Indian Journal of Agricultural Sciences **89** (9): 1456–61, September 2019/Article
https://doi.org/10.56093/ijas.v89i9.93488

Assessment of genetic diversity in West Coast Tall coconut (*Cocos nucifera*)

R SUDHA[1], V NIRAL[2], Y DIWAKAR[3], M K RAJESH[4] and K SAMSUDEEN[5]

ICAR-Central Plantation Crops Research Institute, Kasaragod, Kerala 671 124, India

Received: 11 October 2018; Accepted: 1 March 2019

ABSTRACT

Coconut palm (*Cocos nucifera* L.) is an important perennial oil-yielding plantation crop in the tropics. It is cross-pollinated and exhibits high level of genetic variation among cultivars in terms of colour, size and shape of the fruits. The objectives of the study were to estimate the magnitude of genetic variability, heritability and genetic advance for vegetative, reproductive and fruit component parameters of the eleven parents and progenies (93) of West Coast Tall (WCT) coconut, and analyse genetic diversity using molecular markers. The experiment was undertaken during 2017-2018 at ICAR-Central Plantation Crops Research Institute, Kasaragod, Kerala. Results revealed that, medium phenotypic and genotypic co-efficient of variation (PCV and GCV) were observed for all studied vegetative and reproductive characters except length of the leaves, total number of bunches, number of female flowers/bunch and number of nuts/palm. High heritability and genetic advance as percent of mean was observed for number of leaves, length of leaf, length of spikelet bearing portion, number of female flowers/inflorescence, length of inflorescence, weight of husked fruit and whole fruit, indicating that most likely the heritability is due to additive gene effects and thus the chances of fixing by selection will be more. Thus, these characters are to be given importance in the breeding for yield improvement in coconut. Based on the molecular data, Jaccards similarity coefficient values were generated and it ranged from 0.54 to 0.96. The information provides the quantum of inheritance of genetic makeup in different groups and it could have practical significance in crop improvement programmes.

Key words: Coconut, Genotypic co-efficient of variation, Heritability, Phenotypic co-efficient of variation, Population

Cocos nucifera L. is a member of the monocotyledon family Arecaceae (Palmae) and it is the only species of the genus Cocos. It is diploid, with 2n = 32 chromosomes. It is an important multipurpose palm grown widely in the humid tropics and is referred as Kalpavriksha (tree of life) since it provides all necessities of life. Coconut cultivars are generally classified into Tall and Dwarf types. The tall type is primarily out-crossing while the dwarf type, with some exceptions, is mainly selfing. Since, tall coconut type is a cross pollinated crop, mass selection is the basic method for coconut breeding. Traditional methods of mother palm selection followed by seedling selection continue to be widely practiced by coconut farmers and breeders (Manju and Gopimony 2001). Hence the variability studies play an important role in crop improvement programme. Generally, the variability available in the population could be partitioned in to heritable and non heritable components, using genetic parameters, viz. phenotypic and genotypic coefficients of variation, heritability and genetic advance and based on which selection can be effectively carried out. Heritability estimate provides information on the extent to which a particular character can be transmitted from the parent to the progeny and genetic advance shows the degree of the gain obtained in a character from one cycle of selection. High genetic advance coupled with high heritability estimates offers the most suitable condition to decide the criteria of selection (Syukur *et al.* 2012). However use of molecular markers reveals the variability at DNA level and provides important findings in genetic variability studies. Among many molecular maker techniques currently available, microsatellites or SSRs (Simple Sequence Repeats) are very effective, as they are highly polymorphic, co-dominant, very informative and PCR based (Powell *et al.* 1996). Several authors had already studied the genetic diversity of coconuts at the morphological (N'cho *et al.* 1993), biochemical (Jay *et al.* 1989) and molecular (Konan *et al.* 2007) levels, but, very less information is available about the genetic diversity of the parental and regenerated populations. Hence the study was carried out to estimate the genetic variability of 11 WCT mother palms and their progenies by variability parameters and also investigate the genetic distance of parental palms and their progenies by

[1]Scientist (rsudhahort@yahoo.co.in), [2,4,5]Principal Scientist (niralv@yahoo.com, mkraju.cpcri@gmail.com, samsudeenk@gmail.com), Division of Crop Improvement, ICAR-CPCRI, Kasaragod, Kerala; [3]Scientist (diwakar.icar@gmail.com), Division of Crop Improvement, ICAR-CPCRI Research Centre, Kidu, Karnataka.

molecular markers.

MATERIALS AND METHODS

The study was carried out at ICAR-Central Plantation Crops Research Institute, Kasaragod, Kerala during 2017-2018.

Plant materials: Eleven West Coast Tall parent palms and its 93 progenies were used for the study to estimate the extent of variability in the population. The 93 progenies were planted during 1972 with open pollinated seed nuts collected from 11 WCT mother palms.

Data collection: Data was collected on stem girth, number of leaves, length of leaf, length of inflorescence, length of spikelet bearing portion, length of spikelet, no. of spikelets/inflorescence, no. of female flowers per inflorescence, number of female flowers per spikelet, total no. of bunches on the crown, no. of nuts/bunch, fruit weight, fruit length and girth, polar and equatorial circumference of the fruit, husk thickness, weight of the husked nut, length and girth of husked nut, polar and equatorial circumference of the husked nut and kernel thickness.

Genetic parameters: Collected data were then used for statistical analysis. Mean values were used for the analysis. Phenotypic and genotypic coefficient of variation (GCV) was calculated as suggested by Burton (1952) by estimating the variance components. The PCV and GCV values were categorized as high, medium and low as suggested by Sivasubramanian and Madhava Menon (1973). Heritability (h^2) in broad sense was calculated according to Lush (1949) and expressed as per cent. The heritability per cent was categorized as suggested by Robinson *et al.* (1949). Genetic advance was computed and genetic advance as per cent of mean was categorized according to the method suggested by Johnson *et al.* (1955).

DNA extraction: Fresh spindle leaves were collected from the parents and progenies of WCT palms. DNA was extracted from the total of 104 samples using a modified SDS method as described by Rajesh *et al.* (2013). The quantity and quality of extracted DNA were verified using the spectrophotometer and agarose gel electrophoresis. Extracted DNA was stored at −20 °C till further use.

SSR analysis: A total of 14 highly polymorphic SSR primer pairs specific to coconut from the microsatellite kit developed by Baudouin and Lebrun (2002) were used in the present study. The list of coconut specific SSR primers and their sequences used in the study were given in Table 3. PCR reaction was conducted in volumes of 20 µl containing 35 ng genomic DNA, 0.2 mM each of forward and reverse primers, 50 mM of each dNTPs (M/s Bangalore Genei Pvt. Ltd, Bengaluru), 1 buffer [10 mM Tris–HCl (pH 8.3), 50 mM KCl, 1.5 mM $MgCl_2$] and 0.3 Unit of Taq DNA polymerase (M/s Bangalore Genei Pvt. Ltd., India). SSR analysis was carried out as described by Rajesh *et al.* (2008). The PCR products were separated using 3% Agarose.

Molecular data analysis: Microsatellite loci were scored individually and the different alleles were recorded for each individual and assigned 1 for presence and 0 for absence of an allele. NTSYS pc Package was used and data analysed. Jaccard's similarity coefficient were generated and dendrogram constructed using UPGMA (Unweighed Pair Group Method with Arithmatic Average) and SHAN (Sequential Hierarchical and Nested clustering).

RESULTS AND DISCUSSION

Assessment of extent of variability will be of immense importance in any crop improvement programme. Harland (1957) reported that the low transmission of yield of the mother palms to their progenies can be due to the nature of genetic variation. Hence estimation of variability, heritability and genetic advance for characters with major influence on productivity is important. This will help in the intensification of selection effort on such traits and for stability of performance of these attributes. But expression of these characters can be influenced by environment. Hence the analysis of DNA which is more stable allows a clear assessment of variation in the genotypes. In the present study, variability parameters, viz. PCV, GCV, heritability and genetic advance were analysed using morphological traits and diversity among the parent and progenies were assessed using molecular markers also.

Morphological analysis

Significant variations were observed between the progenies for all the recorded traits. This variation is very important for the plant breeders and selection is effective when magnitude of variability in the breeding population is too enough.

Information on the variability in a population was measured by genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic gain for individual quantitative characters. In the present study, all the studied morphological and reproductive characters recorded medium PCV (10-20%) in WCT population except length of the leaves, number of spikelets per inflorescence, number of female flowers per bunch and number of nuts per palm (Table 1). Medium PCV was recorded for fruit weight, husked nut weight and kernel thickness while all other fruit component characters were recorded high PCV (>20%). GCV was medium in all observed morphological and reproductive parameters except stem girth, length of the leaves, number of bunches on crown, number of female flowers per bunch and number of nuts per palm (Table 1). In fruit component characters, medium GCV was recorded in fruit weight, fruit girth, husked nut weight, length and girth of husked nut and kernel thickness and the entire remaining fruit component parameters were recorded high GCV (Table 2).

Present study revealed that the phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the character, indicating the influence of environment on the genotype for the expression of the characters. The same trend was reported by Manju and Gopimony (2001). They studied the genetic parameters in Komadan (3 generations), West Coast Tall (WCT)

Table 1 Genetic parameters for vegetative and reproductive traits in WCT population

Character	Mean	Range	PCV (%)	GCV (%)	Heritability (%)	GAM (%)
Stem girth (cm)	76.72	61-103	11.06	8.90	64.79	14.77
Total leaves on the crown	28.01	15-37	12.90	12.57	94.93	25.23
Length of leaf (cm)	486.00	300-570	9.68	9.62	98.84	20.00
Length of inflorescence (cm)	108.24	75-180	13.98	11.25	92.26	26.58
Length of spikelet bearing portion (cm)	38.23	22-55	17.77	14.39	65.49	23.98
No. of spikelets per inflorescence	36.11	25-61	20.00	10.47	27.44	11.30
No. of female flowers per inflorescence	22.85	8-48	30.01	23.45	60.71	37.64
Total no. of bunches on crown	15.87	6-21	15.41	8.85	32.97	10.47
No. of nuts/palm/year	122.15	16-180	37.47	20.42	48.75	33.24

Table 2 Genetic parameters for fruit component traits in WCT population

Character	Mean	Range	PCV (%)	GCV (%)	Heritability (%)	GAM(%)
Fruit weight (Kg)	0.80	0.55-1.38	19.60	16.55	71.26	32.08
Fruit length (cm)	19.82	17.00-24.00	42.40	28.81	46.17	9.06
Fruit breadth (cm)	13.65	12.00-19.50	38.16	11.07	8.42	1.79
Polar circumference (cm)	56.88	49.00-66.00	54.86	39.97	53.09	7.95
Equatorial circumference (cm)	48.62	40.00-65.00	63.39	28.54	20.27	3.80
Husk thickness (cm)	2.80	1.6-4.8	38.38	28.34	37.08	23.44
Husked nut wt (Kg)	0.45	0.16-0.74	17.00	14.15	69.33	36.04
Length (cm)	11.10	9.00-13.00	25.49	19.97	61.38	9.68
Breadth (cm)	9.24	7.50-11.00	26.32	12.69	23.26	4.15
Polar circumference (cm)	34.46	30.00-39.00	38.25	28.02	53.67	7.20
Equatorial circumference (cm)	32.05	26.00-38.00	46.57	21.21	20.74	3.51
Kernal thickness (cm)	1.23	0.90-1.50	12.14	10.77	77.93	17.83

and Natural Cross Dwarf (NCD) to estimate the genetic parameters of the mother palm characters revealed that the PCV was higher than the GCV for all the characters. High phenotypic and genotypic coefficients of variation were observed for number of nuts per palm per year and number of female flowers per bunch in the current study. Similar results have been reported by Ganesamoorthy *et al.* (2002) also. High GCV (>20%) indicating the heritable portion of total variation. Since the genotypic coefficient of variation is a measure of genetic variability, the improvement through selection of characters can be effective, provided there is considerable extent of genetic variability available and the characters are also highly heritable.

The characters with high GCV as well as PCV indicating the existence of wide range of genetic variability in the population for these traits. This also indicated broad genetic base, less environmental influence and these traits are under the control of additive genes. The phenotypic and genotypic coefficient of variation for morphological and reproductive characters were studied by Muluk (1987). He reported that high phenotypic and genotypic coefficient of variation were recorded for plant height and number of bunches, while the variation was low for rachis length among various characters studied. Sindhumole and Ibrahim (2000) studied nine coconut cultivars and revealed the economic characters showed higher genotypic coefficients of variation (16 to 22 per cent) compared to vegetative and reproductive characters. These reports were in accordance with the present investigation.

Heritability and genetic advance estimates represent the degree of inheritance of a character from parent to progeny. Heritability estimates of different characters would give information about the contribution by these characters towards yield. Characters having high heritability estimate could be improved through selection since they are less affected by environment (Lush 1940). Genetic advance is another breeding parameter for determining the amount of expected genetic change that could occur due to selection. High heritability along with high genetic gain could be considered to determine the amount of heritable variation with accuracy (Johnson *et al.* 1955). In the present study, low heritability (broad sense) (<30%) was recorded in number of spikelets per inflorescence and medium heritability was recorded in no. of. nuts per palm per year (Table 1). Fruit component parameters, viz. girth of husked and unhusked fruit and equatorial circumference of husked and unhusked fruit recorded low heritability. Medium heritability was recorded in fruit length, polar circumference of the husked and unhusked fruit, husk thickness (Table 2). High heritability (>60%) was recorded in plant girth, number of leaves, length of leaf, length of spikelet bearing portion, length of spikelet, no. of female flowers/inflorescence, length

Table 3 Coconut-specific SSR primers used in the study

Primers	Sequence (5'–3')		Annealing temperature (ºC)	Allele size (bp)
	Forward	Riverse		
CnCir A3	AATCTAAATCTACGAAAGCA	AATAATGTGAAAAAGCAAAG	52	162-174
CnCir A9	AATGTTTGTGTCTTTGTGCGTGTGT	TCCTTATTTTTCTTCCCCTTCCTCA	59	89-103
CnCir B6	GAGTGTGTGAGCCAGCAT	ATTGTTCACAGTCCTTCCA	58	155-179
CnCir B12	GCTCTTCAGTCTTTCTCAA	CTGTATGCCAATTTTTCTA	56	176-210
CnCir C3'	AGAAAGCTGAGAGGGAGATT	GTGGGGCATGAAAAGTAAC	58	228-240
CnCir C7	ATAGCATATGGTTTTCCT	TGCTCCAGCGTTCATCTA	58	157-169
CnCir C12	ATACCACAGGCTAACAT	AACCAGAGACATTTGAA	54	218-236
CnCir E2	TCGCTGATGAATGCTTGCT	GGGGCTGAGGGATAAACC	55	115-177
CnCir E10	TGGGTTCCATTTCTTCTCTCATC	GCTCTTTAGGGTTCGCTTTCTTAG	57	191-211
CnCir E12	TCACGCAAAAGATAAAACC	ATGGAGATGGAAAGAAAGG	58	133-139
CnCir F2	GGTCTCCTCTCCCTCCTTATCTA AC	CGACGACCCAAAACTGAAC	58	196-208
CnCir G11	AATATCTCCAAAAATCATCGAAAG	TCATCCCACACCCTCCTCT	58	232-246
CnCir H4'	TTAGATCTCCTCCCAAAG	ATCGAAAGAACAGTCACG	54	168-188
CnCir H7	GAGATGGCATAACACCTA	TGCTGAAGCAAAAGAGTA	58	154-174

of inflorescence and total no. of bunches denoting the least influence of environmental factors. High heritability and high genetic advance as percentage of mean was recorded in number of leaves, length of spikelet bearing portion, no. of female flowers/inflorescence, length of inflorescence, and weight of husked and unhusked nut.

Parameters with high heritability and high genetic advance indicating that these parameters reflecting the presence of additive gene action for the expression of these traits which is fixable for next generations and selection based on this character would be ideal. Panse (1957) reported that high heritability combined with high genetic advance were observed for nut yield, whole nut weight and dehusked nut weight. Similar findings were reported by Ganesamoorthy *et al.* (2002). Manju and Gopimony (2001) also reported high heritability with high genetic advance for nut yield. High heritability for weight of husked nut was reported by Liyanage and Sakai (1960). They also suggested that selection of seedlings should be based on the heritability of yield attributing economic characters such as number of nuts per year and weight of husked nuts. Charles (1961) reported low heritability for yield of nuts per palm per year and hence suggested that selection based on yield alone was ineffective. Nambiar and Nambiar (1970) reported high heritability values for number of female flowers. They also advocated that these characters be given importance in selection procedure. Louis (1981) estimated high genetic advance for number of leaves per palm, spathes per year, nuts per year and setting per cent. Muluk (1987) reported high heritability estimates for plant height and bunch number and high heritability combined with moderate to high genetic advance was recorded for nut yield per palm per year and number of female flowers per bunch. Sindhumole and Ibrahim (2000) reported maximum heritability for nut yield (45%). Liyanage and Sakai (1960) observed that the heritability of nut weight (0.95) was high and stem girth (0.45), inflorescence production (0.47), female flower production (0.52), number of nuts per bunch (0.50) and yield of nuts (0.48) were intermediate. Bourdeix (1988) stated that number of nuts and copra per tree recorded significantly low heritability. Mathew and Gopimony (1991) noticed extremely high heritability for weight of unhusked nut, whereas thickness of kernal registered low heritability value. Sankaran *et al.* (2015) concluded that 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 yield in coconut. These reports were in line with the result of the current study.

Hence, the characters with high values of genetic coefficient of variation and heritability accompanied by high genetic advance in percentage of mean indicating that they might transmit to progenies and therefore, phenotypic selection based on these characters would be effective.

Molecular analysis

Molecular resemblance between the regenerated and parental populations of WCT palms were investigated using 14 SSR markers (Table 3). The PCR amplification using 14 primers in 11 parents and 93 progenies yielded 30 reproducible amplified bands. The number of amplified bands varied from 5-7. Out of 30 bands, 26 were polymorphic (86.6%). The Polymorphic Information Content (PIC) value as a relative measure of polymorphism level ranged between 0.19-0.23. The similarity matrix was computed using SSR markers based on Jaccard's coefficient using NTSYS-Pc programme and the similarity coefficient ranged from 0.54 to 0.96. In Sequential Agglomerative Hierarchical Non overlapping (SAHN) UPGMA were used to generate dendrogram. Based on the dendrogram, 11 parents and 93 progenies recorded similarity index ranged from 0.68 (Fig.2) to 0.79 (Fig 1).

In general, the tall coconuts are preferentially cross-

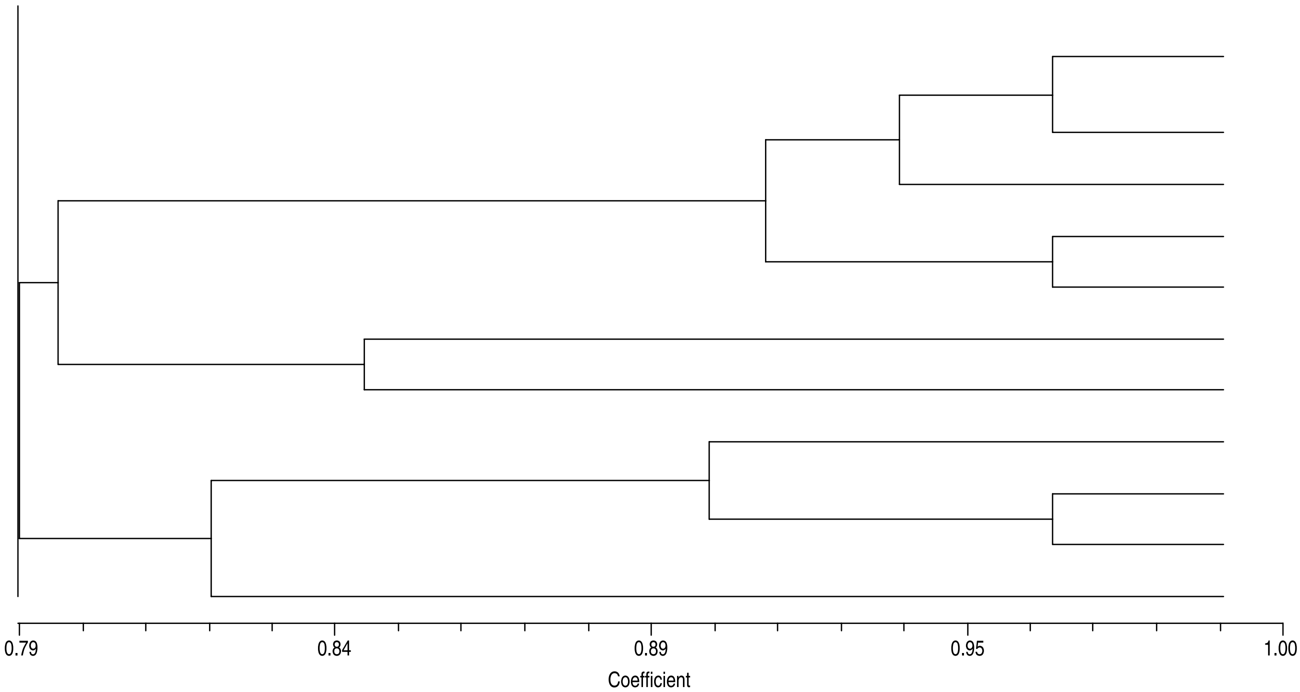

Fig 1 Dendrogram derived from cluster analysis of SSRs markers based on Jaccard's similarity coefficient showing the genetic relationships between parent (2) and its 11 progenies.

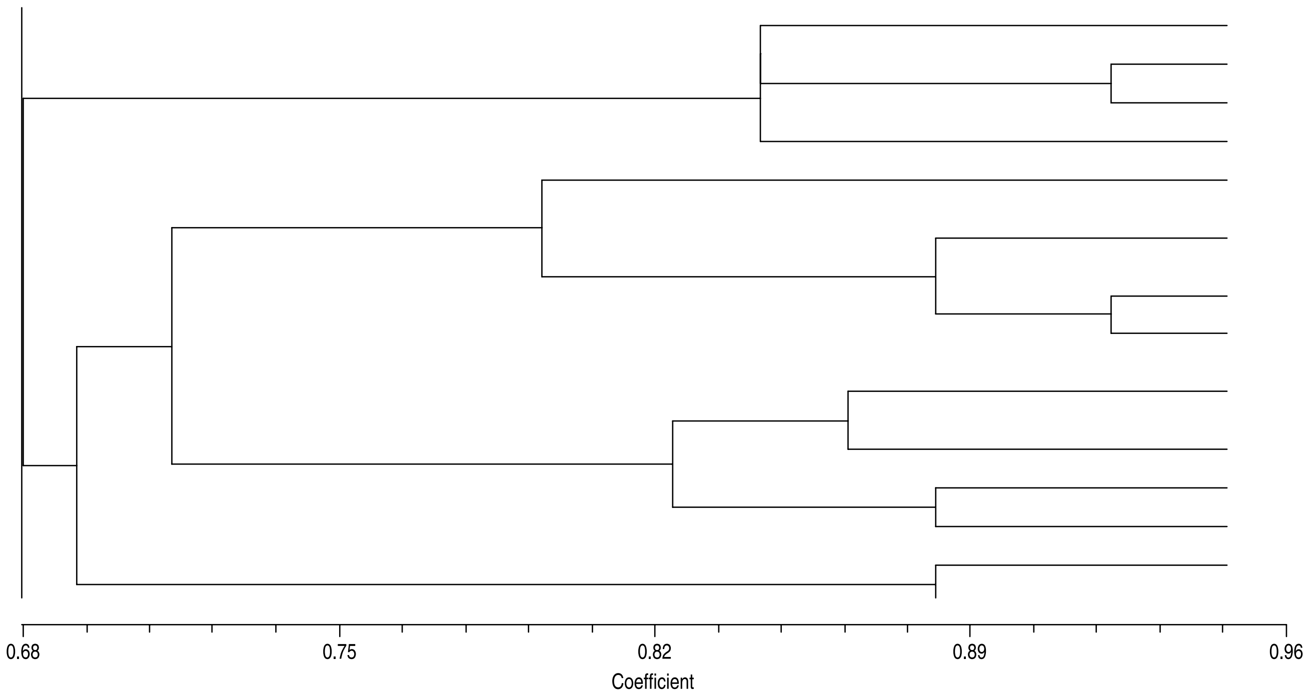

Fig 2 Dendrogram derived from cluster analysis of SSRs markers based on Jaccard's similarity coefficient showing the genetic relationships between parent (3) and its 15 progenies.

pollinated and have high level of genetic diversity within populations (Konan *et al.* 2007). In the present study, there is varied level of genetic relationship and different clustering patterns in different parent and its open pollinated progenies were observed. All the 11 groups of parent and progenies showed some of the progenies distinctly separated. This indicated that there is always a natural phenomenon to derive new variability through random genetic recombination as reported by Asolkar *et al.* (2011). The cross pollination nature coupled with high heterozygosity may contribute to such recombinants in the progenies. The information of quantum of inheritance of genetic makeup in different groups could be of greatest practical significance in crop improvement programmes. Kumar *et al.* (2011) reported about molecular resemblance between South Pacific coconut populations with a similarity index varying from 0.867 to 0.93, compared to that the studied parental and regenerated populations of WCT palms varying from 0.54 to 0.96. The non inheritance of some alleles into the regenerated accessions could be due to the high pressure in parent palms sampling as mentioned by Harlen (1992). Hence, molecular diversity analysis revealed that, the parent genotype contributed more than 50% of its genetic makeup to its progenies with similarity coefficient values in the range of 0.54 to 0.96. This information would be of practical significance for improvement of coconut genotypes.

Identification and propagation of genetically superior (prepotent) palms among the population is the only method for population improvement in coconut. These prepotent palms which can transmit their high yielding capacity to their offspring in spite of open pollination, have an important role to play in future breeding programme of coconut. In the present study, parameters, viz. number of leaves, length of leaf, length of spikelet bearing portion, no. of female flowers per inflorescence, length of inflorescence, and weight of husked and unhusked nut recorded high heritability along with high genetic advance. Hence selection based on these characters is highly effective. Based on the molecular data, Jaccards similarity coefficient values were generated and similarity coefficient values of 0.54 to 0.96 were observed. We hypothesized that the information obtained from this study would help the coconut breeders to efficiently select the promising prepotent palms that have higher potential of producing higher yield and omit the least potential.

REFERENCES

Baudouin Luc and Lebrun Patricia. 2002. The development of a microsatellite kit and dedicated software for use with coconuts. Rome: International Plant Genetic Resources Institute. *Burotrop Bulletin* **17**: 16–20.

Bello O B, Ige S A, Azeez M A, Afolabi M S, Abdulmaliq S Y, Mahamood J. 2012. Heritability and genetic advance for grain yield and its component character in maize (*Zea mays* L.). *International Journal of Plant Research* **2**: 138–145.

Burton G W. 1952. Quantitative inheritance in grasses. *Proceedings of Sixth International Grassland Congress* **7**: 277–83.

Charles A E. 1961. Selection and breeding of coconut palm. *Tropical Agriculture* (Trin) **38**: 283–96.

Ganesamoorthy C, Natarajan S, Rajarathinam S, Vincent and Khan H H. 2002. Genetic variability and correlation of yield and nut characters in coconut. *Journal of plantation Crops* **30**(2): 23–5.

Harland S C. 1957. The improvement of the coconut palm by breeding and selection, p 89. Bull press, Coconut Research Institute, Ceylon.

Harlen J. 1992. Origins and processes of domestication. *Grass Evolution and Domestication,* pp 159-75. Chapman G P (Eds). Cambrige University Press.

Jay M, Bourdeix R, Potier F, Sanlaville C. 1989. Premiers résultats de l'étude des polyphénols foliaires du cocotier. Oléagineux, **44**: 151–61.

Johnson H W, Robinson H F, Comstock R E. 1955. Estimation of genetic and environmental variability in soybean. *Agronomy Journal* **47**: 314–8.

Konan N, Konan J L, Koffi K, Lebrun P and Sangaré A. 2007. Coconut Microsatellite gene diversity analysis technology transfer to Côte d'Ivoire. *Biotechnology* **3**: 383–8.

Kumar S, Manimekalai R and Kumari B. 2011. Microsatellite marker based characterization of South Pacific coconut (*Cocos nucifera* L.) accessions. *International Journal of Plant Breeding and Genetics* **5**(1): 34–43.

Liyanage D V, Sakai K I. 1960. Heritabilities of certain yield characters of the coconut palm. *Journal of Genetics* **57**: 245–52.

Louis I H. 1981. Genetic variability in coconut palm (*Cocos nucifera* L.). *Madras Agricultural Journal* **38**: 388–93.

Lush J L. 1949. Heritability of qualitative characters in farm animals. (*In*) *Proceedings 8th Congress Hereditas (Suppl.),* pp 356–75.

Manju P and Gopimany R. 2001. Variability and genetic parameters of mother palm characters in coconut palm. *Journal of Tropical Agriculture* **39**: 159–61.

Mathew T and Gopimony R. 1991. Influence of seed nut characters on seedling vigour in coconut. Coconut breeding and management. (*In*) *Proceedings of the National Symposium on coconut breeding and management,* held at the Kerala Agricultural University, Thrissur, November 23–26.

Muluk C. 1987. Correlation and heritability among some morphological characters and growth parameters in the oil palm (*Elaeis guineensis* Jacq.). *Buletin Perkebunan* **18**(3): 97–98.

N'cho Y, Sangaré A, Bourdeix R, Bonnot F and Baudouin L. 1993. Evaluation de quelques écotypes de cocotier par une approche biométrique. 1. Etude des populations de grands. Oléagineux **48**(3): 121–32.

Nambiar M C and Nambiar K P P. 1970. Genetic analysis of yield attributes in *Cocos nucifera* var. West Coast Tall. *Euphytica* 19: 543–51.

Panse V G. 1957. Genetics of quantitative characters in relation to plant breeding. *Indian Journal of Genetics and plant breeding* **17**: 318–28.

Powell W, Morgante M, Andre C, Hanagey M, Vogel J, Tingey S and Rafalski A. 1996. The comparison of RFPL, RAPD AFLP and SSR (microsatellite) markers for germplasm analysis. *Molecular Breeding* **2**: 225–38.

Rajesh M K, Jerard B A, Preethi P and Thomas R J. 2013. Development of a RAPD-derived SCAR marker associated with tall-type palm trait in coconut. *Scientia Horticulturae* (Amsterdam) **150**: 312–6.

Rajesh M, Nagarajan P, Jerard B, Arumachalam V and Dhamapal R. 2008. Microsatellite variability of coconut accessions (*Cocos nucifera* L.) from Andaman and Nicobar Islands. *Current Science* **94** (12): 1627–32.

Robinson H F, Comstock R and Harvey P H. 1949. Estimation of heritability and the degree of dominance in corn. *Agronomy Journal* **41**: 353–9.

Sankaran M, Damodaran V, Singh D R, Sankar I and Jerard B A. 2015. Genetic analysis in Pacific and Nicobar Islands coconut collections conserved at Andaman Islands, India. *Indian Journal of Horticulture* **72**: 117–20.

Sindhumole P and Ibrahim K K. 2000. Path analysis of nut yield in cultivars of coconut (*Cocos nucifera* L.). *South Indian Horticulture* **48** (1): 160–2.

Sivasubramanian S and Madhavamenon P. 1973. Genetic analysis of quantitative characters in rice through diallel crosses. *Madras Agricultural Journal* **60**: 1097–102.

Syukur M, Sujiprihati S and Yunianti R. 2012. Teknik Pemuliaan Tanaman. Penebar Swadaya. Jakarta.