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Genetic Analysis in mango (*Mangifera indica* L.) based on fruit characteristics of 400 genotypes

Sankaran M.*, Dinesh M. R.*, Gowda D.C.S. and Venugopalan R.
Division of fruit crops, ICAR-Indian Institute of Horticultural Research
Hesaraghatta Lake post, Bengaluru - 560 089
*Corresponding author Email : drmrdinesh@gmail.com, kmsankaran@gmail.com

ABSTRACT

The analysis of variance for 6 quantitative traits and 30 qualitative traits showed significant differences among the 400 genotypes of mango which indicates the existence of high heterozygosity. Among the 18 clusters formed, the highest fruit weight of 1404.27 g was recorded in cluster 10 followed by cluster 15 with 1280.67g whereas the lowest fruit weight was recorded in cluster 16 (30.94g). The highest fruit length (22.03 cm) was recorded in cluster 10 followed by 17.80 cm in cluster 14. Similarly, the fruit diameter was highest (12.18 cm) in cluster 10 followed by 12.03 cluster 4. The fruit thickness was highest (10.60 cm) in cluster 15 followed by cluster 4 with 9.96 cm. The pulp recovery was maximum (87.16%) in cluster-14 followed by followed by cluster 4 and 18 with 79.28 and 78.41 %, respectively. The clusters 15 had the varieties meant for pickle making and possessed the less TSS whereas the TSS of above 19°B was recorded in cluster 2. The maximum inter cluster (D^2) value was obtained between cluster 10 and cluster 11. These clusters may be used for hybridization programme due to wide variability and possibility of transgressive sergeants. Estimates of phenotypic variance and genotypic variance had only a narrow difference for all six characters studied indicating that these characters are not much influenced by environmental factors and highly heritable which can be exploited by adopting clonal selection or selection of chance seedlings and selection as parents for breeding purpose.

Key words: Biplot analysis, GCV, Genetic analysis, Heritability, Mango and PCV,

INTRODUCTION

Mango (*Mangifera indica* L.*)* is originated from the Indo-Burma region and genus *Mangifera* has more than 60 species world-wide, the highest diversity being found in the Malayan Peninsula, Borneo and Sumatra (Bompard,1993). Mukherjee (1953) opines that mango has been under cultivation for at least 4000 years with over 1000 varieties in cultivation. Almost all these are selections made from open-pollinated seedlings and selection by man from seedlings of unknown parentage has played the most significant role in the development of new mango cultivars (Singh, 1963). Mango is a premier fruit crop in India as well as some other countries in the tropical world with respect to being its eminent place in nutritional security and employment and income generation. The present scenario and expected future need of mangoes necessitate bringing improvement in mango with respect to the productivity not only per tree but also per unit area of land. A need has therefore, arisen to develop high yielding varieties of dwarf plant type, high fruit quality and resistant to biotic and abiotic stresses. Studies have been made for understanding diversity in the genus *Mangifera* and the possibility of its use in improvement of mango through introduction and selection of promising varieties for commercial cultivation and making further improvement in the existing varieties through inter-specific and inter-varietal hybridization and induction of useful mutations.

Mukherjee (1948) has described 72 mango varieties from Bengal, Bihar and Uttar Pradesh.

Simultaneously, Naik and Gangolly (1950) have described 335 varieties of South India. Apart from the fruit characters, they have also laid great stress on the vegetative characters. The list of 1595 cultivars of mango in world (Pandey, 1998) was revised with the names of 1663 cultivars by Pandey and Dinesh (2010). The updated list now contains the names of 1682 cultivars. There are seven centres of diversity exists in India which includes (i) humid subtropical region (Manipur, Tripura, Mizoram and south Assam), (ii) Chhota Nagpur Plateau (trijunction of Madhya Pradesh, Odisha and Bihar), (iii) Santhal Paragana, (iv) Southern Madhya Pradesh (tribal area) adjoining Odisha and Andhra Pradesh, (v) Dhar Plateau of Madhya Pradesh adjoining South Rajasthan and Gujarat, (vi) humid tropical southern peninsular India and (vii) Andaman & Nicobar group of islands (Yadav and Rajan, 1993). A list of the names of cultivars available in the world as probable gene sources for dwarf-ness, fruit size, red peel colour, high pulp content, high content of total soluble solids, long shelf-life of fruit, regularity in fruit bearing, earliness and lateness in fruit maturity and good processing quality have been mentioned by Pandey and Dinesh (2010). Dinesh and Vasugi (2002) catalogued 151 cultivars of mango including *M. zeylanica*. Another lot of 223 varieties of mango were catalogued by Dinesh *et al.,* (2012) using Bioversity International Descriptors and they developed barcodes for these varieties through molecular characterization. There is a great variation in fruit weight in mango. Pandey and Dinesh (2010) categorized mango on the basis of fruit weight as very small (99g and below), small (100-149g), medium large (150-299g), large (300-500g) and very large (more than 500g) fruited varieties. Out of 61 varieties of mango registered in U.S.A., 19 varieties have been reported to bear large to very large fruits (Brooks and Olmo, 1972). The evaluation of genetic variability with in a cultivated crop has important consequences in plant breeding and germplasm management. The yield and its contributing traits improvement in this crop can be achieved through selection of superior genotypes with desirable traits existing in nature. Mahalnobis (D^2) statistics which is based on the multivariate analysis of quantitative trait is powerful tool for measuring genetic divergence among the population. Therefore, an attempt has been made to study the variability of fruit characteristics among 400 mango germplasm.

MATERIALS AND METHODS

The experimental materials consists of 400 mango genotypes belonging to different geographical regions of the world were evaluated for over the three years (2014-17) at ICAR-Indian Institute of Horticultural Research, Bengaluru. The experimental material comprised of 400 mango germplasm belonging to different geographical regions and evaluated in the year 2015, 2016 and 2017. The fruit characteristics such as fruit weight (g), fruit length (cm), fruit diameter (cm), fruit thickness (cm), pulp recovery (%) and TSS (ÚBrix) have been recorded by using the standard procedure. Thirty qualitative characteristics have been used to catalogue 400 varieties as per the standard descriptors given by the Bioversity International (IPGRI, 1997). At the first instance, statistical tools such as ANOVA and F-test were used to evaluate the significant difference ($p<0.05$) among the varieties/hybrid individually for all the traits. Least Significant Difference (LSD) was computed as a Post-hoc test (Cochran and Cox, 1957). SAS GLM was used to develop suitable codes for the statistical analysis (SAS V 9.3 2012).

Biometrical Analysis

With a view to understand the extent of diversity to which the observed variation were due to genetic factors, the phenotypic variance (PV), genotypic variance (GV), phenotypic coefficient of variation (GCV), genotypic coefficient of variation (GCV), broad sense heritability (h2), genetic advance (GA) and genetic advance as per cent over mean (GAM) were computed (Falconer,1985; Venugopalan, 2015).

Estimation of genetic parameters

Genotypic variance (σ_g^2) = $\frac{\text{Treatment MSS} + \text{Error MSS}}{\text{r}}$

Environmental variance (σ_e^2) = Error mean sum of squares

Phenotypic variance (σ_p^2) = $\sigma_g^2 + \sigma_e^2$

Coefficient of variation

The coefficient of variation (CV) being a standardized form of variance is useful for comparing the extent of variation between different characters with different scales. Genotypic and phenotypic coefficients of variation were estimated according to

Burton and Dewane (1953) based on estimate of genotypic and phenotypic variance.

$$\text{Genotypic coefficient of variation} = \frac{\sqrt{\sigma_g^2}}{\bar{x}} \times 100$$

$$\text{Phenotypic coefficient of variation} = \frac{\sqrt{\sigma_p^2}}{\bar{x}} \times 100$$

Where $\bar{x}$ = General mean of the character

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

Heritability (h2)

Heritability in broad sense was calculated as the ratio of genotypic variance to the phenotypic variance and expressed in percentage (Falconer, 1985).

Heritability (h2) =

Where σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

Expected genetic advance

Expected genetic advance (EGA) was calculated using the formula given by Robinson *et al.,* (1949).

EGA = l x h2 x áp

Where i = Selection of differential (2.06) at five per cent selection intensity

h2 = Heritability in broad sense

áp = Phenotypic standard deviation

Genetic advance over mean

Genetic advance as per cent over mean was worked out as suggested by Johnson *et al.,* (1955).

GAM =

Where GA = Genetic advance

= General mean of the character

Correlation

Genotypic (rg) and phenotypic (rp) coefficients of correlation were estimated as suggested by Al-Jibourie *et al.,* (1958).

$$\text{Genotypic correlation} = \frac{C_o V_{xy}(G)}{\sqrt{V_x(G) \times V_y(G)}}$$

$$\text{Phenotypic correlation} = \frac{C_o V_{xy}(P)}{\sqrt{V_x(P) \times V_y(P)}}$$

Where

C0Vxy (G) = Genotypic covariance between x and y

C0Vxy (P) = Phenotypic covariance between x and y

Vx (G) = Genotypic variance of character x

Vx (P) = Phenotypic variance of character x

Vy (G) = Genotypic variance of character y

Vy (P) = Phenotypic variance of character y

Test of significance of correlation was tested by comparing the 'r' value with obtained value.

Estimated heritability (broad sense) was classified as low (< 30 %), medium (30 – 60 %) and high (> 60 %) and the range of genetic advance as a percentage of mean was classified as low (< 10 %), moderate (10 – 20 %) and high (> 20 %) as suggested by Johnson et al. (1955). SAS package was used to develop suitable codes for the statistical analysis (SAS V 9.3 (2012)).

Using quantitative traits, the genetic distance among the populations is calculated using D2 statistics (Rencher, 1995) on the basis of multiple characters. The clustering of genetic groups is done by a method suggested by Tocher (Rao, 1974). The means of all the characters were subjected to Squared Euclidian Cluster analysis and a dendrogram was derived using Ward's method (Rencher, 1995).

RESULTS

The analysis of variance for 6 quantitative traits showed significant differences among the 400 genotypes of mango which indicates the existence of genetic diversity. Means for different qualitative characters of 400 accessions of mango are given as Supplementary Table S1 (Available online). The maximum fruit weight of 1404.27g in variety Sora followed by 1280.67g in variety Amini where as the

minimum fruit weight was of 29,51g in variety Kana Appe followed by 39.31g in variety Halasage. The fruit length was maximum (22.03 cm) in var. Sora followed 16.77cm in hybrid 7/15 where as the minimum fruit length of 4.33cm was recorded in var. Pacharasi. The maximum fruit diameter 13.50 cm was recorded in var. Dorgani Kavi followed by 11.33 cm in var. Maharaja Pasand where as minimum fruit diameter of 3.33 cm was recorded in var. Dodderi Jeerige. The maximum fruit thickness of 11.40cm was recorded in var. Dorgani Kavi followed by 9.87 in var. Amini whereas the minimum thickness was recorded (2,80cm) in Haldotta Appe. The highest pulp recovery (89.67%) was recorded in var. Manoranjan followed by 88.20 % in var. Lahara whereas the lowest pulp recovery was recorded in var. Halasage. The highest TSS (ÚBrix) of 31.00 was recorded in var. Dattatreya local followed by 30.67 in var.K-0-7 where as the lowest was recorded in var. Halasage (5.5%)

The cluster mean analysis (Table 1) reveals that there is a huge variation among the clusters. Highest fruit weight of 1404.27 g was recorded in cluster 10 followed by cluster 15 with 1280.67g. Whereas the lowest fruit weight was recorded in cluster 16 (30.94g). The highest fruit length (22.03 cm) was recorded in cluster 10 followed by 17.80 cm in cluster 14. Similarly, the fruit diameter was highest (12.18 cm) in cluster 10 followed by 12.03 cluster 4. The fruit thickness was highest (10.60 cm) in cluster 15 followed by cluster 4 with 9.96 cm. The pulp recovery was maximum (87.16%) in cluster-14 followed by cluster 4 and 18 with 79.28 and 78.41 %, respectively.

Table 1. Cluster mean for quantitative traits of 400 mango genotypes

Clusters	Fruit w eight (g)	Fruit length (cm)	Fruit diameter (cm)	Fruit thickness (cm)	Pulp (%)	TSS (°Brix)
Cluster 1	376.51	10.81	8.19	7.25	74.48	18.95
Cluster 2	246.93	9.27	7.16	6.43	70.35	19.36
Cluster 3	144.69	8.04	5.94	5.27	63.28	18.31
Cluster 4	1188.69	15.30	12.03	9.96	79.28	14.97
Cluster 5	197.24	8.78	6.62	5.94	68.42	19.23
Cluster 6	527.53	12.60	9.09	7.91	78.60	19.26
Cluster 7	1015.20	16.77	11.07	9.60	79.26	17.47
Cluster 8	452.59	11.20	8.73	7.72	73.79	18.64
Cluster 9	835.55	13.70	10.75	9.26	79.25	17.02
Cluster 10	1404.27	22.03	12.18	9.50	78.78	13.53
Cluster 11	86.84	5.97	5.24	4.62	60.68	17.50
Cluster 12	965.09	15.32	11.08	9.14	79.49	16.27
Cluster 13	305.87	10.09	7.66	6.85	72.30	19.18
Cluster 14	1077.39	17.80	11.00	9.13	87.16	13.60
Cluster 15	1280.67	15.93	11.67	10.60	74.23	11.23
Cluster 16	38.94	6.70	3.40	3.12	27.54	13.98
Cluster 17	625.93	13.25	9.46	8.70	78.37	17.14
Cluster 18	714.91	14.11	9.70	8.41	78.41	17.79
Average	340.525	10.076	7.59	6.7289	70.7	18.581

The maximum inter cluster (D^2) value was obtained between cluster 10 and cluster 11. These clusters may be used for hybridization programme due to wide variability and possibility of transgressive sergeants. The minimum cluster distance was obtained in cluster 2 and cluster 5 which indicates that the accessions belonging to such clusters are relatively close. The selection of parents from genetically close clusters may be due to narrow genetic base and inbreeding depression.

The pattern of distribution of accessions in different clusters indicating the existence genetic diversity which is related to geographical distribution. These 400 genotypes were grouped in to 18 clusters as presented in Table 2 which is apparent that cluster 1 (28 accessions), cluster 2(63 accessions), cluster 3(50 accessions), cluster 4 (3 accessions), cluster 5 (56 accessions), cluster 6 (20 accessions), cluster 7 (1 accessions), cluster 8 (34 accessions), cluster 9 (7 accessions), cluster 10 (1 accession), cluster11 (24 accessions), cluster 12 (6 accessions), cluster 13 (53 accessions) cluster14 (1 accession), cluster15 (1 accession), cluster16 (3 accessions), cluster17 (12 accessions) and cluster 18 (10 accessions).The clusters such as 7, 10, 14 and 15 had 1 accession in each with hybrid 7/15, Sora, Tella Gulabi and Amini, respectively. All these accessions possessed the fruit weight ranged from 1015.20g to 1280.67g which are meant for pickle making.

Table 2. Distribution mango accessions in various clusters

Clusters	Varieties/Hybrids
Cluster 1 (48accessions)	Ananas, Arka Puneet, Ashrafi, Bangalore Sindhura, Bennet Alphonso, Bombay Green, Chambeliwala, Chinnarasam, Cipia, Dalbia, Dilpasand, Dori,Fazrizafrani,H-165,H-85, Himsagar, Kacha Meetha, Kadikai, Kari Ishad, Karkanchavadi Rumani, Keitt, Khazri, Kitchner, Kurd, Lord, Madan Rao Pasand, Mahmood Bahar, Maya, Motichoor, Muffarai, Mulgoa, Mumbaigaro, Murshidabad, Navneet, Nom- Dok-Moi, Nr.25, Pattar, Peddarasam, Potte, Prior, Rangoon Goa, Rumani, Salem, Sanakalu, Santi, Mulgoa, Tatamidi, Tenkasi Banganpalli, Thogarapalli.
Cluster 2 (63accessions)	Almas, Alphonso black, Ambika, Ameer gola, Andamans local, Apple Rumani, Ashruf-Us-Samar, Asiquot, Badami modal, Bhopdya, Borsha, Botlimavu, Brindabani, Chimut, CISH M-2, Devrakhio, Dofasala, Gidagana Mavu, Gopal Bhog, Guruvam, Hindustan Ball,Hy-87, Hyder Sahib, IRS (Long fruit), Jawahar, Kasturi Mamidi (R), Kohinoor, Kottur Konum, Kove Sara, Lal Sundari, Lat Sundari, Mahamoozda, Malai Misri, Malgesh, Mandor Katta, *Mangifera zeylanica*, Manibhatta Appe, Manipur, Manoranjan (Sreddy), Moreh, Muvandan, Nagin, Neelgoa, Olour, Panchavarnam, Papayakhas, Prabhashankar, Puttu, Raja Pasand, Ramphalya, Raspuri, Rosa, Safeda Malihabad, Santhura Collection, Sardar, Sensation, Sepia, Sindhu, Sundar Langra, Sundarshan, Tenkasi Rumani, Tofanchan and Vellaikulamban
Cluster 3 (50accession)	Adderi jeerige, Amrapali, Anfas, Balekoppa appe, Bappakkai, Barbalia, Bombay darsha, Chengavarikai, Coorg Collection, Dattatreya local, Dashehari Clone-51, Ec 95862, Gomavu, H-12 (Arka udaya), H-151, Hamsa Mamidi, Hilario, Hittalahalli Appe, Jeerige, Kalapadi, Kalkuni, Karigal Appe, Kerala Kalapadi, Khas-Ul-Khas, Kintalavenipeta, K-o-22, Kobbe, Kurukkan, Kutumba Appe, La resorce -1, La Resource-2, Lalmuni, Lazzat baksh, Licthi, *Mangifera griffithi*, Narayanasheni, Narela (SR), Nekkare, Paiyur–1, Sabre, Sadamidi, Safeda Lucknow, Siddapura Alavalli, Siroli, Terpentine, Thali, Thumbebeedu, Vattam, Vinayaka Hegde, Willard
Cluster 4 (3 accessions)	DorganiKayi, Maharaja Pasand(L), Safed Mulgoa
Cluster 5 (56 accessions)	Achar Pasand, Agarabathi, Akhadya, Alfazli, All season, Ambalavi, Ananthabhatta appe, AtiMadhuram, Bandariya, Bhutto Bombay, Bobbalipunasa, Bombayno.1, Carabao(g), Carabao(s), Chandanum, Chitanga, Fernandin, Furtad, H-14, IRS (Small fruit), Isagoor Appe, Janardhan Pasand, Java, Kalapara, Kalgundi Koppa Appe, ,Karanjio, Khuddus, Kishen Bhog, Zardalu, KM P7, *Mangifera odorata*, Miranda, Mohammada Vikarabad, Mohandas, Mylupilian, Naati, Nalla Mamidi, Neeleshwari, Neelphonso, Neeluddin, Pacharisi (TN), Panakalu, Peach, PKM-2, Ratnagiri Alphonso, Ratul, Ropeday, Royal Special, Samarbehisht Chausa, Shandariya, Sharbathi Bagri, Shidadakke Appe, Surankundi, Virudhanagar, Yakutti and Zardalu
Cluster 6 (20 accessions)	Arya Samaj, Azam-Us –Samar, Badaaam, Bandar bandal, Chausa, Fakir, Fakirwala, Hansraj, Jalal, Kerala Dwarf, Lahara, Lal Khatra, Manoranjan, Ostin, Padiri, Sai Sugandh, Samparpatti Totapuri, Swathantram, Thatnur and Vanraj.
Cluster 7 (1 accession)	Hybrid 7/15

Cluster 8 (34 accessions)	Abbas, Allampurbaneshan, Aryavarthana Rasalu, Black ceri, Bombay alphonso, Bombay natasala, Bombay peda, Chandrama, Chettalli, Dannalli appe, Danti Mamidi, Fazli, Goa Kodur, H-56, Harsha, Himam Pasand, Hyb-11/14, Intimax (P3), Jehangir, Kalami Hindustani, Kensington, K-o-11, Ku-8, Mage Mavu, Manjeera, Mombasa, Mundappa Black, Navaneetham, Nazukbadan, Neeleshan, Pkm 1, Ruswani, Thorappadi, Warate Gidaga
Cluster 9 (7 accessions)	Arka Aruna, Begum Pasand, Black Andrews, Hamlet, Katta Gola, Rajapuri, Thambva
Cluster 10 (1 accession)	Sora
Cluster 11 (24 accessions)	Appemidi, Chandrakaran, Chanshi, Creeping, DodderiJeerige, Elaichi, Gurumurthy Appe, Hajeera, Heera Chowki, Huli Appekai, Kalakai, Kempikundi, Lalpasand, Malange, Muregeer, Musoore, Mylapuri, Nuha (M), Pacharasi, Rasool, Rubi, Starch, Tenkasi Neelum, Vhout
Cluster 12 (6 accessions)	Himayat Pasand, Kerali Goa, Kothapalli Kobbari, Mutwar Pasand, Shahjahan, Tenneru
Cluster 13 (55 accessions)	Alphonso, Anda, Arka anmol, Arka Neelkiran, Asif Pasand, Au Rumani, Badagulab, Chauthi, Cherukurasam, Chitha, Colaso, Dashehari, Dwarf Rumani, Faluda, Gaddahall Appe, Goa Bunder, Goa Mankurd, Gola, Goran Appe, Hur (SR), Jamedar, K-0–7, Kadari, Kadri, Kalakand, Kalwa Gudda, Kesar, Kirsapati, Kolanka Goa, Krishna, Laddu, Langra, Latif, Lemon, Maharaja of Mysore, Mallika, Mandamane, Nagalapalli Rasalu, Neelum,Nr-34 Local, Panchadara Kalasa, Papayaraju Goa, Peter, Pulihara, Ratna, Rehman, Pasand, Salem Bangalora, Shakkar Gola, Sushan Bhog, Suvarna Rekha, Swarna Jehangir, Taimur Pasand, Tephala, Tokio, Xavier
Cluster 14 (1 accession)	Tella Gulabi
Cluster 15 (1 accessions)	Amini
Cluster 16 (3 accessions)	Halasage, Haldotta Appe, Kana Appe-1
Cluster 17 (17 accessions)	Balakondapari, Balakrishnan, Banganapalli, Cowasji Patel, Ebatti Mavu, Eldon, Elephant Head, K -0-32, Kasturi Mamidi (l), Khudadath, K-0-15, Lily, Maharaja Pasand(rd), Shendriyo, Tommy Atkins, Totapuri, Whiteceri
Cluster 18 (10 accessions)	Anardana,Gaddemar,Kmh-1, Makaram, Mohan Rao Pasand, Mulgoa Black, Nymath, Pahilwan, Papaya (SR), Rebello

Estimates of phenotypic variance and genotypic variance had only a narrow difference for all six characters studied indicating that these characters are not much influenced by environmental factors (Table 3). This also suggests the presence of sufficient genetic variability which can be exploited by adopting clonal selection or selection of chance seedlings. The maximum PCV was recorded for fruit weight followed by fruit length and fruit diameter. This indicates the better scope for phenotypic selection of these traits for improvement.

Heritability and genetic advance for fruit characters varied considerably. The high heritability (0.84 to 0.94) and high estimate of genetic advance recorded for fruit weight, fruit length, fruit diameter, fruit thickness, pulp recovery and TSS. High heritability indicates the effectiveness of selection through phenotypic performance but it does not mean a high genetic gain. However, high heritability associated with high genetic advance proves more useful for efficient improvement of a character through simple selection. In the present study, high heritability estimates with high genetic advance as per cent over mean was observed for the all the fruit traits studied indicating the possible role of additive gene action, whereas moderate heritability with low genetic advance as per cent over mean indicating the non-additive gene action. In the present investigation, the estimates of genotypic correlations in general were higher than phenotypic correlations, indicating the presence of inherent association between various characters.

A total of 30 characters have been used to group the 400 genotypes as per standard descriptor of the Bioversity International (Table 4) which is evident that there are gradations of variations due to the heterozygosity nature of the crop.

Table 3. Genetic parameters for fruit characteristics of 400 mango accessions

Characters	Mean	Range	CV	GCV	PCV	h^2	Genetic advancement as % of mean
Fruit weight (g)	336.61	29.10-1404.2	15.141	63.946	65.714	0.946	128.37
Fruit length (cm)	10.050	4.33-22.03	6.228	25.317	26.072	0.942	50.72
Fruit diameter (cm)	7.57	3.23-13.50	5.589	20.529	21.276	0.930	40.86
Fruit thickness(cm)	6.71	2.80-11.40	8.287	19.346	21.046	0.844	36.68
Pulp recovery (%)	70.76	18.93 -89.67	4.762	13.234	14.065	0.885	25.69
TSS (°Brix)	18.61	5.50-31.00	8.124	20.501	22.052	0.864	39.32

Table 4. Grouping of 400 germplasm of mango based on qualitative traits

Character	Percentage (%)	Character	Percentage (%)	Character	Percentage (%)
1.Fruit shape		**11.Fruit beak type**		1. Slightly Juicy	50.00
1. Oblong	67.5	1.Absent	79.75	2. Juicy	41.75
2. Elliptic	1.50	2. Pointed	14.75	3. Very Juicy	8.25
3. Roundish	30.5	3. prominent	3.75	**21.Pulp aroma**	
4. Ovoid	0.25	4. Mammiform	1.75	1 Mild	55.50
5. Obovoid	0.25	**12.Fruit sinus type**		2. Intermediate	28.75
2.Shape of fruit apex		0. Absent	53.50	3. Strong	15.75
1. Acute	48.75	1. Shallow	38.25	**22.Presence of turpentine flavour**	
2. Obtuse	38.75	2. Deep	8.25	0. Absent	61.00
3. Round	12.50	**13.Fruit skin waxiness**		1. Mild	22.00
3.Fruit attractiveness		1. Waxy	95.50	2. Intermediate	9.50
1. Poor	15.75	2. Non-waxy	4.50	3. Strong	7.50
2. Average	35.25	**14.Pulp colour of ripe fruit**		**23.Veins on stone**	
3. Good	39.00	1. Light yellow	1.00	1. Level with surface	46.75
4. Excellent	10.00	2. Golden yellow	-	2. Depressed	14.50
4.Fruit skin surface texture		3. Yellow orange	66.00	3. Elevated	38.75
1.Smooth	84.75	4. Orange	14.50	**24.Pattern of stone venation**	
2. Rough	15.25	5. Greenish yellow	0.25	1. Parallel	46.00
5.Density of lenticels on fruit skin		6. Yellow	17.50	2. Forked	54.00
3. Spare	21.25	7. Light orange	0.25	**25 Quantity of fiber on stone**	
5. Medium	23.00	8. Dark orange	0.50	3. Low	57.50
7. Dense	55.75	**15.Pulp texture of ripe fruit**		5. Intermediate	27.50
6.Fruit stalks insertion		3.Soft	25.50	7. High	15.00
1.Vertical	71.25	5. Intermediate	40.00	**26.Adherence of fiber to stone**	

2. Oblique	28.75	7. Firm	34.50	3. Weak	12.25
7.Depth of fruit stalk cavity		**16.Adherence of fruit skin to pulp**		5. Intermediate	29.75
0. Absent	41.25	0. Absent (free)	17.75	7. Strong	58.00
1. Shallow	43.75	3. Weak	38.00	**27Space occupied by seed inside the stone (%)**	
2. Medium	6.50	5. Intermediate	27.00	1. < 25	1.75
3. Deep	7.75	7. Strong	17.25	2. 26 - 50	2.25
4. Very deep	0.75	**17.Quantity of fiber in pulp**		3. 51 - 75	19.25
8. Fruit stalks attachment		0. Absent	3.75	4. 76- 100	76.75
3. Weak	6.50	3. Low	48.75	**28.Seed shape**	
5. Intermediate	55.25	5. Medium	32.25	1. Ellipsoid	2.75
7. Strong	38.25	7. High	15.25	2. Oblong	13.75
9.Fruit neck prominence		**18.Adherence of fiber to fruit skin**		3. Reniform	83.50
0. Absent	80.75	3. Low	49.75	**29.Type of embryony**	
1. Slightly	12.75	5. Intermediate	39.25	1. Monoembryony	91.50
prominent					
2. Prominent	5.50	7. High	11.00	2. Polyembryony	8.50
3. Very prominent	1.00	**19. Fiber length in the pulp.**		**30.Eating quality**	
10.Slope of fruit ventral shoulder		3. Short (0.58 -2)	44.25	3. Poor	16.75
1. Slopping abruptly	9.00	5. Medium (2.1-5)	6.50	5. Good	63.50
2. Ending in a long curve	44.75	7. Long (5.1 & above)	49.25	7. Very good	15.50
3. Rising and then rounded	46.25	**20.Pulp juiciness**		9. Excellent	4.25

DISCUSSION

The analysis of variance for 6 quantitative traits exhibited the significant differences among the 400 genotypes of mango which indicates the existence of genetic diversity within the *Mangifera indica*. The maximum fruit weight of 1404.27g in var. Sora followed by 1280.67g in var. Amini whereas the minimum fruit weight was of 29,51g in var. Kana Appe followed by 39.31g in var. Halasage. The results are similar as reported by Pandey and Dinesh (2010). While selecting the parents for hybridization programme, the quantitative characters such as fruit weight, fruit length, fruit thickness, fruit diameter, and pulp recovery should be considered as all of them have high heritability. Transgressive segregation was observed for fruit size in the progeny (Iyer and Subramanyam, 1987) and it appeared to be governed by additive genes (Sharma and Majumder, 1988a). Detailed study conducted by Prabhuram (1998) based on heritability, expected genetic advance and total genetic variance gave useful information on inheritance of different fruit characters. Fruit weight was influenced considerably by the environmental conditions. Equal proportion of the additive and non-additive components of the total genetic variance influenced its genotype. Rajan *et al.,* (2009) found high degree of broad sense heritability in mango varieties for the length and weight of fruit, peel weight and length and weight of stone. The fruit length was maximum (22.03 cm) in var. Sora followed 16.77cm in hybrid 7/15 where as the minimum fruit length of 4.33cm was recorded in var. Pacharasi. Fruit length shows transgressive segregation in either side of the parental limits and therefore, suggested a polygenic control of this character. Also, this character was influenced by environment to a considerable extent (Pandey, 2012). The maximum fruit thickness of 11.40cm was recorded in var. Dorgani Kavi followed by 9.87 in var. Amini whereas the minimum thickness

was recorded (2,80cm) in Haldotta Appe. Fruit thickness showed polygenic control and was highly influenced by environmental factors. For breadth of fruit the genotypic contribution appeared to be comparatively lesser than in most of the traits. The peel colour and attractiveness are considered as important qualitative traits in mango, only 10% of the germplasm possess excellent attractiveness out of 400 germplasm screened. A high frequency of hybrids with red peel or burgundy blush can be recovered from crosses where one of the parents has an intense red blush (Brittell *et al.,* 2004). The highest pulp recovery (89.67%) was recorded in var. Manoranjan followed by 88.20 % in var. Lahara whereas the lowest pulp recovery was recorded in var. Halasage. The highest TSS (ÚBrix) of 31.00 was recorded in var. Dattatreya local followed by 30.67 in var.K-0-7 where as the lowest was recorded in var. Halasage (5.5%). Sharma and Majumder (1988) stated that total Beta carotenoid pigments and T.S.S. content in these two hybrids exceeded the better parent Dashehari suggesting the gene action showing transgressive segregation for this trait. On the other hand, light yellow colour of pulp appeared dominant over orange yellow in the progenies of Alphonso x Neelum cross (Iyer, 1991). According to Prabhuram (1998), total soluble solids (T.S.S.) content in some hybrids transgressed either of the parents Amrapali and Sensation, which suggested a polygenic control for this trait and that it was influenced considerably by environmental factors.

Bretell *et al*., (2004) observed that many important fruit quality aspects such as fruit weight, fruit shape, ground skin colour, fruit width and pulp depth have high heritability, and can therefore be readily selected in a breeding programme. For non-ordered traits scored in discrete categories (blush colour, bloom, lenticel colour, embryo type and flavour), an estimate was made of data consistency from multiple scores for individual hybrids at different times and locations. Relatively high consistency value was recorded for fruit flavour, and in combinations involving Kensington Pride. The analysis of blush colour and fruit flavour in twelve families of hybrids has confirmed that these characters have a strong genetic component, the high frequency of hybrids with red or burgundy blush can be recovered from crosses where one parent has an intense red blush colour. Singh *et al*., (2004) observed wide magnitude of phenotypic coefficient of variation with high genetic advance for yield per plant and fruit weight in 31 chance seedlings of mango.

Biometrical studies

The analysis of variance for 6 quantitative traits showed significant difference among 400 germplasm of mango indicating the existence of diversity. These germplasms have been grouped in to 18 clusters and distribution of germplasm among the clusters varied in numbers which indicates that genetic divergence was related to geographical differentiation. The clustering of genotypes from different eco-geographical locations in to one cluster can be attributed to possibility of free exchange of germplasm. Similar observation was recorded by Singh and Gupta. However, unidirectional selection practiced for a particular trait or a group of linked traits in several places may produce similar phenotype which can be aggregated in to one cluster irrespective of their geographical origin as reported by Singh and Gupta (1968). The maximum inter cluster (D^2) value was obtained between cluster 10 and cluster 11. These clusters may be used for hybridization programme due to wide variability and possibility of transgressive segregants (Singh, 1991; Singh *et al.,* 1991). The minimum cluster distance was obtained in cluster 2 and cluster 5 which indicates that the accessions belonging to such clusters are relatively close. The selection of parents from genetically close clusters may be due to narrow genetic base and inbreeding depression (Singh and Gupta, 1968).

Qualitative characters

Out of 30 qualitative characters studied in 400 germplasm, the fruit shape distribution was observed to be oblong (67.5%), .elliptic (1.50%), roundish (30.5%), ovoid (0.25%), and obovoid (0.25%), fruit attractiveness, fiber free, pulp recovery (>70%) , pulp aroma (mild 55.50 (%), intermediate (28.75%) and strong (15.75%)); TSS and eating quality (poor (16.75%), good (63.50%), very good (15.50%) & excellent (4.25%) are very important for commercial point of view.

Sharma (1987) opined that flesh colour is controlled by additive genes. However, Iyer (1991) observed that light yellow colour is dominant over orange-yellow in the progenies of Alphonso x Neelum cross. Dinesh (2003), carried out using half-sib analysis and found that fruit characters like fruit weight, TSS and

pulp percentage are controlled by non additive factors and heritability is less. Lavi *et al.* (1998) reported that parents should not be chosen on the basis of phenotype since offspring performance is quite unpredictable. With regard to skin colour, it was found that when red-coloured varieties were crossed with green-coloured varieties, gradation of colour in the progenies indicated that it is controlled by a number of loci (Sharma, 1987; Iyer and Subramanyam, 1987). The presence of beak on the fruit seems to be dominant as the entire progenies had beak on their fruits when 'Totapuri' was used as one of the parents (Iyer and Subramanyam, 1979). Bunch bearing was found to be dominant over single fruiting (Sharma *et al*., 1972). Inheritance of red peel colour in the cross Amrapali x Sensation suggested no clear out dominance, as the cross between these parents with yellow and red peel respectively yielded hybrids with yellow, green yellow, fully green and red colouration on peel in various intensities. A high heritability with a high expected genetic advance clearly suggested that the inheritance of this trait was governed more by additive genes (Prabhuram, 1998). Sharma and Majumder (1988) in the crosses involving Totapuri Red Small and Sensation (both red peeled ones) and yellow-peeled varieties Dashehari and Amrapali revealed that the red peel colour was dominant and governed by duplicate genes, thereby showing various gradations of pink blush on the fruits. They reported that a few hybrids bore fruits with green colour which suggested that the red colour is in heterozygous condition. Fruit peel colour was found to be governed by a number of loci (Iyer and Subramanyam, 1987). Red peel colour is dominant over yellow and green and gradation of red peel suggested role of duplicate gene. Fruit quality varied in different hybrids developed at IARI, New Delhi. Fruit pulp colour is governed more by additive genes and that the environmental influence is very low (Prabhuram, 1998). Based on two hybrids, *viz*., Amrapali and Mallika, Fibre in pulp showed high heritability and high expected genetic advance, which suggested the genetic variance to be additive in nature. Aroma in pulp showed high heritability with a moderately high expected genetic advance. This suggested equal contributions of additive and non-additive genetic variance. On the other hand, genetic variance of fruit taste might have been governed mostly by non-additive genes.

Most of the commercially important varieties have been evolved as open pollinated progenies; still there are lot scopes to explore the OP varieties through exploitation of variability by selections. However, the varieties such as Alphonso, Amrapali, Arka Anmol, Arka Puneet, Bobbali punasa, Bombay no.1, Creeping, Danti Mamidi, Dashehari, Goa Kodur, Maharaja of Mysore, Mohammada Vikarabad, Mohan Rao Pasand, Neelgoa, Prabha shankar, Prior and Sardar, possess an excellent eating quality which can be utilized the breeding programme as well as commercial cultivation for table purpose.

CONCLUSION

The analysis of variance for 6 quantitative traits showed significant differences among the 400 genotypes of mango which indicates the existence of genetic diversity. The maximum inter cluster (D^2) value was obtained between cluster 10 and cluster 11. These clusters may be used for hybridization programme due to wide variability and possibility of transgressive sergeants. Estimates of phenotypic variance and genotypic variance had only a narrow difference for all six characters studied indicating that these characters are not much influenced by environmental factors. This also suggests the presence of sufficient genetic variability which can be exploited by adopting clonal selection or selection of chance seedlings.

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