# DIVERSITY AMONG MORPHOLOGICAL TRAITS OF SEGREGATING SWEETPOTATO [*Ipomoea batatas* (L.) LAM] GENOTYPES IN UMUDIKE, NIGERIA.


## ABSTRACT

Sweetpotato (*Ipomoea batatas* (L.) Lam), genotypes frequently display wide variations in terms of their physical traits. In order to identify the morphological diversity among the population of 68 first filial generation (F1) 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 field experiment was conducted at the National Root Crops Research Institute, Umudike, Abia State, Nigeria in 2017. 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 nineteen characters that covered both folial and 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. Based on their morphological traits, all of the genotypes were found to be divided into four separate groups using cluster analysis. This would provide a sizable gene pool for efficient recombination to produce a promising sweetpotato variety with significant agricultural value.



**Keywords:** Characterization,Diversity, Morphological traits, Sweetpotato, Variation.

## 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 (Allemann*et al.*,2004, Ulasi*et al.*, 2021). 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 (Austin, 1977). 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 (FAOSTAT, 2014). Sweetpotatoes are a highly heterozygous and cross-pollinated group in which various attributes show widespread variability (Afuape*et al.*, 2011). 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 (Ulasi*et al.*, 2021). 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 (CIAT, 2007). 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~~ improving crop breeding (Yada *et al.*, 2010). 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~~ that are important economically (Tsegaye*et al.*, 2007). Therefore, the objectives of this research were to characterize the morphological diversity among sweetpotato genotypes obtained from the poly cross system.

## MATERIALS AND METHODS

### Study site

The experiment was carried out at the National Root Crops Research Institute in Umudike, southeast Nigeria, during the planting seasons of 2016 and 2017. Umudike is situated at latitude 05° 29 N, and longitude 07° 33 E, at an elevation of 122 m above sea level. Umudike, located in the humid tropics, receives an average annual rainfall of around 2177 mm, experiences an average annual temperature of about 26 °C, and has sandy loam utisol soil (NRCRI, 2012).

### Planting materials

sixty-eight (68) sweet potato seeds sourced from International Potato Center, Kumasi, Ghana, including two varieties (Umuspo 3 and TIS 87/0087) which served as checks which were obtained from the National Root Crops Research Institute, Umudike, Nigeria, were used for the experiment. The dormancy of the seeds was broken by soaking them in cold water for twenty-four hours before planting.

**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.

**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~~ planted 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.

**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 (120 DAP) and foliar morphology (90 to 100 DAP). Standard descriptors, for morphological and agronomical developed by the "Centro Internacional de la papa" (Human, 1991) 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. An electronic calliper was used to measure the internode diameter (G02022 165). A leaf area measuring system was used to measure the leaf area (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**

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 (Mohammadi and Prasanna, 2003). The results of the analyzed data were represented using tables and pie charts.

**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 (CIP/AVRDC/IBPGR, 1991) CIP code

## 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 (CIAT, 1993). High morphological variation was present in the shoot and storage root characters of the CIP sweet potato genotypes.

### Morphological variation

The morphological traits measured among sweet potato (*Ipomoea batatas*) genotypes ~~is~~ are shown in Figures 1 and 2:

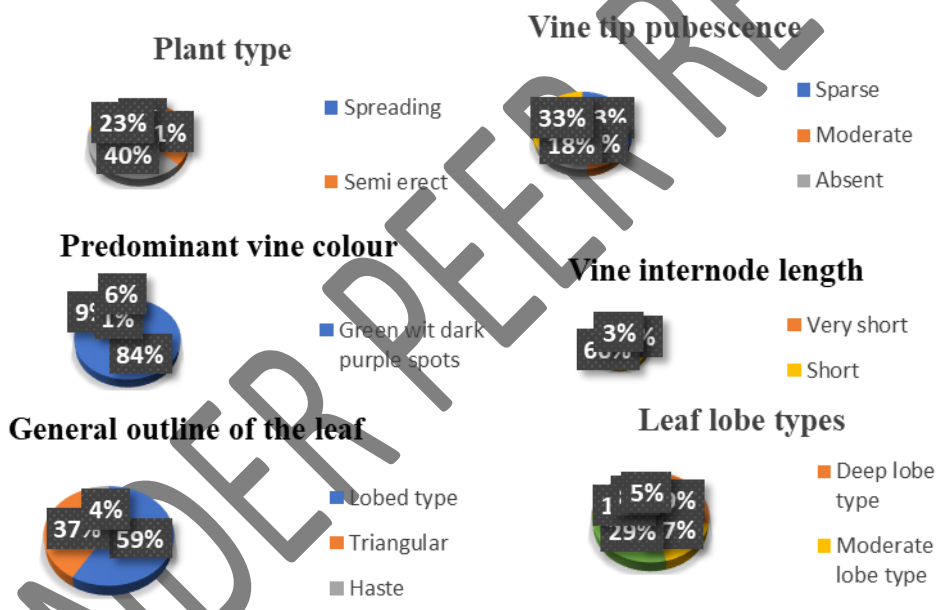
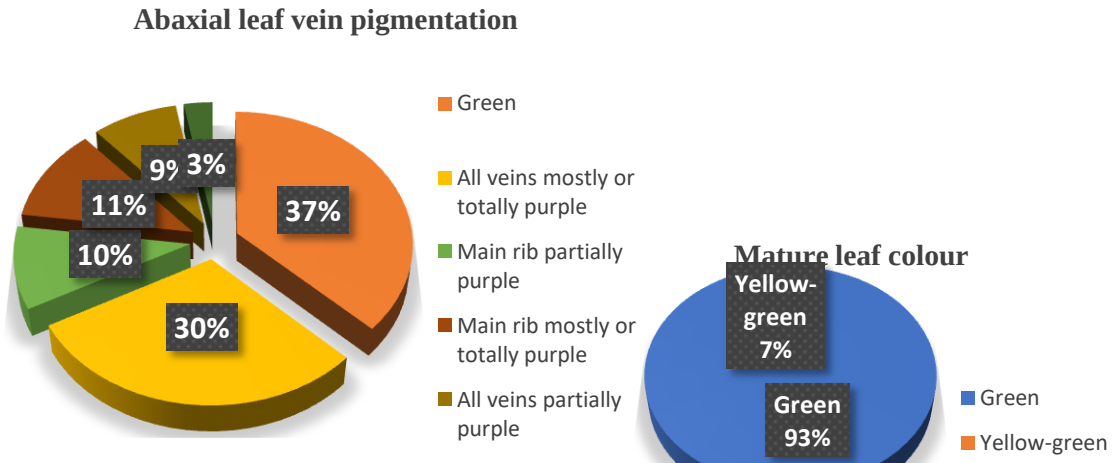



**Figure 1.** Frequency data for different morphological characters of sweet potato genotypes.



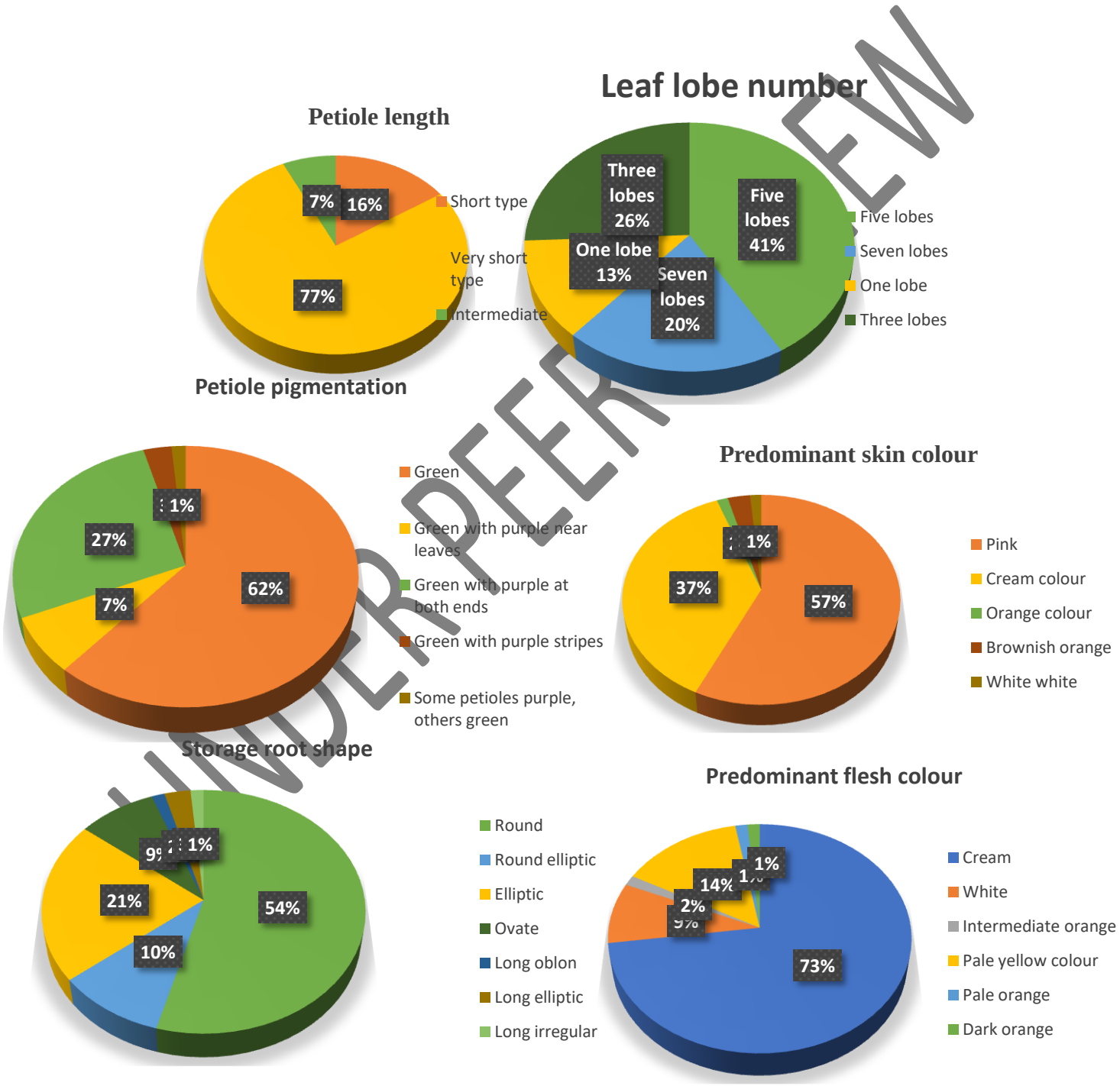



**Figure 2.** Frequency data for different morphological characters of sweet potato genotypes.

Plant type: The frequency distribution for the plant type indicated that the majority of the progenies belonged to extremely spreading (40%), whereas 31% belonged to the semi-erect type. The spreading and erect habits were found to be low (6%) and (23%), respectively.

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%).

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 was observed to vary ranging from absent to heavy. It was observed that the progenies recorded (33%) for sparse pubescence, (16%) for moderate pubescence, (18%) for absent pubescence and (33%) was observed for heavy pubescence.

Predominant vine colour: High variability was observed in vine colour ranging from green to purple. It was observed that the progenies possessed green with dark purple spots (84%). The other vine colours observed in the progenies were mostly purple (9%), mostly dark total purple (1%) and totally dark purple (6%) colourations.

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).

Lleaf lobe types: The leaf lobe types showed that six key characters were identified among the progenies. The frequency distribution of the progenies showed that deep lobe (29%) and very slightly lobe (29%) were the prevalent types, which was followed by moderate lobe (17%). The frequency of other lobe types was very deep lobe (12%), slight lobe (8%) and no lateral lobe (5%).

Abaxial leaf vein pigmentation: The abaxial vine pigmentation showed that six key characters were identified among the progenies. The frequency distribution of the progenies showed that green (37%) and all veins mostly or totally purple (30%) were the prevalent types. The frequency of other abaxial vein pigmentation ~~were~~ was the 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 showed that two key characters were identified among the progenies. The frequency distribution of the progenies showed that green (93%) and yellow-green (7%).

Petiole length: The frequency distribution of the petiole length indicated that majority of the progenies belonged to the very short type (77%), the short and intermediate were found to be 16% and 7% respectively.

Petiole pigmentation: petiole pigmentation showed that five key characters were identified among the progenies. The frequency distribution of the progenies showed that green (62%), green with purple at both ends (27%), green with purple near leaves (7%), green with purple stripes (3%) and some petioles purple, others green (1%).

Storage root shape: The prevalent 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 possessed a variety of tuber skin colour varying from white, cream, orange, brownish orange and pink. Pink colour was predominant (57%), followed by cream colour (37%). Orange colour and brownish-orange colour (3%), orange (2%) and white colour (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 progenies (73%). Others include; intermediate orange colour (2%), pale yellow colour (14%), white (9%), dark orange colour (1%) while pale orange colour was (1%).

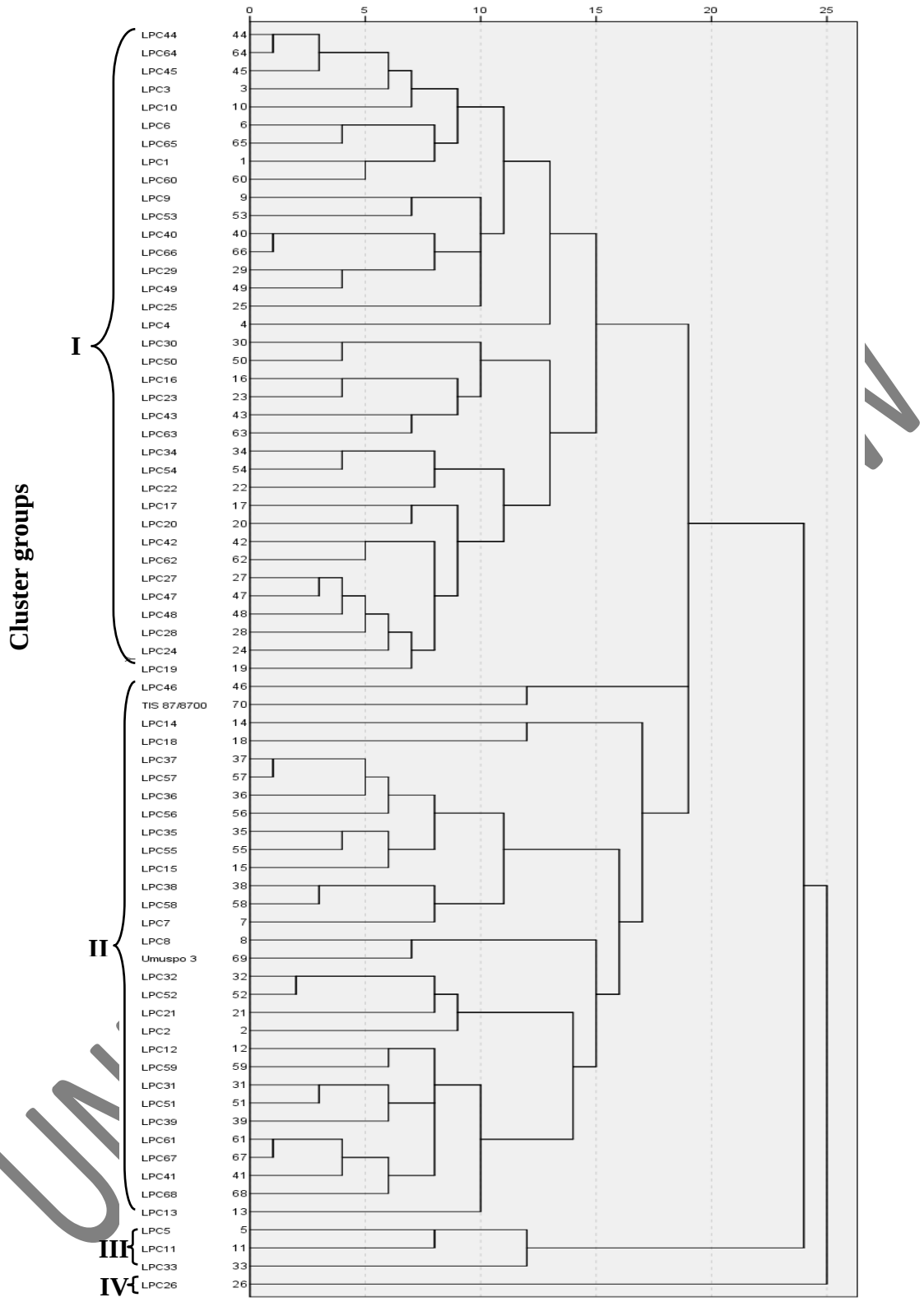



**Figure 3** - Dendrogram of the **Ligri PC (LPC)**sweetpotato genotypes with checks; Umuspo3 and TIS 87/0087 revealed by average linkage cluster analysis based on the twenty one discriminant phenotypic characters.

**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 |

**Ligri Poly Cross Genotypes:**

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

**Cluster Group II:** consisted of 27 genotypes, plant type was extremely spreading (151-250cm), ground cover was high (75-90%), vine internode diameter was very thick (>12mm), vine tip pubescence was heavy, general outline of the leaf was lobed, mature leaf color was green, petiole pigmentation was green with purple at both ends, storage root shape was round, predominant skin color was pink, predominant flesh color was white, storage root formation was an open cluster, ~~variability of~~ storage root shape was slightly variable . , ~~variability of storage root size was slightly variable.~~

**Cluster Group III:** consisted of 3 genotypes, plant type was erect (<75cm), ground cover was low (<50%), vine internode diameter was very thick (>12mm), vine tip pubescence was moderate, a general outline of the leaf was triangular, mature leaf color was green, petiole pigmentation was green with purple at both ends, storage root shape was elliptic, predominant

skin color was pink, predominant flesh color was cream, storage root formation was open cluster, ~~variability of~~ storage root shape was slightly variable. , ~~variability of storage root size was slightly variable.~~

**Cluster Group IV:** consisted of 1 genotype, plant type was extremely spreading (>250cm), ground cover was total (>90%), vine internode length was long (10-12cm), general outline of the leaf was lobed, mature leaf color was green, petiole pigmentation was green with purple at both ends, storage root shape was ovate, predominant skin color was cream, predominant flesh color was cream, storage root formation was an open cluster, variability of storage root shape was moderately variable, variability of storage root size was moderately variable. Among sweet potato varieties, there is a great degree of diversity in both morphological and root characteristics. 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 (Amin and Singla, 2010). 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 (Jindal *et al*., 2010). 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.* (2013), 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~~beta-carotene increases with the intensity of the colour of the tuber flesh (Saraswati*et al.*, 2013). 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 (Ritschell and Huaman, 2002). The evaluation of the morphological characters of 250 hybrid sweet potato progenies resulting from a controlled cross system by Vimala and Binu (2011) reported similar findings. Daros*et al.* (2002) noted substantial morphological variation in their evaluation of 14 sweet potato accessions and came to the conclusion that the vine tip pubescence, the abaxial leaf vein coloring, and the shape of the roots were the most useful descriptors. Ulasi*et al.* (2021) found substantial ~~morphologicalldiversity~~ 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 (Ulasi*et al.*, 2021). 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) should be added in the reference list. 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.* (2008) found two significant groups with low genetic similarity of 0.52. Crop breeding requires an understanding of the morphological variability among genotypes (Acquaah, 2007). In order to develop crosses, plant breeding programs require sufficient materials with widespread genetic diversity.

**CONCLUSION**

This research has presented ~~anagro~~an agro-morphological characterization as a preliminary study of several genotypes of sweetpotato acquired using a poly cross system. The population of sweet potatoes in this study thus exhibits a rich diversity that can serve as a solid foundation for selection in connection to genetic advancement.

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