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The Relationship of Sweet Potato Germplasm Based on Morphological Characters

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Abstract. *Information about the morphological and genetic characteristics of sweet potato (Ipomoea batatas) is important in the variety development program. This experiment aimed to determine the diversity and genetic relationship of sweet potato accessions from NTT based on morphological character data. The research was carried out at Kendalpayak Research Station, Malang, East Java from April - September 2019. The materials used were seventy-one sweet potato germplasm from the ILETRI collection (collected from NTT). Each accession was planted on a 1 m × 5 m plot size, with a spacing of 100 × 20 cm (single row). Fertilization was carried out using a dose of "100 kg urea + 100 kg SP36 + 200 kg KCl ha-1". The observed characters were the vines length, growth type, internode length, leaf length, leaf width, leaf size, leaf bone color, leaf shape, leaf characteristics, lobes number, lobe shape, mature leaf color, shoot color, pigmentation of petiole, young stems pigmentation (dominant and secondary color), young leaves feathers, tuber skin color, tuber flesh color, weight of canopy, number of tubers perplot, weight of tubers perplot, number and weight of tubers perplot. Cluster analysis was carried out using the Minitab 17 program. There was morphological diversity in seventy-one accessions of sweet potato germplasm from NTT. Principal component analysis resulted in seven main components with the proportion of diversity 76.3%. cluster analysis, seventy-one accessions of sweet potato germplasm were divided into fifteen accession groups on the basis of 80% degree. Characteristics of shoot color, mature leaf color, leaf size, petiole pigmentation, and leaf bone color contributed greatly to the total diversity.*

Keywords: *accession, cluster analysis, diversity, sweet potato*

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INTRODUCTION

Sweet potato (*Ipomoea batatas*) is one of the most important food crops (1. wheat, 2. rice, 3. corn, 4. potato, 5. barley, 6. cassava, 7. sweet potato) (FAOSTAT, 2012; Wera et al., 2014). According to Ji et al. (2015), the nutrients contained in sweet potatoes are quite complete, with high carbohydrate content and low glycemic levels. Aywa et al. (2013) stated that they are a source of vitamin A and micronutrients (Ca, Fe, K, and Zn), also antioxidants. Sweet potato is also a source of starch, so it is suitable as a raw material for the food industry (Zhao et al., 2015; Trancoso-Reyes et al., 2016). Therefore, in Indonesia, sweet

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potatoes have the opportunity and prospects to industrial raw materials and guarantee food security.

Sweet potato belongs to the Convolvulaceae family which has a wide genetic diversity. According to Grüneberg et al., (2015) and Wadl et al., (2018), the wide genetic diversity is due to the natural genetic composition of plants classified as hexaploid, the ability to flower, and the incompatibility of plants. High genetic diversity requires good management. Genetic diversity management begins with characterization, evaluation, and documentation, also conservation and rejuvenation (Trustinah & Iswanto, 2014).

Sweet potato germplasm needs to be characterized in order to obtain important trait information to be used as a genetic source that can be utilized in plant breeding programs, as well as to identify duplicated accessions, and structuring populations for conservation purposes. Therefore, in genetic development, conservation, collection, and utilization of germplasm, characterization can be used as a good guideline (Norman et al. 2014).

Morphological and agronomic characterizations were used to analyze diversity in germplasm collections (Ngailo et al., 2016). Principal component analysis (PCA) and cluster analysis can be used to analyze diversity in germplasm collections. Afuape et al. (2011), said that to identify the character that characterizes a variety, PCA is used. This is a way to find out the contribution of a character to diversity. Furthermore, according to de Andrade et al. (2017) and Wadl et al. (2018), information obtained from the analysis can be used as a reference for determining kinship and potential genetic variations that can be produced, so it will facilitate the selection of sweet potato clones with the desired advantages.

However, little research has been done on diversity of ILETRI sweet potato accession, especially collection from NTT exploration. Therfore, this study aimed to obtain information on the morphological and agronomic diversity of sweet potato germplasm (exploration from NTT) using analysis of principal component analysis and cluster analysis.

MATERIALS AND METHODS

The research was carried out at Kendalpayak Research Station, Malang, East Java from April to September 2019. The material used was seventy-one sweet potato accessions from NTT (ILETRI germplasm collection).

Each accession was planted on a 1 m × 5 m plot size and with spacing 100 × 20 cm (single row). Fertilization used a dose of 100 kg urea + 100 kg SP36 + 200 kg KCl ha-^{1}, given entirely at the time of planting. Except Urea given twice, at the time of planting and 1.5 months after planting.

Weeding was done at four, seven, and ten weeks after planting. The irrigation was carried out once every 2-3 weeks to prevent dryness or lack of water. Control of pests and diseases using pesticides. Tubers were harvested four months after planting.

The variables observed included: the vines' length (cm), plant type, length of internode (cm), length and width of leaf, leaf size, leaf color, leaf shape, characteristics of leaf, lobes number, lobe shape, petiole length, mature leaf color, shoot color, Petiole pigmentation , young stems pigmentation (dominant and secondary color), young leaves of feathers, tuber skin color, tuber flesh color, canopy weight per plot, number and the weight of tubers per plot, number of tubers per plant, weight of tubers per plant, and weight per tuber. The code and the abbreviation for each character are presented in table 2 and table 3.

PCA was used to identify the contribu-

tion the diversity of morphological characters. Furthermore, Minitab 17 program was used for cluster analysis of main component values.

Table 1. Accession of sweet potato germplasm used in the study

No. Accession	Origin	Tubers Color		No. Accession	Origin	Tubers Color	
		Skin	Flesh			Skin	Flesh
MLGI 1440	Sumba Timur, NTT	Krem	P O	MLGI 1479	Kupang, NTT	M4	P
MLGI 1441	Sumba Timur, NTT	M4	K2	MLGI 1480	TTS, NTT	Krem	K1 O1
MLGI 1442	Sumba Timur, NTT	M4	P	MLGI 1481	TTS, NTT	Krem	K1 O1
MLGI 1443	Sumba Timur, NTT	M4	K3	MLGI 1482	TTS, NTT	Krem	K3 O
MLGI 1444	Sumba Timur, NTT	M4	K2	MLGI 1483	TTS, NTT	M3	P
MLGI 1445	Sumba Timur, NTT	Krem	K1 O1	MLGI 1484	TTS, NTT	Krem	K2 O2
MLGI 1446	Sumba Timur, NTT	M4	K1	MLGI 1485	TTS, NTT	M3	P
MLGI 1447	Sumba Timur, NTT	M4	K2	MLGI 1486	TTU, NTT	M4	P
MLGI 1448	Sumba Timur, NTT	M5	K2	MLGI 1487	TTU, NTT	M2	P
MLGI 1449	Sumba Barat, NTT	Krem	P	MLGI 1488	Belu, NTT	M3	P
MLGI 1450	Sumba Barat, NTT	M4	K1	MLGI 1491	Sikka, NTT	Krem	K2
MLGI 1451	Sumba Barat, NTT	M5	K3	MLGI 1492	Ende, NTT	Krem	K2 O2
MLGI 1452	Sumba Barat Daya, NTT	Krem	K2 O	MLGI 1493	Ende, NTT	Krem	K2 O2
MLGI 1453	Sumba Barat Daya, NTT	Krem	K3	MLGI 1494	Nagekeo, NTT	Krem	O3
MLGI 1454	Sumba Barat Daya, NTT	Krem	P	MLGI 1495	Ngada, NTT	M5	K1
MLGI 1455	Sumba Barat Daya, NTT	Krem	P	MLGI 1496	Ngada, NTT	Krem	K2
MLGI 1458	Sumba Barat Daya, NTT	M2	P	MLGI 1497	Ngada, NTT	M2	K1
MLGI 1459	Sumba Barat Daya, NTT	Krem	P	MLGI 1498	Ngada, NTT	Krem	K2
MLGI 1460	Sumba Barat Daya, NTT	Krem	K2	MLGI 1499	Sumba Barat, NTT	Krem	K2 O2
MLGI 1461	Sumba Barat Daya, NTT	Krem	P	MLGI 1500	Sumba Barat, NTT	M6	U6
MLGI 1462	Sumba Barat, NTT	Krem	K3	MLGI 1501	Sumba Barat, NTT	M3	K1
MLGI 1463	TTU, NTT	Krem	P	MLGI 1502	Sumba Barat, NTT	M3	K1
MLGI 1464	TTU, NTT	Krem	K2 O	MLGI 1503	Sumba Barat, NTT	M6	U6
MLGI 1465	TTU, NTT	M4	P	MLGI 1504	Sumba Barat, NTT	M5	P
MLGI 1467	TTU, NTT	M1	P	MLGI 1505	Sumba Barat, NTT	Krem	P
MLGI 1468	Belu, NTT	M5	P	MLGI 1506	Sumba Barat Daya, NTT	Krem	P
MLGI 1469	Belu, NTT	M5	P	MLGI 1507	Sumba Barat Daya, NTT	Krem	K2 O3
MLGI 1470	Belu, NTT	M5	P	MLGI 1508	Sumba Barat, NTT	M6	U5
MLGI 1471	Belu, NTT	M5	P	MLGI 1509	Sumba Barat, NTT	M5	P
MLGI 1472	Belu, NTT	M5	K2	MLGI 1510	Sumba Barat Daya, NTT	M2	P
MLGI 1473	TTS, NTT	M5	P	MLGI 1511	Sumba Barat Daya, NTT	Krem	O3
MLGI 1474	TTS, NTT	M3	P	MLGI 1512	Sumba Barat Daya, NTT	M6	U6
MLGI 1475	TTS, NTT	M4	P	MLGI 1513	Sumba Barat Daya, NTT	M3	P
MLGI 1476	TTS, NTT	Krem	P	MLGI 1514	Sumba Timur, NTT	M5	P
MLGI 1477	TTS, NTT	Krem	P	MLGI 1515	Sumba Timur, NTT	M6	P
MLGI 1478	Kupang, NTT	Krem	P				

Note: U= purple; M= red; O= orange; K= yellow; Krem= cream; and P= white,
1 = very pale; 2 = slightly pale; 3 = pale; 4 = bright; 5 = slightly dark; 6 = dark; and 7 = very dark

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Table 2. Quantitative characters observed in the study

Acronym	Trait	Score Code
VL	Vines Length (cm)	Direct measurement (5 plants)
LL	Leaf Length (cm)	Direct measurement (5 plants)
LW	Leaf Width (cm)	Direct measurement (5 plants)
CW	Canopy Weight per plot (kg)	Direct measurement
NT	Tuber Numbers per plot	Direct measurement
NTP	Tuber Numbers per plant	Direct measurement (5 plants)
WT	Tuber Weight per plot (kg)	Direct measurement
WTP	Tuber Weight per plant (g)	Direct measurement (5 plants)
WPT	Weight per tuber	Direct measurement (5 plants)

Table 3. Qualitative characters observed in the study

Acronym	Trait	Score Code
PT	Type of Plant	type 3 = erect; 5 = semi-erect; 7 = spreading; and 9 = extremely spreading
IL	Internode Length	1 = very short; 3 = short; 5 = intermediate; 7 = long; dan 9 = very long
MLS	Mature Leaf ize	3 = small; 5 = medium; 7 = large; 9 = very large
ALVP	Abaxial Leaf Vein Pigmentation	1 = yellow; 2 = green; 3 = purple spot in the base of main rib; 4 = purple spot in several veins; 5 = main rib partially purple (<1/3); 6 = main rib mostly or totally purple (<2/3); 7 = All veins partially purple partially purple; 8 = All veins mostly or totally; 9 = Lower surface and veins totally purple
LS	Mature Leaf Shape	1= rounded; 2= reniform (kidney-shaped); 3= cordate (heart-shaped); 4= triangular; 5= hastate; 6= lobed; dan 7 = almost divided
LLT	Leaf Lobes Type	0=no lateral lobes; 1= very slight; 3= slight; 5= moderate; 7= deep; dan 9= very deep
LLN	Leaf Lobes Number	0= no lobes; 1= 1 lobes; 3= 3 lobes; 5= 5 lobes; 7= 7 lobes; dan 9= 9 lobes
SCL	Central Lobes Shape	0=absent; 1=toothed; 2=triangular; 3=semi-circular; 4=semi-elliptic; 5=elliptic; 6=lanceolate; 7=oblanceolate; 8=linear (broad); 9=linear (narrow)
PL	Petiole Length	1= very short; 3= short; 5= intermediate; 7= long; dan 9= very long
MLC	Mature Leaf Color	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; dan 9= purple both surface
ILC	Immature Leaf Color	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; dan 9= purple both surface
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 spot troughout petiole; 6= green with purple strips; 7=purple with green near leaf; 8= some petioles purple; others green; and 9= totally or mostly purple
PVC	Predominant Vine Color	1= green; 3= green with few purple spots; 4= green with many purple spots; 5= green with many dark purple spots; 6= mostly purple; 7= mostly dark purple; 8= totally purple; dan 9= totally dark purple

SVC	Secondary Vine Color	0= absent; 1= green base; 2= green tip; 3= green nodes; 4= purple base; 5= purple tip; 6= purple nodes; dan 7= other
VTP	Vine Tip Pubescence	0= absent; 3= sparse; 5= moderate; 7= heavy
TSC	Tubers Skin Color	M= red; Krem= cream; O= orange; K= yellow; P= white; U= purple; 1 = very pale; 2 = slightly pale; 3 = pale; 4 = bright; 5 = slightly dark; 6 = dark; 7 = very dark
TFC	Tuber Flesh Color	M= red; Krem= cream; O= orange; K= yellow; P= white; U= purple; 1 = very pale; 2 = slightly pale; 3 = pale; 4 = bright; 5 = slightly dark; 6 = dark; 7 = very dark

RESULTS AND DISCUSSION

Estimation of sweet potato germplasm diversity based on morphological characters using the coefficient of variant (CV) of each character observed shows the level of difference between the observed accessions (Hamida & Parnidi 2019). The results of observations of quantitative characters (Table 4) and qualitative characters (Table 5) show a fairly large coefficient of diversity. In quantitative character, diversity ranges from 21.18% to 81.92%. Characters such as width and length of leaves, length of vine, weight per tuber, and canopy weight had a CV value of less than 50% while the character of the number and weight of tubers had a CV value of more than 50%. CV values between 13.26% (leaf size) to 93.87% (vine tip pubescence) were indicated by qualitative characters.

Table 4. Qualitative characters observed in the study

Quantitative Characters	Min	Max	Average±SD	CV
Vines Length (cm)	89.67	465	241.47±80.04	33.15
Leaf Length (cm)	7.667	19.5	11.113±2.76	24.84
Leaf Width (cm)	7.833	20.667	12.001±2.54	21.18
Canopy Weight per plot (kg)	1.6	13.3	5.668±2.30	40.52
Number of Tubers per plot	3	72	26.54±18.67	70.34
Number of Tubers per plant	0.2	5.75	2.15±1.46	67.84
Weight of Tubers per plot (kg)	0.1	12.9	3.763±3.08	81.92
Weight of Tubers per plant (g)	0.0091	0.9667	0.3076±0.25	81.07
Weight per tuber	25	300	132.29±46.33	35.02

Table 5. Qualitative characters observed in the study

Qualitative Characters	Persentage (%)	CV (%)
Plant Type		17.47
5.Semi-erect	11.27	
7.Spreading	47.89	
9.Extremely spreading	40.85	
Internodes Length		26.65
3.Short	52.11	
5.Intermediate	46.48	
7.Long	1.41	
Mature Leaf Size		13.26
3.Small	1.41	
5.Medium	87.32	
7.Large	11.27	
Abaxial Leaf Vein Pigmentation		49.23

2.Green	33.80	
3.purple spot in the base of main rib	5.63	
4.purple spot in several veins	9.86	
5.main rib partially purple (<1/3)	7.04	
6.main rib mostly or totally purple (<2/3)	9.86	
8.All veins partially purple partially purple	28.17	
9.Lower surface and veins totally purple	8.45	
Mature Leaf Shape		28.97
2.Reniform (kidney-shaped)	282	
3.Cordate (heart-shaped)	28.17	
4.Triangular	28.17	
5.Hastate	9.86	
6.Lobed	30.99	167
Leaf Lobes Type		90.36
0.no lateral lobes	2.82	
1.very slight	56.34	
3.Slight	25.35	
5.Moderate	5.63	
7.Deep	7.04	
9.very deep	2.82	
Leaf Lobes Number		67.73
no lobes	2.82	
1 lobes	42.25	
3 lobes	32.39	
5 lobes	19.72	
7 lobes	2.82	
Shape of Central Lobes		79.42
0.Absent	2.82	
1.Toothed	40.85	
2.Triangular	19.72	
3.semi-elliptic	25.35	
5.Elliptic	5.63	
7.Oblanceolate	1.41	
8.Linear	4.23	
Petiole Length		28.62
1.very short	4.23	
3.Short	74.65	
5.Intermediate	21.13	
Mature Leaf Color		27.17
1.yellow-green	1.41	
2.Green	84.51	
3.green with purple edge	11.27	
5.green with purple veins on upper surface	2.82	
Immature Leaf Color		58.78
1.yellow-green	15.49	
2.Green	2.82	
3.green with purple edge	45.07	
5.green with purple veins on upper surface	7.04	
6.slightly purple	11.27	
7.mostly purple	14.08	
9.purple both surface	8.45	
Petiole Pigmentation		58.33
1.Green	26.76	
2.green with purple near stem	1.41	
3.green with purple near leaf	9.86	
4.green with purple at both ends	30.99	
5.green with purple spot troughout petiole	9.86	
6.green with purple strips	14.08	
7.purple with green near leaf	1.41	
9.totally or mostly purple	5.63	
Predominant Vine Color		81.38
1.Green	66.20	
3.green with few purple spots	5.63	

4.green with many purple spots	16.90	
5.Green with many dark purple spots	5.63	
6.mostly purple	2.82	
7.mostly dark purple	2.82	
Secondary Vine Color		89.47
0.Absent	40.85	
1.green base	1.41	
2.green tip	4.23	
4.purple base	4.23	
5.purple tip	1.41	
6.purple nodes	47.89	
Vine Tip Pubescence		93.87
0.Absent	49.30	
3.Sparse	33.80	
5.Moderate	7.04	
7.Heavy	9.86	

Trustinah & Iswanto (2014) stated that accession classification involving several characters will be more informative using multivariate analysis (principal component analysis and cluster analysis). The principal component Analysis was conducted to determine the diversity of contributing characters (Hetharie et al., 2018). The study on the diversity of morphological characteristics of sweet potatoes using principal component analysis has been carried out by Rahajeng et al. (2018) which got 83.2% diversity that can be explained by five main components. Five main components that can explain the diversity of 96.8% were obtained from the research of Ishaq et al. (2019). While in the research of Mustamu et al. (2021) found three main components that were able to explain the variation of 90.19% of the total diversity among the accessions tested.

Table 6. Analysis of principal component of sweet potato germplasm accession

Variable	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7
VL	0.164	0.057	-0.145	-0.521	0.155	-0.145	-0.002
LL	0.225	0.218	0.343	0.102	0.148	0.001	0.051
LW	0.186	0.199	0.397	0.051	0.124	-0.025	-0.003
CW	0.024	-0.189	0.188	-0.173	0.224	0.331	-0.25
NT	-0.35	0.135	0.046	0.011	0.287	-0.024	0.104
NTP	-0.373	0.139	0.05	0.022	0.179	-0.031	0.114
WT	-0.376	0.124	0.058	-0.01	0.271	-0.02	-0.033
WTP	-0.387	0.123	0.055	-0.01	0.18	-0.022	-0.043
WPT	-0.226	0.028	-0.008	-0.039	0.116	0.079	-0.492
PT	0.156	0.076	-0.045	-0.49	0.145	-0.29	-0.048
IL	0.076	0.128	-0.087	-0.389	0.246	-0.112	0.021
MLS	0.208	0.213	0.343	0.108	0.087	-0.026	0.043
ALVP	0.185	-0.269	-0.094	0.126	0.408	-0.068	0.032
LS	-0.023	-0.397	0.163	-0.029	-0.077	-0.131	-0.106
LLT	-0.076	-0.351	0.312	-0.163	0.004	-0.076	0.137
LLN	-0.142	-0.343	0.285	-0.109	-0.045	-0.039	-0.124
SCL	-0.114	-0.372	0.29	-0.105	0.015	-0.012	0.19
PL	0.166	0.14	0.268	0.184	0.007	-0.278	-0.086

MLC	0.033	-0.16	-0.127	0.094	0.073	-0.392	0.406
ILC	0.227	0.009	0.052	-0.176	-0.041	0.446	-0.158
PP	0.132	-0.184	-0.2	0.287	0.352	0.011	-0.133
PVC	0.078	-0.203	-0.312	0.098	0.154	0.173	0.039
SVC	0.18	-0.077	0.019	0.19	0.46	-0.022	-0.102
VTP	-0.011	-0.04	-0.057	0.114	-0.156	-0.521	-0.594
Eigenvalue	5.38	3.80	2.99	2.24	1.73	1.13	1.05
Proportion	22.4	15.8	12.5	9.3	7.2	4.7	4.4
Cumulative	22.4	38.2	50.7	60.1	67.3	72.0	76.3

Note: PC = principal components

In this study, the results of PCA showed that the observed characters have been reduced to seven main components that have an eigenvalue of more than one, and 76.3% of the diversity of the tested accessions could be explained (Table 5.). PC 1 with an eigenvalue of 5.38 contributed to 22.4% of the total diversity, PC 2 contributed to 38.2% of the total diversity with an eigenvalue of 3.80, 50.7% of the total diversity is contributed by PC 3 which has an eigenvalue of 2.99, PC 4 with eigenvalue of 2.24 contributed to 60.1% total diversity, PC 5 with eigenvalue of 1.73 contributed to 67.3% total diversity, PC 6 with eigenvalue of 1.13 contributed to 72.0% total diversity, and PC 7 with eigenvaluevalue of 1.05 contributed to 76.3% of the total variance among the seventy-one accessions tested.

Haydar et al. (2007), stated that the characters with highest and positive eigenvalues are the characters that contribute the most to the diversity of genetic material. In PC 1, the characters that greatly contributed to the diversity were immature leaf color, leaf length, and leaf size. In PC 2 the diversity was influenced by leaf length. In PC 3, the character contributes to the diversity of leaf width, leaf length, and leaf size. In PC 4, the character that affects the diversity is petiole pigmentation. In PC 5, the Abaxial Leaf Vein Pigmentation character contributed to the diversity. In PC 6 immature leaf color affects the diversity. While mature leaf color is a characteristic that contributes to diversity in PC 7 (Table 6).

The results of Prayudha et al. (2019) obtained the Predominant vine color, the type of lobe, the lobes number, the leaf lobes shape, the type of plant, the size and length of the petiole, tubers per plant number, the tuber length, the tuber diameter, the internodes diameter, and internodes length have major contributions to the diversity of 11 purple sweet potato genotypes. Research by Lestari & Julianto (2020) showed that number of tubers, tuber weight, tuber dry matter, biomass dry matter, and harvest index were the characteristics that contributed greatly to the diversity of the 13 sweet potato genotypes.

Subsequently, seven principal component factors were used for cluster analysis. Seventy-one accessions of sweet potatoes were divided into fifteen groups according to the variable that played a role in the forming factor (Figure 1 and Table 7).

Based on the average character of each cluster presented in Table 7, of the 15 clusters formed, cluster/group 10 showed the best characters compared to other clusters. Group 10 consisting of 4 accessions (MLGI 1494, MLGI 1507, MLGI 1510, and MLGI 1514) had characteristics of the highest number and weight of tubers, with compact plant type, this type of character is the character that is much favored by farmers. Meanwhile, cluster

13, which consisted of two accessions (MLGI 1442 and MLGI 1479), had the lowest number and weight of tubers and had spreading to extremely spreading plant type.

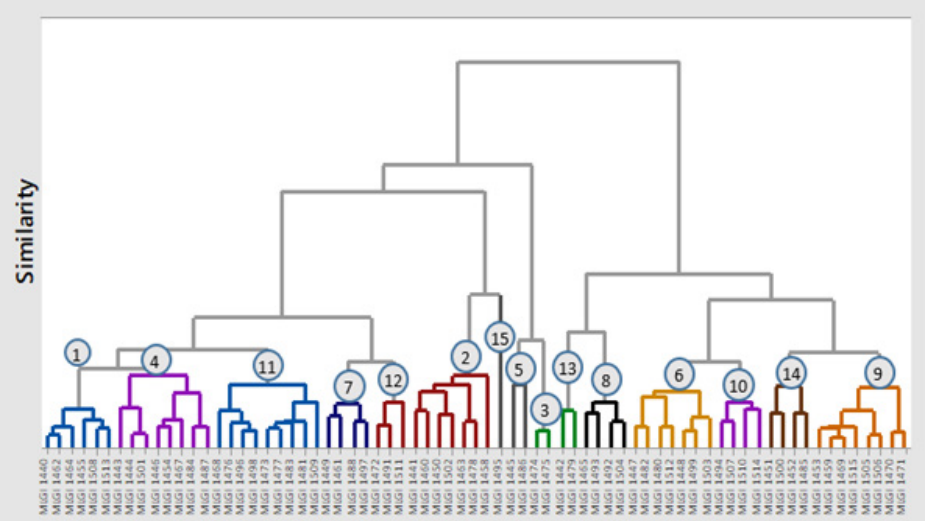

Figure 1. Grouping of seventy-one accessions of sweet potato germplasm

Table 7. The grouping and the average character of seventy-one sweet potato accessions

Variable/ klp	1/6	2/7	3/2	4/8	5/2	6/7	7/4	8/4	9/8	10/4	11/9	12/3	13/2	14/4	15/1
VL	232.39	330.17	139.25	258.08	391.17	188.10	310.50	139.75	182.09	100.08	248.52	320.44	457.50	221.92	338.00
LL	12.53	9.86	12.75	10.40	9.83	9.88	12.42	10.04	11.40	10.13	13.30	13.33	8.50	9.71	10.33
LW	14.17	11.02	11.00	10.75	12.17	11.24	13.00	10.83	12.17	11.83	13.50	13.33	9.42	11.92	10.83
CW	6.40	6.40	4.40	6.48	6.15	4.93	5.78	4.13	7.01	6.08	4.82	4.07	5.45	5.15	4.70
NT	18.50	37.71	23.50	37.50	20.50	42.57	21.00	35.00	13.88	51.25	12.22	19.33	9.00	23.50	3.00
NTP	1.46	3.00	1.85	2.85	1.16	3.41	1.60	2.51	1.04	4.52	1.29	1.45	0.53	2.48	0.50
WT	2.28	6.86	5.40	5.08	1.45	6.43	2.88	4.05	1.48	7.88	1.00	1.73	0.90	4.55	0.90
WTP	0.18	0.55	0.42	0.38	0.08	0.52	0.22	0.28	0.11	0.70	0.11	0.13	0.05	0.48	0.15
WPT	123.15	184.02	228.35	132.65	50.34	152.70	133.60	113.74	101.80	153.37	83.72	83.62	100.00	189.06	300.00
PT	7	9	6	9	9	7	9	6	7	5	8	9	9	7	9
IL	4	4	3	4	4	4	5	3	3	3	4	5	6	4	5
MLS	6	5	5	5	5	5	6	5	5	5	6	6	4	5	5
ALVP	5	5	3	4	7	3	7	6	5	5	5	3	6	3	8
LS	4	5	4	5	5	4	5	5	5	6	4	3	4	5	3
LLT	2	2	1	3	3	1	6	1	2	6	2	1	1	3	1
LLN	2	3	2	3	3	2	4	2	3	6	2	1	1	3	3
SCL	2	2	1	3	3	1	5	3	3	7	2	1	1	3	1
PL	3	3	3	3	3	3	4	3	4	4	4	4	2	3	3
MLC	2	2	2	2	3	2	2	2	2	2	2	2	2	2	3
ILC	6	3	3	4	6	3	3	3	4	2	5	4	8	6	6
PP	3	4	4	3	4	4	6	7	5	3	4	2	5	2	5
PVC	2	1	2	1	4	2	5	5	2	1	2	1	4	3	4
SVC	4	2	3	3	2	2	5	4	5	3	3	2	6	2	6
VTP	2	1	6	2	5	3	1	4	3	0	1	2	0	1	3

CONCLUSION

From the research above, it can be concluded that the diversity of 24 observational variables with a proportion of diversity of 76.3% can be explained by seven main component factors. Based on cluster analysis, seventy-one accessions of sweet potato germplasm were divided into 15 groups with 80% similarity. The characteristics like color of immature leaf, the color of mature leaf, the size of leaf, pigmentation of petiole, and abaxial leaf vein pigmentation contributed the most to the total diversity.

AUTHOR CONTRIBUTION

Data collected, analyzed and written by W.R. Research designed and monitored by F.C.I. and J.R.

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CONFLICT OF INTEREST

All authors have no conflict of interest.

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