

GENETIC DIVERSITY OF COCONUT (*Cocos nucifera* L.) IN BARISAL REGION

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Abstract

Nineteen genotypes of coconut (*Cocos nucifera* L.) of different geographic origins were evaluated for genetic divergence at the Regional Agricultural Research Station, Rahmatpur, Barisal during June 2008 to May 2009. Genetic divergences among 19 genotypes were estimated using D^2 and principal component analysis. All the genotypes were grouped into five clusters. The inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups. The intra-cluster values were lower in all the clusters. Cluster II and V were the largest consisting of five genotypes and cluster I was the smallest with two genotypes. Distribution pattern of the genotypes in clusters indicated geographical distribution, and genetic divergence did not follow the same trend. The highest inter genotypic distance was observed between the genotypes G08 and G12. The inter-cluster distance was the maximum between the clusters I and V. Girth at 50 cm, girth at 20 cm, number of nuts per palm, fruit weight and kernel weight had the highest contribution towards genetic divergence. The intra cluster distance revealed that the genotypes within the same cluster were closely related. Cluster I had the highest fruit weight, nut weight, husk weight, water weight, shell weight, kernel weight and kernel thickness. Utilization of available information on coconut variability would be helpful to improve the fruit and nut qualities through hybridization and selection.

Key words: Coconut (*Cocos nucifera* L.), morphological characters and genetic diversity

Introduction

Coconut is an important economic crop in Bangladesh. It is cultivated in 2598 ha of land producing about 3, 34,047 M. tons per year (Anonymous, 2008). It is grown sporadically throughout the country, but mostly confined to the coastal areas of the southern part. In the Barisal region 1,082 acre area was covered by coconut plants and the production was 54,552 M. tons (Anonymous, 2008). Most of those belong to the tall variety. Recently dwarf and semi-dwarf types from Sri Lanka,

Malaysia and Indonesia have been introduced (Islam and Hossain, 2000). Young/immature coconuts are widely served as beverages and mature endosperm is used as food seasonings. Coconut is also a source of coir, oil and wood. Genetic diversity arises either due to geographical separation or due to genetic barriers to crossability. Genetic diversity plays an important role in plant breeding, because hybrids between lines of diverse origin generally display higher heterosis than those between closely related strains

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(Singh, 1983) which permits to select the genetically divergent parents to obtain the desirable recombination of the segregating generations. Precise information about the extent of genetic divergence and on characters used for discrimination among the population is crucial in any crop improvement program, because selection of parents based on genetic divergence has become successful in several crops (Ashana and Pandey, 1980; Ananda and Rawat, 1984). The multivariate analysis has been established by several investigators for measuring the degree of divergence and ascertaining the relative contribution of different characters to the total divergence

(Golakia and Makne, 1992; Sindhu *et al.*, 1989; Natarajan *et al.*, 1988). However, limited work has been done on the genetic divergence of coconut in Bangladesh. This study was undertaken to understand the genetic divergence in 19 coconut population selected in Barisal region.

Materials and Methods

The experiment was carried out at the Regional Agricultural Research Station, BARI, Rahmatpur, Barisal with 19 genotypes of coconut, collected from home and abroad. The source and the origin of genotypes are presented Table 1.

Table 1. Source and origin of the selected 19 genotypes of coconut.

Genotype	Accession number	Source and type
G 01	CG001	Bakerganj, Tall, Bangladesh
G 02	CG002	Swarupkathi, Tall, Bangladesh
G 03	CG003	Uzirpur, Tall, Bangladesh
G 04	CG004	Bhola, Tall, Bangladesh
G 05	CG005	Lebukhali, Tall, Bangladesh
G 06	CG006	Malayan yellow, tall, Malaysia
G 07	CG007	Babugonj, Tall, Bangladesh
G 08	CG008	Malayan green (BARI Narikal 2), Tall, Malaysia
G 09	CG009	Srilanka, yellow, Srilanka
G 10	CG010	Malayan red, Tall, Malaysia
G 11	CG011	Agailjhara, Tall, Bangladesh
G 12	CG012	Jalokati, Tall, Bangladesh
G 13	CG013	Borguna, Tall, Bangladesh
G 14	CG014	Srilanka red, Srilanka
G 15	CG015	Banaripara, Tall, Bangladesh
G 16	CG016	Pirojpur, Tall, Bangladesh
G 17	CG017	Gaurnadi, Tall, Bangladesh
G 18	CG018	Srilanka green, Srilanka
G 19	CG019	Kalapara, Tall, Bangladesh

The present investigation was done during the period from June 2008 to May 2009. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Weeding was done at an interval of thirty days from fruit set to harvest. Irrigation was continued at an interval of thirty days during dry season. Fertilizer were applied @ 50 kg cow dung, 1 kg urea, 1kg TSP, 1.2 kg MP, 100g zinc sulphate and 50g boric acid per plant.

These 19 genotypes of coconut were considered as the experimental treatments. All cultivars of coconut under study belonged to the typical group of the subcontinent. Age of coconut plants varied from 25 to 30 years. For each treatment, one plant was regarded as a replication. At 6 months interval

morphological and fruit component characters were studied. Number of harvested fruits was recorded after harvest, and mature fruits were randomly collected from each plant for the study. Fifteen fruits were collected from each plant, but final data were recorded from seven randomly selected fruits. Genetic diversity was worked out following Mahalanobis's (1936) generalized distance (D^2) extended by Rao (1952). Clustering of genotypes was done according to Tocher's method (Rao, 1952). All the statistical analyses were done using GENSTAT-5 program.

Results and Discussion

The analysis of variance showed significant variations among the genotypes for all the ten characters studied (Table 2).

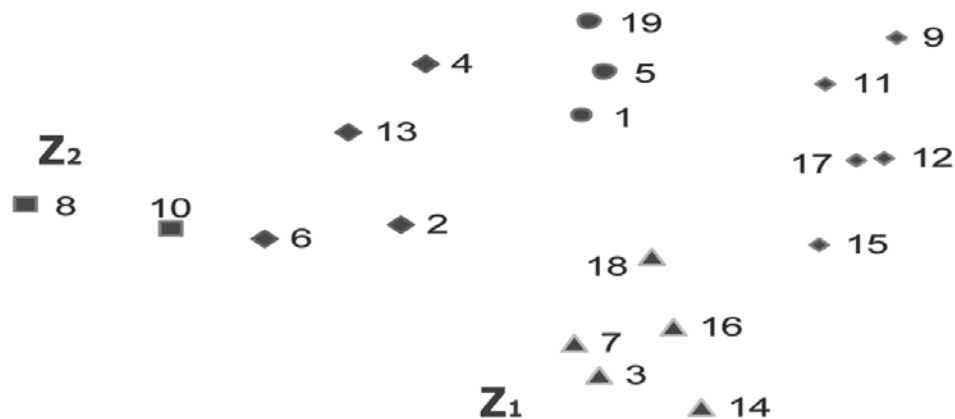
Table 2. Analysis of variance of 22 quantitative characters in coconut.

Gnotype	Girth at 50 cm	Girth at 20 cm	Length of 11 leaf scar	Stem height (m)	Bunches per palm	Nuts per bunch	Nuts per palm	Length of Central Axis (cm)	Spikelet with female flower	Spikelet without female flower	Spikelets per inflorescence
G01	116.33	142.00	2.73	11.17	11.00	8.67	90.00	89.67	9.00	32.00	41.00
G02	117.33	134.67	2.95	12.70	11.67	8.33	97.33	96.67	18.00	30.00	48.00
G03	134.67	157.33	2.78	10.67	10.00	9.00	81.33	101.67	8.67	35.67	44.33
G04	157.00	196.00	3.00	10.53	10.67	6.00	64.67	95.67	6.67	29.00	35.67
G05	119.67	145.00	2.89	13.07	9.00	10.33	87.00	121.33	9.67	30.00	39.67
G06	112.00	134.33	2.80	11.37	9.33	8.33	78.00	113.33	9.33	26.33	35.67
G07	111.67	141.67	3.30	13.06	10.00	7.67	77.00	99.00	8.00	31.67	41.33
G08	145.00	170.00	2.96	14.03	11.00	8.67	85.34	125.20	11.00	25.00	36.00
G09	108.00	130.00	2.89	10.60	8.00	11.67	81.67	89.00	10.00	34.33	44.33
G10	140.00	160.00	3.03	13.33	8.33	6.00	50.67	115.30	9.00	33.33	42.33
G11	82.33	104.67	2.53	8.46	6.33	5.00	32.67	92.67	13.67	24.33	38.00
G12	126.00	150.67	2.93	9.67	13.33	7.67	90.67	113.33	18.33	18.67	39.67
G13	120.33	145.00	2.90	10.43	10.00	9.00	89.67	121.00	11.00	27.67	38.67
G14	133.33	156.67	2.76	8.97	13.00	6.00	85.67	118.00	19.00	17.00	37.67
G15	125.00	160.00	3.36	13.07	9.33	6.00	65.33	86.33	10.00	22.67	32.67
G16	99.67	114.00	3.05	9.63	12.00	7.33	88.00	110.67	13.00	21.00	34.00
G17	130.67	165.00	3.34	13.07	7.00	8.67	64.00	90.67	11.67	24.00	35.67
G18	94.67	105.33	3.47	8.83	10.67	9.67	93.00	95.67	15.33	24.33	39.67
G19	113.00	140.00	3.34	10.87	5.00	9.00	45.33	89.9	6.00	28.00	34.00
Mean	120.35	144.86	3.00	11.17	10.16	8.10	81.67	103.43	11.44	27.10	38.86
CV(%)	9.42	11.25	7.74	11.05	12.59	15.97	19.07	12.34	26.41	13.69	9.86
Level of significance	**	**	**	**	**	**	**	**	**	**	**

** Significant at 1% level of probability.

Table 2. Continued

Gnotype	Female flower per inflorescence	Fruit length (polar view)	Fruit length (equatorial view)	Fruit weight	Nut weight	Husk weight	Volume of water	Shell weight	Kernel weight	Kernel thickness	Total soluble solid
G01	10.67	20.33	17.50	1395.00	890.00	506.67	343.33	166.67	363.33	11.33	8.67
G02	12.33	24.00	18.67	1634.33	1026.67	611.67	370.00	210.00	435.00	11.67	8.50
G03	15.67	24.83	17.00	1420.33	805.00	616.00	286.67	150.00	351.67	9.67	7.50
G04	7.67	23.50	20.33	1581.67	1025.00	554.67	450.00	171.67	443.33	12.33	8.00
G05	10.00	23.77	20.50	1363.33	874.00	472.67	320.00	166.67	406.67	11.67	7.50
G06	9.00	23.53	20.60	1795.67	1110.00	686.67	455.00	273.33	493.33	11.00	6.83
G07	13.67	23.90	18.13	1443.33	817.33	623.33	315.00	181.67	388.33	11.33	8.50
G08	10.67	25.50	21.07	2083.33	1358.33	723.33	510.00	293.33	526.67	12.33	7.00
G09	10.33	20.00	15.50	995.00	620.00	378.33	246.67	150.00	340.00	11.00	7.90
G10	10.00	23.53	19.93	1913.33	1206.33	703.33	470.00	221.67	506.67	12.33	7.18
G11	14.33	20.87	16.37	1073.33	610.00	480.00	370.00	136.67	356.67	11.67	8.33
G12	22.33	21.87	16.83	1035.00	630.00	406.67	210.67	170.00	263.33	10.00	9.50
G13	11.00	23.13	16.87	1686.67	1130.00	560.00	340.00	201.67	463.33	11.67	9.50
G14	10.00	22.63	17.33	1298.33	708.33	590.00	240.00	193.33	320.00	11.00	8.50
G15	10.33	18.03	15.83	1118.33	660.00	600.00	183.33	143.33	253.33	10.00	8.33
G16	13.00	22.53	18.20	1320.00	800.00	520.00	168.33	191.67	330.00	11.33	9.50
G17	11.67	21.00	16.40	1091.67	650.00	423.33	238.00	145.00	265.00	11.00	7.50
G18	15.00	23.83	15.67	1323.33	723.33	606.67	390.00	211.67	385.00	12.33	10.33
G19	6.00	23.17	17.33	1370.00	873.33	493.33	410.00	191.67	381.67	10.33	8.17
Mean	11.79	22.63	17.90	1418.00	869.35	555.61	332.47	187.90	382.81	11.26	7.91
CV(%)	31.94	8.31	6.05	14.11	12.07	13.44	19.10	14.19	12.26	7.08	7.01
Level of significance	**	**	**	**	**	**	**	**	**	**	**

**Figure 1.** Scatter diagram of 19 coconut genotypes based on their principal component scores.

A two-dimensional scatter diagram was constructed using component I in X-axis and component 2 in Y-axis, reflecting in the relative position (Figure 1). As per scatter diagram the genotypes were apparently distributed into five clusters which indicated that there exists considerable diversity among the genotypes.

After comparing D^2 values 19 genotypes were grouped into four clusters. Cluster II and V had the maximum number of (5) genotypes followed by III, I and IV which had 4, 2 and 3 genotypes, respectively (Table 3). These results confirmed the clustering pattern of the genotypes obtained through principal component analysis. Badignavar *et al.*, (2002), Joel and Mysamy (1998), Islam *et al.*, (2000) found similar results in compositions of different clusters with their corresponding genotypes in each cluster. Islam *et al.*, (2007) carried out principal component analysis and cluster analysis in 22 coconut (*Cocos nucifera*.L) genotypes and stated that the 22 genotypes were divided into 6 groups. Genetic diversity is generally associated with geographical diversity, but the former is not necessarily directly related with geographic distribution. The genotypes within the same cluster although formed specific clusters but were collected from different places, which indicated that the geographical distribution and genetic divergence did not follow the same trend.

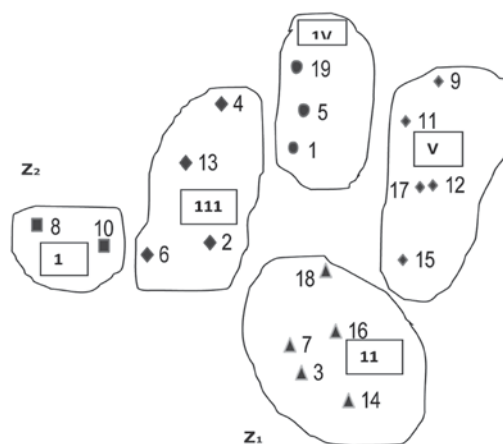


Figure 2. Scatter distribution of 19 coconut genotypes based on their principal component scores super imposed with clustering.

The inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups. Islam *et al* (2007) obtained larger inter-cluster distances than the intra-cluster distances in a multivariate analysis in coconut. The inter-cluster distance was maximum between clusters I and V (19.047) followed by the clusters I and II (14.482), while the distance was minimum between cluster III and IV (5.577) followed by the cluster II and IV (5.927). The maximum value of inter-cluster distance indicated that the genotypes belonging to cluster I was far diverged from those of cluster V. Similarly

Table 3. Distribution of 19 coconut genotypes in five clusters.

Clusters	Number of genotypes	Names of genotypes
I	2	G08, G10
II	5	G03, G07, G14, G16, G18
III	4	G02, G04, G06, G13
IV	3	G01, G05, G19
V	5	G09, G11, G12, G15, G17

Table 4. Average intra and inter cluster distances (D²) for 19 coconut genotypes.

Cluster number	I	II	III	IV	V
I	0.920				
II	14.482	1.097			
III	6.567	8.673	0.898		
IV	12.127	5.927	5.577	1.055	
V	19.047	8.234	12.493	6.920	1.286

the higher inter-cluster values between cluster III and V, clusters I and IV indicated that the genotypes belonging to each pair of clusters were far diverse. The genotypes within the other pair of clusters indicated that they were less diverse. This relationship was also reflected in the scatter diagram. The genotypes belonging to the distant clusters could be used in hybridization program for obtaining a wide spectrum of variation among the segregates. Similar reports were also made by Islam *et al.*, (2007).

The intra-cluster distances were computed by the values of inter-genotypic distance matrix of PCO. There was not marked variation in intra-cluster divergence, which varied from 0.898 to 1.286 (Table 4). The maximum intra-cluster distance was computed for the

cluster V (1.286), consisted of five genotypes of diverse origin followed by the cluster II (1.097), composed of five genotypes, while the minimum distance (0.898) was observed in the cluster III that composed four genotypes. The intra-cluster distances of cluster I and IV were 0.920 and 1.055 consisting of two and three genotypes, respectively. However, the highest values (1.286) of intra-cluster distance in cluster V indicated the genotypes (5) constituted this cluster might have contributed as the diverged characters.

Inter-cluster means for twenty two characters are presented in Table 5. Girth at 50cm had the highest intra-cluster means in cluster I followed by those in cluster III and cluster IV. The lowest intra-cluster mean for this was

Table 5. Cluster means for 22 characters of 19 coconut genotypes.

Character	Cluster				
	I	II	III	IV	V
Girth at 50cm	142.5	114.8	126.67	116.3	114.4
Girth at 20cm	165.0	135.0	152.5	142.3	142.1
Length of 11 leaf scar (cm)	3.0	3.1	2.9	3.0	3.0
Stem height (m)	13.7	9.8	11.3	11.9	11.0
Number of bunches per palm	9.7	11.1	10.4	8.3	8.8
Number of nuts per bunch	8.3	7.9	7.9	9.3	8.0
Number of nuts per palm	75.1	85.8	82.4	74.1	66.1
Length of central axis (cm)	120.3	105.0	106.7	100.3	94.4
Spikelets with female flower	10.0	12.8	9.5	11.3	12.7
Spikelets without female flower	29.2	25.9	30.0	28.2	24.8
Spikelet per inflorescence	39.2	39.4	39.5	38.2	38.1
Female flower per inflorescence	10.5	13.5	10.0	8.9	13.8
Fruit length (polar) cm	24.5	23.5	23.5	22.4	20.4
Fruit length (equate) cm	20.5	17.3	19.1	18.4	16.2
Fruit weight (g)	1998.3	1361.1	1674.6	1376.1	1062.7
Nut weight (g)	1282.3	770.8	1072.9	879.1	634.0
Weight of husk (g)	713.3	591.2	603.3	490.9	457.7
Volume of water (ml)	490.0	280.0	403.8	357.8	249.7
Weight of shell (g)	257.5	185.7	214.2	175.0	149.0
Weight of kernel (g)	516.7	355.0	458.7	383.9	295.7
Kernel thickness (mm)	12.3	11.1	11.7	11.1	10.7
Total Soluble Solid	7.1	8.9	8.2	8.1	8.3

observed in cluster V. Girth at 20cm had the highest group means in cluster I followed by those of cluster III and cluster IV. The lowest mean was in cluster II. Intra-cluster mean for length of 11 leaf scar was highest in cluster II followed by those in cluster IV, cluster V and cluster I. The lowest intra-cluster mean for this was observed in cluster III. Stem height had the highest intra-cluster means in cluster I followed by those in cluster IV and cluster III. The lowest intra-cluster mean for this was observed in cluster II followed by that in cluster V.

Intra-cluster mean for number of bunches per palm was the highest in cluster II followed by those in cluster III and cluster I. The lowest intra-cluster mean was observed in cluster IV. Cluster IV comprised the highest intra-cluster mean for number of nuts per bunch followed by those in cluster I, while the values for this character was the lowest in cluster II and cluster III. Group mean for number of nuts per palm was the highest in cluster II, while it was the lowest in cluster V. Length of central axis showed the highest intra-cluster mean in cluster I. The character had the lowest value for the cluster V. Spikelets with female flower had the highest intra-cluster means in cluster II followed by those in cluster V. The lowest intra-cluster mean for this was observed in cluster IV. Intra-cluster mean for spikelets without female flower was the highest in cluster III. The lowest intra-cluster mean for this was observed in cluster V. Spikelets per inflorescence had the highest group means in cluster III. The lowest mean was in cluster V. Intra-cluster mean for female flower per inflorescence was the highest in cluster V. The lowest was in cluster IV. Cluster I comprised of the highest intra-cluster mean for fruit length

(polar), fruit length (equator), fruit weight, nut weight, husk weight, volume of water, weight of shell, kernel weight and kernel thickness. The lowest intra-cluster mean for fruit length (polar), fruit length (equator), fruit weight, nut weight, husk weight, Volume of water, weight of shell, weight of kernel and kernel thickness was observed in cluster V. Total soluble solid had the highest intra-cluster means in cluster II followed by those in cluster V. The lowest intra-cluster mean for this was observed in cluster I followed by that in cluster IV.

The character contributing the maximum to the divergence are given greater emphasis for deciding on the cluster for the purpose of further selection and the choice of parents for hybridization (Jagadev *et al.*, 1991). Contribution of characters towards divergence obtained from Canonical Variate Analysis is presented in Table 6. The values of vector I and vector II (Table 6) revealed that both the vectors had positive values for girth at 50cm, girth at 20cm, number of nuts per palm, fruit weight and kernel weight. These results indicated that these five characters had the highest contribution towards the divergence among the 19 coconut genotypes. In vector I, the other important characters responsible for genetic divergence in the major axis of differentiation were length of central axis (cm), number of bunches per palm, spikelets with female flower, female flower per inflorescence, nut weight, shell weight and total soluble solid having positive vector values. While in vector II (the second axis of differentiation) stem height, number of nuts per palm, spikelets without female flower, spikelets per inflorescence and husk weight were important.

Table 6. Latent vectors for 22 characters of 19 coconut genotypes.

Character	Vector I	Vector II
Girth at 50cm	0.0542	0.1007
Girth at 20cm	0.0924	0.1673
Length of 11 leaf scar (cm)	0.0187	-0.1640
Stem height (m)	-0.1893	0.2306
Number of bunches per palm	0.0307	-0.4016
Number of nuts per bunch	-0.0335	0.2114
Number of nuts per palm	0.0453	0.2549
Length of central axis (cm)	0.1805	-0.1477
Spikelets with female flower	0.1984	-0.3919
Spikelets without female flower	-0.1830	0.2988
Spikelet per inflorescence	-0.0580	0.0317
Female flower per inflorescence	0.2033	-0.3770
Fruit length (polar) cm	-0.2428	-0.1820
Fruit length (equator) cm	-0.2765	-0.1085
Fruit weight (g)	0.3432	0.1166
Nut weight (g)	0.3390	-0.0850
Weight of husk (g)	-0.2649	0.1267
Volume of water	-0.3073	-0.0072
Weight of shell	0.2740	-0.2604
Weight of kernel (g)	0.3412	0.0757
Kernel thickness	-0.2012	-0.1148
Total Soluble Solid	0.1829	-0.1856

Negative values in both the vectors for fruit length (polar), fruit length (equator), volume of water and kernel thickness indicated these four characters had the lowest contribution to the total divergence. Uddin (2003) reported that nut weight and husk weight contributed significantly to the variation in the coconut population in northern Luzon, Philippines Islands. He also stated that fruit characters are key factors in distinguishing coconut populations. Islam *et al.*, (2007) reported that fruit weight and nut weight had higher contribution to the total divergence in coconut. Considering the magnitude of genetic distance, contribution of different characters toward the total divergence, magnitude of cluster means for different characters and *per se* performance the genotype G08 of cluster I could be selected for length of central axis, fruit length (polar), fruit length (equator), fruit weight, nut weight, husk weight, volume

of water, weight of shell, weight of kernel and kernel thickness. From cluster II the genotype G18 could be selected for length of 11 leaf scar, number of nuts per palm and total soluble solid, G14 for number of bunches per palm, spikelets with female flower and female flowers per inflorescence. The genotype G2 of cluster III could be selected for spikelet per inflorescence. From cluster IV the genotype G05 could be selected for number of nuts per bunch. The genotype G04 of cluster V could be selected for girth at 50cm, G15 for girth at 20cm, G12 for length of central axis and female flowers per inflorescence.

Considering cluster distance and cluster mean, the genotypes G08 and G10 from cluster I, genotypes G14 and G18 from cluster II, genotype G04 from cluster III, genotype G05 from cluster IV, genotype G12 from cluster V may be considered better parents for future hybridization program.

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