



Genetic Diversity in Banana (*Musa* spp.)

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Twenty eight banana genotypes grown at the Instructional Farm, College of Agriculture, Vellayani, Thiruvananthapuram, Kerala were observed for twenty three different morphological characters and the data were subjected to analysis of variance. Significant differences were recorded among the genotypes with regard to different morphological characters. Twenty eight genotypes of banana were grouped into six clusters following the Tocher's method of clustering analysis utilizing data on a set of 23 characters related to yield, vegetative characters and quality characters. Koonoor Ethan (cluster VI), Vellapalayankodan (cluster V) and Quintal banana (cluster IV) formed individual clusters and had the maximum genetic divergence. Cluster II had the maximum of 14 genotypes while cluster I and III had 9 and 2 genotypes respectively. The highest mean performance was recorded by cluster VI for 13 characters whereas cluster V and IV recorded the same for 7 and 3 characters. The intra and inter cluster genetic distance values ranged from 96 (cluster I) to 150 (cluster III). The maximum inter cluster distance was observed between cluster IV and cluster V (803) followed by cluster VI and cluster I (762). Contribution of individual characters towards divergence recorded that maximum contribution to total divergence was recorded by fingers per hand, shelf life of the fruit, fingers per bunch and finger girth whereas the characters which were contributing minimum towards divergence were leaf width, TSS, pseudostem girth, leaves per plant, suckers per plant, hand weight, pulp/peel ratio, fruit volume and acidity.

Key words: banana, genetic divergence, cluster analysis, genotypes.

The use of Mahalanobis D^2 statistics for estimating genetic divergence had been emphasized by many workers (Rekha *et al.*, 2001 Singh *et al.*, 2003 and Rai and Mishra, 2005). Banana (*Musa* spp.) is the most important fruit crop in India. High yielding, disease resistant and delicious banana genotypes with keeping qualities are to be developed for the benefits of the banana cultivars. Simmonds (1962) concluded that the present day cultivars had evolved by the hybridization of two main species, *Musa acuminata* and *M. balbisiana* which were considered the main contributors of A and B genome respectively. All the cultivars were classified into various genomic groups such as AA, AAA, AB, AAB and ABB respectively based on morphological scoring method (Stover and Simmonds, 1987). Morphological characterization has been the major tool for classifying banana cultivars into different genomic groups. The variability and genetic divergence among Indian banana were studied by Valsalakumari *et al.* (1985). The information about the extent of genetic divergence is critical for the improvement programme of any crop. Though clonally propagated, significant variation is observed among banana cultivars (Nayar *et al.*, 1979). The present study was undertaken to estimate the genetic diversity among 28 varieties of banana and to find

out the characters which contribute maximum towards genetic divergence considering 23 characters simultaneously.

Materials and Methods

The experimental materials consisted of 28 banana clones and their intra clones (Table.1). The suckers of each clone were maintained at the Instructional farm, College of Agriculture, Vellayani, Thiruvananthapuram. Suckers of the twenty eight clones and intraclasses of almost uniform size were collected from different parts of Kerala and Tamil Nadu. Suckers of Kaliethan, Koonoor Ethan, Quintal banana, Vellayani Nendran, Monthan, Red banana, Vellakappa and Robusta were collected from the Instructional Farm, College of Agriculture, Vellayani. The suckers of Kadali, Kunnan, Vellapalayankodan, Peyan, Pisang Lilin, Njalipooan and Palode Palayankodan varieties were collected from Banana Farm, Pering amala, Palode, Thiruvananthapuram. Mottapooan, Chandra Bale, Pisang Ceylon, PKNR, Padalamurian, Mysore Ethan, Myndoli, Attu Nendran, Chengazhi kodan, Changanasserri Nendran, Manjeri Nendran and Zanzibar were collected from Banana Research Station (BRS), Kannara. Suckers of about three to four months age were used for planting at a spacing of 2.0 x 2.0 m. The cultural

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Table 1. Cultivars, banana types, ploidy and genomic composition of banana clones

Sl.No.	Clone Name	Type	Ploidy	Genomic Composition
1.	Red banana	Dessert	3x	AAA
2.	Vellakappa	Dessert	3x	AAA
3.	Robusta	Dessert	3x	AAA
4.	Vellayani Nendran	Dessert	3x	AAB
5.	Padalamurian	Dessert /cooking	3x	AAB
6.	Myndoli	Dessert /cooking	3x	AAB
7.	Chengazhikodan	Dessert /cooking	3x	AAB
8.	Attu Nendran	Dessert /cooking	3x	AAB
9.	Kaliethan	Dessert /cooking	3x	AAB
10.	Koonoor Ethan	Dessert /cooking	3x	AAB
11.	Mysore Ethan	Dessert /cooking	3x	AAB
12.	Zanzibar	Dessert /cooking	3x	AAB
13.	Quintal banana	Dessert /cooking	3x	AAB
14.	Changanasserri Nendran	Dessert /cooking	3x	AAB
15.	Manjeri Nendran	Dessert /cooking	3x	AAB
16.	Palode Palayankodan	Dessert	3x	AAB
17.	PKNNR	Dessert	3x	AAB
18.	Chandra Bale	Dessert	3x	AAB
19.	Pisang Ceylon	Dessert	3x	AAB
20.	Mottapoovan	Dessert	3x	AAB
21.	Vellapalayankodan	Dessert	3x	AAB
22.	Monthan	Cooking	3x	ABB
23.	Peyan	Cooking	3x	ABB
24.	Kadali	Dessert	2x	AA
25.	Pisang Lilin	Dessert	2x	AA
26.	Njalipoovan	Dessert	2x	AB
27.	Kunnan	Dessert	2x	AB
28.	Ilavazha	Leaf purpose	2x	BB

practices as per the package of practices recommendation (KAU, 1996) were followed. The experiment was laid out in completely randomized block design with five replications in each genotype. The data on plant morphology, yield and fruit parameters were collected and analysed as per the techniques of Panse and Sukhatme (1967). Observations made on plant height, pseudostem girth, number of leaves, leaf length, leaf width, number of suckers per plant, crop duration, bunch weight, hand per bunch, fingers per bunch, finger per hand, length, girth weight and volume of finger, bunch length, hand weight, pulp/peel ratio, TSS, acidity, total sugars, sugar/acid ratio and shelf life of the fruit. The D^2 statistics, a measure for a group distance based on multiple characters as proposed by Mahalanobis (1936) was estimated. Grouping of variance was done by Tocher's method (Rao, 1952). The relative contribution of characters to divergence at the cluster levels as well as the genotype levels was assessed on the basis of the coefficients of variation of the individual traits (Sharma, 1998). Average intraclasses distances were calculated using the formula $\sum D_i^2/n$ where D_i^2 is the sum of distance between possible combinations (n) of the populations included in the cluster. Average inter-cluster distances were calculated by taking each cluster and their distances from the other cluster. The cluster diagram was drawn with the help of D values showing relationships within and between clusters.

Results and Discussion

The analysis of variance showed highly significant differences between the genotypes for each of the twenty three characters studied. All the 28 genotypes were grouped into six clusters (Table 2). The clusters were based on the 23 quantitative characters were study. The clustering pattern was not influenced by genomic constitution. The same cluster included cultivars belonging to different genomic groups.

Table 2. Group constellations in twenty eight clones of banana

Cluster	Number of clone	Clones
C ₁	9	Palode Palayankodan, PKNNR, Chandra Bale, Pisang Ceylon, Mottapoovan, Kadali, Pisang Lilin, Njalipoovan, Kunnan
C ₂	14	Red banana, Vellakappa, Robusta, Padalamurian, Chengazhikodan, Kaliethan, Myndoli, Attu Nendran, Mysore Ethan, Manjeri Nendran, Changanasserri Nendran, Monthan, Peyan, Ilavazha
C ₃	2	Vellayani Nendran, Zanzibar
C ₄	1	Quintal banana
C ₅	1	Vellapalayankodan
C ₆	1	Koonoor Ethan

Maximum number of genotypes were included in cluster II (14 genotypes) viz., Red banana, Vellakappa, Robusta, Padalamurian, Chengazhikodan, Kaliethan, Myndoli, Attu Nendran, Mysore Ethan, Manjeri Nendran, Changanasserri Nendran, Monthan, Peyan, Ilavazha, followed by cluster I (9 genotypes) namely Palode Palayankodan, PKNNR, Chandra Bale, Pisang Ceylon, Mottapoovan, Kadali, Pisang Lilin, Njalipoovan, Kunnan whereas the cluster IV, (Quintal banana), cluster V (Vellapalayankodan) and cluster VI (Koonoor Ethan) formed individual clusters.

Table 3. Estimation of average intra and inter cluster D for six clusters constructed from 28 clones of banana

	Cluster Number					
	C ₁	C ₂	C ₃	C ₄	C ₅	C ₆
C ₁	96	244	460	408	202	762
C ₂		112	210	310	553	
C ₃			159	536	336	
C ₄				0	427	382
C ₅					0	803
C ₆						0

Bold figures in diagonals are the intra-cluster distances

The cluster III contains only two genotypes namely Vellayani Nendran and Zanzibar. The clones of first cluster were characterized by Palode Palayankodan, PKNNR, Mottapoovan, Chandra Bale and Pisang Ceylon. Another member of Palayankodan that is Vellapalayankodan came into the fifth cluster. The name of this particular clone though resemble Palayankodan in name is characterized by robust growth characters with higher value for crop duration, pseudostem girth,

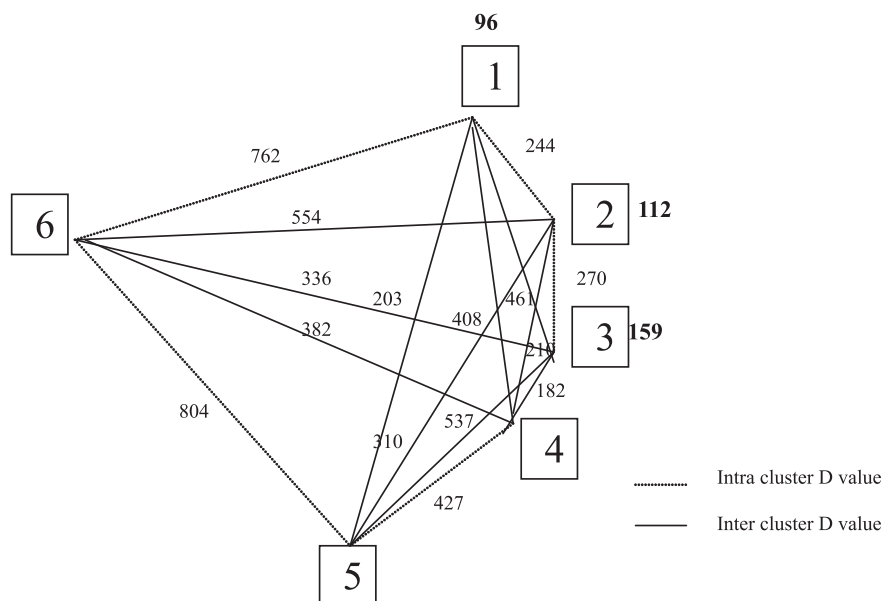


Fig 1. Cluster diagram showing relationships between different clusters

plant height, fingers per bunch, bunch length, suckers per plant, hands per bunch, finger length, sugar/acid ratio and shelf life. It is called vernacularly as Vellapalayankodan because of the ashy white skin colour of the fruit. This group contains genotypes with genomic grouping and also clones of different geographical origin. Second group contains fourteen genotypes of different ploidy and genomic constitution. This group contains all the Nendran intraclones and the culinary varieties like Peyan and Monthan and table varieties like Red banana, Vellakappa and Robusta and BB group like Ilavazha. However, two Nendran clones like Koonoor Ethan and Quintal banana formed a separate cluster.

Table 4. Character means in different clusters of banana accessions

S.No.	Characters	I	II	III	IV	V	VI
1.	Plant height (cm)	287.07	302.87	270.80	387.00	417.20	331.40
2.	Pseudostem girth (cm)	60.80	65.54	59.95	78.68	96.06	66.24
3.	No. of leaves	8.16	8.69	8.39	9.00	8.39	11.00
4.	Leaf length (cm)	210.85	212.68	192.71	253.20	213.98	215.38
5.	Leaf width (cm)	73.24	73.76	66.08	75.54	72.92	81.26
6.	No. of suckers	9.71	9.84	10.40	10.40	15.80	24.80
7.	Crop duration (days)	305.3	363.71	313.90	384.0	407.0	321.20
8.	Bunch weight (kg)	13.72	16.65	13.95	30.40	23.04	19.00
9.	Hands per bunch	9.93	6.70	3.50	7.20	14.60	2.00
10.	Fingers per bunch	165.71	80.54	34.40	102.80	254.20	19.40
11.	Fingers per hand	16.54	11.79	9.73	14.25	18.93	9.70
12.	Finger length (cm)	11.78	20.04	26.30	27.96	13.06	37.26
13.	Finger girth (cm)	9.48	13.65	14.21	15.62	10.52	17.74
14.	Finger weight (g)	94.72	203.10	317.97	294.54	90.08	507.42
15.	Bunch length (cm)	73.06	71.28	57.95	81.74	130.04	58.96
16.	Hand weight (kg)	1.86	2.27	2.68	4.35	1.50	4.50
17.	Pulp peel ratio	3.85	5.84	5.75	3.45	2.53	5.95
18.	Fruit volume (cc)	86.38	191.83	310.83	291.28	82.54	503.90
19.	TSS (°Brix)	25.76	24.95	28.27	30.28	25.40	30.92
20.	Acidity (%)	0.36	0.39	0.38	0.39	0.24	0.32
21.	Total sugars (%)	16.07	22.09	21.31	25.06	16.57	25.61
22.	Sugar/acid ratio	40.80	56.60	57.51	66.16	68.53	79.72
23.	Shelf life (days)	6.73	10.91	11.33	12.32	8.65	12.75

Table 5. Contribution of various characteristics to divergence

S.No.	Characters	Frequency%	Contribution
1.	Plant height (cm)	5	2.98
2.	Pseudostem girth (cm)	2	1.19
3.	No. of leaves	2	1.19
4.	Leaf length (cm)	1	0.60
5.	Leaf width (cm)	4	2.38
6.	No. of suckers	2	1.19
7.	Crop duration (days)	3	1.79
8.	Bunch weight (kg)	11	6.55
9.	Hands per bunch	13	7.74
10.	Fingers per bunch	23	13.69
11.	Fingers per hand	26	15.48
12.	Finger length (cm)	3	1.79
13.	Finger girth (cm)	15	8.93
14.	Finger weight (g)	5	2.98
15.	Bunch length (cm)	5	2.98
16.	Hand weight (kg)	2	1.19
17.	Pulp peel ratio	2	1.19
18.	Fruit volume (cc)	2	1.19
19.	TSS (°Brix)	1	0.60
20.	Acidity (%)	2	1.19
21.	Total sugars (%)	7	4.17
22.	Sugar/acid ratio	7	4.17
23.	Shelf life (days)	25	14.88

Koonoor Ethan was characterized by long crop duration, more suckers per plant, long finger with higher values for girth, weight and volume of fingers and long duration. The Quintal banana was characterized by longer crop duration, higher plant height, more leaves per plant, higher fruit length and bunch weight. These characters made it to occupy a separate cluster with single genotype. The other two Nendran clones like Vellayani Nendran and Zanzibar formed a separate cluster. From the clustering pattern based on morphological characters it is evident that the clones of particular cluster do not follow a definite

pattern in respect of geographical origin, plant and fruit character, crop duration, fruit quality etc. Therefore clustering based on morphological characters may give reliable information.

The absence of grouping based on the genomic constitution is although intriguing, demonstrates that in banana, the genomes 'A' and 'B' might not be contributing specific morphological characters and hence might be of close relatives.

Inter and intra cluster distances among the six clusters were variable (Table 3). The intercluster D values were expressed as the diversification among the groups of genotypes resembling each other based on 23 characters under this study and intra-cluster D values were expressed as the magnitude of divergence between clones within a cluster. The intra cluster genetic distance, D values ranged from 96 (cluster I) to 159 (cluster III) indicating wide divergence. The maximum inter cluster distance was observed between cluster VI and cluster V (803), followed by cluster VI and cluster I (762) while minimum inter cluster distance D (182) was between cluster IV and cluster III. Intercluster distances and their mutual relationship has been depicted in Fig. 1. The intercluster distance was higher than the intracluster distances in all the cases indicating more divergence of genotypes between the clusters. The similar relationships were also observed by Valsalakumari *et al.* (1985) and Mercy and George (1987) in banana; Balasubramanyan *et al.* (2009) in mango. Mean values for different characters in various clusters (Table. 4) provided an interesting picture of the nature of diversity. Considerable differences in cluster mean values were evident for all the characters. Genotypes of cluster VI showing the maximum inter cluster distance with cluster V and cluster VI exhibited higher mean performance in 13 out of 23 characters studied. Number of leaves per plant, leaf width, number of suckers per plant, finger length, finger girth, finger weight, bunch length, pulp /peel ratio, fruit volume, TSS, total sugars, sugar / acid ratio and shelf life of the fruit. In fact cluster V had the highest mean values for plant height, pseudostem girth, crop duration, hands per bunch, fingers per bunch, fingers per hand and bunch length, whereas the cluster IV had the highest in leaf length, bunch weight and acidity.

Contribution of individual character towards divergence (Table 5) revealed that maximum contribution to total differences was recorded by fingers per hand (15.48 %). shelf life of the fruit (14.88 %), fingers per bunch (13.69 %) and finger girth (8.93 %). The lowest contribution of frequency was recorded in leaf width, TSS, pseudostem girth,

leaves per plant, suckers per plant, hand weight, pulp /peel ratio, fruit volume and acidity content. This result indicated that involving cultivars with desirable characters, diseases resistance and high inter-cluster distance would result in highly segregating generation in breeding programmes. While selecting cultivars for hybridization purpose considerable care should be taken to select particular clusters and to select particular cultivars from the selected clusters. The study showed that cultivars belonging to the same genomic group were highly variable since they belonged to different clusters.

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