NIGERIAN AGRICULTURAL JOURNAL
ISSN: 0300-368X
Volume 54 Number 1, April 2023 Pg. 559-565
Available online at: http://www.ajol.info/index.php/naj
https://www.naj.asn.org.ng


# Morphological Characterization of Sweetpotato Genotypes Evaluated at Umudike, Abia State Nigeria

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**Abstract**
Sweetpotato (*Ipomoea batatas* (L.) Lam), dicotyledonous plants belong to the family Convolvulaceae. Collecting and characterizing plant material has been the basis for crop improvement. Twenty-three genotypes of Sweetpotato (*Ipomea batata* (L) Lam were obtained from the Sweetpotato Program of National Root Crops Research Institute Umudike in the 2022 cropping season. This study therefore sought to morphologically characterize these selected sweetpotato genotypes; to identify those important descriptor traits that contributed most to the observed variation among the genotypes. The data generated were analyzed for morphological diversity using principal component analysis (PCA), which was used in identifying the few characters that significantly influenced the observed variation.PCA analysis further indicated that there are variations among the sweetpotato genotypes studied. Predominant skin colour, Mature leaf colour, Secondary vine colour, Vine internode length, Plant type, Mature leaf shape, Leaf lobe number, Shape of central leaf number, Secondary skin colour and Flower habit are the major source of variation and are important descriptors traits that contributed most to the observed variation among all the sweetpotato genotypes studied Among the 23 genotypes of sweetpotato studied, the mean yield performance (t/ha) shows that there is no significant difference (P>0.05) between PGA 14011-43 (6.30t/ha) and LOCAL BEST (FV) (6.13 t/ha). However PGA 14011-43 (6.30 t/ha) is significantly higher in yield compared to all other sweetpotato genotypes Local Best (Fv) 6.13 t/ha, BUTTER MILK 5.87 t/ha, UMUSPO/3 (5.53 t/ha), PGA 14398-4 (5.07 t/ha), PGA 14442-1 (4.90 t/ha), 87/OP/195 (4.50 t/ha ), PGA 14351-4 (4.33 t/ha), CRI – OKUMCOM 3.67 t/ha, CEMSA 74228 3.60 t/ha CRI – DADANYUIE (3.60 t/ha), PO3/116 (2.80 t/ha), TIS 87/0087 (2.67t/ha), OBARE( 2.30t/ha), TU-PURPLE (2.30 t/ha), PO3/35 (2.27 t/ha), PGA 17362-N1 (2.23t/ha), PGA 17265-N1(2.26 t/ha), NWOYORIMA (2.17 t/ha), KWARA (2.1 t/ha), PGN1 6021-39 (2.00 t/ha) and PGA 14008 – 9 (1.97 t/ha).
***Keywords: Sweetpotato, Morphological characterization, and Principal component analysis***

## Introduction

Sweetpotato [*Ipomoea batatas* (L.) Lam] is from Morning Glory (Convolvulaceae), one of the staple root crops in the world, particularly in sub-Saharan Africa (SSA) where its cultivation area covers around 3 million hectares with an estimated annual production of 13 million tonnes (Low and Van Jaarswels, 2008). It is a tuberous root plant and herbaceous perennial vine, with alternate heart-shaped or palmately lobed leaves and sympetalous flowers (Austin 2000). The edible tuberous roots are long with smooth skin whose colour ranges between yellow, orange, red, purple, and beige. Its flesh ranges from beige to white, red, pink, yellow, orange and purple (Gad and George, 2009). Sweetpotato can be used as a raw material for several industrialized products, considering its composition and agricultural potential (Afuape and Nwachukwu, 2005). The major forms by which sweetpotato roots are consumed in Nigeria are by boiling and eating, frying, and as a sweetener in a local non-alcoholic beverage called *kunnu*, which is popular in northern Nigeria. Other lesser forms include pottage and pounding (Agbo and Ene, 1994). The study of botanical characteristics of a particular crop is best done when diversity is maximum (Nwankwo, *et al*., 2010). This will ensure the expression and capturing of all the diversities that exist for a trait in the crop. All the different forms of the leaves, vines, and flowers have been studied and reported (Human, 2002). Morphological characterization is an important tool even in the era of molecular characterization because of its reliability and easy identification with fewer resources for certain stable characters unaltered by environmental interactions (Manamela, 2009). It is also essential to provide information on the traits of accession to enhance the assuming maximum utilization of the morphological description of the plant and its architecture (Hidalgo, 2003). Its descriptions permit relative differences between phenotypes, they are

usually highly inheritable characters that are easily detected by the naked eye and find expression in all environments (Hidalgo, 2003). A descriptor may assume different values; it can be expressed as a numerical value scale code or descriptive quality (Jaramillo and Baena, 2000). This is because descriptors correspond to characteristics or attributes whose expressions are easily detected by the naked eye, be recorded, have high heritability, high taxonomic and agronomic value, easy to measure or evaluate (Hidalgo, 2003). The International Plant Genetic Resources Institute (IPGRI) format is often used for plant characterization (IBPGR, 1997) Characterization of germplasm is essential to provide information on the traits of accessions assuring the maximum utilization of the germplasm collection to the final users (Singletary, 2010). Through characterization, the diversity that exists in a germplasm population can be estimated and effectively studied (Sinha *et al*., 2013). Morphological characterization in sweetpotato is done by assessing variations in the vine, leaf, flower and storage root characteristics (Huaman, 1999). This method has been used for identifying sweetpotato cultivars, detecting unique character traits and correlating with characteristics of agronomic importance (Karuri *et al*., 2010). Standard descriptor lists provide an international format, thereby producing a universally understood language for plant genetic resource data (Huaman, 1991). Therefore, the objectives of this study were to determine the morphological diversity among the sweetpotato genotype and to determine high yielding genotype among the population

**Materials and Methods**

The planting materials consisting of four node vine cuttings of 23 sweetpotato (Table 1) were obtained from the Sweetpotato Program of the National Root Crops Research Institute, Umudike. The field experiment was conducted at the National Root Crops Research Institute, Umudike which is located on Latitude 50' 20" N, Longitude 07' 32"E, and Altitude 122m above sea level. The experiment site was slashed, ploughed, harrowed and ridged with the tractor to a space of 1m apart before the field was marked out into a plot size of $9m^2$ (3m by 3m) containing 30 plants per plot with planting space of 1m by $0.3m^2$. The experiment was laid out in a randomized complete block design (RCBD) with three replicates. The sweetpotato vines were planted on the crest of the ridge slanted at an angle of $45^0$. Planting was done on the 4th of June, 2022 after the soil was sufficiently moist. Fertilizer application was carried out four weeks after planting at the rate of 400kg per hectare of NPK (15:15:15). First weeding was done manually at four weeks after planting before fertilizer was applied. Subsequent weeds found were rogued.

***Data Collection***

Morphological data were collected 60 days after planting based on the average of three measurements from the middle portion of the main stem as recommended by (Huaman, 1991). Qualitative characters were scored using a scale of 0 to 9. The following variables were scored: Plant growth characteristics: plant type (PT), ground cover (GC); mature vine characteristics: vine internode length (VIL), predominant vine colour (PVC), secondary vine colour (SVC), vine tip pubescence (VTP), mature leaf characteristics, a general outline of leaf (GOL), leaf lobes number (LLN), leaf lobed type (LLT), mature leaf size (MLS), shape of central leaf lobe (SCLL), mature leaf colour (MLC), immature leaf colour (ILC), flowering habit (FH), Storage root characteristics, predominant skin colour (PSC), secondary skin colour (SSC), predominant flesh colour (PFC), secondary flesh colour (SFC), distribution of secondary flesh colour (DSFC) and storage root shape (SRS). Measurements were done on three plants chosen randomly from the 30 plants per plot and averaged for the variable in each of the genotypes collected.

***Data Analysis***

The data collected were analyzed for morphological diversity using principal component analysis (Principal components analysis is a procedure for identifying a smaller number of uncorrelated variables, called "principal components", from a large set of data Jolliffe (2002). The goal of principal components analysis is to explain the maximum amount of variance with the fewest number of principal components) which was used in identifying the few characters that significantly influenced the observed variation among the genotypes for both above and below-ground attributes (Abdi and Williams, 2010).

**Results and Discussion**

Morphological characters are predominantly used as markers for easy differentiation of genotypes because the characters are expressed genetically involving one or more genes. Among the 23 sweetpotato genotypes studied, there is a high level of phenotypic variation exhibited in sweetpotato using morphological characters Table 1, the extent and distribution of the variation in sweetpotato is essential for sound conservation strategies whereby conservation and sustainable use of phenotypic resources is essential to meet the demand for future use (Kanuri *et al*., 2010). Morphology diversity and relationship among sweetpotato varieties are very important, not only for germplasm conservation but also for breeding purposes, especially during the selection of varieties having superior qualities (Laurie *et al*., 2013).

Among the 23 genotypes of sweetpotato studied, the mean yield performance (t/ha) shows that there is no significant difference (P>0.05) between PGA 14011-43 (6.30t/ha) and LOCAL BEST (FV) (6.13 t/ha) as shown in Table 2. However PGA 14011-43 (6.30 t/ha) is significantly higher in yield compared to all other sweetpotato genotypes Local Best (Fv) 6.13 t/ha, BUTTER MILK 5.87 t/ha, UMUSPO/3 (5.53 t/ha), PGA 14398-4 (5.07 t/ha), PGA 14442-1 (4.90 t/ha), 87/OP/195 (4.50 t/ha ), PGA 14351-4 (4.33 t/ha), CRI – OKUMCOM 3.67 t/ha, CEMSA 74228 3.60 t/ha CRI – DADANYUIE (3.60 t/ha), PO3/116 (2.80 t/ha), TIS 87/0087 (2.67t/ha), OBARE( 2.30t/ha), TU-PURPLE (2.30 t/ha), PO3/35 (2.27 t/ha), PGA 17362-N1

(2.23t/ha), PGA 17265-N1(2.26 t/ha), NWOYORIMA (2.17 t/ha), KWARA (2.1 t/ha), PGN1 6021-39 (2.00 t/ha) and PGA 14008 – 9 (1.97 t/ha).

***PCA analysis on Morphological Traits***

Table 3 shows the PCA variable loading percentage and cumulative variance for the first six components axis. Out of the nineteen traits, six principal components exhibited more than one eigenvalue and showed 79.63% variability among the characters under investigation (Table 3) PC1 showed 23.78%, PC 2 showed 41.80%, PC 3 showed 56.30%, PC 4 showed 65.88%, PC 5 showed 73.56% and PC 6 showed 79.63% variability among the sweet potato genotype for the character (traits) being studied. Principal component one (PC 1), principal component two (PC2), Principal component three (PC 3), principal component four (PC 4), principal component five (PC 5), principal component 6 (PC 6) had an eigenvalue of 4.519, 3.428, 2.754; 1.820, 1.450 and 1.150 respectively (Table 3). Furthermore in PC1, secondary vine colour, mature leaf shape, leaf lobe number, leaf lobe type, the shape of central leaf number, mature leaf colour, flower habit, vine internode length, secondary skin colour were positively correlated while plant types, predominant vine colour, vine tip pubescence, immature leaf colour, flower colour, root shape, predominant flesh colour, secondary flesh colour and distribution of secondary skin colour were negatively correlated (Table 3). in pc 2, vine tip pubescence, mature leaf shape, leaf lobe type, leaf lobe number, the shape of central leaf number, mature leaf colour, immature leaf colour, flower colour, root shape, predominant flesh colour and Secondary flesh colour were positively correlated while plant types, predominant vine colour, secondary vine colour, flower habit, vine internode length., distribution of secondary skin colour were negatively correlated (Table 3). In PC 3, secondary vine colour, leaf lobe type, leaf lobe number, the shape of central leaf number, immature leaf colour, flower habit, vine internode length, secondary skin colour, predominant flesh colour, secondary flesh colour and distribution of secondary skin colour were positively correlated while plant types, predominant vine colour, vine tip pubescence, mature leaf shape, mature leaf colour, flower colour, root shape, predominant skin colour were negatively correlated (Table 3). in PC 4, plant types, predominant vine colour, secondary vine colour, vine tip pubescence, mature leaf shape, leaf lobe number, the shape of central leaf number, mature leaf shape, flower colour, vine internode length, Secondary skin colour, Secondary flesh colour were positively correlated while leaf lobe type, immature leaf colour, flower habit, root shape, predominant flesh colour, predominant skin colour and distribution of secondary skin colour were negatively correlated (Table 3). In PC 5 Plant type, predominant vine colour, vine tip pubescence, mature leaf shape, leaf lobe number, shape of central leaf number, flower colour, flower habit, vine internode length, root shape, predominant skin colour, predominant flesh colour, secondary flesh colour and distribution of secondary skin colour were positively correlated while secondary vine colour, mature leaf colour, immature leaf colour, secondary skin colour were negatively correlated and lastly in PC 6, secondary vine colour, leaf lobe number, flower colour, flower habit, vine internode length, root shape, predominant skin colour, predominant flesh colour, secondary flesh colour and distribution of secondary skin colour were positively correlated while plant type, predominant vine colour, vine tip pubescence, leaf lobe type, shape of central leaf number, mature leaf colour, immature leaf colour, secondary skin colour were negatively correlated, the first principal component (PC 1) accounted for 23.78% of total variance had factors with high contribution as predominant skin colour, mature leaf shape, leaf lobe number and shape of central leaf number, the second principal component (PC 2), accounting for additional 18.02% of the total variation, had factors with high contribution as mature leaf colour, flower colour, secondary flesh colour and distribution of secondary skin colour, the third principal component (PC3), accounting for 14.50% of total variation had factors with high contribution as secondary skin colour, secondary flesh colour, predominant skin colour, predominant flesh colour and vine tip pubescence. The fourth principal component (PC 4), accounting for an additional 9.58% of the total variation had factors with high contributions as vine internode length, flower habit, secondary skin colour and vine tip pubescence, the fifth principal component (PC 5), accounting for additional 9.68% of total variation and had factors with high contribution as plant type, predominant flesh colour and distribution of secondary colour. Lastly, principal component six (PC 6) accounted for an additional 6.07% of the total variation and had factors with high contributions as mature leaf colour, secondary vine colour, flesh colour and root shape.

***PCA biplot analysis***

The PCA biplot analysis of the twenty-three sweetpotato genotypes assembled into 4 clusters based on the nineteen morphological traits (Fig 1), in the first cluster A, OBARE, PO 3/16, CEMSA 74-228, KWARA, NWOYORIMA, PCA 14398-4 are closely related in Vine internode length, Secondary vine colour, Distribution of secondary skin colour and Flower habit. In the second cluster B, PO3/35, Local Best, 87/OP/195 and CRI- DADANYUIE are closely related in Secondary skin colour, Mature leaf colour, Leaf lobe number, Leaf lobe type, Mature leaf shape and Shape of central leaf number. In the third cluster C, OBARE TIS 87/0087, PG 17362 – N1, PG 14351-4, PGA 14008-9, CR1 APOMUDEN, UMUSPO 3 and BUTTER MILK are closely related in Plant types, Vine tip pubescence and lastly in the fourth cluster D, TU-PURPLE, CR1 OKUMKOM, PGA 14398-4, PGN 16021 – 39, PGA 14442-1 are closely related in predominant skin colour, secondary flesh colour, flower colour, predominant flesh colour, immature leaf colour and predominant vine colour.

**Conclusion**

Results show that the 23 sweetpotato genotype used for

this study have high morphological diversity within both the above (vine, leaf, flower) and below (root) attributes in the population. PCA analysis has proved to be an effective method in grouping sweet potato genotypes that may facilitate effective utilization of the genotypes in crop improvement programs, It helps to identify the trait with the highest variability Moreover, PCA analysis further indicated that there are variations among the sweetpotato genotypes studied, predominant skin colour, mature leaf colour, secondary vine colour, vine internode length, plant type, mature leaf shape, leaf lobe number, the shape of central leaf number, secondary skin colour and flower habit are the major source of variation and are important descriptor traits that contributed most to the observed variation among all the sweetpotato genotypes studied. Morphological diversity and relationships among sweetpotato varieties are very important, not only for germplasm conservation, but also for breeding purposes especially during the selection of varieties having superior qualities (Laurie *et al*., 2004). Morphological characterization of plants is vitally imperative for the detection of desirable peculiar traits, identification of duplication, accessions and structuring of the population for conservation (Manamela, 2009).

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**Table 1**: **Morphological variation among the 23 sweetpotato genotypes (Using sweetpotato descriptor manual)**

| S/N | NAMES | PLANT TYPES | PREDOMINANT VINE COLOUR | SECONDARY VINE COLOUR | VINE PUBESCENCE | MATURE LEAF SHAPE | LEAF LOBE TYPE | LEAF LOBE NUMBER | SHAPE OF CENTRAL LEAF LOBE | MATURE LEAF COMATURE | LEAF COLOUR | FLOWER COLOUR | FLOWER HABIT | VINE INTERNODE LENGTH | STORAGE ROOT SHAPE | PREDOMINANT SKIN COLOUR | SECONDARY SKIN COLOUR | PREDOMINANT FLESH COLOUR | SECONDARY FLESH COLOUR | DISTRIBUTION OF SECONDARY SKIN COLOUR |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | PGA14008-9 | 5 | 1 | 1 | 1 | 4 | 1 | 1 | 1 | 2 | 7 | 4 | 3 | 3 | 2 | 8 | 1 | 6 | 2 | 5 |
| 2 | OBARE | 5 | 1 | 4 | 1 | 4 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 3 | 2 | 3 | 1 | 1 | 1 | 9 |
| 3 | KWARA | 5 | 1 | 1 | 1 | 6 | 5 | 3 | 6 | 2 | 1 | 1 | 1 | 3 | 3 | 1 | 1 | 1 | 1 | 9 |
| 4 | CRI-ADOMYDEN | 5 | 6 | 2 | 1 | 4 | 1 | 1 | 1 | 1 | 9 | 4 | 3 | 3 | 8 | 4 | 2 | 8 | 4 | 9 |
| 5 | PG17362-N1 | 3 | 1 | 4 | 1 | 4 | 1 | 1 | 1 | 1 | 2 | 4 | 3 | 1 | 9 | 2 | 1 | 2 | 4 | 2 |
| 6 | 87/OP/195 | 3 | 1 | 2 | 1 | 5 | 5 | 1 | 2 | 1 | 6 | 4 | 3 | 1 | 5 | 6 | 2 | 7 | 4 | 9 |
| 7 | PGN1602-39 | 3 | 7 | 1 | 1 | 4 | 1 | 1 | 1 | 3 | 7 | 6 | 1 | 1 | 5 | 9 | 1 | 8 | 3 | 4 |
| 8 | CEMSA 74-228 | 5 | 1 | 5 | 1 | 5 | 5 | 3 | 4 | 1 | 3 | 4 | 3 | 5 | 1 | 2 | 6 | 2 | 1 | 9 |
| 9 | TIS 87/0087 (check) | 3 | 1 | 4 | 1 | 4 | 1 | 1 | 1 | 2 | 3 | 6 | 1 | 5 | 2 | 8 | 1 | 1 | 1 | 9 |
| 10 | PGA 14442-1 | 5 | 1 | 4 | 1 | 4 | 1 | 1 | 1 | 2 | 9 | 6 | 1 | 1 | 9 | 8 | 1 | 8 | 4 | 9 |
| 11 | BUTTERMILK | 5 | 1 | 2 | 1 | 4 | 1 | 1 | 2 | 2 | 2 | 6 | 1 | 5 | 9 | 4 | 1 | 2 | 1 | 9 |
| 12 | PGA 14011-43 | 5 | 1 | 4 | 1 | 4 | 1 | 1 | 1 | 2 | 9 | 4 | 3 | 3 | 1 | 1 | 1 | 5 | 3 | 9 |
| 13 | PGA 14398-4 | 5 | 6 | 2 | 1 | 4 | 1 | 1 | 1 | 2 | 9 | 4 | 3 | 1 | 8 | 4 | 1 | 8 | 2 | 4 |
| 14 | CRI-DADANYUIE | 3 | 1 | 1 | 5 | 5 | 5 | 3 | 4 | 5 | 9 | 6 | 1 | 1 | 4 | 8 | 1 | 1 | 2 | 1 |
| 15 | LOCAL BEST (fv) | 3 | 1 | 4 | 1 | 6 | 7 | 5 | 6 | 7 | 3 | 6 | 1 | 3 | 9 | 9 | 1 | 6 | 4 | 2 |
| 16 | CRI-OKUMKOM | 5 | 1 | 2 | 5 | 4 | 1 | 1 | 1 | 2 | 3 | 6 | 1 | 5 | 9 | 9 | 1 | 1 | 2 | 1 |
| 17 | PO3/35 | 5 | 1 | 2 | 1 | 5 | 9 | 5 | 9 | 2 | 3 | 5 | 3 | 3 | 9 | 8 | 1 | 8 | 4 | 9 |
| 18 | PGA 14351-4 | 3 | 1 | 5 | 1 | 6 | 7 | 7 | 6 | 2 | 3 | 4 | 3 | 3 | 3 | 4 | 1 | 2 | 1 | 9 |
| 19 | UMUSPO/3 (check) | 7 | 8 | 2 | 5 | 4 | 1 | 1 | 1 | 2 | 3 | 6 | 1 | 5 | 4 | 4 | 1 | 8 | 4 | 9 |
| 20 | TU-PURPLE | 3 | 8 | 4 | 1 | 5 | 3 | 3 | 4 | 2 | 8 | 6 | 1 | 3 | 1 | 1 | 9 | 10 | 9 | 1 |
| 21 | PG17362-N1 | 3 | 1 | 4 | 1 | 5 | 5 | 3 | 4 | 2 | 3 | 4 | 5 | 1 | 1 | 5 | 8 | 1 | 2 | 2 |
| 22 | NWOYORIMA | 3 | 1 | 2 | 1 | 6 | 5 | 3 | 6 | 2 | 2 | 4 | 3 | 3 | 3 | 1 | 1 | 1 | 1 | 9 |
| 23 | PO3/116 | 3 | 1 | 2 | 1 | 5 | 5 | 3 | 5 | 2 | 2 | 4 | 3 | 5 | 3 | 8 | 1 | 8 | 4 | 9 |

***Note: Each column is a character and rows respective state or genotype***

**Table 2: Mean Yield Performance (T/ha) of 23 Sweetpotato Genotypes evaluated At Umudike**

| Genotypes | Mean t/ha |
|---|---|
| PGA 14011-43 | 6.30 |
| LOCAL BEST (FV) | 6.13 |
| BUTTERMILK | 5.87 |
| UMUSPO/3 (CHECK) | 5.53 |
| PGA 14398-4 | 5.07 |
| PGA 14442-1 | 4.90 |
| 87/OP/195 | 4.50 |
| PGA 14351-4 | 4.33 |
| CRL-OKWUMCOM | 3.67 |
| CEMSA 74228 | 3.60 |
| CRI – DADANYUIE | 3.60 |
| PO3/116 | 2.80 |
| TIS 87/0087 (CHECK) | 2.67 |
| OBARE | 2.57 |
| TU-PURPLE | 2.30 |
| PO3/35 | 2.27 |
| PGA 17362 – N1 | 2.23 |
| PGA 17265 – N1 | 2.26 |
| NWO YORIMA | 2.17 |
| KWARA | 2.01 |
| PG N1 6021-39 | 2.00 |
| PGA 14008 – 9 | 1.97 |
| FLSD 0.05 | 1.28 |

**Table 3: Factors loading on 19 morphological traits for the first six principal components and percentage of variance accounted for each component**

| Character (Traits) | PC 1 | PC 2 | PC 3 | PC 4 | PC 5 | PC 6 |
|---|---|---|---|---|---|---|
| Plant types | -0.182 | -0.235 | -0.054 | 0.137 | 0.489 | -0.811 |
| Predominant vine colour | -0.260 | -0.166 | -0.268 | 0.168 | 0.211 | -0.252 |
| Secondary vine colour | 0.115 | -0.072 | 0.211 | 0.212 | -0.331 | 0.554 |
| Vine Tip pubescence | -0.135 | 0.117 | -0.310 | 0.321 | 0.122 | -0.324 |
| Mature Leaf shape | 0.416 | 0.147 | -0.053 | 0.032 | 0.013 | -0.219 |
| Leaf lobe type | 0.408 | 0.195 | 0.028 | -0.059 | 0.-195 | -0.037 |
| Leaf lobe number | 0.397 | 0.201 | 0.047 | 0.056 | 0.103 | 0.036 |
| Shape of central leaf number | 0.408 | 0.170 | 0.038 | 0.013 | 0.241 | -0.076 |
| Mature leaf colour | 0.092 | 0.392 | -0.249 | 0.049 | -0.103 | -0.677 |
| Immature leaf colour | -0.261 | 0.201 | 0.194 | -0.237 | -0.096 | -0.134 |
| Flower colour | -0.162 | 0.351 | -0.120 | 0.200 | 0.046 | 0.350 |
| Flower habit | 0.123 | -0.137 | 0.246 | -0.405 | 0.120 | 0.071 |
| Vine internode length | 0.075 | -0.180 | 0.096 | 0.511 | 0.299 | 0.254 |
| Root shape | -0.105 | 0.168 | -0.225 | -0.266 | 0.-183 | 0.318 |
| Predominant skin colour | -0.739 | 0.270 | -0.339 | -0.145 | 0.123 | 0.291 |
| Secondary skin colour | 0.004 | 0.106 | 0.438 | 0.376 | -0.119 | -0.005 |
| Predominant flesh colour | -0.181 | 0.253 | 0.317 | -0.160 | 0.394 | 0.116 |
| Secondary flesh colour | 0.127 | 0.379 | 0.358 | 0.080 | 0.099 | 0.106 |
| Distribution of secondary skin colour | -0.118 | -0.351 | 0.077 | -0.088 | 0.364 | 0.188 |
| Eigenvalue | 4.519 | 3.423 | 2.754 | 1.820 | 1.450 | 1.150 |
| % variance contribution | 23.78 | 18.02 | 14.50 | 9.58 | 7.68 | 6.07 |
| % cumulative variance contribution | 23.78 | 41.80 | 56.30 | 65.88 | 73.56 | 79.63 |

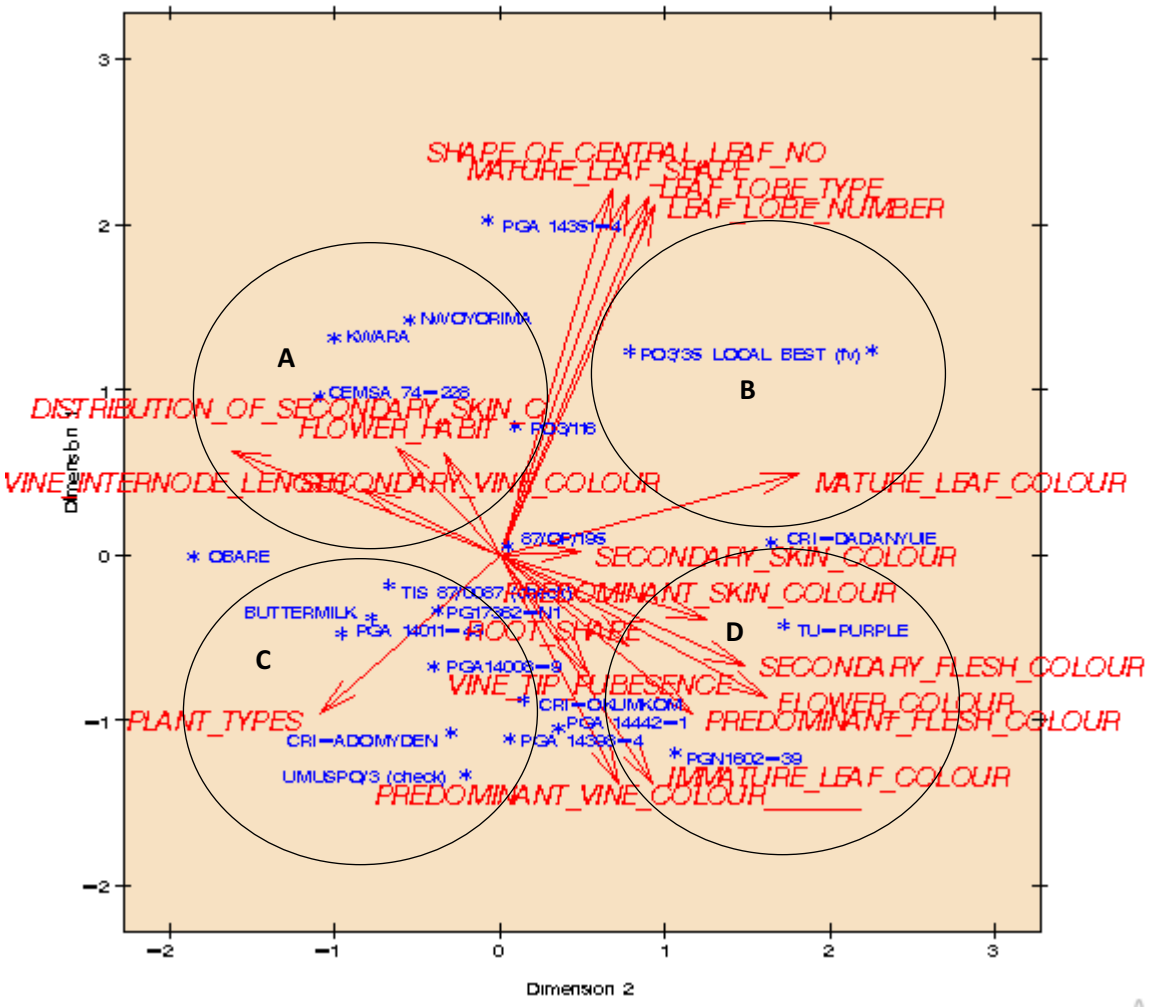


***Fig. 1: The PCA biplot graph of the twenty-three sweetpotato genotypes***