

Short communication

Genetic analysis in Pacific and Nicobar Islands coconut collections conserved at Andaman Islands, India

M. Sankaran*, V. Damodaran, D.R. Singh, I. Jai Sankar and B.A. Jerard*
Division of Horticulture & Forestry, Central Agricultural Research Institute, Port Blair 744 101,
Andaman & Nicobar Islands

ABSTRACT

Characterization and genetic analysis of coconut accessions collected from Pacific Ocean Islands and Nicobar Islands for morphological, physio-chemical traits and fruit component traits resulted into six distinct clusters with maximum inter-cluster distance D^2 value was obtained between cluster IV, V and VI. Cluster VI resulted with high copra yield (244.3 g), dwarfness and other yield attributing characters followed by cluster III. Among the accessions high heritability coupled with high genetic advance was observed for fruit weight, weight of dehusked fruit, kernel weight, shell weight and plant height which had direct influence on the copra yield/palm in coconut. Hence, due weightage for these traits must be given in coconut selections for the improvement of copra yield.

Key words: Coconut, genetic analysis, heritability, cluster analysis.

Coconut palm (*Cocos nucifera* L.) is one of the most important plantation crops of India. Genetic improvement of coconut has been effective through selection and hybridization and 15 hybrids and 18 selections have been released for commercial cultivation in different parts of India. There are two major plant types available in coconut, viz., tall and dwarf based on differences in number of morphological traits such as growth rate, earliness, plant height, pollination behavior and nut characteristics. Dwarf palms are normally low (5%) in frequency (Ganeshamurthy *et al.*, 1). Dwarf palms are mainly cultivated for tender nut purpose and tall cultivars are preferred for copra and oil extraction. The main objective of any coconut breeding is to increase the nut yield, which is a complex character depended on interaction of large number of component characters. The copra yield is the most important economic trait governing the oil yield per unit area, which depends not only on the nut yield but also on the nut characteristics. Several studies (Ganeshamurthy *et al.*, 1; Kumaran *et al.*, 3; Upadhyay *et al.*, 6) indicated that the phenotypic association among the characters. Although correlations are helpful in determining the components of complex traits like yield, they do not provide an exact picture of relative importance of direct and indirect influence of each of the complex characters towards this trait. Utilization of conserved coconut accessions in breeding programmes needs the genetic diversity information and diverse parents. In order to get the genetic diversity in coconut, the

accessions need to be conserved and evaluated for more than 30 years.

An attempt was made to elucidate the genetic parameters of coconut accessions conserved at World Coconut Germplasm Centre. The experimental material comprised of 30 coconut accessions including 24 accessions originally collected from Pacific Ocean Islands and 6 from Nicobar Islands that were conserved and evaluated since 1983 to 2012 in the filed gene banks (Table 1). The analysis of genetic divergence

Table 1. Pacific and Nicobar coconut accessions used for characterization.

Acc. No.	Genotype	Country of origin
WCGC 01	Soloman Tall	Soloman Island
WCGC 02	Rennel Tall	Soloman Island
WCGC 03	Fiji Tall	Fiji Island
WCGC 04	Niu Drau Tall	Fiji Island
WCGC 05	Niu Lekha Green Dwarf	Fiji Island
WCGC 06	Niu Bulavu Tall	Fiji Island
WCGC 07	Local Tall	American Somoa
WCGC 08	Niu Oma Yellow Dwarf	American Somoa
WCGC 09	Local Tall (Tutiala)	American Somoa
WCGC 10	Niuui Tall	American Tonga
WCGC 11	NiuTaukave Tall	American Tonga
WCGC 12	Niu Hake Tall	American Tonga
WCGC 13	Tahiti Tall Tall	French Polynesia

*Corresponding author's E-mail: kmsankaran@gmail.com

**Division of Crop Improvement, ICAR-Central Plantation Crops Research Institute, Kasaragod, Kerala

Contd...

Table 1 Contd...

Acc. No.	Genotype	Country of origin
WCGC 14	Local Tall (Paopao)	French Polynesia
WCGC 15	Local Tall (Haepiti)	French Polynesia
WCGC 16	Local Tall (Bora Bora)	French Polynesia
WCGC 17	Rangiroa Tall (Avaoru)	French Polynesia
WCGC 18	Hari Papua Orange Dwarf	French Polynesia
WCGC 19	Rangiroa Tall (Tiputa)	French Polynesia
WCGC 20	Kiriwana Tall	Papua New Guinea
WCGC 21	Muwa Tall	Papua New Guinea
WCGC 22	Nikkore Orange Dwarf	Papua New Guinea
WCGC 23	Kaveing Tall	Papua New Guinea
WCGC 24	Natava Tall	Papua New Guinea
WCGC 25	Auckchang Tall	Car Nicobar Island
WCGC 26	Tamaloo Tall	Car Nicobar Island
WCGC 27	Kimios Tall	Car Nicobar Island
WCGC 28	Kinmai Tall	Car Nicobar Island
WCGC 29	Katchal	Katchal Island, Nicobar
WCGC 30	Campbell Bay Tall	Great Nicobar Island

was carried out by using Mahalanobis D² statistics (Mahalanobis, 4). The genotypes were grouped in to different clusters as per Tocher's method.

The analysis of variance for 11 quantitative characters showed significant differences among 30 accessions indicated existence of wide genetic diversity. These 30 accessions were grouped in to 6 clusters (Fig. 1). Tocher's method of clustering and combined analysis of variance revealed the cluster I with 20 tall accessions, cluster II with one tall accession, cluster III with 5 accessions (four tall and one dwarf accessions), cluster IV with two dwarf accessions, cluster V with one tall accession and cluster VI with one dwarf accession. The pattern of distribution of accessions in different clusters indicated that it was related to not only geographic differentiation but also related to the morphological and fruit component traits. Clustering of genotypes from different geographic locations into one cluster can be attributed to the possibility of human selection for desirable traits. The unidirectional selection practiced for particular trait or group of linked traits in several places may produce similar phenotype, which can be aggregated in to one cluster irrespective of their geographic origin (Rajesh, 5).

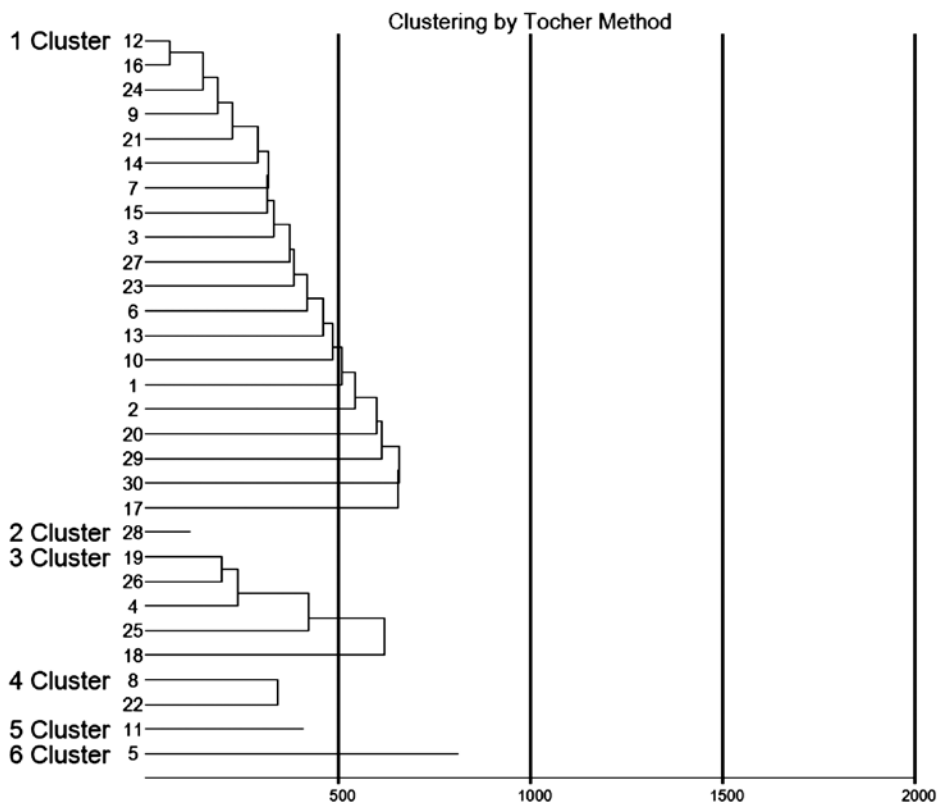
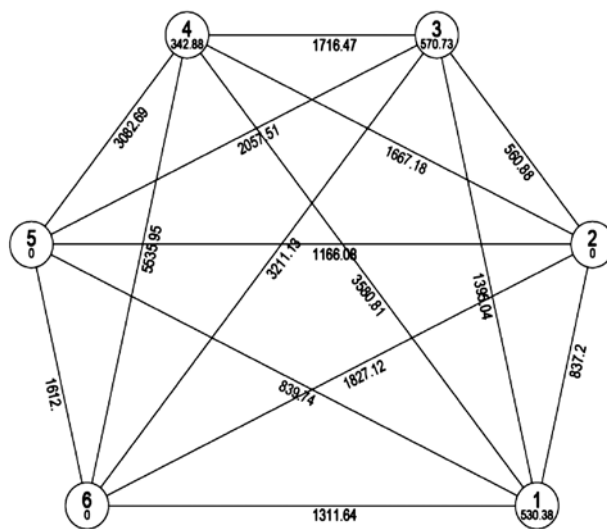


Fig. 1. Clustering of coconut accessions by Tocher's method.

The maximum inter-cluster distance D^2 value was obtained between clusters IV,V and VI (Fig. 2). These three clusters may be used in the hybridization programme due to wide variability and expected generation of transgressive segregants. Among the accessions in the clusters, three accessions were dwarfs and one dwarf WCGC 05 was observed to form a distinct cluster owing to its unique traits of dwarf stature combined with other morphological and fruit traits as tall. The grouping of the dwarf accession WCGC 18 along with tall accessions, indicate the existence of out-crossed progenies in it. The minimum inter-cluster distance was observed between clusters 1 and 2.

The comparison of cluster means revealed that cluster VI gave high values for copra yield, dwarfness and other yield contributing characters followed by cluster III (Table 2). Cluster mean for leaf phenol was highest in cluster VI followed by cluster III which indicates that the higher levels of phenol is negatively correlated with the plant height, which is an important trait. Therefore, these genotypes can be used in hybridization programme to get recombinations with highest value for the all traits under study. The coconut cultivars based on leaf polyphenol (Jay *et al.*, 2) and suggested that the appearance of dwarfism on the species historic scales is relatively recent phenomenon. In this study, the most dwarf cultivar is cluster VI and is considerably distant from other groups which are tall.

The magnitude of variations as represented by range, phenotypic coefficient of variation and



Mahlnobis Euclidean² Distances (Not to the Scale)

Fig. 2. Average cluster distance from cluster centroids.

genotypic coefficient of variation (Table 3) were moderate to high for most of the traits except length of longest leaflet and copra content. The genotypic coefficient of variation is a measure of genetic variability and provides means to compare with other characters facilitating successful isolation of desirable types. Genetic coefficients of variation together with heritability estimates can give the best picture of the amount of genetic advance to the expected selection.

Table 2. Cluster mean for different traits in coconut.

Trait	Group 1	Group 2	Group 3	Group 4	Group 5	Group 6
Plant height (cm)	949.14	587.50	936.60	614.25	787.50	484.25
No. of leaves on the crown	29.80	29.84	27.36	22.38	28.09	32.25
Petiole length (cm)	116.69	108.67	112.31	99.88	101.50	98.00
Length of leaflet bearing petiole (cm)	379.49	369.84	375.40	297.75	347.84	279.50
No. of leaflets on one side of petiole	111.90	115.67	104.14	90.88	111.34	97.75
Length of longest leaflet (cm)	116.86	107.50	113.82	110.00	100.34	103.75
Leaflet breadth (cm)	5.21	5.59	4.85	4.00	4.59	5.50
Trunk girth (cm)	85.30	73.17	76.34	66.63	76.67	103.25
No. of leaf scars	21.89	24.09	21.21	34.50	21.84	33.25
Percentage of nut weight to whole fruit	53.42	51.64	48.89	64.57	64.98	57.64
Kernel thickness (cm)	1.34	1.28	1.29	1.05	1.20	1.38
Shell thickness (cm)	0.51	0.48	0.48	0.41	0.48	0.50
Copra content/nut (g)	209.09	210.50	215.06	86.62	122.50	244.28
Leaf polyphenol (mg/100 g FW)	205.98	182.77	163.62	248.16	240.93	259.86
Leaf nitrogen (%)	0.74	0.58	0.46	0.80	0.52	0.30
Leaf protein (%)	4.61	3.63	2.87	5.00	3.22	1.85

Table 3. Genetic parameters of coconut accessions conserved in Andaman Islands.

Trait	Mean	Range	PCV (%)	GCV (%)	Heritability (h ²)	Genetic Advance as % of Mean
Plant height (cm)	891.784	484.25-1308.14	24.230	21.976	0.823	41.060
No.of leaves on the crown	28.929	20.75-33.91	11.603	9.135	0.620	14.816
Petiole length (cm)	113.443	87.50-130.83	8.808	7.396	0.725	12.795
No. of leaflets on one side of petiole	108.845	82.00-122.00	8.659	7.702	0.791	14.11
Length of longest leaflet (cm)	114.595	100.33-125.00	6.321	4.564	0.521	6.790
Breadth of leaflet (cm)	5.075	3.50-5.91	11.446	8.676	0.575	13.54
Girth of trunk at 1 m (cm)	82.47	66.25-103.25	10.510	9.596	0.834	18.048
No. of leaf scars in 1m	23.071	16.25-35-25	20.142	18.371	0.832	34.516
Fruit length (cm)	22.785	18.08-28.18	11.015	9.964	0.818	18.566
Fruit weight (g)	1469.78	422.09-2099.25	30.544	28.420	0.866	54.475
Husk thickness (cm)	2.465	1.48-3.05	16.860	15.334	0.827	28.728
Dehusked fruit wt. (g)	767.966	267.71-1060	26.967	24.868	0.850	47.243
Kernel weight (g)	372.864	147.71-466.09	21.988	20.872	0.901	40.814
Shell thickness (cm)	0.4986	0.38-0.61	11.427	9.223	0.61	15.334
Kernel thickness (cm)	1.304	0.95-1.55	9.247	8.040	0.756	14.401
Weight of shell (g)	208.752	91.88-260.91	23.072	21.377	0.858	40.814
Copra content/ nut (g)	200.25	71.67-256.71	23.768	21.948	0.53	41.750

The heritability estimates in the present study were observed high for all the traits.

High heritability coupled with high genetic advance was observed for weight of fruit, weight of dehusked fruit, kernel weight, shell weight and plant height. The results indicated that these characters were highly heritable and hence were less affected by the environment. Heritability in conjunction with genetic advance would give a more reliable index of selection value. Hence, selection based on this phenotypic performance would result in considerable genetic gain for these traits. It may be concluded that from the present study that weight of fruit, weight of de-husked fruit, weight of kernel, weight of shell and plant height are important components that showed largest influence directly on the copra yield/ palm in coconut (Ganeshamurthy *et al.*, 1). They also showed higher heritability with appreciable level of genetic gain there by suggesting that an emphasis on these characters in selection programmes would result in improvement of copra yield in coconut.

REFERENCES

1. Ganeshamurthy, K., Natarajan, C., Rajarathinam, S., Vincent, S. and Khan, H.H. 2002. Genetic variability and correlation of yield and nut characteristics in coconut (*Cocos nucifera* L.). *J. Plant. Crops*, **30**: 23-25.
2. Jay, M., Bourdeax, R. and Potier, F. 1991. Polymorphism of coconut leaf phenols. *In: Coconut Breeding and Management* (Eds.), E.G. Silas *et al.* KAU, Vellanikara, Thrissur, pp. 60-68.
3. Kumaran, P.M., Arunachalam, V., Nampoothiri, K.U.K., Pillai, R.V., Ratnambal, M.J., Niral, V. and Nampoothiri, C.G.N. 2006. Evaluation of coconut hybrids in rainfed conditions. *J. Plant. Crops*, **34**: 11-14.
4. Mahalanobis P.C. 1936. On the generalized distance in statistics. *Proc. Nat. Acad. Sci. (India)*, **2**: 49-55.
5. Rajesh, M.K., Nagarajan, P., Jerard, B.A., Arunachalam, V. and Dhanapal, R. 2008. Microsatellite variability of coconut accessions from Andaman and Nicobar islands. *Curr. Sci.* **94**: 1627-31.
6. Upadhyay, A., Jayadev, K., Manimekalai, R. and Parthasarathy, V.A. 2004. Genetic relationship and diversity in Indian coconut accessions based on RAPD markers. *Scientia Hort.* **99**: 353-62.

Received : July, 2013; Revised : October, 2014;
Accepted : December, 2014