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Genetic diversity of sweet yam "*Dioscorea dumetorum* "(Kunth) Pax revealed by morphological traits in two agro-ecological zones of Cameroon

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Genetic diversity of 43 *Dioscorea dumetorum* accessions and two of *Dioscorea cayenensis* Lam as out-group species was evaluated for qualitative and quantitative traits in two different agro-climatic zones Baham (05°20.040' N/010°22.572' E and 1634±3 masl, agro-ecological zone III with rainfall of 1500 to 2000 mm, and mean annual temperature of 19°C) and Ekona (04°12.773'N/009°19.425'E and 445±3 masl, agro-ecological zone IV with rainfall of 2500 to 4000 mm and mean annual temperature of 26°C). Forty one (41) morphological characters according to International Plant Genetic Resources Institute (IPGRI) descriptor, including nine quantitative and 32 qualitative characters were analyzed for multivariate analysis using cluster analysis, principal component analysis (PCA), and analysis of variance. For quantitative characters, cluster analysis revealed three major clusters. The first three components with eigen values > 1 contributed 83% of the variability. The PCA results indicate that traits which largely contributed to the variability within and between the accessions were stem length, leaf length, internode number, leaf width, harvest index, leaf number and internode length. Traits such as harvest index, internode number and stem length showed high heritability and high genetic advance. For qualitative traits, cluster and principal component analysis revealed two major clusters in Baham as well as in Ekona. The traits such as spines on stem base, spines on stem above base, spines length contributed to the variability within and between the accessions. However, the limits of morphological characters in the study of diversity have been detected.

Key words: *Dioscorea dumetorum*, morphological traits, characterization, agro-climatic zone, Cameroon.

INTRODUCTION

Yams constitute a staple food crop for over 100 million people in the humid and sub humid tropics (Mignouna et al., 2003). Yams (*Dioscorea* spp.) belong to the family of *Dioscoreaceae* and are widely distributed throughout the humid and sub humid tropics with about 600 described species (Coursey, 1976). Among the eight yam species

commonly grown and consumed in West Africa, *Dioscorea dumetorum* is the most nutritious (Sefa-Deheh and Afoakwa, 2002). *D. dumetorum*, which belongs to the family *Dioscoreaceae*, originated in tropical Africa and occurs in both wild and cultivated forms but its cultivation is still restricted in West and Central Africa (Degras, 1993). Cultivation of *D. dumetorum*, reported especially in West Africa, is widespread in Western Cameroon (Treche and Delpeuch, 1979). Tubers of *D. dumetorum* are rich in protein (9.6%), fairly balanced in essential amino acids (chemical score of 0.94) and its starch is easily digestible (Mbome Lape and Trèche, 1994; Afoakwa and Sefa-Dedeh, 2001). The use of *D. dumetorum* as famine food is therefore recommended with caution. *D. dumetorum* is not only used for human consumption but also for pharmaceutical purposes. Thus, a novel bio-active compound dioscoretine in *D. dumetorum* has been detected (Iwu et al., 1990), which is acceptable pharma-ceutically and which can be used advantageously as a hypoglycemic agent to reduce the blood glucose level in situations of acute stress such as experienced by patients with hyperthermia, trauma, sepsis and burns and those undergoing general anesthesia (Sonibare et al., 2010). In the practice of folk medicine in West Africa, *D. dumetorum* has been used by herbalists and traditional medical practitioners for the treatment of diabetes and as a topical anesthetic while others have used it as an arrow poison and as bait for monkeys (Corley et al., 1985).

Agronomically, *D. dumetorum* is high-yielding, with yields of 10 and 40 tones/hectare recorded under traditional farming conditions and in agricultural stations, respectively (Lyonga and Ayuk-takem, 1979; Ngong-Nasah et al., 1980; Treche, 1989). It is one of the only two species in which high level of resistance to two major nematode parasites of yam has been reported (Kwoseh, 2000). Unlike the other yams, staking is not necessary to maintain yield (Agbor-Egbe and Treche, 1995) and the tubers grow near the surface of the soil. This saves labour and allows for mechanization of harvest (Sefa-Dedeh and Afoakwa, 2002). Despite these qualities, in general little information is available on *D. dumetorum* diversity but in the case of Cameroon no information is available. Genetic diversity is the prerequisite for any plant breeding program.

Furthermore, the key to success for any genetic improvement programme lies in the availability and measure of genetic variability of desired traits. Morpho-logical characterization is an important first step in description and classification of crop germplasm because a breeding program mainly depends upon the magnitude of genetic variability. However, morphological traits have been widely used in the study of yam germplasm and other yam species, specifically to determine the relation-ships between the various species and landraces, as well as to develop identification keys (Dansi et al., 1999; Mignouna et al., 2002; Norman et al., 2011; Tamiru et al., 2011). Such studies have not been conducted on *D.*

dumetorum species. The aim of this study was to assess the genetic diversity of *D. dumetorum* in two different agro-ecological zones of Cameroon in order to show the influence of environmental conditions on morphological characters.

MATERIALS AND METHOD

Plant materials

A total of 43 accessions of *D. dumetorum* with 2 accessions of *Dioscorea cayenensis* as out-group species are considered in this study (Table 1). 42 are collected from various localities in the main yam growing regions (West, South-West and Nord-west) in Cameroon, 3 from Nigeria. Two accessions of *D. cayenensis* were chosen as out-group species. The accessions were planted in the same period (April 2013) in two experimental fields, one in the West region at ''Ferme Ecole Boukue'' (FEBO) in Baham and the other in the South-West region at ''Institue de Recherche Agricole pour le Developpement'' (IRAD) of Ekona. There was no control over environmental conditions. FEBO is located at latitude 05°20.040' N, longitude 010°22.572 E and an elevation of 1634±3 m asl. FEBO belongs to agro-ecological zone III (Western highlands) characterized by rainfall of 1500 to 2000 mm, with mean annual temperature of 19°C (Anonymous, 2008) whereas, IRAD of Ekona is located at latitude 04°12.773'N, longitude 009°19.425'E, and elevation of 445±3 m and belongs to agro-ecological zone IV (Humid forest with monomodal rainfall) with rainfall of 2500 to 4000 mm and mean annual temperature of 26°C (Figure 1).

Field planting

The tubers were planted in the field at 1 m spacing in each row, and 1 m between rows. The tubers were planted in an arranged randomized complete block with a replicate plot of ten plants per accession. Each plant was supported by an independent stake of *Phyllostachys* to induce good canopy development (Figure 2).

Morphological characterization

The morphological description was done according to International Plant Genetic Resources Institute (IPGRI) and International Institute of Tropical Agriculture (IITA) descriptors for yam (IPGRI/IITA, 1997). These descriptors for yam have been previously used for characterizing cultivated yam (Dansi et al., 1999; Mignouna et al., 2002; Tamiru et al., 2011).

Data collection and analysis

Data was recorded on different types of qualitative and quantitative morphological characters with varying scales of measurements (Table 2). The characters were measured on all the plants in each replication, and mean values from the two replications were used for analysis. Data was analyzed for simple statistic (mean, standard deviation, and variance). Variance components (genotypic δ^2_g and phenotypic δ^2_p) were estimated using Wricke and Weber (1986) formula. Phenotypic (PCV) and genotypic (GCV) coefficient of variation were evaluated as suggested by Singh and Chaudhry (1985). Heritability (broad sense h^2) and genetic advance as percentage of mean were calculated as per Hanson et al. (1956) and Johnson et al. (1955), respectively. Cluster analysis was performed using single linkage with the Euclidean distance. The analyses were made using the computer program IBM/SPSS

Table 1. Accessions of *D. dumetorum* used in this study.

Accessions code	Local name	Area of collection	Altitude (±3 masl.)	Latitude (N)	Longitude (E)
Alou 1	Meleuh	Alou	1606	05°31.240'	009°56.479'
Babadjou1	Neliola	Mbouda	1395	05°37.488'	010°15.668'
Babungo 1	Leueh	Babungo	1182	06°03.984'	010°26.823'
Bafut 1	Nelegha	Bafut	1123	06°05.187'	010°07.094'
Baham cayenensis 1	Leng	Baham	1647	05°20.063'	010°22.118'
Bambalang 1	Leueh	Bambalang	1185	05°53.644'	010°30.814'
Bambui 1	Neleghe-ndongbeu	Bambui	1262	06°00.797'	010°13.635'
Bamendjou1	Chechio	Baham	1647	05°20.063'	010°22.118'
Bamendjou2	Torguem	Baham	1647	05°20.063'	010°22.118'
Bamokonbou1	Nelio	Bafoussam	1414	05°28.781'	010°25.197'
Bana1	Chinchi	Bafang	1167	05°09.365'	010°10.147'
Bandjoun cayenensis 2	Leng	Bandjoun	1509	05°22.392'	010°24.960'
Banga bakundu sweet 1	Sweet yam	Muyuka	62	04°17.314'	009°24.451'
Bangang 1	Neliola	Bangang	1776	05°34.303'	010°09.133'
Bangang 2	Nelio	Bangang	1776	05°34.303'	010°09.133'
Bangangté1	Peule	Bangangté	1350	05°08.379'	010°31.406'
Bangou1	Torgai	Bangangté	1350	05°08.379'	010°31.406'
Batibo 1	Aysoh	Batibo	1127	05°50.144'	009°53.467'
Bayangam1	Chechio	Bayamgan	1560	05°17.930'	010°26.446'
Bayangam 2	Torguem	Bayamgan	1560	05°17.930'	010°26.446'
Bekora 1	Sweet yam	Bekora	60	04°36.114'	009°05.704'
Bekora 2	Sweet yam	Bekora	60	04°36.114'	009°05.704'
Buea sweet 1	Sweet yam	Muea	554	04°10.149'	009°18.149'
Buea sweet white yam 1	Sweet yam	Muea	438	04°12.295'	009°19.912'
Dschang1	Lilio	Dschang	1337	05°26.637'	010°03.404'
Ekona Muyuka sweet white 1	Sweet yam	Muea	401	04°12.740'	009°19.554'
Fenkam-Foto1	Chechio	Bafoussam	1414	05°28.781'	010°25.197'
Fongo-Tongo1	Nloh-nelek	Fongo-Tongo	1460	05°30.118'	009°59.976'
Fonkouankem1	Torga	Bafang	1167	05°09.365'	010°10.147'
Fundong 1	Alim	Fundong	1554	06°16.790'	010°17.075'
Guzang 1	Ndong-mbeck	Guzang	1233	05°49.983'	009°55.278'
Ibo sweet 1	Ibo sweet	Banga Bakondu	56	04°24.103'	009°26.522'
Ibo sweet 2	Ibo sweet	Banga Bakondu	56	04°24.103'	009°26.522'
Ibo sweet 3*	Ibo sweet	Banga Bakondu	56	04°24.103'	009°26.522'
Kumbo 1	Reeg	Kumbo	1722	06°12.386'	010°40.478'
Lysoka sweet 1	Lysoka sweet yam	Lysoka	60	04°11.306'	009°18.745'
Mabondji sweet white 1	Sweet yam mabondji	Mabondji	80	04°33.745'	009°11.806'
Mabondji sweet yellow 1	Sweet yam mabondji	Mabondji	80	04°33.745'	009°11.806'
Mankon 1	Ndong-nebengha	Mankon	1253	05°58.172'	010°08.541'
Mbongue sweet 1	Sweet yam	Muyuka	62	04°17.314'	009°24.451'
Muyuka 1	Sweet yam	Muea	554	04°10.149'	009°18.149'
Muyuka 2	Sweet yam	Muea	554	04°10.149'	009°18.149'
Muyuka 3	Sweet yam	Muyuka	62	04°17.314'	009°24.451'
Nkwen 1	Zolik	Nkwen	1251	05°57.717'	010°10.078'
Penda-boko sweet 1	Penda-boko sweet 1	Muea	554	04°10.149'	009°18.149'

* These accessions collected in Cameroon come from Nigeria.

statistics 20. Quantitative and qualitative characters were analyzed separately to avoid the effect due to the difference in scale. Thus, for quantitative characters, cluster analysis was conducted on the basis of average distance of k-means whereas for qualitative characters, it was on the basis of average linkage. Out-group species was used to give a root to the tree in hierarchical cluster
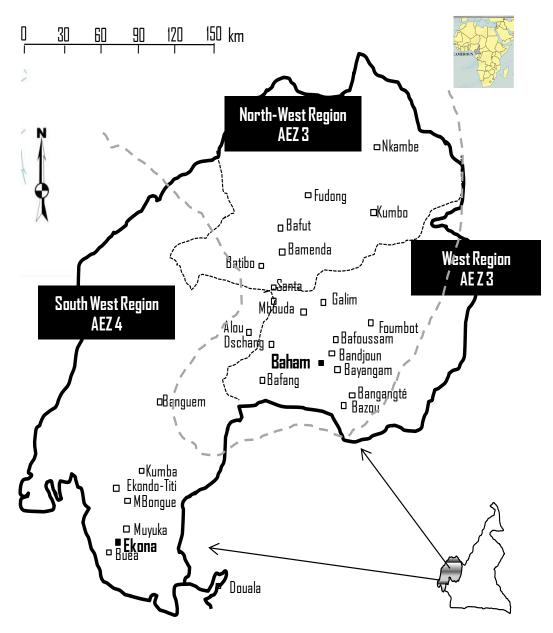
Figure 1. Map of the sample collection areas including the two experimental sites (Baham and Ekona) and some locations where accessions have been collected.

analysis. Principal component analysis was used for variables reduction. Multivariate analyses are a valid system to deal with germplasm collections (Falcinelli et al., 2008).

RESULTS

The estimates of genotypic and phenotypic variance, broad sense heritability and genetic advance in percentages of means and genotypic and phenotypic coefficients of variation are given in Table 3. Variance analysis for characters revealed highly significant differences among genotypes for all the traits evaluated. Genetic advance as percentage of the mean was highest for

harvest index (86.84%, P=0.05), internode number (59.03%, P=0.05), and stem length (53.45%, P=0.05) (Table 3). Broad sense heritability estimates was high for all the characters. The magnitude of phenotypic coefficient of variation (PCV) values for all the traits was higher than the corresponding genotypic coefficient of variation. The highest values of genetic advance as percentage of mean were for harvest index (86.84%), internode number (59.03%) and stem length (53.45%). The first three components with eigen values > 1 contributed 83.26% of the variability, while the first component (PC1) alone accounted for 60% of the total of the variation amongst 45 accessions evaluated for nine

Figure 2. Experimental fields. A: IRAD (Ekona); B: FEBO (Baham).

quantitative traits (Table 4). The first principal component (PC1) was more related to stem length, leaf length, internode number and leaf width. The second principal component (PC2), explaining 18.49% of total variation was associated with harvest index, leaf number and internode length. The third principal component (PC3), explaining 14% of total variation was correlated with day to emergence and stem diameter.

Based on the average distance of k-means, quantitative traits accessions were grouped into three. Group I consisted of five accessions, group II of 10, and group III of 30 accessions. Cluster I was constituted by one accession from the North-West (30), three from South-West (1, 24, 26) and one accession of *D. cayenensis* (12). Cluster II, included three accessions from the West region (8, 15, and 20), two accessions from Nigeria (32, 34), four from South-West region (13, 37, 43, and 45) and one accession from out-group species (5). Cluster II included all the *D. dumetorum* accessions form West, North-West, South-West regions and Nigeria. Mean values along S.D. for each cluster (Table 5) showed that accessions in

Cluster II were highest mean performance for most of the characters studied. Accessions of this cluster gave high yielding and medium number of days to emergence, whereas accessions in cluster I was high yielding but more days to emergence. The first two principal components were plotted to observe relationships between the clusters (Figure 3). Cluster I and III were clearly separated, whereas cluster II was not clearly separated.

Morphology diversity assessed by cluster for qualitative characters

Cluster analysis using single linkage of 32 morphological qualitative characters gave two major groups in Baham (Figure 4) and two major groups in Ekona (Figure 5). Cluster I in Baham was constituted of 34 accessions. It included all the accessions from West and North-West region with six accessions from South-West region (1, 13, 23, 24, 43 and 37) and three from Nigeria (32, 33 and 34). This cluster is characterized by low spines on and

Table 2.Morphological descriptors used for characterization.

Characters	State
Young stem	
Days to emerge*	
Stem length (cm) *	
Internode number*	
Adult stem	
Internode length (cm)*	
Presence/absence of spines	0 absent, 1present
Spine length**	3= short, 5= intermediate,7= long
Spines on stem base**	3= few, 7= many
Spines on stem above base**	3= few, 7= many
Vigour of entire plant**	3=low, 5=intermediate, 7=high
Twining habit**	2= no, 1= yes
Twining direction**	1= clockwise, 2= anticlockwise
Adult stem colour**	1= green, 2= purplish green, 3= brownish green, 4= dark brown, 5= purple
Stem diameter*	
Young leaves	
Leaf number at 20 days after emergence*	
Adult leaves	
Petiole length (cm)**	1= ≤5 cm, 2= 6-9 cm, 3= ≥10 cm
Leaf lenght (cm)*	
Leaf width (cm)*	
Leaf tip (mm)**	1= <2 mm, 2= 2-5 mm, 3= >5 mm
Leaf type*	1= Simple, 2= Compound
Leaf colour**	1= green, 2= purple
Leaf base shape**	1= ovate, 2= cordate, 3= cordate long, 4= cordate broad, 5=sagittate long, 6= sagittate broad, 7= hastate
Leaf density**	3= low, 5= intermediate, 7= high
Leaf margin**	1=entire, 2= serrate
Position of leaves**	1= alternate, 2= opposite, 3= alternate at base/opposite above
Leaf lobation**	1= shallowly lobed, 2= deeply lobed
Leaf Apex shape**	1 Obtuse, 2 Acute, 3 Emarginate
Flowering	
Flowering**	0 no, 1 yes
Fructification**	0 no, 1 yes
Tuber	
Presence/absence of aerial tuber**	0 absent, 1 present
Number of tubers per seedbed**	1= one, 2= few (2-5), 3=several (>5)
Tuber length (cm)**	1= ≤20 cm, 2= 21 - 40 cm, 3 ≥41 cm
Tuber skin colour**	1=Light maroon, 2= dark maroon, 3=greyish
Tuber skin thickness**	1= <1 mm, 2= ≥1 mm
Tuber shape**	1= round,2= oval, 3= oval-oblong,4= cylindrical,5= flattened,6= irregular
Tendency of tuber to branch**	3= slightly branched, 5= branched,7= highly branched
Place where tuber branched**	1= upper third, 2= middle, 3= lower third
Root on the tuber surface**	3= few, 7= many
Place of roots on the tuber**	1= lower, 2= middle, 3= upper, 4= entire tuber
Presence/absence of cracks on the tuber surface**	0= absence, 1= present
Tuber skin thickness**	1= <1mm, 2 ≥1mm
Flesh colour of lower part of tuber**	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
Harvest index*	

*State not specified in IPGRI/IITA, ** Characters used for clustering and principal component analysis.

Table 3. Basic statistics, variance components (δ^2g, δ^2p), genotypic (GCV) and phenotypic (PCV) coefficient of variations, broad sense of heritability (h^2) and genetic advance (GA %, P=0.05) for 43 accessions of *D. dumetorum* and 2 accessions of *D. cayenensis*

Character	Mean ± S.E.	δ^2g	δ^2p	h^2	GCV	PCV	GA (%)
Day to emergence	20.15±0.33	654.74	688.48	0.95	0.53	0.54	44.18
Stem length (cm)	90.47 ±1.22	4751.57	5364.35	0.89	0.50	0.53	53.45
Internode number	10.58±0.21	98.41	118.67	0.83	0.49	0.54	59.03
Number of Leave	11.68±0.23	270.51	287.69	0.94	0.51	0.53	44.34
Leaf length/ leaf width	1.49±0.01	0.42	0.43	0.96	0.73	0.75	44.77
Stem diameter (cm)	0.47±0.01	0.26	0.27	0.97	0.58	0.59	45.28
Internode length (cm)	14.40±0.15	32.38	40.62	0.80	0.29	0.33	37.56
Harvest index (%)	3.40±0.23	64.86	95.77	0.68	0.61	0.75	86.84

Table 4. Principal component (PCs) for nine quantitative characters in 43 accessions of *D. dumetorum* and two accessions of *D. cayenensis*.

Parameter	PC1	PC2	PC3
Eigenvalue	4.57	1.66	1.25
Variance (%)	50.83	18.49	13.94
Cumulative (%)	50.83	69.32	83.26
Stem length	0.90	0.31	0.07
Leaf length	0.85	0.14	0.27
Internode number	0.85	-0.07	-0.14
Leaf width	0.72	0.44	0.22
Harvest index	-0.08	0.79	0.00
Leaf number	0.49	0.78	0.08
Internode length	0.62	0.68	-0.04
Day to emergence	-0.15	0.10	0.96
Stem diameter	0.48	-0.09	0.84

Table 5. Mean and S.D. for three clusters on agronomic traits.

Trait	Cluster I	Cluster II	Cluster III
Stem length (cm)	51.77±8.61	122.60±14.65	82.95±8.29
Leaf length (cm)	8.05±0.46	13.10±1.62	10.85±1.11
Internode number	7.99 ± 2.50	14.54±4.66	9.48±1.60
Leaf width (cm)	5.71±1.48	9.50±1.85	7.13±0.78
Harvest index	5.31±6.69	4.47±1.75	2.51±1.64
Leaf number	9.91±3.80	16.56±7.06	10.14±1.69
Internode length (cm)	8.43±2.33	16.09±2.22	13.71±1.49
Day to emergence	29.33±15.09	25.55±10.43	20.61±7.82
Stem diameter	0.37±0.13	0.66±0.16	0.48±0.15

above stem base. Cluster II contained nine accessions (21, 22, 26, 36, 38, 40, 41, 42 and 45). All the accessions of this cluster were from South-West region. They were characterized by many spines on and above stem base, except accession 36 with low spines on stem base. In

Ekona, Cluster I was constituted by 31 accessions. It included all the accessions from West and North-West regions with six accessions from South-West region (1, 13, 23, 36, 37 and 43). As in Baham, this cluster was characterized by low spines on and above stem base.

Figure 3. Scattered diagram of 43 accessions of *D. dumetorum* and 2 accessions of *D. cayenensis* for two PCs. The digits 1, 2 and 3 represent the cluster number.

Cluster II contained nine accessions from South-West (21, 22, 24, 26, 38, 40, 41, 42 and 45) and three from Nigeria (32, 33 and 34). They were characterized by many spines on and above stem base. It contained the only accession which formed flowers and fruits (32).
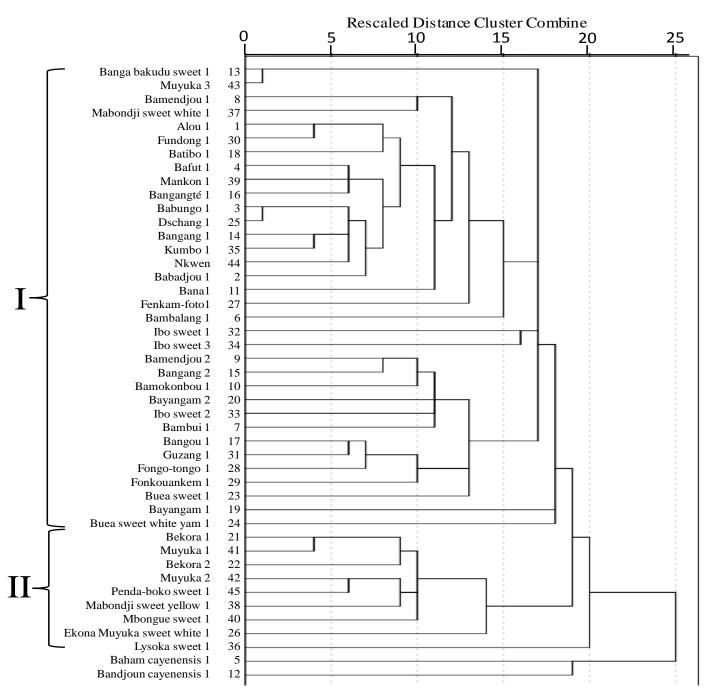
Morphology diversity assessed by principal component for qualitative characters

The result of principal component analysis based on 25 and 26 qualitative characters of 43 accessions of *D. dumetorum* in Baham and Ekona, respectively, are presented in Tables 6 and 7. In Baham six principal components are observed with Eigen-values greater than 1.0 contrary to Ekona with seven principal components. In Baham, the first six principal components explained 71.39% of the variation, while the first principal component (PC1) alone explained 21.60% of the total variation. The PC1 had high loading for tendency of tuber branched, tuber shape, leaf density, number of tuber per seedbed, flowering. The second component (PC2) explaining about 16% of total variation was correlated with spines on stem base, spines on stem above base, spines length and plant vigor. The third component (PC3) explaining about 11% of total variation was mainly associated with characters such as roots on tuber surface, place of roots on the tuber surface, and cracks on the tuber surface.

In Ekona, the first seven principal components explained 77.34% of the variation, while the first principal component (PC1) alone explained about 22% of the total variation. The PC1 had high loading for spines on stem base, spines on stem abovebase, spines length and tuber length. The second component (PC2) explaining about 17% of total variation was correlated with roots on tuber surface, and place of roots on the tuber surface. The third component (PC3) explaining about 12% of total variation was mainly associated with characters such as tuber shape, petiole length and leaf density.

To assess the scores of individual accessions PC1 and PC2 were plotted (Figure 6). In Baham, the biggest set which represented the cluster I in cluster analysis occupied the low corner of the plot with relatively the highest positive and negative values for PC1. Contrary to cluster analysis, PCA analysis detected one sub-group within cluster I. This sub-group was constituted by nine accessions from West (8, 9, 10, 15, and 20), South-West (37 and 43) regions and Nigeria (32 and 33). It constituted the flowering accessions. The second set represented the cluster II which occupied the top corner of the plot with relatively high score for PC2. In Ekona, the biggest set which represented the cluster I in cluster analysis occupied the right corner of the plot with relatively the highest positive and negative values for PC2.

The second set represented the cluster II, and occupied the left corner of the plot with relatively high positive

Figure 4. Relationship of 43 accessions of *D. dumetorum* and 2 accessions of *D. cayenensis* based on single linkage clustering of 32 qualitative characters in Baham.
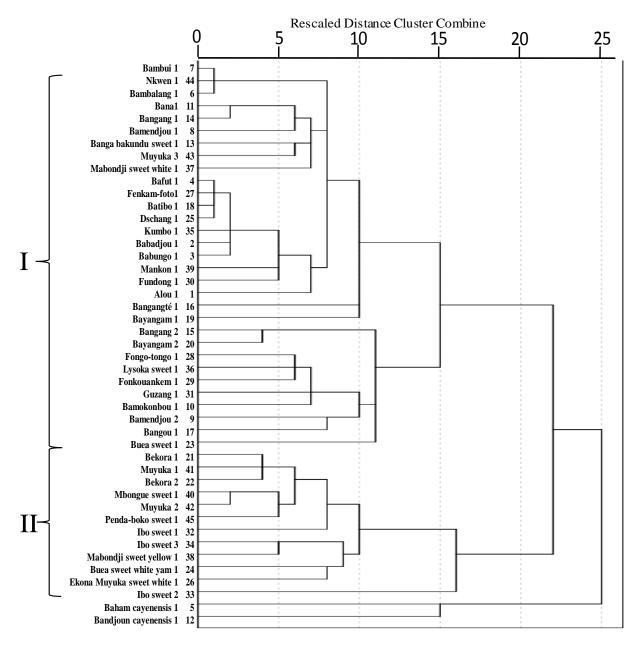
score for PC1.

DISCUSSION

The key to success of any genetic improvement programme lies in the availability of genetic variability of the desired traits (Heller, 1996). Morphological charac-

terization is an important first step in description and classification of crop germplasm because a breeding program mainly depends upon the magnitude of genetic variability (Ghafoor et al., 2001).

Quantitative characters

For all the quantitative characters, the magnitude of

Figure 5. Relationship of 43 accessions of *D. dumetorum* and 2 accessions of *D. cayenensis* based on single linkage clustering of 32 qualitative characters in Ekona.

Table 6. Principal components (PCs) for qualitative characters in 43 accessions of *D. dumetorum* in Baham.

Parameter	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6
Eigenvalue	4.10	3.03	2.13	1.68	1.38	1.23
% of variance	21.60	15.96	11.21	8.86	7.25	6.50
Cumulative (%)	21.60	37.57	48.78	57.64	64.89	71.39
Tendency of tuber branched	0.761	-0.094	0.048	-0.255	0.079	0.187
Tuber shape	0.744	-0.206	0.049	0.222	-0.400	-0.020
Leaf density	0.726	-0.203	0.146	0.137	0.422	0.075
Number of tuber per seedbed	0.658	-0.099	-0.204	0.269	0.231	-0.305

Table 6. Contd.

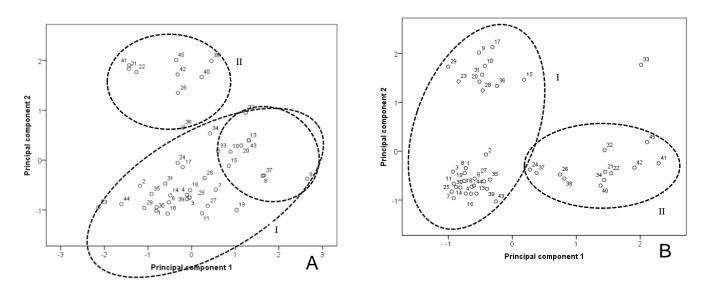| Parameter	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6
Flowering	0.645	0.271	0.208	-0.264	0.264	0.038
Tuber length	0.413	-0.058	0.351	-0.128	-0.164	-0.331
Spines on above stem base	-0.160	0.884	-0.122	0.224	-0.007	-0.019
Spines length	0.013	0.878	-0.152	0.005	-0.024	-0.115
Spines on stem base	-0.269	0.862	-0.108	-0.157	-0.102	-0.115
Plant vigour	0.496	0.638	0.009	-0.222	0.287	-0.086
Roots on tuber surface	0.099	-0.094	0.935	0.093	-0.004	0.109
Place of roots on the tuber surface	0.145	-0.139	0.905	0.077	0.067	0.135
Cracks on the tuber surface	0.031	0.264	-0.609	0.156	-0.191	0.274
Leaf lobation	0.066	0.084	-0.136	0.795	0.084	-0.007
Tuber flesh colour	-0.132	-0.083	0.253	0.694	-0.069	0.090
Petiole length	0.145	0.064	0.250	0.105	0.790	-0.012
Place where tuber branched	0.121	-0.146	-0.405	-0.107	0.509	0.043
Aerial tuber	0.004	-0.151	-0.047	-0.141	-0.137	0.795
Tuber skin thickness	-0.048	0.111	-0.138	-0.279	-0.197	-0.649

Table 7. Principal components (PCs) for qualitative characters in 43 accessions of *D. dumetorum* in Ekona.

Parameter	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7
Eigenvalue	4.40	3.48	2.42	1.53	1.31	1.18	1.14
% of variance	22.01	17.39	12.11	7.65	6.56	5.92	5.69
Cumulative (%)	22.01	39.40	51.50	59.16	65.72	71.65	77.34
Spines on above stem base	0.914	-0.115	-0.166	-0.094	0.086	-0.029	0.086
Spines on stem base	0.914	-0.115	-0.166	-0.094	0.086	-0.029	0.086
Spines length	0.876	-0.117	-0.051	0.198	-0.190	0.030	-0.014
Tuber length	0.712	0.110	0.190	0.357	0.071	-0.064	0.054
Roots on tuber surface	-0.139	0.962	0.002	0.033	0.010	0.059	-0.035
Place of roots on the tuber surface	-0.139	0.962	0.002	0.033	0.010	0.059	-0.035
Tuber shape	0.191	0.311	-0.712	0.198	-0.073	0.263	-0.162
Petiole length	0.164	0.071	0.673	0.140	-0.088	0.394	0.047
Leaf density	-0.228	0.123	0.655	0.434	-0.319	0.151	0.154
Cracks on the tuber surface	0.375	-0.336	-0.486	0.175	0.090	0.251	0.087
Flowering	0.174	0.047	-0.001	0.851	0.049	0.144	-0.009
Number of tuber per seedbed	-0.394	0.050	0.074	0.422	-0.269	0.242	0.268
Tuber flesh colour	-0.041	0.033	-0.179	-0.109	0.812	-0.050	-0.003
Leaf lobation	0.224	-0.092	0.170	0.320	0.738	0.184	-0.157
Plant vigour	0.485	-0.016	0.232	0.274	-0.532	0.289	0.046
Tendency of tuber branched	-0.221	0.041	0.088	0.098	0.032	0.834	0.148
Tuber skin thickness	0.399	0.379	-0.163	0.167	-0.062	0.575	-0.029
Aerial tuber	-0.053	-0.196	0.225	-0.176	-0.056	0.282	0.743
Fruit formation	0.225	0.003	-0.069	0.457	-0.029	-0.282	0.707
Place where tuber branched	0.273	0.467	0.075	0.073	-0.188	0.254	0.536

phenotypic coefficient of variation (PCV) values for all the traits was near the corresponding genotypic coefficient of variation. This indicated a highly significant effect of genotype on phenotypic expression with little effect of the environment (Manju and Sreelathakumary, 2002). High GCV along with high heritability and high genetic advance will provide better information than single parameters alone (Saha et al., 1990; Baye et al., 2005). Hence, traits such as harvest index, internode number and stem length can be improved in the breeding

Figure 6. Plot of the first (PC1) and the second (PC2) principal components for 43 accessions of *D. dumetorum* based on qualitative characters. A: Baham; B: Ekona. The numbers represent the accessions.

program of *D. dumetorum*. However, all the traits of this study showed high heritability, and according to Manju and Sreelathakumary (2002), high heritability estimates indicate the presence of large number of fixable variable additive factors and hence these traits may be improved by selection. The PCA revealed that stem length, leaf length, internode number, leaf width, harvest index, leaf number and internode length were positive, indicating that these traits contributed at their peak towards diversity and can be used in the classification of *D. dumetorum* accession.

Qualitative character

Cluster analysis using single linkage of 32 morphological qualitative characters gave two major groups of *D. dumetorum* accessions in Ekona as well as in Baham with a few differences between the members of these groups, that is, accession 32 formed flowers and fruits in Ekona but has not flowered in Baham. This difference is probably due to environmental effects, in fact plants respond and adapt differently to pressure differences imposed by distinctive agro-climatic zones (Singh et al., 1998). There was no clear separation between accessions and area of collection. The same result has been reported by Sonibare et al. (2010), resulting from the natural migration of populations. Cluster analysis has also clearly separated *D. dumetorum* accessions from *D. cayenensis* accessions in the two areas of cultivation. This observation is explained by the fact that both species belong to two different sections; lasiophyton and Enantiophylum for *D. dumetorum* and *D. cayenensis*, respectively. The section lasiophyton is characterized by the fact that the vines twine to the right, that is, in a

clockwise direction when viewed from the ground upwards, whereas species in section Enantiophylum twine to the left (Onwueme and Winston, 1994).

The PCA analysis is a way of identifying patterns in the data and expressing the data in such a way as to highlight their similarities and differences (Winterota et al., 2008). Traits such as the tendency of the tuber to branch, tuber shape, leaf density, number of tubers per seedbed, flowering, spines on stem base, spines on stem above base, spines length and plant vigor were positive for PC1 and PC2, thus contributing to the maximum diversity of *D. dumetorum* accessions, whereas in Ekona, we had traits such as spines on stem base, spines on stem above base, spines length and tuber length, roots on tuber surface and place of roots on the tuber surface. This difference is related to the fact that plants react differently to varying environmental conditions. That is why morphological and agronomic features cannot be relied upon due to the inconsistency in identification (Muthamia et al., 2013).

The results were consistent between cluster and PCA analysis, but the PC detected in Baham shows that the subgroup of *D. dumetorum* was constituted by the flowering accessions. Thus, grouping accessions by multivariate methods is practical value in the breeding programme, Ghafoor et al. (2001) have already remarked this in blackgram (*Vigna mungo* L.).

Conclusion

This study shows the relatively high genetic diversity of *D. dumetorum* accessions. This diversity could effectively be used in the breeding programme of *D. dumetorum* accessions. Although, morphological traits allowed the

separation of *D. dumetorum* in different clusters, their expression is subjected to agro-climatic variations and thus provide limited genetic information. This is why, molecular markers are recommended with caution to reveal the full extent of existing biodiversity of *D. dumetorum* in Cameroon.

Conflict of interests

The authors did not declare any conflict of interest.

REFERENCES

Afoakwa EO, Sefa-Dedeh S (2001). Chemical composition and quality changes in trifoliate yam *Dioscorea dumetorum* tubers after harvest. J. Food Chem. 75(1):85-91.

Agbor-Egbe T, Treche S (1995). Evaluation of the chemical composition of Cameroonian yam germplasm. J. Food Compost. Anal. 8:274-283.

Anonymous (2008). Second report on the state of plant genetic resources for food and agriculture in Cameroon. Institute of Agricultural Research and Development (IRAD), Yaounde, Cameroon 74 p.

Baye B, Ravishankar R, Singh H (2005). Variability and association of tuber yield and related traits in potato (*Solanum tubersum* L.). Ethiop. J. Agric. Sci. 18(1):103-121.

Corley D, Tempesta MS, Iwu M (1985). Convulsant alkaloids from *Dioscorea dumetorum*. Tetrahedron Lett. 26 (13):1615-1618.

Coursey DG (1976). The origins and domestication of yams in Africa. In: Origins of African domestication. Ed Harlan JR. Mouton Publisher pp. 383-408.

Dansi A, Mignouna HD, Zoundjihékpon J, Sangaré A, Asiedu R, Quin F (1999) Morphological diversity, cultivar groups and possible descent in the cultivated yams (*D. cayenensis / D. rotundata*) complex in Benin Republic. Gen. Res. Crop Evol. 46:371-388.

Degras L (1993). The yam: a tropical root crop (2nd edn.). London: Macmilan Press Ltd. 408 p.

Falcinelli M, Veronesi F, Lorenzetti S (1988). Evaluation of an Italian germplasm collection of *Lolium perenne* L. through a multivariate approach. In: Proceedings of the Eucarpia Fodder Crops Section Meeting, Lusignan, France. pp. 22-24.

Ghafoor A, Sharif A, Ahmad Z, Zahid MA, Rabbani MA (2001). Genetic diversity in blackgram (*Vigna mungo* L. Hepper). Field Crops Res. 69:183-190.

Hanson CH, Robinson HF, Comstock RE (1956). Biometrical studies on yield in segregating population of Korean lespedesa. Agron. J. 48: 268-272.

Heller J (1996). Physic *nut Jatropha curcas* L. Promoting the conservation and use of underutilized and neglected crops. Institute of Plant Genetic and Crop Plant Research, Gatersleben/International Plant Genetic Resource Institute, Rome.

IPGRI/IITA (1997). Descriptors for Yam (*Dioscorea spp.*). International Plant Genetic Resources Institute (IPGRI), Rome), International Institute for Tropical Agriculture (IITA) (Ibadan) 53 p.

Iwu MM, Okunji CO, Ohiaeri GO, Akah P, Corley D, Tempesta MS (1990). Hypoglycaemic activity of dioscoretine from tubers of *Dioscorea dumetorum* in normal and alloxan diabetic rabbits. Planta Med. 56 (3):264-268.

Johnson HW, Robinson HF, Conmstock RE (1955). Estimates of genetic and environmental variability in soybeans. Agron. J. 47:314-318.

Kwoseh CK (2000). Identification of resistance to major nematode pest of yams (*Dioscorea spp.*) in West Africa. PhD thesis. University of Reading, UK. 196 p.

Lyonga SN, Ayuk-takem JA (1979). Collection, selection and agronomic studies on edible yams (*Dioscorea spp.*) in Cameroun. Proceedings of Fifth International Symposium of Tropical Root Crops. pp. 217-243.

Manju PR, Sreelathakumary I (2002).Genetic variability, heritability and genetic advance in hot Chilli *(Capsicum Chinense* Jacq.). J. Trop. Agric. 40:4-6.

Mbome Lape I, Trèche S (1994). Nutritional quality of yams (*D. rotundata and D. dumetorum*) flours for growing rats. J. Sci. Food Agric. 66: 447-455.

Mignouna HD, Abang MM, Fagbemi SA (2003). A comparative assessment of molecular marker assays (AFLP, RAPD and SSR) for white yam (*Dioscorea rotundata*) germplasm characterization. Ann. Appl. Biol. 142:269-276.

Mignouna HD, Dansi A, Zok S (2002). Morphological and isozymic diversity of the cultivated yams (*Dioscorea cayenensis/ Dioscorea rotundata* complex) of Cameroon. Genet. Resour. Crop Evol. 49:21-29.

Muthamia ZK, Morag FE, Nyende AB, Mamati EG, Wanjala BW (2013). Estimation of genetic diversity of the Kenyan yam (*Dioscorea* spp.) using microsatellite markers. Afr. J. Biotechnol. 12(40):5845-5851.

Ngong-Nassah E, Lyonga SN, Ayuk-Takem J (1980).How to grow yams for better yields. Technical Bulletin N° 3, IRA, Bambui, Cameroon.

Norman PE, Tongoona P, Shanahan PE (2011). Diversity of the morphological traits of yam (*Dioscorea* spp.) genotypes from Sierra Leone. J. Appl. Biosci. 45:3045-3058.

Onwueme IC, Winston BC (1994). Tropical Root and Tuber Crops: Production, Perspectives and Future Prospects. Food & Agriculture Org (Ed.), Rome 228 p.

Saha SC, Mishira SN, Mishira RS (1990). Genetic variation in F2 generation of *Chilli capsicum*. NewsLett. 8:29-30.

Sefa-Dedeh S, Afoakwa EO (2002). Biochemical and textural changes in trifoliate yam *Dioscorea dumetorum* tubers after harvest. Food Chem. 79:27-40.

Singh AK, Smart J, Simpson CE, Raina SN (1998). Genetic variation visa-vis molecular polymorphism in groundnut, *Arachis hypogaea* L. Genet. Resour. Crop. Evol. 45:119-126.

Singh RK, Chaudhry BD (1985). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, Ludhiana 303 p.

Sonibare Mubo A, Asiedu R, Albach DC (2010). Genetic diversity of *Dioscorea dumetorum* (Kunth) Pax using Amplified Fragment Length Polymorphisms (AFLP) and cpDNA. Biochem. Syst. Ecol 38:320-334.

Tamiru M, Becker HC, Maass BL 2011. Comparative analysis of morphological and farmers cognitive diversity in yam landraces (*Dioscorea* spp.) from Southern Ethiopia. Trop. Agric. Dev. 55(1):28-43.

Treche S (1989). Nutritional potential of yams (Dioscorea spp.) cultived in Cameroon. Appendices. Thesis, ORSTOM Editions, Collection Studies and Thesis, Paris. 595p.

Treche S, Delpeuch F (1979). Evidence for the development of membrane thickening in the parenchyma of tubers of *Dioscorea dumetorum* during storage. C. R. Hebd. Seances Acad. Sci. 288:67-70.

Winterota R, Mikulikova R, Mazac J, Havelec P (2008). Assessment of authenticity of fruits spirits by gas chromatographic and staple isotope ratio analyses. Czech J. Food Sci. 26:368-375.

Wricke H, Weber WE (1986). Quantitative genetics and selection in plant breeding. Berlin: Walter de Gruyter and Co.