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Diversity among Morphological Traits of Segregating Sweetpotato [*Ipomoea batatas* (L.) Lam] Genotypes in Umudike, 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

Genotypes of the sweet potato (*Ipomoea batatas* (L.) Lam) normally exhibit high variability in their morphological characters. A field experiment was carried out in 2017 at the National Root Crops Research Institute, Umudike, Abia State, Nigeria to assess the morphological diversity among the population of 68 first filial generation (F_1) sweet potato genotypes (Ligri PC) derived from seeds produced through poly cross systems from the International Potato Center, Kumasi, Ghana, including two local check varieties (UMUSPO3 and TIS87/0087). A randomized complete block design with three replicates was used to set up this experiment. The morphology descriptor was used to evaluate the genotypes of sweet potatoes on sixteen characters that covered both folial and fresh storage root morphology. The data were then subjected to an analysis of variance to identify any differences between the measured morphological parameters and agronomic variables. Using cluster analysis, it was established that all of the genotypes could be categorized into four distinct groups based on their physical characteristics. Consequent, a vast gene pool would provide for effective recombination to create a viable sweetpotato variety with high agricultural value.

Keywords: Characterization; diversity; morphological traits; sweetpotato; variation.

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1. INTRODUCTION

"Sweetpotato (*Ipomoea batatas* (L.) Lam), a crop native to tropical America, is a member of the Convolvulaceae family. It is a tropical and warm-temperate herbaceous dicotyledon that is commonly cultivated worldwide" [1,2]. "Sweetpotato is a hexaploid with the chromosome number (2n=6x=90), and is the only species of Ipomoea that is regarded to be of significant commercial relevance" [3]. "With an estimated annual production of 104.02 million tonnes, the sweetpotato is a stable root crop grown on several continents across the world on an area of about 8.21 million hectares" [4]. Sweetpotatoes are a highly heterozygous and cross-pollinated group in which various attributes show widespread variability [5]. "The phenotypic characters of sweet potato cultivars vary widely, and they are typically identified by their morphological traits, which include a wide range of yield potential, root size, shape, flesh color, and skin color, as well as leaf and branch sizes, colors, and shapes" [2]. Morphological descriptors are used to phenotypically characterize the genotypes of sweet potatoes. The ability to measure, assess, and record phenotypic characteristics or features is made possible and simple by descriptors [6]. Phenotypic characterization has been useful for a variety of purposes, including for decreasing the number of accession numbers by identifying and removing duplicates, conservation of the germplasm, and improve crop breeding [7]. New genotypes of sweetpotato are being developed as a result of advancements made by plant breeders and to design efficient breeding programs, it is essential to determine the magnitude of variation across genotypes of sweetpotato for traits which are important economically [8]. Therefore, the objectives of this research were to characterize the morphological diversity among sweetpotato genotypes obtained from the poly cross system.

2. MATERIALS AND METHODS

2.1 Study Site

During the 2016 and 2017 planting seasons, the experiment was conducted at the National Root Crops Research Institute in Umudike, southeast Nigeria. Umudike is positioned 122 meters above sea level at latitude 05° 29ˈ North and longitude 07° 33ˈ East. Umudike, which is in the humid tropics, has sandy loam utisol soil, an average annual rainfall of around 2177 mm, and average annual temperatures of about 26°C [9].

2.2 Planting Materials

Sixty-eight (68) sweetpotato seeds from the International Potato Center in Kumasi, Ghana were utilized for the experiment, including two types (Umuspo 3 and TIS 87/0087) that were used as checks and obtained from the National Root Crops Research Institute in Umudike, Nigeria. By soaking the seeds in cold water for twenty-four hours before to planting, the seeds' dormancy was disrupted.

2.3 Nursery Management

The soil used for the nursery was made up of a 3:2:1 mixture of river sand, topsoil, and organic matter. Polythene bags holding 1 kg of soil were used to prepare the nursery in the National Root Crops Research Institute greenhouse in Umudike and South-eastern, Nigeria. Some of the seeds sprouted after being soaked in cold water for roughly 24 hours to break their dormancy. Individual seeds were carefully removed from the cold-water container and sowed into the moist soil that was kept in plastic bags.

2.4 Land Preparation and Experimental Design

The experimental field was cleared, ploughed, harrowed and ridged. The cleared land was marked out into plots of 1.5 m^2 (1 m × 1.5 m). The field was laid out in a randomized complete block 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 360 m^2. Planting was done on July, 2017 using five vines on each plot. The crops 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.

2.5 Evaluation of Morphological Traits

Using a sweet potato descriptor manual, 16 morphological traits of the progeny sweet potatoes were assessed 90 to 120 Days After Planting (DAP). These characteristics fall into two categories: storage root descriptors

Table 1. Progenies of Sweetpotato and their sources

S/No.	Genotypes	Source	S/No.	Genotypes	Source
1.	Ligri Poly Cross/1	CIP, Kumasi, Ghana	36.	Ligri Poly Cross/36	CIP, Kumasi, Ghana
2.	Ligri Poly Cross/2	CIP, Kumasi, Ghana	37.	Ligri Poly Cross/37	CIP, Kumasi, Ghana
3.	Ligri Poly Cross/3	CIP, Kumasi, Ghana	38.	Ligri Poly Cross/38	CIP, Kumasi, Ghana
4.	Ligri Poly Cross/4	CIP, Kumasi, Ghana	39.	Ligri Poly Cross/39	CIP, Kumasi, Ghana
5.	Ligri Poly Cross/5	CIP, Kumasi, Ghana	40.	Ligri Poly Cross/40	CIP, Kumasi, Ghana
6.	Ligri Poly Cross/6	CIP, Kumasi, Ghana	41.	Ligri Poly Cross/41	CIP, Kumasi, Ghana
7.	Ligri Poly Cross/7	CIP, Kumasi, Ghana	42.	Ligri Poly Cross/42	CIP, Kumasi, Ghana
8.	Ligri Poly Cross/8	CIP, Kumasi, Ghana	43.	Ligri Poly Cross/43	CIP, Kumasi, Ghana
9.	Ligri Poly Cross/9	CIP, Kumasi, Ghana	44.	Ligri Poly Cross/44	CIP, Kumasi, Ghana
10.	Ligri Poly Cross/10	CIP, Kumasi, Ghana	45.	Ligri Poly Cross/45	CIP, Kumasi, Ghana
11.	Ligri Poly Cross/11	CIP, Kumasi, Ghana	46.	Ligri Poly Cross/46	CIP, Kumasi, Ghana
12.	Ligri Poly Cross/12	CIP, Kumasi, Ghana	47.	Ligri Poly Cross/47	CIP, Kumasi, Ghana
13.	Ligri Poly Cross/13	CIP, Kumasi, Ghana	48.	Ligri Poly Cross/48	CIP, Kumasi, Ghana
14.	Ligri Poly Cross/14	CIP, Kumasi, Ghana	49.	Ligri Poly Cross/49	CIP, Kumasi, Ghana
15.	Ligri Poly Cross/15	CIP, Kumasi, Ghana	50.	Ligri Poly Cross/50	CIP, Kumasi, Ghana
16.	Ligri Poly Cross/16	CIP, Kumasi, Ghana	51.	Ligri Poly Cross/51	CIP, Kumasi, Ghana
17.	Ligri Poly Cross/17	CIP, Kumasi, Ghana	52.	Ligri Poly Cross/52	CIP, Kumasi, Ghana
18.	Ligri Poly Cross/18	CIP, Kumasi, Ghana	53.	Ligri Poly Cross/53	CIP, Kumasi, Ghana
19.	Ligri Poly Cross/19	CIP, Kumasi, Ghana	54.	Ligri Poly Cross/54	CIP, Kumasi, Ghana
20.	Ligri Poly Cross/20	CIP, Kumasi, Ghana	55.	Ligri Poly Cross/55	CIP, Kumasi, Ghana
21.	Ligri Poly Cross/21	CIP, Kumasi, Ghana	56.	Ligri Poly Cross/56	CIP, Kumasi, Ghana
22.	Ligri Poly Cross/22	CIP, Kumasi, Ghana	57.	Ligri Poly Cross/57	CIP, Kumasi, Ghana
23.	Ligri Poly Cross/23	CIP, Kumasi, Ghana	58.	Ligri Poly Cross/58	CIP, Kumasi, Ghana
24.	Ligri Poly Cross/24	CIP, Kumasi, Ghana	59.	Ligri Poly Cross/59	CIP, Kumasi, Ghana
25.	Ligri Poly Cross/25	CIP, Kumasi, Ghana	60.	Ligri Poly Cross/60	CIP, Kumasi, Ghana
26.	Ligri Poly Cross/26	CIP, Kumasi, Ghana	61.	Ligri Poly Cross/61	CIP, Kumasi, Ghana
27.	Ligri Poly Cross/27	CIP, Kumasi, Ghana	62.	Ligri Poly Cross/62	CIP, Kumasi, Ghana
28.	Ligri Poly Cross/28	CIP, Kumasi, Ghana	63.	Ligri Poly Cross/63	CIP, Kumasi, Ghana
29.	Ligri Poly Cross/29	CIP, Kumasi, Ghana	64.	Ligri Poly Cross/64	CIP, Kumasi, Ghana
30.	Ligri Poly Cross/30	CIP, Kumasi, Ghana	65.	Ligri Poly Cross/65	CIP, Kumasi, Ghana
31.	Ligri Poly Cross/31	CIP, Kumasi, Ghana	66.	Ligri Poly Cross/66	CIP, Kumasi, Ghana
32.	Ligri Poly Cross/32	CIP, Kumasi, Ghana	67.	Ligri Poly Cross/67	CIP, Kumasi, Ghana
33.	Ligri Poly Cross/33	CIP, Kumasi, Ghana	68.	Ligri Poly Cross/68	CIP, Kumasi, Ghana
34.	Ligri Poly Cross/34	CIP, Kumasi, Ghana	69.	Umuspo 3	NRCRI, Umudike, Nigeria
35.	Ligri Poly Cross/35	CIP, Kumasi, Ghana	70.	TIS 87/0087	NRCRI, Umudike, Nigeria

Table 2. Morphological traits measured among sweetpotato (*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

The traits and measurement methods were based on the International Board for Plant Genetic Resources descriptor list [12] CIP code

Table 3. Classification of the Ligri poly cross genotypes into clusters

Cluster number	Number of genotypes	Genotypes
I	36	LPC44, LPC64, LPC45, LPC3, LPC10, LPC6, LPC65, LPC1, LPC60, LPC9, LPC53, LPC40, LPC66, LPC29, LPC49, LPC25, LPC4, LPC30, LPC50, LPC16, LPC23, LPC43, LPC63, LPC34, LPC54, LPC22, LPC17, LPC20, LPC42, LPC62, LPC27, LPC47, LPC48, LPC28, LPC24, LPC19
II	27	LPC46, TIS87/0087, LPC14, LPC18, LPC37, LPC57, LPC36, LPC56, LPC35, LPC55, LPC15, LPC38, LPC58, LPC7, LPC8, Umuspo3, LPC32, LPC52, LPC21, LPC2, LPC12, LPC59, LPC31, LPC51, LPC39, LPC61, LPC67, LPC41, LPC68, LPC13
III	3	LPC5, LPC11, LPC33
IV	1	LPC26

(120 DAP) and foliar morphology (90 to 100 DAP). Standard descriptors, for morphological and agronomical developed by the "Centro Internacional de la papa" [10] was used for characterization. Internode length, internode diameter, leaf area, and leaf size (the distance between the base and the tip of the leaf) were all measured quantitatively to identify any developmental differences. Morphological character measurements were graded based on the average value obtained from several plants of each genotype. Using the meter rule, the lengths of the petiole, internode, and mature leaf (measured from tip to base) of the leaf were all determined. The internode diameter was measured using an electronic calliper (G02022 165). The leaf area was measured using a leaf area measurement equipment (Delta T devices. Model RS232). From the area in the middle of the stem, the characteristics of the vines and leaves were recorded.

2.6 Data Analysis

Statistical Package for Social Scientists (SPSS) software (Version 22) was used to conduct an analysis of variance on 16 characters in order to evaluate how agronomic and measured morphological parameters varied. The ward's approach was used to perform cluster analysis on all 19 characters based on Euclidean distance [11]. The results of the analyzed data were represented using tables and pie charts.

3. RESULTS AND DISCUSSION

Evaluation of a specific crop's genetic variation is essential for any breeding program to be successful. The identification of duplicates, the analysis of variability patterns, and the correlation with important agronomic characteristics have all been accomplished through the use of morphological characterization [6]. High morphological variation was present in the shoot and storage root characters of the CIP sweet potato genotypes.

3.1 Morphological Variation

The morphological traits measured among sweet potato (*Ipomoea batatas*) genotypes is shown in Figs. 1 and 2.

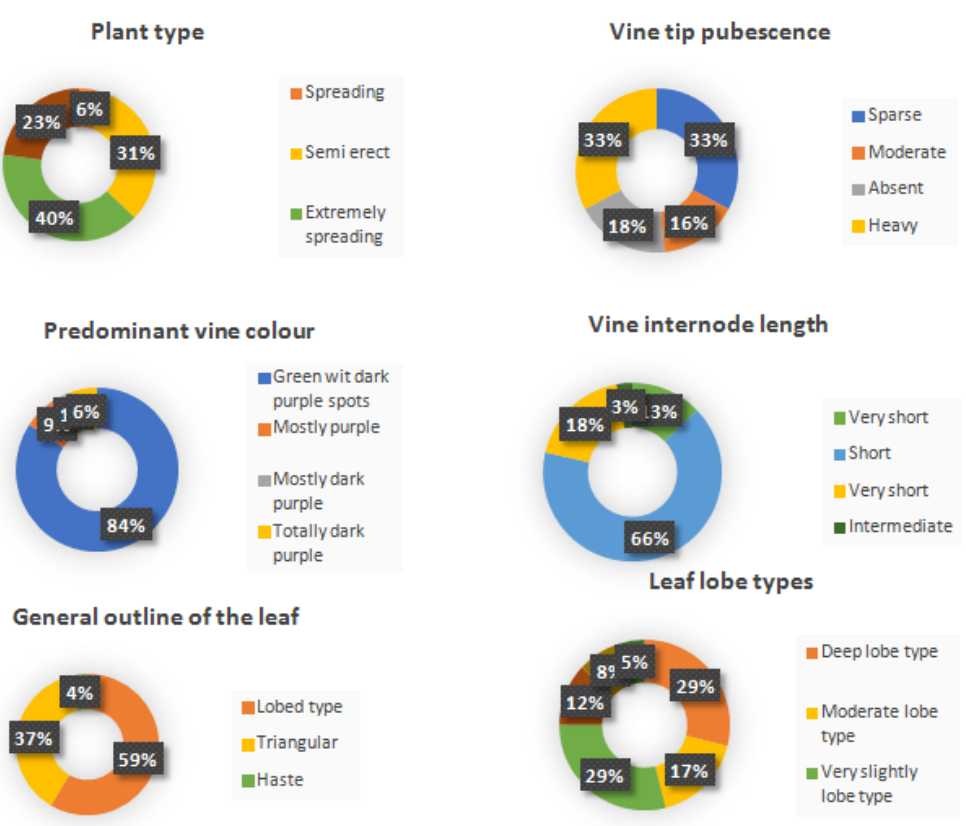

Fig. 1. Frequency data for different morphological characters of sweet potato genotypes

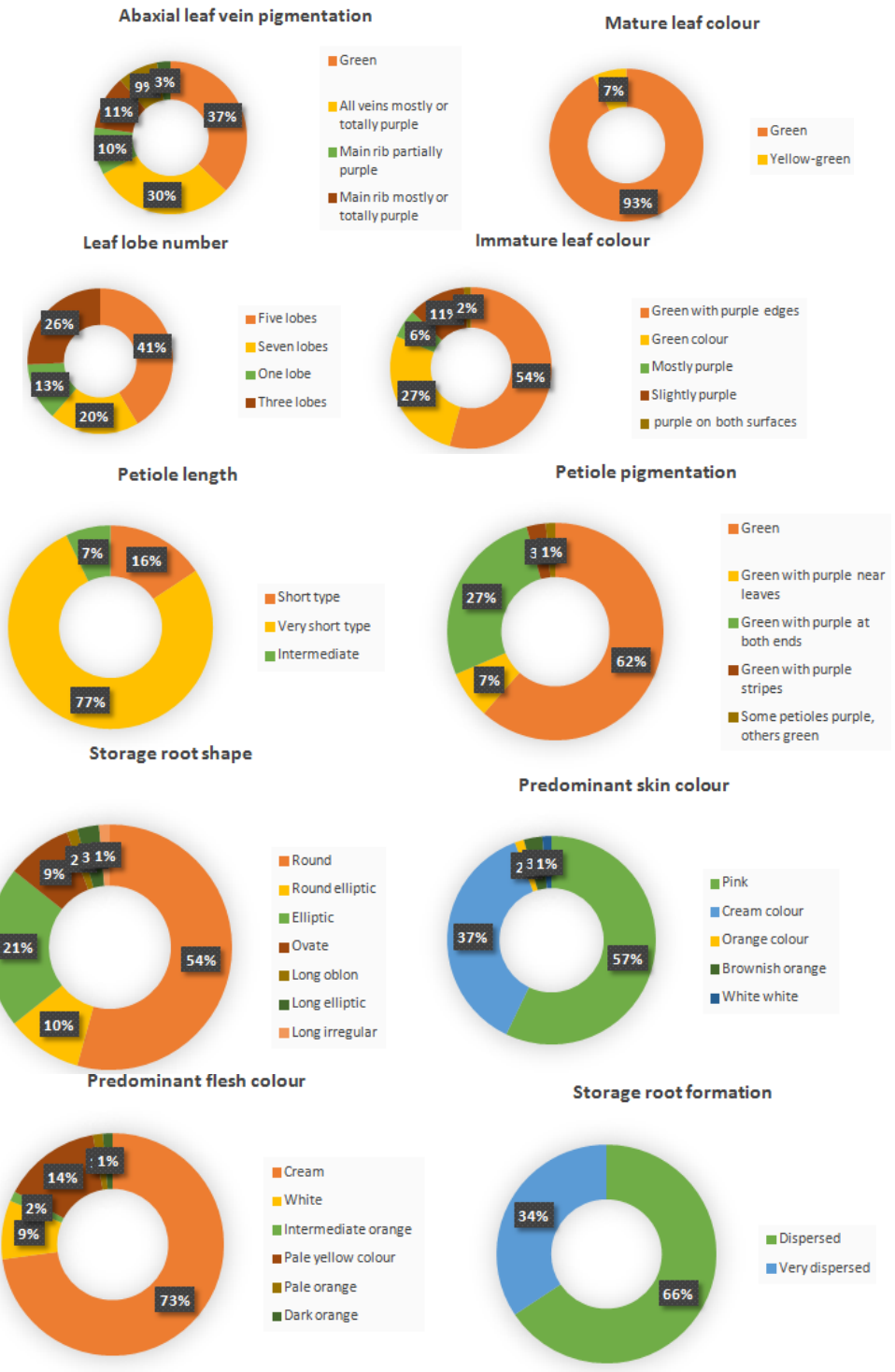

Fig. 2. Frequency data for different morphological characters of sweet potato genotypes

Plant type: According to the frequency distribution for the plant type, the majority of the progeny (40%), while 31%, belonged to the extremely spreading type. It was discovered that the spreading and erect behaviors were both low (6%) and (23%), respectively.

Ground cover: According to the ground cover's frequency distribution, the majority of the progeny (44%), medium (33%) and high (20%) types, as well as the lowest (3%), total type, were all observed.

Vine internode length: The frequency distribution of the vine internode length indicated that majority of the full sib progenies belonged to the short type (66%), the very short and intermediate were found to be 31% and 3% respectively.

Vine tip pubescence: Vine tip pubescence is shown to range from being absent to being heavy. The progenies were found to have (33%) for light pubescence, (16%) for medium pubescence, (18%) for no pubescence, and (33%) for heavy pubescence.

Predominant vine colour: The vine colors, which ranged from green to purple, demonstrated a high level of diversity. It was observed that 84% of the offspring were green with dark purple markings. Other vine colors seen in the progeny included primarily purple (9%), primarily dark complete purple (1%), and entirely dark purple (6%) colorations.

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 (59%). This was followed by triangular (37%) and haste (4).

Leaf lobe types: Six traits were revealed among the progenies, as demonstrated by the leaf lobe types. Deep lobe (29%) and very slightly lobe (29%) were the most common forms, followed by moderate lobe (17%), according to the frequency distribution of the progenies. Other lobe types that were common included very deep lobes (12%), small lobes (8%) and no lateral lobes (5%).

Abaxial leaf vein pigmentation: Six distinct traits were found among the progeny, as evidenced by the abaxial vine pigmentation. The frequency distribution of the progenies revealed that green (37%) and all veins mostly or totally purple (30%) were the predominant types. The frequency of other abaxial vein pigmentation included main rib mostly or totally purpose, main rib partially purple (10%), all veins partially purple (9%) and purple spot in the base of main rib (3%).

Mature leaf color: The mature leaf color indicated that the progenies had two distinct characteristics. Green (93%) and yellow-green (7%), according to the frequency distribution of the progenies.

Petiole length: The majority of the progenies were observed to be of the very short type (77%), while the short and intermediate types were determined to be 16% and 7%, respectively, according to the frequency distribution of the petiole length.

Petiole pigmentation: Petiole pigmentation revealed that the progeny possessed five distinct characters. The progeny's frequency distribution revealed that green predominated (62%), followed by green with purple at both ends (27%), green with purple close to the leaves (7%), green with purple stripes (3%) and some petioles with purple stripes and others with green (1%).

Storage root shape: The most common storage root shape was round (54%), followed by elliptic (21%), round elliptic (10%), ovate (9%), long oblong (2%), long elliptic (3%) and long irregular (1%).

Predominant skin colour: The progenies expressed skin colors ranging from white, cream, orange, brownish orange, and pink on their tubers. In 57% of the cases, pink predominated, with 37% in favor of cream. Orange and brownish-orange hues make up 3% of the color spectrum, followed by orange (2%) and white (1%).

Predominant flesh colour: White, cream, yellow, pale yellow, pale orange, intermediate orange, and dark orange were among the attractive flesh colors that were displayed in the progeny. A majority of the progeny (73%), according to the frequency distribution, were cream-colored. Others are white (9%), dark orange (1%), pale orange (1%), intermediate orange (2%), pale yellow (14%) and pale yellow (9%).

3.2 Ligri Poly Cross Genotypes

Cluster group I: 36 genotypes were identified in the first cluster. The cluster revealed the ground cover was high (75-90%), the vine internode diameter was very thick (>12mm), the general outline of the leaf was triangular, the mature leaf color was green, the petiole pigmentation was green with purple at both ends, the storage root shape was round, the predominant skin and flesh colors were cream, the storage root formation was an open cluster, the variability of the storage root shape was slightly variable, and the variability of the storage root size was slightly variable.

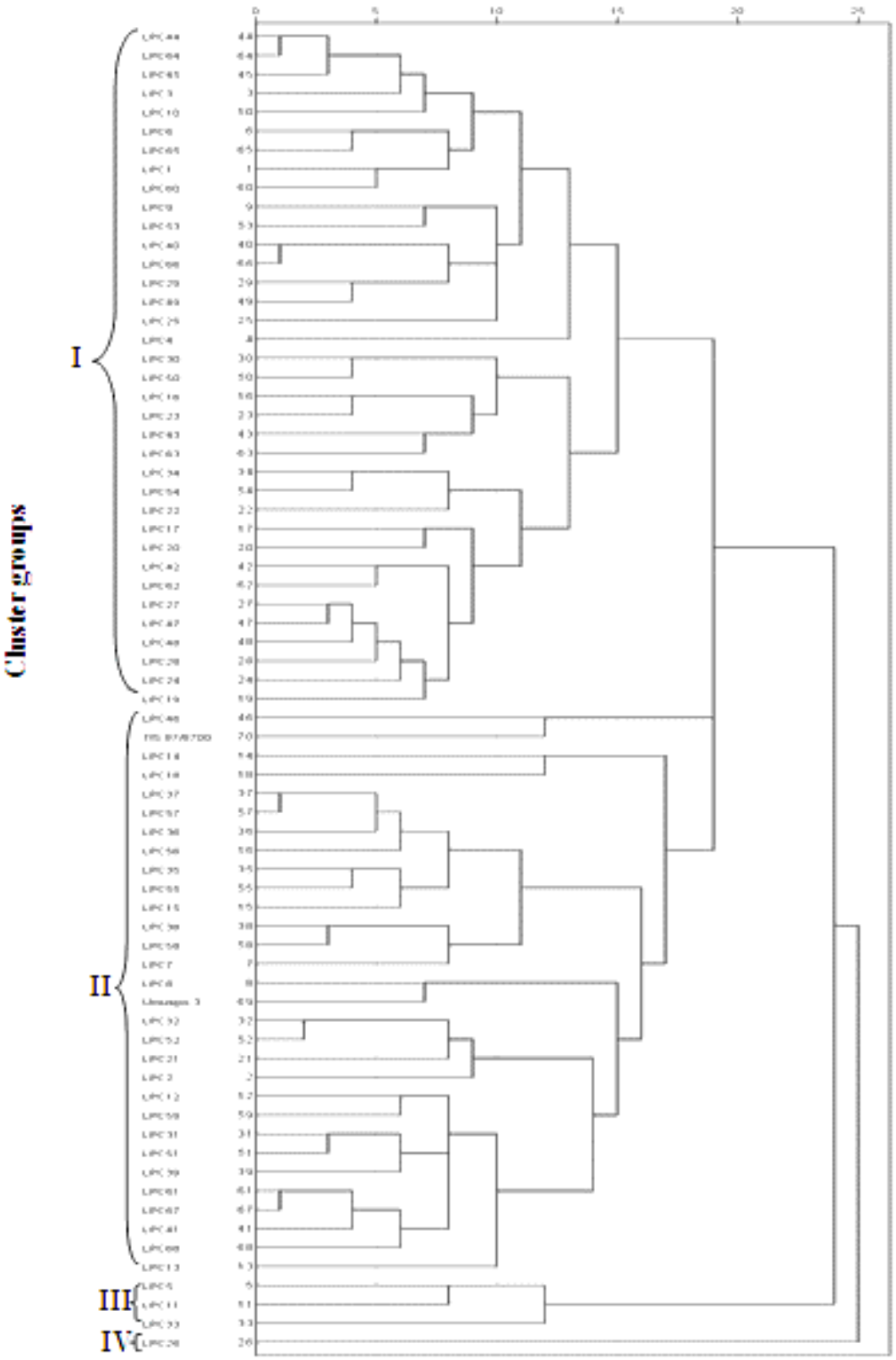

Fig. 3. Dendrogram of the Ligri PC (LPC)sweetpotato genotypes with checks; Umuspo3 and TIS 87/0087 revealed by average linkage cluster analysis based on the twenty one discriminant phenotypic characters

Cluster group II: A total of 27 genotypes made up the second cluster. The plant type was very spreading (151-250cm), the ground cover was high (75-90%), the vine internode diameter was very thick (>12mm), the vine tip pubescence was heavy, the general shape of the leaf was lobed, the mature leaf color was green, the petiole pigmentation was green with purple at both ends, the storage root shape was spherical, the predominating skin color was pink, the predominant flesh color was white, storage root formation was open cluster, variability of storage root shape was slightly variable, variability of storage root size was slightly variable.

Cluster group III: Three genotypes made up the third Cluster. The plant type was erect (75 cm), the ground cover was sparse (50%), the vine internode diameter was very thick (>12 mm), the vine tip pubescence was moderate, the mature leaf color was green, the petiole pigmentation was green with purple at both ends, the storage root shape was elliptic, the predominant skin color was pink, the predominant flesh color was cream, the storage root formation was open cluster, and the variability of storage root shape was slightly variable, variability of storage root size was slightly variable.

Cluster group IV: In the fourth cluster, there was only one genotype. The plant type was extremely spreading (>250 cm), the ground cover was complete (> 90%), the vine internode length was long (10-12 cm), the mature leaf shape was lobed, the petiole pigmentation was green with purple at both ends, the storage root shape was ovate, the predominant skin color was cream, the predominant flesh color was cream, the storage root formation was an open cluster, and the variability of storage root shape was moderate. Both morphological and root traits exhibited a diverse range among different sweet potato cultivars. They differ in a number of vegetative characteristics, including root shape, rooting depth, maturity period, disease resistance, and more. Given that they are polygenically controlled, the environment has a significant impact on most significant features, including yield [13]. The degree of genetic diversity in a crop's attributes determines how likely it is that it may be improved by selection; the more genetic variability a crop has, the more improvement potential it has [14]. The carotenoids and anthocyanin pigments in sweet potatoes give both the skin and the flesh their distinctive colours. Different combinations and intensities of these pigments result in a wide spectrum of skin and flesh tones, including skin that is cream, yellow, orange, pink, or purple. According to Rahman et al. [15], sweet potato clones with yellow, white, or cream coloured tuber flesh are lower in beta carotene and anthocyanins than genotypes with orange and purple coloured tuber flesh. The concentration of pigment contained can also be seen in the colour of the flesh of the tuber. The amount of beta carotene increases with the intensity of the colour of the tuber flesh [16]. Earlier studies on sweet potato's morphological diversity have only focused on germplasm bank collections, which have shown to exhibit a significant degree of phenotypic variety [17]. Similar results were observed by Vimala and Binu [18] in their evaluation of the morphological traits of 250 hybrid sweet potato progenies resulting from a controlled cross system. In their analysis of 14 sweet potato accessions, Daros et al. [19] noticed a significant morphological variation and drawn the conclusion that the vine tip pubescence, the color of the abaxial leaf veins, and the shape of the roots were the most helpful descriptors. Ulasi et al*.* [2] found substantial morphological diversity among the 38 sweetpotato genotypes. Plant type, vine tip pubescence, mature leaf color, immature leaf color, petiole length, root shape, root color distribution, surface defects on storage roots, and predominate storage root flesh colour were the factors that most influenced diversity [2]. Cluster analysis separated 20 genotypes into two main groups in the previous study by Solankey et al*.* (2015), demonstrating a genetic relationship between accessions. However, in another study, cluster analysis of 116 genotypes produced 12 clusters (Mohammed et al. 2015). According to Fongold et al. (2012), a cluster analysis of 19 sweet potato genotypes employing 26 features found three primary groups with similarity indices ranging from 0.42 to 1.00 prior to maturity and 0.34 to 1.00 upon maturity. In a cluster study of Tanzanian elite sweetpotato genotypes for resistance to sweetpotato virus disease and high dry matter content, Tairo et al. [20] found two significant groups with low genetic similarity of 0.52. Crop breeding requires an understanding of the morphological variability among genotypes [21]. In order to develop crosses, plant breeding programs require sufficient materials with widespread genetic diversity [22].

4. CONCLUSION

In this study, numerous genotypes of sweetpotato that were obtained using a poly

cross system were first studied using morphological characterization. The sweetpotato population for this study demonstrated a wide diversity that provides a strong basis for selection in relation to genetic advancement.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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