Hindawi

Research Article

Phenotypic Diversity within Ugandan Yam (*Dioscorea species*) Germplasm Collection

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A proper understanding of the diversity of the available germplasm is an initial step for the genetic improvement of a crop through breeding. However, there is limited information on the diversity of Uganda's yam germplasm. The study sought to characterize the diversity of yam germplasm utilized for decades in Uganda together with germplasm recently introduced from West Africa using phenotypic traits. A germplasm collection of 291 genotypes was characterized using 28 phenotypic traits. Data were subjected to multivariate analysis using principal component analysis and cluster analysis. The traits assessed were informative and discriminating, with 62% of the total variation explained among the first six principal components. Results showed that the important phenotypic traits contributing to most of the variability among the genotypes were leaves, flowering, and tuber traits. Ugandan genotypes were identified with amorphous tuber shapes compared to West African genotypes. The study has shown that there is ample phenotypic variability within the major yam genotypes in Uganda yam germplasm that can be used for genetic improvement. More in-depth molecular and biochemical studies to further understand the diversity are recommended. The preprint was made available by research square in the following link: "https://www.researchsquare.com/article/rs-1518551/v1."

1. Introduction

Yam (*Dioscorea* spp.) is a clonally propagated crop with a large global market, particularly in underdeveloped countries [1]. The crop is cultivated mainly for its tubers and is a major source of food energy for millions in tropical countries including East and West Africa, the Caribbean, South Africa, India, and Southeast Asia [2]. The yam belt region of West Africa, which includes Benin, Ghana, Ivory Coast, Nigeria, and Togo, produces nearly 97.7% of global

production (73.2 million tonnes) with an area harvested of about 8.6 million hectares [3]. Nigeria is the world's leading yam producer, accounting for more than 70% of worldwide production [3]. Farmers in West Africa primarily grow *Dioscorea rotundata*, *Dioscorea alata*, *Dioscorea cayenensis,* and *Dioscorea dumetorum*, even though several species of yams are grown around the world [4].

East Africa accounts for only 0.25% (187, 290 tonnes) of the total production [3]. In Uganda, the cultivation of yams is widespread but farmers mainly grow landraces or old

cultivars, which have low productivity and are susceptible to multiple pests and diseases [5, 6]. The crop is attractive for food security because of its resilience to adverse weather, broad agroecological adaptation, significantly longer shelf life compared to other staple crops, and diverse options for value-added utilization. Yams and yam food products are sold in Ugandan markets and attract high prices.

The lack of knowledge about the origin, diversity, and genetics of crop species extremely limits the effectiveness of genetic improvement programs [7]. Some cytogenetic and marker studies have been used to characterize the diversity of germplasm collections of *Dioscorea rotundata/Dioscorea cyanensis*. The acquisition of knowledge about the genetic diversity of the species at both agronomic and useful traits is essential for an effective genetic improvement program. Hence, in yams, being an essential tuber crop, more research studies based on morphological and molecular markers need to be conducted. A better understanding of the available genetic diversity and the breeding potential of specific accessions is important for the choice of parents for use in breeding programs. Borges et al. [8] recommended that the selection of superior parental lines for crop improvement should be based on both the quantitative measure of the trait evaluated and enough knowledge of the genetic diversity of the germplasm destined for such use.

Knowledge of yam diversity comes from the West African yam belt, primarily through work at the National Agricultural Research Institutes (NARs) and the International Institute of Tropical Agriculture (IITA) [9]. In countries such as Ghana and Nigeria, yams have been widely studied using phenotypic descriptors to classify the different types of yam accessions which are grouped into distinct clusters independent of geographic origin [10]. Similarly, 52 accessions of *Dioscorea species* from Sierra Leone were successfully characterized using 28 morphological descriptors and appreciable differences among the genotypes used were observed [11]. Also, Girma et al. [12] redefined yam core collection using morphological traits. In the study, an attempt was made to redefine the previously developed yam core collection using 56 morphological traits. The Shannon Weaver diversity index and principal component analysis revealed the maximum diversity captured in the base collection in the study. Sartie et al. [13] considered the genetic and phenotypic diversity in a germplasm working collection of cultivated tropical yams (*Dioscorea species*). Working collection of yams (*Dioscorea species*) comprising 53 landraces and seven improved cultivars of four species (*Dioscorea alata, Dioscorea cayenensis* Lam, *Dioscorea dumetorum* Kunth, and *Dioscorea rotundata* Poir.) was evaluated for phenotypic and genetic diversities. The evaluation involved a field assessment of 24 morphological traits and DNA analysis with 32 SSR markers [13]. The study provided an improved understanding of the genetic and phenotypic relatedness among *Dioscorea rotundata, Dioscorea cayenensis, Dioscorea alata,* and *Dioscorea dumetorum*. Interspecific polymorphic SSR markers were identified that may be used for genetic analysis across yam species.

Research to introduce, collect locally, or utilize yam germplasm for genetic improvement in East Africa has been limited, sporadic, and short-lived [5]. Therefore, despite the crop's huge potential for nutrition, food security, income, and economic development, East Africa lags behind West Africa in terms of yams research, production, adoption, and utilization. Information on yam diversity structure within East Africa is limited to two countries in Ethiopia, Kenya, and recent studies in Congo. In Ethiopia, 84 yam accessions were evaluated based on 32 qualitative morphological traits to assess the variation among them [14]. From that study, no clear morphological variations were observed between the genotypes. Such efforts have also been made in Kenya where 22 morphological traits were used to evaluate diversity and reported close relatedness among the yam genotypes [15].

There has been no systematic breeding and selection of yam genotypes for improved traits in Uganda. As such, there is scanty information on yam genotypes grown, their distribution, inherent traits, and diversity at phenotypic and genetic levels [5]. This limits the efficient conservation of these genetic resources and their use in breeding traits [11, 16]. The lack of knowledge on yam diversity has been suggested as a factor in genetic deterioration in several countries [11, 17]. There have been interventions to address these gaps, mainly through germplasm assembly and collaboration with research institutions in West Africa. To understand the diversity of the assembled germplasm, the study sought to characterize the diversity of yam cultivars grown by farmers for decades in Uganda together with germplasm recently introduced from West Africa using phenotypic traits quantifying intrapopulation and interpopulation diversities.

2. Materials and Methods

2.1. Yam Germplasm. The genetic materials used in the study were sourced from Uganda, Nigeria, and Ghana. This included 88 yam cultivars collected from farmers' fields in about forty-five (45) districts/subregions of Uganda (Table 1; Table S1). In addition, 102 yam genotypes were obtained from IITA, Ibadan, Nigeria (Table 1; Table S1). The study also included 101 genotypes from CSIR-SARI, Ghana, comprised of landraces and improved clones routinely used for research at the institute (Table 1; Table S1).

2.2. Phenotypic Evaluation. This study was conducted at National Crops Resource Research Institute (NaCRRI), Namulonge during two cropping seasons, 2020 and 2021. The site is located at latitude 0°5′ N, longitude 32°61′ E, with an elevation of 1,120 meters above sea level (masl), and receives 1,170 mm of rainfall annually [18]. The experiment was laid in an augmented design with each block consisting of 37 genotypes, three local checks, and three plants per genotype. Genotypes were planted on mounds with inter and intrarow spacing of 1.2 m × 1.2 m, respectively. Three presprouted sets (average size of between 100 and 150 g) for each genotype were planted per mound and plots were labeled for data collection. Phenotypic observations were made on leaves, flowers, plant vigour, diseases (yam anthracnose disease and yam virus disease), tubers

TABLE 1: Description of yam germplasm.

Geographical origin	Institution	No. of genotypes sourced	Description of genotypes
Uganda	NARO-NaCRRI	88	Landraces and old cultivars
Nigeria	IITA/Ibadan	102	Improved clones
Ghana	CSIR-SARI	101	Landraces and improved clones

characteristics, and dry matter content. In total, 28 morphological and agronomic descriptors from the standard operating protocol for yam varietal performance evaluation trial [19] were used to characterize the yam genotypes (Table 2).

2.3. Phenotypic Data Analysis. The augmented RCBD function in R package "*agricolae*" (v. 4.1.2) DAU test function [20] was used for the analysis of variance computation to determine differences among genotypes regarding phenotypic traits observed over two cropping seasons. Adjusted means for the different genotypes for the two cropping seasons were obtained and used for further analysis.

Descriptive analysis for qualitative data was performed in R [21] to identify the proportion of plant morphology based on species and the geographical origin of the genotypes. The outputs were presented in bar charts for the three geographical sources of the genotypes.

Principal component analysis (PCA) was performed for all traits using "*factoextra*" and "*vegan*" packages in R [21]. Eigenvalues and load coefficient values were extracted from the PCA result. Six principal components with eigenvalues greater than one with a total cumulated value of 62% were selected. The contribution of each trait to the observed variability was determined using the first two principal components as described by Peres-Nero et al. [22]. With the use of the first two principal components, a biplot plot was generated using the "*ggbiplot*" package in R.

For cluster analysis, a standardized data matrix was used to construct pair-wise genetic similarity values implemented under the "*ape*" package [23] among genotypes using the Gower distance. The genetic distances calculated were used to construct a "*ward.D*" clustering algorithms hierarchical dendrogram and visualized using the FigTree software [24]. These analyses were used to study patterns of variance and relationships among genotypes to determine phenotypic diversity in the collection.

3. Results

3.1. Phenotypic Diversity Based on Morphology. There was considerable variation among the genotypes studied concerning both the underground and aerial morphological parts. Variability among the genotypes in leaf, tuber, inflorescence, and stem morphological parts are presented in Figures 1–4 and classification based on geographical origin is presented in Table 3. Out of the 291 genotypes studied, 218 genotypes (74.9%) were classified as *Dioscorea rotundata* species, and 71 genotypes (24.4%) were observed to be *Dioscorea alata*. Two genotypes

from Uganda were classified as unique based on the trifoliate leaves observed. Generally, *Dioscorea dumetorum* is the species that has trifoliate leaves but this needs to be further confirmed through characterization with an additional number of genotypes having trifoliate leaves or through molecular markers. The majority (175 genotypes, 80.2%) of the *Dioscorea rotundata* genotypes were amongst materials sourced from West Africa (Ghana and Nigeria), with only 47 genotypes (21.6%) collected in Uganda (Table 3). On the other hand, the majority (39 genotypes, 54.9%) of the *Dioscorea alata* genotypes were observed to have been sourced within Uganda.

Four basic leaf forms were identified on yams assessed in this study; ovate (egg-shaped), cordate (heart-shaped), sagittate (arrowhead-shaped), and hastate (spearhead-shaped). The majority of the genotypes (120 genotypes; 41.2%) had cordate leaf form, followed by hastate (96 genotypes; 32.9%), and sagittate (73 genotypes; 25.1%) (Figure 1). Only two genotypes collected from Uganda (0.7%) with ovate leaf form were trifoliate. It was observed that the majority of the hastate and sagittate-shaped genotypes were *Dioscorea alata* from Uganda (39 genotypes; 61.3%). *Dioscorea rotundata* genotypes had cordate-shaped leaves (Figure 1). Leaf colour was generally green among all genotypes assessed, except one *Dioscorea rotundata* genotype (UGY20088) from Ghana, which was characterized by dark purple leaves. Three *Dioscorea alata* genotypes were purplish green in colour and were all introduced from Ghana.

In terms of tuber shape, the majority of genotypes had either cylindrical (59.8%) or irregular (29.2%) tuber shapes. The remaining 13% of the genotype had either spherical/round (7%) or oval shapes (5%). A majority of the genotypes (174 genotypes; 59.8%) with cylindrical-shaped tubers are from West Africa (Ghana and Nigeria), while a majority (85 genotypes; 29.2%) of genotypes with irregularly shaped tubers are from Uganda (Figure 2).

Among the 291 genotypes studied, 192 genotypes (65.9%) did not flower or did not exhibit signs of budding (Figure 3). Nonetheless, of the 99 genotypes (34.0%) that flowered, 92 (92.9%) were *Dioscorea rotundata* genotypes, and 7 (7.0%) were *Dioscorea alata* genotypes. The intensity of flowering among the genotypes that flowered was assessed wherein 12.2% had low flowering intensity, 22.6% had moderate flowering intensity, and the remaining had profuse flowering (Figure 3). The sex among flowering genotypes showed majorly male flowering with 67 genotypes (68.7%), while 31 genotypes (31.3%) were female. The *Dioscorea alata* genotypes (7%) from Uganda that flowered were primarily female. None of the *Dioscorea alata* genotypes sourced from

TABLE 2: Morphological descriptors used for phenotypic characterization of yam genotypes.

| Descriptor	Description	Period of collection
Vine per plant	Counting of the number of vines on each plant	
Spine on sprout	0 = absent and 1 = present	
Vine colour	1 = green, 2 = purplish green, 3 = brownish green, 4 = dark brown, and 5 = purple	
Spines on vine	0 = absent, 1 = few, and 2 = many	
Leaf position	1 = alternate, 2 = opposite, and 3 = alternate at base/opposite above	
Leaf width	Measured (cm)	
Leaf length	Measured (cm)	16 weeks after planting
Leaf area	Calculated (cm)	
Leaf shape	1 = ovate, 3 = cordate, 5 = sagittate, and 7 = hastate	
Leaf density	3 = low, 5 = intermediate, and 7 = high	
Petiole length	Measured (cm)	
Plant vigour	1 = weak, 2 = medium, and 3 = vigorous	
Petiole colour	3 = light green, 5 = dark green, 7 = green purple, 8 = red, and 9 = purple	
Sex of flower	0 = non flowering, 1 = male flowers, 2 = female flower, 3 = monoecious male (predominantly male), and 4 = monoecious female (predominantly female)	
Flower intensity	0 = no flower, 1 = aborted flower, 3 = low, 5 = moderate, 7 = profuse, and 9 = extremely profuse	Two weeks after flowering
Days to flowering	Counting in days (first observation of flower)	
Flower length	The length of the flower (cm)	
Yam anthracnose disease	1 = no visible symptoms, 2 = few on leaves, 3 = mild symptoms, 4 = severe symptoms, and 5 = severe leaf distortion and stunting	Monthly (8 weeks after planting)
Yam virus disease	1 = no visible symptoms, 2 = mosaic on most leaves, 3 = mild symptoms, 4 = severe mosaic, and 5 = severe leaf distortion and stunting	
Tuber weight	Calculated per plot	
Tuber number	Counted per plot	
Tuber circumference	The average circumference length of 3 tubers per plot in cm	
Tuber surface texture	1 = smooth and 2 = rough	
Tuber branching	0. no branching, 3. Slightly branching, 5. Branched, and 7. Highly branched	Between 1 and 14 days after harvesting
Tuber length	The average length of 3 tubers per plot in cm	
Tuber shape	1 = spherical/round, 2 = oval, 3 = cylindrical, and 4 = irregular	
Tuber size	1 = small (less than 15 cm length, 2 = medium (between 15 and 25 cm length), and 3 = big (more than 25 cm length)	
Dry matter content	Calculated using the oven method	

Source: [19]; https://yambase.org/.
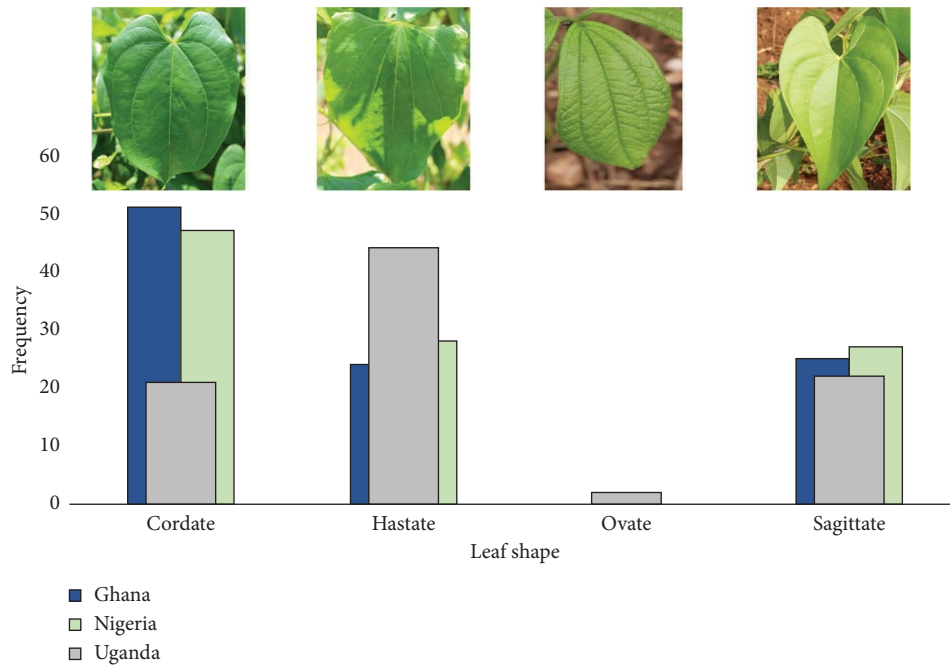
FIGURE 1: Phenotypic variability of plant morphology-based leaf shape and colour.
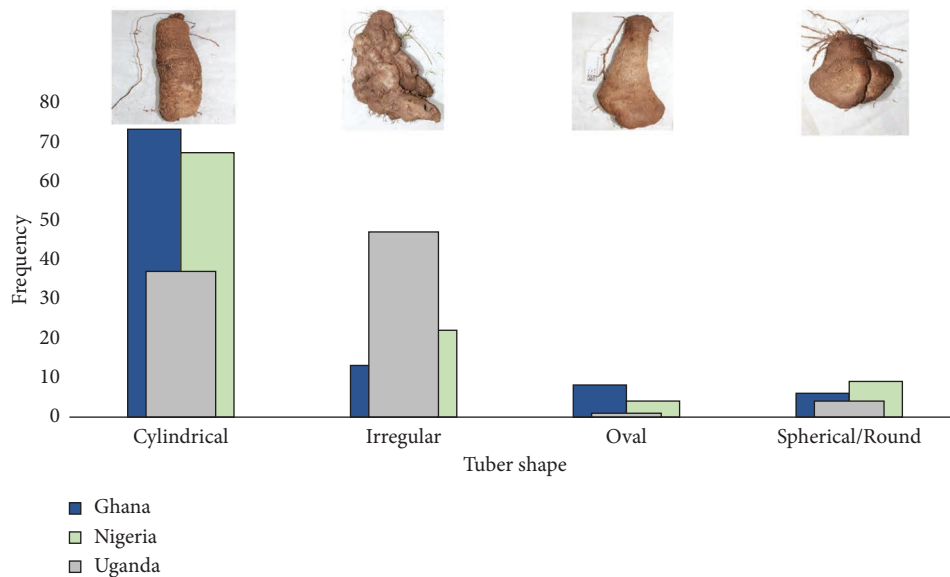

FIGURE 2: Phenotypic variability of plant morphology based on tuber shapes.

Ghana or Nigeria flowered. Moreover, the *Dioscorea rotundata* genotypes that flowered were mainly from West Africa and the two unique trifoliate genotypes from Uganda were male flowering.

The presence or absence of spines and the formation of wings were used to distinguish vine differences observed among the genotypes. Five main variations in vine forms were classified (i) vines without spines, (ii) vines with many spines, (iii) vines with few spines, (iv) winged, and (v) unwinged veins. A total of 122 genotypes (41.9%) were without spines on the vines followed by 132 genotypes (45.4%) with few spines and 39 genotypes (12.7%) with many

spines on the vines (Figure 4). Additionally, most of the thornless genotypes had winged smooth vines and were mainly *Dioscorea alata*. All the genotypes with spines on vines were unwinged and were mainly *Dioscorea rotundata*.

3.2. Contribution of Individual Traits to Phenotypic Variation.
Patterns of variation and the relative importance of each descriptor in explaining the observed variability were assessed through principal component analysis (PCA). Each eigenvalue for the first six principal components (PC) was greater than 1.0 and cumulatively contributed to 62% of the
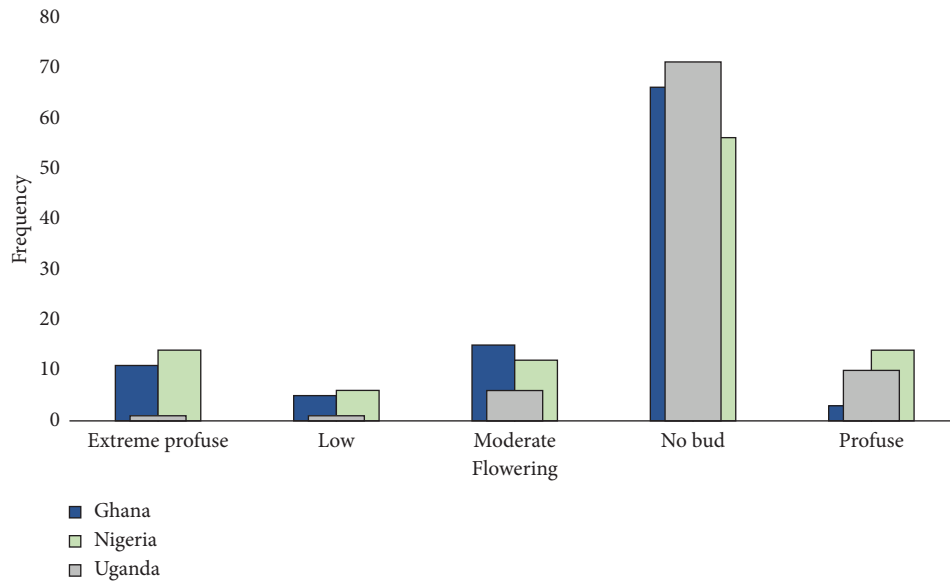
FIGURE 3: Phenotypic variability of plant morphology based on flowering intensity.
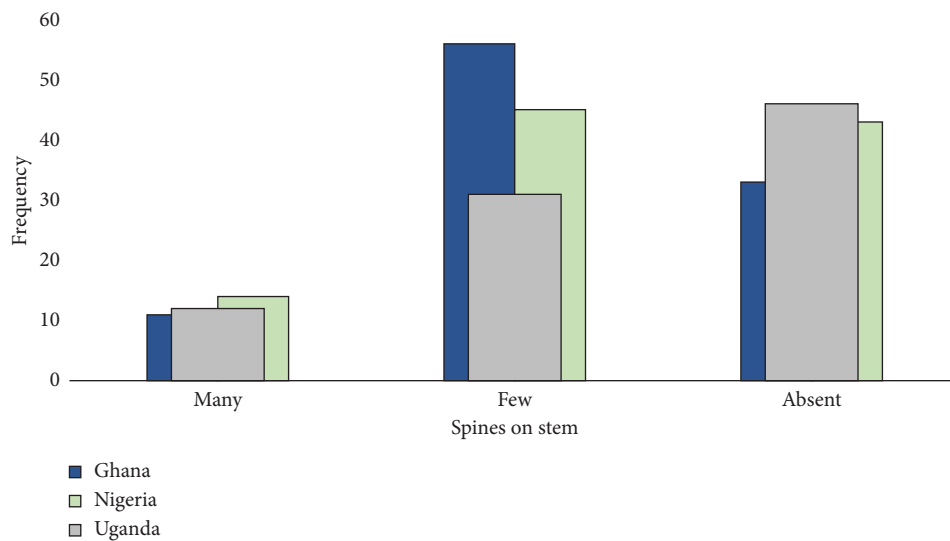

FIGURE 4: Phenotypic variability of plant morphology spines on stem.

TABLE 3: Genotypes are classified based on geographical origin and species.

Origin	*D. alata*	*D. rotundata*	Unique[§]	Total
Ghana	13	88	0	101
Nigeria	19	83	0	102
Uganda	39	47	2	88
Total	71	218	2	291

[§]Trifoliate leaf shape and male flowering.

total morphological variation. Scores of PC1, which accounted for 23% of the total variation, were correlated ($r > 0.45$) to leaf width, leaf length, leaf area, leaf density, petiole length, plant vigour tuber weight, tuber circumference, tuber surface texture, tuber branching, tuber length, tuber shape, and tuber size (Table 4). Scores of PC2

explained 15% of the total variation. Vine characteristics such as sprout spines, vine spines, and vines per plant contributed mainly to the variation in PC3 and PC4, respectively. Considering disease characteristics (Yam mosaic virus and Yam anthracnose disease), at PC4 only yam anthracnose disease was relevant in causing any variation among the genotypes studied. Scores of PC5 contributed to a variation of 5% correlated well with traits such as tuber branching and tuber shape. Based on the contribution of each of the measured traits to the most informative principal components, all 28 traits were found to be relevant in discriminating the yam genotypes.

To assess the clustering/grouping of individual genotypes, the scores of each genotype on the first two principal components, PC1 and PC2, sets were plotted (Figure 5). The genotypes were coloured based on the geographical origin.

TABLE 4: The proportion of the morphological variation and traits contribution explained by the first six principal components.

Traits	PC1[§]	PC2	PC3	PC4	PC5	PC6
Vine per plant	−0.24	0.05	−0.06	0.61	−0.20	0.28
Sprout on spines	0.34	0.39	**0.58**	−0.19	−0.03	0.02
Vine colour	−0.08	0.16	0.29	0.17	−0.35	−0.32
Vine spines	0.16	0.22	**0.58**	−0.44	−0.05	0.12
Leaf position	−0.06	0.05	−0.06	0.33	0.25	−0.29
Leaf width	**−0.81**	−0.22	0.02	−0.19	−0.12	−0.24
Leaf length	**−0.77**	−0.17	−0.28	−0.11	−0.21	−0.24
Leaf area	**−0.84**	−0.24	−0.12	−0.15	−0.18	−0.27
Leaf shape	−0.29	**−0.48**	−0.42	0.11	0.26	−0.02
Leaf density	**−0.68**	0.24	0.06	−0.02	−0.05	0.13
Petiole length	**−0.77**	−0.02	−0.07	−0.24	−0.19	−0.24
Plant vigour	**−0.61**	0.27	0.23	−0.17	0.20	0.11
Petiole colour	0.19	−0.12	−0.34	**−0.54**	−0.24	0.27
Sex of flower	−0.01	**0.85**	−0.35	−0.02	0.01	−0.09
Flower intensity	0.02	**0.83**	−0.40	−0.02	0.03	−0.04
Days to flowering	0.04	**0.87**	−0.38	−0.03	0.02	−0.09
Flower length	0.00	**0.80**	−0.42	−0.04	0.08	−0.05
Yam anthracnose disease	0.01	−0.22	−0.37	**−0.46**	−0.14	0.41
Yam virus disease	0.18	−0.29	−0.36	0.19	−0.06	0.27
Tuber weight per plot	**−0.79**	0.04	0.14	0.14	0.13	0.13
Tuber number per plot	−0.40	0.17	−0.01	0.39	−0.03	0.44
Tuber circumference	**−0.53**	0.28	0.14	0.12	−0.36	0.14
Tuber surface texture	**−0.52**	−0.28	−0.33	0.03	−0.07	0.15
Tuber branching	**−0.56**	0.09	0.14	−0.05	**0.56**	−0.04
Tuber length	**−0.56**	0.36	0.40	0.07	−0.06	0.15
Tuber shape	−0.37	−0.03	−0.07	−0.32	**0.57**	0.15
Tuber size	**−0.68**	0.25	0.20	−0.03	−0.04	0.31
Dry matter content	0.22	0.30	−0.09	−0.15	−0.20	0.04
Eigenvalue	6.34	4.16	2.46	1.76	1.38	1.28
Proportion explained (%)	22.64	14.84	8.78	6.28	4.94	4.57
Cumulative proportion (%)	22.64	37.48	46.26	52.54	57.48	62.05

[§]Principal components (values in bold indicate the most relevant characters (>0.45) that contributed to the variation of the components).

While most of the genotypes clustered around the center of the graph, others were widely scattered along the PC axes. Despite a large amount of overlap between Ghana and Nigeria groups, the dispersion pattern generally separated the species based on the measured morphological traits (Figure 5). The genotypes originating from Uganda clustered at different quadrants with few overlaps with genotypes from West Africa. Most traits such as leaf characteristics and disease-related traits were the main variables associated with the cluster of genotypes of Uganda origin (Figure 5).

3.3. Genetic Relationship among Yam Genotypes. There was considerable variation among the genotypes with regard to the morphological traits used in the study. The analysis of morphological variability based on "ward" hierarchical clustering resulted in two major clusters (cluster A and cluster B (Figure 6)). Cluster A consisted of 194 genotypes (66.7%) with a distance ranging from 28.1 to 188.8 and an average of 52.8. The majority of the genotypes in this cluster

were from Nigeria (69 genotypes; 35.6%), followed by Ghana (67 genotypes; 34.5%), and the remaining from Uganda (58 genotypes; 29.9%).

Based on species, the cluster was mainly made up of *Dioscorea rotundata* (144 genotypes; 74.2%) of which most were sourced from West African genotypes with Nigeria genotypes being the highest (59 genotypes; 49.2%) (Figure 6). Out of the 194 genotypes observed in the cluster, 50 genotypes (25.8%) were identified to be *Dioscorea alata* of which the majority (26 genotypes, 52%) was sourced from Uganda. *Dioscorea alata* genotypes from Ghana in the cluster were only 10 (20%) and Nigeria had 14 genotypes (28%). Within this cluster, most of the genotypes were mainly characterized by cylindrical/oval tubers, hairy tubers, sagittate/cordate-shaped leaves, green with a few purple-colored leaves, and nonwinged vines. The flowering of the genotypes was classified as highly profuse and predominantly female. Two subclusters (A_1 and A_2) were identified within cluster A of which subcluster A_1 had 74 genotypes (38.1%) and subcluster A_2 had 120 genotypes (61.9%) (Figure 6).

In cluster B, the distance ranged from 27.6 to 159.3 with an average distance of 53.0. The cluster was made up of 97 genotypes (33.3%). The highest number of genotypes in this cluster was from Ghana with 45 genotypes (46.3%) while the number of genotypes from Nigeria to Uganda was 19 (19.5%) and 33 (34.2%), respectively (Figure 6). Genotypes in this cluster were characterized by thornless stems, hastate-shaped leaves, green leaf colour, dark green leaves, and a few purple-colored petioles, amorphous shaped, and rough surface tubers.

4. Discussion

Morphological characterization is a highly relevant method to define germplasm or breeding lines and serves as meaningful criteria for selecting materials with desirable traits for breeding activities. In this study, the phenotypic traits used to assess variability in the yam genetic resources were successful in distinguishing the genotypes based on their relationships or groupings. A better understanding of the existing yam germplasm in Uganda is one of the prerequisites for breeding new genotypes with novel or improved characteristics.

Generally, the 28 traits contributed significantly to phenotypic variability, indicating a high degree of morphological polymorphism within the genotypes of *Dioscorea* spp. used in the current study. Similar observations were made by Norman et al. [11] who reported that the observed variations are likely due to sexual recombination and possible mutations [11]. In addition, yams are dioecious with few reported monoecious species, implying that spontaneous hybridization may have contributed to the ancestry of some of the genotypes [11] especially materials obtained from Uganda in this current study.

In the current study, the morphological traits that had a principal role in discriminating between the yam genotypes were tuber and aerial characteristics. These outcomes from the current study were in congruence with reports
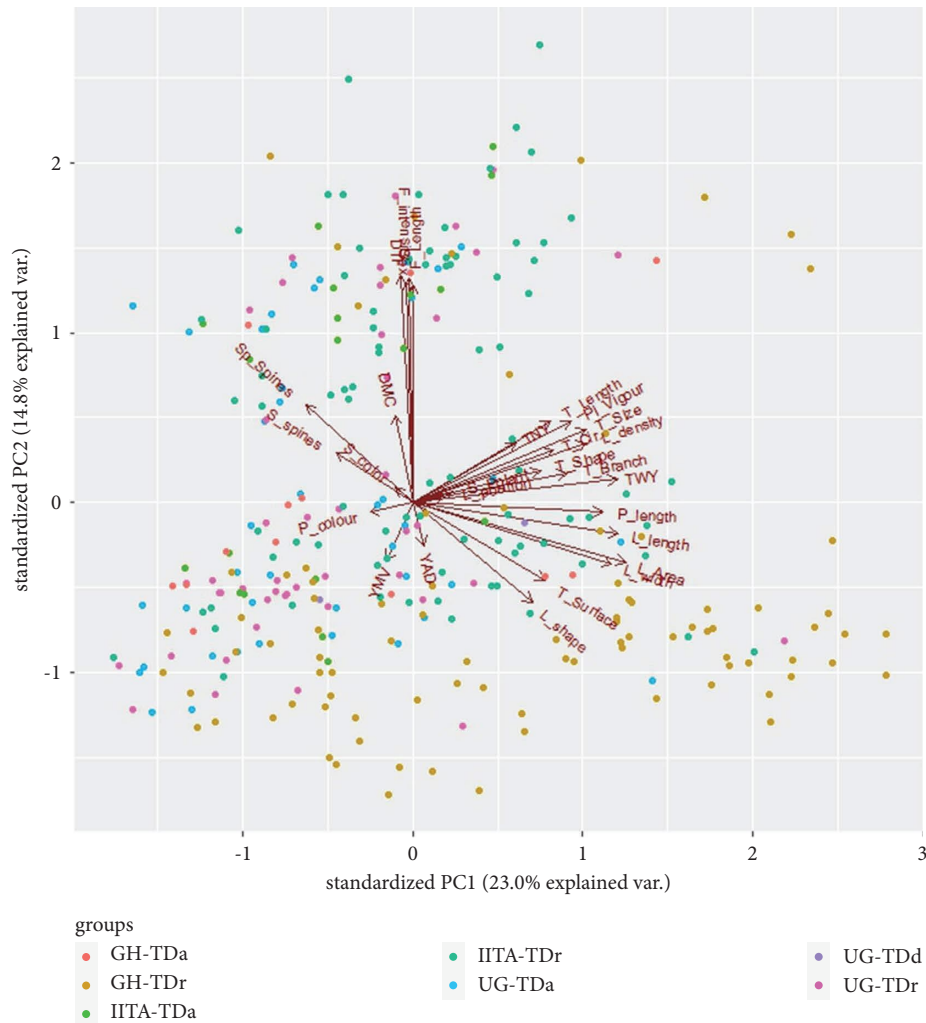
FIGURE 5: The two-dimensional plot of the first two principal components (PC1 and PC2).

obtained by Valentine et al. [15]. In their study, they revealed that the most astute traits were stem colour, leaf margin colour, leaf position, petiole colour, tuber shape, tuber surface texture, and tuber flesh colour. Tuber form is extremely important to both farmers and consumers hence the need to make a proper and careful selection of genotypes for adoption by farmers and end-users. In this study, tuber and leaf shapes revealed significant differences among the different genotypes sourced from different geographical origins which were consistent with studies by Bekele A. and Bekele E. [25] where their research findings reported tuber shape as the key morphological differences among genotypes sourced from different geographical origins. Most of the tubers obtained from Uganda were amorphous and the variations in tuber forms may be attributed to genetic or soil nature.

Progress in yam breeding can be constrained by variable flowering behaviour, making hybridization difficult [26]. The proportion of plants that flower and the flowering intensity also vary with season and location. In this study, varying flowering was observed among the genotypes. The proportion varied which was consistent with reports by

Hamadina et al. [26] where they concluded that the proportion of flowering plants and flowering intensity is strongly influenced by growth potential and environment.

Despite the potential of phenotypic traits in diversity studies, their expression may be partly subjected to environmental variation, thus, providing limited genetic information [9]. The results of the multivariate analysis revealed significant diversity in the current set of yam genotypes based on all phenotypic traits used. The first six principal components contributed 62.05% of the total variation, which was slightly lower than variations observed in Norman et al. [11] and Agre et al. [27] with 74.93% and 71.44% of the total variation, respectively for the first 6 PCs. However, a subgroup of traits including leaf width, leaf length, leaf area, leaf density, petiole length, plant vigour, tuber weight per plot, tuber circumference, tuber surface texture, tuber branching, tuber length, tuber shape, and tuber size had very high contributions to the principal components. This differentiation could be used to assess diversity in future yam collections. Several authors have also reported the importance of phenotypic traits in unraveling the diversity and differentiation in yam [10, 11, 27].
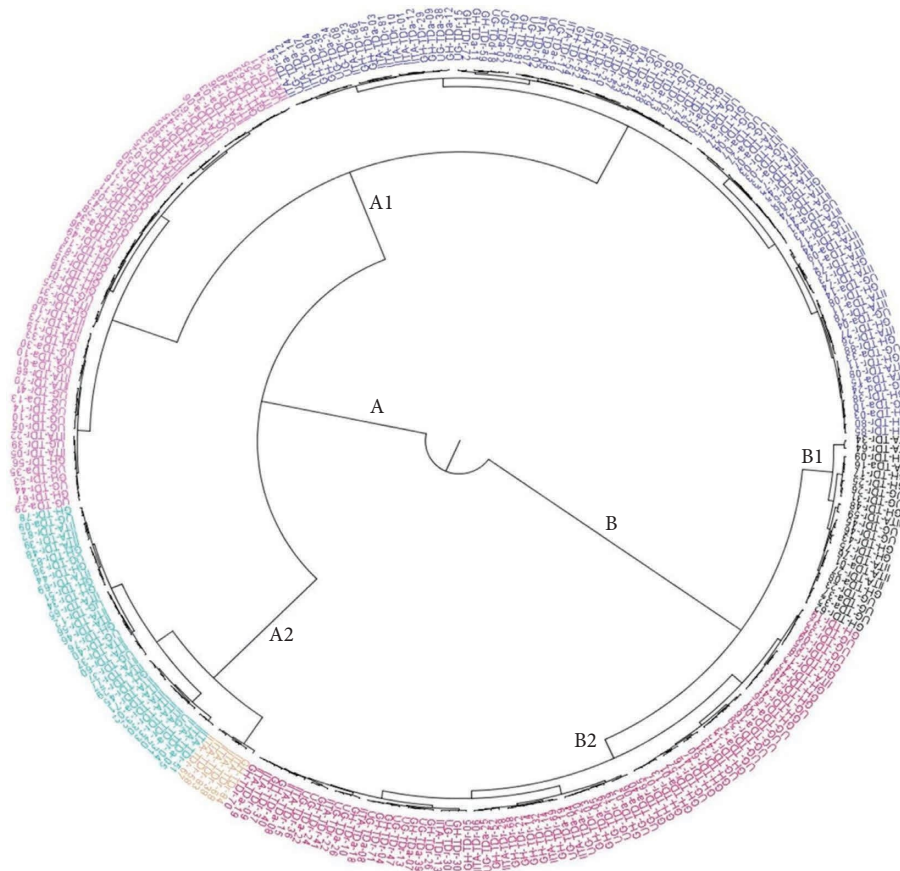
FIGURE 6: A dendrogram showing diversity among 291 yam genotypes based on phenotypic traits.

From the clustering, it was not possible to group all the genotypes based on their geographical origins while it was clear that a majority of the genotypes are related. Also, the clustering pattern did not follow the geographic proximity of the genotypes except in a few cases where some genotype groups were. For example, a majority of genotypes in cluster A were from West Africa and cluster B consisted of a considerable number of genotypes from Uganda. A similar observation was made by Tamiru et al. [9] for geographical origins and reported significant morphological diversity among 84 Ethiopian yam accessions using morphological and farmers' cognitive characteristics. The close proximity of genotypes from Nigeria and Ghana suggests a strong exchange of materials between these two countries, and this may not be the same with Uganda. This is expected considering that both Nigeria and Ghana are neighboring countries and there are several reports of formal and informal exchange of yam materials between these two countries. However, with the introduction of germplasm from these two countries in Uganda, there is a possibility to broaden the genetic base of Uganda yam collection for further use in improvement programs.

5. Conclusion

The study revealed ample phenotypic variability among the yam genetic resources currently available in Uganda. Tuber shape and leaf characters played major roles in distinguishing the genotypes. The significant variability observed in the characters between yam genotypes may be due to the inherent nature of genotypes across each species which can be further determined by genetic analysis. It is therefore prudent to augment the outcome of this study with genetic characterization to accurately identify and classify the major yam genotypes/species grown in Uganda. In this study, two genotypes with trifoliate leaves were observed which could not be classified under white or water yam. There is a possibility that these two genotypes belong to *Dioscorea dumetorum,* but this needs to be further confirmed through the collection of additional genotypes having trifoliate leaves and using molecular characterization. Further, there is a need to conserve and maintain these 291 germplasm collections to ensure that these are not lost due to environmental, social, and economical challenges in the country. Thus, genetic conservation and improvement based on the selected materials should be encouraged with an aim to prevent and/or reverse genetic erosion. With the current information on morphological traits and the identification of some diverse genotypes, there is a possibility that these will be used in establishing a yam breeding program at NaCCRI, Uganda.

Data Availability

The data used to support the findings of this study are available at https://yambase.org/.

Conflicts of Interest

Acknowledgments

Supplementary Materials

Table S1: list of genotypes and their geographical origin. (*Supplementary Materials*)

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