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Full Length Research

Diversity of morphological characters in progenies of sweet potato (*Ipomoea batatas* (L.) Lam) obtained from poly cross and controlled cross systems in Southeastern Nigeria

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ABSTRACT: Sweet potato (*Ipomoea batatas* (L.) Lam.) genotypes frequently exhibits extensive variations in terms of its morphological characteristics. A field experiment was carried out at National Root Crops Research Institute, Umudike, Abia State, Nigeria during 2015 and 2016 cropping seasons, to characterize sweet potato genotypes for morphological diversity. Three different sweet potato families (Sauti X 442162, Sauti X Ligri, Sauti Poly Cross), including two local checks (Umuspo3 and TIS87/8700) were selected for the experiment. This experiment was laid out in a randomized complete block design with three replicates. The sweet potato genotypes were evaluated on nineteen characters covering both folial and storage root morphology using morphology descriptor and data collected were subjected to analysis of variance to determine variation among agronomic and measured morphological parameters. Cluster analysis was done on all the nineteen characters, based on Euclidean distance and similarity matrix and a dendrogram generated using the ward's method. Most of the genotypes had pink skin colour and creamy flesh colour. Cluster analysis revealed that all the genotypes were grouped into 4 different classes based on their morphological traits. The analysis of variance showed a significant ($p \leq 0.05$) difference among the sweet potato genotypes in most of traits observed. This study revealed that yields of total storage roots ranged from 2.07 to 14.96 t/ha. Sauti X 440163/5 recorded the highest total storage root yield of 14.96 t/ha among the genotypes while Sauti X 440163/6 recorded the lowest total storage roots yield of 2.07 t/ha. The results of this study revealed that Sauti X 440163/5 is suitable for cultivation in the environment and could be incorporated into further breeding programs as this would provide a large gene pool for effective recombination to raise promising sweet potato variety of considerable agricultural importance.

Keywords: Diversity, morphological characters phenotypic characterization, sweet potato.

INTRODUCTION

Sweet potato (*Ipomoea batatas* [L.] Lam.) is a stable root crop cultivated in different continents of the world on approximately 8.21 million hectares (ha) with an estimated annual yield of 104.02 million tonnes (FAOSTAT, 2014). Sweet potato is commonly cultivated in Africa, Asia, Latin America, with China accounting for 52% of the crop grown on approximately 4.7 million hectares (FAOSTAT, 2009). It is the third most important tuberous root crop (Gibson and Aritua, 2002) with annual world production of about 131 million tons, on approximately 9 million hectares with mean estimated yields of 13.7 t/ha. In Nigeria, however, farmers have recorded one of the world's lowest average sweet potato yields of 3 t/ha (FAO, 2015).

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Sweet potato cultivars exhibit extensive variations in terms of its botanical characteristics and are commonly distinguished on the basis of morphological traits with a wide range of yield potential, size, shape, flesh and skin colour of roots, as well as sizes, colours and shapes of leaves and branches (Zhang *et al*., 2000). Most varieties of this crop are self-incompatible, and, because of the obligate outcrossing nature of the crop, have high levels of heterozygosity (Zhang *et al*., 2000).

Phenotypic characterization of sweet potato genotypes is achieved using morphological descriptors. This is considered necessary because descriptors make it possible and easy to measure, evaluate and record phenotypic characters or traits. Descriptors acknowledge the discrimination in terms of the phenotypic and morphological description of the plant (CIAT, 2007). Among other uses, phenotypic characterization has proven to be advantageous in duplicates identification, genetic diversity studies as well as correlation with characters of agronomic relevance (CIAT, 2007). This method of evaluating plant diversity is quite easy to use, less expensive and was considered to be the strongest determinant of the agronomic value (Li *et al.,* 2009).

Diverse genotypes of sweet potato are emerging consequent upon advancement being made by plant breeders in Africa. However, adequate information on the diversity of the crop is insufficient. Consequently, there is the need for proper evaluation, identification and follow-up of new progenies which are products of hybridization programmes from research institutes before they are mass-cultivated by farmers. Therefore, the objectives of this study were to determine the morphological diversity among progenies obtained from controlled cross system and to evaluate their yield abilities.

MATERIALS AND METHODS

Study site

The experiment was conducted during the 2015 and 2016 planting seasons at the National Root Crops Research Institute, Umudike, Southeastern Nigeria. Umudike is located at latitude 05° 29′ N, longitude 07° 33′ E and altitude 122 m above sea level. Umudike is in the humid tropics and has a total rainfall of about 2177 mm per annum, annual average temperature of about 26^{o}C and its soil is classified as sandy loam utisol (NRCRI, 2012).

Nursery Management

The soil of the nursery comprised a mixture of topsoil, organic matter and river sand at the ratio of 3:2:1 respectively. The nursery was prepared in the greenhouse of National Root Crops Research Institute, Umudike, and Southeastern, Nigeria using polythene bags containing 1 kg of soil. After soaking the seeds for about twenty four hours in cold water to break dormancy, it was discovered that some of the seeds sprouted. The seeds were carefully isolated from the container of cold water and sown individually into the well-watered soil contained in polythene bags.

Land preparation and experimental design

The land for the experimental site was cleared, ploughed, harrowed and ridged. The prepared land was marked out into plots of 1.5 m^2 (1 m × 1.5 m). The field was laid out in an augmented design with three replications and two check varieties were panted at intervals. The planting distance was 1 m × 0.3 m. This gave five stands of sweet potato per plot which is equivalent to 33,333 stands per hectare. Therefore, the land area for this research was 240 m^2. Planting was done on 21th July, 2015 and 18th April, 2016 using five vines on each plot. The plants were rain-fed. Weeding was done at 6 and 12 weeks after planting (WAP). Compound fertilizer (NPK 15:15:15) was applied at the rate of 400 kg/ha 4WAP using side placement.

Evaluation of morphological traits

Nineteen morphological traits of the sweet potato progenies were scored using a sweet potato descriptor manual (Huaman, 1991) at 90 to 120 days after planting (DAP). These traits can be grouped into foliar morphology (90 to 100 DAP) and storage root (120 DAP) descriptors. Characterization was achieved using standard descriptors; morphological and agronomical descriptors developed by 'Centro Internacional de la papa' (Human, 1991) as shown in Table 1. Quantitative measurements were taken for internode length, internode diameter, leaf area, leaf size (length from the base to the tip of the leaf) to know the differences in their development. Measurement of morphological characters were scored on the basis of the average value obtained from several plants of each genotype. The petiole length, internode length, matured leaf size (distance from the tip to the base) of the leaf were measured using a meter rule. The internode diameter was measured using an electronic caliper (G02022 165). Leaf area measurements were done using a leaf area measuring system (Delta T devices. Model RS232). The characters of vines and leaves were recorded from the section located in the middle portion of the stem.

Data analysis

Nineteen characters were subjected to analysis of variance using Statistical Package for Social Scientists

Table 1. The families of the sweet potato seeds and number of seedlings obtained for the study.

S/No.	Parents	Crosses type	Source
1.	Sauti X 442162/1	Controlled cross	CIP, Kumasa, Ghana
2.	Sauti X 442162/2	Controlled cross	CIP, Kumasa, Ghana
3.	Sauti X 442162/3	Controlled cross	CIP, Kumasa, Ghana
4.	Sauti X 442162/4	Controlled cross	CIP, Kumasa, Ghana
5.	Sauti X 442162/5	Controlled cross	CIP, Kumasa, Ghana
6.	Sauti X 442162/6	Controlled cross	CIP, Kumasa, Ghana
7.	Sauti X Ligri/1	Controlled cross	CIP, Kumasa, Ghana
8.	Sauti X Ligri/2	Controlled cross	CIP, Kumasa, Ghana
9.	Sauti X Ligri/3	Controlled cross	CIP, Kumasa, Ghana
10.	Sauti PC/1	Poly Cross	CIP, Kumasa, Ghana
11.	Sauti PC/2	Poly Cross	CIP, Kumasa, Ghana
12.	Sauti PC/3	Poly Cross	CIP, Kumasa, Ghana
13.	Sauti PC/4	Poly Cross	CIP, Kumasa, Ghana
14.	Sauti PC/5	Poly Cross	CIP, Kumasa, Ghana
15.	Sauti PC/6	Poly Cross	CIP, Kumasa, Ghana
16.	Sauti PC/7	Poly Cross	CIP, Kumasa, Ghana
17.	Sauti PC/8	Poly Cross	CIP, Kumasa, Ghana
18.	Sauti PC/9	Poly Cross	CIP, Kumasa, Ghana
19.	Sauti PC/20	Poly Cross	CIP, Kumasa, Ghana
20.	Umuspo3	Local check variety	NRCRI, Umudike, Nigeria
21.	TIS87/0087	National check variety	NRCRI, Umudike, Nigeria

(SPSS) software (Version 22), which was carried out on all quantitative characters to determine variation among agronomic and measured morphological parameters. Cluster analysis was done on all the nineteen characters, based on Euclidean distance using the ward's method (Mohammadi and Prasanna, 2003). The results of the analyzed data were represented using tables and pie charts.

RESULTS AND DISCUSSION

Critical to the success of any breeding programme is the need to assess genetic variation of a particular crop. Morphological characterization has been used for various purposes including identification of duplicates, variability patterns and correlation with characteristics of agronomic importance (CIAT, 1993). The sweet potato genotypes from CIP exhibited high morphological variability for the shoot and storage root characters.

Morphological variation

The morphological traits measured among sweet potato (*Ipomoea batatas*) genotypes is shown in Table 2 as mentioned below:

Plant type: The frequency distribution for the plant type indicated that majority of the progenies belonged to spreading (33%), whereas 29% belonged to semi-erect type. The extremely spreading and erect habits were found to be low (18%) and (20%), respectively (Figure 1).

Ground cover: The frequency distribution for the ground cover indicated that majority of the progenies belonged to low type (44%), the medium and high types were found to be 33 and 20% respectively, while the total type was found to be the lowest (3%) (Figure 1).

Vine internode length: The frequency distribution of the vine internode length indicated that majority of the full sib progenies belonged to the short type (47%), the very short and intermediate were found to be 35 and 18% respectively, while the long type was found to be completely absent among the progenies (Figure 1).

Vine colour: High variability was observed in vine colour ranging from green to purple. It was observed that the progenies possessed predominantly purple colour (72%). The other vine colours observed in the progenies were green with many dark purple spots (10%), green with few purple spot (6%), mostly purple (5%), mostly dark purple (5%), total purple (1%) and totally dark purple (1%) colouration (Figure 1).

Table 2. Morphological traits measured among sweet potato (*Ipomoea batatas*) genotypes.

Trait acronym	Trait/ descriptor	Score code – descriptor state
PT	Plant type	3–erect (<75 cm); 5–semi-erect (75-150 cm); 7–spreading (151-250 cm); 9–extremely spreading (>250 cm)
GC	Ground cover	3–low (<50%); 5–medium (50-74%); 7–high (75-90%); 9–total (>90%)
VIL	Vine internode length	1–very short (<3 cm); 3–short (3-5 cm); 5–intermediate (6-9 cm); 7–long (10-12 cm); 9–very long (>12 cm)
PVC	Predominant vine colour	1–green; 2–green with few purple spots; 3–green with many purple spots; 4–green with many dark purple spots; 5–mostly purple; 6–mostly dark purple; 7–totally purple; 8–totally dark purple
SVC	Secondary vine colour	0–absent; 1–green base; 2–green tip; 3–green nodes; 4–purple base; 5 – purple tip; 6–purple nodes
GOL	General outline of the leaf	1–rounded; 2–reniform; 3–cordate; 4–triangular; 5–hastate; 6–lobed; 7–almost divided
LLT	Leaf lobes type	0–no lateral lobes; 1–very slight; 3–slight; 5–moderate; 7–deep; 9–very deep
LLN	Leaf lobe number	Direct measurement (1, 3, 5, 7, 9)
SCLL	Shape of central leaf lobe	0–absent; 1–toothed; 2–triangular; 3–semi-circular; 4–semi-elliptic; 5–elliptic; 6–lanceolate; 7–oblanceolate; 8–linear (broad); 9–linear (narrow)
MLC	Mature leaf colour	1–yellow-green; 2–green; 3–green with purple edge; 4–greyish-green; 5–green with purple veins on upper surface; 6–slightly purple; 7–mostly purple; 8–green upper, purple lower; 9–purple both surfaces
ILC	Immature leaf colour	1–yellow-green; 2–green; 3–green with purple edge; 4–greyish-green; 5–green with purple veins on upper surface; 6–slightly purple; 7–mostly purple; 8–green upper, purple lower; 9–purple both surfaces
PL	Petiole length	1–very short (<10 cm); 3–short (10-20 cm); 5–intermediate (21-30 cm); 7–long (31-40 cm); very long (>40 cm)
PP	Petiole pigmentation	1–green; 2–green with purple near stem; 3–green with purple near leaf; 4–green with purple at both ends; 5–green with purple spots throughout petiole; 6–green with purple stripes; 7–purple with green near leaf; 8–some petiole purple, others green; 9–totally or mostly purple
SRS	Storage root shape	1–round; 2–round elliptic; 3–elliptic; 4–ovate; 5– obovate; 6–oblong; 7–long oblong; 8–long elliptic; 9–long irregular
PSC	Predominant skin colour	1–white; 2–cream; 3–yellow; 4–orange; 5–brownish orange; 6–pink; 7–red; 8–purple red; 9–dark purple
PFC	Predominant flesh colour	1–white; 2–cream; 3–dark cream; 4–pale yellow; 5–dark yellow; 6–pale orange; 7–intermediate orange; 8–dark orange; 9–strongly pigmented with anthocyanin
SFC	Secondary flesh colour	0–absent; 1–white; 2–cream; 3–yellow; 4–orange; 5–pink; 6–red; 7–purple-red; 8–purple; 9–dark purple
VSRS	Variability of storage root shape	3-Uniform; 5-slightly variable; 7-moderately variable
VSRS	Variability of storage root size	3-Uniform; 5-slightly variable; 7-moderately variable

The traits and measurement methods were based on the International Board for Plant Genetic Resources descriptor list (CIP/AVRDC/IBPGR, 1991) CIP code.

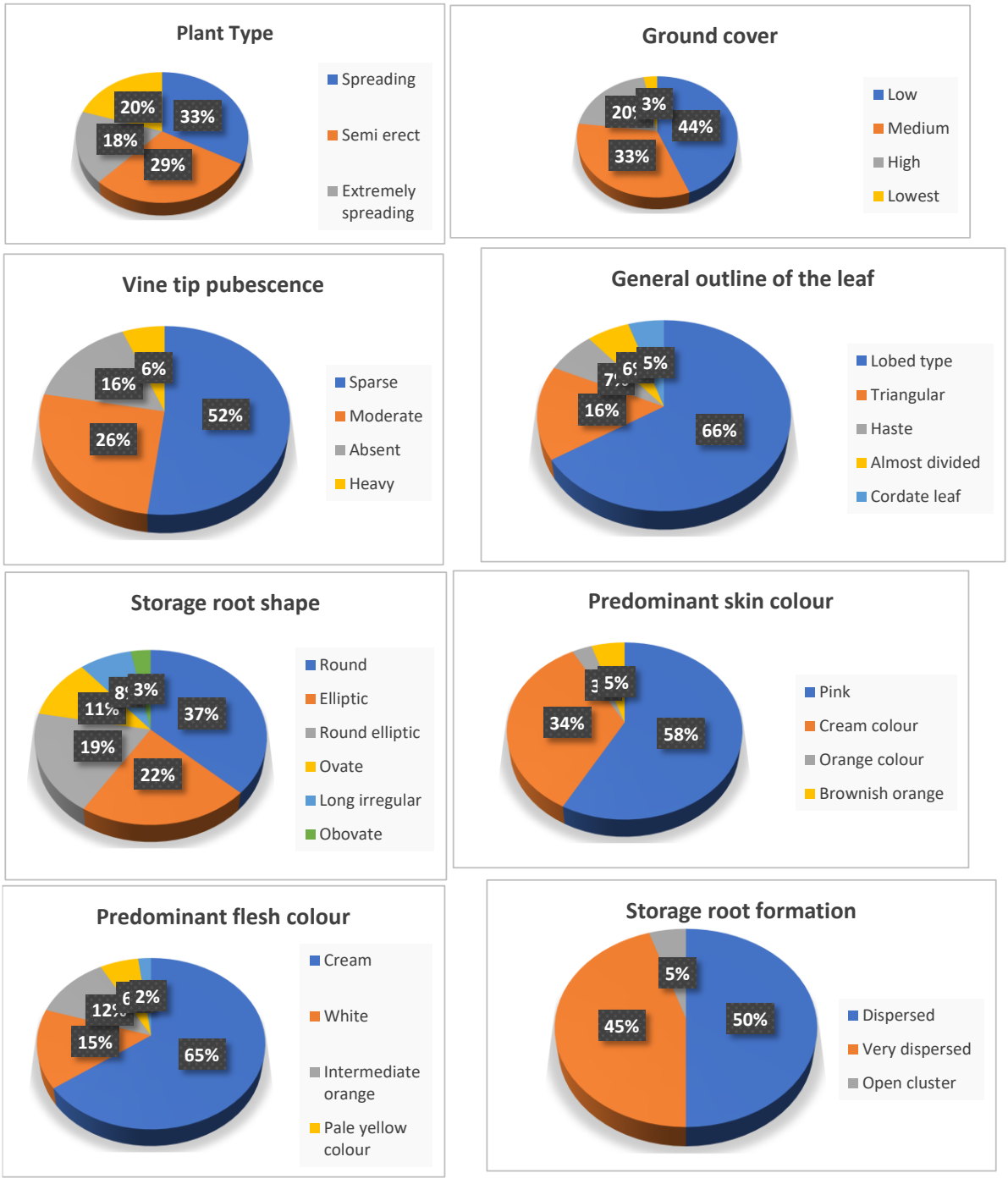

Figure 1. Frequency data for different morphological characters of sweet potato genotypes.

Vine tip pubescence: Vine tip pubescence was observed to vary ranging from absent to heavy. It was observed that the progenies recorded (52%) for sparse pubescence, (26%) for moderate pubescence, (16%) for absent pubescence and (6%) was observed for heavy pubescence (Figure 1).

General outline of the leaves: Sweet potato leaves are reported to be variable in size and shape even within the same plant. The frequency distribution of the general outline of the leaves of the progenies showed that lobed type had the maximum frequency (66%). This was followed by triangular (16%), haste (7%), almost divided

(6%), while the occurrence of the cordate leaf type was lowest (5%) (Figure 1).

Shape of the central leaf lobe: The shape of the central leaf lobe showed that eight key characters were identified among the progenies namely, toothed, triangular, semi-circular, semi-elliptic, elliptic, lanceolate, oblanceolate, and linear (narrow). The frequency distribution of the progenies showed that elliptic (26%) was the prevalent type, which was followed by semi-elliptic (21%). The frequency of other shapes of the central leaf lobe was toothed (15%), lanceolate (13%), triangular (10%), oblanceolate (8%), and linear (5%), while semi-circular had the lowest (2%) (Figure 1).

Storage root shape: The prevalent storage root shape was round (37%) and 48% for both full sib and half sib progenies respectively, followed by elliptic (22%) and (28%), respectively (Figure 1).

Predominant skin colour: The progenies possessed a variety of tuber skin colour varying from white, cream, orange, brownish orange and pink. Pink colour was predominant (58%), followed by cream colour (34%). Orange colour and brownish-orange colour (3%) and white colour was totally absent (0%) (Figure 1).

Predominant flesh colour: Attractive flesh colours were exhibited progenies such as white, cream, yellow, pale yellow, pale orange, intermediate orange and dark orange. The frequency distribution showed that cream colour was prevalent among the full sib (65%). Others include; white colour (15%), intermediate orange colour (12%), pale yellow colour (6%), dark orange colour (2%) while pale orange colour was absent (0%) (Figure 1).

A high level of diversity occurs among the sweet potato cultivars for the morphological as well as root characters. They differ in the shape of roots, depth of rooting, time of maturity, resistance to disease and several other vegetative characters. Most of the important characters including yield are highly influenced by environment, since they are polygenically controlled (Amin and Singla, 2010). The possibility of improvement in any crop is dependent on the variability available in the crop, higher genetic variability in the traits, better the chances of improvement through selection (Jindal *et al*., 2010). In sweet potato, the skin as well as the flesh contains carotenoids and anthocyanin pigments which determines its colour. The combination and intensity of these pigments differs and produces varying intensities of skin and flesh colour, such as, cream, yellow, orange, pink or purple skin. However, with the advent of molecular markers and development of various DNA isolation protocols, these problems have been solved to an extent (Binu *et al*., 2011).

Previous reports on characterization of morphological diversity in sweet potato have been restricted to germplasm bank collections which revealed high phenotypical variability (Ritschell and Huaman, 2002). Similar results were observed in another study by Vimala and Binu (2011) while evaluating the morphological characters of 250 hybrid progenies of sweet potato generated from a controlled cross system. All these studies showed that no clear cut demarcation was visible for any of the morphological traits and all the characters showed continuous variation (Vimala and Lakshmi, 1990). From evaluating 14 sweet potato accessions, Daros *et al*. (2002) observed high morphological variability, concluding that the most informative descriptors were the vine tip pubescence, the abaxial leaf vein pigmentation and the shape of the roots. The traits that most contributed to the diversity were distribution of root flesh color, root shape, storage root surface defects and predominant storage root flesh color.

Cluster analysis of morphological characters

From the hierarchical cluster analysis, number of leaf lobes, leaf lobe type, petiole pigmentation, vine tip pubescence, predominant flesh colour, storage root formation, storage surface defect and storage root surface defect showed a widespread morphological dissimilarity among the genotypes (Figure 2).

Cluster Group I consisted two genotypes, plant type was erect (<75 cm), ground cover was low (<50%), vine tip pubescence was heavy, mature leaf colour was green, storage root shape was round, predominant skin colour was pink, predominant flesh colour was pale orange, variability of storage root shape was slightly variable, variability of storage root size was moderately variable (Table 3).

Cluster Group II consisted six genotypes, plant type was erect (<75 cm), ground cover was low (<50%), vine internode length was short (3 to 5cm), vine internode diameter was very thick (>12 mm), vine tip pubescence was heavy, general outline of the leaf was lobed, mature leaf colour was green, storage root shape was round, predominant skin colour was pink, predominant flesh colour was pale orange, variability of storage root shape was slightly variable, variability of storage root size was moderately variable (Table 3).

Cluster Group III consisted eight genotypes, plant type was spreading (151 to 250 cm), ground cover was high (75 to 90%), vine internode diameter was very thick (>12 mm), vine tip pubescence was sparse, general outline of the leaf was triangular, mature leaf colour was green, petiole pigmentation was green with purple at both ends, storage root shape was round, predominant skin colour was pink,

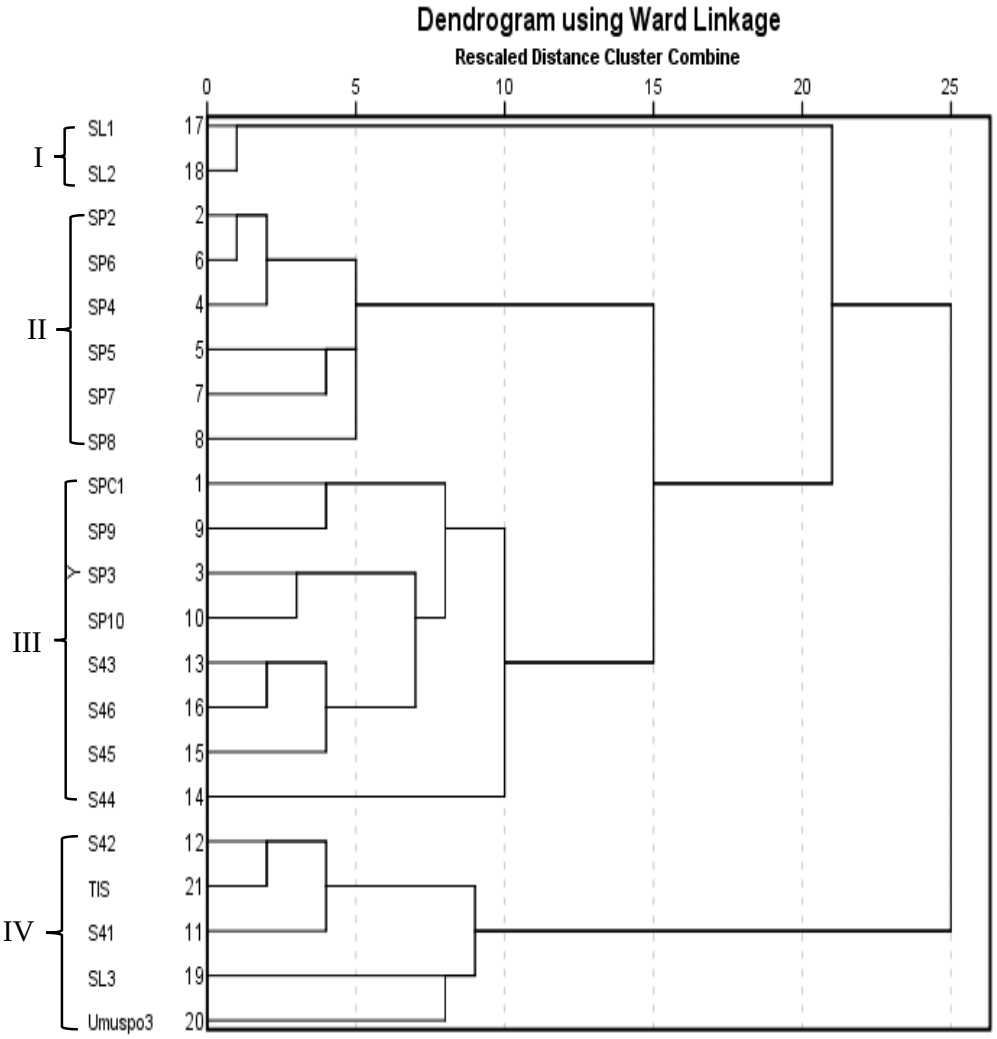

Figure 2. Dendrogram of the sweetpotato genotypes with checks; Umuspo3 and TIS 87/0087 revealed by average linkage cluster analysis based on the nineteen discriminant phenotypic characters.

predominant flesh colour was cream, storage root formation was open cluster, variability of storage root shape was slightly variable, variability of storage root size was slightly variable (Table 3).

Cluster Group IV consisted five genotypes, plant type was semi-erect (<75 cm), vine internode length was short (3 to 5 cm), general outline of the leaf was triangular, mature leaf size was medium (8 to 15 cm), predominant skin colour was orange, predominant flesh colour was cream (Table 3).

Total storage root yield

The results presented in Table 4 showed that in 2015 and 2016 cropping seasons, the analysis of variance revealed there was significant ($p \leq 0.05$) differences among genotypes for marketable root number, unmarketable root number, marketable root weight and unmarketable root weight (Table 4). In 2016 cropping season, analysis of variance showed that there were no significant ($p<0.05$) differences among genotypes for unmarketable root number, marketable root number, unmarketable root weight yield but there was significant difference among the genotypes for marketable root weight (Table 2). Results presented in Table 4 showed that the sweet potato genotypes differed significantly ($p \leq 0.05$) in number of marketable and unmarketable roots for both cropping seasons. Sauti X 440163/5 produced the highest number of marketable root (5.33) in 2015 cropping season while Sauti X 440163/2 produced the highest number of

Table 3. Clusters of the sweet potato genotypes based on morphological variations.

Cluster number	Number of genotypes	Progenies
I	2	Sauti X Ligri/1, Sauti X Ligri/2
II	6	Sauti PC/2, Sauti PC/4, Sauti PC/5, Sauti PC/6, Sauti PC/7, Sauti PC/8
III	8	Sauti PC/1, Sauti PC/3, Sauti PC/9, Sauti PC/10, Sauti X 440163/3, Sauti X 440163/4, Sauti X 440163/5 Sauti X 44016/6
IV	5	Sauti X 440163/1, Sauti X 440163/2, Sauti X Ligri/3, TIS 87/0087, Umuspo 3

Table 4. Mean number of storage root parameters of the sweet potato genotypes evaluated with checks in 2015 and 2016 planting seasons.

Genotype	MRTRTN 2015	UMRTRTN 2015	MRTRTN 2016	UMRTRTN 2016	MRTW/ha 2015	UMRTW /ha 2015	MRTW/ha 2016	UMRTW /ha 2016	Yield (t/ha) 2015	Yield (t/ha) 2016
Sauti PC/1	2.00	2.00	2.66	3.00	5.00	0.53	5.55	0.47	5.53	6.02
Sauti PC/2	1.67	3.67	2.33	4.33	3.33	1.12	5.18	0.88	4.45	6.07
Sauti PC/3	2.00	2.00	2.00	3.33	6.78	1.39	4.90	0.68	8.17	5.59
Sauti PC/4	1.67	2.67	2.66	4.33	4.17	0.91	5.41	0.63	5.07	6.05
Sauti PC/5	2.67	2.00	2.00	4.00	7.82	1.39	4.62	0.88	8.41	5.51
Sauti PC/6	2.67	2.00	2.00	2.66	7.82	0.56	4.44	0.52	8.39	4.97
Sauti PC/7	3.00	2.33	2.33	4.00	6.85	0.89	4.86	0.99	7.74	5.86
Sauti PC/8	2.00	1.67	2.66	2.66	5.48	0.48	6.68	0.52	5.96	7.21
Sauti PC/9	3.33	1.67	2.33	2.33	9.21	0.56	6.61	0.51	9.77	7.13
Sauti PC/10	2.67	4.33	2.00	3.66	5.91	1.19	4.76	0.99	7.09	5.75
Sauti X 440163/1	4.67	2.00	1.66	4.33	8.97	0.25	3.51	0.74	14.33	4.25
Sauti X 440163/2	3.67	4.67	2.33	4.33	10.89	1.44	4.58	0.72	12.33	5.30
Sauti X 440163/3	2.33	1.33	2.66	3.66	5.65	1.39	6.43	0.77	7.04	7.21
Sauti X 440163/4	1.67	1.33	2.33	3.33	5.18	0.37	6.38	0.71	5.56	7.10
Sauti X 440163/5	5.33	1.33	3.00	3.00	14.22	0.74	9.25	0.88	14.96	10.14
Sauti X 440163/6	1.67	3.00	1.66	3.00	1.48	0.59	1.48	0.59	2.07	2.07
Sauti X Ligri/1	3.33	3.33	3.00	4.66	10.81	1.19	7.96	0.75	12.00	8.72
Sauti X Ligri/2	3.00	1.33	2.33	3.33	6.28	0.28	6.48	0.94	6.55	7.42
Sauti X Ligri/3	2.33	1.00	2.33	1.00	7.78	0.96	7.77	0.96	8.74	8.73
TIS 87/0087	4.05	0.99	3.22	2.42	10.62	0.22	8.60	0.66	10.84	9.27
Umuspo3	3.79	1.56	3.04	2.73	11.33	0.30	7.98	0.75	11.63	8.73
Mean	2.83	2.20	2.41	3.34	10.25	0.82	7.02	0.80	8.41	6.62
$LSD_{0.05}$	0.12	0.20	0.12	0.20	0.70	0.08	0.73	0.09	0.71	0.75

MRTRTN = Marketable root number, UMRTRTN = Unmarketable root number, MRTW/ha = Marketable root weight per hectare, UMRTW /ha = Marketable root weight per hectare.

marketable (4.67) in 2016. Sauti PC/4, Sauti X 440163/4 and Sauti X 440163/6 produced the least number of marketable root (1.67) in 2015 while Sauti X 440163/1 and Sauti X 440163/6 produced the least number of marketable root (1.67) in 2016. Sauti X 440163/2 produced the highest number of unmarketable root (4.67) in 2015 cropping season while Sauti X Ligri/1 produced the highest number of unmarketable root (4.66) in 2016 cropping season (Table 4).

Results presented in Table 4 also showed that the sweet potato genotypes differed significantly ($p \leq 0.05$) in marketable root weight and unmarketable root weight for both cropping seasons. Sauti X 440163/5 produced the highest marketable root weight (14.22 kg/ha, 9.25 kg/ha) in 2015 and 2016 cropping seasons, respectively. Sauti X 440163/6 produced the least weight of marketable root (1.48 kg/ha) in 2015 and 2016 cropping seasons, respectively. Sauti X 440163/2 produced the highest unmarketable root weight (1.44 kg//ha) in 2015 cropping season and Sauti PC/7, produced the highest unmarketable root weight (0.99 kg//ha) in 2016 cropping season. TIS 87/0087 (national check variety) produced the least weight of unmarketable root (0.22 kg/ha) in 2015 cropping season while Sauti PC/1 produced the least weight of unmarketable root (0.47 kg/ha) in 2016 cropping season (Table 4).

Table 4 also showed that the mean of genotypes for total storage root yield was 8.41 t/ha while the mean of checks umuspo3 and TIS 87/0087 for total storage roots yield were 11.63 and 10.84 t/ha, respectively (Table 4). Table 4 further revealed that yield of total storage roots ranged from 2.07 to 14.96 t/ha. Sauti X 440163/5 recorded the highest total storage root yield of 14.96 t/ha among the genotypes and check varieties, while Sauti X 440163/6 recorded the lowest total storage roots yield of 2.07 t/ha. Four genotypes performed better for total storage root yield than the check variety UMUSPO3 and the check variety TIS 87/0087. In agreement with the results of this study, Nwankwo *et al*. (2012) also observed none significant differences in number of unmarketable root number per plot among sweet potato varieties in their study. Similarly, Wassu *et al*. (2015) reported significant variations among 116 sweet potato genotypes which included the genotypes tested in this experiment, with a mean total storage fresh root yield of 10.74 t/ha and a range of 2.26 to 28.46 t/ha. According to Andrade *et al.* (2009), the total storage root yields of Sub Saharan African five sweet potato varieties ranged from 0.5 and 65 t/ha. Consistent with the results of this study, Nedunchezhiyan *et al.* (2012) and Mcharo and Ndolo (2013) reported wide variations among sweet potato clones for root yield performance due to genetic variation.

Conclusion

This study has provided preliminary morphological and agronomic characterization of the different genotypes of sweet potato parents. Morphological characterization of the sweet potato genotypes revealed significant variations in the vine, leaf, storage root and floral characters. In this present study, the sweet potato population therefore represents a rich diversity in form, and yield that can form a good basis for selection in relation to transformation. Yield is considered an important factor which determines choice of sweet potato genotype for cultivation. Hence, Sauti X 440163/5 and Sauti X 440163/1 were the genotypes with the highest storage root yield above the world's sweet potato average yield (13.7 t/ha) and adaptable to the environment of the study and could be recommended for incorporation into further breeding program.

CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

REFERENCES

Amin, A., & Single, J. (2010). Genetic variability, heritability and genetic advance studies in Carrot (Daucus carota var. sativa L.). *Electronic Journal of Plant Breeding*, *1*(6), 1504-1508.

Andrade, M., Barker, I., Cole, D., Dapaah, H., Elliott, H., Fuentes, S., Grüneberg, W., Kapinga, R., Kroschel, J., Labarta, R., Lemaga, B., Loechl, C., Low, J., Lynam , J., Mwanga, R., Ortiz, O., Oswald, A., & Thiele, G. (2009). *Unleashing the potential of sweet potato in Sub-Saharan Africa: Current challenges and way forward*. Lima: International Potato Center (CIP).

Binu H., Vimala, B., & Mohan, C. (2011). Efficient DNA isolation and electrophoretic methods for molecular analysis of sweet potato. *Gene Conserve*, 10(40), 87-109.

CIAT (1993). Biotechnology Research Unit. *Annual Report*, Cali, Colombia.

CIAT (2007). *Germplasm characterization. Multi-Institutional distance learning course on the ex-situ conservation of plant genetic resources*. Pineda B., & Hidalgo, R. (eds). CIAT. Pp. 171-184.

Daros, M., Amaral Júnior, A. T., Pereira, T. N. S., Leal, N. R., Freitas, S. P., & Sediyama, T. (2002). Caracterização morfológica de acessos de batata-doce. *Horticultura Brasileira*, *20*, 43-47.

Food and Agriculture Organization Corporate Statistical Database (FAOSTAT) (2009). Food and Agriculture Organization of the United Nations Database. Food and Agriculture Organization of the United Nations.

Food and Agriculture Organization Corporate Statistical Database (FAOSTAT) (2014). Agricultural production statistics. Food and Agriculture Organization of the United Nations.

Food and Agriculture Organisation (FAO) (2015). Agricultural Bulletin Board on Data Collection Dissemination and Quality of Statistics, Rome, Italy. FAOSTAT Database.

Gibson, R. W., & Aritua, V. (2002). The perspective of sweet potato chrolotic Stunt virus in sweet potato production in Africa: A review. *African Crop Science Journal*, *10*(4), 281-310.

Huaman, Z. (1991). Descriptor for sweet potato. *International Board for Plant Genetic Resources* (CIP/AVRDC/IBPGR), Rome, Italy.133p.

Jindal, S. K., Arora, D., & Ghai, T. R. (2010). Variability studies for yield and its contributing traits in okra. *Electronic Journal of Plant Breeding*, 1(6), 1495-1499.

Li, P., Wang, Y., Sun, X., & Han, J. (2009). Using microsatellite (SSR) and morphological markers to assess the genetic diversity of 12 falcata (*Medicago sativa* spp. falcata) populations from Eurasia. *African Journal of Biotechnology*, *8*(10), 2102-2108.

Mcharo, M., & Ndolo, P. (2013). Root-yield performance of pre-release sweet potato genotypes in Kenya. *Journal of Applied Biosciences*, *65,* 4914-4921.

Mohammadi, S. A., & Prasanna, B. M. (2003). Analysis of genetic diversity in crop plants—salient statistical tools and considerations. *Crop Science*, *43*(4), 1235-1248.

National Root Crops Research Institute (NRCRI) (2012). *Annual Report of the National Root Crops Research Institute, Umudike.*

Nedunchezhiyan, M., Byji, G., & Jata, S. K. (2012). Sweet potato agronomy. Fruit, vegetable and cereal science and biotechnology, Global science book. Regional center of centeral tuber crops research institute, bhubaneswwar -751 019, India.

Nwankwo, I. I. M., Bassey, E. E., Afuape, S. O., Njoku, J., Korieocha, D. S., Nwaigwe, G., & Echendu, T. N. C. (2012). Morpho-agronomic characterization and evaluation of in-country sweet potato accessions in southeastern Nigeria. *Journal of Agricultural Science*, *4*(11), 281-288.

Ritschel, P. S., & Huamán, Z. (2002). Variabilidade morfológica da coleção de germoplasma de batata-doce da Embrapa-Centro Nacional de Pesquisa de Hortaliças. *Pesquisa Agropecuária Brasileira*, *37*, 485-492.

Vimala, B., & Hariprakash, B. (2011). Variability of morphological characters and dry matter content in the hybrid progenies of sweet potato (Ipomoea batatas (L) Lam). *Gene conserve*, *10*(39), 65-86.

Vimala, B., & Leksmi, K. R. (1990). Heritability estimates in sweet potato. *Journal of Root Crops*, 17, 35-38.

Wassu, M., Solomon, A., Beneberu, S., & Simret, B. (2015). Genetic diversity of local and introduced sweet potato [*Ipomoea batatas* (L.) Lam.] Collections for agro-morphology and physicochemical attributes in Ethiopia. *Science, Technology and Arts Research Journal, 4*(1), 09-19.

Zhang, D., Cervantes, J., Huamán, Z., Carey, E., & Ghislain, M. (2000). Assessing genetic diversity of sweet potato (*Ipomoea batatas* (L.) Lam.) cultivars from tropical America using AFLP. *Genetic Resources and Crop Evolution*, *47*(6), 659-665.

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