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Principal Component Analysis for Phenotypic Characterization of Sweet Potato (*Ipomoea batatas* (L.) Lam.) Genotypes in Malaysia

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Abstract

A total of 39 sweet potato genotypes (*Ipomoea batatas* (L.) Lam.) were grown at Malaysia Agricultural Research and Development Institute (MARDI), Industrial Crop Research Centre, in Bachok, Kelantan. The aim of the study is to classify sweet potato germplasm for a future breeding programme in Malaysia. Twenty-seven phenotypic characters were graded using the International Potato Centre (CIP) using standard sweet potato descriptors. The principal components analysis (PCA) was performed to identify the main characteristics to be used in phenotyping. PC1, PC2 and PC3 had eigen value of more than 1.0 and accounted for roughly 78.00 % of all the morphological characters. The scree plot clearly shows that the semi-curved line was obtained for vine characters with a high variability of 95.14 %, with a cumulative variability of 89.36 % for leaf and 89.78 % for root characters. These 39 genotypes can be classified into 3 classes. Factor analysis revealed that the main plant habit characteristics in the first group were ground cover, plant type, twining and internode vine length and tip pubescence. The general leaf outline, the form of the leaf lobe, the number of leaf lobes and the shape of the central leaf lobe were the second groups. In the third group, the primary and secondary colours of the skin, as well as the flesh, were two of the storage root's major characteristics. Genotypes with these characteristics can be helpful in determining the appropriate requirements and goals for sweet potato enhancement in breeding strategies. It can also be used to document sweet potato germplasm for passport purposes.

Keywords: *Ipomoea batatas*, Phenotypic characterization, Principal component analysis (PCA), Scree plot, Factor analysis

Abbreviation

TWN = Twining
PTY = Plant type
GB = Ground cover
VIL = Vine internode length
VID = Vine internode diameter
PVC = Predominant vine colour
SVC = Secondary vine colour
VTP = Vine tip pubescence
GLO = General leaf outline
LLT = Leaf lobe type
LLN = Leaf lobe number
SCL = Shape of central leaf lobe
MLS = Mature leaf size
ALVP = Abaxial leaf vein pigmentation
MLC = Mature leaf colour
ILC = Immature leaf colour
PL = Petiole length
PP = Petiole pigmentation
SRS = Storage root shape

SRD = Storage root defects
SRT = Storage root cortex thickness
PSC = Predominant skin colour
IPC = Intensity predominant skin colour
SSC = Secondary storage root skin colour
PFC = Predominant flesh colour
SFC = Secondary flesh colour
DSF = Distribution of secondary flesh colour

Introduction

Sweet potatoes, *Ipomoea batatas* L. (Lam.) is one of the nutritious, high-carbohydrate and vitamin-rich food crops that are beneficial to human health. In developed countries, it is one of the most nutritious and economic food crops [1]. After cassava, sweet potato is the world's second most widely grown tuber crop [2]. Sweet potato production is estimated to be 91.9 million metric tonnes worldwide, with an average yield of 13.4 $t \cdot ha^{-1}$ in a total area of 8.06 million hectares [3]. Asia is the world's leading producer of sweet potatoes, accounting for 67 % of total production [3]. China is the world's largest sweet potato producer, accounting for 51.8 million tonnes of global supply in 2019. Indonesia, after China, is Asia's second-largest producer of sweet potatoes, with 1.8 million tonnes produced compared to Malaysia's production of just 56,323 tonnes [3]. In Malaysia, sweet potato has been declared a cash crop, as stated in the 2011 - 2020 National Agrofood Policy [4]. Cash crops offer farmers reasonably fast economic returns; for example, the sweet potato crop can be harvested as early as 3 months after planting. Since 2014, the sector has contributed RM0.43 million (238 Mt), up 44 % in value and 11.2 % in production. Most cash crops are primarily intended for fresh consumption and agro-based industries [5]. Cash crop production was 215,087.65 Mt with a total cultivated area of 19,028 ha and a production value of RM389,886.50, according to vegetable and cash crop statistics [6].

Sweet potato is genetically a hexaploidy (2n = 6x = 90), a dicotyledonous root-tuber crop belonging to the *Convolvulaceae* family [7], which is inherently perennial and widely grown as an annual crop. It is grown using either storage roots or stem cuttings by vegetative propagation [8]. Sweet potato can be found in different colours, shapes and sizes of tubers' morphological features, as well as their physiological properties. The edible plant parts are leaves, storage roots and vines. Varieties are available in various skin and flesh colours, from white to yellow-orange and deep purple [9]. Morphological characterization activities make accessible knowledge about the stored germplasm, placing it in the most effective form for use, and it is important to emphasize that as it becomes established and documented, the quality of the germplasm increases [10,11]. The phenotypic diversity for important morpho-agronomic traits, which are not known, typically shows important traits of interest to plant breeders [12]. In addition, morphological characterization can help to remove duplicate accessions, thereby reducing the cost of conservation. The characterization will also promote the effective synthesis of breeding populations to achieve desired outcomes. The principal component analysis (PCA) is one of the statistical methods commonly used to identify phenotypic traits in crop germplasm which can be deployed to group genotypes based on their similarities. The PCA directs parents' selection for genetic improvement [13,14]. Wiley and Lieberman [15] pointed out that the PCA reduces the original variables to a new set of non-correlated variables known as principal components (PCs). These PCs explain the linkages between the traits and split the total variance of the original traits into a small number of uncorrelated new variables.

The purpose of this study was to morphologically classify 39 sweet potato genotypes. As a result, the pattern of variation, as well as the relationship between individuals and their characteristics, are established. The PCA was used to see if there were any conditions that differentiated the sweet potato genotypes. The findings provide information for researchers, especially breeders, to use in improving sweet potato genetics by defining traits that can be suggested for improving specific traits such as yield and other agronomic traits that contributed to yield.

Materials and methods

Planting material and experiment location

The experiment used a total of 39 sweet potato genotypes, including introduced hybrids, and traditional and released varieties, together with breeding lines acquired from MARDI. **Table 1** shows the origin of 39 sweet potato accessions. During the growing season, the experiment was conducted at Tuber Crops Research Centre, MARDI Bachok, Kelantan, from January to May 2019. The location is located at latitude 5°58' N and longitude 2°25' E. The field is dominated by BRIS (Beach Ridges Interspersed with

Swales) Soils, which are sand-like soils. Up to 150 cm below the soil level, the soils on the beach ridges are sandy (95 % sandy). In the topsoil, coarse sand and fraction are common; however, very fine sand is widespread in the subsoil [16]. The pH level of the soil is between 5.5 and 6.0.

Table 1 List of 39 sweet potato genotypes and their origin used to be characterized in the study.

No.	Accession No.	Genotypes	Origin	No.	Accession No.	Genotypes	Origin
1	MIb-01	PASAR BORONG 2	Malaysia	21	MIb-29	VitAto	MARDI
2	MIb-02	CN-2067-7	AVRDC	22	MIb-30	BIRU	Malaysia
3	MIb-03	PEJABAT	Malaysia	23	MIb-31	Anggun 2	MARDI
4	MIb-08	SABAH B	Malaysia	24	MIb-32	V6 D2 15	IC01
5	MIb-09	M/BAYENG		25	MIb-33	C 76	Unknown
6	MIb-10	PASAR BORONG 1	Malaysia	26	MIb-34	GUNTUNG 2	Malaysia
7	MIb-11	PISANG KAPAS	Malaysia	27	MIb-35	JEPUN ASAL	Malaysia
8	MIb-12	SB-031	Malaysia	28	MIb-36	SABAH K	Malaysia
9	MIb-14	CN-94517-17	AVRDC	29	MIb-37	KARAK BAKAR	Malaysia
10	MIb-16	CN-254-13	AVRDC	30	MIb-38	SUNGAI CHUA 2	Malaysia
11	MIb-17	GUNTUNG 1	Malaysia	31	MIb-39	PH 4 (PURPLE)	Indonesia
12	MIb-19	TANJUNG SEPAT 1	Malaysia	32	MIb-40	Anggun 3	MARDI
13	MIb-20	V6 D1 13	IC01	33	MIb-41	BATU PAHAT 1	Malaysia
14	MIb-22	TANJUNG SEPAT 2	Malaysia	34	MIb-42	BATU PAHAT 2	Malaysia
15	MIb-23	TANJUNG SEPAT 3	Malaysia	35	MIb-43	BATU PAHAT 4	Malaysia
16	MIb-24	GENDUT	Malaysia	36	MIb-44	BANTING	Malaysia
17	MIb-25	OREN 2	Indonesia	37	MIb-45	CAMERON HIGHLAND 1	Malaysia
18	MIb-26	18G-257	Unknown	38	MIb-46	CAMERON HIGHLAND 2	Malaysia
19	MIb-27	UBI CAIRO	Egypt	39	MIb-47	CAMERON HIGHLAND 3	Malaysia
20	MIb-28	MERODA INTA	Indonesia				

*MARDI - Malaysia Agriculture research and Institute; AVRDC - Asian Vegetable Research and Development Center; MIb - MARDI *Ipomoea batatas* (accessions number of sweet potato germplasm collected in MARDI); IC01 - Breeding lines accessions derived from Industrial Crops breeding program)

Experimental design

The experiment was designed in a randomized complete block design (RCBD) with 3 replicates. Each plot was 1.20×6.00 m^2 with a planting distance of 0.30×1.20 m^2 in a single row having 20 plants per plot. Sweet potato cuttings approximately 0.30 m long from each genotype were planted at each point of the ridges. Each accession was planted on a different plot.

Crop field practices

The field was ploughed to produce fine tilth. To ensure soil fertility, a substantial quantity of organic manure should be applied at the time of planting. Organic manure at a rate of 5 to 10 $t \cdot ha^{-1}$ was added to

BRIS soil. Fertilizer was applied 3, 5 and 8 weeks after planting. Nitrogen (N), phosphorus (P_2O_5), and potassium (K_2O) in the ratio of 12:12:17 accumulated at a rate of 200 kg·ha^{-1} to yield 600 kg·ha^{-1}. Fertilizer was given by each plant at a rate of 6 g per plant. Furthermore, the crop was grown in accordance with the required cultural practices. Weeds like *Cyperus* sp. and *Damaranthus* sp. will start growing wild as soon as a week after planting. Herbicides must also be used to monitor and inhibit weed growth. Isoproturon had been applied as a pre-emergence weedicide at a rate of 1 kg a.i. ha^{-1} 2 days after planting, followed by hand weeding 30 days later. Weeds were regulated with pesticides, pesticides and diseases were controlled with pesticides. Hence, sufficient soil moisture must be provided at the time of planting to ensure proper vine sprouting and establishment. Irrigation with 50 mm water was given at an IW/CPE ratio of 1.2. The sweet potato weevil, *Cylas formicarius* Fab. is a major pest in most sweet potato-growing countries [2]. The weevil was controlled using CIP's integrated pest management (IPM) technique. After 2 months of planting, the ridge was re-ridged, and synthetic sex pheromone traps were installed at 1 trap 100 m^{-2} area to collect and kill the weevils.

Evaluation of morphological characteristic

The International Potato Centre (CIP) standard sweet potato descriptors [8] were used to determine the morphological characterization of 39 sweet potato accessions (**Table 2**). At 90 days after planting, vine characteristics like plant habit, ground cover, vine internode length, diameter and colour as well as leaf characteristics like general leaf shape, type of leaf lobe, central lobe shape, number of lobes, leaf colour and pigmentation and petiole length and pigmentation, were reported [8]. All of the characters were derived from a random sample of 15 plants from each plot, which was then labelled. At harvest 120 days after planting, qualitative data such as storage root shape, storage root defect, storage root cortex thickness, storage root colour, and skin and flesh colour were reported. Fifteen fresh medium-sized roots (100 - 150 g) were randomly picked from each replication's 5 plants. It was carried out in accordance with the descriptor's specifications.

Table 2 List of morphological characteristics as described by CIP-standard descriptor assessed for 39 accessions of sweet potato genotypes.

Code	Descriptor	Phenotypes
		Vine characteristics
4.1.1	Twining (TWN)	0 Non-twining; 3 Slightly twining; 5 Moderately twining; 7 Twining; 9 Very twining
4.1.2	Plant type (PTY)	3 Erect (< 75 cm); 5 Semi-erect (75 - 150 cm); 7 Spreading (151 - 250 cm); 9 Extremely spreading (> 250 cm)
4.1.3	Ground cover (GB)	3 Low (< 50 %); 5 Medium (50 - 74 %); 7 High (75 - 90 %); 9 Total (> 90 %)
4.1.4.1	Vine internode length (VIL)	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)
4.1.4.2	Vine internode diameter (VID)	1 Very thin (< 4 mm); 3 Thin (4 - 6 mm); 5 Intermediate (7 - 9 mm); 7 Thick (10 - 12 mm); 9 Very thick (> 12 mm)
4.1.5.1	Predominant vine colour (PVC)	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
4.1.5.2	Secondary vine colour (SVC)	0 Absent; 1 Green base; 2 Green tips; 3 Green nodes; 4 Purple base; 5 Purple tip; 6 Purple nodes; 9 Other (specify in the descriptor Notes)
4.1.6	Vine tip pubescence (VTP)	0 Absent; 3 Sparse; 5 Moderate; 7 Dense
		Leaf characteristics
4.1.7.1	General leaf outline (GLO)	1 Rounded; 2 Reniform (kidney-shaped); 3 Cordate (heart-shaped); 4 Triangular; 5 Hastate; 6 Lobed; 7 Almost divided
4.1.7.2	Leaf lobe type (LLT)	0 No lateral lobes (entire); 1 Very slight (teeth); 3 Slight; 5 Moderate; 7 Deep; 9 Very deep
4.1.7.3	Leaf lobe number (LLN)	Generally, sweet potatoes have 1, 3, 5, 7 or 9 leaf lobes. If the leaf has no lateral lobes but shows a central tooth this number is 1. If the apical portion of the leaf is rounded this number is 0
4.1.7.4	Shape of central leaf lobe (SCL)	0 Absent; 1 Toothed; 2 Triangular; 3 Semi-circular; 4 Semi-elliptic; 5 Elliptic; 6 Lanceolate; 7 Oblanceolate; 8 Linear (broad); 9 Linear (narrow)
4.1.8	Mature leaf size (MLS)	3 Small (< 8 cm); 5 Medium (8 - 15 cm); 7 Large (16 - 25 cm); 9 Very large (> 25 cm)

Code	Descriptor	Phenotypes
4.1.9	Abaxial leaf vein pigmentation (ALVP)	1 Yellow; 2 Green; 3 Purple spots at the base of the main rib; 4 Purple spots in several veins; 5 Main ribs partially purple; 6 Main ribs mostly or totally purple; 7 All veins partially purple; 8 All veins mostly or totally purple; 9 Lower surface and veins totally purple
4.1.10.1	Mature leaf colour (MLC)	1 Yellow-green; 2 Green; 3 Green with a purple edge; 4 Greyish-green (due to dense pubescence); 5 Green with purple veins on upper surface; 6 Slightly purple; 7 Mostly purple; 8 Green upper surface, purple lower surface; 9 Purple on both surfaces
4.1.10.2	Immature leaf colour (ILC)	1 Yellow-green; 2 Green; 3 Green with a purple edge; 4 Greyish-green (due to dense pubescence); 5 Green with purple veins on upper surface; 6 Slightly purple; 7 Mostly purple; 8 Green upper surfaces; purple lower surface; 9 Purple on both surfaces
4.1.11	Petiole length (PL)	1 Very short (< 10 cm); 3 Short (10 - 20 cm); 5 Intermediate (21 - 30 cm); 7 Long (31 - 40 cm); 9 Very Long (> 40 cm)
4.1.12	Petiole pigmentation (PP)	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 petioles purple, some others green; 9 Totally or mostly purple
	Storage root characteristics	
4.2.1	Storage root shape (SRS)	1 Round - almost a circular outline with a length to breadth (L/B) ratio of about 1:1; 2 Round elliptic - a slightly circular outline with acute ends. L/B ratio not more than 2:1; 3 Elliptic - symmetrical outline with about the maximum breadth at equal distance from both ends which are slightly acute. L/B ratio not more than 3:1; 4 Ovate - outline resembling the longitudinal section of an egg. The broadest part is at the distal end (i.e., away from the root stalk); 5 Obovate - inversely ovate outline. The broadest part is at the proximal end (i.e., close to the root stalk); 6 Oblong - almost rectangular outline with sides nearly parallel and corners rounded. L/B ratio about 2:1; 7 Long oblong - oblong outline with a L/B ratio of more than 3:1; 8 Long elliptic - elliptic outline with a L/B ratio of more than 3:1; 9 Long irregular or curved
4.2.2	Storage root defects (SRD)	0 Absent; 1 Alligator-like skin; 2 Veins; 3 Shallow horizontal constrictions; 4 Deep horizontal constrictions; 5 Shallow longitudinal grooves; 6 Deep longitudinal grooves; 7 Deep constrictions and deep grooves; 8 Other
4.2.3	Storage root cortex thickness (SRT)	1 Very thin (< 1 mm); 3 Thin (1 - 2 mm); 5 Intermediate (2 - 3 mm); 7 Thick (3 - 4 mm); 9 Very thick (> 4 mm)
4.2.4.1	Predominant skin colour (PSC)	1 White; 2 Cream; 3 Yellow; 4 Orange; 5 Brownish orange; 6 Pink; 7 Red; 8 Purple-red; 9 Dark purple
4.2.4.2	Intensity predominant skin colour (IPC)	1 Pale; 2 Intermediate; 3 Dark
4.2.4.3	Secondary storage root skin colour (SSC)	0 Absent; 1 White; 2 Cream; 3 Yellow; 4 Orange; 5 Brownish orange; 6 Pink; 7 Red; 8 Purple-red; 9 Dark purple
4.2.5.1	Predominant flesh colour (PFC)	1 White; 2 Cream; 3 Dark creams; 4 Pale yellow; 5 Dark yellow; 6 Pale orange; 7 Intermediate orange; 8 Dark orange; 9 Strongly pigmented with anthocyanins
4.2.5.2	Secondary flesh colour (SFC)	0 Absent; 1 White; 2 Cream; 3 Yellow; 4 Orange; 5 Pink; 6 Red; 7 Purple-red; 8 Purple; 9 Dark purple
4.2.5.3	Distribution of secondary flesh colour (DSF)	0 Absent; 1 Narrow ring in the cortex; 2 Broad rings in the cortex; 3 Scattered spots; 4 Narrow rings in flesh; 5 Broad rings in flesh; 6 Ring and other areas in flesh; 7 In longitudinal sections; 8 Covering most of the flesh; 9 Covering all flesh

Data analysis

The SAS computer software [17] was used to interpret qualitative data that had been "converted" to quantitative data by using the scale values in **Table 2**. To classify the principal of each trait to be used in phenotyping sweet potato accessions, a principal component analysis (PCA) was performed. The PCA was conducted on the mean values recorded for 27 phenotypic traits related to vine, leaf and storage roots. The FACTOR procedure has been used to perform a variety of common factor and component analyses. The following output data provided common data-revealed factors, which are more variables required for accurate analysis. The squared multiple correlations (SMCs) for the prior communality estimates (PRIORS = SMC) are all reasonably large; thus, the loading factor does not vary significantly from the

principal component analysis. To determine the number of factors, the Scree plot (SCREE) of the eigen values was needed, as well as the PREPLOT option plots the unrotated factor pattern [17]. The PCs that had eigen values greater than 1 were selected, and those characters that had load coefficient values greater than 1.0 were considered as relevant scores for the PC, which significantly contributed to distinguishing between the genotypes as proposed by Jeffers [18].

Results and discussion

Correlation matrix using principal component analysis (PCA)

A principal component of this analysis is estimated from the correlation matrix. When variables are measured in different units, the effects of scales may affect the composition of the derived components. In such cases, it is desirable to standardize the variables. The results of the PCA were presented in **Table 3**. The characteristics of the vine resulting from the 8 traits tested, 3 main components displaying more than one eigen value with a total variability of 78.01 %. PC1, PC2 and PC3 displayed an eigen value of 3.1344, 1.8984 and 1.2081, respectively. The quantitative characteristics that contributed to PC1 are ground cover, plant type and twining. In the leaf characteristics, PC1 had 3.3813, PC2 had 2.999, and PC3 had 1.5054, with a total percentage of 78.87 %. Most of the leaf characteristics that positively contributed to PC1 are the form of the leaf lobe, the shape of the central leaf lobe, the general outline of the leaf, the number of the leaf lobe, the mature and immature colour of the leaf. The analysis demonstrated that there is a 9 eigen value for storage root characteristics. Each of the first 4 principal components had an eigen value greater than 1.0 and together accounted for 77.98 % variance in the data collection. The PC1, PC2, PC3 and PC4 registered eigen values of 2.9107, 1.8620, 1.1921 and 1.0535, respectively. Most storage root characters are contributed to PC1 except for storage root cortex thickness, storage root shape and storage root defect. Afuape *et al.* [13] reported that within the genotype group, PCA is a useful technique for identifying the plant traits that contribute most to the variation observed. PCA has helped to establish the relationship between the traits and the independent principal components that are effective for plant traits [14]. The cumulative variance of 79.00 % for the first 4 axes with the eigen values of > 1.0 indicates that the traits identified within these axes had a great influence on the phenotype of accessions and could be effectively used for selection among them. Haydar *et al.* [19] concluded that the maximum characters that contribute to the diversity of genetic material are characteristics that have the greatest value and the most positive trait vector. The principal components of eigen value with a value greater than 1.0 are suggested to be used in the factor analysis. The higher the eigen value of the variable, the more representative it is of the data. The percentage of variance explained depends on how well all the components summarize the data [20]. Placide *et al.* [21] have used PCA to analyse the heterogeneity between 54 sweet potato genotypes and found that the average variance of 77.83 % was extracted from the first 7 main component axes. In comparison, Solankey and Singh [22] stated that the first main component (PC1) accounted for 26.00 % of the total variance. The characteristics that contributed most favourably to PC1 were the length of the vine, the length of the internal vine and the length of the petiole.

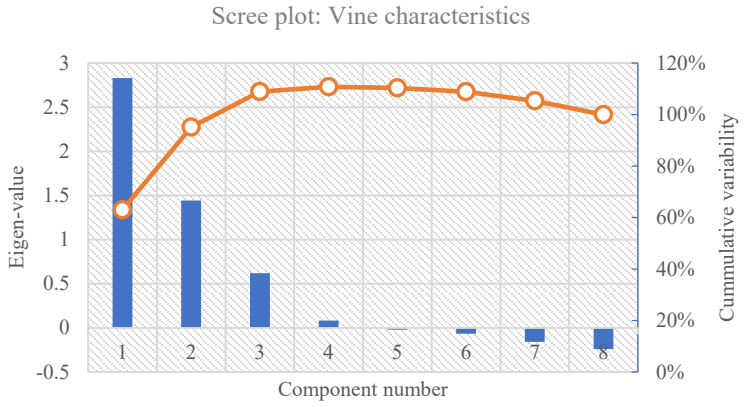
Table 3 Principal component analysis (PCA): Correlation matrix. Eigen values, the variance of each component (%) and accumulation of variation (%) values of 39 sweet potato accessions.

Principle component (PC)		Eigen values	Total of Variance (%)	Cumulative (%)
Vine characteristics				
Twining (TWN)	1	3.1344	39.18	39.18
Plant type (PTY)	2	1.8984	23.73	62.91
Ground cover (GB)	3	1.2081	51.0	78.01
Vine internode length (VIL)	4	0.6805	8.51	86.52
Vine internode diameter (VID)	5	0.5251	6.56	93.08
Predominant vine colour (PVC)	6	0.2634	3.29	96.38
Secondary vine colour (SVC)	7	0.1774	2.22	98.60
Vine tip pubescence (VTP)	8	0.1123	1.40	100
Leaf characteristics				
General leaf outline (GLO)	1	3.3813	33.81	33.81
Leaf lobe type (LLT)	2	2.9999	30.00	63.81
Leaf lobe number (LLN)	3	1.5054	15.05	78.87

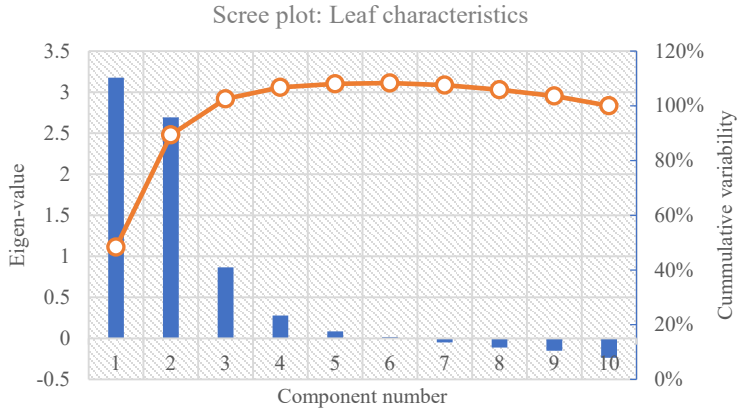
Principle component (PC)		Eigen values	Total of Variance (%)	Cumulative (%)
Shape of central leaf lobe (SCL)	4	0.6633	6.63	85.50
Mature leaf size (MLS)	5	0.5021	5.02	90.52
Abaxial leaf vein pigmentation (ALVP)	6	0.3442	3.44	93.97
Mature leaf colour (MLC)	7	0.2156	2.16	96.12
Immature leaf colour (ILC)	8	0.1831	1.83	97.95
Petiole length (PL)	9	0.1505	1.51	99.46
Petiole pigmentation (PP)	10	0.0540	0.54	100
Storage root characteristics				
Storage root shape (SRS)	1	2.9107	32.34	32.34
Storage root defects (SRD)	2	1.8620	20.69	53.03
Storage root cortex thickness (SRT)	3	1.1921	13.25	66.28
Predominant skin colour (PSC)	4	1.0535	11.71	77.98
Intensity predominant skin colour (IPC)	5	0.6518	7.24	85.23
Secondary storage root skin colour (SSC)	6	0.4622	5.14	90.36
Predominant flesh colour (PFC)	7	0.4028	4.48	94.84
Secondary flesh colour (SFC)	8	0.2910	3.23	98.07
Distribution of secondary flesh colour (DSF)	9	0.1733	1.93	100

Scree plot: Reduced correlation matrix

A Scree plot is a line plot of the eigen values of the factors or the principal components of the analysis. The scree plot was used to evaluate the number of factors to be retained in the exploratory factor analysis (FA) or principal components to be maintained in the principal component analysis (PCA) (**Figure 1**). Eigen values have clearly shown the 2 common factors that are present for all morphological characters. Two broads positive eigen values of the vine characteristics with 2.83104 (PC1) and 1.4435 (PC2) together account for 95.14 % of the common variance, which is as near as 100 % (**Figure 1(A)**). The semi-curved line was also obtained for the characteristics of the leaf (**Figure 1(B)**). Principal component one (PC1) showed eigen values were 3.1772 with high variability, 48.37 %, while PC2 had eigen value of 2.6931 contributed with 43.00 % variability, with a cumulative percentage of 89.36 %. Storage root characteristics also revealed the first 2 common axes influences (**Figure 1(C)**). The PC1 has eigen value of 2.4125 accounted for 56.67 % of the total variability and the PC2 recorded 1.4094 eigen values of approximately 33.11 % of the standardized variance with a cumulative percentage of 89.78 % of the 39 sweet potato accessions studied. A sharp bend at the third eigen value can be seen in the scree plot, confirming the previous inference. Thus, the first 2 principal components provide a sufficient description of the data for most purposes. The same trend was also shown in Laurie *et al.* [23], the scree plot displaying that all 29 characters measured played a role in explaining the variability of the 57 accessions. The first 6 factors (F1 to F6) accounted for 58.00 % of the total variability.



(A)



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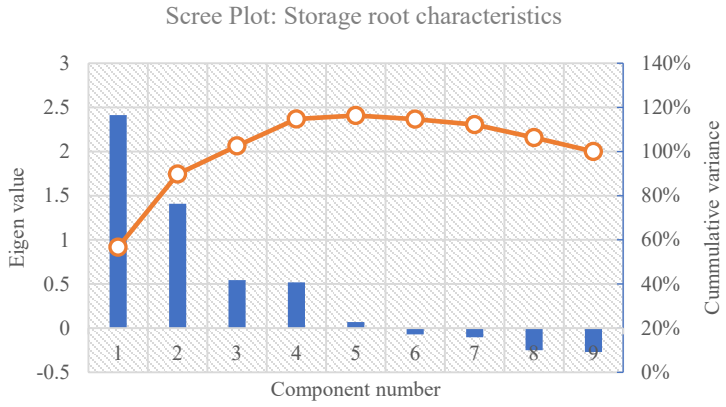

(C)

Figure 1 Scree plot of principal component analysis of sweet potato accessions indicating the relative contribution of each factor in explaining the variability (A) scree plot for vine characteristics, (B) scree plot for Leaf characteristics and (C) scree plot for storage root characteristics of 39 sweet potato accessions studied.

Factor pattern: Matrix and communalities

The consequences of variables as component functions or factors in general the factor loading matrix are shown in **Table 4**. The factor pattern is also referred to as the factor loading matrix in factor analysis. The elements of the loading matrix are called factor loadings. The principal component eigen value greater than 1.0 in **Table 3** is used for factor analysis [20]. Characteristics of the vine: Factor 1 has significant positive loads for the characteristics of the ground cover, plant type and twining with loading factors was 0.89546, 0.88423 and 0.87767, respectively. In comparison, the loading factors in Factor 2 for the ground cover and twining characteristics were negative (−0.0368 and −0.1074, respectively) while the plant type characteristics showed that the lowest loading factor value was 0.0187. Factor 3 indicates an intermediate variation of loading factors varying from 0.5334 for vine internode diameter characteristics to −0.4483 for vine internode length characteristics.

Characteristics of the leaf: Factor 1 was high loaded with a type of leaf lobe (0.94475), a central leaf lobe shape (0.93861), a general leaf shape (0.85991) and a leaf lobe number (0.71874). The characteristics of mature leaf size, petiole length and abaxial leaf vein pigmentation were negatively affected (−0.10416, −0.02738 and −0.07196, respectively). In contrast, Factor 2 was strongly loaded with mature leaf colour (0.86338), abaxial leaf vine (0.85022), petiole pigmentation (0.78943) and immature leaf colour (0.72451), while the remaining leaf characteristics were negative. Factor 3 was poor for all leaf characters (< 0.25).

Characteristics of the storage root: Factor 1 was high loaded with predominant flesh colour (0.78433), followed by predominant skin colour (0.66997) and predominant skin colour intensity (0.62396). Factor 2 was an intermediate loading factor with storage root cortex characteristics (0.59271) and intensity predominant skin colour (0.40620) while the rest was low. Factor 3, only storage root shape was the intermediate loading factor (0.58775) while the rest was poor (< 0.25). According to Yong and Pearce [24], the large and moderate value of the loading factors indicated how the characteristics were related to the factors. The loading factor value below 0.25 was considered essential and emboldened. Laurie *et al.* [23] found that predominant colour pigmentation of the vine, petiole pigmentation and immature leaf foliage were predominant characteristics associated with the second principal component (PC2).

Table 4 Loadings of common and specific factors of 27 agro-morphological characteristics of 39 sweet potato (*Ipomoea batatas* L.) accessions analysed by principal factor analysis.

Traits	Factor 1	Factor 2	Factor 3	Communality
Factor loadings: Vine characteristics				
GB	0.8954	−0.0368	0.1275	0.8194
PTY	0.8842	0.0187	0.0014	0.7822
TWN	0.8776	−0.1074	0.3054	0.8751
VTP	0.4743	0.3388	−0.1313	0.3570
SVC	−0.07938	0.8338	0.0687	0.7063
PVC	0.0548	0.7597	0.0564	0.5833
VID	−0.2330	−0.1525	0.5334	0.3622
VIL	0.4340	−0.1407	−0.4483	0.4092
Factor loadings: Leaf characteristics				
LLT	0.94475	−0.13487	0.04068	0.9123
SCL	0.93861	−0.14968	0.07542	0.9090
GLO	0.85991	−0.09660	−0.06529	0.7530
LLN	0.71874	−0.07325	0.07615	0.5277
MLC	0.21471	0.86338	−0.04540	0.7935
ALVP	−0.07196	0.85022	0.16780	0.7562
PP	0.07602	0.78943	0.04408	0.6309
ILC	0.28117	0.72451	−0.01988	0.6043
PL	−0.02738	−0.02530	0.64138	0.4127
MLS	−0.10416	−0.14415	0.63541	0.4353
Factor loadings: Storage root characteristics				
PFC	0.78433	0.27568	0.04069	0.6928
PSC	0.66997	0.07185	0.12003	0.4684
IPC	0.62396	0.40620	0.00219	0.5543

Traits	Factor 1	Factor 2	Factor 3	Communality
SFC	0.56571	−0.08812	−0.22752	0.3795
SRD	−0.54169	0.03848	0.16781	0.3230
SRT	0.11046	0.59271	0.17884	0.3954
DSF	0.40123	−0.53184	0.10169	0.4541
SSC	0.40506	−0.70957	0.24567	0.7279
SRS	−0.09213	0.12789	0.58775	0.3702

Extraction method: Principal component analysis

The plot of factor pattern between factors

Figures 2 - 4 display the graphical plot of the rotated factor loadings in the different characteristics of the vine, leaf and storage root. It is clear that the traits of twining, plant type, ground cover, vine tip pubescence and vine internode length were closed to Factor 1, while the characteristics of primary and secondary vine colour were regulated by Factor 2 (**Figure 2**). Meanwhile, for the leaf characteristics, the general leaf outline, the type of leaf lobe, the number of leaf lobes and the shape of the central leaf lobe were grouped together, which is influenced by Factor 1. Traits of mature leaf size and petiole length were grouped together, while the others were similar to Factors 2 and 3 (**Figure 3**). Characteristics of predominant and intensity storage root skin colour and predominant and secondary flesh colour were closely grouped into Factor 1. Secondary storage root skin colour was significantly controlled by Factor 2 and the distribution of secondary flesh colour was controlled by Factor 3 (**Figure 4**).

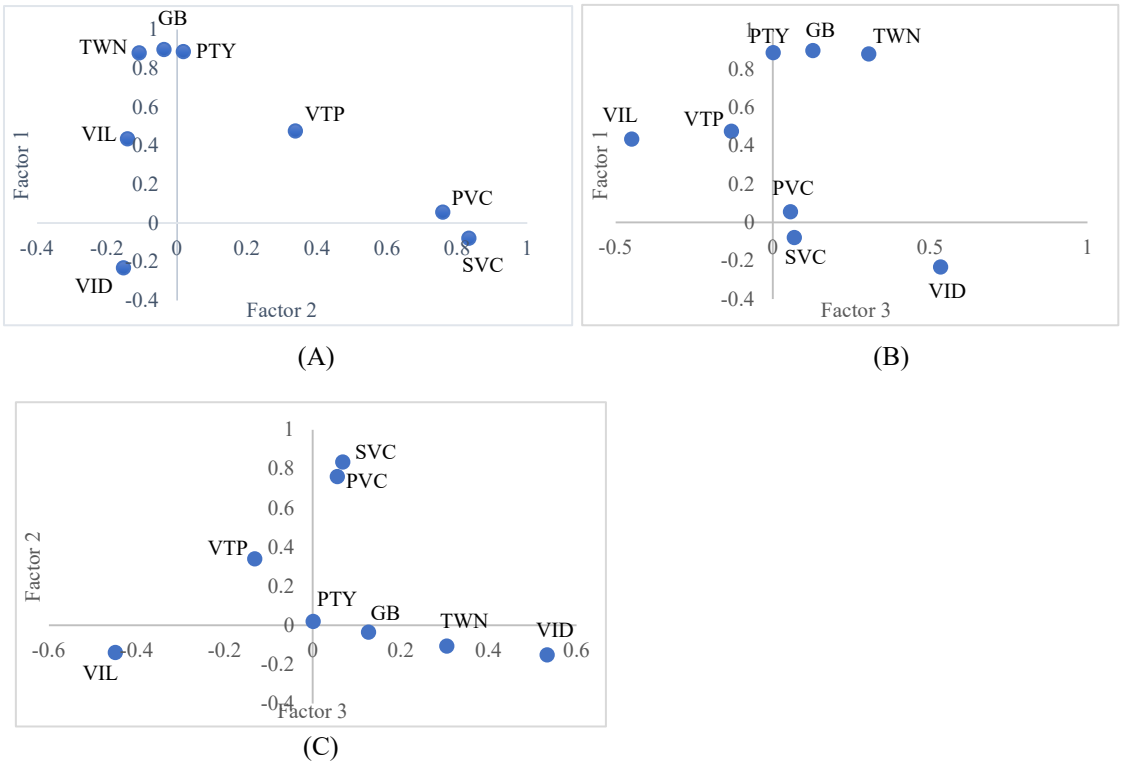

Figure 2 Graphical plot representation of rotated factor loadings in different traits of vine characteristics (A) plot of factor pattern for factor 1 and factor 2, (B) plot of factor pattern for factor 1 and factor 3, and (C) plot of factor pattern for factor 2 and factor 3 of 39 sweet potato accessions studied.

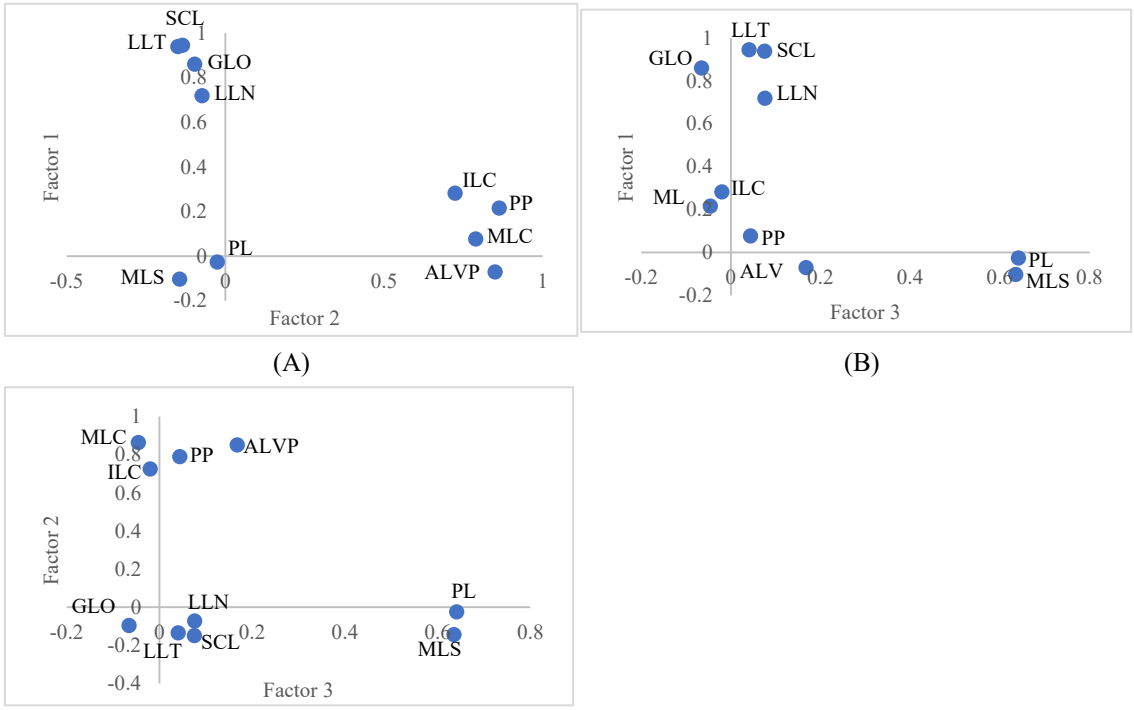

Figure 3 Graphical plot representation of rotated factor loadings in different traits of leaf characteristics. (A) the plot of factor pattern for factor 1 and factor 2, (B) plot of factor pattern for factor 1 and factor 3 (C) plot of factor pattern for factor 2 and factor 3 of 39 sweet potato accessions studied.

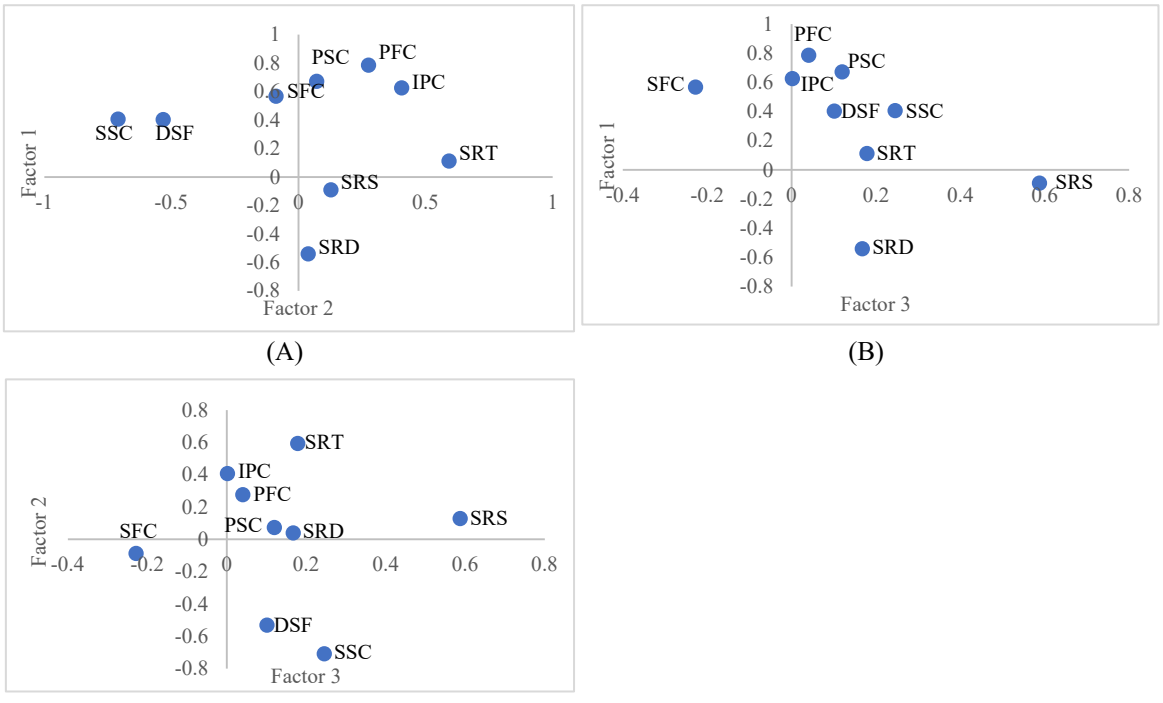

Figure 4 Graphical plot representation of rotated factor loadings in different traits of storage root characteristics (a) Plot of Factor Pattern for Factor1 and Factor2 (b) Plot of Factor Pattern for Factor1 and Factor3 (c) Plot of Factor Pattern for Factor2 and Factor3 of thirty-nine sweet potato accessions studied.
Note: **Figures 2, 3** and **4** refer to the abbreviation for the full description of the agro-morphological characteristics.

The results revealed that the sweet potatoes genotypes could be divided into 3 classes. Group 1 consists of 18 genotypes. MIb2, MIb11, MIb12, MIb14, MIb16, MIb17, MIb24, MIb25, MIb26, MIb28, MIb29, MIb30, MIb37, MIb38, MIb41, MIb42, MIb44 and MIb47 were mostly showed a bushy type of plant, the majority of which were very twining, strongly spreading (> 250 cm) and completely covered with ground cover (90.00 %). The general outline of the leaves was cordate and hastate, with 3 to 5 lateral lobes in number. The colour of the stored root skin ranged from white, cream to yellow to brownish, while the colour of the flesh ranged from cream to yellow to pale orange.

Group 2, approximately 12 genotypes consist of MIb1, MIb3, MIb8, MIb9, MIb10, MIb19, MIb22, MIb23, MIb27, MIb35, MIb36 and MIb46. They were small to medium mature leaf size and short (10 - 20 cm) petiole length with green predominant and secondary vine colour. The storage root's dominant skin colour ranged from pink to dark purple, while the flesh was cream to light yellow and some pigmented with anthocyanin.

In Group 3, there are 3 genotypes were grouped together. MIb20, MIb31, MIb32, MIb33, MIb34, MIb39, MIb40, MIb43 and MIb45 were slightly twining, semi-erect to spreading, short vine internode length, and green vine colour was the plant habit. The outline of the leaf shape was cordate, hastate, and lobed with 3 to 5 lobes as well. Most of the leaves were green. The skin colour of the storage root was brownish to pink to dark purple and the flesh colour was cream and strongly pigmented with anthocyanin. A similar result was found by Tairo *et al.* [25], where a total of 136 accessions of sweet potatoes were divided into 3 major classes. Solankey and Singh [22] discovered that 20 sweet potato genotypes had a genetic association, suggesting a genetic relationship between accessions where the sweet potato genotypes studied have a narrow genetic basis due to a high level of genetic erosion and selection pressure by farming communities. It might be due to farmers using the same parents and seed source for crop production. Thus, the 20 sweet potato genotypes were divided into 2 main classes. In other studies, the cluster analysis of 116 genotypes resulted in 12 clusters [26].

Conclusions

The results of the PCA identified 3 main components for each vine, leaf and root trait explained more than 78.00 % of the total variance in genotypes. The main characteristics of the vines which have contributed to the diversity are the ground cover, the plant type, and the twining, while the leaf characteristics are the type of leaf lobe, the shape of the central leaf lobe, the general leaf shape, the number of the leaf lobe and the mature and immature leaf colour. Most root characters are contributed to the PC except for storage root cortex thickness, storage root type and defect. Of the 39 sweet potato genotypes, it can be classified into 3 groups based on total variation; the first group consists of 18 genotypes which were clustered based on major characteristics; the second group consists of 12 genotypes and the remaining genotypes fall into the third group. The results of this study may be useful in the breeding program for the improvement of varieties as well as the development of more genetic variations in sweet potatoes, especially in Malaysia.

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