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Variability studies for yield and yield attributing characters in Palmyrah accessions (*Borassus flabellifer* L.) under Killikulam condition of Tamil Nadu

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Abstract

Palmyrah (*Borassus flabellifer* L.), the state tree of Tamil Nadu of south India is grown for its multitude of food and economic uses. Breeding efforts in this crop is minimal due to its very long duration to maturity and dioecious nature. We aim to fill this gap by first studying the variability and fruiting behaviour in 16 genotypes of the 265 germplasms being maintained under the ICAR-All India Coordinated Research Project in Plantation Crops at the Department of Horticulture, VOC Agricultural College and Research Institute, Killikulam, Tamil Nadu, India. These palmyrah accessions were collected from different states of India viz., Tamil Nadu, Andhra Pradesh, Karnataka, Bihar, West Bengal and Odisha. Nine fruit morphology characters were observed on the accessions and used to assess the diversity. Wide variability was observed for the different traits studied. Number of fruits ranged from 12 (acc.252) to 410 (acc.41). The highest fruit weight (1.440 kg), flesh weight with epicarp (0.605 kg) and nut weight per fruit (0.835 kg) was recorded in the accession no. 41. Accession 3 recorded highest weight per nut (0.182 kg). Similarly, variation in other fruit traits was observed. High heritability of these traits indicated the suitability of selection in this population. The selected germplasm accessions will be used as parents in further breeding programmes.

Keywords: Palmyrah, mean performance, fruit, seed, heritability, variability, and yield

Introduction

Palmyrah (*Borassus flabellifer* L.; Botanical family: Arecaceae), is a tree that is native to tropical Africa that is also spread in the drier parts of India, Sri Lanka, Thailand, Malaysia, Vietnam, and Indonesia. In India, where almost 102 million palms are found, nearly half of them are located in the south Indian state of Tamil Nadu. It has been designated as the state tree of Tamil Nadu since 1978. Out of 51.9 million palms in Tamil Nadu, over 50% can be found in the southern districts of Thoothukudi, Tirunelveli, Virudhunagar, and Ramnad, with Thoothukudi district alone having a major share of 10 million palms. Palmyrah trees are tall that can grow up to a height of 13-14 meters, dioecious with separate male and female trees and are perennials that may take 15 years to attain sexual maturity to produce fruits (Krishnaveni *et al.*, 2020)^[11]. Its trunk is black, cylindrical, and has a circumference of 1.5 meters, and it is able to withstand adverse climate conditions (Mohan *et al.*, 2016)^[13]. The tree's flowers are small and densely clustered on spikes, developing into large, brownish, round fruits. The male flowers are typically smaller than the female flowers. The fruits of this palm is large and fibrous, consisting of nut-like portions containing seeds. When young, the fruits are three-sided, eventually becoming semi-spherical to spherical in shape and covered with sepals at the base (Gummadi *et al.*, 2016)^[9]. When ripe, the fruit turns a deep brown to black color (Ramachandran *et al.*, 2004)^[17]. Each part of the palmyrah tree has unique pharmaceutical and health-beneficial properties. Palmyrah roots are high in calories and rich in Vitamin E. They also contain phytochemicals such as flavonoids and phenolic acids that exhibit antioxidant activity (Sahni *et al.*, 2014)^[19]. Its trunk is used as timber and leaves are used for thatching and for handy crafts; endosperm of young fruits are nutrient-rich and famous as a summer delicacy; the inflorescence sap, known as

'neera' is consumed raw or processed into palm sugar. Thus palmyrah is vital for the livelihoods of many people in the state, especially those from economically and socially disadvantaged sections.

Therefore, it is crucial to make the most of large Palmyrah population available in the state. Unfortunately, due to its extremely long duration to sexual maturity (~15 years), its dioecious nature and other botanical traits such as tall stature research in this crop has been minimal. And, there is currently no database regarding their natural variability present in the state and elsewhere. As a result, efforts have been made to study the variation in Palmyrah based on their morphology, flower biology and yield potential (Kumari *et al.*, 2020) [12]. We aim to fill this gap by assessing variability between different accessions of palmyrah currently being maintained at the field genebank of VOC Agricultural College and Research Institute, Killikulam. We studied different traits with special attention to the fruit characters.

Materials and Methods

The experiment was conducted at the field gene bank under ICAR-All India Coordinated Research Project in Plantation Crops of the Department of Horticulture, VOC Agricultural College and Research Institute, Killikulam, Thoothukudi district (longitude 77.8624, latitude 8.7038) to study the variability in palmyrah accessions for yield and yield attributing characters. The germplasm consisted of 265 accessions collected from different parts of India viz., Tamil Nadu, Andhra Pradesh, Karnataka, West Bengal, Bihar and Odissa. Of these, fruit samples were collected from sixteen bearing accessions in the month of August and September during the year 2023-24. Observations were recorded for nine characters viz., number of fruits per tree, fruit weight, flesh weight with epicarp, nut weight per fruit, weight per nut, seed length, fruit length, fruit diameter, and seed circumference. The list of accessions studied and their source is given in Table 1.

Table 1: Different accessions of Palmyrah and their source of collection being maintained at VOC AC&RI, Killikulam

S. No.	Genotypes	Source of collection
1.	Accession 1	Killikulam, Tamil Nadu
2.	Accession 2	Killikulam, Tamil Nadu
3.	Accession 3	Killikulam, Tamil Nadu
4.	Accession 10	Killikulam, Tamil Nadu
5.	Accession 17	Ananthanambikurichi, Tamil Nadu
6.	Accession 22	Ananthanambikurichi, Tamil Nadu
7.	Accession 26	Ananthanambikurichi, Tamil Nadu
8.	Accession 27	Ananthanambikurichi, Tamil Nadu
9.	Accession 41	Seerudaiyarpuram, Tamil Nadu
10.	Accession 48	Anaikudi, Tamil Nadu
11.	Accession 51	Anaikudi, Tamil Nadu
12.	Accession 52	Anaikudi, Tamil Nadu
13.	Accession 63	Thisaiyanvilai, Tamil Nadu
14.	Accession 65	Ampalacherry, Tamil Nadu
15.	Accession 91	Pillayarapuram, Andhra Pradesh
16.	Accession 252	Orissa

Statistical analyses

Mean, Standard Error, Critical Difference (CD) and coefficient of variation (CV) were estimated as per standard protocols (Gomez and Gomez, 1984) [10]. Phenotypic and genotypic variances were obtained from the ANOVA according to Comstock and Robinson (1952) [6]; phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated by following Singh and Chaudhury (1985) [21]; heritability in broad sense was estimated according to Falconer (1989) [7] and genetic advance as percent of mean was estimated

according to Allard (1960) [1]. All the statistical analyses were performed using SAS software version 4.0.

Principal component analysis

The phenotypic data were subjected to the principal component analysis (PCA) to identify the major components responsible for higher variability within the population. Principal Components Analysis (PCA) was used to extract the major components of variability and to measure the relative discriminative power of the primary axes; Single Linkage Cluster Analysis (SLCA) was followed to cluster and plot the genotypes on principal component axes.

D² analysis and clustering of genotypes

Data were analysed using SAS software (SAS software for Microsoft windows 9.2) (SAS Institute, 2011) by following the method reported earlier (Steel & Torrie, 1980). Mahalanobis' D² analysis is a technique to measure the degree of divergence among different genotypes of a population. It uses multiple quantitative observations made on these genotypes to calculate genetic distance with which we can estimate the closeness or distant genetic relationship between them. Genetic diversity of the strawberry population was estimated (Mahalanobis, 1936); generalized distance (D²) between the genotypes and clusters were estimated as extended by Rao, 1952. Average intra-cluster distance was calculated by the formula suggested by Singh & Choudhary, 1985 [21]. Average intra-cluster:

$$D^2 = \sum D^2 i/n$$

Where, $\sum D^2$ = Sum of distances between all possible combination) n (of the varieties/lines included in a cluster; n = all possible combinations to assess genotypes position in distinct group.

Results

Mean performance for yield and yield attributing traits

Wide variability for all the fruit morphology traits was observed (Table 2). Number of fruits per palm ranged between 12 (acc. 252) to 410 (acc. 41) with a mean of 142 fruits per palm. Average fruit length was 15.19 cm which ranged from 14.25 cm (acc. 52) to 16.92 cm (acc. 2). Fruit diameter ranged between 33.18 cm (acc. 52) to 36.67 cm (acc. 2). Mean fruit weight was 1.01 kg and ranged between 0.52 kg (acc. 252) to 1.28 kg (acc. 1). In these fruits, flesh weight with epicarp ranged between 0.21 kg (acc. 252) to 0.61 kg (acc. 41). Average nut weight per fruit and weight per nut was 0.62 and 0.16 kg respectively. Seed length ranged from 11.03 cm (acc. 52) to 13.84 cm (acc. 2) with an average of 12.37 cm; seed circumference ranged from 16.00 cm (acc. 52) to 18.75 cm (acc. 2). Highest critical difference (CD) value was observed for the trait number of fruits per palm (9.09). Similarly, highest coefficient of variation was observed for the trait number of fruit per tree (3.84%).

Genetic variability parameters

Genetic variability parameters also varied between the traits (Table 3). High PCV and GCV was recorded for the trait number of fruits per tree. Moderate PCV and GCV was observed for the traits fruit weight, flesh weight with epicarp and nut weight per fruit. For the other traits PCV and GCV was low (<10%). Broad sense heritability (H²) was in the high category (>60%) for all the traits except fruit diameter (46.51%). Genetic advance (as percent of mean) was high for fruit weight, flesh weight with epicarp, nut weight per fruit and number of fruits per tree; moderate for weight per nut, seed length and fruit length; low for other traits.

Table 2: Mean Performance for Yield and Yield Attributing Characters in Palmyrah Germplasm under Killikulam Condition

Sl. No	Genotypes	Traits								
		Fruit weight (kg)	Flesh weight with epicarp (kg)	Nut weight per fruit (kg)	Weight per nut (kg)	Seed Length (cm)	Fruit Length (cm)	Fruit Diameter (cm)	Seed Circumference (cm)	Number of fruits per tree
1	Acc.1	1.28	0.40	0.64	0.17	13.10	16.05	36.14	18.44	240.00
2	Acc.2	1.04	0.40	0.64	0.16	13.84	16.92	36.67	18.75	196.00
3	Acc.3	1.04	0.40	0.64	0.18	13.15	16.18	36.01	18.11	84.00
4	Acc.10	1.05	0.39	0.65	0.18	13.51	16.63	36.08	18.47	110.00
5	Acc.17	1.04	0.40	0.64	0.17	13.25	16.21	35.52	18.00	99.00
6	Acc.22	1.01	0.39	0.62	0.17	12.22	15.11	35.35	17.56	24.00
7	Acc.26	0.91	0.31	0.60	0.15	12.86	11.05	35.99	17.91	352.00
8	Acc.27	1.00	0.34	0.65	0.16	12.23	15.27	35.67	17.65	240.00
9	Acc.41	1.44	0.61	0.83	0.18	12.59	15.54	35.78	17.79	410.00
10	Acc.48	0.97	0.34	0.64	0.16	12.00	14.90	34.49	17.79	104.00
11	Acc.51	1.02	0.40	0.62	0.17	12.18	15.06	35.14	17.25	35.00
12	Acc.52	0.95	0.30	0.65	0.15	11.03	14.25	33.18	16.00	138.00
13	Acc.63	0.93	0.41	0.55	0.15	11.41	15.10	34.22	17.10	144.00
14	Acc.65	0.94	0.30	0.64	0.15	12.14	15.12	35.28	17.46	24.00
15	Acc.91	1.01	0.40	0.61	0.17	11.30	14.92	33.99	16.95	60.00
16	Acc.252	0.52	0.21	0.31	0.15	11.11	14.77	33.42	16.50	12.00
Mean		1.01	0.38	0.62	0.16	12.37	15.19	35.18	17.61	142.00
Std. Dev		0.18	0.08	0.10	0.01	0.88	1.32	1.29	0.78	114.29
S.E.		0.01	0.01	0.01	0.00	0.17	0.22	0.54	0.24	3.15
C.D. (5%)		0.04	0.02	0.03	0.01	0.50	0.62	1.57	0.68	9.09
CV (%)		2.30	2.43	3.00	3.29	2.44	2.47	2.67	2.33	3.84

Table 3: Genetic Parameters for Yield and Yield Attributing Characters in Palmyrah Germplasm under Killikulam Condition

Traits	Genetic Parameters			
	Phenotypic coefficient of variation	Genotypic coefficient of variation	Heritability	Genetic Advance Percent of Mean (GAM)
Fruit weight (kg)	18.74	18.60	98.50	38.02
Flesh weight with epicarp (kg)	22.41	22.27	98.83	45.61
Nut weight per fruit (kg)	16.26	15.98	96.59	32.36
Weight per nut (kg)	7.32	6.54	79.83	12.04
Seed Length (cm)	7.32	6.90	88.86	13.40
Fruit Length (cm)	8.96	8.61	92.40	17.05
Fruit Diameter (cm)	3.65	2.49	46.51	3.50
Seed Circumference (cm)	4.55	3.91	73.76	6.92
Number of fruits per tree	83.12	83.03	99.79	170.86

Phenotypic and genotypic correlation between the traits

High significant phenotypic correlation existed between all the traits except nut weight per fruit with fruit length, weight per nut with number of fruits per tree, fruit length with fruit diameter and fruit length with number of fruits per tree (Table 4). All the significant correlations were positive. Highest positive correlation existed between fruit weight and nut weight per fruit (0.887) followed by fruit weight and flesh weight with epicarp (0.874), and seed length and seed circumference.

To nullify the effect of environment on traits, genotypic correlation was estimated. Similar pattern of correlation was

observed here (Table 5). Correlation between the traits except nut weight per fruit with fruit length, weight per nut with number of fruits per tree and fruit length with number of fruits per tree were highly significant. All these significant correlations were positive. Highest correlation existed between fruit diameter and seed circumference (1.181), seed length and fruit diameter (1.158) and seed length and seed circumference (1.013). This was followed by the correlation between fruit weight and nut weight per fruit (0.909) and fruit weight and flesh weight with epicarp (0.885).

Table 4: Estimation of Genotypic Correlation Coefficient for Yield and Yield Attributing Characters in Palmyrah Germplasm under Killikulam Condition

Traits	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉
X ₁	0.885**	0.909**	0.648**	0.494**	0.343*	0.664**	0.545**	0.571**
X ₂		0.783**	0.690**	0.397**	0.390**	0.535**	0.437**	0.487**
X ₃			0.528**	0.430**	0.204 ^{NS}	0.600**	0.434**	0.537**
X ₄				0.530**	0.609**	0.586**	0.514**	0.030 ^{NS}
X ₅					0.418**	1.158**	1.013**	0.339*
X ₆						0.362*	0.428**	-0.265 ^{NS}
X ₇							1.181**	0.516**
X ₈								0.364*

Note: X₁: Fruit Weight (kg); X₂: Flesh Weight with Epicarp (kg); X₃: Nut Weight per Fruit (kg); X₄: Weight per Nut (kg); X₅: Seed Length (cm); X₆: Fruit Length (cm); X₇: Fruit Diameter (cm); X₈: Seed Circumference (cm); X₉: Number of Fruits per Tree

Table 5: Estimation of Phenotypic Correlation Coefficient for Yield and Yield Attributing Characters in Palmyrah Germplasm under Killikulam Condition

Traits	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉
X ₁	0.874**	0.887**	0.580**	0.471**	0.324*	0.440**	0.462**	0.566**
X ₂		0.763**	0.622**	0.373**	0.376**	0.360*	0.380**	0.484**
X ₃			0.467**	0.400**	0.187 ^{NS}	0.380**	0.378**	0.528**
X ₄				0.485**	0.526**	0.339*	0.432**	0.022 ^{NS}
X ₅					0.355*	0.680**	0.831**	0.321*
X ₆						0.209 ^{NS}	0.367*	-0.255 ^{NS}
X ₇							0.653**	0.343*
X ₈								0.316*

Note: X₁: Fruit Weight (kg); X₂: Flesh Weight with Epicarp (kg); X₃: Nut Weight per Fruit (kg); X₄: Weight per Nut (kg); X₅: Seed Length (cm); X₆: Fruit Length (cm); X₇: Fruit Diameter (cm); X₈: Seed Circumference (cm); X₉: Number of Fruits per Tree

Path coefficient analysis

Path analysis showed the relationship between the variables on number of fruits per tree (dependent variable) (Table 6). It was separated into direct and indirect effects. Highest positive direct effect was observed for seed circumference (0.833). Highest positive indirect effect was observed for fruit diameter through seed circumference. Traits nut weight per fruit, fruit diameter and seed length showed negative indirect relationship with the seed circumference.

Table 6: Estimation of Path Coefficient Analysis for Yield and Yield Attributing Characters in Palmyrah Germplasm under Killikulam Condition

Traits	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈
X ₁	0.441	0.367	-0.042	-0.269	-0.255	-0.164	0.040	0.454
X ₂	0.390	0.414	-0.036	-0.287	-0.205	-0.186	0.032	0.364
X ₃	0.401	0.324	-0.046	-0.220	-0.222	-0.098	0.036	0.361
X ₄	0.286	0.286	-0.024	-0.416	-0.274	-0.291	0.035	0.428
X ₅	0.218	0.165	-0.020	-0.220	-0.516	-0.200	0.069	0.844
X ₆	0.151	0.161	-0.009	-0.253	-0.216	-0.478	0.022	0.357
X ₇	0.293	0.221	-0.028	-0.244	-0.598	-0.173	0.060	0.984
X ₈	0.240	0.181	-0.020	-0.214	-0.523	-0.205	0.071	0.833

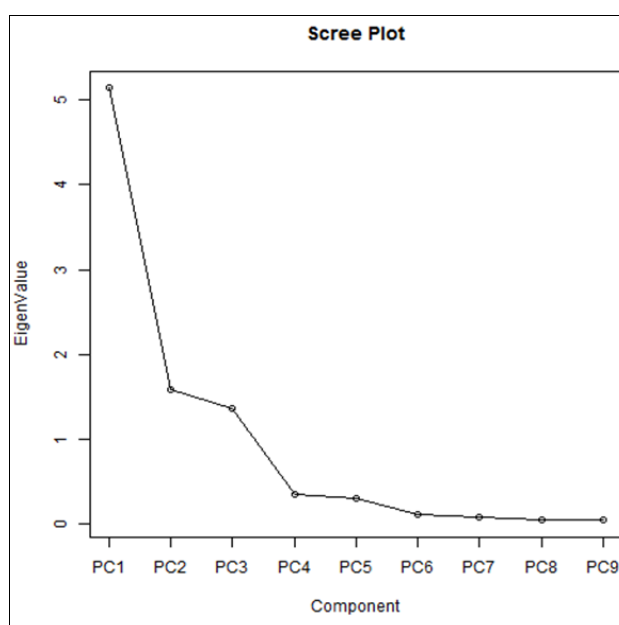
Note: X₁: Fruit Weight (kg); X₂: Flesh Weight with Epicarp (kg); X₃: Nut Weight per Fruit (kg); X₄: Weight per Nut (kg); X₅: Seed Length (cm); X₆: Fruit Length (cm); X₇: Fruit Diameter (cm); X₈: Seed Circumference (cm); X₉: Number of Fruits per Tree

Principal component analysis

From the principal components analysis three major components (above an Eigen value of 1) was extracted (Table 7; Fig. 1). Together these components explained about 89.99 percent of the total variation. PC1 was the largest component (Eigen value: 5.142) that explained about 57% of the variation. However, all the traits have negatively contributed to this trait. PC2 (Eigen value: 1.582) explained about 17.6% of the variation and was positively contributed by weight per nut, seed length, fruit length, fruit diameter and seed circumference.

Table 7: Estimation of Principal Component Analysis (PCA) for Yield and Yield Attributing Characters in Palmyrah Germplasm under Killikulam Condition

Variables	PC1	PC2	PC3
Fruit weight (kg)	-0.386	-0.278	0.203
Flesh weight with epicarp (kg)	-0.358	-0.244	0.335
Nut weight per fruit (kg)	-0.347	-0.348	0.159
Weight per nut (kg)	-0.326	0.195	0.380
Seed Length (cm)	-0.360	0.293	-0.349
Fruit Length (cm)	-0.209	0.477	0.428
Fruit Diameter (cm)	-0.373	0.176	-0.379
Seed Circumference (cm)	-0.363	0.284	-0.337
Number of fruits per tree	-0.230	-0.529	-0.339
Eigen Values	5.142	1.582	1.363
Proportion of Variance	0.571	0.176	0.151
Cumulative Proportion	0.571	0.747	0.899

**Fig. 1:** Estimation of Principal Component Analysis (PCA) of Scree Plot for Yield and Yield Attributing Characters in Palmyrah Germplasm under Killikulam Condition

Genetic dissimilarity between the genotypes

The genotypes were clustered based on D² analysis (Tables 8&9; Fig. 2; Supplementary Table 1). The average genetic distance between the genotypes was 3.866. Highest genetic distance of 10.15 was observed between acc. 9 and acc. 16. This was followed by the distance between acc. 9 and acc. 16 (7.77) and between acc. 41 and acc. 252 (7.66). Lowest genetic distance was observed between acc.22 and acc. 51 (0.5) and between acc. 3 and acc. 10 (0.77). Based on these distances the genotypes were grouped in two major clusters and five clusters. Cluster II was the largest with eight genotypes followed by cluster I with

five genotypes. Other clusters had one genotype each. Mean values of the traits varied between the clusters. Highest mean fruit weight and highest mean number of fruits per tree was observed in cluster IV (acc.41). Highest fruit length, fruit diameter and seed circumference were observed in cluster I. Acc. 252, the sole genotype in the cluster V recorded relatively lower agronomic performance with lowest fruit weight, flesh weight with epicarp, nut weight per fruit, weight per nut, seed length, fruit length, fruit diameter, seed circumference and number of fruits per tree.

Table 8: Genotypes in the five clusters based on D² analysis

Sl. No	Cluster	Number of genotypes	Name of the genotypes
1	I	5	Acc.1, Acc.2, Acc.3, Acc.10 & Acc.17
2	II	8	Acc.22, Acc.27, Acc.48, Acc.51, Acc.52, Acc.63, Acc.65 & Acc.91
3	III	1	Acc.26
4	IV	1	Acc.41
5	V	1	Acc.252

Table 9: Mean trait values of genotypes of different clusters in D² analysis

Cluster	Fruit weight (kg)	Flesh weight with epicarp (kg)	Nut weight per fruit (kg)	Weight per nut (kg)	Seed Length (cm)	Fruit Length (cm)	Fruit Diameter (cm)	Seed Circumference (cm)	Number of fruits per tree
I	1.09	0.40	0.64	0.17	13.37	16.40	36.08	18.35	145.80
II	0.98	0.36	0.62	0.16	11.81	14.97	34.66	17.22	96.12
III	0.91	0.31	0.60	0.15	12.86	11.05	35.99	17.91	352.00
IV	1.44	0.61	0.84	0.18	12.59	15.54	35.78	17.79	410.00
V	0.52	0.21	0.31	0.15	11.11	14.77	33.42	16.50	12.00

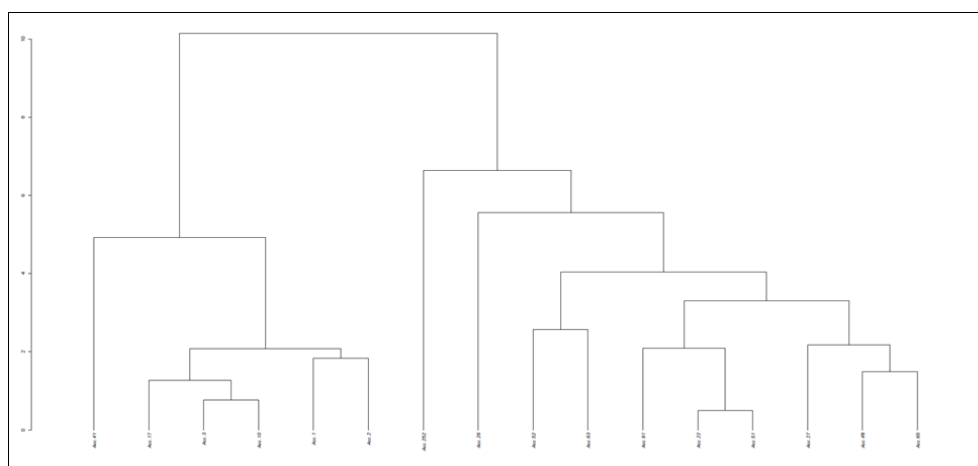


Fig 2: Dendrogram showing the clustering of genotypes based on D² analysis

Discussion

Genetic variability studies in crops are important to understand the genetic basis of different traits and to know if selection will be effective in the population. In crops like palmyrah, that take decades to come into sexual maturity, such studies could open new possibilities for genotype selection and breeding improvement. Our study shows the presence of variability in fruit morphology traits. In our present study, the ANOVA highlighted the significance of mean squares for all the traits under investigation. This suggests the presence of variability for all the characters, which can be further leveraged for future breeding programme in Palmyrah (Sivakumar *et al.*, 2020) [23]. Natarajan *et al.* (2010) [14] reported a high degree of variability in coconut for nut yield, whole nut weight, dehusked nut weight, and copra weight.

Presence of variability is the pre-requisite for genetic

improvement. The variability parameters assessed here showed scope for improvement in Palmyrah palms. Generally, the phenotypic variance and the phenotypic coefficient of variation are higher than the genetic variance and genotypic coefficient of variation, respectively. However, the difference is less-indicating less influence by the environment. Therefore, selection based on the phenotype of different traits will likely be effective. The genotypic coefficient of variation (GCV) showed the potential for a particular trait to respond to selection pressure.

Palmyrah has multiple uses and different parts of the palm can be considered as the economic part based on the utility. Considering the fruits as the major economic part, number of fruits per palm, fruit weight and flesh weight with epicarp are the major yield contributing traits. High variability existed for these traits. Number of fruits per palm ranged from 12 (in acc.

252) to 410 (acc. 41). Kumari *et al.*, (2020)^[12] and Bhaskar (2017)^[5] observed similar results in which palmyrah trees produced fruits which ranging from 50 to 300. This shows that selection could be applied based on this trait. This trait was also characterized with high PCV, GCV, heritability and genetic advance indicating additive gene action and less environmental influence. Selection based on this trait will be highly effective.

Accession 41 recorded the highest fruit weight (1.44 kg), flesh weight (0.61 kg) with epicarp and nut weight per fruit (0.83 kg) and weight per nut (0.18 kg) along with the highest number of fruits. Accession 41 collected from Seerudaiyarpuram, Tamil Nadu during the year 1997 stands promising for its unique trait of bearing highest number of triple nuts (350 nos), double nuts (50 nos.) and single nut (15 nos) on an average in a single tree. The fruit weight bearing triple nuts ranged from 1200 to 1500 grams, double nuts from 750 to 900 grams, single nuts from 210 to 350 grams. Hence, these accessions can be considered as the best accessions for agronomic performance with vigorous fruits. Acc. 252 recorded lowest performance in all the agronomic traits and remained as the sole genotype in the cluster V. However, under field conditions Acc. 252 recorded early flowering within 8 years as compared to the usual flowering period in Palmyrah which enter into reproductive phase after 12-15 years. Hence, accession 252 can be studied for traits other than the agronomic qualities. Aman *et al.* (2018)^[2] used fruit weight to develop selection index. The study reported that among the fifteen accessions under study, the accession collected from Kunjaravalasai in the Mandapam block of Ramanathapuram district has exerted superiority over other accessions for fruit weight. Similar findings were also revealed by Ponnuswami and Chitra (2011)^[15]. Fruit weight was characterized with high heritability and genetic advance (as percent of mean). Selection based on this trait shall be highly effective. Likewise, the flesh weight with epicarp, another yield contributing trait was also highly variable (ranging between 0.21 and 0.4) offering a chance for selection. This character was also under genetic control characterized with high heritability and genetic advance.

The fruit dimensions between genotypes varied considerably. Accession 2 recorded the highest fruit length (16.92 cm), fruit diameter (36.67 cm) and seed circumference (18.75 cm). While lowest fruit length (11.05 cm) in acc. 26 and fruit diameter (33.18 cm) and seed circumference (16.00 cm) in acc. 52 was observed. Similar results were also reported by Ponnuswami and Chitra (2011)^[15].

The relationship between the different traits was revealed by the correlation and path analysis. Generally, all the trait combinations except three (table 4) recorded positive genotypic correlation. Fruit weight was highly influenced by flesh weight with epicarp and nut weight per fruit evident by the high positive correlation. Number of fruits per tree, another yield contributing character, has medium levels of significant positive correlation with fruit weight, nut weight per fruit and fruit diameter. Accession 26 collected from Ananthanambikurichi, Tamil Nadu during the year 1995 stands promising for its unique trait more number of fruits (352) in a single tree and the average fruit weight was 960 grams. Accession 1 collected from Killikulam, Tamil Nadu during the year 1995 stands promising for its unique trait maximum fruit weight (1250 to 1300 grams) coupled with more number of fruits per bunch (48) and bunch weight (11.8 kg). Keeping this trait as the dependent variable, highest direct effect on this trait was recorded by seed circumference. Highest indirect effects through the traits fruit diameter and seed circumference indicates that improving these traits would

improve the yield contributing traits. Similar observations on the final yield of palms were reported for coconut palms (Geethanjali *et al.*, 2014; Sivakumar *et al.*, 2021)^[8, 22]. Such trait relationship studies in palmyrah have been limited and hence a thorough study on other traits of palmyrah would be beneficial to fix the breeding objectives.

Heritability is the proportion of phenotypic variance that is due to genetic factors. High heritability indicates the higher possibility of the particular trait to appear unchanged in the offspring. In this study, heritability was high for all the traits (>60%). Hence, selections based on these traits are possibly effective. This may also indicate the presence of additive gene action in these traits. Genetic advance is an indicator of an efficient and effective selection process that can be expected from the process of selection (expected genetic gain under selection). High genetic advance (>20%) generally indicates the presence of additive gene action. High genetic advance was observed for the traits fruit weight, flesh weight with epicarp, nut weight per fruit and fruits per tree. Similar trends were observed in coconut by Augustine Jerard (2002)^[3] and Suchithra and Paramaguru (2018)^[24]. These traits were also combined with high heritability. Selection based on these traits will be highly effective. For other traits however, high heritability was combined with either moderate (weight per nut, seed length and fruit length) or low (fruit diameter and seed circumference) genetic advance. This generally indicates high environmental effect. However, in palmyrah this may be due to the dioecious and high cross pollination behavior. Similar results were highlighted by Balakrishnan *et al.*, (1991)^[4], Renuga (1999)^[18], Augustine Jerard (2002)^[3], Suchithra and Paramaguru (2018)^[24] and Sivakumar *et al.* (2020)^[23].

Principal components analysis (PCA) generally indicated the major contributors to variability. From the first two principal components it is clear that the traits weight per nut, seed length, fruit length, fruit diameter and seed circumference are the positive contributors to the overall variance. Selection based on these traits will be highly effective. Apart from concentrating on the fruit characters, seed characters may indicate the development of a vigorous offspring. This indicator is highly valuable as the performance of palmyrah cannot be evaluated until sexual maturity which may take 15 to 20 years (Siju and Sabu, 2021)^[20].

The D² analysis revealed the genetic divergence between the accessions. Five clusters indicate a good divergence and within clusters the genotypes are expected to be highly similar. Accession 252 recorded with high diversity values with many other genotypes indicate its high divergence from the other genotypes. Agronomically, this is not an ideal genotype, however it can be used as a source of genes after evaluation of other traits. Previously, a group of genotypes from the palmyrah germplasm has been analysed using inter simple sequence repeat (ISSR) markers to show molecular level divergence. However, phenotype based diversity from the population is lacking (Ponnuswami *et al.*, 2009)^[16]. The data from this research show the divergence based on yield contributing traits which has immediate utility for selection. Phenotypic data can further strengthen the marker based genotype data to aid in future breeding programmes.

Conclusion

It can be concluded that a wide range of variability and significant differences between accessions for various traits existed in the material studied. The results presented in this paper indicated that the Palmyrah accessions collected from all

over India are important genetic reservoir of variability. This paper also shows the first step towards the scientific breeding of this underutilized horticultural crop, the Asian palmyrah. While some traits with high heritability combined with high genetic advance indicated immediate use as selection indices, other traits indicate requirement of further research to improve these characters. Molecular markers shall be inevitable to improve these traits as palmyrah has a long breeding duration and cycle. Accession 41 from the germplasm is the best in terms of yield and yield related traits. Further research into other traits of the palmyrah would shed more light on the germplasm genotypes.

References

1. Allard RW. Principles of plant breeding. New York: John Wiley and Sons; 1960.
2. Aman A, Sengupta S, Prasad M, Sinha S, Kumari S. Evaluation of the fruit characteristics of some accession of palmyrah palm grown in Bhagalpur district of Bihar. J Pharmacogn Phytochem. 2018;7(3):459-61.
3. Augustine Jerard B. Studies on the mean performance, variability, association analysis, stability and diversity in Coconut (*Cocos nucifera* L.) genotypes [PhD thesis]. Coimbatore: Tamil Nadu Agricultural University; 2002.
4. Balakrishnan PC, Sumangala, Nambiar S, Rajan KM. Selection indices in Coconut. In: Abstracts of papers presented in the International Symposium on Coconut Research and Development; Kasaragod. 1991. p. 28.
5. Bhaskar K. India *Borassus flabellifer* L. A tree behind the forest with multiple uses in rural areas: A case study from Nellore district, Andhra Pradesh, India. Imp J Interdiscip Res. 2017;3(5):1486.
6. Comstock RR, Robinson HF. Genetic Parameters, their estimation and significance. In: Proc 6th Int Grassland Congr. Washington DC: Nat. Pub. Co.; 1952. Vol 1. p. 248-91.
7. Falconer DS. Introduction to quantitative genetics. 3rd ed. Essex, England: Longman Scientific and Technical; 1989.
8. Geethanjali S, Rajkumar D, Shoba N. Correlation and path coefficient analysis in coconut (*Cocos nucifera* L.). Electron J Plant Breed. 2014;5(4):702-7.
9. Gummedi VP, Battu GR, Diyya MSK, Manda K. A review on palmyrah palm (*Borassus flabellifer*). Int J Curr Pharm Res. 2016;8:17-20.
10. Gomez KA, Gomez AA. Statistical procedures for agricultural research. 2nd ed. New York: John Wiley & Sons; 1988.
11. Krishnaveni TR, Arunachalam R, Chandrakumar M, Parthasarathi G, Nisha R. Potential review on palmyrah (*Borassus flabellifer* L.). Adv Res. 2020;21(9):29-40.
12. Kumari S, Rani R, Sengupta S, Aftab A, Kumari N, Aman A. Study of genetic variability of Palmyrah palm on the basis of tree morphology and yield parameters in Bihar. Int J Curr Microbiol Appl Sci. 2020;9:2522-8.
13. Mohan CHK, Soundarya V, Kumar RV, Kiran LK, Sharathnath K, Vamshi. *In vitro* anti-inflammatory activity of dried leaves of *Borassus flabellifer* L. Indo Am J Pharm Sci. 2016;3:809-13.
14. Natarajan C, Ganesamurthy K, Kavitha M. Genetic variability in Coconut (*Cocos nucifera*). Electron J Plant Breed. 2010;1(5):1367-70.
15. Ponnuswami V, Chitra S. Variability and association among fruit traits in Palmyrah (*Borassus flabellifer* L.). Electron J Plant Breed. 2011;2(4):589-91.
16. Ponnuswami V, Janarthani D, Priya R, Ramesh Kumar A, Prabhu M, Senthamizh Selvi B. Molecular characterization for genetic diversity of palmyrah (*Borassus flabellifer*) accessions using ISSR markers. Asian Australas J Plant Sci Biotechnol. 2009;3(1):11-5.
17. Ramachandran VS, Swarupanandan K, Renuka C. A traditional irrigation system using Palmyrah palm (*Borassus flabellifer* L.) in Kerala, India. Palms. 2004;48:175-81.
18. Renuga M. Studies on indexing economic characters of varieties and hybrids for the genetic improvement of coconut (*Cocos nucifera* L.) through selection [PhD thesis]. Coimbatore: Tamil Nadu Agricultural University; 1999.
19. Sahni C, Shakil NA, Jha V, Kumar Gupta R. Screening of nutritional, phytochemical, antioxidant and antibacterial activity of the roots of *Borassus flabellifer* (Asian palmyra Palm). J Pharmacogn Phytochem. 2014;58(34):58-68.
20. Siju S, Sabu KK. Genetic resources of Asian palmyrah palm (*Borassus flabellifer* L.): a comprehensive review on diversity, characterization and utilization. Plant Genet Resour. 2021;18(6):445-53.
21. Singh RK, Chaudhary BD. Biometrical methods in Quantitative Analysis. New Delhi: Kalyani Publishers; 1985.
22. Sivakumar V, Geethanjali S, Subramanian A, Praneetha S, Maheshwarappa HP, Rajkumar D. Correlation and path coefficient studies for fruit component traits in coconut (*Cocos nucifera* L.). Electron J Plant Breed. 2021;11(1):224-7.
23. Sivakumar V, Subramanian A, Geethanjali S, Praneetha S, Maheshwarappa HP. Assessment of genetic variability for growth, floral, yield and its component traits in Coconut (*Cocos nucifera* L.). Electron J Plant Breed. 2020;11(3):809-13.
24. Suchithra M, Paramaguru P. Variability and Correlation studies for vegetative, floral, nut and yield characters in Indigenous and Exotic Coconut Genotypes. Int J Curr Microbiol Appl Sci. 2018;7(7):3040-54.