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Research Article

Genotypic variation and hierarchical clustering of Palmyrah (*Borassus flabellifer* L.)

V. Ponnuswami* and S. Chitra
Horticultural College and Research Institute, Periyakulam – 625 604
*Email: swamyvp2002@yahoo.co.in

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Abstract:
The genotypic divergence and hierarchical clustering based on morphological, fruit and seed traits was studied in 48 palmyrah genotypes of diverse genetic background. Significant differences were recorded for morphological, fruit and seed characters among genotypes. Highest variability was observed in fruit weight followed by Neera yield and Tree height. Multivariate hierarchical cluster analysis was done to classify genotypes according to their degree of similarity in morphological, fruit seed and pooled traits.

Key words: *Borassus flabellifer* L. , genotypes, variability hierarchical clustering.

Introduction:

Palmyrah (*Borassus flabellifer* L.) palms are found in abundance in the peninsula. In some places they grow wild and in others they are cultivated as bund or border crop. Increasing exploitation of the palmyrah indiscriminately threatens the future availability of palm raw materials so important to rural populations. Palmyrah genotypes are distributed in many part of India and exhibit high variability in morphological characters (Kavoor 1983).

It has been reported that the genetic variation in the traits is probably due to the joint action of many genes/quantitative trait loci (QTLs). Multivariate statistical techniques have been suggested to measure genetic and phenotypic divergence among genotypes to aid in identifying potential parents for hybridization programme (Rai *et al.* 2003). Genetic diversity studies in palmyrah was already reported by Louis *et al.* 1991; Sankaralingam *et al.* 1999; Sankaralingam and Khan 2001; Paramaguru and Venkatraman 2004. In the present paper we describe the genetic variability and hierarchical clustering of genotypes based on morphological, fruit traits and neera the sweet sap yield. The present investigation was undertaken to assess the genetic variability and hierarchical clustering of palmyrah genotypes based on morphological, trait seed and pooled traits of palmyrah.

Materials and Methods

About 281 different palmyrah genotypes were collected from different palm growing regions of India. Out of which forty eight palmyrah were identified as elite genotypes that represented different palm growing regions of India were taken for this study during 2005-2008.

The height of the palm was measured from ground level to the crown and expressed in centimeters (cm). The trunk girth (cm) was measured at one metre height from the ground level. The total number of photosynthetically active green leaves were counted at the time of neera collection and expressed as number/tree. The petiole length (cm) was measured from the point of clasping with trunk to the starting the previous season was counted and expressed in numbers per palm. Number of fruits per bunch was computed by dividing the total number of fruits in a tree by total number of bunches produced in the current year. The various fruit parameters viz, fruit length (cm), fruit circumference (cm), fruit weight (g) and flesh weight (g) were quantified at random for five fruits in each bunch in a palm and the average was derived. The different seed parameters like individual seednut weight (g), seed length (cm) and seed circumference (cm) were taken for 25 seeds per palm at random and the average was derived. During the survey, the sequential neera yield (litres per palm) per season of 90 to 100 days was recorded by collecting in earthen containers with inside lime coating (Davis and Johnson, 1987). The number of traits observed was 15 with break down of five morphological attributes related to plant type, six fruits traits related to fruit parameters and four seed traits including Neera yield.

The number of traits observed was 15 with break down of 5 morphological, 6 fruit and 4 seed traits including neera yield. Morphological traits includes tree height, trunk girth, total number of leaves, length of petiole, total length of leaves (cm). Fruit traits includes number of bunches/tree, number of fruits/bunch, fruit length (cm) fruit weight (g), flesh weight (g) of shreds while seed traits include seed weight (g), seed length (cm), circumference of seed (cm) and neera yield (l/season/tree).

The differences in mean values between the accessions were tested using one-way analysis of variance (ANOVA) and differences were considered to be significant at $P < 0.05$. The data on all the traits were computed and agglomerative hierarchical clustering was done using SAS software version 4.0. The clustering was based on the squared Euclidean distances and the average linkage between groups was taken as the average of the distance between all pairs of cases with one member of each group.

Results and discussion

The analysis of data for all the component characters studied showed considerable variation among the genotypes is presented in Table 2 with the increasing diversity of germplasm collected from various sources. Hierarchical cluster analysis was conducted for morphological, fruit, seed and pooled traits. Authority distance between all pairs of genotypes was calculated using squared Euclidean distance method and genotypes were clustered based on ward's method.

Since these clusters are group of individuals possessing similar characters mathematically gathered into the same cluster, these individuals are supposed to exhibit higher external heterogeneity. Cluster analysis of genotypes based on morphological traits expressed 2 clusters at first node with 24 and 24 genotypes **(Fig.1A).** The first cluster further subdivided into 2 clusters with 9 and 15 genotypes and the second cluster further subdivided into two clusters with 16 and 8 genotypes. When we observed the morphological grouping, the genotypes collected from West Bengal and Kerala were distantly different fromeach other.

On the basis of fruit traits, forty eight genotypes were divided into 2 clusters at first node with 30 and 18 genotypes **(Fig. 1B).** These 30 genotypes were further divided into clusters of 19 and 11 genotypes and the 18 genotypes were further subdivided into 8 and 10 genotypes. However, in seed traits, clustering the forty eight palmyrah genotypes were divided into 2 clusters at first node with 42 and 6 genotypes **(Fig. 1C).** These 42 genotypes further divided into 14 and 28 genotypes. When we observed the morphological clustering the genotypes were collected from same location/state are in the same cluster group. So, this morphological clustering indicated that the prevalence of geographical diversity among these evaluated palmyrah genotypes. Clustering based on seed traits including neera (the sweet sap) yield, the genotypes K3, BFPU 23, BFPU 25, TNS 20, BFPU 26 and BFPU 27 were entirely different from other genotypes. Further as an exercise, all the three types of traits were considered together to study the overall multivariate picture of palmyrah genotypes. It was surprising to observe more or less the same clustering pattern, which was based on morphological traits (Fig. 1D). In other words the differences observed in fruit and seed behaviour of genotypes were masked by morphological traits. So the selection based on morphological characters will be of much useful for the palm breeders to select highly diversified parents for their future breeding programme.

The information obtained through clustering analysis will assist palmyrah breeders in identifying a limited number of highly differentiated elite genotypes useful in developing dwarf, high neera yielding varietie/s or hybrids

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Table 1. List of elite genotypes with place of collection

Genotype	Name of the cluster	Village	District	State
TNPO 01	Pollachi	Sendrampalayam	Coimbatore	Tamil Nadu
TNPO 02		Sendrampalayam		
TNPO 08		Jameen kaliapuram		
TNPM 06	Pillai Madam	Pillai madam	Ramnad	Tamil Nadu
TNPM 08		Adaikalappattinam		
TNPM 09		Adaikalappattinam		
TNPM 10		Adaikalappattinam		
TNTK 01	Tenkasi	Adhioothu	Trinelveli	Tamil Nadu
TNTK 02		Keelachsurandai		
TNTK 06		Parankunrapuram		
TNTK 08		Maruthupuram		
TNT 01	Tuticorin	Vadamalaipalayam	Tuticorin	Tamil Nadu
TNT 06		Soorianallor		
TNT 08		Thiranchendur		
TNT 10		Thiranchendur		
KVIC 02	KVIC	KVIC	Chennai	Tamil Nadu
KVIC 07				
KVIC 09				
KVIC 10				
K2	Kerala	Palakkad	Palakkad	Kerala
K3		Palakkad		
K4		Kadumthuruthi		
BFNAM 01	Nambiyur	Nambiyur	Erode	Tamil Nadu
BFNAM 02		Nambiyur		
BFNAM 07		Piliyampalayam		
BFNAM 09		Piliyampalayam		
BFNAM 12		Sanar Pudur		
BFNAM 17		Kasipalayam		
BFNAM 22		Kasipalayam		
BFNAM 27		Elathur		
BFNAM 31		Kadathur		
BFNAM 32		Puduchooripalayam		
BFPU 15	Puduchery	Thethampakkam	Puduchery	Puduchery UT
BFPU 23		Shompet		
BFPU 24		Shompet		
BFPU 25		Shompet		

Table 1. Contd…

Genotype	Name of the cluster	Village	District	State
BFPU 26	Sub-hub of Kolkata	Shompet	Kolkata	West Bengal
BFPU 27		Shompet		
WBP 08		Dostopur		
WBP 09		Dostopur		
WBP 12		Dauli		
WBP 14		Ramgar		
TNS 05	Sankagiri	Rayalur	Salem	Tamil Nadu
TNS 13		Rayalur		
TNS 15		Chinnagoundanur		
TNS 17		Chinnagoundanur		
TNS 18		Varuthampatti		
TNS 20		Varuthampatti		

Table 2. Descriptive statistics of morphological, fruit and seed traits of palmyrah genotypes

Statistical parameters	**Tree height (cm)**	**Trunk girth (cm)**	**No. of leaves**	**Length of petiole (cm)**	**Length of leaves (cm)**	**No. of bunches /tree**	**No. of fruit bunch**	**Fruit length (cm)**	**Fruit Cir. (cm)**	**Wt. of fruit (g)**	**Wt. of flesh (g)**	**Wt. of seed (g)**	**Length of seed (cm)**	**Cir of seed (cm)**	**Neera yield (lt/season)**
Average	576.87	92.12	24.66	81.68	150.56	10.27	14.41	17.87	31.22	524.10	119.69	128.52	15.00	17.70	396.53
Standard error	9.99	4.56	1.49	33.11	6.51	0.41	0.93	0.44	0.73	28.14	6.72	5.05	0.39	0.55	11.07
Median	565.00	93.50	26.50	80.00	140.00	10.00	13.50	17.50	31.00	500.50	110.30	136.90	14.60	17.80	394.00
Standard deviation	69.22	31.60	10.34	21.55	45.16	2.90	6.47	3.08	5.09	194.96	46.60	35.03	2.76	3.84	76.69
Minimum	450.00	25.00	8.00	45.00	80.00	6.00	1.00	11.00	19.00	175.00	32.40	53.60	10.00	11.50	214.75
Maximum	750.00	150.00	43.0	125.00	250.0	16.00	32.0	24.50	42.00	1039.00	240.50	171.20	24.60	30.00	540.50

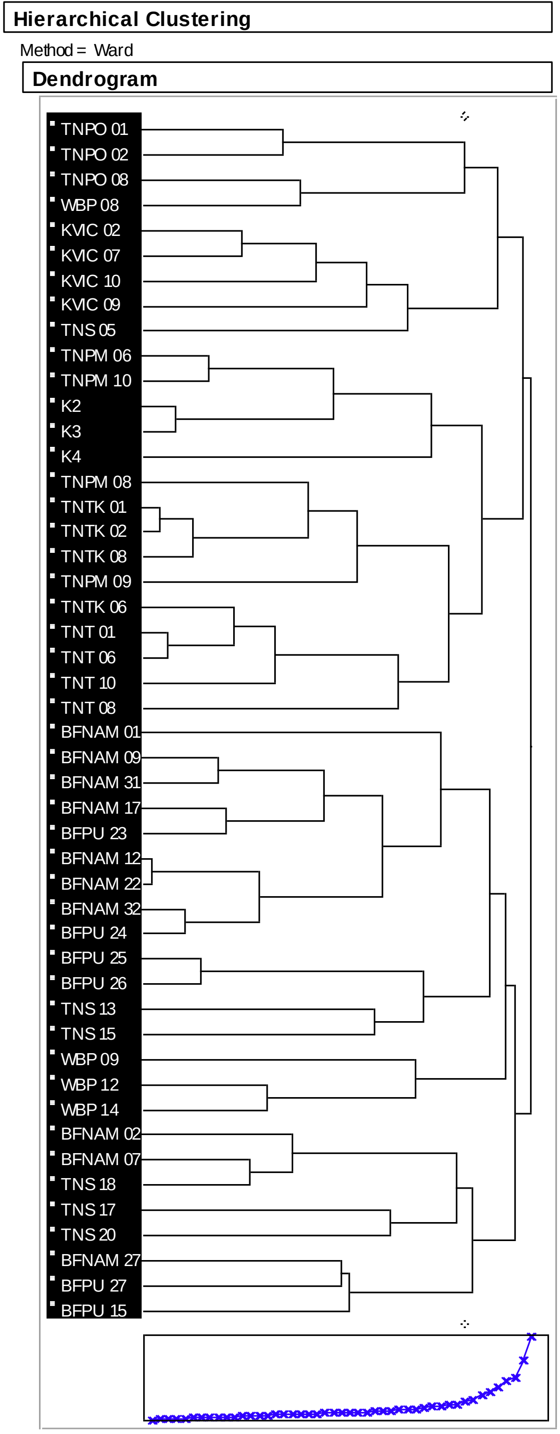

Fig. 1A. Dendrogram based on multivariate hierarchical cluster analysis for morphological traits

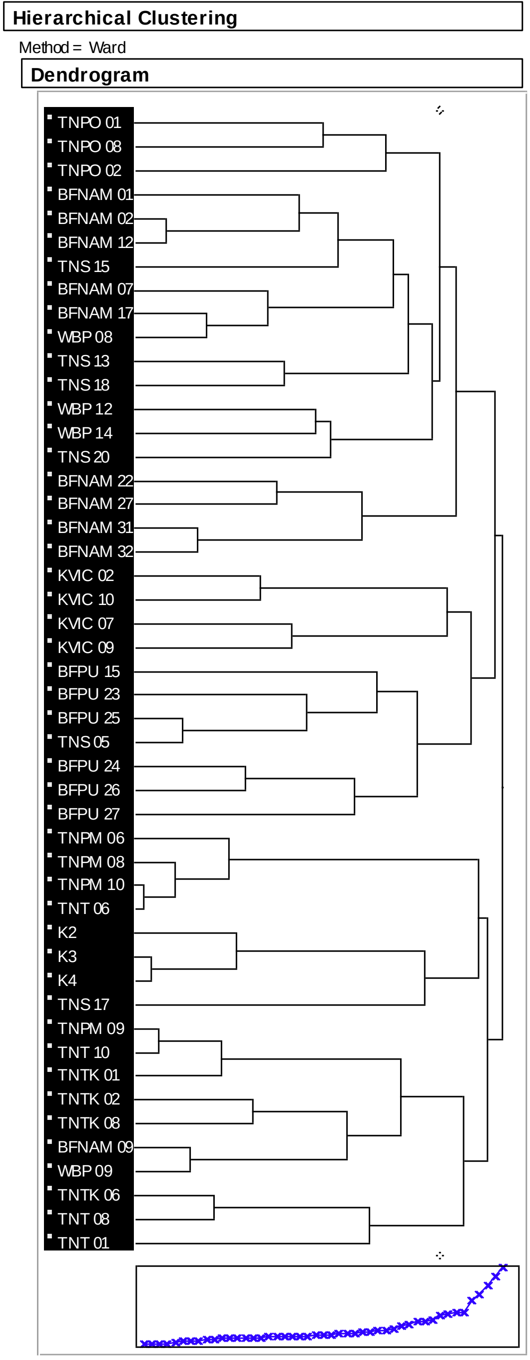

Fig. 1B. Dendrogram based on multivariate hierarchical cluster analysis for fruit traits

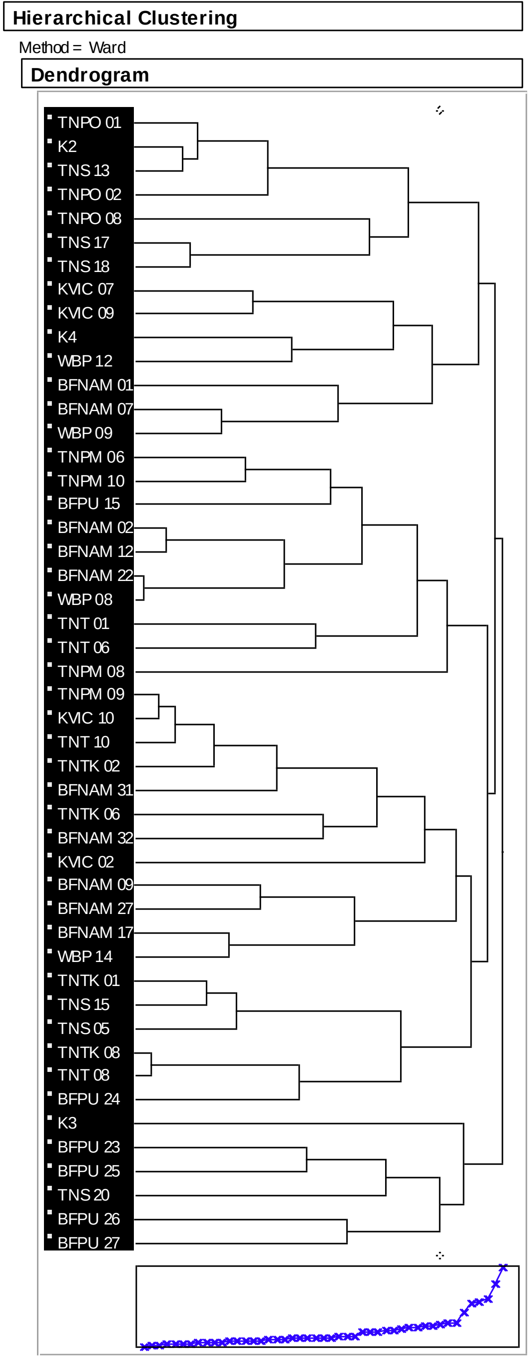

Fig. 1C. Dendrogram based on multivariate hierarchical cluster analysis for neera yield

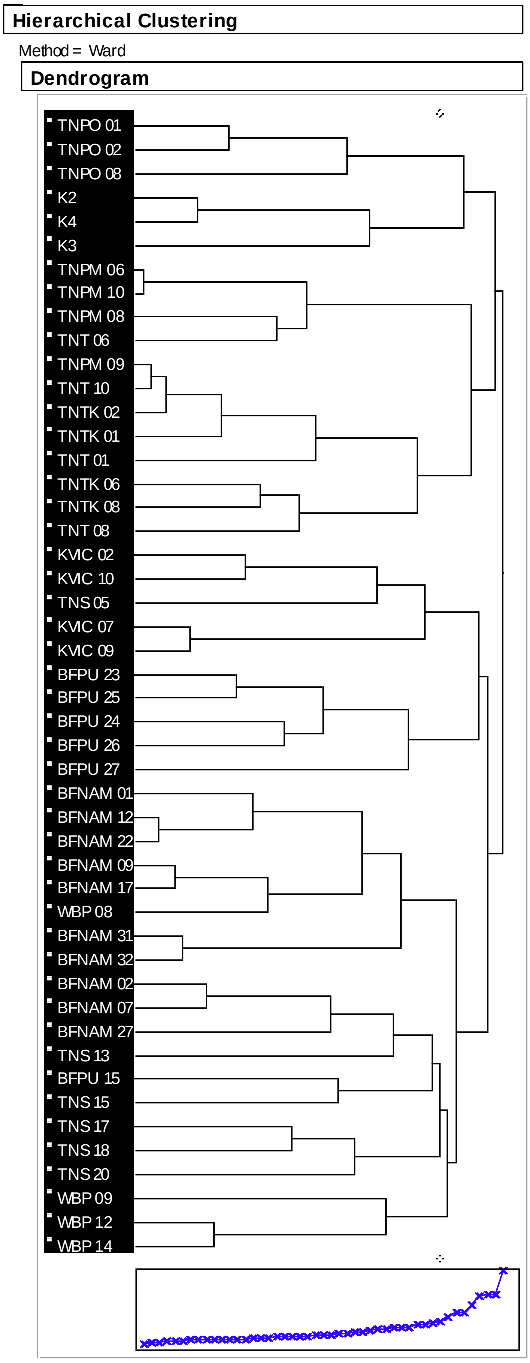

Fig. 1D. Dendrogram based on multivariate hierarchical cluster analysis for pooled traits