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Morphological Characterization of Greater Yam (*Dioscorea alata* L.) Landraces in Kerala

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Abstract

Yams belonging to Dioscoreaceae family are important climate resilient food security crops widely cultivated in India and Africa. In India, one of the major cultivated yam species is greater yam (*Dioscorea alata* L.). It provides a good source of dietary carbohydrates in tropical and subtropical regions. In the present study, 45 accessions conserved in the National repository of tuber crops germplasm at ICAR-CTCRI were characterized based on 25 qualitative and 13 quantitative traits including the major yield components and four biochemical characteristics. Traits like tuber shape, tuber flesh colour, tuber skin texture, tuber cortex colour, leaf shape and young leaf colour were all found to be of great importance in distinguishing the accessions. These traits were considered for Principal Component Analysis (PCA) with a measure of Sample Adequacy greater than 0.5. The first six principal components of data accounted for 50.12% of the total variance among accessions. The cluster dendrogram based on morphological data revealed that the *D. alata* accessions exhibited greater degree of genetic variation for the 42 different morphological traits observed. According to the morphological data, there were no duplicate accessions and Da 331, Da 390 and Da 340 were found be the highly divergent among the accessions studied.

Key words: *Dioscorea alata*, greater yam, landraces, Kerala, characterization, morphological, biochemical, principal component analysis.

Introduction

Yam plant is a vine cultivated for its large, edible underground tubers. More than 600 *Dioscorea* species exist worldwide. Their habitat is mainly in tropical or subtropical areas of Africa, America, Asia and Polynesia, where some *Dioscorea* species represent economically important tuber crops (Coursey, 1967). Yams are cultivated as a food source by more than 100 million people especially in many developing countries (Lebot, 2009). It is usually associated with traditional agriculture systems, known to maintain a wide genetic reservoir represented by several varieties bearing several vernacular names (Siqueira et al., 2014). Yam is primarily eaten for its carbohydrates (Tetchi et al., 2007), as well as protein, vitamins, potassium, sodium, magnesium, copper and zinc (Baah et al., 2009). Yam also has medicinal properties such as the steroidal sapogenins, used in the production of cortisone and synthetic steroid hormones (Narula et al., 2007).

Annual statistical data available from FAO (2014) shows that over 60.2 million tons of yams were produced in the World in 2013 and the area harvested in the world has increased from 1.15 million hectare in 1961 to 5.05 million hectare in 2013. Yield also increased from 72.35 thousand metric tons in 1961 to 119.12 thousand metric tons in 2013. Popular *Dioscorea* species grown are *Dioscorea rotundata* (white /guinea yam), *D. alata* (water yam), *D. bulbifera* (aerial potato), *D. opposita* (Chinese yam), *D. esculenta* (lesser yam) and *D. dumetorum* (trifoliate yam).

Greater yam (*Dioscorea alata* L.,) also known as “water yam” is probably the cultivated species with the largest world distribution and one of the oldest cultivated yam species. It constitutes an important staple food crop for millions of people in the humid and sub humid tropics. *D. alata* is superior to most edible yam species in terms of high yield potential especially under low to average soil fertility, ease of propagation (production of bulbils and reliability of sprouting), early vigor for weed suppression and storability of tubers. Wu et al. (2005) analyzed the consumption of *D. alata* by post-menopausal women and concluded that although the mechanisms are not yet fully understood, its consumption reduces the risk of breast cancer and cardiovascular disease.The development of *D. alata* varieties with improved food quality and resistance to pests and diseases would encourage its widespread cultivation and significant increase in production. Genetic improvement programs at the ICAR-Central Tuber Crops Research Institute (ICAR-CTCRI, India) aims at developing high yielding greater yam varieties with resistance to pests and diseases to meet farmers' requirements. Accurate information on genetic diversity is critical to the success of breeding programs, since genetic divergence produces high heterotic effects and, therefore, desirable segregants for selection.

In this study, the multivariate techniques of principal components and cluster analyses were used to determine the levels of morphological diversity in 45 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 germplasm of yams collected from different districts of Kerala. The exploitation of the genetic diversity so determined serves to facilitate the development of better varieties through combination and marker assisted breeding program.

Materials and Methods

The plant materials used for morphological studies comprises of forty five accessions of *D. alata* conserved in the National repository of tuber crops germplasm at ICAR-CTCRI, Sreekariyam, Thiruvananthapuram. The details of materials used for the study is given in Table 1.

Table 1. List of accessions of greater yam used

Sl. no.	Accession no.	Vernacular name	Place of collection
1	Da 340	*Kalakkompan*	Idukki
2	Da 240	*Kachil*	Paravatty, Thrissur
3	Da 8	*Nadan chappan*	Thrissur
4	Da 13	*Nadan chappan*	Malappuram
5	Da 343	*Kavathu*	Malappuram
6	Da 215	*Nadan kachil*	Kallada, TVPM
7	Da 278	*Pal kachil*	Omalloor, Pattanamthitta
8	Da 289	*Kachil*	Omalloor, Pattanamthitta
9	Da 243	*Kachil*	Mala, Thrissur
10	Da 303	*Anakkompan*	TVPM
11	Da 287	*Pulinthodan*	Sarkara, TVPM
12	Da 222	Da 5	NBPGR, Thrissur
13	Da 313	*Kachil*	Pathanapuram
14	Da 312	*Kachil*	Pathanapuram
15	Da 308	*Kachil*	Pathanamthitta
16	Da 122	*Kachil*	Wayanad
17	Da 209	*Kachil*	Nedumangad, TVM
18	Da 21	*Chuvanna muramchari*	Vellayani, TVM
19	Da 28	*Kachil*	Ernakulam
20	Da 52	*Aanakkalan kachil*	Palode, TVPM
21	Da 65	*Kachil*	Pariyaram
22	Da 40	*Elivalan*	Kallar
23	Da 68	*Bharani kachil*	Kumali
24	Da 53	*Pathi kachil*	Arippa
25	Da 33	*Kachil*	Ernakulam
26	Da 70	*Thekkan kachil*	Kaladi
27	Da 27	*Kuda kachil*	Ponkunnam
28	Da 102	*Nadu chuvappan*	Nedumkandam, Idukki
29	Da 114	*Erachi kavithu*	Kunnappally, Malappuram
30	Da 241	*Kachil*	Vadanappally, Thrissur
31	Da 73	*Muramchari*	Chowara
32	Da 58	*Kolla kachil*	Aalancheri
33	Da 120	*Wayanad*	Wayanad
34	Da 56	*Ezhankulam*	Ezhankulam
35	Da 84	*Vazhakulam*	Vazhakulam
36	Da 113	*Ottapalam*	Ottapalam
37	Da 88	*Alapuzha*	Alapuzha
38	Da 85	*Nedumkandam*	Nedumkandam
39	Da 118	*Kaduvakkayyan*	Wayanad
40	Da 69	*Kaduvakkayyan*	Kumali
41	Da 99	*Vettu kachil*	Kaladi
42	Da 81	*Parisakodan*	Vazhakulam
43	Da 390	*Kavithu*	Kasargod
44	Da 331	*Neela kachil*	Pathanamthitta
45	Da 391	*Neela kachil*	Pathanamthitta

The tubers of the collected accessions were planted on the field at the end of April. Tuber cuttings were planted on mounds prepared at a spacing of 1m × 1m. The vines were supported on a stake of about 2m height. Harvest was done during January-February by manually digging out the tubers and the tubers were cleaned free of soil and kept in ventilated yam storage house till the next planting season.

The accessions were characterized based on 25 qualitative and 13 quantitative traits including the major yield components and four biochemical characteristics. 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.

The quantitative data were analyzed for analysis of variance (ANOVA) and LSD test was performed to identify genotypes that were significantly different from each other. Cluster analysis was used to estimate pair-wise genetic similarity values based on qualitative traits among accessions using Jaccard's similarity coefficient. The similarity matrix was then used to construct a dendrogram using Darwin 5.1.531 software (http://darwin.cirad.fr/darwin/Home.php). Correlation and principal component analysis (PCA) was done using SAS 9.3 software (SAS, 2011)

Genetic parameters were estimated to identify genetic variability among accessions and determine genetic and environmental effects on characters. The genotypic and phenotypic components of variance, coefficients of variability, broad sense heritability and genetic advance were estimated by adapting the formulae suggested by Allard (1960) and Singh and Chaudhary (1977).

Results and Discussion

Variation in qualitative traits assessed

The use of qualitative traits in the classification of crops is very essential due to their relative stability over quantitative traits. Wide variation was observed in various qualitative characters used in the differentiation of the accessions *viz*., tuber shape, tuber flesh colour, tuber skin texture, tuber cortex colour, leaf shape and young leaf colour. Similar observations have been reported in the studies done by Demuyakor et al. (2013) and Anokye et al. (2014). The variation observed on major qualitative traits in germplasm collected from different districts of Kerala is given below

a. Young leaf colour

There were six different colours observed namely, yellowish green, pale green, dark green, light brown, purplish green and purple colour. In all, 71.1% showed pale green colour, 13.3% had yellowish green, 6.7% showed dark green, 4.4% showed purplish green, 2.3% had light brown and 2.2% had purple colour.

b. Leaf shape

Five different shapes of leaves were observed among *D. alata* accessions. It was observed that 51.0% was cordate, 26.7% observed as cordate long, 8.9% had cordate broad, 6.7% showed sagitate broad and 6.7% exhibited sagitate long leaves.

c. Tuber shape

Tuber shape variation among the greater yam accessions studied is presented in Fig. 1. that shows different types of shapes observed in *D. alata*. The *D. alata* accessions examined phenotypically based on their tuber shape exhibited variation with round (11.1%), oval (11.1%), oval-oblong (31.1%), cylindrical (8.9%), conical (8.9%), spindle shape (13.3%), digitate (11.1%) and irregular (4.5%) shapes.

d. Tuber cortex colour

The tuber cortex colour showed high variability among the accessions studied and six different cortex colours were observed. Among the accessions, majority (49.0%) had light purple, followed by light cream (22.2%), light yellow (11.1%), dark purple (8.9%), purple (4.4%) and greenish yellow (4.4%) cortex colour.

e. Tuber flesh colour

Wide variation was observed in tuber flesh colour among 45 accessions of *D. alata* landraces studied. Majority of the accessions (86.7%) had off-white colour, 8.9% showed white colour, 2.2% had yellow colour and 2.2% exhibited purple coloured flesh.

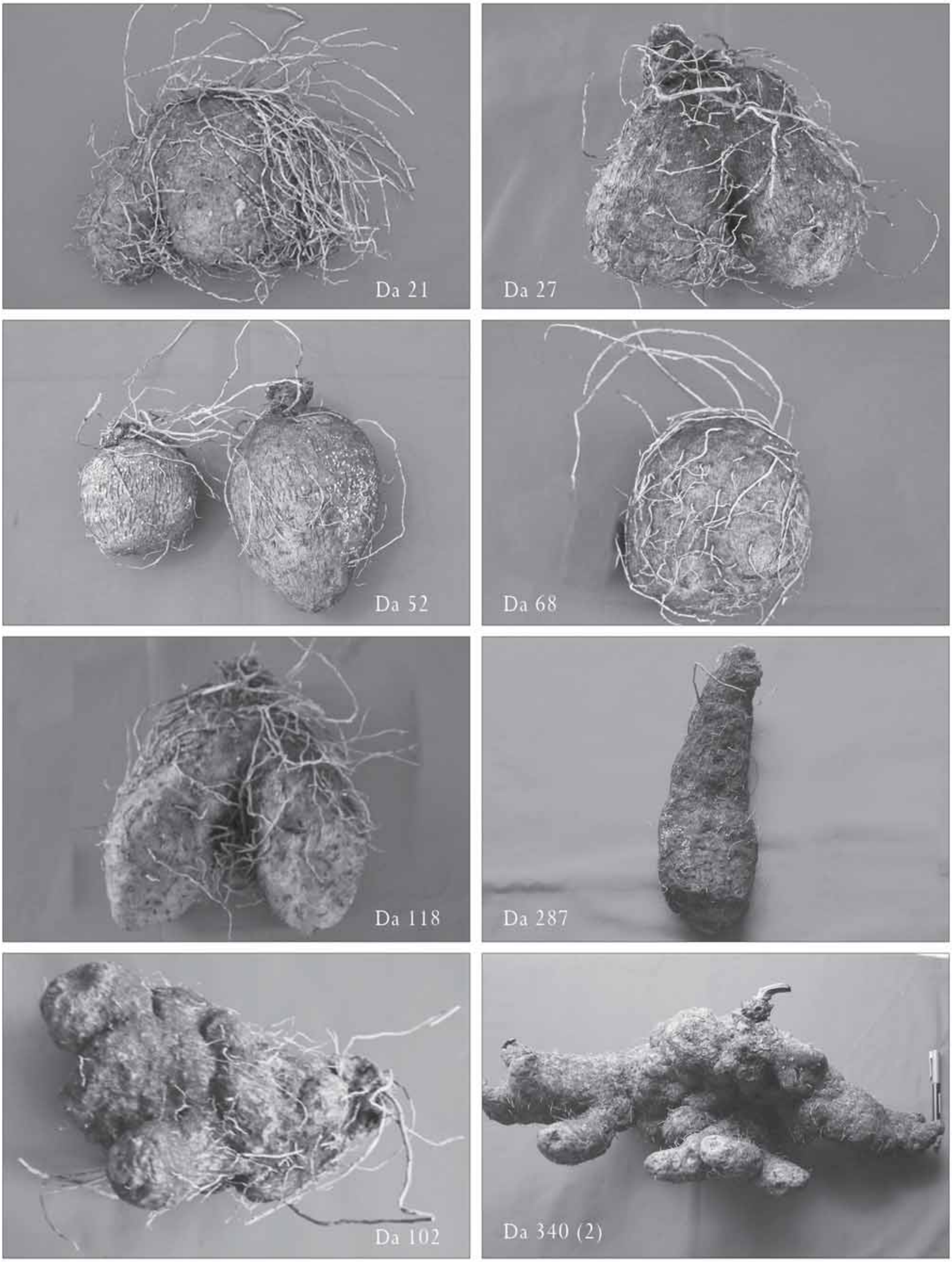

Fig. 1. Variation in tuber shape

Table 2. Evaluation of genetic parameters in greater yam

Character	GCV (%)	PCV (%)	Heritability	GA 5%	GA as % of mean
Mature stem diameter	13.85	19.18	0.5215	0.58	20.61
Leaf length	12.94	16.32	0.6291	3.10	21.16
Leaf breadth	13.85	21.98	0.3970	1.56	17.99
Petiole length	19.61	27.97	0.4916	2.37	28.33
Length of tuber	36.51	37.78	0.9338	13.64	72.69
Girth of tuber	31.14	32.83	0.8999	17.62	60.87

Where, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, GA = Genetic advance

Table 3. Phenotypic correlation among agronomic traits in greater yam

Character	X1	X2	X3	X4	X5	X6	X7
X1	1						
X2	-0.0545	1					
X3	-0.1376	0.5622**	1				
X4	-0.0908	0.3517*	0.4766**	1			
X5	0.0617	0.1222	0.1404	0.2184	1		
X6	0.1792	-0.128	-0.1816	0.0067	-0.0114	1	
X7	0.1231	-0.0601	0.0092	0.2247	0.3512*	0.0680	1

Where, X1 = Mature stem diameter, X2 = leaf length, X3 = leaf breadth, X4 = petiole length, X5 = tuber length, X6 = tuber girth, X7 = tuber weight

Table 4. Genotypic correlation among agronomic traits in greater yam

Character	X1	X2	X3	X4	X5	X6	X7
X1	1						
X2	-0.0017	1					
X3	-0.0845	0.4912**	1				
X4	-0.1052	0.253	0.5062**	1			
X5	-0.0524	0.1489	0.2111	0.3324*	1		
X6	0.2261	-0.1963	-0.3349	-0.0286	0.0075	1	
X7	0.1663	-0.0699	0.0247	0.3364*	0.3636*	0.7153**	1

Where, X1 = Mature stem diameter, X2 = leaf length, X3 = leaf breadth, X4 = petiole length, X5 = tuber length, X6 = tuber girth, X7 = tuber weight

f. Tuber skin texture

Significant phenotypic variability was identified among the individual accessions with respect to texture of tuber. Four types of skin texture were recorded - smooth, moderately smooth, warty and highly warty. Among the accessions 44.4% had warty skin, 33.3% had moderately smooth skin, 20% had skin texture which was highly warty in nature while 2.3% exhibited smooth skin.

g. Cooking quality/culinary quality

One important character taken for the study was cooking quality. There were four characters recorded under cooking quality/culinary quality *viz.* softness, stickiness, colour and taste. On examining the cooking quality, 75.5% exhibited soft flesh while 48.9% had non-sticky flesh. In case of taste of the tuber, 57.8% had good, 33.3% had excellent, 6.7% had average taste and 2.2% exhibited poor cooking quality.

Variation in quantitative characters

Among the 45 *D. alata* accessions, seven quantitative data was recorded and performed ANOVA (Analysis of Variance). Analysis was also done for estimation of genetic parameters, genotypic and phenotypic correlation between the selected quantitative characters. Among the agronomic traits evaluated, highest genotypic coefficient of variation (GCV) was recorded for length of tuber (36.51) followed by girth of tuber (31.15) while lowest GCV was recorded by leaf length (12.95) (Table 2). Among the traits studied, tuber characters recorded very high heritability as compared to shoot characters. The highest heritability was recorded by length of tuber

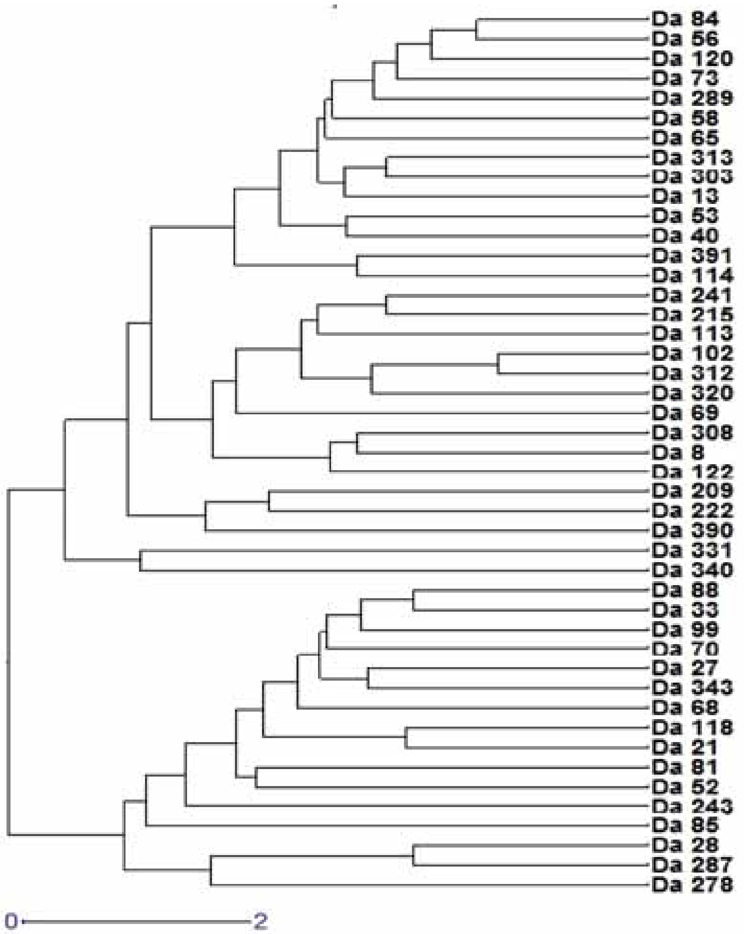

Fig.2. Dendrogram based on the cluster analysis of greater yam genotypes through distance matrix based on morphological traits

Table 5. Eigen values and cumulative variance of the first fifteen PCs representing variability of greater yam accessions.

	Eigen values of the correlation matrix			
	Eigen value	Difference	Proportion	Cumulative
1	5.7028	1.5674	0.1358	0.1358
2	4.1354	0.6519	0.0985	0.2342
3	3.4835	0.6348	0.0829	0.3172
4	2.8487	0.3340	0.0678	0.3850
5	2.5146	0.1492	0.0599	0.4449
6	2.3654	0.1051	0.0563	0.5012
7	2.2602	0.3082	0.0538	0.5550
8	1.9520	0.0389	0.0465	0.6015
9	1.9130	0.4444	0.0455	0.6470
10	1.4686	0.1006	0.0350	0.6820
11	1.3679	0.0523	0.0326	0.7146
12	1.3155	0.0834	0.0313	0.7459
13	1.2321	0.1088	0.0293	0.7752
14	1.1233	0.1634	0.0267	0.8020
15	0.9598	0.0681	0.0229	0.8248

followed by girth of tuber. Highest genetic gain (%) was recorded for girth of tuber (17.62) followed by tuber length (13.64).

The phenotypic as well as genotypic correlations among the traits were also studied (Table 3 and 4). Among the traits studied, highest genotypic correlation was recorded for girth of tuber with weight of tuber (0.7153). However, phenotypic correlation of girth of tuber with weight of tuber (0.0680) was found to be negligible. Phenotypic correlation was found to be maximum among the petiole characters, leaf length with leaf breadth (0.5622) and leaf length with leaf breadth (0.4766). These characters also recorded significantly high genotypic correlation also. For length of tuber, both phenotypic (0.3512) and genotypic (0.3636) correlation with weight of tuber was found to be significant.

Cluster and Principal Component Analysis (PCA)

Observations recorded for the morphological characters of greater yam was used for clustering with tree analysis concept based on Jaccard's index genetic similarity matrix. It revealed that the *D. alata* accessions exhibited greater degree of genetic variation for the 42 different morphological traits observed (Fig. 2). The 45 greater yam accessions were grouped into two major clusters with Cluster I having maximum number of accessions (29) and Cluster II with 16 accessions. The Cluster I and II again formed three sub clusters. The major cluster was divided into two sub clusters and Da 331 and Da 340 showed the maximum divergence among the accessions and grouped as a separate sub cluster. Among the accessions none were found to be completely similar. However maximum similarity was obtained between Da 102 and Da 312 followed by Da 56 and Da 84.

The morphological traits were considered for PCA analysis with a Measure of Sample Adequacy greater than 0.5. The Eigen values and cumulative variance of the first fifteen components is given in Table 5 and variability

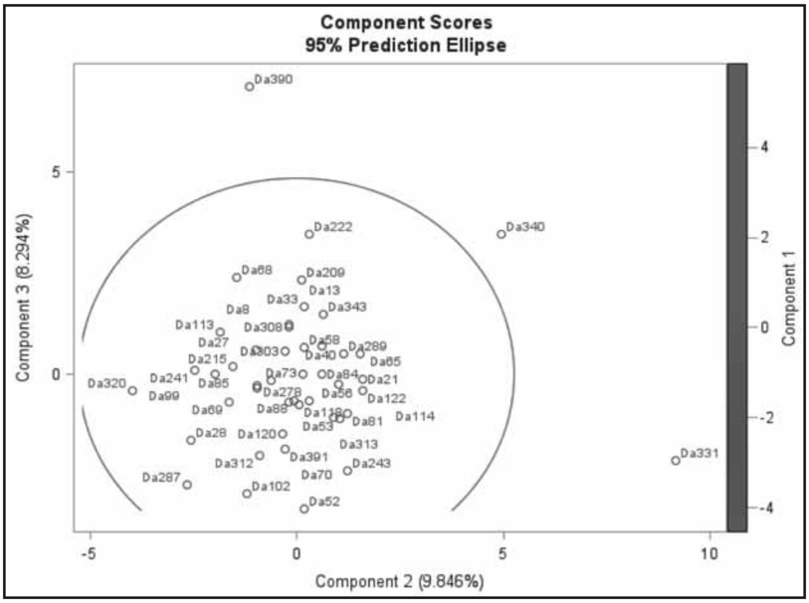

Fig. 3. Scatter plot for the first three principle components (PCs) for morphological traits

is depicted in Fig. 3. The first six principal components of data accounted for 50.12% of the total variance among accessions. The first principal component (PC1) explained 13.58% of the total variance, which was contributed mainly by young vein colour, colour of young leaves, leaf shape, petiole length, young leaf vein colour, tuber shape, tuber cortex colour and starch content. The distribution of accessions in the scatter plot revealed high divergence of Da 340, Da 331 and Da 390.

The use of qualitative traits in the classification of crops is very essential due to their relative stability over quantitative traits. Wide range of variation was observed in various qualitative characters used in the characterization of the greater yam accessions namely, tuber shape, tuber flesh colour, tuber skin texture, tuber cortex colour, leaf shape and young leaf colour. Similar observations have been reported in the studies done by Demuyakor et al. (2013) and Anokye et al. (2014) also. Among the genotypes evaluated yellowish white/off-white emerged as the predominant character among the flesh colour of the accessions. It was followed by purple colour, white and yellow had the lowest relative frequency. Islam et al. (2012) assessed 59 *Dioscorea alata* accessions from Bangladesh and observed white, yellow, off white, red, purple and yellow orange flesh colour. Similarly, on the study conducted on *Dioscorea alata* landraces by Bressan et al. (2011), he also observed that white, purple and yellow coloured flesh of tubers exist. In this study, the higher number of white, yellow and purple coloured tuber flesh observed were in agreement with Bressan et al. (2011), while red types were absent as reported by Islam et al. (2012). Light purple tuber cortex colour was in the majority among the accessions studied followed by light cream, light yellow, dark purple, purple colour and greenish colour. Regarding the tuber skin texture, majority of the germplasm had warty skin while others have moderately smooth and smooth skin. Regarding the tuber shape, it showed a wide range of morphological variation for the accessions. The observed tuber shapes were oval-oblong, spindle shape, round, oval, cylindrical, conical and irregular shapes. In the diversity pattern study of *D. alata* in Brazil (Siqueria et al., 2014) three tuber shapes, namely irregular, oblong and round were found. But in the present study more than three shapes were found indicating more variability for this crop in India.

For other qualitative characters, wide variation was observed in terms of the shape of the leaves. Most of the materials had cordate leaf shape varying between cordate long and cordate broad. Very few accessions had sagitate leaf shape also. The present study have similar observation in the study of morphological characterization of *D. alata* in Ghana (Anokye et al., 2014).

The results obtained from the PCA indicated that the characters that most contributed to the species variability were related to tuber shape, flesh colour and tuber cortex colour. Further clustering of the morphological data with tree analysis concept and tree construction using Jaccard's similarity matrix approach gave two main clusters. In the cluster formation, tuber flesh colour contributed maximum polymorphism. The accessions with purple coloured flesh (Da 340 and Da 331) were found to be highly divergent from other landraces. Similar observations were reported in the study of genetic diversity analysis in greater yam native to India (Sheela et al., 2016). Mahalakshmi et al., (2007) also reported the use of morphological traits to obtain a core collection for *Dioscorea alata* by evaluating a total of 772 accessions.

Conclusion

In the present study, 45 landraces of greater yam collected were morphologically analyzed using the descriptors of yam. According to the present study, there were no duplicate accessions identified based on the morphological classification and it can be maintained as core collection because it depicts wide spectrum of variability and also represent landraces representing different yams growing regions of the Kerala state. Morphological traits like tuber shape, tuber flesh colour, tuber skin texture, tuber cortex colour, leaf shape and young leaf colour were all found to be of great importance in distinguishing the accessions in greater yam. Among the traits studied, tuber characters recorded very high heritability as compared to shoot characters. Highest genetic gain (%) was recorded for girth of tuber (17.62) followed by tuber length (13.64). The 45 greater yam accessions were grouped into two major clusters with Cluster I having maximum number of accessions (29) and Cluster II with 16 accessions. Principal component analysis showed that the eigen values of the first six principal components of data accounted for 50.12% of the total variance among accessions. The cluster dendrogram based on morphological data revealed that the *D. alata* accessions exhibited very high genetic variation and no duplicate accessions were observed among the landraces studied. Scatter plot for the first three principle components (PCs) for morphological traits identified Da 331, Da 390 and Da 340 as the highly divergent landraces and could be used in future breeding programmes for the genetic improvement of yams.

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