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Phenotypic diversity within yam (*Dioscorea spp.*) germplasm collection in Uganda

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Abstract

A deeper understanding of the morphology of available germplasm is an indispensable initial step for yam genetic improvement and enhanced production in Uganda. However, there is limited information in Uganda on the diversity of yam. The objective of this study was to characterize the diversity of yam cultivars farmers have utilized for decades in Uganda together with germplasm recently introduced from West Africa using phenotypic traits. A germplasm collection of 291 genotypes was characterized based on 28 phenotypic variables. The phenotypic traits data were subjected to multivariate analysis using principal component analysis (PCA) and cluster analysis. Phenotypic traits assessed were informative and discriminating, with 62% of total variation explained among the first six principal components. Our results showed that the important phenotypic traits contributing to most of the variability among the genotypes were leaf characteristics, flowering characteristics, and tuber traits. In general, most genotypes collected within Uganda were identified with amorphous tuber shapes compared to material sourced from West Africa. Dendrogram generated using “ward” hierarchical clustering revealed two major clusters with few of the genotypes sharing similarities. 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. The results are also useful with regard to the identification and conservation of elite genotypes for future genetic improvement of yam in Uganda. More in-depth molecular and biochemical studies to further understand the diversity are recommended.

Introduction

Yam (*Dioscorea spp.*) is a clonally propagated crop with a large global market, particularly in underdeveloped countries (Girma et al. 2014). The crop is cultivated mainly for its tubers and are major source of food energy for millions in tropical countries including East and West Africa, the Caribbean, South Africa, India, and Southeast Asia (Yang et al. 2009). Yam is the world's fourth most important tuber crop (IITA 2006). The yam belt region of West Africa, which includes Benin, Ghana, Ivory Coast, Nigeria, and Togo, produces nearly 96% of global production (72.6 million tonnes) (FAOSTAT 2017). Nigeria is the world's leading yam producer, accounting for more than 65% of worldwide production (FAOSTAT 2017). Farmers in West Africa primarily grow *D. rotundata*, *D. alata*, *D. cayenensis*, and *D. dumetorum*, even though several species of yams are grown around the world (Girma et al. 2016). In Uganda, the cultivation of yams is widespread but farmers mainly grow landraces or old cultivars, which have low productivity, are susceptible to multiple pests and diseases (Mudiope et al. 2012). The crop is attractive for food security because of its resilience to adverse weather, broad agro-ecological 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.

Knowledge on yam diversity comes from the West African yam belt, primarily through work at the National Agricultural Research Institutes (NARs) and International Institute of Tropical Agriculture (IITA) (Tamiru et al. 2011). 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 (Anokye et al. 2014). 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 (Norman et al. 2011).

Previous work to introduce, collect locally or utilize yam germplasm for genetic improvement of the crop in Eastern Africa have been limited, sporadic, and short-lived (IITA 2000). Therefore, despite the crop's huge potential for nutrition, food security, incomes, and economic development, Eastern Africa lags behind West Africa in terms of yams research, production, adoption, and utilization. Information on yam diversity structure within Eastern Africa is limited to two studies in Ethiopia and Kenya. In Ethiopia, 84 yam accessions were evaluated based on 32 qualitative morphological traits to assess the variation among them (Tamru 2006). 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 close relatedness among the yam genotypes was reported (Valentine et al. 2020).

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 in Uganda, their distribution, inherent traits, and diversity at phenotypic and genetic levels. This limits efficient conservation of these genetic resources and their use in breeding traits (Asiedu et al. 2003; Norman et al. 2011). The lack of knowledge on yam diversity has been suggested as a factor in genetic deterioration in several countries (Norman et al. 2011; Dansi et al. 2001). There have been interventions to address these gaps, mainly through germplasm assembly and collaboration with research institutions in West Africa. Understanding the diversity of the assembled germplasm is an indispensable initial step for yam genetic improvement and enhanced production in Uganda. Therefore, the main objective of the current study was 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.

Materials And Methods

Yam germplasm

The genetic materials used in the study were sourced from Uganda, Nigeria, and Ghana. This included 88 yam cultivars were collected from farmers' fields in about forty-five (45) districts/sub-regions of Uganda (Table 1; S1 Table). In addition, 102 yam genotypes were obtained from IITA, Ibadan, Nigeria (Table 1; S1 Table). 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; S1 Table).

Table 1. Description of yam germplasm

Phenotypic evaluation

This study was conducted at NaCRRI, Namulonge during two cropping seasons, 2020 and 2021. The site is located at latitude 0˚5` N, longitude 32 ˚61` E, elevation of 1,120 meters above sea level (masl), and receives 1,170 mm rainfall annually (Nsubuga et al. 2011). 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 intra-row spacing of 1.2 m x 1.2 m, respectively. Three pre-sprouted setts (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, yam virus disease), tubers characteristics, and dry matter content. In total, 28 morphological and agronomic descriptors from the Standard Operating Protocol for Yam Varietal Performance Evaluation Trial (Asfaw 2016) were used to characterize the yam genotypes (Table 2).

Table 2. Morphological descriptors used for phenotypic characterization of yam genotypes

Phenotypic data analysis

The augmented RCBD function in R package "*agricolae"* (v. 4.1.2) DAU test function (de Mendiburu F 2015) for Analysis of variance computation to determine differences among genotypes regarding phenotypic traits observed over two (2) cropping seasons. Descriptive analysis for qualitative data was performed in R (R Core Team 2020) to identify the proportion of plant morphology based on species and geographical origin of the genotypes.

Principal Component Analysis (PCA) was performed using *"factoextra"* and *"vegan"* packages in R (R Core Team 2020). 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 (Peres-Neto et al. 2003).

For cluster analysis, the standardized data matrix was used to generate pair-wise genetic similarity values among genotypes using the Gower distance under the *"ape"* package (Paradis and Schliep 2019). The genetic distances calculated were used to construct a "ward" clustering algorithms hierarchical dendrogram using the R statistical package. These analyses were used to study patterns of variance and relationships among genotypes in order to determine phenotypic diversity in the collection.

Results

Phenotypic diversity based on morphology

There was considerable variation among the genotypes studied with regard to both the underground and aerial morphological parts. Variability among the genotypes in leaf, tuber, inflorescence, and stem morphological parts are presented in Fig 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 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.

Table 3. Genotypes classified based on geographical origin and species

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%) (Fig 1A). Only two genotypes collected from Uganda (0.7%) with ovate leaf form were trifoliate. It was observed that majority of the hastate and sagittate-shaped genotypes were *Dioscorea alata* from Uganda (39 genotypes; 61.3%). *Dioscorea rotundata* genotypes had cordate-shaped leaves (Fig 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 color and were all introduced from Ghana.

Fig 1. Phenotypic variability of plant morphology-based leaf shape and colour

In terms of tuber shape, 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%). Majority of the genotypes (174 genotypes; 59.8%) with cylindrical-shaped tubers are from West Africa (Ghana and Nigeria) while majority (85 genotypes; 29.2%) of genotypes with irregularly shaped tubers are from Uganda (Fig 2).

Fig 2. Phenotypic variability of plant morphology based on tuber shapes

Among the 291 genotypes studied, 192 genotypes (65.9%) did not flower or did not exhibit signs of budding (Fig 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 (Fig 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 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.

Fig 3. Phenotypic variability of plant morphology based on flowering intensity

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) vine 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 (Fig 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*.

Fig 4. Phenotypic variability of plant morphology spines on stem

Contribution of individual traits to phenotypic variation

Patterns of variation and relative importance of each descriptor in explaining the observed variability were assessed through principal components analysis (PCA). Each eigenvalue for the first six principal components was greater than 1.0 and cumulatively contributed to 62% of 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 were

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.

Table 4: Proportion of morphological variation and traits contribution explained by first six PCs

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

Fig 5. Two-dimensional plot of the first two principal components (PC1 and PC2)

Genetic relationship among yam genotypes

There was considerable variation among the genotypes with regards 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 (Fig 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 remaining from Uganda (58 genotypes; 29.9%) (Fig 6). Genotypes within this cluster are mainly characterized by cylindrical/oval tubers, hairy tubers, sagittate/cordate-shaped leaves, green with a few purple-colored leaves, and non-winged 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%).

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 were from Ghana with

40 genotypes (41.3%) while the number of genotypes from Nigeria and Uganda was 37 (27.8%) and 30 (30.9%), respectively (Fig 6). Genotypes in this cluster were characterized by thornless stems, hastate-shaped leaves, green leaf color, dark green leaves, and a few purple-colored petioles, amorphous shaped and rough surface tubers.

Fig 6. Dendrogram showing diversity among 291 yam genotypes based on phenotypic traits

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. (2011) where they reported that the observed variations are likely due to sexual recombination and possible mutations (Norman et al. 2011). 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 (Norman et al. 2011) 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 obtained by Valentine et al. (2020). 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 shape revealed significant differences among the different genotypes sourced from different geographical origins which were consistent with Bekele and Bekele (2020) study 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 (Hamadina et al. 2009). The proportion of plants that flower and the flowering intensity also vary with season and locations. In this study, varying flowering was observed among the genotypes. The proportion varied which was consistent with reports by Hamadina et al. (2009) 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 (Tamiru et al. 2011). The results of the multivariate analysis revealed significant diversity in the current set of yam genotypes based on all with phenotypic traits used. The first six principal components contributed 62.05% of the total variation, which were slightly lower than variations observed inNorman et al. (2011) andAgre et al. (2019) with 74.93 % and 71.44 % of the total variation, respectively forthe first 6PC's. 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 (Norman et al. 2011; Anokye et al. 2014; Agre et al. 2019).

From the clustering, it was not possible to group all the genotypes based on their geographical origins while it was clear that 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. For example, 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. (2011) for geographical origins and reported significant morphological diversity among 84 Ethiopian yam accessions using morphological and farmers' cognitive characters. 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 introductions of germplasm from these two countries in Uganda, there is a possibility to broaden the genetic base of Ugandan yam collection for further use in improvements programs.

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 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 couldn't 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 leave 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 economic 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 identification of some diverse genotypes, there is a possibility that these will be used in establishing a yam breeding program at NaCCRI, Uganda.

Declarations

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Conflict of interests

The authors have not declared any conflict of interests.

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Authors contribution

All authors contributed to the study conception and design. Material preparation, data collection and analysis were performed by Emmanuel Amponsah Adjei, Thomas L Odong, Williams Esuma and Isaac Onziga Dramadri*. The first draft of the manuscript was written by Emmanuel Amponsah Adjei and all authors commented on previous versions of the manuscript. All authors read and approved the final manuscript.*

Data availability

The datasets generated during and/or analysed during the current study are available in the YamBase repository, https://yambase.org/*.*

Supplementary table

S1 Table: List of genotypes and their geographical origin

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Tables

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

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	16 weeks after planting
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, 3 = Alternate at Base/Opposite Above	
Leaf width	Measured (cm)	
Leaf length	Measured (cm)	
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) 4 = Monoecious female (Predominantly female)	Two weeks after flowering
Flower intensity	0 = No flower, 1 = Aborted flower, 3 = Low, 5 = Moderate, 7 = Profuse and 9 = Extremely profuse	
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	Between 1 to 14 days after harvesting
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
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 - 25 cm length) and 3 = Big (more than 25 cm length)
Dry matter content	Calculated using the oven method

(Asfaw 2016); https://yambase.org/

Table 3. Genotypes classified based on geographical origin and species

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

[a]Trifoliate leaf shape and male flowering.

Table 4: Proportion of morphological variation and traits contribution explained by first six PCs

Traits	PC1[a]	PC2	PC3	PC4	PC5	PC6
Vine [b]	-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 [c]	**-0.79**	0.04	0.14	0.14	0.13	0.13
Tuber number [c]	-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

[a] Principal Components, [b] per plant, [c] per plot bases, values in bold indicates the most relevant characters **(>0.45)** that contributed to the variation of the components

Figures

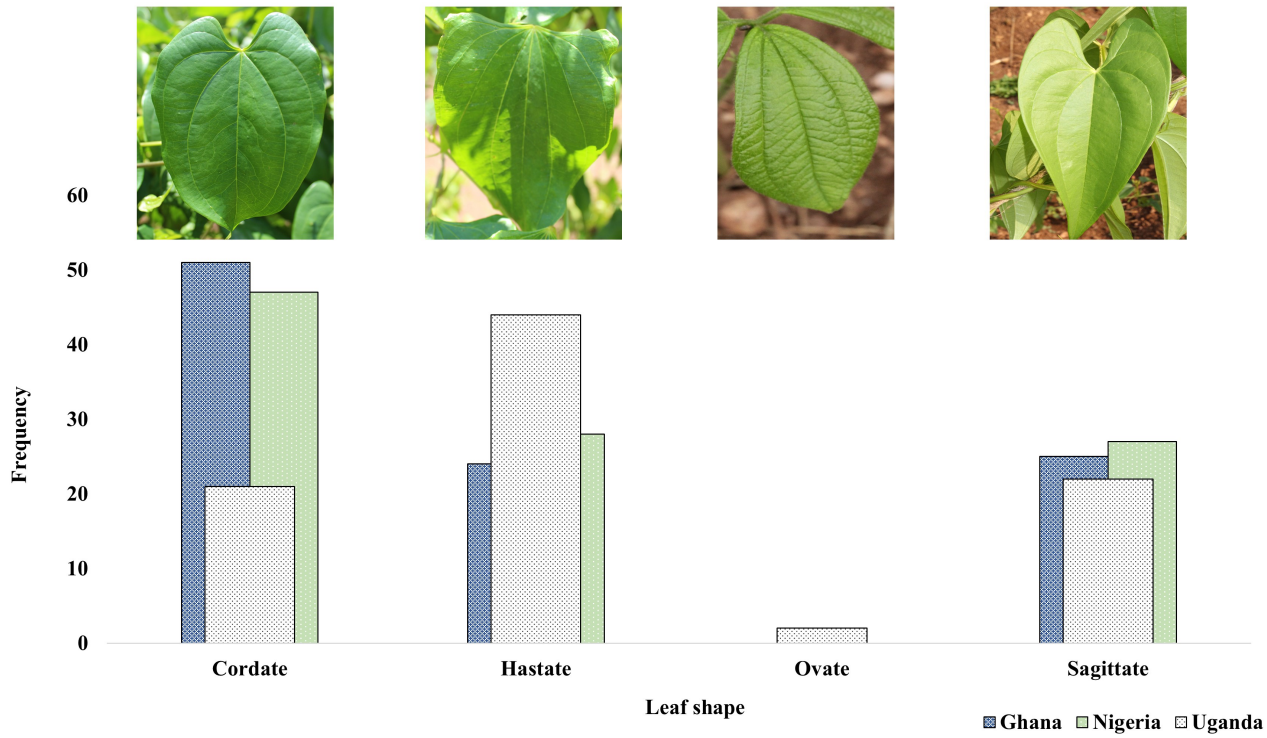

Figure 1

Phenotypic variability of plant morphology-based leaf shape and colour

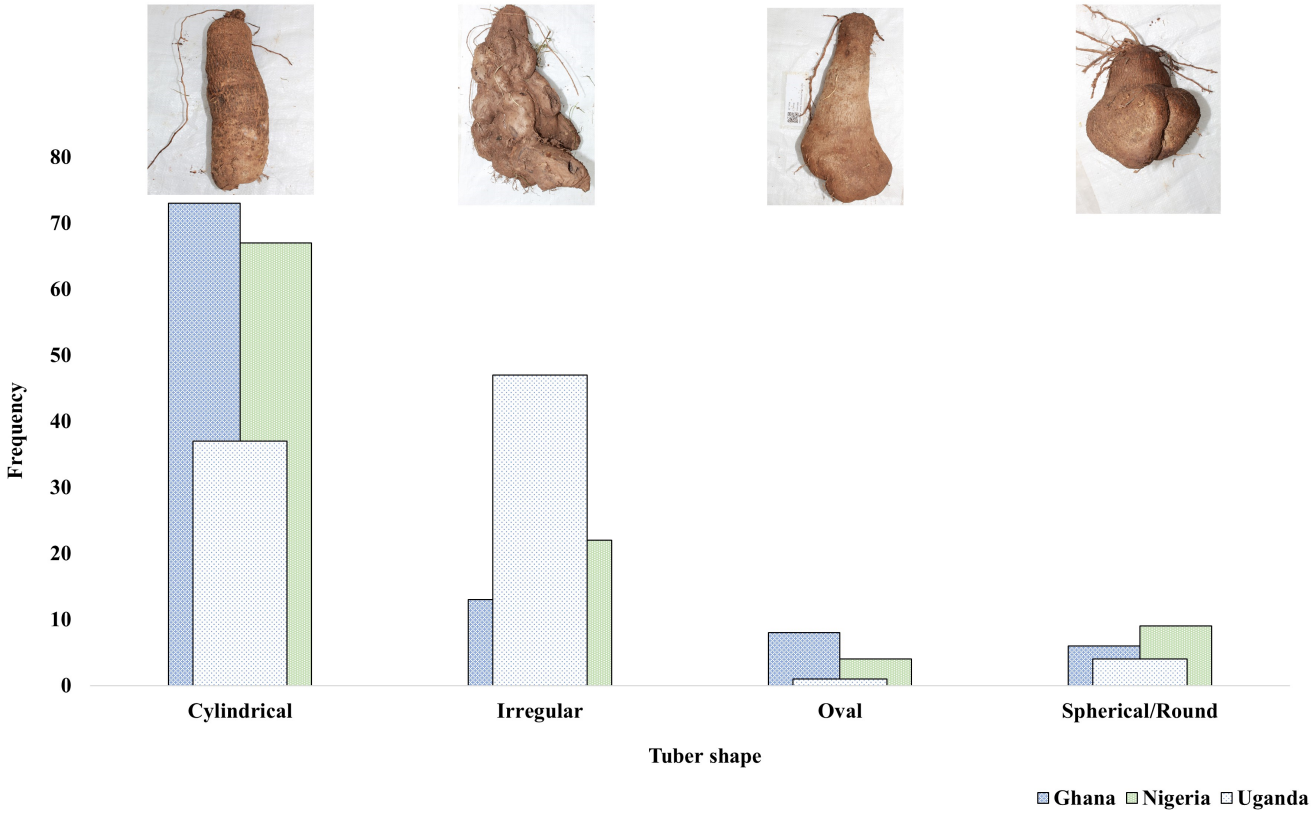

Figure 2

Phenotypic variability of plant morphology based on tuber shapes

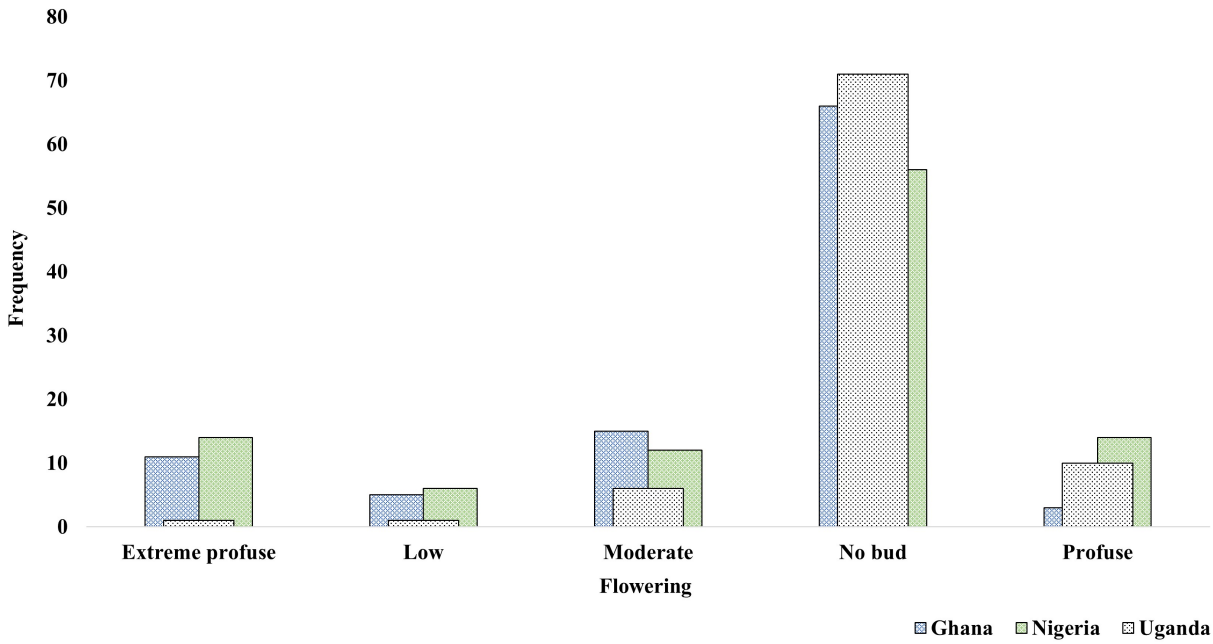

Figure 3

Phenotypic variability of plant morphology based on flowering intensity

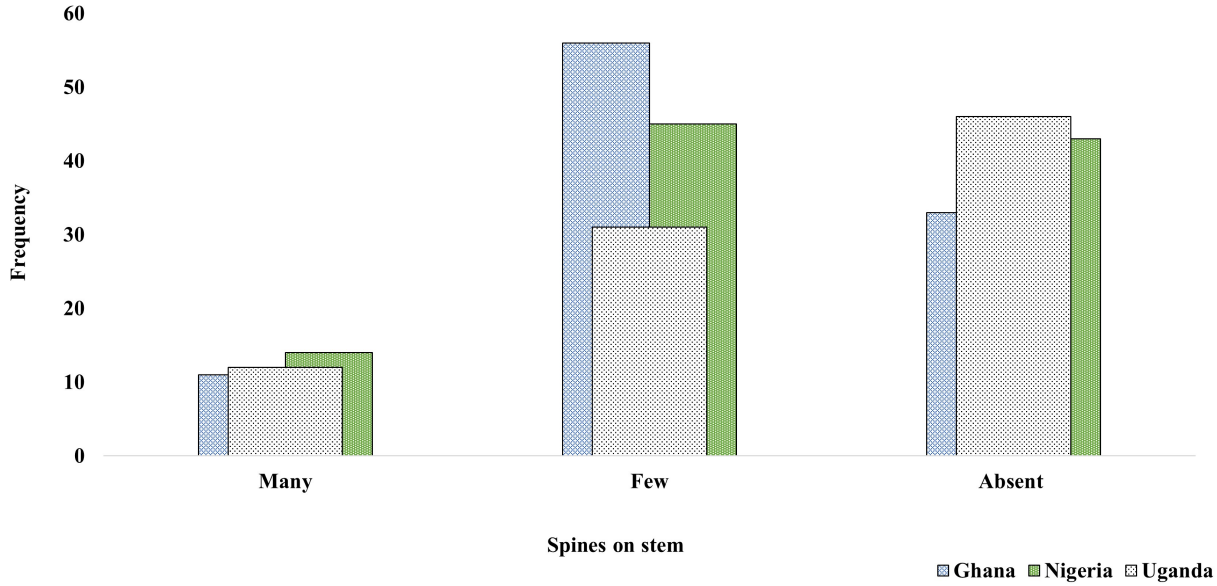

Figure 4

Phenotypic variability of plant morphology spines on stem

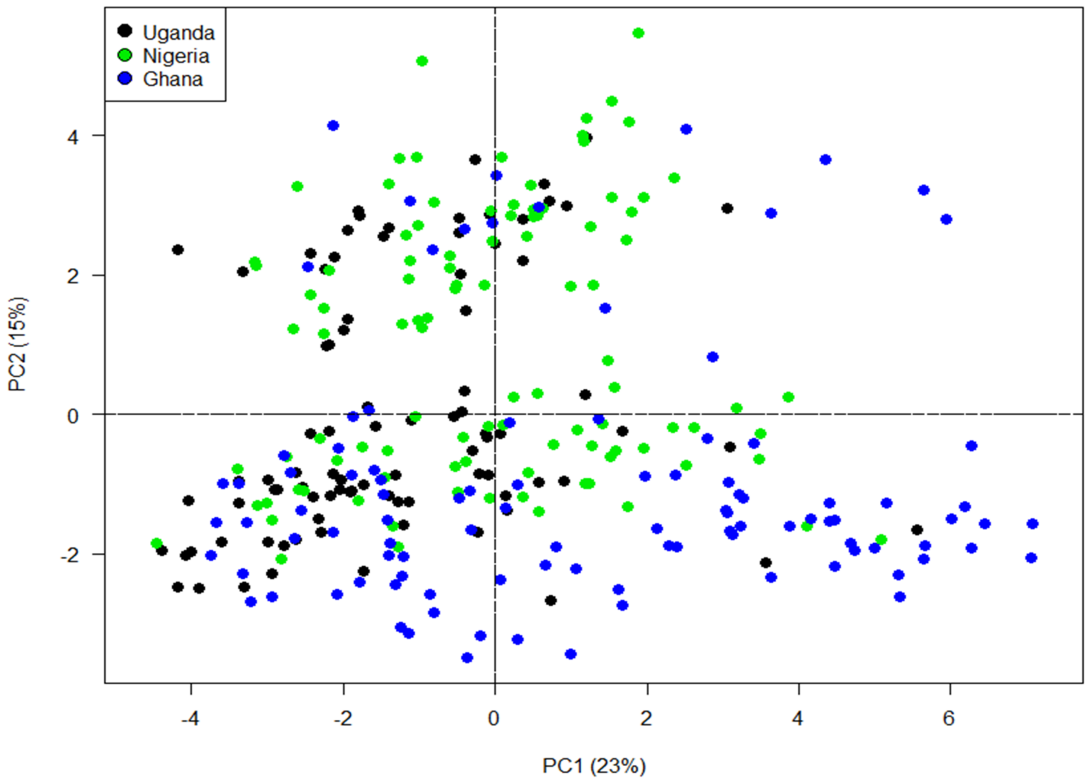

Figure 5

Two-dimensional plot of the first two principal components (PC1 and PC2)

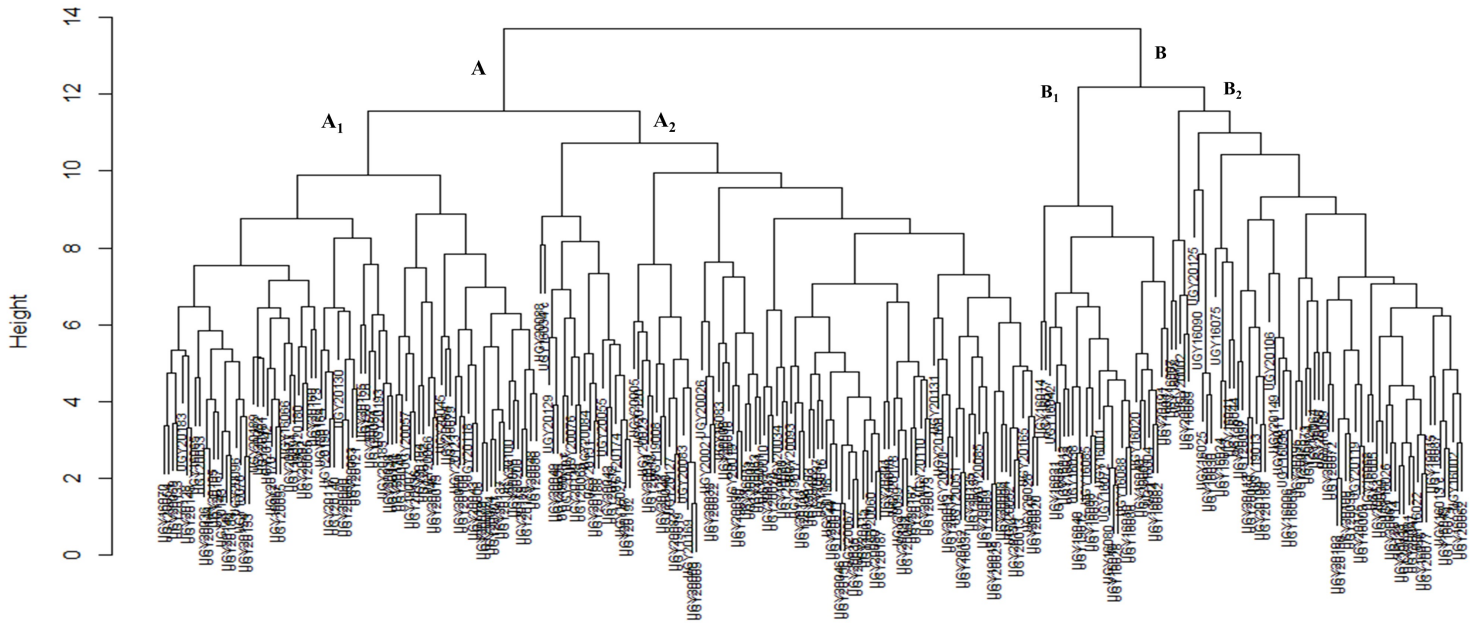

Figure 6

Dendrogram showing diversity among 291 yam genotypes based on phenotypic traits

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- S1Table.docx