

Morphometric Characterization of Coconut Germplasm Conserved at Bari

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Abstract: An experiment was conducted at the Pomology Research Field, HRC of BARI, Gazipur, Bangladesh during the period from September 2011 to February 2012 to evaluate the morphometric characterization of coconut germplasm. PCA revealed that days to spathe opening, days to male phase and number of nuts per palm contributed for 66.73% of the observed variation. Twenty seven entries of coconut were grouped into 7 clusters. The largest cluster VII included 9 palms, cluster VI, V and II included 8, 4 and 3 palms respectively while cluster I, III and IV included 1 palm. The inter-cluster values were maximum in between clusters III and VII (82.455) while it was minimum in between II and IV (22.351). The intra-cluster distance was maximum in cluster VII (13.210) while the clusters I, III and IV showed no distance. So, the clusters between III and VII could be used as germplasm for future breeding.

Key words: Morphometric characterization % Coconut germplasm

INTRODUCTION

Coconut (*Cocos nucifera* L.) is a monocotyledonous plant species belonging to the family Palmaceae (Arecaceae), subfamily Cocoideae and the monospecific genus *Cocos* [1]. It is widely distributed throughout the tropics between 20° N and 20° S latitude covering about 11.6 million hectares over 86 countries [2]. Asia and the Pacific produce 85 % of the total world coconut production. Bangladesh produces about 100 million nuts annually weighing about 90,000 tons in an area of 30,000 hectares [3]. About 80% of coconut in Bangladesh consumed as fresh fruit and tender nut for drink purpose. Only 9 % is available for processing in oil mills [3].

Coconut palm is capable of sequestering carbon-dioxide and causing soil bio-diversification of farm product and nutrient recycle. It is a food source which provides supplement for body fluids and minerals. Bangladesh hardly can produce 5000 tons of coconut oil against its yearly demand of 30,000 tons [3]. The yield of nut in Bangladesh is very low on an average 21 nuts per palm per year as compared to many other coconut growing countries in the world [3]. Tall type cross pollinated coconut is grown in Bangladesh for its long productive life and nut quality. Collection, conservation and evaluation of germplasm offer an opportunity of

exploiting advantages of natural diversity for crop improvement. Hence, an initial study on the diversity of coconut of the country is essential for documenting the genetic diversity of coconut in Bangladesh. Therefore, the study was undertaken for characterization and evaluation of coconut germplasm.

MATERIALS AND METHODS

The experiment was conducted at the Pomology Research Field, Horticulture Research Centre of Bangladesh Agricultural Research Institute (BARI), Gazipur under the agro-ecological zone of Modhupur Tract (AEZ No. 28) during the period from September 2011 to February 2012. Soil of the experimental field was silty clay loam in texture and acidic in nature. Coconut germplasm were collected from different Agro Ecological Zone of Bangladesh which was planted at BARI campus in 1998-2001 among which 27 palms of different population was selected. Coconut palms were about 10 years. Data on bole category, stem, leaf, flowers and nut were recorded and subjected to diversity analysis by SPSS-12 computer packages. Principal component analysis (PCA) and clustering were carried to assess the pattern of morphological variation. To assess the relationships within genotypes or classes of the population, a dendrogram was developed.

RESULTS AND DISCUSSION

Principal Component Analysis (PCA): To examine the relationship among quantitative variables, principal component analysis (PCA) was carried out. First three components contributed 66.73% of the observed variation (Table 1). The rest of the components contributed for 33.27% of variation.

In Prin1, number of nuts per palm and number of nuts per bunch contributed to the highest loading 87% followed by 77%, 66% and 58% for girth of peduncle, number of female flowers and length of central axis of inflorescence respectively. In Prin2, girth at stem contributed highest loading 83% followed by 82% and 59% for girth at bole and width of leaflet respectively (Table 2). Contributions of characters towards divergence were estimated through canonical variate analysis. The coefficients pertaining to the different characters in the first two canonical roots presented in Table 2. The positive absolute values of the two vectors revealed that days to spathe opening, days to male phase, number of nuts per palm, number of nuts per bunch, length of central axis of inflorescence, number of spikelets per inflorescence, number of female flowers and girth of peduncle had the greatest contribution to genetic divergence. On the other hand, the negative absolute values of vector-1 and positive absolute value for vector-2 for the characters of Girth at bole, Girth at stem, Width of leaflet and Width of petiole indicated the responsibility of secondary differentiation.

Cluster Analysis

Number of Clusters and Cluster Members: Twelve variables of 27 palm collections were selected on the basis of principal component analysis subjected to Unweighted Paired Group Method Arithmetic Average (UPGMA) for cluster analysis using SPSS.

From the resulting dendrogram in 1-5 scale measurement (Fig. 1), the populations were grouped into seven clusters, which were presented in the Table 3. The cluster VII was the largest, containing nine palms followed by cluster VI, which included 8 palms. Cluster V consisted of 4 palms while cluster II included 3 and cluster I, III and IV represents 1 palm (Table 3). Similarity in many phenotypic characters of the genotypes brought them in a particular group. The observed diversities in the collections might be resulted from natural and human intervention [4].

Average intra and inter cluster distance of seven clusters were presented in Table 4. The magnitude of intra cluster distances indicated the extent of genetic diversity among genotypes within the cluster whereas inter cluster distances depicted the extent of diversity among genotyped between the clusters. It was reported that clusters with lesser magnitude of divergence showed instability, while widely divergent clusters remained distinct in different environments [5-7].

The higher value of inter cluster distances than intra cluster distances indicated that diversity presents more in between clusters than within clusters. Genetically distant parents usually able to produce higher heterosis [8-12]. Keeping this in view, the findings from the present study indicated that the maximum inter-cluster distance was obtained in between clusters III and VII (82.455) indicated the wider genetic divergence between these two clusters. It was followed by the distance between the clusters I and III (72.894), III and IV (70.825), III and V (58.362), II and III (64.855). It was observed that, the cluster III had the highest distance from the rest indicated that the genotype in the cluster III was distinctly different from others. Parental material selection from these clusters would give high manifestation of heterosis as well as wide spectrum of variation when they are hybridized. Endang *et al.* [13] stated that the clustering pattern could be utilized in

Table 1: Eigenvalues of the Covariance Matrix of 10 principal components for quantitative characters of coconut population

	Eigenvalues	Difference	Variance (%)	Cumulative (%)
PRIN1	3.400	0.765	28.336	28.336
PRIN2	2.635	0.662	21.955	50.290
PRIN3	1.973	0.906	16.443	66.734
PRIN4	1.067	0.160	8.892	75.626
PRIN5	0.907	0.045	7.561	83.187
PRIN6	0.862	0.362	7.184	90.371
PRIN7	0.500	0.161	4.165	94.537
PRIN8	0.339	0.109	2.829	97.365
PRIN9	0.230	0.144	1.917	99.282
PRIN10	0.086	0.06	0.718	100.000

Prin = Principal component

Table 2: Eigenvector of 12 characters in the first three Principal Component

Variable	PRIN1	PRIN2	PRIN3
Days to spathe opening	0.114	0.570	-0.781
Days to male phase	.0114	0.570	-0.781
Number of nuts per palm	0.870	0.013	-0.159
Number of nuts per bunch	0.870	0.013	-0.159
Length of central axis of inflorescence (cm)	0.578	0.172	0.250
Number of spikelets per inflorescence	0.434	0.359	0.292
Number of female flowers	0.661	0.092	0.423
Girth of peduncle (cm)	0.770	0.239	0.192
Girth at bole (cm)	-0.310	0.823	0.294
Girth at stem (cm)	-0.299	0.834	0.145
Width of leaflet (cm)	-0.152	0.596	0.467
Width of petiole (cm)	-0.317	0.178	0.116

Prin = Principal component

Table 3: Cluster grouping of 27coconut population

Cluster Number	Palm Number	Total Genotypes
I	22	1
II	2, 8, 17	3
III	25	1
IV	24	1
V	13, 14, 18, 21	4
VI	1, 3, 9, 12, 20, 23, 26, 27	8
VII	4, 5, 6, 7, 10, 11, 15, 16, 19	9

Table 4: Intra and inter cluster distances among the various clusters of coconut population

Cluster	I	II	III	IV	V	VI	VII
I	0.00	26.021	72.894	16.808	16.204	49.530	25.014
II		12.910	64.855	22.351	24.226	37.471	23.486
III			0.00	70.825	58.362	27.690	82.455
IV				0.00	23.896	46.903	18.435
V					11.550	35.654	33.177
VI						4.472	56.378
VII							13.210

Table 5: Intra-cluster means for 12 characters of coconut population

Characters	Cluster number						
	I	II	III	IV	V	VI	VII
Days to spathe opening	31.00	34.33	30.00	33.00	31.50	32.00	43.55
Days to male phase	31.00	34.33	30.00	33.00	31.50	32.00	43.55
Number of nuts per palm	40.00	38.33	50.00	20.00	23.75	31.87	33.33
Number of nuts per bunch	8.00	7.67	10.00	4.00	4.75	6.87	6.67
Length of central axis of inflorescence (cm)	70.00	53.33	29.00	36.00	34.50	50.00	45.33
Number of spikelets per inflorescence	37.00	48.00	43.00	31.00	40.00	40.87	38.77
Number of female flowers	109.00	82.00	45.00	15.00	42.50	30.75	39.22
Girth of peduncle (cm)	17.00	15.00	13.00	10.00	11.50	13.25	13.44
Girth at bole (cm)	150.00	128.33	170.00	150.00	150.75	147.50	153.77
Girth at stem (cm)	96.00	85.00	99.00	91.00	91.50	92.25	96.11
Width of leaflet (cm)	5.40	4.93	5.00	4.00	5.00	4.72	4.80
Width of petiole (cm)	3.00	3.10	3.20	3.00	3.20	3.32	3.24

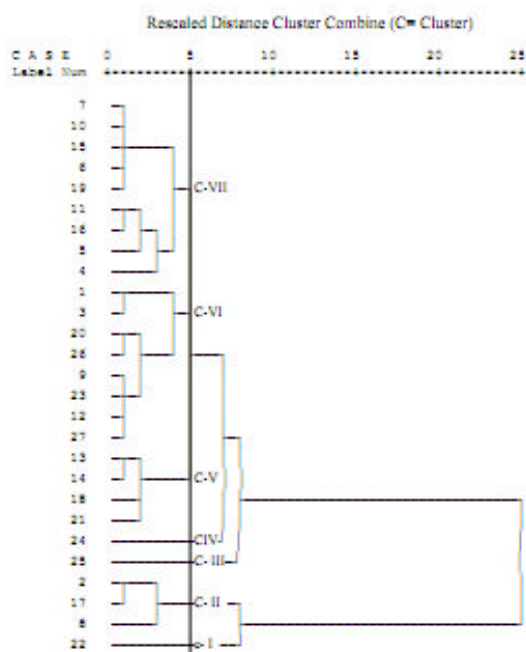


Fig. 1: Dendrogram using average linkage between the conserved genotypes at BARI

choosing parents for cross combinations which likely to generate the highest possible variability for effective selection of various economic traits.

Parents for hybridization could be selected on the basis of large inter-cluster distance for isolating useful recombinants in the segregating generations. Increasing parental distance implies a greater number of constraining alleles at the desired loci and then to the extent that these loci recombining in the F_2 and F_3 generations, following a cross of distantly related parents, the greater will be the opportunities for successful selection for any character of yield interest [14].

The minimum distance was obtained in between clusters II and IV (22.351) indicated that the genotypes belonging to these clusters were comparatively less diverse. Thus crossing of genotypes from these two clusters may not produce high level of heterotic expression in the F_1 's and broad spectrum of variability in segregating (F_2) population. The maximum intra-cluster distance was in cluster VII (13.210) while the clusters I, III and IV showed no distance because each of them included only one palm in each cluster (Table 4).

Girth at bole, girth at stem and number of female flowers in all the clusters were found to contribute maximum diversities (Table 5). The cluster mean of 170.00 cm was recorded maximum for girth at bole in cluster III followed by 153.77 cm in cluster VII, 150.75 cm in cluster

V and minimum of 128.33 cm in cluster II. The cluster mean of 99.00 cm was highest for girth at stem in cluster III followed by 96.11 cm in cluster VII, 96.00 cm in cluster I and least of 85.00 cm in cluster II. Cluster means 109.00 for the number of female flowers was highest in cluster I followed by 82.00 in cluster II, 45.00 in cluster III and minimum of 15.00 in cluster IV. In cluster IV, number of nuts per palm, number of nuts per bunch and number of female flowers were minimum for 20, 4 and 15 respectively.

CONCLUSION

PCA and cluster analysis revealed that inflorescence and nut characters are the most important components contributing to the observed variation. So, nut yield and quality improvement in coconut would be achieved through selection of these characters. But these collections not yet reached in full bearing stage. So, further studies should be conducted to evaluate the nut characters, bearing habit and yield of selected entries of coconut.

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