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Morphological Variabilities and Identification of Yam (*Dioscorea* spp.) Genotypes from Major Growing Regions in Tanzania

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Abstract

Yam (*Dioscorea* spp.) is a vegetatively propagated crop that belongs to the family Dioscoreaceae. In Tanzania, yam is mainly grown as a source of food and income generation, especially for smallholder farmers. In this study, an assessment of morphological variations among 74 genotypes of *Dioscorea* spp. collected from six major growing regions was conducted. Yam genotypes were maintained and planted at Tanzania Agricultural Research Institute-Kibaha for characterization. Data from fifty morphological variables were subjected to multivariate analysis using principal component analysis and cluster analysis. The first nine principal components with Eigenvalues > 1 accounted for 86.28% of the total variations. Some traits that contributed to the variabilities include stem length, leaf margin colour, vein colour, absence/presence of wings, wing colour, hairiness, spines on stem base, aerial tubers, and inner skin colour. The dendrogram separated the 74 yam genotypes into two major clusters with six sub-clusters. Based on the results, four yam species were identified from the collected genotypes, and these included *D. alata*, *D. bulbifera*, *D. cayenensis*, and *D. dumetorum*. The results revealed high morphological variabilities among the yam genotypes. Information obtained in this study is very useful in yam breeding programs in Tanzania.

Keywords: Cluster analysis, multivariate analysis, phenotypic variabilities, yam in Tanzania

Introduction

Yam (*Dioscorea* spp.) is a perennial, polyploid rhizome crop that belongs to the genus *Dioscorea* and the family Dioscoreaceae (Girma et al. 2016). The genus *Dioscorea* consists of more than six hundred species, ten species and many other wild species are used for food (Kumar et al. 2017). Yam ranks as the fourth most economically important edible tuber crop in the world after sweet potatoes, cassava and Irish potatoes (Srivastava et al. 2012). The crop is mainly grown in tropical and sub-tropical regions, particularly in West Africa, tropical America, and South-East Asia (Rao et al. 2019).

Yam serves as a source of food due to its richness in carbohydrates, minerals, and vitamins (Bhattacharjee et al. 2018). Yam is usually consumed as boiled, fried, or baked (Atieno et al. 2020). In West Africa, tubers are also often dried and later milled into flour to reconstitute a stiff paste (fufu/amala), a famous traditional food, especially in Nigeria (Ikwebe et al. 2020). Yam is also used as feed for livestock and socio-cultural purposes, such as marriage ceremonies (Sanginga and Mbabu 2015). Wild yams are used as food sources, especially during famine, while

providing active pharmacological compounds in traditional medicine (Xu et al. 2008, Fan et al. 2020).

The total annual production of yam is estimated to be more than 74.8 million tons globally, whereby more than 96% of the world production occurs in Africa, with Nigeria being the leading producer accounting for 66.8%, which is more than 50 million tons (FAOSTAT 2021). In eastern Africa, yam is commonly grown in Tanzania, Kenya, Sudan, Uganda, and Ethiopia, with Sudan being the leading producer accounting for 166,843 tons annually (FAOSTAT 2021).

In Tanzania, there is limited data on yam production, diversity, or even types of yam species that are grown. In 2011, a non-government organization (NGO) surveyed some regions and reported production of 6 MT/ha and a total annual production of 9,800 tons (Kilimo-Trust 2013). Otherwise, there is hardly any published data on yam production in Tanzania. However, the major yam growing regions are Mtwara, Lindi, Morogoro, Arusha, Kilimanjaro, and Kagera. In all these regions, yam is mainly produced for food consumed after boiling, roasting, frying, grilling and sometimes is processed into flour mixed with cassava flour and used to make bites. The crop also contributes to the income generation of farmers who sell whole fresh tubers in the local markets. In various communities, yam scores different social values whereby many consider it a famine food, while some use it as medicinal food (especially *D. bulbifera*) for various diseases, including diabetes.

Despite its production and use within the country, there is hardly any published data on the types of yams, cultivars/landraces, or varieties that are grown in Tanzania. It is possible that farmers only cultivate a few species due to the unavailability of improved yam varieties, a situation that may lead to genetic erosion and loss of ecotypes and diversity. Without efforts to undertake research on yam, the risk of extinction of yam landraces in the country is inevitable. In addition, little information on the available genetic resources impedes breeding and conservation strategies efforts. To improve the yam germplasm available in the country, collection, characterization, and genetic diversity studies are crucial.

Morphological characterization is vital for the initial identification of yam species, followed by further in-depth characterization using protein and or/DNA markers. The studies by Hasan et al. (2008) and Anokye et al. (2014) established the genetic relationships of *D. alata* genotypes in Malaysia and Ghana using morphological traits and were able to classify the genotypes into four and three groups, respectively. Similarly, Mwirigi et al. (2009) and Norman et al. (2011) established morphological variabilities of yam in Kenya and Sierra Leone and revealed wide genetic diversity with four and six major groups of yams, respectively. In Tanzania, traditional cultivars grown by farmers have never been characterized; thus, the variabilities within the cultivated and even wild genotypes is unknown. The present study used agronomical traits to characterize and identify yam genotypes grown in Tanzania, to facilitate its conservation and breeding.

Materials and Methods

Collection of plant materials and planting

A field survey was conducted during the harvesting season (August-October 2019) in six major growing regions (Figure 1, Table 1), whereby 74 yam genotypes were collected. A total of three to five underground and/or aerial tubers were collected from every single plant or stand. All yam genotypes were planted and maintained at Tanzania Agricultural Research Institute (TARI) Kibaha experimental plot. Large tubers were sliced into minisetts of about 60 g, while small tubers (mainly aerial tubers) were planted as a whole. All tubers were planted on ridges with three replications. The distance between rows and plants within a row was 1 m. Cow dung manure and other standard cultural agronomic practices, including hand weeding and stacking, were employed as necessary. All plants were manually irrigated in the first three months using a field sprinkler once per day, three times a week.

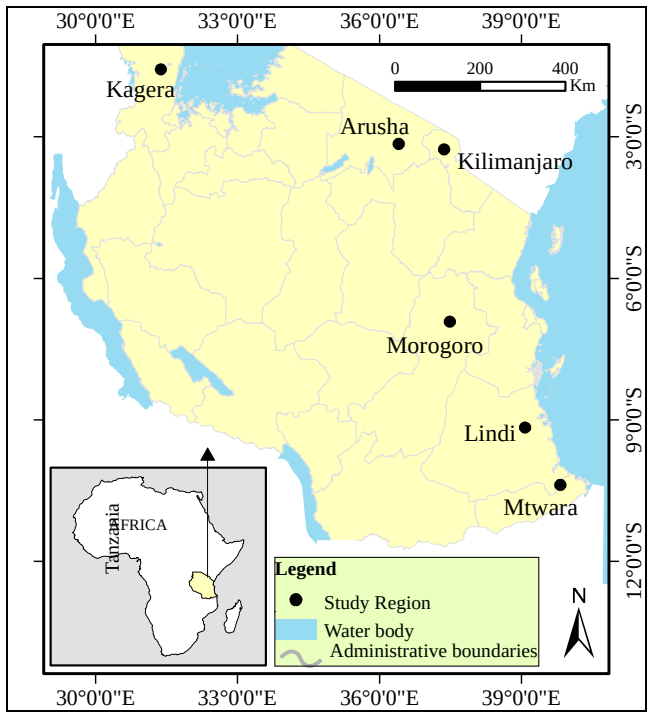

Figure 1: Map of Tanzania showing regions and study sites where yam samples were collected.

Table 1: Yam genotypes used in the present study, their uses and places of collection

Genotype No.	Local names	Species	Common uses	Locations (Village, District, Region)
1	Fikwa	*D. cayenensis*	Food	Akeri, Arumeru, Arusha
2	Hamandeke	*D. alata*	Food	Milongodi, Tandahimba, Mtwara
3	Hamandeke	*D. alata*	Food	Miule, Tandahimba, Mtwara
4	Hangadi pori	*D. dumetorum*	Food during famine	Nammbali, Newala, Mtwara
5	Hangadi pori	*D. dumetorum*	Food during famine	Lupota, Nachingwea, Lindi
6	Ifure	*D. alata*	Food	Katangara, Rombo, Kilimanjaro
7	Ifure	*D. alata*	Food	Katangara, Rombo, Kilimanjaro
8	Ifure	*D. alata*	Food	Imbaseni, Arumeru, Arusha
9	Ifure	*D. alata*	Food	Kirongo juu, Rombo, Kilimajaro
10	Ifure	*D. alata*	Food	Sangananu, Arumeru, Arusha
11	Kiraira	*D. alata*	Food	Bujuruga, Karagwe, Kagera
12	Kiraira	*D. alata*	Food	Kassambya, Missenyi, Kagera
13	Kiraira	*D. alata*	Food	Minziro, Missenyi, Kagera
14	Kiraira	*D. alata*	Food	Ngando, Missenyi, Kagera
15	Kashuri	*D. cayenensis*	Food	Maruku, Bukoba Rural, Kagera
16	Kashuri	*D. cayenensis*	Food	Kishanje, Bukoba Rural, Kagera
17	Kashuri	*D. cayenensis*	Food	Ngando, Missenyi, Kagera
18	Kitundi	*D. alata*	Food	Mmalachi, Newala, Mtwara
19	Kitundi	*D. alata*	Food	Namajani, Masasi, Mtwara
20	Kijabo	*D. alata*	Food	Mungurumo, Liwale, Lindi

Genotype No.	Local names	Species	Common uses	Locations (Village, District, Region)
	zambarau			
21	Mgendagenda	*D. alata*	Food	Mtamba, Morogoro Rural, Morogoro
22	Mgendagenda	*D. alata*	Food	Tambuu, Morogoro Rural, Morogoro
23	Msagala	*D. alata*	Food	Mtamba, Morogoro Rural, Morogoro
24	Matui	*D. bulbifera*	Food	Mtombozi, Morogoro rural, Morogoro
25	Mkonga	*D. alata*	Food	Matogoro, Tandahimba, Mtwara
26	Mamaya	*D. bulbifera*	Food and	Kirongo juu, Rombo, Kilimanjaro
27	Mamaya	*D. bulbifera*	Food and medicinal	Katangara, Rombo, Kilimanjaro
28	Mamaya	*D. bulbifera*	Food and medicinal	Katangara, Rombo, Kilimanjaro
29	Mnangilangi	*D. alata*	Food	Matogoro, Tandahimba, Mtwara
30	Mnangilangi	*D. alata*	Food	Nammbali, Newala, Mtwara
31	Mnangilangi	*D. alata*	Food	Mhoha, Newala, Mtwara
32	Mnangilangi	*D. alata*	Food	Mmalachi, Newala, Mtwara
33	Mnangilangi	*D. alata*	Food	Chiwata, Masasi, Mtwara
34	Mnangilangi	*D. alata*	Food	Matogoro, Tandahimba, Mtwara
35	Mnangilangi	*D. alata*	Food	Matogoro, Tandahimba, Mtwara
36	Mapeta	*D. alata*	Food	Chiwata, Masasi, Mtwara
37	Mapeta	*D. alata*	Food	Chiwata, Masasi, Mtwara
38	Mapeta	*D. alata*	Food	Chiwata, Masasi, Mtwara
39	Mapeta	*D. alata*	Food	Ikungu, Nachingwea, Lindi
40	Mapeta	*D. alata*	Food	Ikungu, Nachingwea, Lindi
41	Mapeta	*D. alata*	Food	Lupota, Nachingwea, Lindi
42	Mapeta	*D. alata*	Food	Lupota, Nachingwea, Lindi
43	Mapeta	*D. alata*	Food	Mpiruka, Nachingwea, Lindi
44	Mapeta	*D. alata*	Food	Mpiruka, Nachingwea, Lindi
45	Mikirachi	*D. alata*	Food	Mpiruka, Nachingwea, Lindi
46	Isoma	*D. bulbifera*	Food	Kishaka, Bukoba rural, Kagera
47	Isoma	*D. bulbifera*	Food	Bujuruga, Karagwe, Kagera
48	Isoma	*D. bulbifera*	Food	Bujuruga, Karagwe, Kagera
49	Isoma	*D. bulbifera*	Food	Kassambya, Missenyi, Kagera
50	Isoma	*D. bulbifera*	Food	Kassambya, Missenyi, Kagera
51	Isoma	*D. bulbifera*	Food	Ngando, Missenyi, Kagera
52	Matu	*D. bulbifera*	Food	Matogoro, Tandahimba, Mtwara
53	Matu	*D. bulbifera*	Food	Miule, Tandahimba, Mtwara
54	Matu	*D. bulbifera*	Food	Nammbali, Newala, Mtwara
55	Matu	*D. bulbifera*	Food	Mmalachi, Newala, Mtwara
56	Matu	*D. bulbifera*	Food	Mmalachi, Newala, Mtwara
57	Matu	*D. bulbifera*	Food	Mmalachi, Newala, Mtwara
58	Matu	*D. bulbifera*	Food	Chiwata, Masasi, Mtwara
59	Matu	*D. bulbifera*	Food	Chiwata, Masasi, Mtwara
60	Nduu	*D. bulbifera*	Food and medicinal	Lukura, Moshi Rural, Kilimanjaro
61	Nduu	*D. bulbifera*	Food and medicinal	Kiala, Moshi Rural, Kilimanjaro
62	Nyuvele	*D. alata*	Food	Matogoro, Tandahimba, Mtwara

Genotype No.	Local names	Species	Common uses	Locations (Village, District, Region)
63	Nyuvele	*D. alata*	Food	Mting'inda, Tandahimba, Mtwara
64	Nyuvele	*D. alata*	Food	Mhoha, Tandahimba, Mtwara
65	Vibere	*D. bulbifera*	Food and medicinal	Shari, Hai, Kilimanjaro
66	Vijabo	*D. alata*	Food	Makata, Liwale, Lindi
67	Vijabo	*D. alata*	Food	Mkundi, Liwale, Lindi
68	Vijabo	*D. alata*	Food	Makata, Liwale, Lindi
69	Vimbelete	*D. alata*	Food	Makata, Liwale, Lindi
70	Vinyamilwa	*Dioscorea* spp.	Food	Matogoro, Tandahimba, Mtwara
71	Vinyamilwa	*Dioscorea* spp.	Food	Mmalachi, Newala, Mtwara
72	Vipandwa	*D. bulbifera*	Food	Ikungu, Nachingwea, Lindi
73	Vitungula	*D. alata*	Food	Chiwata, Masasi, Mtwara
74	Vigonzo ubwabwa	*D. alata*	Food	Mtamba, Morogoro Rural, Morogoro

Morphological characterization

Morphological characterization was done under experimental field conditions using 50 morphological traits (Table 2) described by IPGRI-IITA (1997). A total of forty five qualitative data were recorded using a one to nine scale or as a binary recording (0 = absent and 1 = present), while five quantitative data were recorded and scaled one to nine. The characters were measured on at least three different visually healthy plants per genotype and then averaged for analysis.

Table 2: Description of morphological traits used in characterization of 74 yam genotypes in this study. The method of data measurements was according to IPGRI-IITA (1997).

SN	Descriptor	Score scale
1	DE	0-14 days = 0 Late, 15 < days = 1 early
2	SLE	1 ≤ 10 cm, 2 = 11-50 cm, 3 = 51-100 cm, 4 = > 101 cm
3	SPN	0 = Absent, 1 = Present
4	LMC	1 = Green, 2 = Purple
5	VCL	1 = Yellowish, 2 = Green, 3 = Pale purple, 4 = Purple
6	TDI	1 = Clockwise (climbing to the left), 2 = Anticlockwise (climbing to the right)
7	SC	1 = Green, 2 = Purplish green, 3 = Brownish green, 4 = Dark brown, 5 = Purple
8	WG	0 = Absent, 1 = Present
9	WC	1 = Green, 2 = Green with purple edge, 3 = Purple
10	HR	3 = Sparse, 7 = Dense
11	SSB	3 = Few, 7 = Many
12	SSA	3 = Few, 7 = Many
13	PLV	1 = Alternate, 2 = Opposite, 3 = Alternate at base/opposite above
14	LTY	1 = Simple, 2 = Compound
15	NCL	1 = Mainly 3 (trifoliate), 2 = Mainly 5 (quinate), 3 = More than 5
16	LHR	0 = No, 1 = Yes
17	LCM	1 = Yellowish, 2 = Pale green, 3 = Dark green, 4 = Purplish green, 5 = Purple
18	HPS	3 = Sparse, 7 = Dense
19	HLS	3 = Sparse, 7 = Dense
20	LSH	1 = Ovate, 2 = Cordate, 3 = Cordate long, 4 = Cordate broad, 5 = Sagittate long, 6 = Sagittate broad, 7 = Hastate
21	W1	1 ≤ 5 cm, 2–5.1 = 8 cm, 3 = 8.1-11 cm, 4 = 11.1-14 cm, 5 ≥ 14.1

SN	Descriptor	Score scale
22	W2	1 ≤ 2 cm, 2 = 2.1–5 cm, 3 = 5.1–8 cm, 4 = > 8.1 cm
23	L2	1 ≤ 5 cm, 2 = 5.1–8 cm, 3 = 8.1–11cm, 4 = 11.1–14 cm, 5 ≥ 14.1
24	L3	1 ≤ 2 cm, 2 = 2.1–5 cm, 3 = 5.1–8 cm, 4 > 8.1 cm
25	PWC	1 = Green, 2 = Green with purple edges, 3 = Purple
26	SPT	3 = Sparse, 7 = Dense
27	FL	0 = No flowering, 1 = Flowering in some years, 2 = Every year
28	DFE	1 > 120 days, 2 ≤ 120 days
29	SX	1 = Female, 2 = Male, 3 = Female and male (predominantly female), 4 = Male and female (predominantly male)
30	IPO	1 = Pointing upwards, 2 = Pointing downwards
31	NFF	1 ≤ 10, 2 = 11–25, 3 = 26–100, 4 ≥ 101
32	FCL	1 = Purplish, 2 = White, 3 = Yellowish
33	FFL	1 ≤ 2.5 cm, 2 = 2.6-5 cm, 3 ≥ 5.1 cm
34	ATU	0 = Absent, 1 = Present
35	ATS	1 = Round, 2 = Oval, 3 = Irregular (not uniform), 4 = Elongate
36	SCL	1 = Greyish, 2 = Light brown, 3 = Dark brown
37	STX	1 = Smooth, 2 = Wrinkled, 3 = Rough
38	FCL	1 = White, 2 = Yellowish white or off-white, 3 = Yellow, 4 = Orange, 5 = Light purple, 6 = Purple, 7 = Purple with white, 8 = White with purple, 9 = Outer purple/inner yellowish
39	ISC	1 = Green, 2 = Purple with white, 3 = White purple, 4 = Purple, 5 = Cream
40	UGT	0 = Absent, 1 = Present
41	MTE	1 = Up to 6 months, 2 = 7–8 months, 3 = 9–10 months
42	TSH	1 = Round, 2 = Oval, 3 = Oval-oblong, 4 = Cylindrical, 5 = Flattened, 6 = Irregular
43	NTH	1 = One, 2 = Few (2–5), 3 = Several (> 5)
44	CTS	0 = Absent, 1 = Present
45	UFC	0 = No, 1 = Yes
46	FCC	1 = White, 2 = Yellowish white or off-white, 3 = Yellow, 4 = Orange, 5 = Light purple, 6 = Purple, 7 = Purple with white, 8 = White with purple, 9 = Outer purple/inner yellowish,
47	ITSC	1 = Light brown, 2 = Brown, 3 = Dark brown, 4 = Purple, 5 = Off-white, 6 = Orange
48	HTB	1 = Hard, 2 = Easy
49	SCH	1 = White, 2 = Yellowish white or off-white, 3 = Yellow, 4 = Orange, 5 = Light purple, 6 = Purple, 7 = Purple with white, 8 = White with purple, 9 = Outer purple/inner yellowish
50	TXT	1 = Smooth, 2 = Grainy, 3 = Very grainy

DE = Days to emergence, SLE = Stem length, SPN = Absence/presence spines, LMC = Leaf margin colour, VCL = Vein colour, TDI = Twinning direction, SC = Stem colour, WG = Absence/presence of wings, WC = Wing colour, HR = Hairiness, SSB = Spines on stem base, SSA = Spine on stem above the base, PLV = Position of leaves, LTY = Leaf type, NCL = Number of the leaflet in compound leaf, LHR = Leatheriness, LCM = Leaf colour, HPS = Hairiness of the lower surface, HLS = Hairiness of the upper surface, LSH = Leaf shape, W1, W2, L2 and L3 = Leaf measurement, PWC = Petiole wing colour, SPT = Spininess of the petiole, FL = Flowering, DFE = Days to flowering, SX = Sex, IPO = Inflorescence position, NFF = Number of female flowers per inflorescence, FCL = Flower colour, FFL = Female flower length, ATU = Presence/absence of Aerial tuber, ATS = Aerial tuber shape, SCL = Skin colour, STX = Surface texture, FCL = Flesh colour, ISC = Inner skin colour, UGT = Underground tuber, MTE = Maturity of tubers after emergence, TSH = Tuber shape, NTH = Number of tubers per hill, CTS = Absence/presence of crack on the tuber surface, UFC = Uniformity of flesh colour, FCC = Flesh colour at the central transverse cross-section, ITSC = Inner tuber skin colour, HTB = Hardness of tuber, SCH = Skin colour at the head of the tuber and TXT = Texture of flesh.

Data analysis

Principal component analysis (PCA)

PCA was performed in R software using the FactorMiner package (Lê et al. 2008). The PCA data was used to generate eigenvalues, cumulative variability, and load coefficient values. The principal components (PC) with eigenvalues > 1.0 were selected, and those traits that had load coefficients ≥ 0.6 were considered relevant scores for the PC and considered as valuable traits for distinguishing between the genotypes (Jeffers 1967). For cluster analysis, a dissimilarity matrix was generated using the Euclidean method in cluster and graphics R packages, while the final hierarchical cluster was generated using the ward.D2 method in cluster R packages (Maechler et al. 2019).

Results

Phenotypic variabilities of yam genotypes

A wide range of morphological variabilities was observed in leaves, stems, flowering, aerial bulbils, aerial tubers, and underground tubers between the 74 genotypes. Among the 74 yam genotypes, 72 (97.3%) were simple leaves, while 2 (2.7%) were compound leaves. The simple leaves were of three types, 65 (90.3%) were cordate, 4 (5.6%) were ovate, while 3 (4.1%) were sagittate. Simple, cordate leaves had three types of petioles; 27 (41.5%) were green with a purple base, 26 (40%) were green and 12 (18.5%) were green with purple on both ends. The stems were of three types: 42 (56.8%) had quadrangular winged stem, 22 (29.7%) had soft and round stem and 10 (13.5%) had spiny and round stem. A total of 20 (27%) yam genotypes flowered, 14 (70%) being male flowers and 6 (30%) female. Male flowers appeared four to five months post-planting, while female flowers appeared six months post-planting. Of the 74 yam genotypes, 34 (45.9%) had aerial bulbils and 22 (29.7%) produced aerial tubers. Both aerial tubers and bulbils displayed varied shapes; 16 (72.7%) genotypes produced irregular aerial tubers with dark and light-brown outer skin colour, whereas 6 (27.3%) had round with dark-brown outer skin colour. For aerial bulbils, 20 (58.8%) were round with dark-brown colour, while 14 (41.2%) were oval with dark-brown colour. The flesh colours of aerial tubers were of three types; 13 (59.1%) were yellow, 5 (22.7%) were white with purple and 4 (18.2%) were purple with white. Three types of aerial bulbils flesh colour were observed; 22 (64.7%) were white-yellowish, 8 (23.5%) were purple and 4 (11.8%) were white with a purple layer colour. Of 74 yam genotypes used in this study, 52 (70.3%) yam genotypes had underground tubers. The underground tubers displayed six different shapes and were of different colours. Among the 52 yam genotypes, 18 (34.6%) had irregular finger-like shapes with brown colour, 10 (19.2%) had an elongated finger-like shapes with dark brown colour and 10 (19.2%) had round shapes with brown colour. Furthermore, 8 (15.4%) had oval shapes with brown colour, 4 (7.7%) had elongated shapes with a brown exterior colour and 2 (3.9%) had cylindrical shapes with light brown colour and fused at the head. The underground tuber flesh colour at the central transverse cross-section was of six colours; 18 (34.6%) were purple, 10 (19.2%) were white, 8 (15.4%) were purple-white, 7 (13.5%) were cream, 5 (9.6%) were orange and 4 (7.7%) were yellow flesh colour.

Based on this study, four *Dioscorea* spp. were identified, and these included *D. alata*, *D. bulbifera*, *D. cayenensis* and *D. dumetorum* (Table 3).

Table 3: *Dioscorea* spp. identified in this study and their distinguishing phenotypic traits

SN	Species identified	Phenotypic traits
1	*Dioscorea bulbifera*	Simple and cordate leaves, smooth, green stem and aerial tubers.
2	*Dioscorea alata*	Simple, cordate and sagittate leaves, quadrangular winged stem, small aerial bulbils and underground tuber with white and purple flesh colour.
3	*Dioscorea dumetorum*	Compound leaves, spiny petiole and stem, and small cylindrical tuber shape fused at the head with white underground tuber flesh colour.
4	*Dioscorea cayenensis*	Simple and ovate leaves, spiny stem, and yellow underground tuber flesh colour.
5	*Dioscorea* spp.	Simple and cordate leaves, brown spiny petiole and stem, oval tuber shape, and white underground tuber flesh colour.

Morphological variabilities observed in *Dioscorea bulbifera* and *Dioscorea alata* are presented in Figure 2:I and Figure 2:II, respectively.

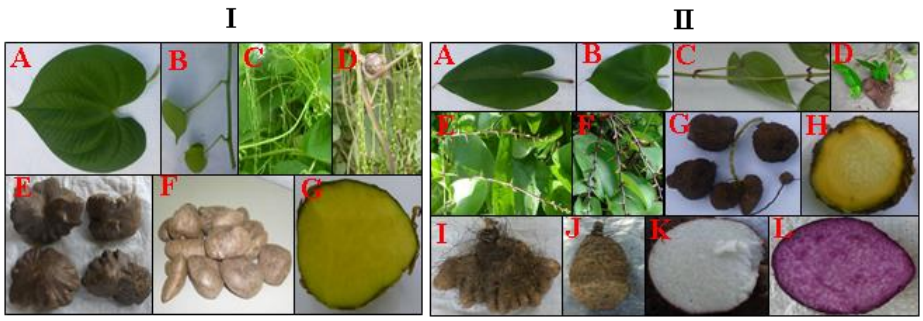

Figure 2: Morphological variabilities in yam genotypes: *D. bulbifera* and *D. alata.*
I. Variabilities in genotypes identified as *D. bulbifera*. A. Simple cordate leaf, B. Green, soft and round stem, C. Male flowers, D. Male flowers, reference genotype (Overholt et al. 2014), E. Irregular shapes of aerial tubers with dark brown colour, F. Round aerial tubers with dark brown, reference genotype (Overholt et al. 2014) and G. Yellow tuber flesh. **II.** Variabilities in genotypes identified as *D. alata*. A. Simple cordate leaf, B. Simple sagittate broad leaf, C. Quadrangular winged stem, D. Cordate leaf and irregular underground tuber, reference genotype (Makiyah and Djati 2018). E. Female flowers, F. Female flowers, reference genotype (Rojas-Sandoval and Acevedo-Rodríguez 2013), G. Small aerial bulbils, H. Aerial bulbils with white-yellowish, I. Irregular finger-like tuber shape, J. Oval tuber shape with brown colour, K. White flesh colour and L. Purple flesh colour.

Morphological variabilities observed in *Dioscorea dumetorum, Dioscorea cayenensis* and one *Dioscorea* spp. that could not be correctly assigned to its specific species are presented in Figures 3:I, 3:II and 3:III, respectively.

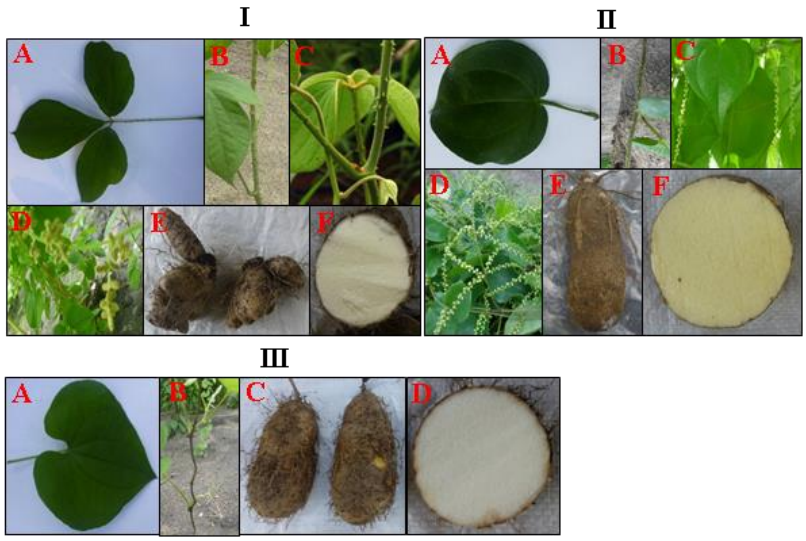

Figure 3: Morphological variabilities in yam genotypes: *D. dumetorum* and *D. cayenensis*. **I.** Variabilities in yam genotypes identified as *D. dumetorum.* A. Compound leaf with spiny petiole, B. Green, round, stem with spiny, C. Compound leaf and spiny stem, reference genotype (Laly et al. 2019), D. Male flowers, E. Cylindrical light brown tubers fused at the head and F. Cream flesh colour. **II.** Variabilities in yam genotypes of *D. cayenensis*. A. Simple cordate broad leaf, B. Green, round stem with spiny, C. Male flowers, D. Male flowers, reference genotype (Loko et al. 2015) E. Elongated tuber shape with brown colour, F. Yellow flesh colour, and **III.** A. Simple cordate leaf, B. Round, brown stem with spiny, C. Oval tuber shape with brown colour and D. White flesh colour. This yam genotype could not be assigned to a known *Dioscorea* spp.

Principal component analysis

Among the fifty characters used in this study, 34 (68%) were the most discriminating characters for the yam genotypes evaluated. The first nine principal components (PC) gave eigenvalues greater than 1 and accounted for 86.28% of the total variations (Table 4). Scores on the first principal component (PC-1), which explained 26.65% of the total variations, were highly correlated (correlation coefficient > 0.6) to stem length, leaf margin colour, vein colour, absence/presence of wings, wing colour, hairiness, spines on stem base, and spines on stem above the base (Table 5). Moreover, PC-1 was also correlated (correlation coefficient > 0.6) to the position of leaves, leaf type, number of the leaflet in compound leaf, leaf colour, hairiness of upper surface, leaf measurement, petiole wing colour, Spininess of the petiole, skin colour, surface texture, inner skin colour and absence/presence of crack on the tuber surface (Table 5). The PC-2, which accounted for 13.86% of the total variations, was highly correlated (correlation coefficient > 0.6) with twinning direction and skin colour at the head of the tuber (Table 5). The PC-3 that described 12.38% of the total variations was correlated (correlation coefficient > 0.6) to flowering, days to flowering, sex, inflorescence position, number of female flowers per inflorescence, flesh colour, and female flower length (Table 5). The rest of the PCs correlated to traits considered less important as their percentage contribution to the total variations was small.

Table 4: Eigenvalues, percentage variations and cumulative variability explained by each component of the first nine principal components (PCs)

Principal component	Eigenvalue	Variation of each component	Cumulative variability
1	13.326	26.651	26.651
2	6.932	13.864	40.515
3	6.191	12.382	52.897
4	4.956	9.912	62.809
5	4.054	8.108	70.917
6	2.744	5.488	76.404
7	2.268	4.536	80.941
8	1.414	2.827	83.768
9	1.259	2.518	86.286

Table 5: First nine principal components of the 50 variables in 74 yam genotypes. The most discriminating traits and their load coefficient values are bolded.

No	Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
1	DE	0.564	0.130	-0.142	0.053	-0.053	0.578	0.077	-0.332	-0.104
2	**SLE**	**0.624**	0.235	-0.115	0.122	-0.169	**0.650**	0.104	-0.270	-0.097
3	SPN	-0.241	0.221	-0.026	-0.091	0.291	0.570	-0.126	-0.034	-0.068
4	**LMC**	**0.668**	0.406	-0.089	0.119	-0.203	0.473	0.148	-0.081	0.031
5	**VCL**	**0.643**	0.318	-0.145	0.141	-0.158	0.508	0.159	-0.119	0.145
6	**TDI**	0.473	**0.736**	0.324	-0.193	-0.094	-0.141	0.111	0.072	0.092
7	SC	-0.470	0.227	0.238	-0.246	0.446	0.481	0.020	0.248	-0.161
8	**WG**	**0.723**	0.601	0.145	-0.067	-0.125	-0.148	-0.076	-0.072	0.081
9	**WC**	**0.723**	0.601	0.145	-0.067	-0.125	-0.148	-0.076	-0.072	0.081
10	**HR**	**-0.711**	0.455	-0.214	0.445	-0.116	-0.014	0.015	-0.035	-0.032
11	**SSB**	**-0.641**	0.360	0.281	-0.231	0.286	0.157	0.193	0.325	-0.049
12	**SSA**	**-0.652**	0.359	0.260	-0.213	0.277	0.172	0.161	0.328	-0.035
13	**PLV**	**0.618**	0.618	0.337	-0.153	-0.046	-0.001	0.056	0.096	0.069
14	**LTY**	**-0.609**	0.393	-0.152	0.470	-0.251	-0.243	0.156	-0.069	0.048
15	**NCL**	**-0.609**	0.393	-0.152	0.470	-0.251	-0.243	0.156	-0.069	0.048
16	LHR	-0.207	0.162	0.342	-0.418	0.335	-0.019	0.437	-0.082	-0.064
17	**LCM**	**0.690**	-0.418	0.240	-0.151	0.005	-0.171	0.016	-0.116	0.075
18	**HPS**	**-0.711**	0.455	-0.214	0.445	-0.116	-0.014	0.015	-0.035	-0.032
19	**HLS**	**-0.694**	0.435	-0.230	0.355	0.013	0.159	-0.104	-0.001	-0.102
20	LSH	0.409	0.395	0.402	-0.428	0.260	-0.049	0.403	-0.130	-0.009
21	W1	0.360	-0.341	0.301	-0.213	0.362	-0.044	-0.050	-0.102	-0.284
22	W2	-0.363	0.317	0.179	0.066	0.157	-0.440	0.326	-0.420	-0.071
23	**L2**	**0.710**	-0.154	0.290	-0.319	0.246	-0.086	0.054	-0.258	0.084
24	L3	0.557	-0.067	0.348	-0.237	0.108	-0.007	-0.445	0.283	-0.125
25	**PWC**	**0.678**	0.556	0.108	-0.024	-0.228	-0.059	-0.321	0.118	0.126
26	**SPT**	**-0.689**	0.439	-0.237	0.349	0.029	0.202	-0.118	0.002	-0.100
27	**FL**	-0.354	-0.207	0.839	0.193	-0.248	0.121	0.038	0.013	0.042
28	**DFE**	-0.263	-0.156	0.802	0.180	-0.265	0.134	-0.001	-0.099	0.073
29	**SX**	-0.465	-0.048	0.799	0.093	-0.114	0.113	0.176	0.097	0.034
30	**IPO**	-0.354	-0.207	0.839	0.193	-0.248	0.121	0.038	0.013	0.042
31	**NFF**	-0.083	-0.395	0.667	0.293	-0.387	0.099	-0.186	-0.120	0.041
32	**FCL**	-0.345	0.098	0.795	0.150	-0.189	0.087	0.175	0.088	0.014
33	**FFL**	-0.083	-0.395	0.667	0.293	-0.387	0.099	-0.186	-0.120	0.041
34	ATU	0.583	-0.528	-0.110	0.450	-0.040	-0.005	0.278	0.154	-0.172
35	ATS	0.403	-0.636	-0.152	0.389	-0.055	0.007	0.148	0.101	-0.207

No	Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
36	**SCL**	**0.670**	-0.217	-0.161	0.425	-0.030	0.049	0.286	0.240	-0.112
37	**STX**	**0.702**	-0.296	-0.056	0.452	-0.052	-0.007	0.303	0.191	-0.175
38	FLC	0.404	-0.322	-0.280	0.251	-0.016	0.171	0.217	0.261	0.201
39	**ISC**	**0.710**	0.218	0.096	0.318	-0.061	-0.049	0.321	0.154	-0.182
40	**UGT**	0.098	-0.004	0.255	0.601	0.659	-0.096	-0.208	-0.100	-0.055
41	**MTE**	0.098	-0.004	0.255	0.601	0.659	-0.096	-0.208	-0.100	-0.055
42	TSH	0.393	0.280	0.123	0.550	-0.021	-0.080	0.231	0.091	-0.182
43	NTH	0.080	0.011	-0.009	0.283	0.444	0.517	-0.175	-0.136	0.246
44	**CTS**	**0.662**	0.508	0.170	0.097	-0.022	-0.234	-0.015	**0.610**	-0.041
45	UFC	-0.251	-0.013	-0.149	0.043	0.464	-0.038	0.336	0.036	0.405
46	**FCC**	0.326	-0.194	-0.076	0.435	0.101	-0.006	0.134	0.154	**0.670**
47	ITSC	0.574	0.346	0.253	0.336	0.332	-0.084	-0.337	0.196	-0.087
48	**HTB**	-0.039	-0.396	0.094	0.151	**0.692**	0.012	0.002	0.043	0.239
49	**SCH**	0.384	**0.719**	0.238	0.328	0.158	-0.136	-0.265	0.121	0.048
50	TXT	0.117	0.028	0.220	0.481	0.432	-0.143	0.045	-0.315	-0.106

Cluster analysis

The dendrogram of hierarchical cluster analysis (Figure 4) separated the 74 genotypes into two distinct clusters regardless of geographical locations with Euclidean dissimilarity distances ranging from 0 to 30. At the dissimilarity distance of 15, two major clusters, I and II, containing 4 and 70 genotypes, respectively, were observed. Cluster I separated yam genotypes into one sub-cluster (A), containing only 4 genotypes. All 4 genotypes clustered according to the presence of spines and hairiness on the upper and lower surfaces of the leaf. Cluster II had five sub-clusters, B, C, D, E, and F containing 10, 27, 14, 15, and 4 genotypes, respectively. Sub-cluster B had yam genotypes clustered according to the white flesh colour at the central transverse cross-section. Sub-cluster C had 27 genotypes, which clustered according to stem length, vein colour, wing colour, absence/presence of crack on the tuber surface, inner skin colour and skin colour at the head of the tuber. Sub-cluster D had 14 genotypes clustered according to flowering abilities, while sub-cluster E had 15 genotypes grouped according to abilities to produce aerial bulbils. The final sub-cluster F had 4 genotypes with no common morphological characters.

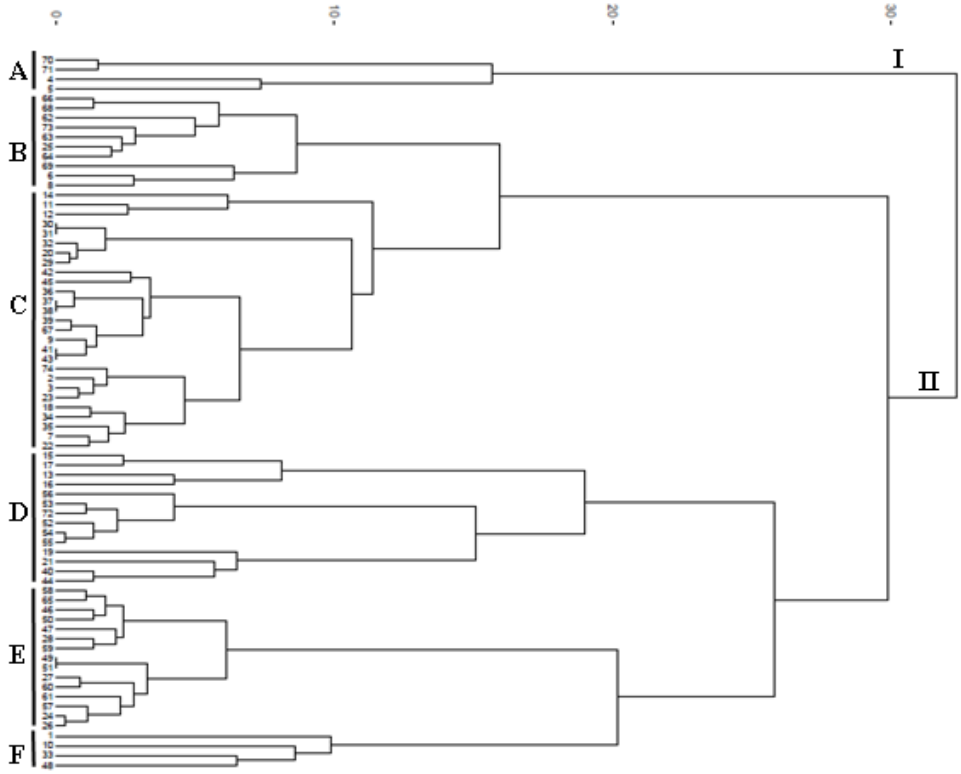

Figure 4: The hierarchical dendrogram based on Euclidean dissimilarity showing the relationships among 74 yam genotypes from Tanzania based on morphological characters.

Discussion

A better understanding of the existing yam germplasm available in the country is among the prerequisites for the conservation and breeding of new varieties with novel traits. This study used morphological traits to identify yam genotypes that are grown in selected regions in Tanzania.

Cordate leaf shape was a dominant shape observed among all the *Dioscorea* spp. identified in this study. Similar results were obtained by Anokye et al. (2014) and Munaweera et al. (2020) while studying the morphological variations of *Dioscorea* spp. in Ghana and Sri Lanka, respectively.

In our study, only 20 (27%) yam genotypes flowered. The flowering aspect is advantageous to breeders since genotypes that flower can produce seeds for sexual reproduction to enhance genetic improvements (Denadi et al. 2020). Several factors have been attributed to the absence of flowering in yams. The type of planting materials used (seed or tuber), environmental conditions and photoperiod (Ile et al. 2007) can contribute to flowering. Flowering in *D. alata*, *D. bulbifera*, *D. dumetorum* and *D. cayenensis* has been reported in previous studies. However, flowering among cultivated yams has generally been reported to be low (Mondo et al. 2020). Sartie and Asiedu (2014) observed that about 45% of *D. alata* genotypes produced flowers with the male being 49% and the female 19.9%, while Wu-Wenqiang et al. (2019) reported about 41.5% flowering in *D. alata* genotypes in China. Similarly, Girma et al. (2018) reported moderate flowering in *D. rotundata*, *D. cayenensis* and *D. dumetorum* genotypes and low flowering in *D. bulbifera*, *D. alata* and *D. esculenta*, with dominant male flowers. Likewise, Siadjeu et al. (2015), Bekele and

Bekele (2020) also reported low flowering in *D. rotundata*, *D. cayenensis* and *D. dumetorum*.

In the present study, aerial tubers of *D. bulbifera* had either round or irregular shapes with dark-brown and light-brown outer skin colour, similar to the findings of Islam et al. (2011) and Mulualem and Weldemichel (2013). Most tuber fleshes of *D. bulbifera* genotypes were yellow, a similar observation by (Prasetia and Setiadi 2018). However, some had white with purple and purple with white flesh colours. Variabilities in shapes and colours of aerial tubers are very important in selecting preferred genotypes by farmers and breeders for cultivation and genetic improvements, respectively.

Based on our study, most of the *D. alata* genotypes produced aerial bulbils. The formation of aerial bulbils in *D. alata* has also been reported (Sanada et al. 2018, Wu et al. 2019). Bulbils are usually formed on the axil of the stem and have the potential of being used as seeds for propagation (Sanada et al. 2018). *D. alata* genotypes had irregular, oval, cylindrical, or round tuber shapes, a result that is similar to that of Jyothy et al. (2017) in which oval, round, cylindrical, and irregular tuber shapes were also observed in *D. alata* genotypes from India. The dominant cream (off-white), purple-white, and purple flesh colours observed in *D. alata* genotypes were congruent to the observations in the study by Jyothy et al. (2017) which observed that 86.7% of yam accessions had off-white while 2.2% were purple flesh colour. Cream and purple flesh colours were also dominant colours reported by Trimanto and Hapsari (2015). Yam genotypes identified in this study as *D. cayenensis* and *D. dumetorum* had yellow and white flesh colours, respectively. Similar results have been reported while studying the phenotypic diversity of *D. cayenensis* and *D. dumetorum* in Nigeria and Ethiopia, respectively (Nwankwo et al. 2017, Bekele and Bekele 2020).

The most discriminating characters identified in our study were 34 (68%) out of 50. Our results are slightly different from others. For instance, Anokye et al. (2014) reported only 23 (21.5%) out of 107 characters as the most discriminating traits. Similarly, Hasan et al. (2008) reported that only 25 (53.2%) out of 47 characters were the most discriminating. Despite using many characters, only a few characters might be necessary to discriminate among genotypes of different yam species. The most discriminating characters such as presence of wings, shape of the leaves, presence of aerial tubers, spines on the stem and underground tuber flesh colours can be used by farmers and breeders to preliminary identify and distinguish yam genotypes.

The cluster analysis results that formed two groups explain the patterns of relationships among genotypes, whereby genotypes with close genetic distances are placed close in the dendrogram. Yam genotypes that farmers regarded as different were grouped together with no clear morphological variabilities despite different local names and geographical origin. This is because the same community may use different names to refer to the same yam genotype. Upon exchange of the same genotype to another community, that genotype may be given a different name and referred to as a new or different cultivar. Our results correspond to the findings of Asfaw et al. (2021) who reported that the same cultivar might be known by different names within the same community and vice versa which might cause an ambiguity during cultivar identification.

In the dendrogram, most yam genotypes clustered randomly regardless of geographical locations, except for cluster I, which had four yam genotypes. Yam genotypes in cluster I were only found in Mtwara and Lindi regions and are poisonous wild types usually used for food only during famine, hence limiting their exchange to other regions of Tanzania**.** Grouping the yam genotypes regardless of their geographical locations suggests that most of the yam genotypes found in the study areas are closely related. The close relationship between genotypes could be due to limited research on yam in Tanzania that renders unavailability of more planting materials, hence most

farmers freely exchange yam tubers for planting. This practice may explain the situation observed in this study whereby there was no clear discrimination of yam genotypes based on the study areas. Furthermore, lack of breeding and conservations programs could have contributed to the similarity of yam genotypes between the regions. This was also observed by Atieno et al. (2020), whereby yam genotypes collected from different regions of Kenya were grouped together despite their geographical locations.

Conclusion

In this study, it was possible to group 74 yam genotypes into two major clusters with six sub-clusters. Four *Dioscorea* spp., *D. alata*, *D. bulbifera*, *D. cayenensis*, and *D. dumetorum* were identified based on at least 34 morphological agronomic traits. One genotype could not be assigned to any species due to limited distinct traits. More in-depth identification using molecular techniques could confirm the identity of all the genotypes. Information obtained from this study contributes to the knowledge of yam genetic resources available in Tanzania that is very important in planning for the conservation, use, and breeding programs of yam in the country.

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