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Original article

Genetic variability and multivariate analysis to assess phenotypic diversity of coconut (*Cocos nucifera* L.) germplasm

R. Sudha[1,a], V. Niral[1], K. Samsudeen[1], G.N. Khadke[2] and M.K. Rajesh[1]

[1] Division of Crop Improvement, ICAR, Central Plantation Crops Research Institute, Kasaragod-671 124, Kerala, India
[2] Division of Crop Improvement, ICAR, Central Plantation Crops Research Institute, Research Centre, Kidu, Karnataka, India

Summary

Introduction – **Coconut is a perennial plantation crop grown extensively throughout the tropics. Characterization of conserved coconut germplasm has been undertaken globally for identification of specific traits of different genotypes. Exploitation of those identified genetic variability forms the primary step in coconut crop improvement program.** *Materials and methods* – **In this study, 16 coconut germplasms, comprising of eight tall and eight dwarf coconut populations maintained under International Coconut Gene Bank for South Asia & Middle East, CPCRI (Central Plantation Crops Research Institute) Research Centre, Kidu, Karnataka, were evaluated. Observations were recorded on morphological traits, reproductive traits and fruit component traits for two years (2017–18 and 2018–19).** *Results and discussion* – **Results revealed that the genotype West Coast Tall (WCT) recorded statistically significant mean value for nut yield. Highest mean value for copra content was observed in SanRamon Tall (SNRT). A total of three principal component axes explained the total variability. Cluster analysis showed that it would be advantageous to utilize the coconut genotypes in cluster I, II and cluster IV in breeding programmes. The results obtained from this study will be useful in the selection among these conserved coconut accessions for specific traits for future utilization in crop improvement initiatives.**

Keywords
coconut germplasm, genetic variability, characterization, cluster analysis, principal component analysis

Significance of this study

What is already known on this subject?

- The assessment of genetic diversity and structure of germplasm is essential for the efficient organization and utilization of breeding material. Morphological characterization is valuable for assessing and comparing diversity patterns within and among populations. Selection of coconut based on available genetic variability has been reported to augment the performance in first generation to the tune of 25–35%. Multivariate analysis, which includes PCA, dendrogram and discriminant analysis can be used to reveal the relationship between variables and categorize the genotypes. Multivariate analyses have proved important in classifying germplasm, ordering variability for large numbers of accessions or analyzing genetic relationships among traits in any breeding materials.

What are the new findings?

- There is wide variability for vegetative, reproductive and fruit component traits in studied coconut germplasm (LMT, SNRT, JSBT, WCT, ADOT, FJT, PHOT, LCT, GUGD, CGD, MGD, CRD, MOD, MYD, COD, GBGD). Populations that are genetically distant from each other have been identified and these can be used for selection of coconut palm with hybrid vigour.

What is the expected impact on horticulture?

- Coconut germplasm with a good amount of genetic divergent and superior characters identified from the study can be used for future crop improvement programmes to derive superior offspring.

Introduction

Coconut (*Cocos nucifera*) is an economically important plantation crop of various tropical countries of the world. It is cultivated around 93 countries of the world with a total production of 67,128 million nuts per year (APCC, 2015). It is cultivated in an area of 20.82 Lakh ha with a production of 23,904 million nuts and productivity of 11,481 nuts palm^{-1} year^{-1} in India (Coconut Development Board, 2016). Coconut is a monotypic species belonging to the genus *Cocos* (Beccari, 1916). Generally, the palms are classified in to two groups, *viz*., Talls and Dwarfs (Narayana and John, 1949). Prominent boles, tall stem, long leaves and thick endosperm/kernel are the typical characteristics of the tall coconut types whereas in dwarf types, boles are less prominent and nuts are with thin leathery endosperm. Tall palms are principally cross pollinated because of non-overlapping of male and female phase in the inflorescence whereas in dwarf palms, the female phase occurs within the male phase, ensures self-pollination (Liyanage, 1949). Because of cross pollination, tall coconut palms are highly heterozygous and store house of a lot of genetic variability.

The effectiveness of any crop improvement programme depends on the utilization of different genetic resources from around the world. Morphological characterizations of coconut accessions need to be undertaken to make these genetic resources useful for plant breeders and farmers throughout the world. Characterisation of conserved coconut germplasm is key area to be focused on for effective utilization of genetic

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[a] Corresponding author: rsudhahort@yahoo.co.in.

resources. Characterisation favours identification of trait-specific accessions among the conserved genetic resources for commercial cultivation. In addition, characterisation is vital in selecting parents for future breeding programs, identification of the duplications in conserved accessions, need of further collection to strengthen the germplasm, management of the conserved germplasm and planning programmes for the future conservation (Perera *et al*., 2009). In coconut, morphological characterization of different germplasm was reported by Bourdeix *et al*. (1993), Harries (1978), Sangare *et al*. (1978), Ratnambal *et al*. (2003), N'Cho *et al*. (1993) and Arunachalam *et al*. (2005). Morphological characterization is valuable for assessing and comparing diversity patterns within and among populations. Selection of coconut based on available genetic variability has been reported to augment the performance in first generation to the tune of 25–35% (Jack, 1930). At present many statistical procedures are used for grouping of genotypes. Multivariate analysis, which includes PCA, dendrogram and discriminant analysis can be used to reveal the relationship between variables and categorize the genotypes. Multivariate analyses have proved important in classifying germplasm, ordering variability for large number of accessions or analyzing genetic relationships among traits in any breeding materials (Zafar *et al*., 2008). Principal components analysis and clustering are mostly used multivariate technique to classify germplasm materials (Li-Hammed *et al*., 2016). Principal component analysis (PCA) generates the general relationship between variables while clustering is an exploratory data analysis tool for grouping accessions (Richard and Wichern, 2007).

Therefore, a study was undertaken to document the genetic diversity among the selected coconut germplasms conserved at International Coconut Gene Bank for South Asia & Middle East, CPCRI (Central Plantation Crops Research Institute), Research Centre, Kidu, Karnataka, in order to explore the possibility of utilizing these genotypes for further conservation, multiplication and in future breeding programmes.

Materials and methods

Plant material

Sixteen coconut genotypes established in *ex-situ* International Coconut Gene Bank for South Asia & Middle East, CPCRI (Central Plantation Crops Research Institute), Research Centre, Kidu, Karnataka, India were used in this study. The details of the genotypes used in the study are given in Table 1. Among the 16 genotypes, 8 were of the 'Tall' types and 8 were of the 'Dwarf' types. Eight accessions were indigenous to India and eight accessions were exotic collections.

The germplasm populations maintained at ICAR (Indian Council of Agricultural Research), CPCRI, Regional Centre, Kidu, is geographically located in the Kidu Reserve Forest and lies at 12.30°N lat. and 75.20°E long. Its altitude is 291.0 m above MSL (Mean Sea Level). The average maximum temperature is 40 °C in summer and 33 °C in winter while the average minimum temperature is 24 °C in summer and 18 °C in winter. The annual rainfall varies between 2,800 mm and 4,200 mm. The soil is red laterite or sandy laterite with high organic matter content.

Morphological analysis

The age of the palms selected for the study was between 40–50 years. A total of 96 palms identified for observations from 16 genotypes. Hence, the observations from six palms were treated as three replications in RBD (Randomized Block Design) with two palms per replication. Morphological and reproductive characters such as plant height, stem girth at base, stem girth at 0.5 m, stem girth at 1 m, total number of leaves, length of petiole, length of leaflet bearing portion, number of leaflets, girth of petiole, length and breadth of leaflet, length of single internode, length of inflorescence, stalk, spikelet bearing portion and spikelet, girth of inflorescence stalk, number of spikelets and female flowers per inflorescence, number of bunches per year, number of nuts per palm,

Table 1. Details of 16 coconut genotypes used in this study.

Abbreviation	Name of the genotype	Country/province	Region
Dwarf genotypes			
COD	Chowghat Orange Dwarf	Kerala (India)	South Asia
CGD	Chowghat Green Dwarf	Kerala (India)	South Asia
GBGD	Gangabondam Green Dwarf	Andhra Pradesh (India)	South Asia
GDGD	Gudanjali Dwarf	Gujarat (India)	South Asia
MGD	Malayan Green Dwarf	Malaysia	South-East Asia
MOD	Malayan Orange Dwarf	Malaysia	South-East Asia
MYD	Malayan Yellow Dwarf	Malaysia	South-East Asia
CRD	Cameroon Red Dwarf	Cameroon	Africa
Tall genotypes			
LMT	Laccadive Micro Tall	Lakshadweep Islands (India)	South Asia
LCT	Laccadive Ordinary Tall	Lakshadweep Islands (India)	South Asia
MYD	Malayan Yellow Dwarf	Malaysia	South-East Asia
PHOT	Philippines Ordinary Tall	Philippines	South-East Asia
SNRT	SanRamon Tall	Philippines	South-East Asia
FJIT	Fiji Tall	Fiji Islands	Oceania
JSBT	Jamaica Sanblas Tall	Jamaica	Indo-Atlantic
ADOT	Andaman Ordinary Tall	Andaman & Nicobar Islands (India)	South Asia
WCT	West Coast Tall	Kerala (India)	South Asia

weight, length and girth of the fruit, husk and shell thickness, length and girth of the nut, weight of copra and shell were recorded. Fully matured nuts were harvested from the identified palms for fruit component analysis. Morphological characters were observed on the basis of coconut descriptors (Ratnambal *et al*., 1995).

Statistical analysis

The mean values of all the traits were subjected to Analysis of Variance (ANOVA) on the basis of model proposed by Panse and Sukhatme (1969). The above data analyses were performed using WASP (Web Based Agricultural Software Package) data analysis software. Principal component analysis was done using the MVSP 3.2 (Multi-Variate Statistical Package) software (Kovach, 2007). The dendrogram was made using the technique of Unweighted Pair Group Method using arithmetic average (UPGMA), using the MVSP software v. 3.2.

Results and discussion

A total of thirty morphological parameters, including nine fruit component characters, were studied from 96 palms of 16 genotypes. The results obtained from the above studies were statistically analyzed and are presented in Tables 2–4. The morphological, reproductive and fruit component characters showed a wide range of variation among the accessions studied.

Vegetative characters

Morphological characters are generally used for assessment of genetic resources for classification of pooled germplasm and use in further trait specific selection. All the studied genotypes exhibited a high variability for most of the morphological characteristics (Table 2).

The highest average plant height and leaflet breadth value recorded was 1,097.8 cm and 6.1 cm, respectively, for WCT. JSBT (Jamaica Sanblas Tall) showed highest mean value for length of the leaflet bearing portion (595.8 cm) followed by ADOT (Andaman Ordinary Tall) (576.3 cm). The highest plant girth at 1.0 m of 97.2 cm was observed in SNRT. Maximum plant girth at base (155.5 cm) and total number of leaves (31) was observed in FJT (Fiji Tall). Length of petiole was high in LMT (Laccadive Micro Tall) (143.3 cm) which is on par with FJT (143.2 cm). Number of leaflets was maximum in PHOT (Philippines Ordinary Tall) (416.7). Lowest length of single internode of 3.2 cm was noted in GUGD (Gudanjali Dwarf). The results revealed that quantitative variations among the genotypes and these variations may be due to the wide range of collection sites and possible preferential collection or human selection for different traits such as dwarfness, nut and copra yield. The inheritance of these traits can be observed without using specialized biochemical or molecular techniques. Kumar (1999) reported that morphological traits that are controlled by a single locus can be used as genetic markers if their expression is reproducible over an array of environments. Among the morphological traits, *viz*., the number of leaves and leaf length are significant characters since these traits decide the ability of the leaf for supporting fruit bunches in its axils and also augment the efficiency of photosynthesis. The increase in plant height with simultaneous increase in leaf number contributed to the overall increased yield of the palm (Iyer, 1980). Shorter internode indicates the dwarfness of palm whereas larger stem girth is a typical character of tall varieties. Stem height, girth and number of leaves were the important parameters to decide the yield of the palm. Similar results of the current study were reported by Pillai *et al*. (1991), Ratnambal *et al.* (2001), Jerard (2002), Jayalakhmi and Sree Rangasamy (2002), Basavaraju *et al.* (2011), and Suchitra (2014).

Reproductive characters

Floral characters are considered to be the key factors for nut yield in coconut. In a coconut palm which has reached a normal bearing stage, every leaf axil produces a spadix or inflorescence. The inflorescence characters showed wide range of variation among the genotypes studied (Table 3). Length of the inflorescence (134.7 cm), length of spikelet bearing portion (48.8 cm) and number of spikelets per in-

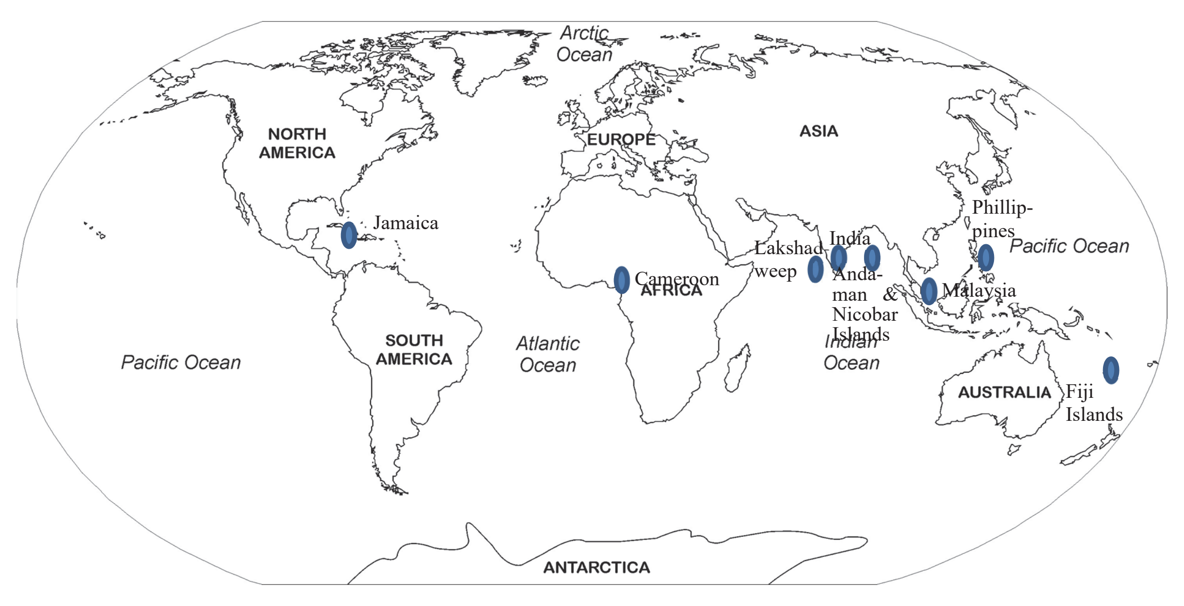

FIGURE 1. Geological distribution of the coconut genotypes used in the study.

Table 2. Morphological and foliar traits of 16 coconut genotypes.

Accession	Plant height (cm)	Stem girth at base (cm)	Stem girth at 0.5 m (cm)	Stem girth at 1 m (cm)	Total number of leaves	Length of petiole (cm)	Length of leaflet bearing portion (cm)	Number of leaflets	Girth of petiole (cm)	Length of the leaflet (cm)	Breadth of the leaflet (cm)	Length of single internode (cm)
GBGD	508.8	66.8	59.3	57.8	24.0	93.8	390.0	270.8	14.3	186.5	3.9	4.3
MGD	283.0	116	88.8	77.8	26.4	135.4	485.2	331.4	18.0	206.2	5.4	4.8
COD	375.6	65.6	62.0	64.4	24.8	114.4	471.0	327.8	15.8	194.4	5.0	4.3
MOD	255.0	82.8	72.8	68.5	22.0	107.3	458.8	304.5	15.0	187.3	5.8	3.4
MYD	325.4	73.2	62.4	60.8	23.0	103.6	426.0	285.4	13.6	186.0	4.5	3.8
CGD	306.2	66.2	62.4	59.4	20.2	101.6	400.4	276.0	14.8	193.4	4.8	3.8
CRD	284.7	84.0	71.7	68.2	22.3	142.8	477.2	313.5	15.4	215.7	5.4	4.5
GUGD	369.2	57.7	52.8	54.0	20.0	92.3	383.7	268.0	10.8	184.7	3.9	3.2
LCT	688.5	125.7	91.5	80.7	27.3	131.5	546.5	380.3	20.3	218.2	5.2	5.8
PHOT	889.3	139.5	103.7	90.0	27.2	135.3	544.0	416.7	20.0	224.3	4.7	4.8
FJT	738.7	155.5	115.7	95.0	31.0	143.2	530.0	347.8	16.2	202.8	5.2	5.0
JSBT	819.0	155.3	113.0	94.2	28.8	142.3	595.8	413.0	19.3	229.8	6.1	8.0
ADOT	759.3	144.5	112.0	91.5	29.2	141.2	576.3	398.2	17.7	230.2	6.0	5.9
SNRT	540.7	135.5	108.7	97.2	28.3	138.5	572.0	390.0	16.2	224.5	5.6	6.4
LMT	854.0	139.2	117.5	91.8	24.8	143.3	555.7	412.2	19.0	230.2	4.8	6.7
WCT	1,097.8	103.3	87.0	77.8	30.0	115.0	482.8	345.3	17.0	227.0	6.1	6.5
Mean	568.4	106.9	86.3	76.8	25.6	123.8	493.5	342.6	16.5	208.8	5.2	5.1
CD (P = 0.05%)	174.0	29.5	21.7	15.2	4.9	51.9	55.6	5.2	19.2	18.0	NS	1.8

CD: Critical difference.

florescence (38.8) were significantly higher in JSBT. Highest mean value for length of the spikelet (43.3 cm) was observed in FJT. Highest mean value for length of the inflorescence stalk (67.8 cm) was observed with FJT which was on par with ADOT. Mean value for number of female flowers per inflorescence (34.4) was higher in CGD (Chowghat Green Dwarf). Highest mean value for number of nuts per palm (127.0) was observed in LMT. The variation in reproductive parameters might be due to the genetic makeup of the individual genotypes. The higher number of nuts per palm may be due to the increased number of inflorescence production per palm per year and number of leaves production per year which might have contributed for higher photosynthetic accumulation towards the reproductive phase. The increased length of the inflorescence or stalk did not have any significant influence on the yield, however these characters are important for characterization of coconut genotypes. Short stalks always help the bunches to rest on the leaf which will avoid buckling of

TABLE 3. Reproductive and yield characters of 16 coconut genotypes.

Accession	Length of inflorescence (cm)	Length of spikelet bearing portion (cm)	Length of stalk (cm)	Girth of the stalk (cm)	Length of spikelet (cm)	Number of spikelets inflorescence^{-1}	Number of female flowers inflorescence^{-1}	Number of bunches year^{-1}	Number of nuts palm^{-1}
GBGD	86.8	26.5	36.0	9.6	32.5	20.8	21.5	11.0	51.2
MGD	115.6	36.8	62.0	7.0	37.4	28.8	18.6	10.2	50.4
COD	95.2	31.8	47.2	9.7	29.8	26.6	14.2	11.0	55.0
MOD	79.0	30.3	34.8	8.1	25.3	28.3	11.2	10.8	53.5
MYD	79.0	26.2	36.4	9.3	28.6	25.2	12.4	11.0	50.2
CGD	90.6	30.0	45.6	9.5	30.2	20.4	24.4	10.6	63.2
CRD	98.5	31.2	52.3	7.3	35.2	27.2	13.7	10.8	34.4
GUGD	77.0	22.8	36.3	8.8	25.8	19.3	31.2	10.3	56.3
LCT	127.7	42.7	63.0	8.0	40.0	33.8	16.2	12.5	74.7
PHOT	126.7	47.5	67.0	8.3	41.8	33.5	20.3	14.8	95.6
FJT	115.3	43.8	67.8	8.0	43.3	32.5	23.8	11.2	84.0
JSBT	134.7	48.8	62.3	9.7	39.0	38.8	15.2	10.7	46.8
ADOT	131.7	45.8	67.8	10.3	39.5	32.5	29.2	12.8	98.8
SNRT	128.2	45.0	63.8	9.8	36.8	31.8	15.5	12.2	38.8
LMT	121.0	41.3	61.0	8.7	40.0	37.2	29.7	11.8	127.0
WCT	112.5	33.3	53.3	9.8	41.8	36.8	21.3	12.9	81.0
Mean	107.5	36.5	53.5	8.9	35.4	29.6	19.9	11.5	66.3
CD (P=0.05%)	18.6	9.2	11.9	NS	10.0	8.1	19.3	4.7	64.2

CD: Critical difference.

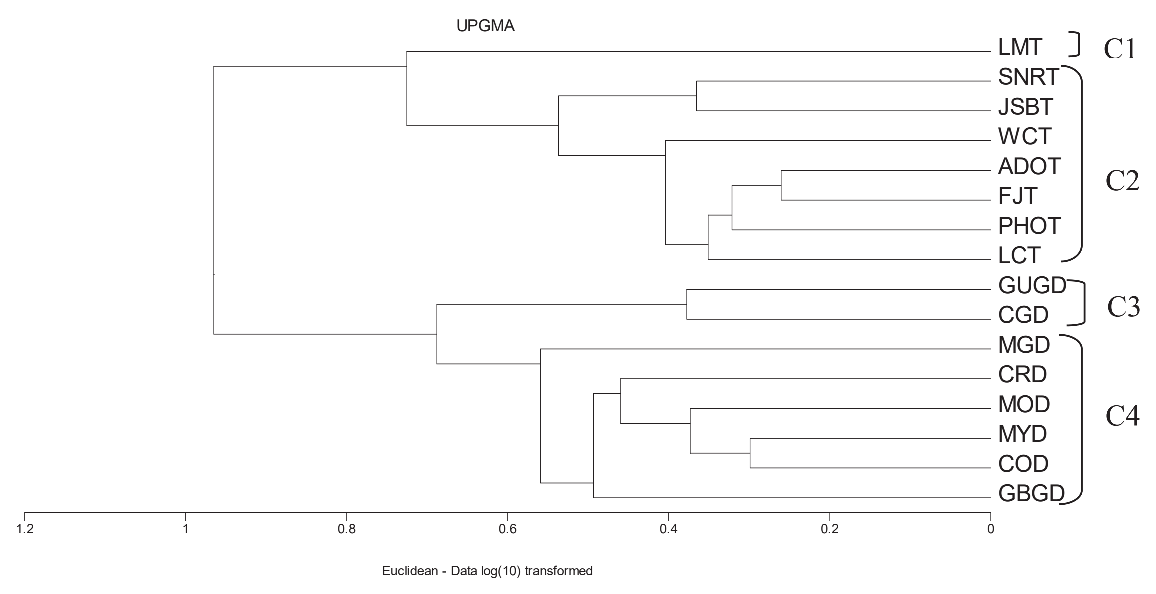

FIGURE 2. Grouping of sixteen coconut germplasms. LMT: Laccadive Micro Tall; SNRT: SanRamon Tall; JSBT: Jamaica Sanblas Tall; WCT: West Coast Tall; ADOT: Andaman Ordinary Tall; FJT: Fiji Tall; PHOT: Philippines Ordinary Tall; LCT: Laccadive Ordinary Tall; GUGD: Gudanjali Dwarf; CGD: Chowghat Green Dwarf; MGD: Malayan Green Dwarf; CRD: Cameroon Red Dwarf; MOD: Malayan Orange Dwarf; MYD: Malayan Yellow Dwarf; COD: Chowghat Orange Dwarf; GBGD: Gangabondam Green Dwarf.

bunches. Variations in reproductive parameters in different coconut genotypes were reported by Ratnambal *et al*. (1995, 2001), Selvaraj *et al*., (2017), Samarasinghe *et al*. (2018), and Suchithra and Paramaguru (2018).

Fruit component characters

Different components of the fruit provide major economically important produce of the coconut palm such as kernel, husk and shell. Thus the quantitative assessment of each of these fruit components by weight is an extremely important aspect of morphological characterization as it is directly influencing the yielding capacity of the coconut palm. Different fruit components along with nut yield of the palm provide the actual yield of the coconut palm.

In the present study, fruit weight (979 g), fruit length (31 cm), husk thickness (3.6 cm), nut length (21 cm) and weight of copra (260.8 g) was significantly higher in SNRT. Highest mean value for fruit girth (18.3 cm), nut girth (12.1 cm) and shell weight (171.4 g) was observed with JSBT and shell thickness (0.4 cm) was maximum in ADOT (Table 4).

Higher copra content might be due to the higher kernel weight. Kernel and husk along with shell are the three most important components of the mature coconut and any commercially grown cultivar should ideally possess satisfactory production capacities of these components. The current study provides ample evidence for SNRT, JSBT and ADOT possessing these characteristics, indicating the suitability of these phenotypes as candidates in a hybridization programme to transmit the characters. The results are in agreement with Pillai *et al.* (1991), Ratnambal *et al.* (2001), Jerard (2002), Basavaraju *et al.* (2011), Suchitra (2014), Ramanandam *et al.* (2017), and Tripura *et al*. (2018).

Cluster analysis

Cluster analysis shows four major clusters (C1, C2, C3 and C4) with eight distinct sub clusters (Figure 4). The first group (C1) consists of tall genotype LMT. The second group comprised of three sub-clusters (C2.1, C2.2 and C2.3). The first sub-cluster (C2.1) comprised of tall genotypes SNRT and JSBT. Sub-cluster C2.2 consists of one tall genotype WCT. The third sub-cluster (C2.3) consists of ADOT, FJT, PHOT and LCT. They were all tall palms with high boles. The third group (C3) comprised of two dwarf cultivars (GUGD and CGD). The fourth group comprised of six genotypes that can be divided into three sub-clusters. The first sub-cluster (C4.1) consists of one dwarf genotype (MGD) and the second sub-cluster (C4.2) included four dwarf genotypes (CRD, MOD, MYD and COD). The third sub-cluster (C4.3) consists of one dwarf genotype (GBGD). Under the clusters C3 and C4, all were dwarf and had the same leaf, stem and nut parameters. Dwarf genotypes formed a distinguishable aggregate in the coconut population, which was distinct from the tall genotypes with a broad variation. The tall genotypes were further classified into various subgroups. The grouping of genotypes had been found to be based on certain morphological, reproductive and fruit component traits which will further assist the breeders in planning future selections within these coconut populations. The clustering pattern has not reflected the geographical diversity of the studied genotypes. This is in conformity with the findings of Perera *et al*. (1998), Teulat *et al*. (2000), and Upadhyay *et al*. (2002). Similarity in many phenotypic characters of the genotypes brought them in a particular group. The observed diversities in the collections might be resulted from natural and human intervention and also due to a reflection of genetic drift and the selection of plants in different environments, rather than geographic location (Foale, 1992). The magnitude of intra-cluster distances indicated the extent of genetic diversity among genotypes within the cluster whereas inter-cluster distances depicted the extent of diversity among genotypes between clusters. It was reported that clusters with lesser magnitude of divergence showed instability while widely divergent clusters remained distinct in different environments

Table 4. Fruit component traits of 16 coconut genotypes.

Accession	Fruit weight (g)	Fruit length (cm)	Fruit girth (cm)	Husk thickness (cm)	Nut length (cm)	Nut girth (cm)	Copra weight (g)	Shell weight (g)	Shell thickness (cm)
GBGD	473.5	21.0	12.0	2.4	16.2	6.5	110.7	76.0	0.2
MGD	600.0	18.5	14.0	2.4	12.9	10.0	149.6	120.6	0.2
COD	407.7	19.3	12.0	1.8	15.3	8.8	142.5	110.5	0.3
MOD	521.0	25.3	12.2	2.7	10.2	9.2	116.8	104.0	0.3
MYD	388.7	20.5	12.8	3.0	14.6	7.3	132.0	98.0	0.2
CGD	274.2	21.1	14.8	2.6	10.9	7.9	77.8	47.8	0.2
CRD	394.5	17.8	11.3	2.0	10.5	9.0	83.2	83.1	0.2
GUGD	233.8	17.4	10.3	3.3	8.2	7.3	80.3	49.7	0.2
LCT	647.2	27.4	16.2	2.8	12.0	10.0	162.0	114.6	0.2
PHOT	962.2	25.2	14.3	2.7	11.76	10.5	216.0	170.7	0.2
FJT	828.5	26.4	13.8	3.3	11.3	10.2	188.9	130.9	0.3
JSBT	902.5	28.2	18.3	3.5	12.2	12.1	218.9	171.4	0.3
ADOT	720.0	29.3	15.6	3.0	9.62	9.5	160.4	128.6	0.4
SNRT	979.0	31.0	16.0	3.6	21.0	11.0	260.8	156.4	0.3
LMT	430.0	17.9	12.1	1.8	9.9	7.4	90.9	78.1	0.3
WCT	800.0	21.8	13.6	2.8	11.1	9.2	181.3	159.7	0.3
Mean	597.6	17.9	14.0	2.8	10.3	9.6	143.8	108.1	0.3
CD (P = 0.05%)	281.6	NS	3.3	0.8	NS	NS	62.4	57.9	0.09

CD: Critical difference.

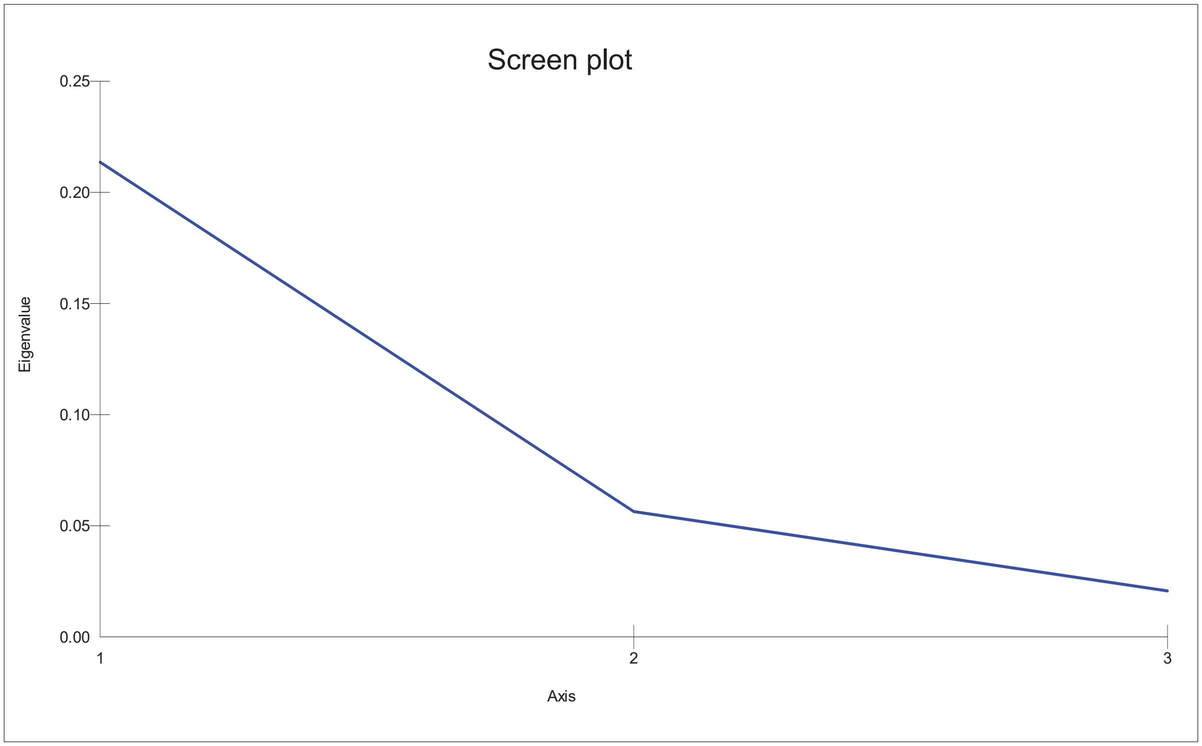

FIGURE 3. Screen plot showing eigen value variation.

TABLE 5. Eigen values, factor scores and contribution of principal component axes.

Principal components	PC1	PC2	PC3
Eigen values	0.214	0.056	0.021
Percentage of variance	64.093	16.925	6.202
Cumulative percentage	64.093	81.018	87.220
Plant height	0.368	-0.401	-0.498
Stem girth at base	0.310	-0.052	0.286
Stem girth at 0.5 m	0.239	-0.067	0.236
Stem girth at 1 m	0.177	-0.014	0.152
Total number of leaves	0.116	0.013	-0.055
Length of leaves	0.118	0.007	0.279
Length of leaflet bearing portion	0.124	0.009	0.137
Length of petiole	0.136	-0.031	0.107
Number of leaflets	0.118	-0.013	0.140
Length of leaflet	0.067	0.066	0.112
Breadth of leaflet	0.174	-0.038	0.054
Length of single internode	0.171	-0.039	0.141
Length of inflorescence	0.205	-0.009	0.196
Length of spikelet bearing portion	0.198	-0.065	0.274
Length of spikelet	0.140	-0.076	0.064
Number of spikelets inflorescence^{-1}	0.178	-0.006	0.116
Number of nuts bunch^{-1}	0.135	-0.518	-0.074
Fruit weight	0.387	0.220	-0.155
Fruit length	0.122	0.095	-0.095
Nut length	0.034	0.249	-0.192
Nut girth	0.110	0.118	0.118
Copra weight	0.300	0.280	-0.315
Shell weight	0.319	0.288	-0.156

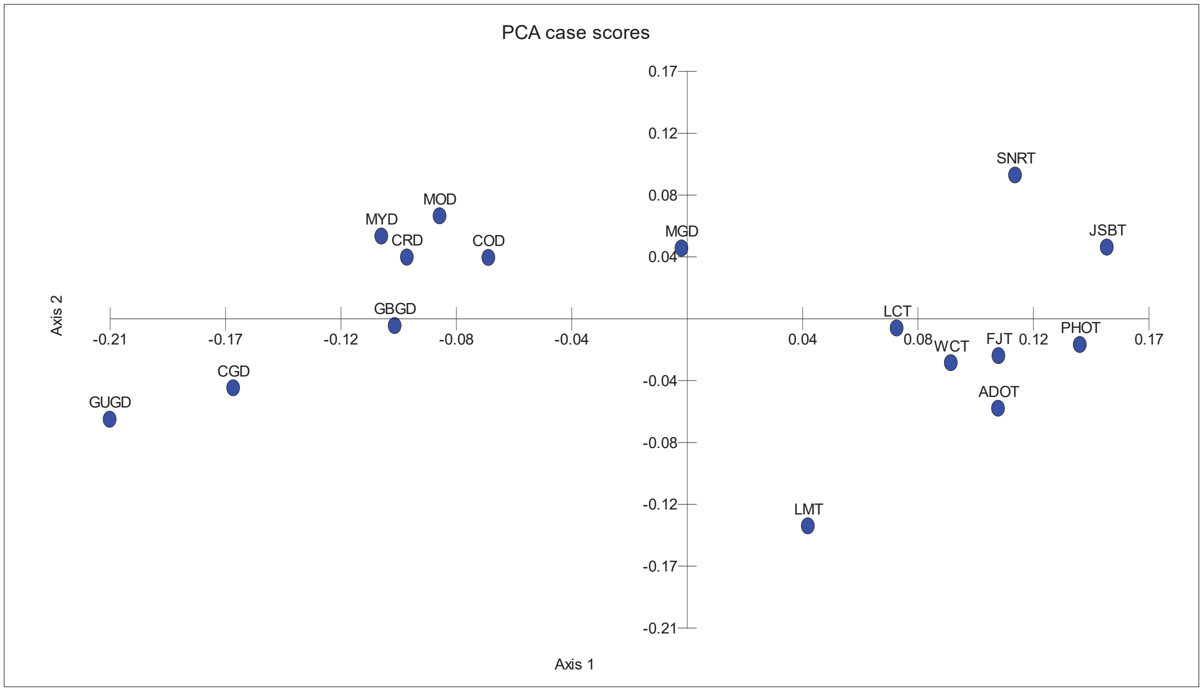

FIGURE 4. Distribution of various traits and genotypes across two components. LMT: Laccadive Micro Tall; SNRT: SanRamon Tall; JSBT: Jamaica Sanblas Tall; WCT: West Coast Tall; ADOT: Andaman Ordinary Tall; FJT: Fiji Tall; PHOT: Philippines Ordinary Tall; LCT: Laccadive Ordinary Tall; GUGD: Gudanjali Dwarf; CGD: Chowghat Green Dwarf; MGD: Malayan Green Dwarf; CRD: Cameroon Red Dwarf; MOD: Malayan Orange Dwarf; MYD: Malayan Yellow Dwarf; COD: Chowghat Orange Dwarf; GBGD: Gangabondam Green Dwarf.

(Raut *et al*., 1985; Singh *et al*., 1980). According to the distance matrix (Euclidean), cluster I, II and cluster IV has the maximum variation in the present study. Hence, it would be advantageous to utilize the coconut genotypes in cluster I, II and IV in breeding programmes. Parents for hybridization could be selected on the basis of large inter-cluster distance for isolating useful recombinants in the segregating generations. Increasing parental distance implies a greater number of constraining alleles at the desired loci and then to the extent that these loci recombine in the F_2 and F_3 generations following a cross of distantly related parents, the greater will be the opportunities for successful selection for any character of interest (Ghaderi *et al*., 1984).

Principal component analysis

Principal component analysis quantifies each parameter to calculate the Principal Components (PCs) which help in describing the variation in the dataset. In the present study, the first three principal components (PC1, PC2 and PC3) accounted for 64.09%, 16.93% and 6.2% of the variation, respectively, accumulating to a total of 87.22% of the total variability among the coconut accessions evaluated (Table 5, Figure 3). Plant height, stem girth at base, stem girth at 0.5 m, stem girth at 1 m, total leaves on the crown, length of the leaf, length of the leaflet bearing portion, number of leaflets, breadth of leaflet, length of single internode, length of inflorescence, length of spikelet bearing portion, length of spikelet, number of spikelets/inflorescence, number of nuts per palm, fruit weight, fruit length, nut girth, copra weight and shell weight were highest loading on PC1. In second principal component (PC2), variables, *viz*., fruit weight, nut length, nut girth, copra weight and shell weight had positive loading. In third principal component (PC3), stem girth at base, stem girth at 0.5 m, stem girth at 1 m, length of the leaf, length of the leaflet bearing portion, number of leaflets, length of leaflet, length of inflorescence, length of spikelet bearing portion, length of spikelet, number of spikelets/inflorescence and nut girth had positive loading. Hence, the characters that came in different principal component axes have the tendency to remain together. Similar variations in the contribution pattern towards principal components were also reported by Nazirul Islam *et al*. (2009), Mohanlal *et al*. (2018), and Subramanian *et al*. (2019).

Conclusion

The wealth of any germplasm collection is quantified in terms of the extent of genetic variability of the accessions it contains. It can be concluded from this study that there is wide variability for vegetative, reproductive and fruit component traits in studied coconut germplasm. Also, populations that are genetically distant from each other have been identified and these can be used for selection of coconut palm with hybrid vigour. Populations with good amount of genetic divergent and superior characters will be of practical use and can be used to derive superior offspring. The variation in this coconut genotypes may be only a portion of the variability in coconut worldwide, and subsequent evaluation may be needed to conserve these valuable genetic materials. Subsequent breeding programmes need to further exploit the existing coconut germplasm variation to broaden the coconut narrow genetic base. The use of multivariate tools will help to explore the unutilized genetic diversity for future generation.

Authors' contribution

Conceptualization of research (R. Sudha and V. Niral); designing of the experiments (R. Sudha and V. Niral); contribution of experimental materials (R. Sudha, V. Niral,

K. Samsudeen and M.K. Rajesh); execution of field/lab experiments and data collection (R. Sudha, K. Samsudeen and G.N. Khadke); analysis of data and interpretation (R. Sudha and M.K. Rajesh); preparation of the manuscript (R. Sudha, V. Niral, K. Samsudeen and M.K. Rajesh).

Declaration

The authors declared that they do not have any conflict of interest.

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