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Diversity of the morphological traits of yam (*Dioscorea* spp.) genotypes from Sierra Leone

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ABSTRACT

Objective: The aim of this study was to explore morphological variability existing within germplasm and to characterize 52 yam genotypes using 28 morphological traits.

Methodology and results: A total of 52 yam genotypes from Sierra Leone were grown in a randomized complete block design with three replications during year 2010 at the University of KwaZulu-Natal, Pietermaritzburg, South Africa. Twenty-eight morphological traits measured from the genotypes were analysed using principal component analysis (PCA) and cluster analysis (CA). The first 10 principal components (PCs), which had eigen-values >0.6 explained 86.61% of the total variability. The PCA results indicating traits that largely contributed to the variability within and between the species included: number of days to shoot emergence, shoot traits (position, shape, size, density, vein colour and measurements of leaves; shoot growth rate) and tuber traits (shape and flesh colour). The two-dimensional plots of the first two PCs grouped the accessions according to their species, whereas some of the genotypes within species were grouped according to the various tuber shapes: irregular, oblong, oval-oblong, round and cylindrical. Genotypes WR 07/024, SR 07/075, 07/073, ER 07/032 and NR 07/042 overlapped in sub-groups B_1 and B_2; whereas genotypes WR07/010, NR 07/041, ER 07/038 and NR 07/067 overlapped in sub-groups B_1 and B_3. This indicated the possibility of duplication of genotypes in the germplasm. The dendrogram of the CA showed six major groups, which also supported groupings in the PCA.

Conclusion and potential application of results: This study revealed that wide genetic diversity exists in yam production cultivars grown in Sierra Leone which could be used to breed high yielding genotypes and other desired traits such as resistance to local pests and diseases. Findings would also be useful for genetic improvement and conservation planning of yams using molecular techniques to confirm the diversity observed.

Key words: *Dioscorea*, agro-morphological diversity, genotypes, characterization

INTRODUCTION

Dioscorea species (yams) are food security crops that sustain many livelihoods in the tropics and subtropics especially West Africa where large commercial scale production is practiced (Mwiringi *et al*., 2009). The crop serves as a source of food, medicine and income for many small scale farmers in Africa. Despite their importance, breeding and selection of yam genotypes with improved traits is currently inhibited by the lack of adequately characterized native genotypes at the morphological and molecular level (Asiedu *et al*., 1998). This is due to the fact that the distribution of

genotypes and their characteristics are not well documented, which constraints the efficient conservation of these genetic resources thereby limiting their use in breeding programmes. This dearth of knowledge has significantly contributed to genetic erosion of yams (Dansi *et al*., 1997).

In Sierra Leone, for instance, despite the importance of yams, there is little knowledge of the existing level of diversity among the various species or varieties within species under cultivation. Also, pests and diseases are among major factors constraining production and causing genetic erosion in yams. Genetic erosion can be overcome by collecting, characterizing and conserving existing germplasm for diversity studies and breeding work (Mignouna *et al*., 2002).

Several morphological diversity studies have been carried out between and within yam populations to catalogue existing diversity (Dansi *et al*., 2001; Hasan *et al*., 2008). However, yams are heterogeneous perennials with many shared morphological, physiological and chemical attributes. The efficient utilization of large genetic variability can be optimized when it has been systematically evaluated, quantified and characterized (Amurrio *et al*., 1995). The use of one or more systematic methods to determine the extent of variability present in yam has provided better understanding in countries like Cote d'Ivoire (Hamon, 1987), Benin (Dansi *et al*., 1999), Cameroon (Mignouna *et al*., 2002) and Malaysia (Hasan *et al*., 2008).

In this study, the multivariate techniques of principal components and cluster analyses were used to determine the levels of phenotypic diversity in 52 yam accessions. The objectives of this study were to determine the relationships between the accessions, and to identify duplicates and groupings of genotypes in the accessions of *Dioscorea* spp. from Sierra Leone.

MATERIALS AND METHODS

Plant material: A total of 52 genotypes which included 50 landraces collected in various locations within four regions (southern, northern, eastern and western) of Sierra Leone, and two improved checks of *D. rotundata* from the International Institute of Tropical Agriculture (IITA) were morphologically characterized (Table 1; Figure 1). The collections were made during the 2007 harvest season (November to December). Two to five tubers of each genotype were collected and assigned an accession number. The accessions were maintained in experimental plots at the Njala Agricultural Research Centre (NARC), Sierra Leone. Minisetts each weighing 50 g were established in 25 cm (diameter) x 20 cm (height) pots in a green-house at the University of KwaZulu-Natal, Pietermaritzburg, South Africa in January 2010. The temperature and relative humidity within the green-house ranged between 20 and 33°C, and between 60 and 85% respectively, typical of the Sierra Leone weather. The pots were filled with composted seedling mix, and water was supplied by drip irrigation. The pots were arranged in a three replicate, randomized complete block design.

Table 1: Accession numbers, collection sites and main tuber traits of 52 yam (*Dioscorea* spp.) accessions.

Accession no.	Local name	Source (village, district/ division, province)	Main tuber traits
WR 07/001	Water Yam	Waterloo, Koya, Western Rural	Oval-white
WR 07/004	Yamsiguwi	Waterloo, Koya, Western Rural	Oval-white
WR 07/007	Water Yam	Waterloo, Koya, Western Rural	Round-white
WR 07/008	Water Yam	Waterloo, Koya, Western Rural	Irregular-white
WR 07/010	Water Yam	Waterloo, Koya, Western Rural	Irregular-white
WR 07/013	Water Yam	Waterloo, Koya, Western Rural	Oblong-white
WR 07/014	Water Yam	Waterloo, Koya, Western Rural	Oval-oblong-white
WR 07/015	Water Yam	Waterloo, Koya, Western Rural	Oval-oblong-white
WR 07/016	Water Yam	Waterloo, Koya, Western Rural	Oval-oblong-white
WR 07/020	Yamsiguwi	Waterloo, Koya, Western Rural	Oval-white
WR 07/022	Unknown	Waterloo, Koya, Western Rural	Round-white
WR 07/024	Water Yam	Waterloo, Koya, Western Rural	Oblong-white
WR 07/025	Water Yam	Waterloo, Koya, Western Rural	Oblong-white

WR 07/028	Water Yam	Waterloo, Koya, Western Rural	Oblong-white
ER 07/029	Yamsiegbamie	Blama, Small Bo, Kenema	Round-white
ER 07/030	Gbuheyamsie	Blama, Small Bo, Kenema	Oval-white
ER 07/031	Gbogboi	Gofor, Dama, Kenema	Round-white
ER 07/032	Yamsigbamie	Gofor, Dama, Kenema	Oval-white
ER 07/033	Water Yam	Levuma, Kando Leppeama, Kenema	Oval-white
ER 07/034	Mende Yamsie	Levuma, Kando Leppeama, Kenema	Oval-white
ER 07/036	Yamsieguwi	Nganyagwehun, Nongowa, Kenema	Oval-white
ER 07/037	Yamsiegbamie	Kenema, Nongowa Kenema	Oval-white
ER 07/038	Yamsieguwi	Kenema, Nongowa Kenema	Round-white
ER 07/039	Njayamsi	Kenema, Nongowa Kenema	Oval-oblong-white
NR 07/040	Mowonmiyim	Ro-Bolie, Magbema, Kambia	Round-yellow
NR 07/041	Mowonmiferra	Rokupr, Magbema, Kambia	Round-white
NR 07/042	Mowomiferra	Masorie, Magbema, Kambia	Round-white
NR 07/043	Mabonk	Makassa, Magbema, Kambia	Round-light purple
NR 07/045	Mowonmiferra	Kalangba, Magbema, Kambia	Round-yellow
NR 07/047	Mawonmiyalla	Ro-thain, Magbema, Kambia	Oblong-white
NR 07/052	Mabonk	Simbeck, Magbema, Kambia	Cylindrical-white
NR 07/054	Eneyi	Makoloh, Pakimasabong, Makeni	Oblong-white
NR 07/057	Anayeyim	Makoloh, Pakimasabong, Makeni	Oval-white
NR 07/059	Anayeyim	Mangay Loko, Makari Gbanti, Makeni	Round-white
NR 07/060	Mawonmiyella	Mangay Loko, Makari Gbanti, Makeni	Cylindrical-white
NR 07/067	Water Yam	Makeni, Bombali Shebora, Makeni	Round-white
NR 07/068	Mawonmiyim	Makeni, Bombali Shebora, Makeni	Oblong-white
NR 07/069	Mawonmiyim	Makeni, Bombali Shebora, Makeni	Round-white
NR 07/071	Water Yam	Makeni, Bombali Shebora, Makeni	Cylindrical-white
SR 07/072	Agbanie	Nguabu, Kaiyamba, Moyamba	Cylindrical-white
SR 07/073	Yamsiegboi	Nguala, Kaiyamba, Moyamba	Oval-white
SR 07/074	Yamsieguwi	Nguala, Kaiyamba, Moyamba	Cylindrical-white
SR 07/075	Jakenakie	Nguabu, Kaiyamba, Moyamba	Round-white
SR 07/076	Agabi	Yayema, Kaiyamba, Moyamba	Cylindrical-light purple
SR 07/079	Njayamsie	Lungi, Kaiyamba, Moyamba	Round-white
SR 07/080	Njamagha	Pelewahun, Kamajeh, Moyamba	Round-white
SR 07/081	Njayamsie	Pelewahun, Kamajeh, Moyamba	Oblong-white
SR 07/082	Njayamsie	Mosongo, Kori, Moyamba	Round-white
SR 07/084	Njamagha	Mokonde, Kori, Moyamba	Round-white
SR 07/085	Darvie	Mokonde, Kori, Moyamba	Round-light purple
TDr 95/00005	Improved check	IITA, Nigeria	Cylindrical-white
TDr 95/18544	Improved check	IITA, Nigeria	Cylindrical-white

Key: WR=Western Region, ER=Eastern Region, NR=Northern Region, SR=Southern Region and TDr=Tropical *Dioscorea rotundata*.

Figure 1: Regional map of Sierra Leone showing germplasm collection districts

The planting distance between pots was 0.25 m. Each pot was fertigated at the rate of 200 kg ha^{-1} of NPK (40:40:60) daily throughout the growing period. Hand weeding was done as necessary.

Morphological characterization: Morphological characterization was conducted by measuring 28 agro-morphological characters from at least three healthy plants (Table 2). Traits measurement and data collection procedure used was based on those presented in the International Plant Genetic Resources Institute's descriptor list for yam (IPGRI/ IITA, 1997) with slight modifications. Only those descriptors or traits that discriminated between genotypes were used in this study. Data were the average of at least three different healthy plants per genotype.

Principal component analysis: Multivariate analysis of the 52 x 28 data matrix comprising of correlation and PCA was performed in Genstat 12.1 (Payne *et al*., 2009) for Windows statistical software package. In the PCA, eigen-values and load coefficient values were generated from the data set. The PCs that had eigen-values > 0.7 were selected, and those traits that had load coefficient values > 0.25 were considered as relevant scores for the PC, which significantly contributed to distinguish between the genotypes (Jeffers, 1967).

Table 2: Morphological traits measured in 52 yam (*Dioscorea* spp.) accessions from Sierra Leone. The traits and measurement methods were based on the International Plant Genetic Resources Institute descriptor list (IPGRI/ IITA, 1997)

IPGRI code	Trait acronym*	Trait/ descriptor	Score code – descriptor state
		Shoot traits	
7.1.1	DE	Number of days to emergence	Direct measurement
7.1.17	NS	Number of stems per plant	1 – 1 stem; 3 – 3 stem; 5 – 5 stem; 7 – 7 stem
7.1.18	SC	Stem colour	1 – green; 2 – purplish green; 3 – brownish green; 4 – purple
7.1.19	NB	Number of internodes to first branching	Direct measurement
7.1.23	IL	Internode length	1 - ≤2.9 cm; 2 – 3-6.9 cm; 3 – 7-10.9 cm; 4 – 11-14.9 cm; 5 -≥15 cm
7.1.25	APW	Absence or presence of wings	0 – absent; 1 – present
7.1.27	WC	Wing colour	1 – green; 2 – green with purple edge; 3 – purple
7.2.9	PL	Position of leaves (mature leaves)	1 – alternate, 2 – opposite, 3 – alternate at base/ opposite above
7.2.10	LD	Number of leaves (density) per plant	3 – low; 5 – intermediate; 7 – high
7.2.12.2	LL	Leaf lobation	1 – shallowly lobed; 2 – deeply lobed
7.2.15	LC	Leaf colour	1 – yellowish; 2 – pale green; 3 – dark green; 4 – purplish green; 5 – purple
7.2.16	LVCUS	Leaf vein colour (upper surface)	1 – yellowish; 2 – green; 3 – pale purple; 4 – purple
7.2.17	LVCLS	Leaf vein colour (lower surface)	1 – yellowish; 2 – green; 3 – pale purple; 4 – purple
7.2.18	LMC	Leaf margin colour	1 – green; 2 – purple
7.2.22	LS	Leaf shape	1–ovate; 2–cordate; 3–cordate long; 4–cordate broad; 5–sagittate long; 6–saggitate broad; 7–hastate
7.2.23	LAS	Leaf apex shape	1 – obtuse; 2 – acute; 3 – emarginated; 4 – acuminate; 5 – aristate; 6 – caudate; 7 – cuspidate
7.2.25	DBL	Distance between lobes	1 – no distance; 5 – medium; 9 – very distant
7.2.30.1	LL1	Leaf length-1	1 - ≤5 cm; 2 – 5.1-8 cm; 3 – 8.1-11 cm; 4 – 11.1-14 cm; 5 – 14.1-18 cm
7.2.30.2	LL2	Leaf length-2	1 – ≤2 cm; 2 – 2.1-4 cm; 3 – 4.1-6 cm; 4 – 6.1-8 cm
7.2.30.3	LW1	Leaf width-1	1 - ≤5 cm; 2 – 5.1-8 cm; 3 – 8.1-11 cm; 4 – 11.1-14 cm; 5 – 14.1-18 cm
7.2.30.4	LW2	Leaf width-2	1 – ≤2 cm; 2 – 2.1-4 cm; 3 – 4.1-6 cm; 4 – 6.1-8 cm; 5 – 8.1-10 cm
7.2.32	TLM	Tip length of mature leaves	1 – ≤4 mm; 2 – 5-9 mm; 3 – 10-14 mm; 4 – 15-19 mm; 5 – 20 mm
7.2.33	TC	Tip colour	1 – light green; 2 – dark green; 3 – purple/ green; 4 – red; 5 – yellowish green; 6 – greenish yellow; 7 – greenish purple
7.2.34	PLM	Petiole length of mature leaves	1 - ≤2.9 cm; 2 – 3-6.9 cm; 3 – 7-10.9 cm; 4 – 11-14.9 cm; 5 -≥15 cm
7.2.37	PC	Petiole colour	1 – green with purple base; 2 – green with purple leaf junction; 3 – green with purple with purple at both ends; 4 – purplish green with base; 5 – purplish green with purple leaf junction; 6 – purplish green with purple at both ends; 7 – green; 8 – purple
7.2.38	PWC	Petiole wing colour	1 – green; 2 – green with purple; 3 – purple
		Underground tuber traits	
7.6.14	TS	Tuber shape	1–round; 2–oval; 3–oval oblong; 4–cylindrical; 5–flattened; 6 – irregular
7.6.30	FCCCS	Flesh colour at central cross section of tuber	1 – white; 2 – yellow; 3 – light purple

**Dioscorea alata* genotypes are identified by presence of wings on stem, while *D. bulbifera* and *D. rotundata* are wingless. This trait was visually assessed.

The first two PCs which accounted for the higher proportion of the total variation were used to present a two-dimensional scatter plot of the groupings of the accessions.

Cluster analysis : For cluster analysis (CA), the standardized data matrix was used to generate pair-wise genetic similarity values among accessions, i.e. the Euclidean dissimilarity coefficient, and then used to generate a hierarchical dendrogram through an unweighted pair-group method average (UPGMA) (Sokal and Michener, 1958) using Genstat 12.1 (Payne *et al*., 2009). This analysis was used to study patterns of variance and relationships among accessions, where accessions with close genetic distances were placed in close proximity in the dendrogram.

RESULTS

Principal component analysis: The multivariate analysis based on the 28 morphological traits revealed considerable diversity among the 52 accessions evaluated in this study (Figures 2, 3 and 4). Each of the first 10 PCs had eigen-value greater than 0.6 and together explained 86.61% of the total variance in the data set (Table 4). Scores of PC1, which accounted for 27.40% of the total variation, were correlated (r > 0.25) with traits related to the shoot (absence or presence of wings, distance between lobes, leaf margin colour, leaf length-2 and tip length of mature leaf) (Table 3). Scores of PC2, which explained 17.95% of the total variation, were correlated (r > 0.25) with shoot traits such as leaf colour, leaf density per plant, leaf length-1, leaf vein colour of lower surface and number of stems per plant; and flesh colour of central cross section of tuber.

Table 3: First 10 principal components (PCs) scores of 28 traits across 52 yam genotypes in Sierra Leone.

No.	Traits+	PC-1	PC-2	PC-3	PC-4	PC-5	PC-6	PC-7	PC-8	PC-9	PC-10
1	APW	**0.274**	-0.093	-0.205	0.213	0.127	0.099	-0.152	0.057	0.044	-0.071
2	DBL	**-0.251**	-0.149	0.071	**0.301**	0.043	-0.039	0.113	-0.125	0.024	-0.086
3	DE	-0.055	0.048	**0.252**	0.060	**0.431**	0.089	**0.284**	**-0.435**	-0.084	**0.357**
4	IL	0.130	0.248	0.142	-0.036	**0.326**	**0.258**	0.072	0.055	**-0.264**	-0.214
5	LAS	0.239	-0.055	0.067	-0.246	**-0.293**	0.007	**0.401**	-0.044	-0.051	-0.028
6	LC	-0.217	**0.273**	-0.035	0.191	-0.102	0.007	0.204	-0.036	0.043	0.002
7	LD	-0.138	**0.333**	0.002	-0.182	-0.002	0.135	0.021	0.150	-0.134	0.084
8	LL	0.214	-0.024	-0.213	0.052	0.109	0.086	0.065	0.121	0.007	**0.653**
9	LMC	**-0.264**	0.226	-0.110	0.157	-0.068	-0.086	0.182	-0.064	0.064	0.033
10	LL1	0.182	**0.258**	0.226	0.105	0.105	0.074	-0.017	-0.040	-0.034	-0.069
11	LL2	**0.271**	0.169	0.061	-0.071	0.119	0.045	-0.154	-0.088	0.193	0.081
12	LW1	0.129	0.226	**0.329**	0.007	-0.198	0.022	-0.169	-0.025	0.089	0.214
13	LW2	0.090	0.091	**0.425**	0.093	0.025	-0.116	-0.015	0.082	**0.280**	-0.223
14	LS	-0.139	-0.163	**0.259**	**0.266**	-0.045	0.248	**0.251**	0.148	-0.209	-0.172
15	LVCLS	-0.001	**0.282**	**-0.295**	0.078	0.102	-0.076	-0.161	-0.040	0.063	-0.148
16	LVCUS	-0.211	0.225	-0.076	0.019	0.183	-0.192	-0.236	-0.138	0.239	-0.071
17	NB	-0.216	0.211	0.172	-0.205	0.062	0.129	-0.198	0.109	0.013	0.013
18	NS	-0.192	**0.265**	0.005	0.027	0.023	0.032	-0.116	0.204	**-0.265**	0.107
19	PC	0.110	-0.075	0.022	**0.446**	-0.008	0.010	**-0.427**	-0.155	**-0.487**	0.028
20	PL	-0.078	-0.048	0.014	0.170	**0.334**	**-0.474**	0.169	**0.623**	-0.038	0.118
21	PLM	0.166	0.109	**0.313**	0.160	-0.229	-0.067	-0.088	0.225	0.244	0.145
22	PWC	0.214	0.156	-0.178	0.208	0.197	0.004	**0.259**	-0.132	**0.274**	0.009
23	SC	-0.238	0.075	0.048	**0.264**	**-0.295**	-0.193	0.039	**-0.274**	0.072	0.158
24	TC	0.171	0.237	-0.025	0.038	**-0.345**	-0.236	0.060	0.014	**-0.336**	0.182
25	TLM	**0.274**	0.108	0.105	0.176	0.065	-0.151	0.211	0.001	-0.089	-0.181
26	TS	-0.131	-0.002	-0.082	**0.278**	-0.128	**0.620**	0.016	**0.272**	**0.258**	0.126
27	WC	0.232	0.119	-0.225	**0.272**	-0.155	0.040	0.034	0.029	0.085	-0.190
28	FCCCS	0.019	**0.328**	**-0.266**	-0.086	-0.090	0.080	0.226	0.029	-0.145	-0.160

+Details of each trait acronym are provided in Table 2. Values in bold indicate the most important traits (>0.25) that had large contributions to the total variance of a particular principal component

a) SR 07/074: Saggitate light green

b) NR 07/052: Cordate green-purple

c) ER 07/038: Saggitate long green

d) WR 07/013: Cordate long green

e) WR 07/025: Saggitate long light green

f) SR 07/085: Cordate long dark green

g) NR 07/041: Cordate long dark green

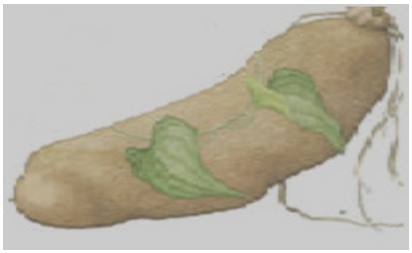
h) NR 07/040: Cordate broad light green

Figure 2: Variation in leaf colour, type and shape among yam (*Dioscorea* spp.) germplasm with a-b, and c-g, and h representing accessions of *D rotundata*, *D. alata*, and *D. bulfifera* respectively

a) WR 07/010: Irregular

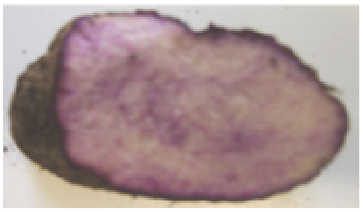
b) SR 07/079: Round shape

c) ER 07/039: Oval-oblong shape

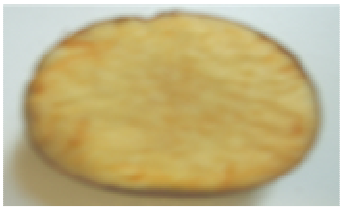


d) Cylindrical shape

Figure 3: Variation in tuber shape among yam (*Dioscorea* spp.) germplasm with a-d, representing accessions of *D. alata*, and *D rotundata*, respectively



a) NR 07/043: light purple flesh



b) NR 07/045: yellow flesh

c) SR 07/072: white flesh

Figure 4: Variation in flesh colour of central cross section of tuber among yam (*Dioscorea* spp.) germplasm with a, b and c representing accessions of *D. alata*, *D. bulbifera* and *D rotundata*, respectively

Table 4: Eigen-value, percentage variation and accumulated variation explained by each component of the first 10 principal components (PCs).

Principal component (PC)	Eigen-values*	Variation of each component (%)	Accumulated variation (%)
1	7.672	27.40	27.40
2	5.025	17.95	45.35
3	3.419	12.21	57.56
4	2.161	7.72	65.28
5	1.636	5.84	71.12
6	1.067	3.81	74.93
7	0.992	3.54	78.47
8	0.869	3.10	81.57
9	0.711	2.54	84.11
10	0.701	2.50	86.61

*[The total of all the variances of the PCs is known as trace. Trace (Λ) = $\sum_{i=1}^{p} \mathrm{Var}\,(Yi) = 28.00$]

The scores of PC3, which explained 12.21% of the total variation, were correlated (r > 0.25) with days to emergence; shoot traits (leaf width-1, leaf width-2, leaf shape, leaf vein colour of lower surface and petiole length of mature leaf); and flesh colour of central cross section of tuber. The scores of PC4, which explained 7.72% of the variation, were mainly correlated (r > 0.26) with shoot traits (distance between lobes, leaf shape, petiole colour, stem colour and wing colour) and the tuber shape trait. The scores of PC5, which explained 5.84% of the total variation, were correlated (r > 0.29) with days to emergence, internode length, leaf apex shape, petiole length, stem colour and tip colour. The scores of PC6, which explained 3.81% of the total variation, were correlated (r > 0.25) with the shoot traits: internode length, petiole length and below ground trait (tuber shape). The scores of PC7, which explained 3.54% of the total variation, were correlated (r > 0.25) with days to emergence, leaf apex shape, leaf shape, petiole and petiole wing colour. The scores of PC8, which explained 3.10% of the total variation, were correlated (r > 0.27) with shoot traits (days to emergence, petiole length, stem colour and tuber shape) and the below ground trait (tuber shape). The scores of PC9, which explained 2.54% of the total variation, were correlated (r > 0.25) with shoot traits (internode length, leaf width-2, number of stems, petiole colour, petiole wing colour, tip colour) and tuber shape. The scores of PC10, which explained 2.50% of the total variation, were correlated (r > 0.35) with internode length and leaf lobation. The PC11 and subsequent PCs were considered to be less significant since their percentage contribution to the total variation were small (Table 4).

Graphical presentation of principle component and cluster analysis: The first two most important principal components, (PC1 and PC2), which contributed 45.35% of the total variance in the data set were plotted in a graph (Figure 5). The 28 morphological traits classified the 52 genotypes into five main clusters, i.e. groups A, B, C, D and E. While most of the genotypes clustered around the centre of the graph (Figure 5), others were widely scattered along both PC axes. Despite the small amount of overlap between sub-groups B_1 and B_2, the dispersion pattern generally separated the species based on the measured morphological traits (Figure 5). Of the 52 genotypes studied, five (WR 07/024, SR 07/075, SR 07/073, ER 07/032 and NR 07/042) overlapped in sub-groups B_1 and B_2, whereas four genotypes (WR07/010, NR 07/041, ER 07/038 and NR 07/067) overlapped in sub-groups B_1 and B_3 implying the possibility of ion of duplicate genotypes in the germplasm collection.

Accessions of group D (NR 07/043 and NR 07/059) had purple wings, purplish-green young leaves, intermediate lobes and cylindrical and branched tubers. Accessions of group E (WR 07/013 and SR 07/085) sprouted in a period of a month had purple leaf margins, purplish-green petioles with purple at both ends. Whereas WR 07/013 had an oblong shaped tuber with white flesh colour, SR 07/085 had round tubers with light purple flesh colour of central cross section of tubers.

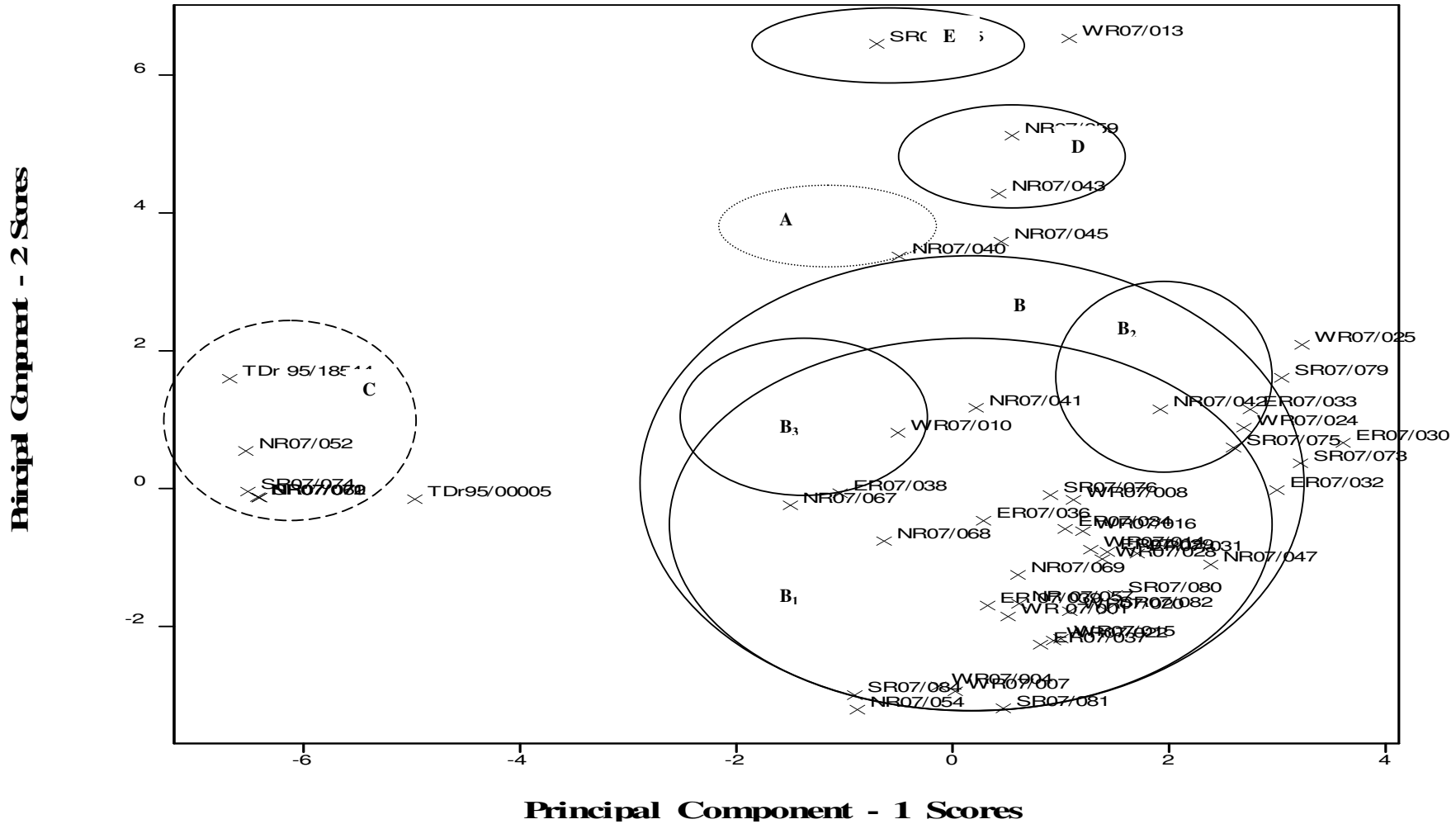


Figure 5. Two-dimensional plot of the first two principal components (PC-1 and PC-2). Accessions that are encircled by the dotted (group A = *D. bulbifera*), dashed (group C = *D. rotundata*), and solid (groups B, D and E = *D. alata*) lines

Accessions of group C (NR 07/052, NR 07/060, NR 07/071, SR 07/072, SR 07/074, TDr 95/00005 and TDr 95/18544) belong to *D. rotundata*, and except for TDr 95/00005 were characterized by wingless vines. Most exhibited saggitate broad leaf shape, purplish green stems, cylindrically shaped tubers, with white flesh colour of central cross section of tubers. They had delayed sprouting, but produced fairly intermediate leaf density due to their profuse branching habit.

Cluster analysis: The dendrogram of the hierarchical cluster analysis (HCA) separated the 52 genotypes into different clusters with Euclidean distance dissimilarities ranging between 0.8 and 1.0 (Figure 6). At the dissimilarity distance of 0.90, the dendrogram identified six main clusters, A, B, C, D, E and F. Clusters A, E and F had two genotypes each, cluster B consisted of 38 genotypes and cluster C consisted of one genotype and cluster D had seven genotypes. Genotypes of cluster A belong to *D. bulbifera*, while genotypes of clusters B, C, E and F belong to *D. alata*, and genotypes of cluster D belong to *D. rotundata*. At the 0.95 dissimilarity distance, cluster B was further divided into three sub-clusters: B_1, B_2 and B_3, each consisting of 5, 30 and 3 genotypes, respectively. The dendrogram of the hierarchical cluster analysis (Figure 6) produced a similar grouping of genotypes as did the PCA scatter plot (Figure 5). The clustering patterns of the various genotypes in the dendrogram revealed the proximity of their genetic distance.

The 43 genotypes of *D. alata* exhibited different leaf traits ranging from saggitate long green leaf to cordate long dark green leaf. Of the 43 gentotypes, 17 had round, 11 oval, seven oblong, five oval-oblong, two irregular and one cylindrical tuber shape; while the flesh colour of central cross section of tuber of 40 genotypes was white, three exhibited light purple colour. Genotypes of *D. bulbifera* exhibited cordate light green leaf and cuspidate leaf apex shape. The tuber shape of both genotypes was round. The bulbils of NR 07/045 were larger than those of NR 07/040. The flesh colour of central cross section of tuber of both genotypes was yellow. Members of *D. rotundata* exhibited mainly saggitate light green leaf, cordate green purple leaf and saggitate long green leaf. The tuber shape of all genotypes was cylindrical possessing white flesh colour of central cross section of tuber.

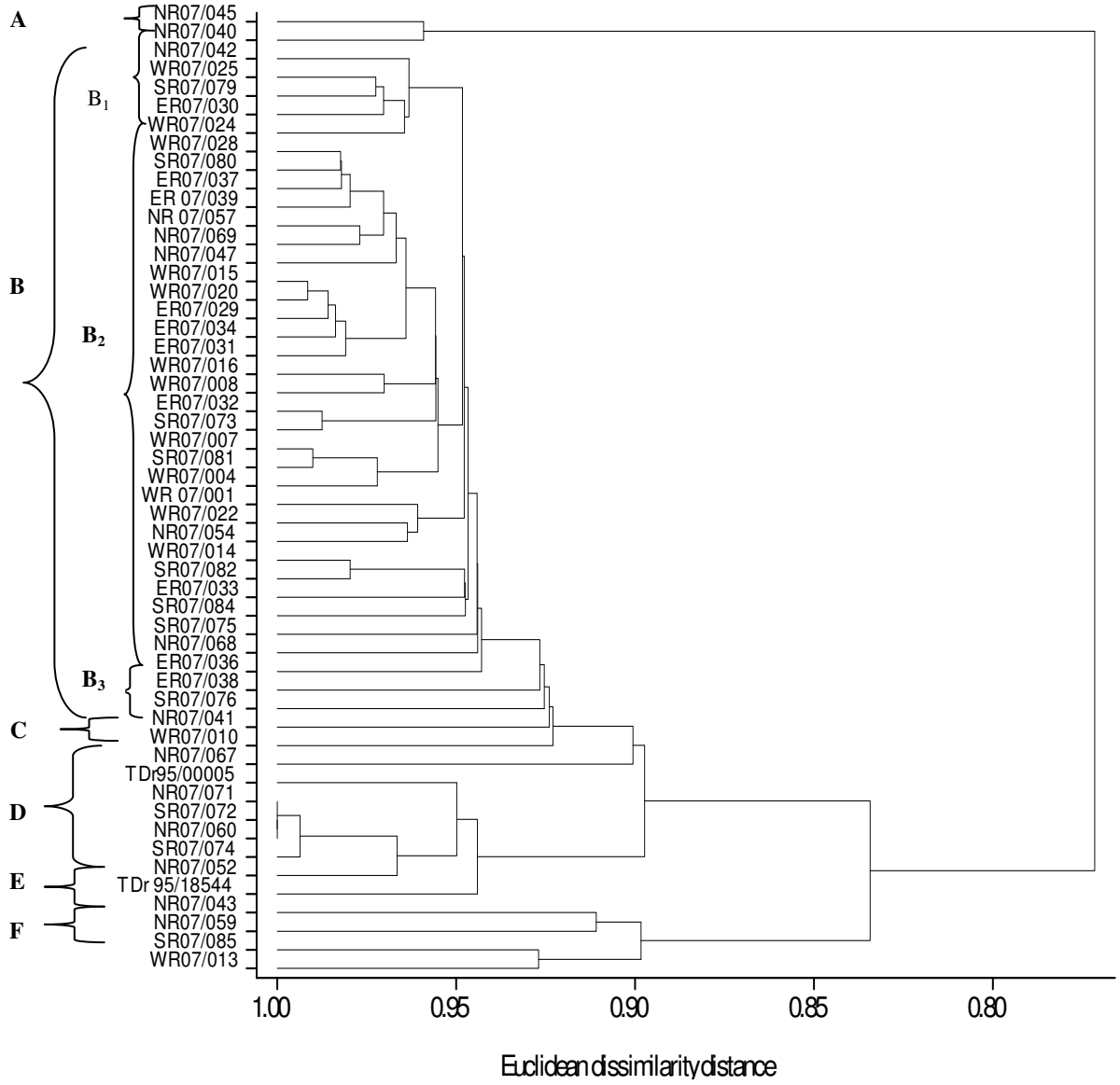


Figure 6. Dendrogram showing genetic diversity among 52 yam accessions from Sierra Leone (43 each of *D. alata*, two each of *D. bulbifera* and seven each of *D. rotundata*) based on morphological traits

DISCUSSION AND CONCLUSION

The standard yam descriptor list (IPGRI/ IITA, 1997) was a useful tool for assessing the available variation among Sierra Leone accessions. The polymorphism showed for 16 qualitative descriptors and 12 quantitative traits confirm that the selected descriptors are appropriate for appraising yam diversity. A better understanding of the existing traditional yam cultivars in Sierra Leone is one of the prerequisites for breeding new cultivars with novel or improved characteristics.

Generally, all 28 traits contributed towards phenotypic variability, which indicated high degree of morphological polymorphism within the accessions of *Dioscorea* species studied. The variation in morphological traits within and between landraces of *D. alata, D. bulbifera* and *D. rotundata* is likely due to sexual recombination and possibly mutation (Martin, 1976).

The variation in morphological traits within and between landraces of *D. alata, D. bulbifera* and *D. rotundata* is likely due to sexual recombination and possibly mutation. Yams are dioceous implying that spontaneous hybridization may have contributed to the

ancestry of some of the accessions, and improvement may have been far more often by selection of somatic mutants In addition (Velayudhan *et al*., 1989). In the present study, however, only two genotypes of *D. bulbifera*, NR 07/040 and NR 07/045, flowered. Thus, the interspecific variation across species was possibly due to the fact that *D. alata* and *D. rotundata* form part of the section Enanthiophylum while *D. bulbifera* belongs to Opsophyton.

Accessions placed in group A (NR 07/045 and NR 07/040), based on PCA, belong to *D. bulbifera* and were characterized by wingless stems and petioles, and sharp angled bulbils with depressions containing preformed buds. Accessions placed in groups B, D and E belong to *D. alata*. Accessions of group B were highly variable with irregular, oblong, oval-oblong and round tuber shapes, with flesh colour of central cross section of tubers ranging from light purple and white. This suggests that tuber shape alone is not sufficient to define taxonomic units in *D. alata*.

Accessions of three sub-groups within group B, namely: B_1, B_2 and B_3 overlapped in the PC1 versus PC2 graph (Figure 5). Overlap between species for morphological traits generally make characterization difficult (MacLean *et al*., 1993). This suggests the need for use of molecular techniques to augment morphological classification to resolve issues of overlap and confirm morphological associations. However, the overlap among the sub-groups of the B group was within the same species rather than different species.

A detailed characterization of the genotypic diversity within the germplasm evaluated should contribute to effective conservation and utilization of the yam genetic resources available in Sierra Leone. The overlap in sub-groups B_1 and B_2 of genotypes WR 07/024, SR 07/075, 07/073, ER 07/032 and NR 07/042, and between sub-groups B_1 and B_3 of genotypes NR 07/041, WR 07/010, ER 07/038 and NR 07/067, indicated the possibility of duplicate genotypes in the germplasm collection.

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REFERENCES

Amurrio JM, Ron de A, Zeven, AC, 1995. Numerical taxonomy of Liberian pea landraces based on quantitative and qualitative characters. *Euphytica* 82: 195-205.

Asiedu R, Ng SYC, Bai KV, Ekanayake IJ, Wanyera NMW, 1998. Genetic Improvement. In: Orkwor GC, Asiedu R, Ekanayake IJ (eds.) *Food yams: Advances in research*, Ibadan, Nigeria: IITA and NRCRI. pp. 63-104.

Dansi A, Zoundjihekpon J, Mignouna HD, Quin FM, 1997. Collecte d'ignames cultivées du Complexe *Dioscorea cayenensis - rotundata* au Benin. *Plant Genetic Resources Newsletter* 112: 81-85.

Dansi A, Mignouna HD, Zoundjihekpon J, Sangare A, Asiedu R, Quin FM, 1999. Morphological diversity, cultivar groups and possible descent in the cultivated yams (*Dioscorea cayenensis-Dioscorea rotundata* complex) of Benin Republic. *Genetic Resources and Crop Evolution* 46: 371-388.

Dansi A, Mignouna HD, Pillay M, Zok S. 2001. Ploidy variation in the cultivated yams (*Dioscorea cayenensis-Dioscorea rotundata* complex) from Cameroon as determined by Flow cytometry. *Euphytica* 119: 301-307.

Hamon P, 1987. Structure, origine genetique des Ignames en Afrique de l'Ouest. These de Doctorat es-Sciences. Université Paris XI, Centre d'Orsay. 223 pp.

Hasan SMZ, Ngadin AA, Shah RM, Mohamad N, 2008. Morphological variability of greater yam (*Dioscorea alata* L.) in Malaysia. *Plant Genetic Resources*: *Characterization and Utilization* 6: 52-61.

International Plant Genetic Resources Institute (IPGRI/ IITA), 1997. *Descriptors for yam* (*Dioscorea* spp.) IPGRI, Rome, Italy: International Plant Genetic Resources Institute (IPGRI)/ International Institute of Tropical Agriculture (IITA), Ibadan Nigeria. 61 pp.

Jeffers JNR, 1967. Two case studies in the application of principal component analysis. *Applied Statistics* 16: 225-236.

MacLean DJ, Bronthwaite KS, Manners JM, Irwing JAG, 1993. How do we identify and classify

fungal pathogens in the era of DNA analysis? *Advances in Plant Pathology* 10: 207-244.

Martin FW, 1976. Tropical yams and their potential. Series – Part 3. *Dioscorea alata*. USDA Agriculture Handbook No. 495 ARS, USDA. 40 pp.

Mignouna HD, Dansi A, Zoc S, 2002. Morphological and isozymic diversity of the cultivated yams (*Dioscorea cayenensis/ Dioscorea rotundata* complex) of Cameroon. *Genetic Resources and Crop Evolution* 49: 21-29.

Mwiringi PN, Kahangi EM, Ngende AB, Mamati EG, 2009. Morphological variability within the Kenyan yam (*Dioscorea* spp.). *Journal of Applied Biosciences* 16: 894-901.

Payne RW, Murray DA, Harding SA, Baird DB, Souter DM, 2009. Genstat for Windows (12th Edition) Introduction VSN International, Hemel Hempstead.

Sokal RR. and Michener CP, 1958. A statistical method for evaluating systematic relationships. *University of Kansas Science Bulletin* 38: 1409-1438.

Velayudhan KC, Muralidharan VK, Amalraj VA, Thomas TA, Soudhamini P, 1989. Studies on the morphotypic variability, distribution and genetic divergence in an indigenous collection of greater yam (*Dioscorea alata* L.). *Journal of Root Crops* 15: 79-89.