

Selection of elite seedling clones of mango (Mangifera indica L.) exposed by phylogenetic relationship and morpho-taxonomic traits

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Abstract

Almost all the current commercial mango cultivars in India are the result of selection from the natural seedling population and majority of them have been selected by the farmers. The conventional breeding system with traditional knowledge is evolving more and more towards preservation of genetic diversity. In Pusa site of the UNEP/GEF sponsored project in the Bihar state of India, many mango seedlings are found growing in the orchards as well as in the backyards. Mango being a highly cross-pollinated fruit crop exhibits a lot of variability in morpho-physico-chemical traits of fruits in these seedling plants. For selection of the elite seedling genotypes, farmers play an important role and with the help of the breeder they can pave the way for maintaining the local germplasm. Hence, in order to study the genetic variability among mango seedlings and to select elite mango genotypes and to conserve them, a survey was conducted in the four project communities and the surrounding villages. A total of 74 seedling types of mango were characterized using morpho-taxonomic parameters. Physico-chemical characterization of fruit samples revealed the existence of a great variability in the seedling mango plants, which not only contributes to biological diversity, but can also be used for crop improvement or for varietal selection. Based on this physico-chemical characterization, principal component and cluster analysis and grouping of seedling clones on the basis of possession of desirable characters by them, six seedling clones, having the majority of desirable fruit characteristics were selected. These selected clones will definitely broaden the genetic base of mango in the Pusa site as well offer the scope for choice of selection of varieties by the farmers and ultimately the conservation of the valuable germplasm.

Key words: Clone, cluster analysis, local seedling population, genetic variability, mango, morpho-taxonomic traits.

Introduction

Mango (Mangifera indica L.) is an ever green dicot angiosperm. The genus Mangifera belongs to order Sapindales of the family Anacardiaceae 1. The major mango producing countries of the world are India, China, Thailand, Indonesia and Pakistan. India is the largest producer of mango in the world, with an annual production of 15.03 million tons from an area of 2.31 million hectares, contributing about 56% of the total world production ². Despite immense commercial potential and great demand of mango fruit and its products, its full utilization is needed ³. Knowledge of a diverse genetic gene pool is important to design and tailor future breeding strategies for sustainability in mango production ⁴. If a population of a species has a very diverse gene pool, then there will be more variety of the traits of individuals of that population and consequently more traits for natural selection to act upon to select the fittest individuals to survive. India is the centre of origin for mango and numerous seedlings of known and unknown varieties are available in the farmer's fields and many of them are of importance locally as they are being maintained particularly for special purposes. Exploitation of natural variability through selection of superior seedlings of mango has been done by several

workers. Naik ⁵ and Oppenheimer ⁶ observed significant variation among the same clone. These variations may be due to bud mutation, reported in 'Alphonso' 7. In Punjab province of India, old mango plantations, predominantly from seedling origin are established naturally or propagated through selected stones from superior indigenous mango plants on the basis of fruit quality characteristics by local fruit lovers during 19th and early 20th century8. Seedling mangoes not only provide a wealth of variability for carrying out selections of desirable strains but also ensure continuous supply of novel genetic material for future crop improvement 9. Moreover, the seedling population offers a very good breeding population of natural crosses, from which desirable selections can be sorted out.

It is well documented that mango cultivars/strains/landraces/ clones are developed from open-pollinated seedling progenies viz. 'Neldawn', 'Neldica', 'Heidi' and 'Ceriese' in South Africa¹⁰; 'Manipur-I' and II mango clones in North-Eastern region of India 11; 'Paiyur-1' from 'Neelum' mango cultivar 12; 'Rumang'a chance seedling of 'Xiangmang' mango in China 13; 'Gangian Sindhuri'14 and 'Ataulfo' from 'Manila' mango in Mexico15.

Rajwana et al. 16 reported that most of the mango cultivars grown in Pakistan have been selected from the seedling population of 'Chausa' or hybrids developed by using it as one of the parents. Similarly clonal selections have led to identification of superior clones viz. 'Dashehari 51' 17 from Lucknow, 'Banarasi Langra' 18 'Cardozo Mankurad' 19 from different locations in India. High yielding clones of Langra 18 and Kensington 20 with resistance to black spot are also mentioned in literature. In perennial fruit trees like mango, clonal propagation coupled with traditional clonal selection methods have proven to be most efficient methods for capturing genetic potential including dominance, additive and epistatic interactions ²¹. Clonal selection for high yield and quality led to collection of 50 clones from Malihabad, Rahimabad and Kakori areas of mango growing belts in Lucknow 22. Pusa is one of the important places in the Bihar state of India where large number of seedling varieties is conserved by the farmers over generations. The orchards in the Pusa site and surrounding areas are rich in unique mango varieties and features ecological, genetic, economic, scientific and social values as also benefits to the society. There is a need to identify the kinds of varieties that can/cannot survive in the course of economic development interventions. Morphological characterization is the first step that should be done before advanced biochemical or molecular studies are carried out ²³. In view of the above it is interesting to explore the potential of the existing variability in the seedling populations of mango with the specific goals of the study were (1) to demonstrate the utility of morphotaxonomic traits for the study of seedling variability and selection of elite seeding clones; (2) to study the phylogenetic relationship within and among seedling populations of mango.

Materials and Methods

Plant material and physico-chemical parameter analysis: A survey was carried out in the project communities viz., Mahmada, Dhobgama, Murliyachak and Jagdishpur and surrounding villages of the Pusa site by National Research Centre on Litchi, Muzaffarpur, Bihar (India) under the UNEP/GEF Project "Conservation and sustainable use of cultivated and wild tropical fruit diversity: promoting sustainable livelihoods, food security and ecosystem services" for the characterization of seedling population of mango and the identification of elite genotypes. More than 2500 bearing seedling mango trees were screened in the Pusa site of the project and this served a very good source for the identification and selection of superior clones of mango. Four cell analyses were performed to know the extent of variability and the causes of loss of variability and how to conserve the diminishing variability. Fruit samples from more than seventy four, apparently phenotypically different mango seedling trees, locally popular for their high performance and peculiar quality fruit as per the information provided by focused group discussion, baseline survey, and feedback from local villagers etc., were selected before harvesting period. Ten fruits from marked trees were collected randomly at the time of their respective harvesting period and five fruits were analysed for various morpho-physico-chemical traits in the laboratory. These identified mango seedling trees were evaluated on site using some of the IPGRI descriptors for mango²⁴. The observations were recorded on the fruits for physico-chemical characteristics viz., fruit length (cm), fruit width (cm), fruit weight (g), peel (%), pulp (%), stone weight and total soluble solids (TSS) (°Brix) following standard analytical procedures. Physical qualitative characters, i.e. fruit rind colour (surface colour of ripened fruit was recorded matching with the Royal Horticultural Society, Colour Chart)²⁵. Percent peel; pulp and stone were calculated by the weight of the peel, pulp and stone, respectively, divided by total weight of the fruit multiplied by 100. In each sample, quantitative trait like TSS was recorded with hand-held digital refractometer. Juice acidity was estimated by titration method against 0.1 N NaOH using phenolphthalein as indicator²⁶.

Statistical analysis: Experiment was conducted in Completely Randomized Design (CRD) with five replications. Data were subjected to analysis of variation to one way ANOVA. P values ≤ 0.05 were considered as significant. All the thirteen physicochemical characters were converted into bi- and multi-state code. A pair-wise similarity matrix was generated based on simple matching coefficient method using NTSYS ver. 2.10e software ²⁷. A cluster analysis was performed using the unweighted pair group method with arithmetic average (UPGMA) based on simple matching coefficient in NTSYS software. Principal Components Analysis (PCA) of all clones was done by NCSS 2007 v 07.1.18²⁸. The principal component score with Eigen-values > 1 were used as new variable for cluster analysis.

Results and Discussion

The results presented in this study are particularly important because they represent morpho-physico-chemical traits, which are highly heritable. The fruit traits studied in mango seedling plants, resulted in the characterization of 74 variants for fruit color, fruit weight, fruit length, fruit width, seed weight, skin weight, skin percent, pulp weight, utilization purposes, etc. and this characterization of mango seedlings indicates a great diversity exiting at the site among the natural mango seedlings (Online Resource 1 and 2). This data could be utilized to identify and conserve elite germplasm for sustainable fruit production and also to identify genes for abiotic and biotic stresses, because these seedling trees are being grown under natural conditions with a minimum use of inputs and care taken by the farmers. The existence of variability in the natural seedling population of mango was also reported by many other workers 29. Further, it was opined that morphological characterization of quantitative characteristics would follow the pattern of molecular characterization in mango³⁰ and the same can be used for confirming the phylogeny of these seedlings.

Morpho-taxonomic characterization of mango clones: Morphotaxonomic parameters like fruit color, fruit weight, fruit length, fruit width, seed weight, skin weight, pulp weight, percent edible portion and total soluble solids of 74 clonal samples of mango were analyzed (Table1, Online Resource 1 and 2). A large variation was observed for all the physico-chemical fruit characteristics studied. The fruit colour varied from completely green fruits at maturity to red coloured fruits in the selections 3 and 25, respectively. The fruit weight ranged from 83.4 g in selection no. 40 to 585.4 g in selection no. 27. Other important characteristics, viz; TSS, seed weight and rind weight also exhibited large variation as is evident from the range and coefficient of variation values amongst these selected clones (Table 1). Higher pulp percentage is a favourable character in mango and it varied between 35.21 in clone no. 18 to 82.60 in clone no. 27. This attribute can be used for

Table 1. Variability parameters in 74 mango clones for different fruit characteristics.

Fruit character	Range	Mean	SE (m)	SE (d)	CV (%)
1. Fruit colour	1(3)-13(25)	4.58	0.103	0.145	5.011
2. Fruit weight (g)	83.4(40)- 585. 40 (27)	227.22	15.936	22.54	15.685
3. Fruit length (cm)	6.16(40)- 13.52 (27)	9.19	0.282	0.399	6.876
4. Fruit width (cm)	4.88 (20)- 9.18 (27)	6.64	0.189	0.267	6.348
5. Length: Width	1.104 (22)- 1.696 (66)	1.38	0.042	0.059	6.715
6. T.S.S. (⁰ Brix)	10.32 (12)- 25.66 (70)	17.62	0.568	0.804	7.215
7. Seed weight (g)	17.40 (41)- 118.80 (69)	43.96	3.387	4.789	17.226
8. Seed (%)	8.146(27)-34.876(18)	20.63	1.496	2.116	16.214
9. Rind weight (g)	15.00(68)-84.60(3)	43.31	3.18	4.497	16.414
10. Rind (%)	7.65(51)- 33.81 (20)	20.64	1.464	2.07	15.856
11. Pulp weight (g)	34.60(18)-561.2(14)	146.11	49.836	70.479	76.272
12. Pulp (%)	35.21(18)- 82.60(27)	58.73	2.627	3.715	10.002
13. TSS: Acidity	8.29 (7)- 148.0 (74)	44.28	1.981	2.801	10.002

selection of varieties that have potentiality for exploitation for juice and canning industry ⁸. All these observations clearly exhibited the existence of large variation in the selected clones, which offers a chance for the selection of superior clones. In the past also, most of the mango cultivars have originated as openpollinated seedlings in nature ³¹. High heterozygosity, crosspollination ability and vegetative propagation for preservation of true-to-type characters made possible to evolve high quality and highly productive cultivars of mango ^{32, 33}.

The selected mango clones were characterized on the basis of six commercially important characteristics, *viz*; fruit weight (>200 g), fruit colour (>6), TSS (>19 °Brix), pulp content (>60.00%), seed content (<20.00%) and rind content (<20.00%) as shown in Table 2. These selected clones were further characterized on the basis of number of desirable characteristics possessed by them (Table 3). The clone no. 51 was possessing maximum desirable characteristics (6 characteristics) followed by clone no. 25, 46, 56, 67 and 72 (all having 5 desirable characteristics) (Fig. 1). Hence, these six clones were identified as superior clones and can be considered for further detailed evaluation. From these groupings,

it is again evident that a wide variation is present in the existing seedling plantations of mango and from this variation, superior clones can be identified and they can further be conserved through vegetative propagation.

Raising large seedling population is quite cumbersome in mango because it requires a long juvenile period along with large areas. The existing seedling plantations offer a good scope for the selection of superior clones owing to cross-fertilization in this crop, as large segregating population is already available

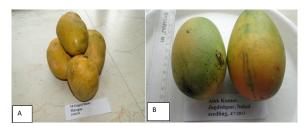




Figure 1. Mature fruits of elite seedling material collected from different farmer fields: (A) clone 51, (B) clone 25 and (C) clone 46 (mature whole fruit).

Table 2. Mango clones identified for different fruit characteristics.

Fruit character	Clone
1. Fruit weight (>200 g)	1, 2, 3, 5, 7, 8, 10, 12, 14, 19, 24, 25, 26, 27, 28, 29, 31, 33, 34, 36, 43, 44, 46, 47, 51, 52, 53, 55,
	57, 59, 60, 61, 62, 63, 65, 66, 67, 69, 72, 73, 74
2. Fruit colour (>6)	6, 8, 12, 25, 26, 28, 46, 51, 54, 56, 57, 58, 62, 65, 68, 69, 70, 73, 74
3. T.S.S. (>19.00 ⁰ Brix)	6, 20, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 58, 59, 60, 61, 64, 66, 67, 68, 69, 70, 71, 72, 73, 74
4. Pulp content (>60.00%)	3, 4, 8, 10, 12, 24, 25, 26, 27, 28, 29, 32, 41, 43, 44, 45, 46, 47, 50, 51, 52, 55, 56, 60, 63, 65, 66,
	67, 68, 71, 72
5. Seed content (<20.00%)	1, 2, 3, 4, 7, 8, 10, 12, 19, 24, 25, 26, 27, 28, 29, 30, 31, 33, 34, 35, 38, 41, 42, 43, 44, 45, 46, 47,
	49, 51, 52, 53, 56, 63, 65, 66, 67, 72
6. Rind content (<20.00%)	4, 10, 15, 18, 19, 20, 25, 27, 30, 28, 44, 51, 52, 55, 59, 60, 67, 68, 69, 71, 72, 73

Table 3. Characteristics of identified superior clones with five or more desirable fruit traits of mango.

S. No.	Clone	Farmer's name	Desirable fruit	Clonal characteristics
	No.		characteristics*	
1	25	Alok Kumar, Jagdishpur, Sukul seedling	1, 2, 4, 5, 6	Red fruit colour, suitable for pickle making due to high fibre content and also good for sucking.
2	46	Sumit, Mehmudpur, Bombay seedling	1, 2, 3, 4, 5	Reddish green colour with reddish orange flesh, fibre content very less and juice is very thick.
3	51	Gopal Ram, Mirapur	1, 2, 3, 4, 5, 6	Acceptable colour, less fibre, but thick skinned fruit and suitable for table purpose.
4	52	Sukund Prasad Singh, Mahmada, Malda seedling	1, 3, 4, 5, 6	Very sweet fruits, flesh colour orange with good eating quality and is suitable for juice purposes.
5	67	VinodRai, Jagdishpur, PaharpurSinduria	1, 3, 4, 5, 6	Orange colored fruits with dark orange pulp colour, very sweet with very less fibre.
6	72	Surya Prasad, seedling	1, 3, 4, 5, 6	Pulp colour is dark orange, suitable for table purpose owing to very less fibre.

^{*1-} Fruit weight (>200.00g), 2**- Fruit colour (>6), 3- T.S.S. (>19.00 Brix), 4- Pulp content (>60.00%), 5. Seed content (<20.00%), 6- Rind content (<20.00%)

^{**} Fruit colour- I- Green, 2- Light green, 3- Green yellow, 4- Light yellow/yellow green, 5- Yellow, 6- Dark yellow, 7- Yellow orange, 8- Orange, 9- Dark orange, 10- Red green, 11- Red yellow, 12- Red orange, 13- Red

in the farmer's field. Conservation of seedling mango varieties also ensures conservation of a diversity associated with non-commercial varieties. The lesser known varieties like Chinia, Ghivia, Madhukupia, Bhadaiya, Kuneila, SafedMalda, LalMalda, SonaMalda, HazipurMalda etc., were evolved through seedling selection by the farmers and these varieties are being cultivated by the farmers on a very limited scale.

Cluster analysis: In order to see the relationship, percentage similarities and display position of clones used in this study, a dendrogram was constructed from the pairwise distance matrices

(Fig. 2). A dendrogram generated based on morpho-physico-chemical data grouped all the 74 clones of mango into one major cluster A and one out group B at similarity value of 0.73. Major cluster A comprised most of the studied clones and further sub-divided into three sub-clusters as A1, A2 and A3 cluster at 63% similarity value. All the clones except clone no 14 were present in major cluster A. Cluster A1 shared 82.5%, A2 9.45% and A3 6.75% clones. Cluster A1 further subdivided into cluster I to VIII, cluster A2 from IX to X and cluster A3 into XI whereas, out-group B comprised only clone no 14 showing as cluster XII (Table 4).

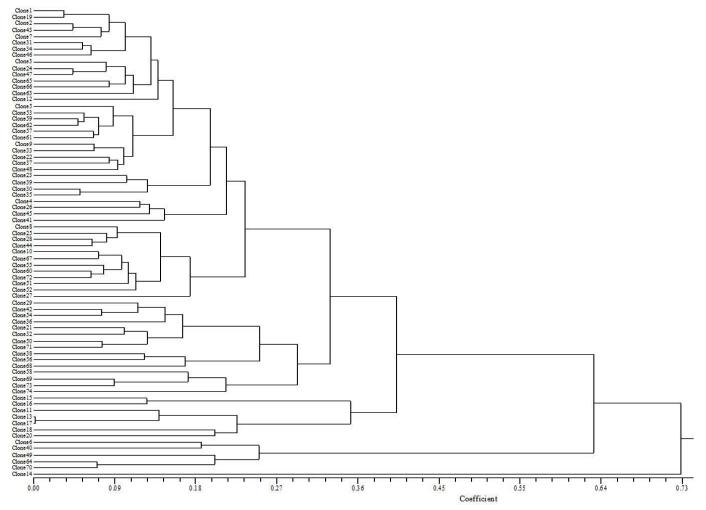


Figure 2. Dendrogram of 74 indigenous seedling clones of mango based on morpho-physico-chemical traits using the UPGMA method.

Table 4. Cluster details of 74 clones using various morpho-physico-chemical parameters.

Cluster name	Sub-	Total no	Percent clones	Clone number
and percent	cluster	of	in sub-cluster	
clone		clones		
A1 (82.5)	I	15	20.27	1,19,2,43,7,31,34,46,3,24,47,65,66,63,12
	II	11	14.86	5,53,59,62,57,61,9,33,22,37,48
	III	4	5.40	23,39,30,35
	IV	4	5.40	4,26,45,41
	V	12	16.21	8,25,28,44,10,67,55,60,72,51,52,27
	VI	8	10.81	29,42,54,36,21,32,50,71
	VII	3	4.05	38,56,68
	VIII	4	5.50	58,69,73,74
A2(9.45)	IX	2	2.70	15,16
	X	5	6.75	11,13,17,18,20
A3(6.75)	XI	5	6.75	6,40,49,64,70
B(1.35)	XII	1	1.35	14

Principal Component Analysis (PCA) for morpho-physicochemical traits: The PCA was used to determine the extent of the variation and percentage similarity within accessions. Eigen-values and factor scores were obtained from PCA, which were used to determine the relative discriminative power of the axis and their associated characters. In principal component analysis, one of the most commonly used criteria for solving the number-ofcomponents problem is the eigenvalue-one criterion, also known as the Kaiser criterion 34. With this approach, any component with an Eigen-value greater than 1.00 should be retained and interpreted. Cumulative percent of variance accounted for the percent of variance accounted for by the present component, as well as all preceding components. The result of the PCA showed that nine of the thirteen Principal Component Axis (PCA) had Eigen-values greater than one and all together accounted for over 99% of the total variability (Table 5). The first PCA (fruit color) accounted for 87.14% of the total variation while the second PCA 2 (fruit weight) accounted for 6.78% of the total variation. The cumulative percent of variance varied from 87.14% to 99.99% for the PCA which had Eigen-value more than 1. The relative discriminating capacity of the PCA is shown by their Eigen-values. The PCA 1 had the highest discriminating power as revealed by its highest Eigen-value of 17315.20 followed by PCA 2 with Eigen-value of 1347.62. The characters contributed the maximum to the divergence should be

Table 5. Principal Component Analysis among seventy-four clones of mango showing the correlations of the first nine principal components with the variables observed in mango clones.

Principal	Fruit traits	Eigen-value	%Variance	% Cumulative
component				variance
PC1	Fruit color	17315.20	87.14	87.14
PC2	Fruit weight (g)	1347.62	6.78	93.93
PC3	Fruit length (cm)	788.89	3.97	97.90
PC4	Fruit width (cm)	213.58	1.07	98.97
PC5	Fruit length: Fruit width	158.44	0.80	99.77
PC6	TSS (°Brix)	25.17	0.13	99.89
PC7	Seed weight (g)	9.46	0.05	99.94
PC8	Seed (%)	7.99	0.04	99.98
PC9	Skin weight (g)	2.32	0.01	99.99

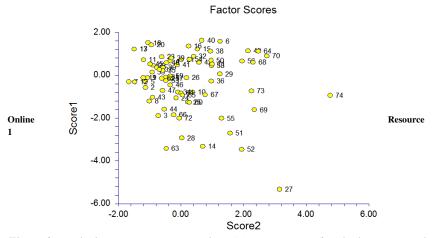


Figure 3. A principal components analysis (PCA) scatter plot of 74 indigenous seedling clones of mango using fourteen morpho-physico-chemical parameters.

given greater emphasis for selection in breeding 35. PCA has successfully found linear combinations of the different morphophysico-chemical parameters, which separate out different clusters of mango clones. The clones were classified into one major and three minor distinct cluster groups (Fig. 3). When we compared the cluster analysis (CA) and principal component analysis (PCA) graph then many similarities were found that both the analysis grouped the accession in one major cluster and other minor clusters. Clone no 13 and 17 showed 100% genetic similarity (Fig. 2) and PCA results also showed closeness of both the clones (Fig. 3). Moreover, clone no 14 presented as out group (Fig. 2) and also it has shown separately in Fig. 3. Cluster analysis revealed that all the six superior clone viz; 25,46,51,52,67 and 72 (Table 3) were part of major cluster A, if we see further categorization then we have found that except clone 46 all were part of subgroup V. Similarly PCA analysis indicated that majority of elite clones were part of major group except clone 51 and 52. Cluster analysis also showed the similarity with statistical parameters like clone no. 6, 18 and 40 showed fruit weight < 100 g and they formed cluster X and XI which were very close. Clone no. 27 was superior in terms of fruit weight (>500 g) and pulp % (> 80%), came with major 5 superior clones in cluster V in terms of parameter fruit colour, clone no 25 was the superior and it is also presented with other superior clones in cluster V.

Conclusions

Present study is interesting to explore the potential of existing variability in the seedling populations of mango and demonstrate the utility of morpho-taxonomic traits for the study of seedling variability along with the phylogenetic relationship within and among seedling populations of mango. The study points out that there is excellent scope for locating useful seedling diversity in mango, which may be the result of the cultivation of many commercial cultivars. These studies clearly showed that there is an existence of a great amount of variability among different seedling clones of mango, which can be exploited for the selection of elite genotypes in future after evaluating their performance. Finally, six clones, having the majority of desirable fruit characteristics were selected for further multiplication and detailed evaluation. Potentially from extant variability, researchers can identify many more mango cultivars based on consumer's preferences and the researchers, farmers and nurserymen can work together for the popularization of these varieties.

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Online Resource 1. Morpho-physico-chemical characters of 74 clones of mango.

Clone	Fruit colour	Fruit wt. (g)	Fruit length (cm)	Fruit width (cm)	L:B	TSS (⁰ Brix)	Seed wt. (g)	Seed (%)	Skin wt.	Skin (%)	Pulp wt.	% edible portion	TSS: acidity
1	5	220.2	9.5	6.92	1.372	17.56	31.4	14.308	61.2	28.018	128	56.6	23.41
2	6	256.0	9.9	7.05	1.406	12.75	45	17.578	59	23.114	152	59.368	17.00
3	1	356.8	10.3	8.76	1.178	14.38	43	11.978	84.6	23.938	229.2	64.082	27.70
4	6	150.2	7.9	6.232	1.272	14.5	26.6	18.092	20.4	13.788	102	64.084	30.72
5	1	234.2	10.8	6.44	1.686	15.2	51.4	21.908	45	19.328	137.8	58.758	12.66
6	9	89.2	6.6	5.28	1.258	19.08	29.8	33.37	18.6	20.914	40.8	45.818	74.53
7	1	237.2	7.5	6	1.27	11.94	40	17.32	63	27.042	134.2	55.632	8.29
8	9	283.2	9.5	7.8	1.238	13.6	37.6	13.302	54.8	19.358	219.2	70.25	12.50
9	1	181.6	9.1	6.22	1.47	16.6	37.2	20.654	38	20.868	106.2	58.436	24.41
10	4	262.2	8.8	7.732	1.14	15.6	39.2	14.956	37.8	14.42	184.4	64.546	44.31
11	1	161	8.2	6.16	1.334	17.58	49.4	30.916	39	24.358	72.6	44.726	16.15
12	9	227.8	8.8	5.5	1.614	10.32	26	11.428	51.6	22.71	150.6	66.05	9.08
13	1	116.2	7.3	5.36	1.38	14.16	32.6	28.28	34.2	29.718	54.6	44.324	12.46
14	3	274.2	8.1	6.832	1.27	16.18	56.4	21.102	68.2	25.736	561.2	54.994	21.98
15	1	126.8	7.8	5.32	1.482	16.42	40	31.602	41.6	32.566	45.2	35.832	64.14
16	5	109.4	6.9	5.1	1.358	18.9	34.2	31.552	30.2	27.772	45	40.672	53.69
17	1	116.2	7.3	5.36	1.38	14.16	32.6	28.28	34.2	29.718	54.6	44.124	12.46
18	5	98.2	6.6	5	1.296	16.96	34.4	34.876	29.2	30.224	34.6	35.214	23.04
19	5	223.0	11.0	6.62	1.67	14.16	33.2	14.844	64.4	30.596	125.2	54.442	21.85
20	1	103.2	7.6	4.88	1.556	20.46	24.8	24.016	34.8	33.814	43.6	42.166	28.41
21	1	152.2	7.3	6.24	1.17	15.7	30.6	20.196	32.6	21.39	89	58.414	44.60
22	1	178.8	8.6	6.58	1.104	19	41.6	22.556	45.6	25.734	91.6	50.51	25.00
23	1	148.6	7.7	5.88	1.31	16.52	39.6	26.932	38.8	26.33	70.2	46.738	32.26
24	5	288.2	9.6	7.632	1.262	17.668	40.332	14.11	58.068	20.396	190	65.668	36.80
25	13	290.4	11.0	6.7	1.65	12.5	37.5	12.982	37	12.776	220	75	36.76
26	10	211.4	8.4	6.58	1.282	18.38	31.4	14.964	37.2	17.658	144	68	43.76
27	1	585.4	13.5	9.18	1.474	14.48	47.2	8.146	55.4	9.57	484	82.6	88.50
28	11	417.2	10.2	8.7	1.178	12.65	44.5	10.66	49	11.744	318	76.5	25.81
29	1	207.8	9.6	6.6	1.448	14.02	33	15.99	53.4	25.282	122	63	77.88
30	1	186	9.4	6.54	1.438	11.26	32.6	17.35	56	30.868	100	53.8	37.53
31	1	218.2	9.4	7.02	1.338	12.66	35.2	16.144	55.8	25.848	128	58.4	36.17

Online Resource 1. Morpho-physico-chemical characters of 74 clones of mango.

Clone	Fruit colour	Fruit wt. (g)	Fruit length (cm)	Fruit width (cm)	L:B	TSS (⁰ Brix)	Seed wt. (g)	Seed (%)	Skin wt. (g)	Skin (%)	Pulp wt. (g)	% edible portion	TSS: acidity
32	4	137.2	7.7	6.04	1.292	16	27.2	20.202	28.2	19.234	84	60.4	53.33
33	1	200.8	9.2	6.42	1.446	13.12	36.6	18.654	49	24.846	114	55.6	24.29
34	2	273.8	10.7	7.32	1.474	14.34	45.8	16.654	71	26.108	164	59.8	44.81
35	2	199.8	9.6	6.46	1.492	13.1	38.2	19.12	57.2	28.852	102	50.8	36.38
36	5	234.8	11.2	6.68	1.68	11.68	50.8	22.096	46.2	20.164	138	57.8	64.88
37	4	193.6	9.7	6.3	1.542	12.34	51.6	26.76	40.8	21.08	104	53.4	25.71
38	4	119.4	7.2	5.82	1.238	16.36	21.6	18.15	26	21.96	72	59.8	68.15
39	2.2	149.4	8.2	5.88	1.406	14.46	32.8	21.8	42	28.242	78	52	41.31
40	1.8	83.4	6.1	4.88	1.304	15.32	21.2	25.424	21.2	26.412	40	47.8	63.83
41	1	164.4	8.7	6.2	1.412	13.46	17.4	10.56	35	21.438	112	68	42.06
42	5	167	7.8	6.06	1.268	16.08	30.6	18.554	36.6	22.152	90	56.6	59.55
43	1	292	11.7	7.46	1.568	14.8	45	15.388	66.8	23.034	178.8	61.14	22.28
44	1	313.2	10.3	7.62	1.358	13.88	36	12.206	37	12.352	242	76.2	16.92
45	4	163.8	7.8	6.14	1.278	14.68	28	17.236	32	19.596	104	63.4	18.82
46	10	246.6	10.1	7.1	1.424	19.12	31.6	12.872	66.8	27.102	148.2	60.232	40.50
47	5	259.6	9.9	7.1	1.398	20.48	32.4	12.446	54.4	20.932	172.8	66.624	27.82
48	3	166	9.2	6.3	1.464	20.8	41.4	24.936	33	19.908	91.6	55.154	30.58
49	4	118.4	7.3	5.62	1.278	24.4	23.4	19.73	24	20.424	71	59.848	95.77
50	3	153	8.2	5.9	1.394	22.04	35.2	22.962	23.8	15.582	94	61.458	62.61
51	9	400.8	9.8	7.8	1.266	20.14	59.8	14.93	35.2	7.648	305.8	76.43	57.21
52	3	477.2	11.6	8.28	1.412	23.34	84.2	17.584	71.8	14.994	321.2	67.422	72.98
53	2	233.2	9.4	6.6	1.434	21.88	51.6	18.088	48.4	20.746	133.2	57.164	29.72
54	12	155.4	7.5	5.5	1.376	22.18	33	21.236	39.8	25.63	82.6	53.134	52.81
55	4	360.00	9.7	8.2	1.204	19.18	77.2	21.558	36	10.06	246.8	68.384	54.49
56	7	155.2	7.6	5.62	1.368	22.98	30.8	19.958	27.6	17.994	96.8	62.052	88.38
57	9	222.4	8.5	6.56	1.302	17.78	59.4	26.67	33.8	15.242	129.2	58.086	27.43
58	9	187	9.7	6.3	1.544	22.8	61.4	32.806	38.8	20.656	86.8	46.536	64.77
59	6	214	10.0	6.68	1.492	22.12	51.6	23.902	39.4	18.19	123	57.91	30.66
60	4	299.4	10.5	7.22	1.47	21.06	62	20.712	28.4	9.442	209	69.846	32.22
61	6	280.8	10.0	7.4	1.352	20.22	71.6	25.452	49.4	17.466	159.8	57.082	36.10

Online Resource 1. Morpho-physico-chemical characters of 74 clones of mango.

Clone	Fruit colour	Fruit wt. (g)	Fruit length (cm)	Fruit width (cm)	L:B	TSS (⁰ Brix)	Seed wt. (g)	Seed (%)	Skin wt. (g)	Skin (%)	Pulp wt.	% edible portion	TSS: acidity
62	10	221.6	9.4	6.68	1.416	17.66	49.2	22.172	41.4	18.602	131	59.628	24.52
63	1	468	12.4	8.36	1.482	18.7	61.4	13.114	83.4	17.816	323.2	69.07	21.25
64	6	129	7.2	5.82	1.248	25.4	34.4	26.032	32.2	24.936	62.4	48.436	105.83
65	9	284	10.7	7.3	1.47	18.86	53.8	18.87	56.2	19.726	174	61.402	40.64
66	4	352	12.2	7.24	1.696	23.36	68.6	19.47	57.2	16.216	226.2	64.314	26.54
67	5	269	10.1	7.2	1.41	20.58	50.4	18.668	25.6	9.416	193	71.918	46.77
68	9	159	8.4	6.06	1.394	19.84	41	25.236	15	8.824	103	65.71	90.18
69	8	354	10.3	7.88	1.322	24.34	118.8	33.532	47.4	13.368	187.8	53.1	82.69
70	8	146.6	7.8	6.22	1.256	25.66	38.4	26.158	35.2	23.942	73	49.9	111.56
71	4	163	8.1	5.84	1.4	22.58	33.8	20.632	20.8	12.682	108.4	66.686	61.02
72	4	357.4	10.7	8.44	1.296	23.82	65	18.178	44.8	12.526	247.6	69.298	25.34
73	7	274.6	9.7	7.26	1.342	23.74	89.6	32.59	29.4	10.678	155.6	56.734	81.86
74	9	303.6	11.0	7.74	1.422	23.68	101	33.254	48.4	15.886	154.2	50.86	148.00
C.D.	0.286	44.383	0.78	0.525	0.116	1.583	9.431	4.167	8.854	4.076	138.777	7.315	5.51
SE(m)	0.103	15.938	0.282	0.189	0.042	0.568	3.387	1.496	3.18	1.464	49.836	2.627	1.98
SE(d)	0.145	22.54	0.399	0.267	0.059	0.804	4.789	2.116	4.497	2.07	70.479	3.715	2.80
C.V.	5.011	15.685	6.876	6.348	6.715	7.215	17.226	16.214	16.414	15.856	76.272	10.002	10.00

Online Resource 2. Grouping of 74 mango clones for six major fruit traits.

Fruit	No. of Clones (Clone no.)
characteristics	
	1. Fruit weight (g)
<100	3(6, 18, 40)
100.01-200.00	30 (4, 9, 11, 13, 15, 16, 17, 20, 21, 22, 23, 30, 32, 35, 37, 37, 39, 41, 42, 45, 48, 49, 50, 54, 56, 58, 64, 68, 70, 71)
200.01-300.00	29 (1, 2, 5, 7, 8, 10, 12, 14, 19, 24, 25, 26, 29, 31, 33, 34, 36, 43, 46, 47, 53, 57, 59, 60, 61, 62, 65, 67, 73) 7 (3, 44, 55, 66, 69, 72, 74)
300.01-400.00	4(28, 51, 52, 63)
400.01-500.00	1 (27)
>500.01	
	2. Fruit colour
<3.00	30 (3, 5, 7, 9, 11, 13, 14, 15, 17, 20, 21, 22, 23, 27, 29, 30, 31, 33, 34, 35, 39, 40, 41, 43, 44, 48, 50, 52, 53 63)
3.01-6.00	25 (1, 2, 4, 10, 16, 18, 19, 24, 32, 36, 37, 38, 42, 45, 47, 49, 55, 59, 60, 61, 64, 66, 67, 71, 72) 13 (6, 8, 12, 51, 56, 57, 58, 65, 68, 69, 70, 73, 74)
6.01-9.00	5 (26, 28, 46, 54, 62)
9.01-12.00	1 (25)
>12.01	
	3. T.S.S. (⁰ Brix)
<15.00	25 (2, 3, 4, 7,8, 12, 13, 17, 19, 25, 27, 28, 29, 30, 31, 33, 34, 35, 36, 37, 39, 41, 43, 44, 45)
	12 (5, 9, 10, 14, 15, 18, 21, 23, 32,38, 40, 42)
15.01-17.00	10 (1, 11, 16, 22, 24, 26, 57, 62, 63, 65)
17.01-19.00	10 (6, 20, 46, 47, 48, 51, 55, 61, 67, 68)
19.01-21.00	8 (50, 53, 54, 56, 58, 59, 60, 71)
21.01-23.00	9 (49, 52, 64, 66, 69, 70, 72, 73, 74)
>23.01	
	4. Pulp (%)
<40.00	2 (15, 18)
40.01-50.00	11 (6, 11, 13, 16, 17, 20, 23, 40, 58, 64, 70)
50.01-60.00	30 (1, 2, 5, 7, 9, 14, 19, 21, 22, 30, 31, 33, 34, 35, 36, 37, 38, 39, 42, 48, 49, 53, 54, 57, 59, 61, 62, 69, 73, 74)
60.01-70.00	24 (3, 4, 10, 12, 24, 26, 29, 32, 41, 43, 45, 46, 47, 50, 52, 55, 56, 60, 63, 65, 66, 68, 71, 72,) 6 (8, 25, 28, 44, 51, 67)
70.01-80.00	1 (27)
>80.01	
	5. Seed (%)
<10.00	1 (27)
10.01-20.00	37 (1, 2, 3, 4, 7, 8, 10, 12, 19, 24, 25, 26, 28, 29, 30, 31, 33, 34, 35, 38, 41, 42, 43, 44, 45, 46, 47, 49, 51, 52, 53, 56, 63, 65, 66, 67, 72)
20.01-30.00	27 (5, 9, 13, 14, 17, 20, 21, 22, 23, 32, 36, 37, 39, 40, 48, 50, 54, 55, 57, 59, 60, 61, 62, 64, 68, 70, 71) 9 (6, 11, 15, 16, 18, 58, 69, 73, 74)
30.01-40.00 >40.01	
	6. Rind (%)
<10.00	5 (27, 51, 60, 67, 68)
10.01-15.00	12 (4, 10, 25, 28, 44, 52, 55, 59, 69, 71, 72, 73)
15.01-20.00	15 (5, 8, 26, 32, 45, 48, 50, 56, 57, 61, 62, 63, 65, 66, 74)
20.01-25.00	21 (2, 3, 6, 9, 11, 12, 21, 24, 33, 36, 37, 38, 41, 42, 43, 47, 49, 53, 58, 64, 70)
25.01-30.00	16 (1, 7, 13, 14, 16, 17, 22, 23, 29, 31, 34, 35, 39, 40, 46, 54)
>30.01	5 (15, 18, 19, 20, 30)