rainforest belt followed by Solo-2 and PYT/12/105 with yield levels of 27.67 and 26.33 t/ha, respectively. At Otobi, same PYT/12/074 had the highest root yield of 27.74 t/ha followed by Kwara and PYT/12/105 with yield levels of 27.67 and 26.33 t/ha, respectively. The principal component analysis identified marketable root weight, number of marketable roots, SPVD incidence and severity as the most important traits that influenced the observed variation among the genotypes. The biplot analysis further identified most of the orange-fleshed genotypes as highly susceptible to SPVD. Genetic studies of the traits showed that while broad-sense heritability estimates ranged from moderate to high for the important agronomic and SPVD traits, the high GCV and genetic advance observed portends a high genetic gain and good breeding progress in the breeding program using the genotypes.

Keywords: Genetic advance; GCV; genotypic variance; heritability; principal component analysis; trait-genotype relationship.

1. INTRODUCTION

Sweetpotato is an important food security crop with increasing importance in the food chain of many communities in Nigeria. Nigeria is the second highest sweetpotato producer in Africa and the third highest producer in the world with production of 3.87 million metric tones (FAOSTAT, 2020). The crop is adapted and planted in all agro-ecologies in Nigeria though with different intensities [1]. Though production has increased in the last 20 years, yield per hectare has remained low due to various factors which include biotic, abiotic and socio-cultural. Of the biotic factor, the sweetpotato virus disease (SPVD) is the most damaging disease of sweetpotato, causing yield loss of as high as 90 - 98% [2,3]. Diseased plants are severely stunted, small and narrow (strap-like); leaves are often with distorted edge; puckering, vein clearing and mottling may occur [4]. The use of old virus-infected planting materials sourced from previous years' fields, a common source of planting material in many developing countries especially in sub-Sahara Africa, is one of the critical reasons for poor root yield in sweetpotato. To increase root yield per unit area, new sweetpotato varieties with increased potential for high root yield and high resistance to SPVD must be developed.

The success of crop variety development depends on the existence and extent of variability within the available crop germplasm [5]. The existence of wide variability for almost all important traits in sweetpotato is a known occurrence [6], and are due to the hexaploid (2n = 6x = 90) and outcrossing nature of the crop. Wide variability for root yield, yield components, SPVD resistance and food quality attributes has been reported [7-9. Also, the existence of medium to high heritability and high genotypic coefficient of variation for the traits [9] suggest that breeding new varieties combining these traits is possible. The first step in the development of new sweetpotato varieties, as it is in other crops, is the evaluation of available elite germplasm to identify genotypes expressing traits of interest for use in the development of progeny population through hybridization [10]. Phenotyping for yield and SPVD resistance is commonly done on the field. Feld phenotyping is one of the most effective and cost efficient ways of identifying genotypes with broad resistance to different strains of viruses, especially when carried out in divergent environments where the genotypes are exposed to varied strains of disease pathogens and growing conditions. Authors such as Koussao et al. [11] and Gibson et al. [4] have variously used this approach. The objective of this work, therefore, was to identify sweetpotato genotypes with combinations of good agronomic traits and sweetpotato virus disease resistance that can be extended to farmers for increased productivity, and/or for breeding purposes.

2. MATERIALS AND METHODS

2.1 Experimental Layout

The field trials were carried out in two locations – the National Root Crops Research Institute (NRCRI), Umudike (high rainforest belt); and Otobi, Benue State (humid guinea savannah). The characteristics of the two locations are presented in Table1. Fifty-two genotypes were evaluated at Umudike and forty-eight genotypes at Otobi during the raining season. The names of the genotypes used are presented in Table 2. The trials were established using 6 X 9 and 6 X 8 alpha lattice design at Umudike and Otobi respectively with three replications. At each location, each genotype was planted on a plot of.

Table 1. Characteristics of the two locations involved in the evaluation of sweet potato genotypes

Location characteristics						
Location	**Longitude**	**Latitude**	**Altitude**	**Soil Type**	**Total Annual Rainfall (mm)**	**Average monthly Temperature (^{0}C)**
Umudike	$07^0$0331′E	$05^0$0291′N	122 m	Ultisol	2079.8	25-32
Otobi	$08^0$0632′E	$07^0$0696′N	141 m	Alfisol	1250.0	25-36

Sources: Umudike: Agro-meteorological Unit, National Root Crops Research Institute, Umudike, Abia State

Table 2. Characteristics of the sweetpotato genotypes evaluated for their agronomic and root quality traits in two diverse agro-ecologies

S/No	Genotype	Source	Flesh colour	Location(s) planted
1	AYT/08/055	NRCRI, Umudike	White	Umudike and Otobi
2	AYT/11/095	NRCRI, Umudike	Light orange	Umudike and Otobi
3	Agege	Landrace	White	Umudike and Otobi
4	Butter milk	Landrace	Light yellow	Umudike and Otobi
5	Centennial	CIP, Kenya	Orange	Umudike and Otobi
6	CIP 199004.2	CIP, Kenya	Light orange	Umudike
7	CIP 420068	CIP, Kenya	White	Umudike and Otobi
8	EA/11/002	NRCRI, Umudike	White	Umudike and Otobi
9	EA/11/003	NRCRI, Umudike	White	Umudike and Otobi
10	EA/11/022	NRCRI, Umudike	White	Umudike and Otobi
11	EA/11/025	NRCRI, Umudike	White	Umudike and Otobi
12	Ex-Igbariam	NRCRI, Umudike	Yellow	Umudike and Otobi
13	Ex-Oyunga	CIP, Kenya	Orange	Umudike
14	Kwara	Kwara state	Light orange	Umudike and Otobi
15	NRSP/11/095	NRCRI, Umudike	Cream	Umudike and Otobi
16	NRSP/11/097	NRCRI, Umudike	Yellow	Umudike and Otobi
17	NRSP/12/095	NRCRI, Umudike	White	Umudike
18	PYT/12/010	NRCRI, Umudike	White	Umudike and Otobi
19	PYT/12/012	NRCRI, Umudike	White	Umudike and Otobi
20	PYT/12/025	NRCRI, Umudike	White	Umudike and Otobi
21	PYT/12/036	NRCRI, Umudike	White	Umudike and Otobi
22	PYT/12/044	NRCRI, Umudike	White	Umudike and Otobi
23	PYT/12/049	NRCRI, Umudike	Yellow	Umudike and Otobi

S/No	Genotype	Source	Flesh colour	Location(s) planted
24	PYT/12/051	NRCRI, Umudike	White	Umudike
25	PYT/12/053	NRCRI, Umudike	White	Umudike and Otobi
26	PYT/12/055	NRCRI, Umudike	Yellow	Umudike and Otobi
27	PYT/12/060	NRCRI, Umudike	Light orange	Umudike and Otobi
28	PYT/12/061	NRCRI, Umudike	White	Umudike
29	PYT/12/063	NRCRI, Umudike	White	Umudike and Otobi
30	PYT/12/068	NRCRI, Umudike	White	Umudike and Otobi
31	PYT/12/074	NRCRI, Umudike	White	Umudike and Otobi
32	PYT/12/078	NRCRI, Umudike	Yellow	Umudike and Otobi
33	PYT/12/086	NRCRI, Umudike	White	Umudike and Otobi
34	PYT/12/094	NRCRI, Umudike	White	Umudike
35	PYT/12/095	NRCRI, Umudike	Light orange	Umudike and Otobi
36	PYT/12/104	NRCRI, Umudike	White	Umudike and Otobi
37	PYT/12/105	NRCRI, Umudike	White	Umudike and Otobi
38	PYT/12/106	NRCRI, Umudike	White	Umudike and Otobi
39	PYT/12/118	NRCRI, Umudike	White	Umudike and Otobi
40	PYT/12/121	NRCRI, Umudike	White	Umudike and Otobi
41	PYT/12/050	NRCRI, Umudike	White	Otobi
42	PYT/12/082	NRCRI, Umudike	White	Otobi
43	PYT/12/098	NRCRI, Umudike	White	Otobi
44	SOLO 1	NRCRI, Umudike	Yellow	Umudike and Otobi
45	SOLO 2	NRCRI, Umudike	Light orange	Umudike and Otobi
46	TIS 2532.OP.1.13	NRCRI, Umudike	White	Umudike
47	TIS 8164	NRCRI, Umudike	White	Umudike and Otobi
48	TIS 86/0356	NRCRI, Umudike	White	Umudike and Otobi
49	TIS 87/0087	NRCRI, Umudike	White	Umudike and Otobi
50	UM/11/001	NRCRI, Umudike	White	Umudike and Otobi
51	UM/11/015	NRCRI, Umudike	White	Umudike and Otobi
52	UM/11/022	NRCRI, Umudike	White	Umudike and Otobi
53	UMUSPO/1	NRCRI, Umudike	Light orange	Umudike and Otobi
54	UMUSP/2	NRCRI, Umudike	White	Umudike and Otobi
55	UMUSPO/3	CIP, Kenya	Deep orange	Umudike and Otobi

2.0 m X 3.0 m with inter-plot spacing of 1.0 m. Planting distance was I.0 m between rows and 0.3 m within row, amounting to 20 plants per plot and 33,333 per hectare. Four node vine cuttings were planted at the crest of the ridges in a slanting manner with two nodes buried in the soil. First weeding was carried out at four weeks after planting (WAP) while 400 kg/ha of NPK 15:15:15 was applied to the field using the side banding method immediately after weeding. The trials were harvested at four months after planting

2.2 Data Collection

The sweetpotato genotypes were screened for SPVD only at Umudike as the location is a known hotspot for SPVD. Sweetpotato virus disease incidence and severity data were collected at 8 weeks after planting (WAP) using the infection severity scale of 1 – 5, where 1= no apparent symptom; 2 = mild/very little symptom; 3 = moderate symptom; 4 = severe symptom; and 5 = very severe symptom according to Mwanga et al. [12] and Yada et al. [7]. At harvest, agronomic data which included number of marketable roots, number of unmarketable roots, weight of marketable roots and weight of unmarketable roots were collected per plot with number of marketable roots taken as the number of roots $\geq$100g; number of unmarketable roots taken as number of roots 100g; weight of marketable roots taken as the weight (kg/plot) of the marketable roots class; and weight of unmarketable roots taken as the weight (kg/plot) of the unmarketable roots according to Levette, [13] .

2.3 Data Analyses

The data collected were subjected to analysis of variance using the Generalized Linear Model procedure of SAS 9.2. The data were analyzed on location basis since the number of genotypes were not equal, and the variances of the two locations were significant following a Bartlet's test for homogeneity of the variances of the two locations. As such, genotype was treated as a fixed factor while replication was treated as random variable according to Steel and Torrie [14]. The ANOVA model used for the single-site analysis is stated below:

$$\mathrm{Yij} = \mu + \alpha i + bj + eij$$

Where, y_{ij} = observation on experimental unit in block j assigned treatment i; μ = over all mean averaged over all treatments and all blocks; α_i = effect of treatment *I,* considered as fixed variable; b_j = effect of block j, considered as random variable; e_{ij} = random error associated with experimental units assigned to treatment *i* in block *j*. Least Square (LS) means of the genotypes in each location were estimated and separated using standard errors of difference (SED). Principal Component Analysis (PCA) was also performed on the data based on correlation matrix using XLSTAT software to estimate the contribution of the traits to the variation within the genotypes.

For genetic analyses, the Expected Mean Squares approach was used to calculate phenotypic, genotypic and environmental variances and broad sense heritability estimates from the linear function of the mean squares of the ANOVA according to Allard [15] as follows:

Environmental variance, $\delta^2 e = MSe$;
Genotypic variance, $\delta^2 g = (MSg - Mse)/r$;
Phenotypic variance, $\delta^2 p = \delta^2 g + \delta^2 e$;
Broad sense heritability, $H_B = \delta^2 g / \delta^2 p$;

where: MSe = mean square of error; MSg = Mean squares of genotypes; and r = number of replications).

Genotypic (GCV) and phenotypic (PCV) coefficients of variation, and Genetic Advance (GA) were estimated according to the methods of Burton [16], using the following equations: Phenotypic coefficient of variation, PCV = (√Vp)/X*100; Genotypic coefficient of variation, GCV = (√Vg)/X*100 (where √Vp and √Vg are the phenotypic and genotypic standard variation, respectively; X is the grand mean of the trait). Genetic advance (GA) expected, and genetic advance as percent of the mean assuming selection of the superior 5% of the genotypes, were estimated in accordance with the methods illustrated by Fehr [17] as follows:

GA (expected) = K (Sp)*H_B;

GA (as % of the mean) = (GA/ X)*100 (where K is a constant which varies depending upon the selection intensity and, if the latter is 5%, it stands at 2.06, Sp is the phenotypic standard deviation (√Vp);

H_B is the broad sense heritability ratio, and X refers to the mean of the character).

Table 3. Mean squares of the analysis of variance of agronomic traits of 48 sweetpotato genotypes evaluated in Otobi, humid guinea savannah

Sources of variation	Degrees of freedom	Mean squares				
		Number of marketable roots	Number of unmarketable roots	Weight of marketable roots (kg/plot)	Weight of unmarketable roots (kg/plot)	Root yield (tons/ha)
Replication	2	125.0542	44.5733	14.3975	0.5065	286.9505
Genotype	47	191.9736***	68.2499***	14.1555***	1.0661ns	147.3006***
Error	94	65.1034	22.3106	4.4187	0.9783	44.1536
Total	143					

*** = p<0.001; ns = p>0.05*

Table 4. Mean squares of the analysis of variance of agronomic traits of 52 sweetpotato genotypes evaluated in Umudike, high rainforest belt

Sources of variation	Degrees of freedom	Mean squares of analysis of variance (ANOVA)						
		Number of marketable roots	Number of unmarketable roots	Weight. of marketable roots (kg/plot)	Weight. of unmarketable roots (kg/plot)	Root yield (tons/ha)	SPVD incidence	SPVD severity
Replication	2	22.9465	429.1600	6.9772	0.9317	162.0642	0.7262	0.0938
Genotype	51	211.6039***	118.9022***	24.1385***	0.2222ns	148.7014***	11.3886***	3.2005***
Error	102	61.9878	49.3747	5.1940	0.1705	41.7249	1.3718	0.2424
Total	155							

*** = p<0.001%; ns = p>0.05*

Table 5. Means of yield and other important traits of 52 sweet potato genotypes evaluated in Umudike, rain forest belt

Genotype	Root yield (t/ha)	Weight of marketable roots (kg/plot)	Weight of unmarketable roots (kg/plot)	Number of marketable roots	Number of unmarketable roots	Percent incidence	Mean SPVD severity
PYT/12/074	29.33	9.90	0.27	29.33	7.33	3.35	1.33
SOLO 2	27.67	5.03	0.53	27.67	13.33	3.35	1.67
PYT/12/105	26.33	7.67	0.43	26.33	9.00	0.00	1.00
PYT/12/053	26.00	9.27	0.33	26.00	7.00	3.35	1.33
EA/11/025	25.69	9.00	0.30	20.33	4.67	0.00	1.00
UMUSPO/3	23.44	6.20	0.43	20.67	12.00	43.35	4.33

Genotype	Root yield (t/ha)	Weight of marketable roots (kg/plot)	Weight of unmarketable roots (kg/plot)	Number of marketable roots	Number of unmarketable roots	Percent incidence	Mean SPVD severity
TIS 8164	23.00	8.33	0.17	23.67	4.67	0.00	1.00
TIS 87/0087	23.00	8.43	0.27	23.00	6.00	0.00	1.00
UMUSPO/1	20.92	9.73	0.20	29.00	7.00	0.00	1.00
UM/11/015	19.00	7.20	1.03	19.00	3.33	3.35	1.33
PYT/12/061	18.93	8.88	0.07	18.93	0.46	0.05	1.01
SOLO 1	18.67	3.67	0.10	18.67	5.33	11.65	4.00
Butter milk	18.54	6.40	0.23	27.67	7.67	0.00	1.00
PYT/12/086	18.33	3.30	0.30	18.33	9.00	0.00	1.00
Agege	18.28	4.70	1.13	26.00	29.67	1.65	1.33
TIS 86/0356	17.67	2.43	0.50	17.67	10.00	0.00	1.00
PYT/12/025	17.51	7.27	0.77	36.00	18.67	0.00	1.00
NRSP/12/095	17.01	5.88	0.33	18.74	7.21	0.05	0.99
PYT/12/104	17.00	8.47	0.17	17.00	2.33	0.00	1.00
PYT/12/036	16.33	2.23	1.27	16.33	26.67	0.00	1.00
PYT/12/118	16.33	6.00	0.57	16.33	6.33	0.00	1.00
PYT/12/044	14.33	1.73	0.37	14.33	12.33	0.00	1.00
PYT/12/121	14.00	5.53	0.17	14.00	6.00	8.35	2.00
EA/11/002	13.75	5.87	0.13	20.67	12.00	0.00	1.33
NRSP/11/095	13.09	6.23	0.30	17.33	7.00	0.00	1.00
PYT/12/060	13.00	2.43	0.70	13.00	17.33	6.65	1.67
TIS 2532.OP.1.13	12.86	2.56	0.01	12.86	0.11	0.20	0.98
PYT/12/051	12.74	4.42	0.43	12.74	11.21	3.25	1.65
PYT/12/063	12.33	1.67	0.10	12.33	6.33	0.00	1.00
PYT/12/012	12.21	4.47	0.40	23.67	10.00	11.65	1.67
PYT/12/106	11.67	4.60	0.27	11.67	3.33	0.00	1.00
UM/11/001	11.33	4.07	0.13	11.33	3.33	0.00	1.00
CIP 1990044.2	11.09	2.67	0.50	19.00	15.33	23.35	4.33
Kwara	11.08	3.47	0.50	17.33	12.67	11.65	1.67
AYT/11/095	9.88	4.35	0.53	24.93	18.79	0.05	1.01
EA/11/022	9.67	3.33	0.30	13.33	8.67	0.00	1.00
PYT/12/068	9.33	2.33	0.33	9.33	7.67	5.00	1.33
PYT/12/078	9.33	1.30	0.37	9.33	11.33	6.65	1.67

Genotype	Root yield (t/ha)	Weight of marketable roots (kg/plot)	Weight of unmarketable roots (kg/plot)	Number of marketable roots	Number of unmarketable roots	Percent incidence	Mean SPVD severity
Centennial	9.25	1.80	0.80	16.00	21.00	23.35	3.00
AYT/08/055	8.62	3.47	0.27	24.00	12.67	1.65	1.33
EA/11/003	8.03	3.43	0.20	10.33	11.33	0.00	1.00
PYT/12/094	6.33	2.60	0.10	6.33	2.33	3.35	1.67
Ex-Igbariam	5.85	1.93	0.43	12.00	9.00	11.65	1.67
UM/11/022	5.67	1.77	0.13	5.67	2.33	0.00	1.00
NRSP/11/097	5.62	2.40	0.23	6.00	11.00	23.35	3.00
Ex-Oyunga	5.14	1.50	0.04	10.53	2.33	38.35	4.67
CIP 420068	5.09	1.50	0.02	8.33	5.00	0.00	1.00
UMUSP/2	3.91	1.53	0.20	6.33	3.67	0.00	1.00
PYT/12/010	3.83	1.07	0.33	9.67	18.33	0.00	1.00
PYT/12/055	3.00	0.13	0.03	3.00	1.67	0.00	1.00
PYT/12/049	0.00	0.00	0.03	0.00	3.33	21.65	4.67
PYT/12/095	0.00	0.00	0.40	0.00	11.00	0.00	1.00
SE	3.51	1.24	0.23	2.47	0.23	3.20	0.27

SE = Standard Error

Table 6. Means of yield and other important traits of 48 genotypes of sweet potato genotypes evaluated in Otobi, humid guinea savannah

Genotype	Root yield (t/ha)	Weight of marketable roots (kg/plot)	Weight of unmarketable roots (kg/plot)	Number of marketable roots	Number of unmarketable roots
PYT/12/074	27.74	5.30	0.67	20.33	12.33
Kwara	25.31	4.20	1.30	25.33	20.33
PYT/12/105	24.03	7.03	0.43	20.00	7.33
PYT/12/078	23.09	6.17	0.87	23.67	10.00
UMUSPO/1	22.9	9.33	1.00	38.33	22.67
PYT/12/060	21.38	7.92	1.02	29.64	15.52
PYT/12/012	16.51	4.40	0.50	18.33	9.67
SOLO 2	16.27	5.87	0.23	15.00	3.33
PYT/12/053	15.18	5.13	0.30	19.00	3.33
PYT/12/050	15.05	5.00	0.10	6.00	0.00
EA/11/003	14.3	5.10	0.37	15.33	6.33

Genotype	Root yield (t/ha)	Weight of marketable roots (kg/plot)	Weight of unmarketable roots (kg/plot)	Number of marketable roots	Number of unmarketable roots
SOLO 1	14.06	3.27	0.13	10.00	2.33
EA/11/025	12.37	5.17	0.57	17.00	8.67
EA/11/002	11.03	3.10	0.50	12.67	6.67
UMUSPO/3	10.97	4.50	0.46	14.31	6.48
PYT/12/104	10.89	4.20	0.36	13.33	4.67
TIS 86/0356	10.41	0.77	3.93	3.67	4.67
PYT/12/025	10.28	3.37	0.67	17.67	10.33
PYT/12/121	10.00	2.63	0.37	9.33	4.33
TIS 8164	9.80	2.97	0.27	11.67	4.67
PYT/12/095	9.43	2.47	0.10	7.00	1.33
AYT/11/095	8.44	3.13	0.27	13.67	6.67
PYT/12/118	7.90	1.80	1.10	6.00	15.00
EA/11/022	7.51	2.60	0.40	10.00	6.33
PYT/12/082	6.65	2.03	0.10	7.00	2.67
UMUSP/2	6.65	2.40	0.27	7.67	4.33
UM/11/001	6.10	1.92	0.13	6.14	2.52
Ex-Igbariam	6.02	2.00	0.43	8.67	2.33
Butter milk	5.44	1.40	0.47	5.33	7.67
Agege	4.99	1.03	0.20	5.00	4.67
PYT/12/068	4.86	0.87	1.13	2.64	5.52
TIS 87/0087	4.79	1.53	0.27	6.00	4.33
Centennial	4.39	1.48	0.31	8.55	5.00
PYT/12/044	3.99	1.23	0.33	7.00	5.67
PYT/12/063	3.94	1.17	0.33	5.33	6.33
NRSP/11/095	3.89	0.47	0.13	1.33	2.00
PYT/12/036	3.81	0.23	0.73	1.00	9.33
AYT/08/055	3.52	1.10	0.23	7.33	4.00
PYT/12/086	3.48	0.70	0.23	3.33	4.00
PYT/12/010	2.98	0.40	0.47	3.31	8.67
CIP 420068	2.62	0.92	0.08	3.64	3.02
PYT/12/049	2.46	0.93	0.10	2.00	1.33
UM/11/015	2.32	0.77	0.13	2.67	2.33
PYT/12/106	1.98	0.57	0.00	3.00	0.00

Genotype	Root yield (t/ha)	Weight of marketable roots (kg/plot)	Weight of unmarketable roots (kg/plot)	Number of marketable roots	Number of unmarketable roots
UM/11/022	1.16	0.43	0.00	1.67	0.33
PYT/12/055	0.96	0.22	0.02	0.64	0.52
PYT/12/098	0.91	0.20	0.10	1.67	3.67
NRSP/11/097	0.30	0.10	0.03	0.33	0.33
SED	3.62	0.85	0.54	4.39	2.57

SED = Standard Error Difference

3. RESULTS AND DISCUSSION

According to the mean squares of the analyses of variance (ANOVA) of the root traits presented in Tables 3 and 4, respectively, significant ($p<0.001$) differences exist among the genotypes for the root traits evaluated in both locations.

For the mean trait performances of the genotypes in each location, all the traits except weight of unmarketable roots exhibited significant ($P<0.05$) variation among the genotypes (Tables 5 and 6). At Umudike, fresh root yield ranged between 0.00 – 29.33 tons/ha for PYT/12/049/PYT/12/095 and PYT/12/074, respectively. Nine of the genotypes had yields > 20 tons/ha, while all the genotypes with this level of yield (>20 tons/ha) also had relatively high weight of marketable roots of 5.03 – 9.90 kg/plot. For weight of unmarketable roots, only UM/11/015 (1.03 kg/plot), Agege (1.13 kg/plot) and PYT/12/036 (1.27 kg/plot) had weight of unmarketable roots of more than 1.00 kg/plot, others had less. Number of marketable roots was high for some of the genotypes, while others had abysmally low values for the trait. With a range of 0.00 – 36.00, only PYT/12/025 had number of marketable roots up to 30 per plot with other genotypes having less. All the genotypes with yield >20 tons/ha also had high number of marketable roots above 20 and lower of unmarketable roots except in Agege. This relationship between root yield and number of marketable roots had earlier been reported by Afuape et al. [8], Yahaya et al. [18] and Ebem et al. [9] who found marketable root number as one of the important components of root yield. Genotypes Agege, PYT/12/036 and Centennial with mean number of unmarketable roots of 29.67, 26.67 and 21.00 respectively had the highest mean number of unmarketable roots. Unmarketable roots do not usually command good prices in the market due to the small root size that falls outside food processors' preference in Nigeria and many African countries where manual processing predominates. As such, genotypes that produce more of small roots (roots with <100g) are usually not adopted by farmers, and so are often selected against during the breeding process. The most devastating disease of sweetpotato in Nigeria is the sweetpotato virus disease (SPVD) [2]. The observed mean incidence and severity of SPVD ranged 0.00 – 43.35%, and 1.00 - 4.67, respectively. The variety UMUSPO/3 had the highest mean percent SPVD incidence of 43.35%, followed by Ex-Oyunga with mean percent incidence of 38.35%. The mean SPVD severity showed that PYT/12/049 (yellow-fleshed) and Ex-Oyunga (orange-fleshed) had the highest mean score of 4.67 and so were highly susceptible to SPVD. UMUSPO/3 (OFSP) ranked third with mean severity score of 4.33. Most of the CIP-introduced genotypes had SPVD severity scores above 3.00.

At the humid savannah location of Otobi, the root yields ranged 0.30 – 27.74 tons/ha. Only six genotypes had yields $\geq$ 20.00 t/ha, and apart from Kwara with mean weight of marketable roots of 4.2 kg/plot, all other genotypes with mean root yields $\geq$ 20.0 tons/ha also had mean weight of marketable roots > 5.00 kg/plot. Mean number of marketable roots had a range of 1.67 – 38.33. As observed in Umudike, genotypes with high root yield also had high mean number of marketable roots in Otobi. The genotype UMUSPO/1 had the highest mean number of marketable roots of 38.33, followed by PYT/12/060 with 29.64 for the trait. PYT/11/097 had the lowest mean number of marketable roots of 0.33 at Otobi. However, unlike the trend observed at Umudike, most of the genotypes with high mean root yield and high mean number of marketable roots also had the highest mean number of unmarketable roots with UMUSPO/1 exhibiting the highest number of unmarketable roots of 22.67. This can always be so when sweetpotato production is done on a fertile, well-drained sandy-loam soil which the humid savannah location of Otobi presented.

3.1 Trait-genotype Relationship

As ANOVA measures the existence of variability among the genotypes for each trait, the Principal Component Analysis (PCA) also identifies traits that define the observed variation among the genotypes. Table 7 presents the principal component analyses of the agronomic traits of the genotypes evaluated. Of the seven component axes, only three principal components (PC) axes had eigen values > 1.0, which cumulatively explained 90.99% of the total observed variability. Principal component axis 1 (PC1) had the highest eigen value of 3.14, and also explained 44.92% of the variations among the genotypes. Mean fresh root yield with eigen vector of 0.90, mean weight of marketable roots (eigen vector of 0.88), and mean number of marketable roots (eigen vector of 0.94) explained most of the 44.92% variation of PC1. It is clear that PC1 identified the important agronomic traits of the crop which were marketable root weight

and number of marketable roots. Principal component axis 2 (PC2) explains 26.70% of the total variability among the genotypes. The two SPVD traits, mean SPVD incidence (with vector 0.92) and mean SPVD severity (with vector 0.90), were responsible for most of the effects of PC2. Similarly, the mean number and weight of unmarketable root with loadings of 0.64 and 0.77 were responsible for PC3. This PC analysis suggests that phenotypic selection of the genotypes for these traits can lead to significant progress.

Principal component biplot can also been used to show trends among genotypes and traits, especially in the grouping of genotypes into trait classes. From the PC1 – PC2 biplot (Fig. 1), mean root yield, mean number of marketable roots, and weight of marketable roots are closely related, suggesting that there is strong and positive relationship between the traits. Mean number and weight of unmarketable roots are also found in the same quadrant as yield, suggesting that they could also positively influence root yield, even if nominally. Mean SPVD incidence and severity are located in another quadrant, and so are negatively related to root yield. However, both SPVD-related traits have very strong relationship with each other. It is interesting to observe that most of the CIP-sourced genotypes clustered around SPVD traits, showing that they exhibited high values for the disease traits, while most of the developed breeding lines appeared more resistant. Mwanga et al*.* [12] had earlier observed the susceptibility of CIP sweetpotato germplasm imported to Africa to SPVD. Incidentally, all the deep orange-fleshed sweetpotato genotypes (UMUSPO/3, CIP 199004.2, Centennial, Ex-Oyunga) were highly susceptible to SPVD. While the relationship between high beta-carotene content that confers orange colour on the flesh and virus disease severity has not been reported, the existence of such relationship could be worth investigating, especially as this inverse relationship has been observed among cassava transgenic lines with elevated beta-carotene content (data unpublished). The grouping of the genotypes into trait classes will enable an efficient selection of parents that give higher chances of developing good progeny populations with high yield and SPVD resistance. The use of PCA procedures in studying genetic relationships among sweetpotato genotypes have been reported [8,11,19].

3.2 Genetic Analyses of Agronomic and SPVD Traits

Understanding the genetics of the traits to be improved is a good guide for the effective selection of parent lines. Table 8 shows the genotypic, phenotypic and environmental variances and the broadsense heritability estimates (H_B) of the agronomic traits in Otobi and Umudike. In both locations, phenotypic variances (Vp) were higher than genetic variances (Vg) for all the traits due to the influence of the environments on trait expression. Heritability estimates were therefore either moderate or low for all the agronomic traits except SPVD incidence and severity with H_B of 0.71 and 0.80 respectively, depending on the extent of environment on each trait. Root yield and root yield component are quantitative traits

Table 7. Principal component analyses of agronomic traits of sweetpotato genotypes evaluated in two locations

	Principal component axes		
Traits	**PC1**	**PC2**	**PC3**
SPVD INC	-0.30	0.92	-0.13
UNMKTWT	0.43	0.15	0.77
Yld ton/ha	0.90	0.15	-0.33
MKTWT	0.88	0.02	-0.45
SPVD SEV	-0.35	0.90	-0.18
MKTNO	0.94	0.18	-0.08
UNMKTNO	0.53	0.37	0.64
Eigenvalue	3.14	1.87	1.36
Variability (%)	44.92	26.70	19.38
Cumulative %	44.92	71.61	90.99

MKTNO = Number of marketable storage roots; UNMKTNO = Number of unmarketable storage roots; MKTWT = Weight (kg/plot) of unmarketable storage roots; UNMKTWT = Weight of unmarketable storage roots; SPVD SEV = Incidence of sweet potato virus disease; SPVD INC = Severity of sweet potato virus disease; Yld = Fresh root yield (tons/ha)

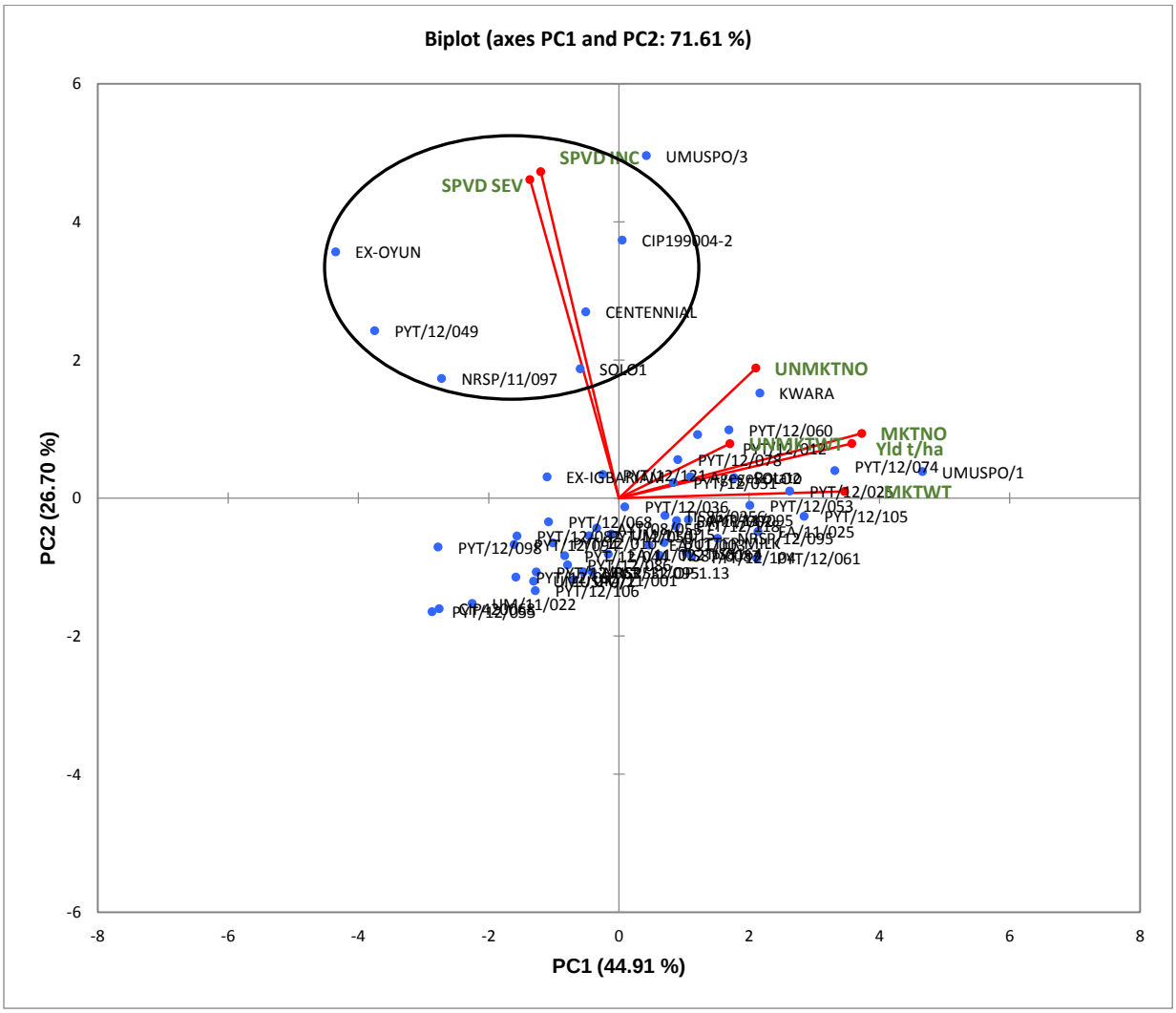

Fig. 1. Biplot of principal components 1 and 2 showing intrinsic relationships between genotypes and important agronomic traits in Umudike

MKTNO = Number of marketable storage roots; UNMKTNO = Number of unmarketable storage roots; MKTWT = Weight (kg/plot) of unmarketable storage roots; UNMKTWT = Weight of unmarketable storage roots; SPVD SEV = Incidence of sweet potato virus disease; SPVD INC = Severity of sweet potato virus disease; Yld = Fresh root yield (tons/ha)

that are largely influenced by the environment, resulting often in large genotype-by-environment interaction and low/moderate heritability estimates observed. As observed by Tumwegamire et al. [20], moderate heritability is often deemed acceptable for such traits.

Genetic variability is usually measured using genetic parameters such as genotypic (GCV) and phenotypic coefficients of variation (PCV) and heritability estimates. The GCV is a measure of the amount of variation within a population for a particular trait [5]. The PCV and GCV, expected genetic advance (GA) and genetic gain as percent of mean (GA (%X)) for both locations are presented in Table 9. The PCV were higher than GCV for all the traits because of environmental influence. At Otobi, GCV had a range of 34.45 – 66.94% with weight of unmarketable roots having the lowest GCV, and weight of marketable roots having the highest GCV. The PCV at Otobi were large with a range of 95.58 – 216.22%. The expected genetic advance (GA) of 0.06 for unmarketable root weight was the lowest, while number of marketable roots had the highest GA of 8.33. The GA (% of mean X) for each trait was high. While 13.6% gain of the general mean of weight of unmarketable roots can be made, 88.96% gain of the mean weight of marketable roots can be

Table 8. Variance components and broad sense heritability of agronomic traits of sweetpotato genotypes evaluated in Umudike and Otobi

Trait	Genotypic variance		Phenotypic variance		Broad-sense heritability	
	Umudike	Otobi	Umudike	Otobi	Umudike	Otobi
Number of marketable roots	49.87	42.29	111.86	107.39	0.45	0.39
Number of unmarketable roots	23.18	15.31	72.55	37.62	0.32	0.41
Weight of marketable roots (kg/plot)	6.31	3.25	11.50	7.67	0.55	0.42
Weight of unmarketable roots (kg/plot)	0.02	0.03	0.19	1.01	0.11	0.03
Fresh root yield (tons/ha)	35.66	34.38	77.38	78.53	0.46	0.44
SPVD incidence	3.34	n.a	4.71	n.a	0.71	n.a
SPVD severity	0.99	n.a	1.23	n.a	0.80	n.a

n.a = not applicable – SPVD was only evaluated at Umudike that is known as hotspot for sweetpotato virus disease

Table 9. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and genetic advance (expected and as percent mean) of agronomic traits of sweetpotato genotypes evaluated in Umudike and Otobi

Trait	Means of traits		Genotypic coefficient of variation		Phenotypic coefficient of variation		Genetic advance (expected)		Genetic advance (% of X)	
	Umudike	Otobi	Umudike	Otobi	Umudike	Otobi	Umudike	Otobi	Umudike	Otobi
MKTNO	16.05	10.01	43.99	64.98	65.89	103.55	9.80	8.33	61.08	83.19
UNMKTNO	9.18	5.90	52.44	66.34	92.77	104.00	5.61	5.18	61.16	87.84
MKTWT (kg/plot)	4.27	2.69	58.90	66.94	79.51	102.82	3.84	2.40	90.09	88.96
UNMKTWT (kg/plot)	0.35	0.46	40.22	37.45	123.97	216.22	0.10	0.06	28.09	13.44
Yld (tons/ha)	11.48	9.27	52.03	63.24	76.65	95.58	8.34	8.03	72.63	86.63
SPVD INC	1.05	n.a	174.86	n.a	207.65	n.a	3.17	n.a	303.71	
SPVD SEV	1.57	n.a	63.21	n.a	70.45	n.a	1.83	n.a	116.12	

MKTNO = Number of marketable storage roots; UNMKTNO = Number of unmarketable storage roots; MKTWT = Weight (kg/plot) of unmarketable storage roots; UNMKTWT = Weight of unmarketable storage roots; SPVD SEV = Incidence of sweet potato virus disease; SPVD INC = Severity of sweet potato virus disease; Yld = Fresh root yield (tons/ha). n.a = not applicable – SPVD was only evaluated at Umudike that is known as hotspot for sweetpotato virus disease

achieved selecting for the trait. At Umudike, the trend was the same with PCV being higher than GCV. The GCV at Umudike had a range of 40.22 – 174.86%, expected GA range of 0.10 – 9.80%, and GA (%X) of 28.09 – 303.71. As observed at the Otobi location, weight of unmarketable roots had the lowest GCV of 40.22%, lowest GA of 0.10, as well as the lowest GA (%X) of 28.09% compared to other traits.

The phenotypic and genotypic coefficients of variation estimated in this study were high enough to permit effective selection for genetic gain in the evaluated agronomic traits. According to Madawal et al. [21], GCV of 10 - 25% is deemed high. The recorded genetic advance as percent of mean (GA %X) of 13.44 – 90.09% for the root yield components and 116.12 - 303.71% for SPVD incidence and severity were big enough gains to be made using the genetic materials based on traits evaluated. While the high GCV suggests that large variation that can ensure rapid improvement of the traits exist, the prediction of response to selection is more reliable when GCV, heritability and genetic advance are combined [22]. Important traits evaluated in this study such as number of marketable roots, weight of weight of marketable roots, root yield, SPVD incidence and severity have moderate to high heritability, high GCV and high genetic advance, and it is expected that effective selection should lead to high genetic gain in the use of this germplasm [23-25].

4. CONCLUSION

The germplasm evaluation carried out during this study revealed that there was wide variability among the genotypes evaluated for all the agronomic and virus disease traits to aid parent line selection. Traits such as fresh root yield, number and weight of marketable roots, and sweetpotato virus disease (SPVD) incidence and severity were identified as important traits that characterized the variability observed among the various genotypes. The genetic studies of the traits showed that while broad-sense heritability estimates ranged from moderate to high for the important agronomic traits, the high GCV and genetic advance observed portends a high genetic gain and good breeding progress in the next generation using the genotypes. The low resistance among all the CIP-sourced genotypes suggests that imported germplasm from other countries need to be well-screened for SPVD before deployment for use. The seeming relationship between high beta-carotene content (orange-fleshed sweetpotato class) and susceptibility to SPVD needs to be further studied for confirmation.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Anderson L, Gugerty MK, Bergh K, Orozco P. Sweetpotato value chain: Nigeria. Evans School Policy Analysis and Research (EPAR) Brief No. 220. Prepared for the Agricultural Policy Team of the Bill and Melinda Gates Foundation; 2012.
2. Hahn SK. Effect of virus (SPVP) on growth and yield of sweetpotato. Experimental Agriculture. 1979;15:252-256.
3. Grüneberg WJ, Ma D, Mwanga ROM, Carey EE, Huamani K, Diaz F, Eyzaguirre R, Guaf E, Jusuf M, Karuniawan A, Tjintokohadi K, Song YS, Anil SR, Hossain M, Shofiur Rahaman EHM, Attaluri S, Some K, Afuape S, Adofo K, Lukonge E, Karanja L, Ndirigwe J, Ssemakula G, Agili S, Randrianaivoarivony JM, Chiona M, Chipungu F, Laurie S, Ricardo J, Andrade M, Rausch Fernandes F, Mello AS, Khan A, Labonte DR, Yencho GC. Advances in Sweetpotato Breeding from 1992 to 2012. In: J. Low, M. Nyongesa, S. Quinn and M. Parker (eds.). Potato and Sweetpotato in Africa: Transforming the Value Chains for Food and Nutrition Security. CABI. 2015;3-68.
4. Gibson RW, Mpembe I, Alicai T, Carey EE, Mwanga ROM, Seal SE, Vetten HJ. Symptoms, aetiology and serological analysis of sweet potato virus disease in Uganda. Plant Pathology. 1998;47(1):95-102.
5. Patil AS, Punewal AA, Nandanwar HR, Shah KP. Estimation of variability parameters for yield and its component trats in groundnut (*Arachis hypogaea*. L.). The Bioscan. 2014;9(2):633-638.
6. Tsegaye E, Nigussie D, Devakara S. Genetic variability for yield and other agronomic traits in sweetpotato. Journal of Agronomy. 2007;6:94-99.
7. Yada B, Tukamuhabwa P, Alajo A, Mwanga ROM. Field evaluation of Ugandan sweetpotato germplasm for yield, dry matter and disease resistance. South African Journal of Plant and Soil. 2011;28(2):142-146.

8. Afuape SO, Okocha PI, Njoku D. Multivariate assessment of the agromorphological variability and yield components among sweetpotato (*Ipomoea batatas* (L.) Lam) landraces. African Journal of Plant Science. 2011;5(2):123-132.
9. Ebem EE, Afuape SO, Chukwu SC, Ubi BE. Genotype x environment interaction and stability analysis for root yield in sweet potato (*Ipomoea batatas* (L.) Lam). Frontiers in Agronomy. 2021;3:665564. DOI:10.3389/fagro.2021.665564.
10. Shumbusha D, Tusiime G, Edema R, Gibson P, Mwanga ROM. Diallel analysis of root dry matter content in sweetpotato. In Second Ruforum Biennial Meeting Ruform, Entebbe, Uganda. 2010:1113-1117.
11. Koussao S. Genetic improvement of sweetpotato (*Ipomoea batatas* [L.] Lam) for beta-carotene and yield in Burkina Faso. (Ph.D Thesis submitted to the University of Ghana, Legon); 2012.
12. Mwanga RO, Yencho GC, Moyer JW. Diallel analysis of sweetpotatoes for resistance to sweetpotato virus disease. Euphytica. 2002;128:237-248.
13. Levette MP. The effects of methods of planting cuttings of sweetpotato (*Ipomoea batatas* (L.) Lam.) on yield. Tropical Agriculture. 1993;70(2):110-115.
14. Steel RGD, Torrie TH. Principles and Procedures of Statistics: A Biometrical Approach. 2nd Edition. Mcgraw Hill book Co. Inc., New York; 1980.
15. Allard RW. Principles of plant breeding. (2nd Edition). John Wiley & Sons, New York; 1999.
16. Burton GW. Quantitative inheritance in grasses. Proc. 6th Int. Grassland Cong. 1952;1:277-283.
17. Fehr WR. Heterosis. In: principles of cultivar development: Theory and Techniques. Macmillan Publishing Company. New York. 1987:1.
18. Yahaya SU, Saad AM, Mohammed SG, Afuape SO. Growth and yield of sweet potato (*Ipomoea batatas* L. Lam) and their relationships with root yield. American Journal of Experimental Agriculture. 2015;9(5):1-7.
19. Tairo F, Mukasa SB, Jones RA, Kullaya A, Rubaihayo PR, Valkonen J. Unravelling the genetic diversity of the three main viruses involved in sweetpotato virus disease (SPVD), and its practical implications. Molecular Plant Pathology. 2005;6:199-211.
20. Tumwegamire S, Kapinga R, Rubaihayo PR, LaBonte DR, Grüneberg WJ, Mwanga RO. Evaluation of dry matter, protein, starch, sucrose, β-carotene, iron, zinc, calcium, and magnesium in East African sweetpotato [*Ipomoea batata*s (L.) Lam] germplasm. Hort Science. 2011;46(3): 348-357.
21. Madawal SI, Madarakhandi TBS, Narasannavar A. Genetic variability study in sweetpotato (*Ipomoea batatas* L.) genotypes. International Journal of Tropical Agriculture. 2015;33(2):279-282.
22. Meshram MP, Ali RI, Patil AN, Meena S. Variability studies in M3 Generation of Blackgram (*Vigna mungo* (L.) Hepper). The Bioscan. 2013;8(4):1357 – 1361.
23. Afuape SO, Tongoona PB, Asante IK, Egesi CN, Nwaigwe G, Offei SK. Breeding new sweetpotato genotypes combining elevated content of two antagonistic traits of high dry matter and beta-carotene content in a high root yield background. *Euphytica* 2019;215**:**211. Available: https://doi.org/10.1007/s10681-019-2532-0
24. Food and Agriculture Organization of the United Nations (FAO). Production Year Book for 2018. Rome, Italy; 2018.
25. SAS Instittute. SAS System for Personal Computers 1002-SAS Institute Inc., Carry, NC 27512-8000, USA; 1992.

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