Electronic Journal of Plant Breeding, 8(3): 772-778 (September 2017)
ISSN 0975-928X
DOI: 10.5958/0975-928X.2017.00119.3

Research Article

Genetic diversity for fruit morphological and biochemical characters of indigenous mango (*Mangifera indica* L.) cultivars of coastal districts in Andhra Pradesh using principal component analysis

A. Himabindu[1], D. Srihari, M. Rajasekhar, V. Sudhavani, P. Subbarammamma, K. Uma Krishna and M. Paratpara Rao
Horticultural Research Station, Dr. Y.S.R Horticultural University, Venkataramannagudem, West Godavari, Andhra Pradesh – 534101
E-mail: himabindu291188gmail.com

(Received: 26 Dec 2016; Revised: 10 Sep 2017; Accepted: 25 Sep 2017)

Abstract
An experiment was conducted at Horticultural research station, Venkataramannagudem, Andhra Pradesh to analyze the genetic diversity among thirty four cultivars using principal component analysis for thirty quantitative characters in mango. In the present investigation, the first seven principal components with eigen values more than one contributed to 82.04 per cent of cumulative variability among the 34 mango cultivars. The thirty four mango cultivars were grouped into 6 clusters. Among all the clusters, clusters I was the largest containing 19 cultivars followed by the cluster II with 8 cultivars, cluster III, IV and V with 2 cultivars each and cluster VI was mono genotypic. The mutual relationships between the clusters revealed that inter-cluster distance values were greater than intra-cluster values. The intra-cluster D^2 values ranged from 0.00 (Cluster VI) to 4253.23 (Cluster IV). The inter-cluster D^2 values varied from 1445.00 (between cluster I and II) to 17367.81 (between cluster III and VI). The high intra and inter cluster distances indicating the presence of substantial amount of genetic diversity in the genetic material.

Key words
Cluster, Genetic divergence, Mango, Principal component analysis

Introduction

Mango (*Mangifera indica* L.) is an important member of the family Anacardiaceae in order Sapindales and is the most important fruit crop in India having a great cultural, socio-economic and religious significance since ancient times. Andhra Pradesh is considered as a centre of diversity for mango with a rich diversity of named local cultivars and unnamed local land races. Mango is considered to be an allopolyploid, most probably amphidiploid and out breeding species having chromosome number 2n=40 (Mukherjee, 1950). It is highly heterozygous as performance varies with the climate which resulted in a high level of genetic diversity. Further, confusion exists in the nomenclature of mangoes due to different local names for the same variety. Therefore, to identify superior parents, genetic characterization is a basic requirement for effective selection within the existing population or population arising out of hybridization. However, it is desirable to select suitable and genetically divergent parents, based on information about the genetic variability and genetic diversity present in the available germplasm. Therefore, the present work was undertaken to study the genetic characterization in 34 mango cultivars (*Mangifera indica* L.) and to identify suitable donors having wider genetic base for a successful breeding programme in this crop. Principal component analysis is a sort of multivariate analysis recognized as a powerful tool in quantifying the degree of genetic divergence based on multiple characters.

Material and methods

The present work was conducted to study the performance of mango cultivars of coastal districts in Andhra Pradesh at Horticultural Research Station, Venkataramannagudem during the subsequent years from 2012 to 2014. A well-planned germplasm collection survey based on diversity richness was conducted in coastal districts of Andhra Pradesh which includes Horticultural Research Station and private owned mango orchards. Random sampling strategy was followed for collection of samples. Three plants in each cultivar were taken as sample size. The experimental material consists of 34 indigenous mango cultivars and variants within them obtained from the coastal districts of Andhra Pradesh. The indigenous mango cultivars used are: Banganapalli – 1, Banganapalli – 2, Banganapalli – 3, Banglora –1, Banglora – 2, Baramasi, Cherukurasam, Chinnarasam, Chinna Suvarnarekha, Elamandala, Hyder, Imampasand, Jalal, Jehangir, Kolanka Goa, Kottapalli Kobbari, Kowsuri Pasand, Nalla Andrews, Nalla Rasalu, Navaneetam, Nuzividu Tiyya Mamidi, Nuzividu Rasalu, Panchadara Kalasa, Pandurivari Mamidi, Paparao Goa, Peddarasam, Panukula Mamidi, Royal Special, Rajamanu, Sora Mamidi, Suvarnarekha, Tella Gulabi, Tella Rasalu and Rajamamidi

The characters considered for the study were TSS (^{o}Brix), total sugars (%), reducing sugars (%), non-reducing sugars (%), titratable acidity (%), β-carotene (µg/100g), ascorbic acid (mg/100g),

DOI: 10.5958/0975-928X.2017.00119.3

TSS: acid ratio, total phenols (mg of gallic acid/100g), fruit length (cm), fruit diameter (cm), fruit weight (g), fruit skin thickness (mm), peel weight (g), peel per cent (%), fruit to pulp ratio, pulp to stone ratio, pulp to peel ratio, pulp weight (g), pulp per cent (%), stone weight (g), stone per cent (%), stone length (cm), stone width (cm), stone thickness (cm), embryo length (cm), embryo width (cm), embryo weight (g), shape index and edible to non-edible ratio. The genetic divergence was worked out among the cultivars using principal component analysis and cultivars were grouped into different clusters by employing Ward's minimum variance method as outlined by Banfield (1978) using WINDOWSTAT software package version 8.1.

Results and Discussion

The Analysis of variance indicated sufficient variability in the cultivars under study indicating considerable genetic diversity among 34 mango cultivars. The principal components, eigen values, per cent variability and cumulative per cent of variability of different fruit morphological and bio-chemical characters studied are furnished in table 1. The principal components with eigen values less than one were considered as non-significant as per the procedure.

In the present investigation, the first seven principal components with eigen values more than one contributed to 82.04 per cent of cumulative variability among the 34 mango cultivars. The character loading values for principal components represented the weights defining the contribution of different characters for the respective principal components (Table 2). The first principal component (PC I) contributed highest variability (27.93%). Characters like peel per cent (0.23), fruit to pulp ratio (0.19), stone per cent (0.18), ascorbic acid (0.17), titratable acidity (0.13), edible to non-edible ratio (0.09), pulp to peel ratio, peel and stone weight (0.07), TSS (0.06), reducing sugars, non-reducing sugars and embryo length (0.01) showed positive loadings whereas negative loadings were recorded for fruit weight (-0.33), pulp to stone ratio (-0.31), fruit length (-0.29), shape index (-0.28), pulp per cent (-0.27), embryo width (-0.27), stone length (-0.25), pulp weight (-0.24), fruit diameter (-0.23), embryo weight (-0.23), stone width (-0.17), total sugars (-0.11), β-carotene (-0.09), fruit skin thickness (-0.08), total phenols (-0.05) and stone thickness (-0.03) in decreasing order of the elements and explained about variability in the first principal component. The second principal component was noticed to explain 14.85 per cent of variability and showed high positive loadings for titratable acidity (0.39) followed by TSS: acid ratio (0.37), fruit diameter (0.30), ascorbic acid (0.27), peel per cent and pulp weight (0.16), embryo weight (0.15), pulp to stone ratio (0.130), pulp per cent (0.11), stone weight (0.10) and TSS (0.08) were noted to explain the maximum variability.

The third principal component explained 12.50 per cent variability and showed high positive correlation for pulp to peel ratio and edible to non-edible ratio (0.40), peel weight (0.38), stone weight (0.33), TSS (0.25), non-reducing sugars (0.22), total phenols (0.15), stone width (0.14), total sugars (0.12), β-carotene and fruit skin thickness (0.07), ascorbic acid (0.06), TSS: acid ratio (0.02), pulp weight and shape index (0.01). The fourth principal component contributed 9.35% variability and showed high positive loadings for non-reducing sugars (0.43), TSS (0.35), fruit skin thickness (0.31), embryo length (0.26), embryo weight (0.24), fruit to pulp ratio (0.23), stone thickness and embryo width (0.20), peel per cent (0.19), peel weight (0.17), TSS: acid ratio (0.11), stone width (0.10), fruit diameter and shape index (0.08), fruit weight (0.05), fruit length and titratable acidity (0.04), stone weight and stone length (0.01).

The fifth principal component explained 8.24% variability and showed high positive correlation for total sugars (0.36) followed by total phenols (0.30), TSS (0.29), stone width (0.25), shape index (0.20), non-reducing sugars, fruit skin thickness and fruit to pulp ratio (0.13), peel per cent (0.09), embryo width (0.06), pulp per cent (0.03), β-carotene (0.01). The sixth principal component contributed 4.93% variability and showed high positive loadings for pulp per cent (0.31), non-reducing sugars (0.30), shape index (0.26), ascorbic acid (0.13), stone thickness (0.12), pulp to peel ratio (0.10), total phenols (0.08), TSS (0.02), pulp to stone ratio (0.01). The seventh principal component explained 4.24% variability and total sugars contributed positively (0.46) to the diversity followed by non-reducing sugars and β-carotene (0.24), stone per cent (0.18), TSS: acid ratio (0.15), TSS and titratable acidity (0.14), pulp weight (0.12), pulp to peel ratio and embryo width (0.10), pulp per cent (0.07), embryo length (0.05), fruit weight (0.04), embryo weight (0.02) in decreasing order of the elements have contributed for genetic divergence and explained about variability in this vector.

The thirty four mango cultivars was grouped into six distinct clusters using Ward's minimum variance method as illustrated in Table 3 and Fig. 1. Cluster I was the largest cluster consisting of 19 cultivars (Banganapalli-1, Cherukurasam, Banglora-1, Nalla Rasalu, Navaneetam, Nalla Andrews, Panchadara Kalasa, Peddarasam, Hyder, Panukula Mamidi, Rajamanu, Banganapalli-3, Tella Rasalu, Banglora -2, Kottapalli Kobbari, Pandurivari Mamidi, Rajamamidi, Nuzividu Tiyya Mamidi and Tella Gulabi) followed by cluster II with 8 cultivars (Banganapalli-2, Suvarnarekha,

DOI: 10.5958/0975-928X.2017.00119.3

Paparao Goa, Chinna Suvarnarekha, Chinnarasam, Nuzividu Rasalu, Imam Pasand and Kolanka Goa), cluster III with 2 cultivars (Baramasi and Royal Special), cluster IV with 2 cultivars (Jalal and Jehangir), cluster V with 2 cultivars (Elamandala, Kowsuri Pasand) and cluster VI with only 1 cultivar (Sora Mamidi) showing nil intra-cluster D^2 values. The pattern of distribution of cultivars from different eco-geographical regions into different clusters with different divergence values was at random supporting the view that geographical diversity is related to genetic diversity. Cultivars with high fruit weight could be utilized in a crossing programme to realize the broad spectrum of genetic variability in segregating generations to effect selection for fruit weight improvement. Kumar *et al.* (2006) and Rathod (2007) also reported that large sized table fruit cultivars have grouped into one cluster in mango.

The average intra- and inter- cluster D^2 values were presented in Table 4 and Fig 2. The highest intra cluster distance was observed in cluster IV (4253.23) indicated the presence of wide genetic diversity among the cultivars *viz.*, Jalal and Jehangir while the lowest intra cluster distance was observed in cluster VI (0.00) indicated the grouping of single cultivar *viz.*, Sora Mamidi in a cluster. The inter-cluster distance was minimum between the cluster I and II (1445.00) while it was maximum between the cluster III and VI (17367.81 indicating presence of substantial amount of genetic diversity in the genetic material.

Higher mean values for total phenols were seen in cluster II (66.74), higher mean values for TSS, titratable acidity and ascorbic acid (20.86, 0.96 and 78.49 respectively) were seen in cluster III, higher mean values for total sugars, reducing sugars, non-reducing sugars, TSS: Acid ratio and fruit skin thickness were seen in cluster V (14.17, 4.87, 9.30, 92.81 and 0.13 respectively), higher mean values for β-carotene, fruit length, fruit diameter, fruit weight, pulp percent, pulp weight and edible to non- edible ratio (17.56, 11.96, 1395.45, 84.43, 1178.24 and 5.59) were seen in cluster VI and higher mean values for fruit skin thickness (0.11) was seen in cluster V which are major contributors in improving quality of mango (Table 5).

Based on these studies crosses may be made between the cultivars from clusters that are far apart genetically to obtain new recombinants in mango since the magnitude of heterosis depends largely on the degree of genetic diversity of parents. Therefore, it is proposed to evolve the hybrids involving cultivars from the clusters with high inter cluster distance to isolate superior segregants in advanced generations with high yield potential and desirable characters. Singh (2005), Rufini *et al.* (2011), Barhate *et al.* (2012) and Sandra *et al.* (2013) studied the utilization of Ward's minimum variance method in genetic divergence studies of mango and reported maximum diversity in the cultivars studied.

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Electronic Journal of Plant Breeding, 8(3): 772-778 (September 2017)
ISSN 0975-928X
DOI: 10.5958/0975-928X.2017.00119.3

Table 1. Eigen values, per cent variability and cumulative variability for principal components of morphological and bio-chemical characters in mango

Principal component	Eigen value (Root)	Per cent variation extracted	Cumulative variation explained
1 Vector	8.38	27.93	27.93
2 Vector	4.46	14.85	42.78
3 Vector	3.75	12.50	55.27
4 Vector	2.80	9.35	64.62
5 Vector	2.47	8.24	72.87
6 Vector	1.48	4.93	77.80
7 Vector	1.27	4.24	82.04
8 Vector	0.94	3.13	85.16

Table 2. Character loading of principal components for fruit morphological and bio-chemical characters in mango

S.No.	Characters	1 Vector	2 Vector	3 Vector	4 Vector	5 Vector	6 Vector	7 Vector	8 Vector
1	TSS	0.06	0.08	0.25	0.35	0.29	0.02	0.14	0.06
2	Total Sugars	-0.11	-0.11	0.12	-0.05	0.36	-0.04	0.46	0.15
3	Reducing Sugars	0.01	-0.02	-0.05	-0.34	0.21	-0.46	-0.06	0.35
4	Non-reducing Sugars	0.01	0.04	0.22	0.43	0.13	0.30	0.24	-0.16
5	Titratable Acidity	0.13	0.39	-0.04	0.04	-0.06	-0.16	0.14	-0.16
6	β-carotene	-0.09	-0.26	0.07	-0.07	0.01	-0.23	0.24	0.04
7	Ascorbic Acid	0.17	0.27	0.06	-0.07	-0.08	0.13	-0.27	-0.10
8	TSS: acid Ratio	0.13	0.37	0.02	0.11	-0.02	-0.20	0.15	-0.09
9	Total Phenols	-0.05	-0.05	0.15	-0.23	0.30	0.08	-0.31	-0.49
10	Fruit Length	-0.29	-0.16	0.00	0.04	0.00	-0.03	-0.06	-0.14
11	Fruit Diameter	-0.23	0.30	-0.01	0.08	-0.04	-0.17	-0.07	-0.06
12	Fruit Weight	-0.33	0.07	-0.04	0.05	-0.12	-0.10	0.04	-0.05
13	Fruit Skin Thickness	-0.08	-0.08	0.07	0.31	0.13	-0.02	-0.48	0.33
14	Peel Per cent	0.23	0.16	-0.15	0.19	0.09	-0.18	-0.12	0.13
15	Peel Weight	0.07	-0.17	0.38	0.17	-0.04	-0.12	-0.13	0.10
16	Fruit to Pulp Ratio	0.19	-0.06	-0.32	0.23	0.13	-0.08	-0.09	0.05
17	Pulp to Stone Ratio	-0.31	0.13	0.07	-0.06	-0.09	0.01	-0.01	0.06
18	Pulp to Peel Ratio	0.07	-0.11	0.40	-0.15	-0.12	0.10	0.10	0.14
19	Pulp Per cent	-0.27	0.11	-0.11	-0.15	0.03	0.31	0.07	0.19
20	Pulp Weight	-0.24	0.16	0.01	-0.04	-0.27	-0.01	0.12	0.10
21	Stone Per cent	0.18	-0.19	-0.15	0.08	-0.23	-0.11	0.18	-0.34
22	Stone Weight	0.07	0.10	0.33	0.01	-0.30	-0.08	-0.10	0.23
23	Stone Length	-0.25	-0.20	-0.08	0.01	-0.13	-0.17	-0.11	-0.23
24	Stone Width	-0.17	-0.02	0.14	0.10	0.25	-0.37	-0.14	-0.21
25	Stone Thickness	-0.03	-0.24	-0.08	0.20	-0.33	0.12	-0.09	0.07
26	Embryo Length	0.01	-0.32	-0.26	0.26	-0.04	-0.07	0.05	0.06
27	Embryo Width	-0.27	0.05	0.00	0.20	0.06	-0.19	0.10	-0.06
28	Embryo Weight	-0.23	0.15	0.00	0.24	-0.22	-0.14	0.02	0.04
29	Shape Index	-0.28	0.07	0.01	0.08	0.20	0.26	-0.16	0.04
30	Edible to Non-edible Ratio	0.09	-0.12	0.40	-0.02	-0.21	-0.18	-0.04	-0.17

 DOI: 10.5958/0975-928X.2017.00119.3

Table 3. Distribution of mango cultivars in different clusters (Ward's minimum variance method)

Cluster No.	Number of cultivars	Name of the cultivars
I	19	Banganapalli-1, Cherukurasam, Banglora-1, Nalla Rasalu, Navaneetam, Nalla Andrews, Panchadara Kalasa, Peddarasam, Hyder, Panukula Mamidi, Rajamanu, Banganapalli-3, Tella Rasalu, Banglora -2, Kottapalli Kobbari, Pandurivari Mamidi, Rajamamidi, Nuzividu Tiyya Mamidi and Tella Gulabi
II	8	Banganapalli-2, Suvarnarekha, Paparao Goa, Chinna Suvarnarekha, Chinnarasam, Nuzividu Rasalu, Imam Pasand and Kolanka Goa
III	2	Baramasi and Royal special
IV	2	Jalal and Jehangir
V	2	Elamandala and Kowsuri Pasand
VI	1	Sora Mamidi

Table 4: Intra and inter-cluster distances for fruit morphological and bio- chemical characters in mango cultivars (Ward's minimum variance method)

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	1038.91	**1445.00**	**3957.72**	**5037.93**	**4530.10**	**13979.96**
Cluster II		913.49	**4096.73**	**5536.88**	**3525.04**	**12998.77**
Cluster III			2478.34	**8461.61**	**8219.92**	**17367.81**
Cluster IV				4253.23	**6222.18**	**13297.47**
Cluster V					2181.97	**6146.38**
Cluster VI						0.00

Figures in bold indicate intra-cluster distances

Electronic Journal of Plant Breeding, 8(3): 772-778 (September 2017)
ISSN 0975-928X
DOI: 10.5958/0975-928X.2017.00119.3

Table 5. Cluster means of fruit morphological and bio-chemical characters (Ward's minimum variance method)

Clusters	TSS	Total Sugars	Reducing Sugars	Non Reducing Sugars	Titratable Acidity	β-carotene	Ascorbic Acid	TSS:acid Ratio	Total Phenols	Fruit Length	Fruit Diameter	Fruit Weight	Fruit Skin Thickness	Peel Per cent	Peel Weight
Cluster I	18.47	12.54	4.41	8.13	0.25	1157.43	29.57	80.21	37.37	9.91	6.99	298.33	0.09	13.21	39.67
Cluster II	17.76	11.84	4.22	7.62	0.26	1080.95	33.18	72.87	66.74	10.80	7.67	373.52	0.11	11.11	41.30
Cluster III	20.86	12.12	4.61	7.51	0.96	809.51	78.49	23.11	57.49	7.22	7.18	191.18	0.06	14.96	28.41
Cluster IV	16.14	10.89	3.97	6.92	0.31	978.23	26.18	53.33	48.65	13.74	9.05	665.20	0.09	13.46	42.14
Cluster V	19.57	14.17	4.87	9.30	0.24	1171.86	22.50	92.81	57.19	14.25	11.42	930.22	0.13	11.58	105.95
Cluster VI	15.05	9.90	3.06	6.84	0.31	1232.73	26.00	49.84	19.90	17.56	11.96	1395.45	0.06	8.39	117.12

Clusters	Fruit to Pulp Ratio	Pulp to Stone Ratio	Pulp to Peel Ratio	Pulp Per cent	Pulp Weight	Stone Per cent	Stone Weight	Stone Length	Stone Width	Stone Thickness	Embryo Length	Embyo Width	Embryo Weight	Shape Index	Edible to Non-edible Ratio
Cluster I	1.40	4.92	5.60	71.61	215.92	15.13	42.56	8.05	3.84	2.12	6.22	3.11	20.82	1.42	2.58
Cluster II	1.30	6.83	7.23	76.98	289.03	11.66	42.56	8.19	3.82	1.96	6.17	2.86	21.99	1.42	3.48
Cluster III	1.40	5.13	4.84	71.41	137.13	14.05	26.38	4.52	3.44	1.49	3.58	2.34	12.70	1.01	2.48
Cluster IV	1.48	4.09	4.37	71.42	476.24	14.08	44.92	11.02	4.11	2.43	7.32	3.36	25.75	1.56	2.11
Cluster V	1.25	9.28	7.03	80.36	747.74	8.69	81.26	10.27	5.26	2.45	6.78	4.41	33.29	1.24	3.98
Cluster VI	1.18	12.87	10.07	84.43	1178.24	6.80	94.96	14.58	5.30	2.28	7.53	3.93	36.25	1.47	5.59

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ISSN 0975-928X
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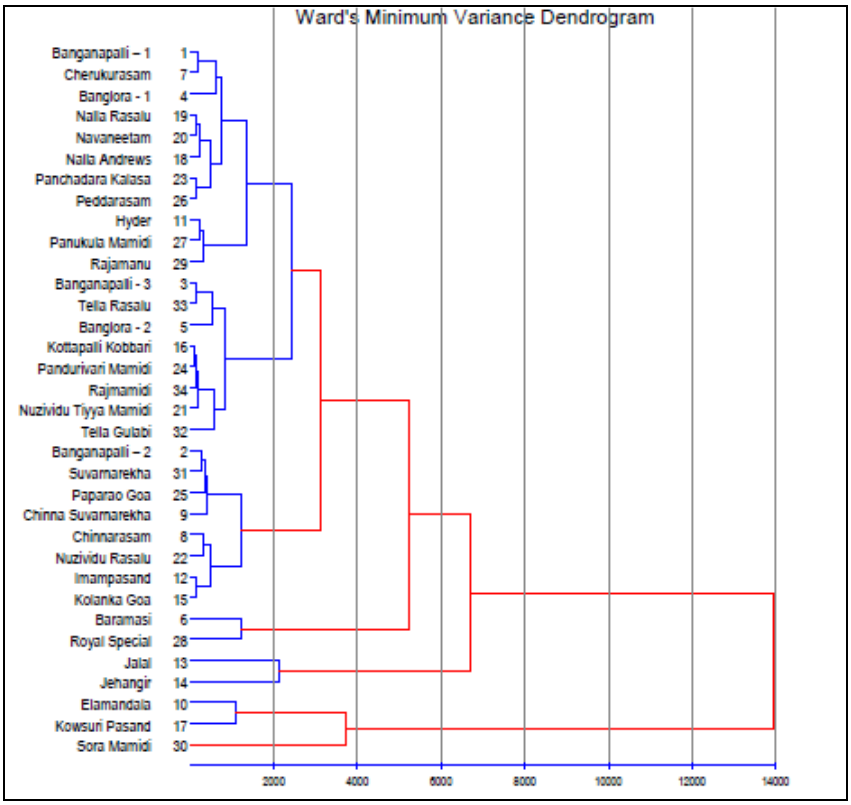

Fig. 1. Clustering pattern of mango cultivars based on fruit morphological and bio-chemical characters (Ward's minimum variance dendrogram)

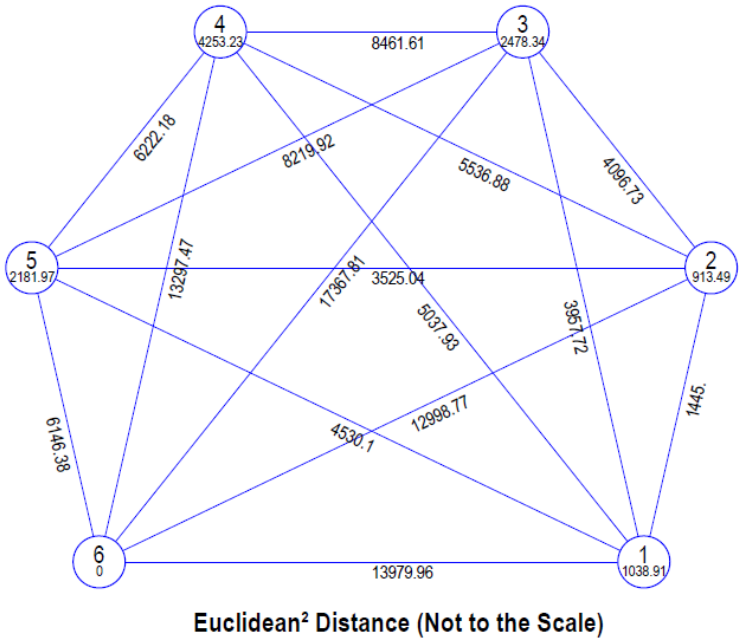

Fig. 2. Intra and inter cluster distances for fruit morphological and bio-chemical characters in different mango cultivars (Ward's minimum variance method)