



Determination of interrelationships among agromorphological traits of yams (*Dioscorea* spp.) using correlation and factor analyses

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ABSTRACT

Objective: To determine the interrelationships existing among agro-morphological traits of yams using correlation and factor analyses.

Methodology and results: A total of 52 yam genotypes from Sierra Leone were grown in a randomized complete block design with three replications in 2010 at the University of KwaZulu-Natal, Pietermaritzburg, South Africa. Twenty-eight morphological traits measured from the genotypes were analysed using correlation and factor analysis (FA). Traits that discriminated the most between the accessions were: the number of days to emergence, shoot traits (absence or presence of wings, leaf colour, density, lobation, position, shape and size of leaf, number of stems and branches) and below ground traits (tuber shape and flesh colour of central cross section of tuber). Factor analysis had six factors, which explained 75% of the total genetic variation in the dependence structure. Factor 1 was strongly associated with absence or presence of wings, distance between lobes, leaf apex shape, leaf colour, leaf density, leaf margin colour, leaf length-2 leaf vein colour of the upper surface, number of branch, number of stem, stem colour and tip length of mature leaf; factor 2 with leaf density, leaf length-1, leaf vein colour of lower surface, petiole wing colour, tip colour, wing colour and flesh colour of central cross section of tuber; factor 3 with absence or presence of wings and leaf width-1; factor 4 with leaf width-2; factor 5 with stem colour; and factor 6 with number of days to emergence. Other factors (≥ 7) explained the rest of the genetic variation and may not be important in yam breeding programmes.

Conclusion and potential application: This study revealed that wide genetic diversity exists in yam 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 variation observed.

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

INTRODUCTION

The distribution of yam genotypes in Sierra Leone and their characteristics is not well documented, which constrains their efficient conservation and use in breeding programmes. This dearth of knowledge of existing germplasm in some of the

countries where yams are cultivated has significantly contributed to genetic erosion of yams (Dansie *et al.*, 1997). In Sierra Leone for instance, despite the importance of yams as a source of food and income, there is lack of knowledge on the

level of diversity within existing genotypes and desired market traits such as yield and tuber shape.

In experiments where large amounts of data are obtained such as diversity studies, data mining (knowledge discovery) is relevant in data reduction or structural simplification, sorting and grouping, investigation of the dependence among variables, prediction and hypothesis construction and testing (Manly, 1994). Principal component analysis is used to reduce dimensionality in data by analyzing covariance between factors. Factor analysis is used to describe variability among observed variables in terms of lower number of unobserved variables known as factors. Factor analysis is related to PCA, but the two are different. Principal component analysis performs a variance-maximizing rotation of the variable space, taking

into account all variability present in the traits (Manly, 1994).

Conversely, FA estimates how much of the variability is due to common factors (communality) and specific factors (specificity). The two techniques may only be on equal terms if the error in the FA model is assumed to have constant variance (Manly, 1994). The use of one or more systematic methods to determine the extent of variability present in yam has provided better understanding in countries like Benin (Dansi *et al.*, 1999), Cameroon (Mignouna *et al.*, 2002) and Malaysia (Hasan *et al.*, 2008).

In this study, correlation and factor analyses were used to determine the interrelationships among 28 phenotypic traits in 52 yam accessions from Sierra Leone.

MATERIALS AND METHODS

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 used. Minisetts each weighing 50 g were sown in pots measuring 25 cm (diameter) x 20 cm (height) and placed in a green-house at the University of KwaZulu-Natal, Pietermaritzburg, South Africa in January 2010. Morphological data collected during the experiment were: number of days to emergence (number of days between planting and emergence), number of stems per plant, number of internode to first branching, stem colour, internode length, absence or presence of wings,

wing colour, position of leaves, leaf density, leaf lobation, leaf colour, leaf margin colour, leaf vein colour of upper and lower surfaces, leaf shape, leaf apex shape, distance between lobes, leaf length and width measurements, tip length of mature leaf, tip colour, petiole length of mature leaf, petiole colour, petiole wing colour, tuber shape and flesh colour of central cross section of tuber.

Multivariate analysis of the 52 x 28 data matrix (Table 1) comprising of correlation and factor analyses was performed in Genstat 12.1 (Payne *et al.*, 2009) for Windows. Correlation analysis was done in order to determine the interrelationship of the metric traits which are essential for designing breeding strategies.

For factor analysis (FA), the general model formula was used:

$$\text{Var}(X_i) = \text{Var}(a_iF + e_i) = \text{Var}(a_iF) + \text{Var}(e_i) = a_i^2\text{Var}(F) + \text{Var}(e_i) \dots\dots\dots(\text{Eqn 1});$$

Where F and e_i are independent and the variance of F and X_i are assumed to be unity (Manly, 1994).

Thus, $1 = a_i^2 + \text{Var}(e_i)$.

The communality (variance due to common factors) and specificity (variance due to specific factors) were estimated from the relationship:

$$\text{Specificity} = 1 - \text{communality} \dots\dots\dots(\text{Eqn 2});$$

and their respective percentages were estimated:

$$\%F_1 = a_1^2 \times 100\% \text{ or } \%F_2 = a_2^2 \times 100\% \dots\dots\dots(\text{Eqn 3});$$

$$\text{and } \% \text{ specificity} = (1 - \text{communality}) \times 100 \% \dots\dots\dots(\text{Eqn 4}); (\text{Manly, 1994}).$$

RESULTS

Correlation analysis: Generally, all the traits whose correlations were greater than or equal to 0.5 significantly ($p < 0.05$) influenced the phenotypic expression of the various genotypes (Table 1). The correlation between absence or presence of wings and leaf colour was negative ($r = -0.517$). Similar negative correlations were also observed between absence or presence of wings and leaf margin colour ($r = -0.562$), between absence or presence of wings and number of branches ($r = -0.684$) and between absence or presence of wings and stem colour ($r = -0.556$). On the other hand, absence or presence of wings was positively correlated with leaf lobation ($r = 0.612$), petiole wing colour ($r = 0.628$) and wing colour of stems ($r = 0.714$).

Wingless genotypes had mostly shallow leaf lobation, which contrasts with *D. alata* genotypes with predominantly deep lobation and winged stems and petioles (Figures 1 and 2). Distance between lobes was negatively correlated ($r = -0.549$) with leaf apex shape (Table 1). The distance between lobes in *D. bulbifera*

cultivars was so small that the lobes of most leaves overlapped (Figure 1). Genotypes of this species had a peculiar cuspidate leaf apex shape. Also, the correlations between distance between lobes and leaf length-2 ($r = -0.601$), and distance between lobes and tip colour of mature leaves ($r = -0.503$) were negative. This contrasts with the positive correlations between distance between lobes and leaf shape ($r = 0.613$) and distance between lobes and stem colour ($r = 0.578$). The expansive lobation expressed by most *D. rotundata* genotypes gave them a peculiar saggitate broad leaf shape and purplish to brownish-green vine colour. The correlation between leaf lobation and petiole wing colour was positive ($r = 0.520$). Some *D. alata* cultivars with purple petiole wing colour were mostly deeply lobed. The correlation between internode length and leaf length-1 was positive ($r = 0.634$). Petiole length of mature leaf had a positive ($r = 0.502$) correlation with tip length of mature leaves.

Table 1. Correlation matrix of the 28 trait means across 52 yam genotypes from Sierra Leone used in factor analysis. The traits and measurement methods were based on the International Plant Genetic Resources Institute descriptor list (IPGRI/ IITA, 1997)

	AP W	DB L	DE	IL	LA S	LC	LD	LL	LM C	LM L1	LM L2	LM W1	LM W2	LS	LVC LS	LVC US	NB	NS	PC	PL	PL M	PW C	SC	TC	TL M	TS	WC	Tfles hc	
APW	-																												
	0.3																												
DBL	82	-																											
	0.2	0.2																											
DE	57	17	-																										
	0.1	0.4	0.3																										
IL	14	20	26	-																									
	0.2	0.5	0.1	0.1																									
LAS	55	49	47	08	-																								
	0.5	0.3	0.1	0.0	0.4																								
LC	17	30	38	46	76	-																							
	0.4	0.0	0.0	0.3	0.2	0.5																							
LD	81	81	92	27	30	58	-																						
	0.6	0.4	0.1	0.0	0.2	0.3	0.2																						
LL	12	33	34	58	34	24	16	-																					
	0.5	0.4	0.0	0.1	0.5	0.8	0.6	0.3																					
LMC	62	20	91	31	51	72	02	42	-																				
	0.1	0.4	0.2	0.6	0.1	0.0	0.2	0.1	0.1																				
LL1	74	20	30	34	94	35	05	23	16	-																			
	0.4	0.6	0.0	0.4	0.3	0.2	0.0	0.4	0.4	0.6																			
LL2	38	01	44	99	83	91	20	07	35	67	-																		
	0.0	0.3	0.1	0.3	0.2	0.0	0.2	0.0	0.1	0.6	0.5																		
LW1	92	75	76	67	94	53	28	36	26	84	33	-																	
	0.0	0.0	0.2	0.3	0.1	0.0	0.0	0.1	0.1	0.5	0.3	0.61																	
LW2	93	43	29	61	37	54	16	86	93	62	34	2	-																
	0.2	0.6	0.2	0.1	0.1	0.1	0.1	0.3	0.1	0.1	0.4	0.08	0.20																
LS	88	13	46	70	62	24	80	55	10	01	70	5	4	-															
	0.1	0.2	0.1	0.1	0.2	0.3	0.3	0.0	0.4	0.1	0.2	0.00	0.27	0.4															
LVC	16	64	19	84	68	74	42	93	15	73	18	8	4	34	-														
	0.4	0.2	0.1	0.0	0.6	0.6	0.4	0.3	0.6	0.0	0.1	0.07	0.07	0.1	0.46														
LVC	26	20	41	71	05	30	89	62	73	76	91	2	3	68	4	-													
US																													

NB	0.6	0.1	0.2	0.1	0.4	0.5	0.6	0.4	0.5	0.0	0.1	0.24	0.13	0.1	0.08	0.52	-																				
NS	0.4	0.2	0.1	0.1	0.4	0.5	0.6	0.2	0.6	0.1	0.1	0.10	0.01	0.0	0.40	0.54	0.5																				
PC	0.4	0.0	0.0	0.0	0.1	0.1	0.3	0.1	0.2	0.1	0.0	0.12	0.06	0.1	0.04	0.20	0.3	0.2																			
PL	0.0	0.2	0.1	0.0	0.2	0.0	0.0	0.0	0.1	0.2	0.21	0.02	0.1	0.01	0.14	0.0	0.0	0.0																			
PLM	0.1	0.2	0.0	0.2	0.3	0.0	0.0	0.0	0.2	0.5	0.4	0.71	0.63	0.0	0.14	0.23	0.0	0.0	0.1	0.0																	
PWC	0.6	0.3	0.0	0.3	0.2	0.0	0.0	0.5	0.0	0.4	0.5	0.10	0.06	0.4	0.38	0.06	0.3	0.1	0.1	0.0	0.1																
SC	0.5	0.5	0.0	0.3	0.4	0.6	0.2	0.4	0.7	0.1	0.5	0.00	0.02	0.2	0.05	0.41	0.3	0.3	0.0	0.0	0.0	0.2															
TC	0.1	0.5	0.2	0.2	0.4	0.1	0.1	0.2	0.0	0.4	0.4	0.47	0.12	0.3	0.26	0.06	0.1	0.1	0.1	0.1	0.4	0.3	0.0														
TLM	0.4	0.4	0.0	0.4	0.4	0.1	0.2	0.3	0.3	0.6	0.5	0.42	0.45	0.1	0.09	0.33	0.3	0.2	0.2	0.0	0.5	0.5	0.3	0.4													
TS	0.0	0.3	0.0	0.0	0.3	0.3	0.0	0.0	0.3	0.2	0.2	0.12	0.20	0.3	0.06	0.13	0.0	0.1	0.0	0.0	0.0	0.0	0.2	0.2	0.3												
WC	0.7	0.4	0.3	0.1	0.2	0.0	0.1	0.4	0.1	0.3	0.4	0.14	0.03	0.3	0.41	0.26	0.5	0.1	0.3	0.1	0.2	0.7	0.1	0.5	0.0												
Tiles hc	0.0	0.3	0.2	0.3	0.0	0.5	0.5	0.1	0.4	0.2	0.2	0.08	0.23	0.4	0.64	0.26	0.1	0.3	0.2	0.1	0.1	0.3	0.0	0.4	0.1	0.0	0.4	0.1	0.0	0.4	0.1	0.0	0.4				

Where APW = absence or presence of wings, DBL = distance between lobes, DE = number of days to emergence, IL = internode length, LAS = leaf apex shape, LC = leaf colour, LD = leaf density, LL = leaf lobation, LMC = leaf margin colour, leaf length and width measurements, LS = leaf shape, LVCUS = leaf vein colour of upper leaf surface, LVCLS = leaf vein colour of lower surface, NB = number of internode to first branching, NS = number of stems per plant, PC = petiole colour, PL = position of leaves, PLM = petiole length of mature leaf, PWC = petiole wing colour, SC = stem colour, TC = tip colour, TLM = tip length of mature leaf, TS = tuber shape, WC = wing colour and FCCCS = flesh colour of central cross section of tuber.



a) SR 07/074: Saggitate light green



b) NR 07/052: Cordate green-purple leaf



c) ER 07/038: Saggitate long green leaf



d) WR 07/013: Cordate long green leaf



e) WR 07/025: Saggitate long light green leaf



f) SR 07/085: Cordate long dark green leaf



g) NR 07/041: Cordate long dark green leaf



h) NR 07/040: Cordate broad light green leaf

Figure 1: Variation in leaf colour, type and shape among yam (*Dioscorea* spp.) germplasm with a-b, and c-g, and f representing accessions of *D. rotundata*, *D. alata*, and *D. bullifera* respectively

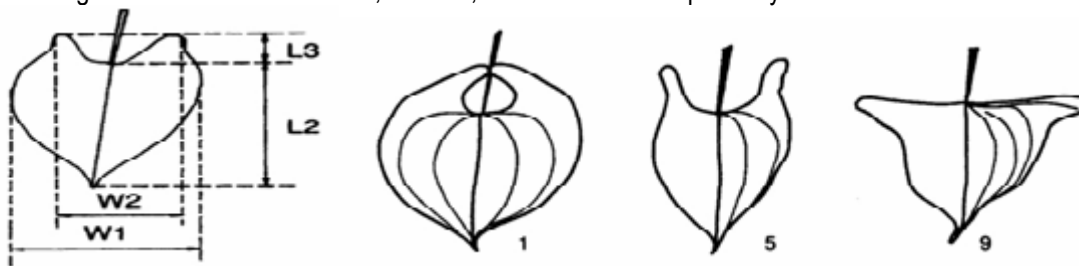


Figure 2: Variation in leaf measurement (L₂=leaf length-1, L₃=leaf length-2, W₁=leaf width-1 and W₂=leaf width-2) and distance between lobe (1=shallow, 5=intermediate and 9=very distant)

Leaf colour had a strong, positive correlation ($r = 0.872$) with leaf margin colour, and a positive correlation with leaf density ($r = 0.558$); leaf vein colour of upper leaf surface ($r = 0.630$); number of branches per plant ($r = 0.510$); number of stems per plant ($r = 0.593$); stem colour ($r = 0.627$); and flesh colour of central cross section of tuber ($r = 0.520$) (Table 1). The correlations between leaf margin colour and leaf vein colour of upper leaf surface ($r = 0.673$), between leaf margin colour and number of stems per plant ($r = 0.628$), between leaf margin colour and stem colour ($r = 0.718$) and between leaf margin colour and number of branches per plant ($r = 0.503$) were positive. The correlations between leaf vein colour of upper leaf surface and number of branches per plant ($r = 0.520$) and between leaf vein colour of upper leaf surface and number of stems per plant ($r = 0.544$) were positive. Most of the genotypes that produced stem with one or few branches had green upper surface leaf venation, whereas pale purple to purple venation was common among profuse branching genotypes.

The correlations between leaf vein colour of lower leaf surface and flesh colour of the central cross section of tuber ($r = 0.644$) were positive. Leaf apex shape was negatively correlated ($r = -0.551$) with leaf margin colour, and leaf vein colour of upper surface ($r = -0.605$). The correlations between: leaf length-1 and leaf length-2 ($r = 0.667$); leaf length-1 and leaf width-1 ($r = 0.684$); leaf length-1 and tip length of mature leaves ($r = 0.620$); leaf length-1 and leaf width-2 ($r = 0.562$); and leaf length-1 and petiole length of mature leaves ($r = 0.535$) were all positive. In the main, genotypes with larger leaf length-2, leaf width-1, leaf width-2, and tip length of mature leaves, also exhibited larger leaf length-1. The correlations between: leaf length-2 and leaf width-1 ($r = 0.533$); between leaf length-2 and petiole wing colour ($r = 0.504$); and between leaf length-2 and tip length of mature leaves ($r = 0.599$) were positive.

The correlation between leaf length-2 and stem colour ($r = -0.502$) was negative. It was evident that genotypes which exhibited larger leaf width-1 and tip length of mature leaves with characteristic green with purple petiole wing also had larger leaf length-2. Both leaf width-2 ($r = 0.612$) and petiole length of mature leaves ($r = 0.718$) were positively correlated with leaf width-1. Genotypes which had larger leaf width-2 and petiole length of mature leaves, also exhibited larger leaf width-1. Petiole length of mature leaf had a positive ($r = 0.636$) correlation with leaf width-2. Genotypes with

larger petiole length of mature leaves also had larger leaf width-2.

Number of branches per plant was positively correlated ($r = 0.572$) with number of stems per plant (Table 1). Apparently, some genotypes with high number of stems also branched profusely. On the contrary, wing colour was negatively correlated ($r = -0.509$) with number of branches per plant. Among genotypes of *D. alata*, profuse branching was most common in genotypes with wing colour ranging from green with purple edge to purple. The correlations between: leaf density and number of branches per plant ($r = 0.685$); leaf density and number of stems per plant ($r = 0.693$); leaf density and leaf margin colour ($r = 0.602$); and between leaf density and flesh colour of the central cross section of tuber ($r = 0.571$) were all positive. Petiole wing colour was positively correlated with tip length of mature leaves ($r = 0.565$) and wing colour ($r = 0.708$).

Among *D. alata* genotypes, many which had tip length of mature leaves ≥ 1.0 cm and green wing with purple edge also exhibited green with purple edge petiole wing colour. Tip colour was positively correlated ($r = 0.500$) to wing colour, but had a weak, negative correlation ($r = -0.207$) with tuber shape. The correlation between tip length of mature leaf and wing colour of stem was positive ($r = 0.532$); but the correlation between tip length of mature leaf and tuber shape was weak, negative ($r = -0.331$).

Factor analysis: The six principal component eigenvalues that were greater than 1.0 (Table 2) suggest the use of six factors in the factor analysis (Biabani and Pakniyat, 2008). Factor loadings with coefficients greater than or equal to 0.5 (ignoring the sign) were considered important and emboldened. These large and moderate loadings indicate how the traits are related to the factors (Manly, 1994).

The contributions by the communalities were fairly high with 24 traits exhibiting higher communality over the specificity (four traits) (Table 2). Factor 1 was heavily loaded with: absence or presence of wings (0.7010); distance between lobes (-0.6071); leaf apex shape (0.7589); leaf colour (-0.7714); leaf density (0.5178); leaf margin colour (-0.8797); leaf length-2; leaf vein colour of upper surface (0.7061); number of branches per plant (-0.6407); number of stems (-0.6472); stem colour (-0.7118); and tip length of mature leaves (0.6008). Factor 2 was loaded with: leaf density (0.5270); leaf length-1 (0.6210); leaf vein colour of lower surface (0.6135); petiole wing colour (0.5824); tip colour (0.6545); wing colour (0.5780); and flesh colour of central cross section of tuber (0.7674).

Factor 3 was loaded with: absence or presence of wings (0.6355); and leaf width-1 (-0.5539). Factor 4 was loaded with leaf width-2 (-0.5799). Factor 5 was loaded with stem colour (0.5070); and factor 6 with number of days to emergence (-0.4793). Most of the variation in the traits was accounted for by factor 1, with moderate (-0.5178) to large (-0.8797) loadings compared to the traits loaded in the other factors. This makes rotating the factors to further explore the variables unnecessary. The variation in absence or presence of wings (APW) was strongly influenced by communality (92.56%) compared to the specificity (7.44%). Factor 1 (50.14%) contributed most of the variation in the communality compared to factors 2 (0.92%), 3 (40.39%), 4 (0.80%), 5 (0.30%) and 6 (0.01%). The variation in distance between lobes (DBL) was largely due to communality (80.51%) compared to specificity (19.49%).

Factor 1 (36.86%) contributed most to the variation in the communality compared to 21.15, 1.19, 0.75, 17.25 and 3.31% contributions by factors 2, 3, 4, 5 and 6, respectively. The variation in leaf apex shape (LAS) was strongly influenced by the communality (95.70%) compared to the specificity (4.30%). Factor 1 (57.59%) accounted for the largest variation in the communality compared to factors 2 (1.57%), 3 (17.53%), 4 (17.51%), 5 (1.18%) and 6 (0.30%). The variation in leaf colour (LC) was largely due to the

communality (83.87%) compared to the specificity (16.13%). Factor 1 (59.51%) contributed most of the variation in the communality compared to factors 2 (21.29%), 3 (0.12%), 4 (0.29%), 5 (2.31%) and 6 (0.36%). The variation in leaf density (LD) was more influenced by the communality (73.29%) compared to the specificity (26.71%). Factor 2 (27.77%) contributed most of the variation in the communality compared to factors 1 (26.81%), 3 (6.79%), 4 (0.18%) 5 (11.71%) and 6 (0.02%).

The variation in leaf margin colour (LMC) was strongly influenced by the communality (95.69%) of which factor 1 (77.39%) contributed the most compared to factors 2 (12.50%), 3 (0.30%), 4 (3.22%), 5 (1.98%) and 6 (0.30%). The specificity contributed 4.31%. The variation in leaf length-1 (LL1) was explained by 78.44% contribution from communality of which factor 2 (36.97%) contributed most compared to factors 1 (8.60%), 3 (4.44%), 4 (24.12), 5 (0.10%) and 6 (2.62%). The specificity accounted for 21.56%. The variation in leaf length-2 (LL2) was largely due to communality (72.35%) of which factor 1 (35.15%) contributed highest compared to 23.99, 0.23, 9.04, 3.94 and 0.00% contributions by factors 2, 3, 4, 5 and 6, respectively. The specificity accounted for 27.65%. The variation in leaf width-1 (LW1) was strongly influenced by the communality (86.01%) compared to the specificity (13.99%).

Table 2. Loadings of common and specific factors of 28 traits of 52 yam (*Dioscorea* spp.) accessions from Sierra Leone analyzed by factor analysis.

Traits	Factor loadings						Communality	Specificity	% variation						
	F1	F2	F3	F4	F5	F6			F1	F2	F3	F4	F5	F6	Specificity
APW	0.7081	0.0959	0.6355	-0.0895	0.0544	0.0116	0.9256	0.0744	50.14	0.92	40.39	0.80	0.30	0.01	7.44
DBL	-0.6071	-0.4599	0.1090	-0.0871	0.4153	-0.1819	0.8051	0.1949	36.86	21.15	1.19	0.75	17.25	3.31	19.49
DE	-0.1707	-0.0351	-0.2377	-0.3440	0.0036	-0.4793	0.4350	0.5650	2.91	0.12	5.65	11.83	0.00	22.97	56.50
IL	0.2065	0.4953	-0.1399	-0.3618	-0.3238	-0.3424	0.6605	0.3395	4.26	24.53	1.96	13.09	10.49	11.72	33.95
LAS	0.7589	0.1253	-0.4187	0.4185	0.1088	-0.0552	0.9570	0.0430	57.59	1.57	17.53	17.51	1.18	0.30	4.30
LC	-0.7714	0.4614	-0.0352	0.0539	0.1519	-0.0603	0.8387	0.1613	59.51	21.29	0.12	0.29	2.31	0.36	16.13
LD	-0.5178	0.5270	-0.2606	0.0425	-0.3422	0.0143	0.7329	0.2671	26.81	27.77	6.79	0.18	11.71	0.02	26.71
LL	0.4938	0.1671	0.3904	0.0571	-0.0900	-0.0084	0.4355	0.5645	24.38	2.79	15.24	0.32	0.81	0.01	56.45
LMC	-0.8797	0.3536	0.0550	0.1795	0.1409	-0.0545	0.9569	0.0431	77.39	12.50	0.30	3.22	1.98	0.30	4.31
LL1	0.2932	0.6210	-0.2106	-0.4911	0.0313	-0.1619	0.7844	0.2156	8.60	38.56	4.44	24.12	0.10	2.62	21.56
LL2	0.5929	0.4898	-0.0479	-0.3006	-0.1985	-0.0060	0.7235	0.2765	35.15	23.99	0.23	9.04	3.94	0.00	27.65
LW1	0.2297	0.4974	-0.5539	-0.4343	0.1314	0.2173	0.8601	0.1399	5.28	24.74	30.68	18.86	1.73	4.72	13.99
LW2	0.1835	0.1602	-0.4571	-0.5799	0.2321	-0.1628	0.6849	0.3151	3.37	2.56	20.89	33.63	5.39	2.65	31.51
LS	-0.2516	-0.4091	-0.1940	-0.1737	0.4500	-0.2334	0.5554	0.4446	6.33	16.73	3.76	3.02	20.25	5.45	44.46
LVCLS	-0.2240	0.6135	0.4010	0.0706	-0.2413	0.1101	0.6627	0.3373	5.02	37.64	16.08	0.50	5.82	1.21	33.73
LVCUS	-0.7061	0.2404	0.0803	-0.1019	-0.2164	-0.0011	0.6201	0.3799	49.86	5.78	0.65	1.04	4.68	0.00	37.99
NB	-0.6407	0.1444	-0.4200	-0.2204	-0.3513	0.0745	0.7854	0.2146	41.05	2.09	17.64	4.86	12.34	0.56	21.46
NS	-0.6472	0.3306	-0.0796	-0.1323	-0.1660	0.0726	0.5848	0.4152	41.89	10.93	0.63	1.75	2.75	0.53	41.52
PC	0.2376	-0.0312	0.3677	-0.3925	0.3608	0.1730	0.5068	0.4932	5.65	0.10	13.52	15.40	13.02	2.99	49.32
PL	-0.2157	-0.1560	0.1515	-0.1395	0.0482	-0.2189	0.1635	0.8365	4.65	2.43	2.30	1.95	0.23	4.79	83.65
PLM	0.3678	0.3192	-0.3449	-0.4519	0.3484	0.1847	0.7158	0.2842	13.53	10.19	11.89	20.42	12.14	3.41	28.42
PWC	0.3863	0.5824	0.4338	-0.0107	0.0818	-0.3023	0.7748	0.2252	14.92	33.92	18.82	0.01	0.67	9.14	22.52
SC	-0.7118	0.0528	-0.1052	0.0524	0.5070	0.1731	0.8103	0.1897	50.67	0.28	1.11	0.28	25.70	2.99	18.97
TC	0.2988	0.6545	-0.1452	0.1123	0.1465	0.2340	0.6276	0.3724	8.93	42.84	2.11	1.26	2.15	5.47	37.24
TLM	0.6008	0.4542	-0.0002	-0.2410	0.2048	-0.2553	0.7325	0.2675	36.10	20.63	0.00	5.81	4.19	6.52	26.75
TS	-0.3410	-0.0226	0.1976	0.0232	0.1983	0.0809	0.2023	0.7977	11.63	0.05	3.90	0.05	3.93	0.65	79.77
WC	0.4650	0.5780	0.4900	0.0734	0.2476	0.1236	0.8723	0.1277	21.62	33.41	24.01	0.54	6.13	1.52	12.77
FCCCS	-0.1542	0.7674	0.1247	0.3606	-0.2693	0.0013	0.8308	0.1692	2.38	58.89	1.56	13.00	7.25	0.00	16.92

*Details of each acronym/ trait are provided in Table 1. Values in bold indicate the most important traits (>0.25) that contributed much to the total variance of the particular component

Factor 3 (30.68%) contributed most to the variation in the communality compared to factors 1 (5.28%), 2 (24.74%), 4 (18.86%), 5 (1.73%) and 6 (4.72%). The variation in leaf width-2 (LW2) was explained by 68.49% contribution from communality of which factor 4 (33.63%) contributed most compared to factors 1 (3.37%), 2 (2.56%), 3 (20.89%), 5 (5.39%) and 6 (2.65%). The specificity contributed 31.51%.

The variation in leaf shape (LS) was explained by 55.54% contribution from communality of which factor 5 (20.25%) contributed higher than factors 1 (6.33%), 2 (16.73%), 3 (3.76%), 4 (3.02%) and 6 (5.45%). The specificity accounted for 44.46%. The variation in leaf vein colour lower surface (LVCLS) was largely due to communality (66.27%) than the specificity (33.73%). Factor 2 (34.27%) contributed highest compared to 5.02, 16.08, 0.50, 5.82 and 1.21% inputs by factors 1, 3, 4, 5 and 6, respectively. The variation in leaf vein colour upper surface (LVCUS) was explained by 62.01% contribution from communality of which factor 1 (49.86%) contributed most compared to factors 2 (7.58%), 3 (0.65%), 4 (1.04%), 5 (4.68%) and 6 (0.00%). The specificity accounted for 37.99%. The variation in number of branches (NB) was more influenced by communality (78.54%) compared to the specificity (21.46%). Factor 1 (41.05%) contributed the highest to the variation in the communality compared to 2.09, 17.64, 4.86, 12.34 and 0.56% inputs by factors 2, 3, 4, 5 and 6, respectively.

The variation in number of stems (NS) was explained by 58.48% contribution from communality of which factor 1 (41.89%) contributed most compared to factors 2 (10.93%), 3 (0.63%), 4 (1.75%), 5 (2.75%) and 6 (0.53%). The specificity accounted for 41.52%. The variation in petiole length of mature leaf (PLM) was explained by 71.58% contribution from communality of which factor 4 (20.42%) contributed most compared to factors 1 (13.53%), 2 (10.19%), 3 (11.89%), 5 (12.14%) and 6 (3.41%). The specificity accounted for 28.42%. The variation in petiole wing colour (PWC) was strongly

influenced by 77.48% contribution from communality compared to 22.52% input by the specificity. Factor 2 (33.92%) contributed most compared to factors 1 (14.92%), 3 (18.82%), 4 (0.01%), 5 (0.67%) and 6 (9.14%). The variation in stem colour (SC) was more due to communality (81.03%) than the specificity (18.97%). Factor 1 (50.67%) contributed most to the variation in the communality compared to 0.28, 1.11, 0.28, 25.70, and 2.99% contributions for factors 1, 3, 4, 5 and 6, respectively.

The variation in tip colour (TC) was explained by 62.76% contribution from communality of which factor 2 (42.84%) contributed most compared to factors 1 (8.93%), 3 (2.11%), 4 (1.26%), 5 (2.15%) and 6 (5.47%). The specificity accounted for 37.24%. The variation in tip length of mature leaf (TLM) was explained by 73.25% contribution from communality of which factor 1 (36.10%) contributed most compared to factors 2 (20.63%), 3 (0.00%), 4 (5.81%), 5 (4.19%) and 6 (6.52%). The specificity accounted for 26.75%.

The variation in wing colour (WC) was strongly influenced by the common factors (87.23%) compared to the specificity (12.77%). Factor 2 (33.41%) accounted for most of the variation in the communality compared to factors 1 (21.62%), 3 (24.01%), 4 (0.54%), 5 (6.13%) and 6 (1.52%). The variation in flesh colour of central cross section of tuber (FCCCS) was explained by 83.08% contribution from communality of which factor 2 (58.89%) contributed most compared to factors 1 (1.38%), 3 (1.56%), 4 (13.00%), 5 (7.25%) with no contribution by factor 6. The specificity accounted for 16.92%.

Generally, all the traits measured were useful in determining variability in the 52 accessions. The six factors considered distinguished the traits into six groups. The highest weightings by factor 1 were given to leaf colour (-0.7719) and leaf margin colour (-0.8797). These traits were not only highly positively correlated ($r = 0.872$), but also served as important components in distinguishing between the accessions.

DISCUSSION AND CONCLUSION

A correlation coefficient quantifies the degree to which the variation in one trait is mirrored by or "affects" variation in another i.e. it provides a measure of the intensity of the biological or other association between the two traits. The sign of the correlation coefficient provides an indication of either a positive or negative association between two traits. Correlation coefficients provide guidance with regard to the execution of direct

or indirect selection of traits and the consequences thereof for other traits (Biabani and Pakniyat, 2008).

In this study, it was considered that quantification of the biological associations between morphological traits in yams would provide invaluable information to current and future breeding programmes. The interrelationships between internode length, leaf length-1, petiole length and tip length were particularly significant in the classification of the genotypes. For instance the higher

internode length noted in some accessions was associated with a corresponding increase in leaf length-1. It appeared that as the leaves were better spaced apart on vines, thereby improving the harnessing of solar radiation for photosynthesis, there was an associated increase in leaf length-1 that consequently enhanced high yields in some genotypes. Some genotypes which had mature leaves with larger tip length also had larger petiole length of the mature leaves. The positive association revealed by Pearson's correlation for the morphological traits: leaf colour, leaf margin colour, leaf vein colour of upper surface and leaf shape was the probable cause of the unique colour venation in the leaves of some genotypes. The variation in morphological traits within and between landraces of *D. alata*, *D. bulbifera* and *D. rotundata* is likely due to initial sexual recombination and possibly mutation. This is often followed by intensive selection by isolated human communities in diverse environments (Martin, 1976).

In Malaysia for instance, Hasan *et al.* (2008) noted a male: female sex ratio of 7.15: 2.85, which was a probable cause of diversity in that germplasm. Also, Velayudhan *et al.* (1989) suggested that continuous vegetative propagation and selection within germplasm may contribute to phenotypic variation in the species. In the present study, however, only two genotypes of *D. bulbifera*, NR 07/040 and NR 07/045, flowered.

The FA indicated significant contributions in the factor loadings of the 28 traits which underpins their relevance in determining the variability among the 52 accessions. Six factors which had eigen-values greater than 1.0 were retained (c.f. Manly, 1994; Biabani and Pakniyat, 2008). These factors accounted for 75% of the total genetic variability. Factor 3 had the highest negative associations (19 traits) whereas factor 4 had the least (10 traits). The sign on the loadings indicates the direction of the relationship between the factor and the trait measured (Biabani and Pakniyat, 2008). Two traits with high weighting in the same factor are expected to be highly correlated. This suggests that these traits could probably be influenced by similar gene(s) and may be used to identify variation among accessions (Biabani and Pakniyat, 2008).

Other factors (7, 8, 9 and 10) explained 25% of the genetic variation, and were considered to be not as important in characterizing the yam accessions. Factor 1 had moderate, positive loading for leaf length-2, tip length of mature leaf, absence or presence of wing and

leaf apex shape on one hand; and moderate (leaf density, distance between lobes, number of branches, number of stems, leaf vein colour, stem colour and leaf colour) to high (leaf margin colour) negative influence on characterization of the accessions. It therefore measured the importance of leaf shape and size attributes against shoot growth and colour traits in distinguishing the accessions. Factor 2 (leaf density, wing colour, petiole wing colour, leaf length-1, tip colour and flesh colour of central cross section of tuber) had a moderate, positive influence in the classification of the accessions. Factor 3 had a moderate, positive loading for absence or presence of wing, and a moderate, negative loading for leaf width-1. It measured the contrast between wing production ability of the various genotypes and leaf width-1. Factor 4 had a moderate, negative loading for leaf width-2. It measured the contribution of leaf growth parameter to genotype classification. Factor 5 had a moderate, positive loading for stem colour, whereas factor 6 exhibited low, negative loading for days to emergence.

Days to emergence contributed the highest weighting in factor 6 compared to the other characters. Among traits that heavily loaded as specificity were days to emergence and tuber shape. The significance of these traits in yam breeding programme is crucial. For instance, the development of early maturing genotype may require the reduction in the number of days to emergence. Early emergence enhances the full utilization of the active growth period, which in turn affords tubers the opportunity to attain their normal size and shape. The longer the number of days to emergence, the shorter the active growth period. Additionally, infertile and poorly irrigated and diseased soils on one hand, coupled with diseased planting material on the other, could affect normal tuber shape. Yam tuber shape is one of the desirable traits in market-oriented breeding.

Of the four traits that loaded as specificity, number of days to emergence and tuber shape are crucial in breeding for market-oriented traits. A major breeding objective is the development of early establishment in yams through a reduction in the number of days to emergence. The characterization of the accessions will facilitate the identification and genetic combining of parental genotypes in order to attain the apex breeding objectives of developing high yielding yam genotypes with desirable market size and shape.

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