# Assessment of Genetic Diversity in Morphological Traits of Mango Genotypes Using D² Statistics

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***Authors' contributions***

*This work was carried out in collaboration among all authors. Authors SSD and KK designed the study, performed the statistical analysis, wrote the protocol, and wrote the first draft of the manuscript. Authors SSD,KK, DS and DL managed the analyses of the study. Authors KK, DKD and DL managed the literature searches. All authors read and approved the final manuscript.*

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## ABSTRACT

An experiment was conducted during 2018-2020 to study the genetic diversity in 24 morphological traits using D² statistics in mango genotypes of eastern tropical region of India. Present study reveals that the clustering pattern based on D² statistics grouped 40 genotypes of mango into 7 clusters, out of which cluster VI (7397.45) shows the highest intracluster value followed by cluster III (5346.99) and cluster V (4130.4), indicating considerable genetic divergence among the accessions of this cluster. While maximum inter- cluster distance was observed between the cluster VI and VII (300180) followed by cluster II and VI (289267.7) and cluster I and VI (214380.5) indicated that the accessions belonging to these groups were genetically most diverse and can be used as a parent in hybridization programme. Wide range of genetic diversity observed among cluster VI and cluster VII, can either be utilized for breeding programmes for genetic improvement in mango or directly adopted as a variety. Fruit yield exhibited significant contribution towards the genetic divergence (60.77%) followed by fruit weight (26.79%), stone percentage (4.74%), peel percentage (2.31%) and pulp percentage (2.05%).

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## 1. INTRODUCTION

Mango *(Mangifera indica* L.) is one of the ancient fruits of India, and its cultivation dates back to 4000 years [1]. The genus *Mangifera* originated from the Indo-Burma region [2,3]. The primary centre of origin is Myanmar (Burma)-Siam-Indochina or the Malay Archipelago and the secondary centre in the Sunda island (Java, Sumatra, Borneo)-the Philippines and Celebes-Banda-Timor group [4]. It is considered the "King of fruits" due to consumers' preference, production scale, exquisite flavour, savoury taste, appealing colour, and high nutritive value. The genus *Mangifera* comprises about 133 species, out of which only ten species have reported as valid (The plant list, 2013). Being a centre of diversity, India is blessed with more than 1000 cultivars originating as chance seedlings. Although India is home to mango, the exploitation of variability in the local germplasm is still lacking. Local mango germplasm, which are the natural heritage of India are under the threat of genetic erosion due to the gradual replacement of traditional local mango genotypes with commercial mango cultivars and high yielding cultivars. Some of the local genotypes possess highly nutritional value and thrive well in adverse climate, but due to anthropogenic effect, these valuable resources are on the verge of extinction. Eastern region of India is bestowed with diverse agroclimatic conditions and rich mango diversity, the huge genetic diversity in these areas has not been thoroughly exploited either by using them directly through selection or indirectly by using them as parents in mango breeding. Therefore, in the present study an attempt was made to study the divergence among local mango germplasm of Eastern India. Genetic diversity studies are essential because the selection of individual plants is solely dependent on variability. Increased diversity will improve opportunities to improve the economic characteristics of the resulting offspring. Diversity studies are an essential step and prerequisite in plant breeding [5].

Therefore, before initiating any breeding programme, the extent of phenotypic/morphological variability present must be assessed so that the breeding programme could yield the desired results. To exploit the available variability present in the genetic material in the form of some specific groups or classes, the divergence studies based upon some desirable characters is of utmost significance. In light of the above, the present study was carried out to estimate the genetic divergence in twentyfour morphological characters of mango genotypes of eastern tropical region of India using $D^2$ statistics to assess the variability present among the mango genotypes. The study will help in identification of parents possessing high genetic divergence which can be used in the breeding program.

## 2. MATERIALS AND METHODS

### 2.1 Experimental Location

The experiment was conducted at Central Horticulture Experiment Station (ICAR-IIHR), Aiginia, Bhubaneswar from 2018-2020. The experimental site is located at an altitude of 45 m above mean sea level, latitude 20° 27′N and longitude 85° 40′E.

### 2.2 Experimental Material

The experimental materials for present investigation were comprised of 40 local mango germplasm collected from different parts of Eastern India. The list of germplasm with indigenous collection (IC) number is given in Table 1. All the germplasm were provided with standard agronomic practices such as nutrient and pest management. The field experiments on various morphological characters were carried out under Randomized Block Design (RBD) with three replications. At the beginning of experiment, the age of varieties/accessions was 12-15 years.

### 2.3 Experimental Data

The observation was recorded on three randomly selected plants per replication for each accession on 24 morphological characters, i.e., leaf length (mm), leaf width (mm), petiole length (mm), inflorescence length (mm), inflorescence width (mm), sex ratio, fruit weight (g), fruit length (mm), fruit width (mm), peel weight (g), peel thickness (mm), stone weight (g), stone length (mm), stone width (mm), pulp weight (g), pulp to stone ratio, length of stone fibre (mm), seed weight (g), seed length (mm), seed width (mm), pulp percentage (%), peel percentage (%), stone percentage (%), yield (Kg/plant). Measurement on leaf length, leaf width, petiole length, inflorescence length, inflorescence width was performed in ten leaves

from each treatment with the help of measuring scale; however, for measuring fruit length, fruit width, peel thickness, stone length, stone width, length of the stone fibre, seed length, seed width five fruits from each replication were selected and measured by measuring scale. Peel weight, stone weight, seed weight was measured with weighing balance. The ratio of hermaphrodite flowers to the male flowers from the tagged panicle was observed for measuring the sex ratio. The yield per plant has been recorded over the study period. The data were calculated by following formulas.

1. Pulp per centage (%) = $\frac{\text{Pulp weight}}{\text{Fruit weight}}$ x 100

2. Stone percentage (%) = $\frac{\text{Stone weight}}{\text{Fruit weight}}$ x 100

3. Peel percentage (%) = $\frac{\text{Peel weight}}{\text{Fruit weight}}$ x 100

Analysis of variance was performed to test the significance of difference among the genotypes for the morphological characters studied, as suggested by Panse and Sukhatme (1985). The morphological quantitative data collected were subjected to multivariate analysis utilizing Mahalanobis $D^2$ statistic as suggested by Mahalanobis [6] and Rao [7]. Accessions were grouped into various clusters following Tocher's method as suggested by Rao [7]. Average intra-cluster $D^2 = \Sigma\ Di^2/n$

where, $\Sigma\ D_i^2$ = sum of all distances between all possible combinations (n) of the genotypes included in the cluster.

Average inter-cluster distance $D^2 = \Sigma\ D_{ij}2/n_i.....n_j$

where, $\Sigma\ D_{ij}^2$ = sum of all distances between all possible combinations $(n_i.n_j)$ of the genotypes between the clusters ($n_i$ = number of genotypes in ith cluster, $n_j$ = number of genotypes in jth cluster). Using $D^2$ values, different genotypes were grouped into various clusters following Ward's minimum variance method. The average $D^2$ value of all possible combination of genotypes in one cluster with those in other was computed and its square root was used to represent the "Statistical distance" between two clusters.

The contribution of individual character to the total divergence and cluster means of mango genotypes falling under different clusters were also calculated by the method employed by Singh and Choudhary [8]. Percentage contribution of each character was calculated as under:

$$\text{Percentage contribution of X character} = \frac{N(X) \times 100}{n(n-1)/2}$$

Where, N (X) = number of genotypic combinations which were ranked for character X out of the total genotypic combinations of n (n-1)/2; n(n-1)/2 = total possible genotypic combinations among 'n' number of genotypes.

**Table 1. Accession number and indigenous collection number of mango germplasm**

| Sl. No. | Accession No. | IC No. | Sl. No. | Accession No. | IC No. |
|---|---|---|---|---|---|
| 1 | IIHR-B-M-2 | 0598378 | 21 | IIHR-B-M-31 | 0598399 |
| 2 | IIHR-B-M-3 | 0598379 | 22 | IIHR-B-M-33 | 0598400 |
| 3 | IIHR-B-M-4 | 0598380 | 23 | IIHR-B-M-34 | 0598401 |
| 4 | IIHR-B-M-5 | 0598381 | 24 | IIHR-B-M-35 | 0598402 |
| 5 | IIHR-B-M-7 | 0598382 | 25 | IIHR-B-M-36 | 0598403 |
| 6 | IIHR-B-M-9 | 0598383 | 26 | IIHR-B-M-37 | 0598404 |
| 7 | IIHR-B-M-10 | 0598384 | 27 | IIHR-B-M-39 | 0598405 |
| 8 | IIHR-B-M-11 | 0598385 | 28 | IIHR-B-M-41 | 0598406 |
| 9 | IIHR-B-M-12 | 0598386 | 29 | IIHR-B-M-43 | 0598407 |
| 10 | IIHR-B-M-13 | 0598387 | 30 | IIHR-B-M-45 | 0598408 |
| 11 | IIHR-B-M-14 | 0598388 | 31 | IIHR-B-M-48 | 0598409 |
| 12 | IIHR-B-M-15 | 0598389 | 32 | IIHR-B-M-49 | 0598410 |
| 13 | IIHR-B-M-18 | 0598390 | 33 | IIHR-B-M-50 | 0598411 |
| 14 | IIHR-B-M-19 | 0598391 | 34 | IIHR-B-M-51 | 0598412 |
| 15 | IIHR-B-M-20 | 0598392 | 35 | IIHR-B-M-54 | 0598413 |
| 16 | IIHR-B-M-21 | 0598393 | 36 | IIHR-B-M-56 | 0598414 |
| 17 | IIHR-B-M-23 | 0598394 | 37 | IIHR-B-M-58 | 0598415 |
| 18 | IIHR-B-M-25 | 0598395 | 38 | IIHR-B-M-60 | 0598416 |
| 19 | IIHR-B-M-26 | 0598396 | 39 | IIHR-B-M-61 | 0598417 |
| 20 | IIHR-B-M-28 | 0598397 | 40 | IIHR-B-M-68 | 0598418 |

## 3. RESULTS AND DISCUSSION

### 3.1 Genetic Divergence Using Cluster Analysis (Tocher's Method)

On basis of morphological observations, the genetic diversity of 40 mango genotypes was estimated. The Mahalanobis $D^2$ statistics was computed for all possible 780 pairs of mango genotypes under study. The variability of morphological characters in leaf, inflorescence, fruit and yield traits of mango genotypes were presented in Table 2 and Table 3 respectively. On the basis of $D^2$ values, forty accessions were grouped into seven clusters. (Table 4 and Fig. 1), indicating adequate genetic diversity for selecting superior and diverse parents which can be exploited for breeding program. The cluster divergence was proved by the high inter-cluster and low intracluster $D^2$ values. Forty mango germplasm was grouped into seven distinct clusters using the Ward's method (Table 4 in such a manner that the average intra-cluster $D^2$ values should be less than the average inter-cluster $D^2$ values. The distribution of 40 genotypes into seven clusters was illustrated in Fig. 2. The perusal of data (Table 5) depicted that clusters I had the maximum number of accessions (14) followed by cluster II (8), cluster V (7), cluster III (6), cluster VI (3) and cluster IV and VII are solitary consisting of only one accessions each. Majumder et al., [9] grouped 60 diverse mango genotypes into 8 clusters based on morphological traits. Dinesh et al. [10] attempted to study the genetic diversity in some indigenous mango varieties of seedling origin and carried out evaluation of morphological traits in the Chittoor area of Andhra Pradesh in India. Himabindu et al., [11] also grouped 34 mango cultivars into 6 clusters.

From the clustering pattern of the present study, it was observed that the accessions were collected from same geographical region i.e., from Eastern India, but these accessions were distributed into different clusters, indicating that accessions with same geographic origin could have under gone change for different characters under selection. This could be due to distribution of different gene constellations within a geographical region or due to differences in adaptation, selection criteria, selection pressure and environmental conditions or may be due to factors like heterogeneity, genetic architecture of the populations and developmental traits. This finding is in conformity with the findings of Murty & Arunachalam [12]; Pawar et al. [13].

The divergence within the cluster (intra cluster distance) indicates the divergence among the accessions falling in the same cluster. On the other hand, inter cluster divergence suggests the distance (divergence) between the accession of different clusters. The intra and inter cluster $D^2$ values among 40 accessions presented in Table 3 and Fig. 2 revealed that cluster IV and VII showed minimum intra-cluster $D^2$ value (0) followed by cluster II (2430.91), whereas, maximum intra-cluster $D^2$ value (7397.45) was shown by cluster VI followed by cluster III (5346.99) and cluster V (4130.4), indicating considerable genetic divergence among the accessions of this cluster and was due to both natural and artificial selection forces among the accessions [14]. Minimum inter-cluster $D^2$ value was observed between the cluster IV and V (3985.33) followed by cluster I and IV (5996.85) indicated close relationship among the accessions. The selection of parents from genetically close clusters may be due to narrow genetic base and inbreeding depression (Singh and Gupta, 1968). Maximum inter-cluster $D^2$ value was observed between the cluster VI and VII (300180) followed by cluster II and VI (289267.7), cluster I and VI (214380.5), cluster I and VII (21395.64) indicated that the accessions belonging to these groups were genetically most diverse and can be used as a parent in hybridization programme. This type of hybridization would be useful for obtaining transgressive segregants [15]. The result of the present study was in line with the findings of Barhate et al., [16]; Barholia & Yadav [17]; Indian et al., [18].

### 3.2 Cluster Means

The cluster means for 24 morphological characters under study revealed considerable differences between the groups (Table 4). Cluster I was characterized with minimum length of stone fibre (9.72 mm). The minimum fruit weight (109.21 g), stone weight (29.61 g), stone width (36.11 mm), pulp weight (56.22 g), seed weight (3.36 g), seed width (18.42 mm) was observed in cluster II. The maximum leaf length (24.39 mm), leaf width (5.92 mm), peel thickness (1.83 mm), pulp to stone ratio (7.45) and pulp percentage (77.33%) and minimum inflorescence length (21.45 mm) and stone percentage (11.1%) was found in cluster III. The highest mean value for inflorescence length (27.63 mm), inflorescence width (15.43 mm) sex ratio (1.48) and lowest value for leaf length (13.7 mm), leaf width (4.1 mm), petiole length (1.3 mm), Peel

weight (20.8 g), stone length (63.81 mm), seed length (37.21 mm), peel percentage (10.17 %), yield (13.2 Kg/Plant) was observed in cluster IV. Cluster V contain neither the maximum nor minimum value for any character. Cluster VI was characterized with only maximum value for petiole length (3.08 mm), fruit weight (516.57 g), fruit length (133.42 mm), fruit width (90.74 mm), peel weight (61.18 g), stone length (119.84 mm), stone width (50.67 mm), Pulp weight (386.06 g), seed width (27.64 mm). Cluster VII was characterized by maximum value for stone

weight (69.73 g), length of stone fibre (42.11 mm), seed weight (11.8 g), seed length (61.41 mm), peel percentage (34.25%), stone percentage (53.76%), yield (35.2 Kg/Plant) and minimum value for inflorescence width (10.8 mm), sex ratio (0.09), fruit length (78.61 mm), fruit width (57.39 mm), peel thickness (0.95 mm), pulp to stone ratio (0.22), pulp percentage (11.99%). Manchekar et al. [19]; Shazia et al. [20] reported similar observations in their experiment.

**Table 2. Variability on leaf and inflorescence/flowering traits among mango genotypes**

| SI. No. | Germplasm accession no. | Leaf characters | | | Inflorescence and flowering characters | | |
|---|---|---|---|---|---|---|---|
| | | Leaf length (cm) | Leaf width (cm) | Petiole length (cm) | Inflorescence length (cm) | Inflorescence width (cm) | Sex ratio |
| 1 | IIHR-B-M-2 | 22.60 | 5.30 | 2.90 | 28.40 | 12.83 | 2.88 |
| 2 | IIHR-B-M-3 | 20.30 | 5.70 | 4.20 | 26.13 | 10.60 | 1.58 |
| 3 | IIHR-B-M-4 | 18.20 | 4.80 | 2.30 | 23.53 | 12.16 | 0.26 |
| 4 | IIHR-B-M-5 | 15.20 | 4.30 | 1.80 | 24.53 | 9.06 | 0.44 |
| 5 | IIHR-B-M-7 | 17.10 | 4.40 | 1.90 | 23.76 | 14.16 | 1.42 |
| 6 | IIHR-B-M-9 | 19.50 | 5.30 | 2.90 | 18.90 | 10.20 | 1.73 |
| 7 | IIHR-B-M-10 | 28.50 | 7.40 | 3.00 | 29.13 | 17.70 | 0.07 |
| 8 | IIHR-B-M-11 | 13.70 | 4.10 | 1.30 | 27.63 | 15.43 | 1.48 |
| 9 | IIHR-B-M-12 | 17.90 | 5.20 | 3.60 | 19.26 | 10.26 | 0.14 |
| 10 | IIHR-B-M-13 | 18.80 | 5.60 | 2.60 | 23.73 | 10.80 | 0.09 |
| 11 | IIHR-B-M-14 | 16.00 | 3.40 | 1.60 | 23.33 | 13.65 | 0.20 |
| 12 | IIHR-B-M-15 | 28.60 | 10.00 | 2.90 | 15.93 | 10.73 | 0.35 |
| 13 | IIHR-B-M-18 | 18.00 | 5.00 | 4.00 | 27.90 | 11.86 | 0.37 |
| 14 | IIHR-B-M-19 | 23.90 | 6.90 | 2.40 | 21.50 | 10.16 | 0.15 |
| 15 | IIHR-B-M-20 | 20.60 | 5.80 | 2.50 | 24.35 | 9.75 | 0.15 |
| 16 | IIHR-B-M-21 | 13.50 | 3.70 | 2.00 | 25.03 | 11.06 | 0.05 |
| 17 | IIHR-B-M-23 | 19.45 | 5.00 | 2.20 | 24.00 | 16.42 | 0.13 |
| 18 | IIHR-B-M-25 | 22.00 | 6.90 | 2.40 | 29.40 | 15.60 | 0.38 |
| 19 | IIHR-B-M-26 | 21.50 | 6.15 | 2.90 | 29.28 | 11.15 | 0.13 |
| 20 | IIHR-B-M-28 | 18.15 | 5.25 | 1.65 | 29.28 | 11.15 | 0.13 |
| 21 | IIHR-B-M-31 | 24.20 | 5.30 | 2.46 | 33.16 | 18.16 | 0.35 |
| 22 | IIHR-B-M-33 | 26.10 | 6.20 | 3.65 | 32.45 | 12.35 | 0.49 |
| 23 | IIHR-B-M-34 | 16.70 | 4.10 | 1.50 | 21.60 | 10.50 | 0.04 |
| 24 | IIHR-B-M-35 | 19.10 | 5.00 | 3.70 | 29.06 | 15.36 | 0.44 |
| 25 | IIHR-B-M-36 | 15.70 | 4.10 | 1.90 | 20.80 | 10.70 | 0.33 |
| 26 | IIHR-B-M-37 | 25.60 | 6.00 | 2.00 | 26.93 | 14.22 | 0.47 |
| 27 | IIHR-B-M-39 | 27.30 | 6.50 | 3.40 | 21.42 | 17.85 | 0.77 |
| 28 | IIHR-B-M-41 | 37.60 | 8.90 | 1.70 | 26.60 | 13.46 | 0.04 |
| 29 | IIHR-B-M-43 | 23.55 | 6.15 | 1.95 | 17.56 | 13.80 | 0.46 |
| 30 | IIHR-B-M-45 | 16.50 | 4.80 | 1.80 | 25.46 | 12.16 | 0.73 |
| 31 | IIHR-B-M-48 | 18.35 | 5.20 | 2.50 | 17.53 | 9.78 | 0.02 |
| 32 | IIHR-B-M-49 | 26.90 | 7.60 | 4.80 | 36.1 | 18.6 | 0.29 |
| 33 | IIHR-B-M-50 | 19.40 | 4.30 | 2.30 | 18.75 | 8.30 | 0.28 |
| 34 | IIHR-B-M-51 | 21.50 | 7.60 | 1.70 | 20.76 | 12.63 | 0.63 |
| 35 | IIHR-B-M-54 | 22.35 | 6.60 | 3.15 | 21.86 | 12.93 | 0.31 |
| 36 | IIHR-B-M-56 | 25.60 | 6.00 | 2.75 | 28.76 | 17.86 | 0.33 |
| 37 | IIHR-B-M-58 | 18.30 | 4.50 | 2.10 | 23.16 | 11.30 | 0.18 |
| 38 | IIHR-B-M-60 | 22.70 | 5.40 | 2.50 | 23.85 | 14.28 | 0.31 |
| 39 | IIHR-B-M-61 | 22.35 | 4.80 | 1.55 | 19.53 | 15.48 | 0.05 |
| 40 | IIHR-B-M-68 | 19.30 | 4.30 | 1.90 | 16.10 | 14.15 | 0.80 |
| | Mean | 21.07 | 5.59 | 2.51 | 24.41 | 12.96 | 0.49 |
| | Maximum | 37.60 | 10.00 | 4.80 | 36.10 | 18.60 | 2.88 |

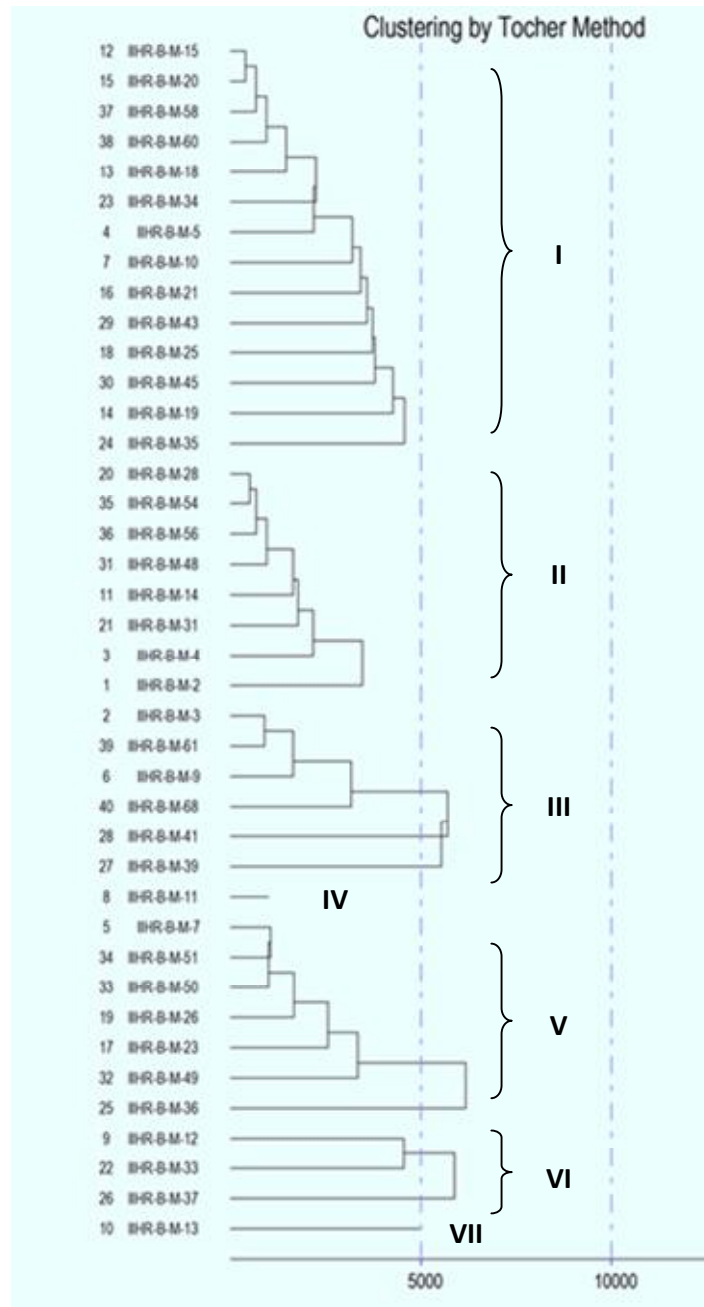| SI. No. | Germplasm accession no. | Leaf characters | | | Inflorescence and flowering characters | | |
|---|---|---|---|---|---|---|---|
| | | Leaf length (cm) | Leaf width (cm) | Petiole length (cm) | Inflorescence length (cm) | Inflorescence width (cm) | Sex ratio |
| | Minimum | 13.50 | 3.40 | 1.30 | 15.93 | 8.30 | 0.02 |
| | C.D. (p=0.05) | 3.265 | 1.388 | 0.723 | 3.148 | 2.174 | 0.075 |
| | SE(m) | 1.158 | 0.492 | 0.256 | 1.116 | 0.771 | 0.026 |
| | C.V. (%) | 9.518 | 15.25 | 17.688 | 7.919 | 10.296 | 9.402 |



**Fig. 1. Dendrogram showing the clusters of different mango varieties on the basis of morphological characteristics according to Mahalnobis' Euclidean distance**

**Table 3. Variability of fruit characters and yield among mango genotypes**

| Sl No | Germplasm accession no. | Fruit weight (g) | Fruit Length (mm) | Fruit width (mm) | Peel weight (g) | Peel thickness (mm) | Stone weight (g) | Stone length (mm) | Stone width (mm) | Pulp weight (g) | Pulp: Stone ratio | Length of stone fibre (mm) | Seed weight (g) | Seed length (mm) | Seed width (mm) | Pulp (%) | Peel (%) | Stone (%) | Yield (kg/tree) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | IIHR-B-M-2 | 103.90 | 79.92 | 51.95 | 36.46 | 1.34 | 34.87 | 101.19 | 36.93 | 32.58 | 0.93 | 8.85 | 1.80 | 45.48 | 17.24 | 31.36 | 35.09 | 33.56 | 45.3 |
| 2 | IIHR-B-M-3 | 301.10 | 94.39 | 82.27 | 20.21 | 1.44 | 36.72 | 71.54 | 39.31 | 244.17 | 6.65 | 19.15 | 7.50 | 46.72 | 23.31 | 81.09 | 6.71 | 12.20 | 17.4 |
| 3 | IIHR-B-M-4 | 122.70 | 92.95 | 56.03 | 29.42 | 1.50 | 36.30 | 87.22 | 55.91 | 56.97 | 1.57 | 21.20 | 6.70 | 51.26 | 22.82 | 46.43 | 23.98 | 29.59 | 27.8 |
| 4 | IIHR-B-M-5 | 175.25 | 77.54 | 66.63 | 30.53 | 2.18 | 23.12 | 63.51 | 41.24 | 121.60 | 5.26 | 7.15 | 2.60 | 41.06 | 19.99 | 69.39 | 17.42 | 13.19 | 31.4 |
| 5 | IIHR-B-M-7 | 235.30 | 98.87 | 74.23 | 38.51 | 3.09 | 23.70 | 78.15 | 39.67 | 173.09 | 7.30 | 12.60 | 3.70 | 39.73 | 23.61 | 73.56 | 16.37 | 10.07 | 26.5 |
| 6 | IIHR-B-M-9 | 313.15 | 103.35 | 78.29 | 47.88 | 1.97 | 39.94 | 81.01 | 39.14 | 225.33 | 5.64 | 24.07 | 4.00 | 46.11 | 24.54 | 71.95 | 15.29 | 12.76 | 23.1 |
| 7 | IIHR-B-M-10 | 179.40 | 94.92 | 59.80 | 22.80 | 0.84 | 26.42 | 87.07 | 34.28 | 130.18 | 4.93 | 5.35 | 2.20 | 42.84 | 19.02 | 72.57 | 12.71 | 14.73 | 45.6 |
| 8 | IIHR-B-M-11 | 204.50 | 78.96 | 70.76 | 20.80 | 1.10 | 31.61 | 63.81 | 40.90 | 152.09 | 4.81 | 16.40 | 4.10 | 37.21 | 23.60 | 74.37 | 10.17 | 15.46 | 13.2 |
| 9 | IIHR-B-M-12 | 529.80 | 126.44 | 91.98 | 64.85 | 1.24 | 72.48 | 110.79 | 47.94 | 392.48 | 5.42 | 27.97 | 6.10 | 51.62 | 28.11 | 74.08 | 12.24 | 13.68 | 13.3 |
| 10 | IIHR-B-M-13 | 129.70 | 78.61 | 57.39 | 44.42 | 0.95 | 69.73 | 111.40 | 46.42 | 15.55 | 0.22 | 42.11 | 11.80 | 61.41 | 27.38 | 11.99 | 34.25 | 53.76 | 35.2 |
| 11 | IIHR-B-M-14 | 115.30 | 73.91 | 55.70 | 21.39 | 0.65 | 32.66 | 74.77 | 35.78 | 61.25 | 1.88 | 9.05 | 3.20 | 40.01 | 24.84 | 53.12 | 18.55 | 28.33 | 50.4 |
| 12 | IIHR-B-M-15 | 151.30 | 87.46 | 56.67 | 15.81 | 0.53 | 27.11 | 73.30 | 33.78 | 108.38 | 4.00 | 10.86 | 6.30 | 47.57 | 17.18 | 71.63 | 10.45 | 17.92 | 15.3 |
| 13 | IIHR-B-M-18 | 140.50 | 71.68 | 58.30 | 22.30 | 1.08 | 38.60 | 69.86 | 46.57 | 79.60 | 2.06 | 10.37 | 7.30 | 40.09 | 27.32 | 56.65 | 15.87 | 27.47 | 25.4 |
| 14 | IIHR-B-M-19 | 188.70 | 79.96 | 70.67 | 11.21 | 1.27 | 32.42 | 63.16 | 39.97 | 145.07 | 4.47 | 5.28 | 8.30 | 51.83 | 25.24 | 76.88 | 5.94 | 17.18 | 19.2 |
| 15 | IIHR-B-M-20 | 148.70 | 83.54 | 57.19 | 15.51 | 0.69 | 24.02 | 70.93 | 35.29 | 109.17 | 4.54 | 6.82 | 2.20 | 35.05 | 16.39 | 73.42 | 10.43 | 16.16 | 15.3 |
| 16 | IIHR-B-M-21 | 162.90 | 70.52 | 62.41 | 22.91 | 1.25 | 18.00 | 54.69 | 32.55 | 121.99 | 6.78 | 0.20 | 2.90 | 32.66 | 15.73 | 74.89 | 14.06 | 11.05 | 64.3 |
| 17 | IIHR-B-M-23 | 202.90 | 93.94 | 60.75 | 20.70 | 0.75 | 28.62 | 80.85 | 31.22 | 153.58 | 5.37 | 18.03 | 9.90 | 56.47 | 23.18 | 75.69 | 10.20 | 14.10 | 38.7 |
| 18 | IIHR-B-M-25 | 177.40 | 86.54 | 53.92 | 23.01 | 0.34 | 56.32 | 78.89 | 41.09 | 98.07 | 1.74 | 13.31 | 15.75 | 61.10 | 29.41 | 55.28 | 12.97 | 31.75 | 41.3 |
| 19 | IIHR-B-M-26 | 261.00 | 90.31 | 72.10 | 50.98 | 1.10 | 37.02 | 72.39 | 33.05 | 173.00 | 4.67 | 19.47 | 16.30 | 57.11 | 24.18 | 66.28 | 19.53 | 14.18 | 33.3 |
| 20 | IIHR-B-M-28 | 103.50 | 73.40 | 55.35 | 21.21 | 1.73 | 21.61 | 63.21 | 32.92 | 60.68 | 2.81 | 12.00 | 4.40 | 39.38 | 17.57 | 58.63 | 20.49 | 20.88 | 14.6 |
| 21 | IIHR-B-M-31 | 122.70 | 90.89 | 40.90 | 19.41 | 1.52 | 32.63 | 82.04 | 28.99 | 70.65 | 2.17 | 24.75 | 2.60 | 45.16 | 16.45 | 57.58 | 15.82 | 26.60 | 33.8 |
| 22 | IIHR-B-M-33 | 500.30 | 120.55 | 92.31 | 42.51 | 1.68 | 94.40 | 109.20 | 59.35 | 363.40 | 3.85 | 40.26 | 20.60 | 82.36 | 32.45 | 72.64 | 8.50 | 18.87 | 21.6 |
| 23 | IIHR-B-M-34 | 173.50 | 98.58 | 62.86 | 21.42 | 1.32 | 32.60 | 74.11 | 38.01 | 119.48 | 3.66 | 5.46 | 12.50 | 48.53 | 18.64 | 68.86 | 12.35 | 18.79 | 20.8 |
| 24 | IIHR-B-M-35 | 189.20 | 95.08 | 65.24 | 23.62 | 1.64 | 59.87 | 85.18 | 43.02 | 105.71 | 1.77 | 22.18 | 14.00 | 65.77 | 25.07 | 55.87 | 12.48 | 31.65 | 19.4 |
| 25 | IIHR-B-M-36 | 181.50 | 112.04 | 58.93 | 20.70 | 0.47 | 33.55 | 100.87 | 36.28 | 127.26 | 3.79 | 17.02 | 4.40 | 86.89 | 25.42 | 70.11 | 11.40 | 18.48 | 42.3 |
| 26 | IIHR-B-M-37 | 519.60 | 153.27 | 87.92 | 76.19 | 1.15 | 41.11 | 139.54 | 44.72 | 402.30 | 9.79 | 24.04 | 3.20 | 40.12 | 22.35 | 77.43 | 14.66 | 7.91 | 59.5 |
| 27 | IIHR-B-M-39 | 376.00 | 106.82 | 84.12 | 57.94 | 2.70 | 33.81 | 77.03 | 42.56 | 284.25 | 8.41 | 10.62 | 14.20 | 60.52 | 28.96 | 75.60 | 15.41 | 8.99 | 35.4 |
| 28 | IIHR-B-M-41 | 369.75 | 104.45 | 78.17 | 41.41 | 0.44 | 56.45 | 84.56 | 44.27 | 271.89 | 4.82 | 26.58 | 23.90 | 64.53 | 32.20 | 73.53 | 11.20 | 15.27 | 13.6 |
| 29 | IIHR-B-M-43 | 184.00 | 80.00 | 58.97 | 23.00 | 0.89 | 27.02 | 64.16 | 29.84 | 133.98 | 4.96 | 22.10 | 11.30 | 52.47 | 20.63 | 72.82 | 12.50 | 14.68 | 56.7 |
| 30 | IIHR-B-M-45 | 161.00 | 78.54 | 63.14 | 30.84 | 1.10 | 51.11 | 61.10 | 37.72 | 79.05 | 1.55 | 5.43 | 11.70 | 49.49 | 27.03 | 49.10 | 19.16 | 31.75 | 51.2 |
| 31 | IIHR-B-M-48 | 115.35 | 73.94 | 50.15 | 23.02 | 2.10 | 36.05 | 70.36 | 35.54 | 56.28 | 1.56 | 19.07 | 4.10 | 41.58 | 17.30 | 48.79 | 19.96 | 31.25 | 19.55 |
| 32 | IIHR-B-M-49 | 214.45 | 81.54 | 67.65 | 35.98 | 1.63 | 47.03 | 70.12 | 40.77 | 131.44 | 2.79 | 22.43 | 12.40 | 55.88 | 24.69 | 61.29 | 16.78 | 21.93 | 40.5 |
| 33 | IIHR-B-M-50 | 243.80 | 99.92 | 65.89 | 35.18 | 1.57 | 35.18 | 84.92 | 44.00 | 173.44 | 4.93 | 13.08 | 24.00 | 69.12 | 27.76 | 71.14 | 14.43 | 14.43 | 21.3 |
| 34 | IIHR-B-M-51 | 224.90 | 99.96 | 69.41 | 20.24 | 0.63 | 32.31 | 90.22 | 42.16 | 172.34 | 5.33 | 13.68 | 9.60 | 52.65 | 26.91 | 76.63 | 9.00 | 14.37 | 23.6 |
| 35 | IIHR-B-M-54 | 92.20 | 69.32 | 49.57 | 15.21 | 1.72 | 23.40 | 55.21 | 35.17 | 53.58 | 2.29 | 6.31 | 3.00 | 37.88 | 17.11 | 58.12 | 16.50 | 25.38 | 18.9 |
| 36 | IIHR-B-M-56 | 98.00 | 86.73 | 48.51 | 20.94 | 1.35 | 19.33 | 79.70 | 27.67 | 57.73 | 2.99 | 12.57 | 1.07 | 36.83 | 14.03 | 58.91 | 21.37 | 19.72 | 11.2 |

| Sl No | Germplasm accession no. | Fruit weight (g) | Fruit Length (mm) | Fruit width (mm) | Peel weight (g) | Peel thickness (mm) | Stone weight (g) | Stone length (mm) | Stone width (mm) | Pulp weight (g) | Pulp: Stone ratio | Length of stone fibre (mm) | Seed weight (g) | Seed length (mm) | Seed width (mm) | Pulp (%) | Peel (%) | Stone (%) | Yield (kg/tree) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 37 | IIHR-B-M-58 | 145.11 | 78.02 | 63.09 | 29.08 | 1.61 | 22.02 | 66.40 | 37.09 | 94.01 | 4.27 | 12.85 | 3.00 | 43.49 | 20.06 | 64.79 | 20.04 | 15.17 | 24.5 |
| 38 | IIHR-B-M-60 | 124.30 | 79.68 | 52.67 | 14.71 | 0.83 | 21.32 | 68.01 | 29.31 | 88.27 | 4.14 | 8.71 | 4.60 | 41.74 | 20.24 | 71.01 | 11.83 | 17.15 | 20.6 |
| 39 | IIHR-B-M-61 | 303.50 | 96.96 | 80.72 | 14.20 | 1.60 | 31.52 | 73.70 | 40.72 | 257.78 | 8.18 | 30.11 | 11.30 | 62.22 | 31.42 | 84.94 | 4.68 | 10.38 | 26.1 |
| 40 | IIHR-B-M-68 | 336.40 | 94.23 | 84.10 | 54.26 | 2.80 | 23.51 | 69.79 | 39.79 | 258.63 | 11.00 | 5.96 | 1.20 | 29.27 | 14.10 | 76.88 | 16.13 | 6.99 | 38.6 |
| | Mean | 215.564 | 90.94 | 65.42 | 30.02 | 1.35 | 36.64 | 79.10 | 39.02 | 148.91 | 4.33 | 15.84 | 7.99 | 49.78 | 22.84 | 65.38 | 15.17 | 19.44 | 29.89 |
| | Maximum | 529.80 | 153.27 | 92.31 | 76.19 | 3.09 | 94.40 | 139.54 | 59.35 | 402.30 | 11.00 | 42.11 | 24.00 | 86.89 | 32.45 | 84.94 | 35.09 | 53.76 | 64.30 |
| | Minimum | 92.20 | 69.32 | 40.90 | 11.21 | 0.34 | 18.00 | 54.69 | 27.67 | 15.55 | 0.22 | 0.20 | 1.07 | 29.27 | 14.03 | 11.99 | 4.68 | 6.99 | 11.20 |
| | C.D. (p=0.05) | 11.816 | 6.223 | 4.182 | 3.804 | 0.289 | 2.533 | 5.667 | 2.785 | 7.988 | 0.335 | 3.154 | 1.971 | 3.602 | 3.366 | 3.070 | 3.072 | 6.948 | 3.681 |
| | SE(m) | 4.189 | 2.206 | 1.483 | 1.348 | 0.102 | 0.898 | 2.009 | 0.987 | 2.832 | 0.119 | 1.118 | 0.699 | 1.277 | 1.194 | 1.089 | 1.089 | 2.463 | 1.306 |
| | C.V. (%) | 3.366 | 4.201 | 3.925 | 7.780 | 13.181 | 4.246 | 4.399 | 4.381 | 3.294 | 4.751 | 12.232 | 15.150 | 4.445 | 9.053 | 2.885 | 12.418 | 21.939 | 7.565 |

**Table 4. Distribution of mango cultivars in different clusters (Ward's method)**

| Cluster | No. of mango genotypes | Name of the genotypes |
|---|---|---|
| I | 14 | IIHR-B-M-15, IIHR-B-M-20, IIHR-B-M-58, IIHR-B-M-60, IIHR-B-M-18, IIHR-B-M-34, IIHR-B-M-5, IIHR-B-M-10, IIHR-B-M-21, IIHR-B-M-43, IIHR-B-M-25, IIHR-B-M-45, IIHR-B-M-19, IIHR-B-M-35 |
| II | 8 | IIHR-B-M-28, IIHR-B-M-54, IIHR-B-M-56, IIHR-B-M-48, IIHR-B-M-14, IIHR-B-M-31, IIHR-B-M-4, IIHR-B-M-2 |
| III | 6 | IIHR-B-M-3, IIHR-B-M-61, IIHR-B-M-9, IIHR-B-M-68, IIHR-B-M-41, IIHR-B-M-39 |
| IV | 1 | IIHR-B-M-11 |
| V | 7 | IIHR-B-M-7, IIHR-B-M-51, IIHR-B-M-50, IIHR-B-M-26, IIHR-B-M-23, IIHR-B-M-49, IIHR-B-M-36 |
| VI | 3 | IIHR-B-M-12, IIHR-B-M-33, IIHR-B-M-37 |
| VII | 1 | IIHR-B-M-13 |

**Table 5. Intra and inter cluster distance of forty mango genotypes with respect to morphological characters**

| | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI | Cluster VII |
|---|---|---|---|---|---|---|---|
| Cluster I | 3739.68 | 9292.65 | 55731.96 | 5996.85 | 10070.48 | 214380.5 | 21395.64 |
| Cluster II | | 2430.91 | 96771.53 | 21038.25 | 27842.72 | 289267.7 | 10370.08 |
| Cluster III | | | 5346.99 | 31524.87 | 26485.46 | 59897.23 | 112790.1 |
| Cluster IV | | | | 0 | 3985.33 | 165389.9 | 36555.25 |
| Cluster V | | | | | 4130.4 | 148147.6 | 39558.54 |
| Cluster VI | | | | | | 7397.45 | 300180 |
| Cluster VII | | | | | | | 0 |

*Intra (bold) and inter cluster D² values for 24 morphological quantitative characters*
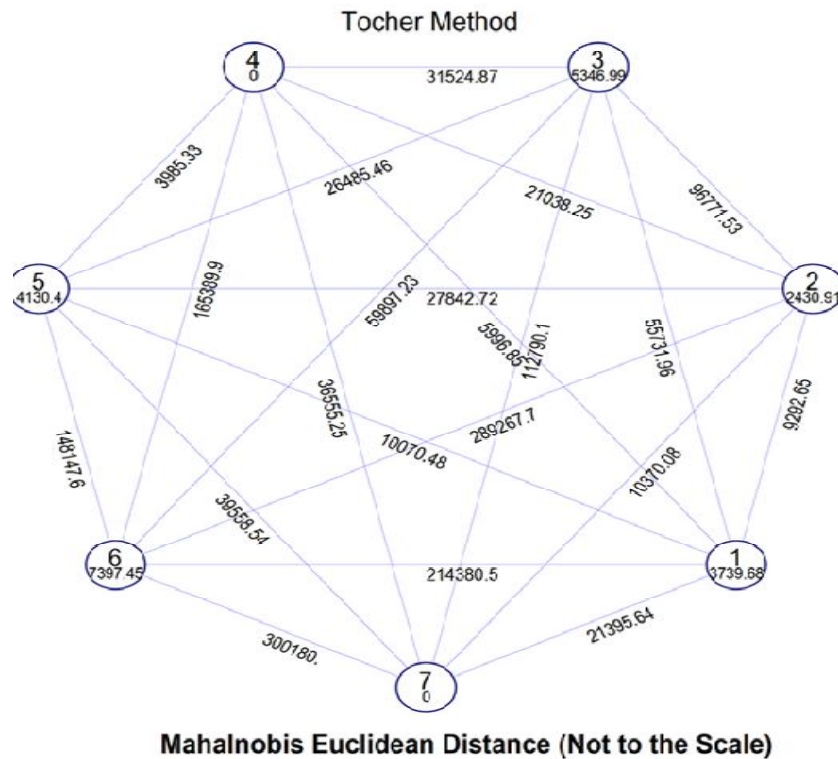


**Fig. 2. Mahalanobis Euclidean distances showing inter-relationship among clusters in different mango genotypes including new accessions for different morphological tr**

**Table 6. Cluster means of forty mango genotypes for morphological characters by Tocher's method**

| Characters | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI | Cluster VII |
|---|---|---|---|---|---|---|---|
| Leaf length (mm) | 20.51 | 20.68 | 24.39 | 13.7 | 20.22 | 23.2 | 18.8 |
| Leaf width (mm) | 5.71 | 5.23 | 5.92 | 4.1 | 5.59 | 5.8 | 5.6 |
| Petiole length (mm) | 2.47 | 2.41 | 2.61 | 1.3 | 2.53 | 3.08 | 2.6 |
| Inflorescence length (mm) | 24.18 | 25.73 | 21.45 | 27.63 | 24.78 | 26.21 | 23.73 |
| Inflorescence width (mm) | 12.38 | 13.57 | 13.62 | 15.43 | 13.14 | 12.28 | 10.8 |
| Sex ratio | 0.29 | 0.56 | 0.83 | 1.48 | 0.46 | 0.37 | 0.09 |
| Fruit weight (g) | 164.38 | 109.21 | 333.32 | 204.5 | 223.41 | 516.57 | 129.7 |
| Fruit length (mm) | 83 | 80.13 | 100.03 | 78.96 | 96.65 | 133.42 | 78.61 |
| Fruit width (mm) | 60.83 | 51.02 | 81.28 | 70.76 | 66.99 | 90.74 | 57.39 |
| Peel weight (g) | 21.91 | 23.38 | 39.32 | 20.8 | 31.76 | 61.18 | 44.42 |
| Peel thickness (mm) | 1.11 | 1.49 | 1.83 | 1.1 | 1.32 | 1.36 | 0.95 |
| Stone weight (g) | 32.85 | 29.61 | 36.99 | 31.61 | 33.92 | 69.33 | 69.73 |
| Stone length (mm) | 70.03 | 76.71 | 76.27 | 63.81 | 82.5 | 119.84 | 111.4 |
| Stone width (mm) | 37.13 | 36.11 | 40.97 | 40.9 | 38.16 | 50.67 | 46.42 |
| Pulp weight (g) | 109.61 | 56.22 | 257.01 | 152.09 | 157.74 | 386.06 | 15.55 |
| Pulp to stone ratio | 3.87 | 2.03 | 7.45 | 4.81 | 4.88 | 6.35 | 0.22 |
| Length of stone fibre (mm) | 9.72 | 14.23 | 19.42 | 16.4 | 16.62 | 30.76 | 42.11 |
| Seed weight (g) | 7.48 | 3.36 | 10.35 | 4.1 | 11.47 | 9.97 | 11.8 |
| Seed length (mm) | 46.69 | 42.2 | 51.56 | 37.21 | 59.69 | 58.03 | 61.41 |
| Seed width (mm) | 21.57 | 18.42 | 25.76 | 23.6 | 25.11 | 27.64 | 27.38 |
| Pulp percentage (%) | 66.65 | 51.62 | 77.33 | 74.37 | 70.67 | 74.72 | 11.99 |
| Peel percentage (%) | 13.44 | 21.47 | 11.57 | 10.17 | 13.96 | 11.8 | 34.25 |
| Stone percentage (%) | 19.9 | 26.91 | 11.1 | 15.46 | 15.37 | 13.49 | 53.76 |
| Yield (Kg/Plant) | 32.21 | 27.69 | 25.7 | 13.2 | 32.31 | 31.47 | 35.2 |

**Table 7. Relative contribution of different morphological characters towards genetic divergence**

| Sl. No. | Character | % contribution | Number of times ranked 1st |
|---|---|---|---|
| 1 | Fruit weight | 26.79 | 209 |
| 2 | Peel weight | 0.51 | 4 |
| 3 | Stone width | 0.38 | 3 |
| 4 | Length of stone fibre | 0.13 | 1 |
| 5 | Seed length | 1.79 | 14 |
| 6 | Seed width | 0.51 | 4 |
| 7 | Pulp percentage | 2.05 | 16 |
| 8 | Peel percentage | 2.31 | 18 |
| 9 | Stone percentage | 4.74 | 37 |
| 10 | Yield | 60.77 | 474 |

## 3.3 Relative Contribution of Morphological Characters towards Genetic Divergence

The components of $D^2$ due to each character were ranked which would help to provide per cent contribution of each character towards genetic divergence. These per cent contributions of different characters are presented in Table 5 and Fig. 3. The yield per tree contributed higher towards the genetic divergence (60.77%) followed by fruit weight (26.79%), stone percentage (4.74%), peel percentage (2.31%), pulp percentage (2.05%), seed length (1.79%), peel weight (0.51%), seed width (0.51%), stone width (0.38%) and length of stone fibre (0.13%) however, all other characters had no contribution towards total divergence. Rajan et al., [21] in their study reported that Pulp weight contributed maximum towards the genetic divergence (34.03%) followed by peel weight (22.65%), TSS (10.22%) stone weight (7.90%) and width (5.46%). Clemilton et al. [22] also reported contribution of different characters towards genetic divergence in papaya genotypes.

**Percentage contribution of morphological characters towards genetic divergence**
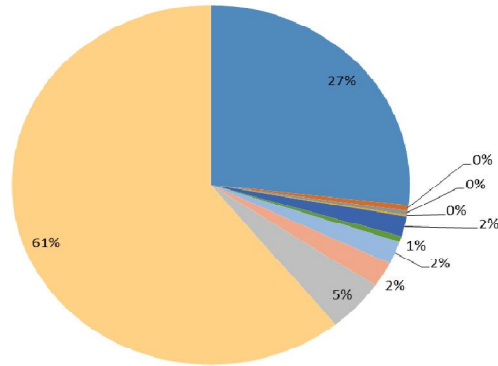


**Fig. 3. Percentage contribution of different morphological characters towards genetic divergence**

## 4. CONCLUSION

It is evident from study, the cluster VI (IIHR-B-M-12,IHR-B-M-33, IIHR-B-M-37) and Cluster VII (IIHR-B-M-13) mango genotypes with high inter-cluster distances are better suited to most morphological characteristics and have characteristics that contribute to maximum genetic diversity, such as fruit weight, peel weight, stone width, seed width, length of stone fibre, seed length, peel percentage, stone percentage and yield can be used as a parent in hybridization programme as these genotypes were genetically most diverse and could generate transgressive segregants by crossing with each other. Genotypes of cluster-VI could also be crossed with genotypes of cluster I and cluster II due to high inter-cluster distance for improvement of desired characters in these genotypes. Apart from, genotypes of clusters VI and VII, cluster III with genotypes IIHR-B-M-3, IIHR-B-M-61, IIHR-B-M-9, IIHR-B-M-68, IIHR-B-M-41, IIHR-B-M-39 possessing maximum intra-cluster distance and highest pulp percentage that contributes maximum towards genetic diversity, could also be used as parent in breeding programme due to considerable genetic divergence among the accessions of this cluster.

## DISCLAIMER

The products used for this research are commonly and predominantly use products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by the producing company rather it was funded by personal efforts of the authors.

## COMPETING INTERESTS

Authors have declared that no competing interests exist.

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