RESEARCH ARTICLE

STUDIES ON GENETIC DIVERGENCE IN UNIQUE INDIGENOUS MANGO ACCESSIONS OF WESTERN GHATS

*[1]Vasugi, C., [2]Sekar, K., [1]Dinesh, M. R., and [3]Venugopalan, R.

[1]Division of Fruit Crops, Indian Institute of Horticultural Research, Hessaraghatta Lake Post, Bangalore-560089, India
[2]Department of Horticulture, Annamalai University, Annamalai Nagar, Tamil Nadu
[3]Section of economics and statistics, IIHR, Bangalore

ARTICLE INFO	ABSTRACT
	Studies carried out on the genetic divergence in 43 unique indigenous mango accessions using 19 quantitative traits exhibited high phenotypic and genotypic variance for fruit weight (12909.38, 12661.92) followed by vitamin 'C' (1231.71 and 1221.023). The genotypic coefficient of variation was more than 60 per cent for the characters fruit weight, vitamin C and sugars indicating that selection procedure can be applied in the improvement of characteristics, which is confirmed by the findings of heritability in broad sense and was observed to be high (>90 per cent) for all the fruit parameters except for pulp per cent, which recorded a moderate heritability estimate of 76 per cent, indicating the influence of environment on this character. The genotypic correlation coefficients were higher than phenotypic correlation coefficients and the fruit weight was observed to have high positive phenotypic and genotypic correlation with pulp per cent, pH, total sugars, non-reducing sugars reducing sugars and stone weight, indicating that selection of medium sized fruits will lead to good pulp recovery.

INTRODUCTION

The mango (*Mangifera indica* L.) popularly called as the 'King of fruits' is one of the choicest fruit crops of tropical and sub-tropical regions of the world. As on today more than 1000 mango cultivars are available in the country, representing the biggest mango germ pool in the world, but only 25-30 are of commercial importance and still an ideal mango variety is lacking. Hence, breeding attempts to develop an ideal mango variety would be dwarf, regular bearer with medium size fruits (250–300 g). Additionally, it should be highly tolerant to various fungal and bacterial diseases. In a highly cross pollinated crop like mango, the knowledge on the magnitude of genetic variation for fruit characteristics among the varieties and its heritability is essential to take up desired crossing programme. Hence, breeding and development of superior varieties through hybridization requires prior quantitative assessment of genetic divergence in the available gene pool especially in the parental lines to be used in the hybridization. If the parents are diverse for the characters, then there is a greater chance of getting wide spectrum of recombinants. As the information on genetic divergence of unique indigenous types are lacking in mango, the present investigation was carried out to group these genotypes based on their genetic distances.

MATERIALS AND METHODS

The present study was carried out at Indian Institute of Horticultural Research, Hessaraghatta, India. The material consisted of 35 pickling accessions, five commercial accessions and three polyembryonic accessions conserved in the Field Gene Bank (FGB) of the Institute.

Corresponding author: Vasugi C., Division of Fruit Crops, Indian Institute of Horticultural Research, Hessaraghatta Lake Post, Bangalore-560089, India

In each accession, one tree was selected to represent one replication and the statistical analysis was carried out by adopting randomized block design. Ten randomly selected leaves/ flowers/ fruits and stones were used for bio-metric observation in each accession and replication. Data from 19 important quantitative characters with three replications were analyzed (Singh and Chaudhury, 1977) to assess the variability, correlation and heritability as detailed below. The analysis of variance for the 19 traits were carried out (Panse and Sukhatme,1985) and the average performance among accessions was compared pair-wise using the critical difference (CD) values derived from the statistical analysis of randomized complete block design (RBD) with three replications. Phenotypic and genotypic coefficients of variability for all characters were calculated (Burton and De Vane, 1953). The ratio of genotypic variance to phenotypic variance was calculated and expressed in percentage (Hanson *et al.*, 1956) as heritability. Mahalanobis D^2 statistic was used for estimating the genotypic divergence among forty three genotypes. For grouping the genotypes into different clusters, a method suggested by Tocher (Rao, 1952) was followed.

RESULTS AND DISCUSSION

Variability

The perusal of data presented in Table 1 indicated that phenotypic variance ranged from 0.43 (leaf width) to 12909.39 (fruit weight) and the genotypic variance ranged from 0.67 (leaf width) to 12661.91 (fruit weight). This was followed by vitamin 'C' (1231.71 and 1221.023 phenotypic and genotypic respectively). This indicates that there is ample scope for improvement in such characters. The phenotypic co-efficient of variation (PCV) ranged from 14.12 (pulp per cent) to 88.53 (per cent acidity) and the GCV ranged from

12.33 (pulp per cent) to 88.45 (per cent acidity). High GCV was observed for acidity (88.45 per cent) and bisexual flower (84.32 per cent) followed by sugars, fruit weight and vit.C with GCV of more than 60 per cent. The higher GCV recorded in this study indicates that this trait can be improved by way of selection. Similar results were also obtained(Rajan *et al.*, 2009) where the PCV and GCV were high for pulp weight, fruit, peel and stone, pulp to stone ratio, length of fruit and stone and medium to low for other traits in mango.

Heritability

The perusal of data presented in Table 1 indicated that the heritability values ranged from 76.2 (pulp per cent) to 99.8 (acidity per cent). High heritability was observed for all traits except for pulp per cent which recorded a moderate heritability estimate of 76.2 per cent. Heritability is the heritable portion of phenotypic variance and is a good index of the transmission of characters from parent to offspring (Falconer, 1989). The heritability in broad sense recorded in the present investigation was high (>90 per cent) for all the fruit parameters except for pulp per cent, which recorded a moderate heritability estimate of 76 per cent, indicating the influence of environment on this character. High heritability for fruit characters like length (98.4 per cent), breadth (99.5 per cent), weight (99.4 per cent) and pulp (90.0 per cent) was also recorded (Singh, 2002), which confirms the findings of the present study. If the heritability of a character is very high, selection for this character would be more effective as there is a close correspondence between genotype and phenotype (Singh, 1991). Since, pulp per cent is indirectly governed by stone thickness, selection for pulp per cent would lead to fruits with less stone.

D^2 analysis

Group constellations

The 43 accessions were grouped into seven clusters using clustering technique (Table 4). The cluster I comprised of 20 accessions. This was followed by cluster II with 18 accessions, while the clusters III, IV, V, VI and VII had only one accession in each. The intra cluster distance ranged from 0.00 to 41.79. Cluster II showed the maximum intra cluster distance and it was found to be the lowest in clusters III, IV, V, VI and VII (Table 5). Maximum inter cluster distance (136.57) was found between clusters V (Aruna Gowda Appe) and VI (Himsagar) which revealed that these genotypes are more diverse. The minimum intercluster distance (56.11) was observed between cluster II and IV. Hence, selection of parents from these diverse clusters will result in heterotic F$_1$s with wide spectrum of recombinants.

Character contribution towards divergence and Cluster means

The contribution of characters towards divergence and cluster means (Table 6) revealed that the traits titrable acidity (38.98) followed by total sugar (15.39), pH (11.19) and stone weight (10.41) contributed more towards divergence. The fruit characters like pulp weight (34.03 %), peel weight (22.65 %) and TSS (10.22 %) contributed more towards the genetic divergence (Rajan *et al.*, 2009). The cluster II recorded maximum leaf width (3.9 cm) and the cluster III recorded the maximum petiole length (3.0 cm), bisexual flower per cent (25.47) and minimum stone weight (7.00 g). The cluster mean for the trait pH was maximum (5.61) and minimum (0.31) for the trait

Table 1. Phenotypic variance, Genotypic variance, Phenotypic coefficient of variation, Genotypic coefficient of variation, heritability estimates

Characters	Phenotypic variance (Vp)	Genotypic variance (Vg)	Heritability (h2)	Phenotypic coefficient of variation (%) (PCV)	Genotypic coefficient of variation (%) (GCV)
1	4.49	4.12	91.78	24.98	23.93
2	2.12	2.02	95.21	23.50	22.93
3	1.53	1.38	90.05	22.60	21.44
4	12909.39	12661.91	98.08	63.59	62.97
5	78.82	60.07	76.21	14.12	12.33
6	4.82	4.81	99.82	88.53	88.45
7	0.67	0.67	99.65	22.04	22.00
8	1231.71	1221.02	99.13	62.20	61.93
9	18.51	18.45	99.65	66.73	66.61
10	6.37	6.31	99.00	66.40	66.07
11	2.95	2.91	98.78	66.08	65.67
12	25.05	24.85	99.18	35.83	35.68
13	5.94	5.20	87.49	16.53	15.46
14	0.43	0.37	87.18	17.42	16.26
15	0.46	0.43	92.66	30.25	29.12
16	41.68	39.33	94.36	24.93	24.22
17	2.45	2.43	99.18	23.00	22.90
18	56.34	52.37	92.96	87.46	84.32
19	101.28	100.45	99.18	34.41	34.27

1.Fruit Length (cm), 2.Fruit Breadth (cm), 3.Fruit thickness (cm), 4.Fruit weight (g), 5.Pulp (%),6.Titrable Acidity (%), 7.pH,   8.Vitamin C (mg 100g $^{-1}$) 9.Total sugar (%), 10.Non reducing sugar (%), 11.Reducing sugar (%), 12.TSS (^{o}B),13.Leaf length (cm),14.Leaf width (cm),15.Petiole length (cm), 16.Inflorescence length (cm), 17.Stone length (cm), 18.Bisexual flower (%), 19.Stone weight (g)

Correlation studies

In the present investigation, the genotypic correlation coefficients were higher than phenotypic correlation coefficients (Table 2, 3), showing a high level of genotypic influence in character expression and a lesser environmental effect. The fruit weight was observed to have high positive phenotypic and genotypic correlation with pulp per cent (0.552, 0.614), pH (0.553, 0.539), total sugars (0.520, 0.526), non-reducing sugars (0.518, 0.527) and reducing sugars (0.518, 0.525) and stone weight (0.564, 0.571). Hence, selection of medium-sized fruits will lead to good pulp recovery with a good sugar content, which is beneficial for evolving new progenies. Similar results were obtained in the correlation of fruit characters in mango (Yadav, 2003).

titrable acidity was recorded in the cluster IV. The cluster V recorded maximum cluster mean for the trait vitamin C (89.90 mg 100g $^{-1}$) and minimum mean value for the trait titrable acidity (0.13 %). The cluster VI recorded maximum cluster mean for more number of traits *viz.,* fruit breadth (7.40 cm), fruit weight (322.50 g), pulp per cent (67.00), total reducing and non reducing sugars (16.47, 9.87, 6.6 per cent respectively), TSS^{0}B (23.13), inflorescence length (32.50 cm) and stone length (10.47 cm). The cluster VII recorded maximum values for the traits fruit thickness (7.30 cm), fruit weight (246.20 g), leaf length (17.18 cm) and petiole length (3.00 cm). Though the accessions selected in the present study were broadly grouped into acidic types (20) in the first cluster and less acidic types (18) in the second cluster, the accessions *viz.,* Alphonso, Dashehari, Himsagar, Kana Appe 1 and Aruna Gowda Appe were distinctly separated from each other and formed mono clusters. Out of

Table 2. Phenotypic correlation between 19 morphological characters in mango germplasm

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	1	0.741**	0.661**	0.713**	0.426**	-0.204	0.286	-0.182	0.224	0.219	0.231	0.061	0.154	-0.049	0.027	0.170	0.829**	-0.134	0.680**
2		1.000	0.852**	0.791**	0.593**	-0.432**	0.424**	-0.311*	0.377*	0.378*	0.364*	0.263	0.047	-0.149	0.059	0.332*	0.506**	-0.314*	0.569**
3			1.000	0.838**	0.695**	-0.496**	0.451**	-0.283	0.414**	0.408**	0.394**	0.307*	0.201	-0.039	0.199	0.299	0.443**	-0.354*	0.428**
4				1.000	0.552**	-0.554**	0.533**	-0.374*	0.520**	0.518**	0.518**	0.366*	0.179	-0.072	0.174	0.198	0.662**	-0.229	0.564**
5					1.000	-0.347*	0.323*	-0.246	0.261	0.261	0.255	0.213	0.141	0.082	0.280	0.186	0.277	-0.187	0.136
6						1.000	-0.813**	0.484**	-0.832**	-0.831**	-0.835**	-0.752**	-0.360*	-0.204	-0.470**	-0.173	-0.112	-0.117	-0.136
7							1.000	-0.507**	0.841**	0.847**	0.839**	0.683**	0.411**	0.134	0.437**	0.238	0.258	0.171	0.157
8								1.000	-0.543**	-0.538**	-0.543**	-0.414**	-0.109	-0.051	-0.105	-0.039	-0.111	-0.031	0.021
9									1.000	0.995**	0.986**	0.788**	0.347*	0.145	0.360*	0.232	0.189	0.191	0.158
10										1.000	0.973**	0.805**	0.353*	0.143	0.363*	0.231	0.188	0.183	0.164
11											1.000	0.764**	0.327*	0.154	0.340*	0.229	0.209	0.237	0.169
12												1.000	0.321*	0.150	0.405**	0.140	0.007	0.238	0.083
13													1.000	0.657**	0.834**	0.120	0.158	0.042	0.118
14														1.000	0.600**	0.043	-0.102	0.126	-0.118
15															1.000	0.079	0.031	0.100	0.038
16																1.000	0.083	0.105	0.226
17																	1.000	-0.076	0.774**
18																		1.000	-0.185
19																			1.000

1.Fruit Length (cm), 2.Fruit Breadth (cm), 3.Fruit thickness (cm), 4.Fruit weight (g), 5.Pulp (%), 6.Titrable Acidity (%), 7. pH, 8.Vitamin C (mg $100g^{-1}$) 9.Total sugar (%), 10.Non reducing sugar (%), 11.Reducing sugar (%), 12.TSS (^{o}B),13.Leaf length (cm),14.Leaf width (cm),15.Petiole length (cm), 16.Inflorescence length (cm), 17.Stone length (cm), 18.Bisexual flower (%), 19.Stone weight (g)

Table 3. Genotypic correlation between 19 morphological characters in mango germplasm

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	1	0.749**	0.687**	0.730**	0.435**	-0.209	0.303	-0.187	0.235	0.232	0.243	0.059	0.180	-0.051	0.028	0.189	0.866**	-0.149	0.708**
2		1.000	0.880**	0.808**	0.620**	-0.439	0.437	-0.316*	0.386*	0.388*	0.374*	0.270	0.054	-0.173	0.056	0.345*	0.517**	-0.334*	0.586**
3			1.000	0.890**	0.748**	-0.517**	0.478**	0.395**	0.435**	0.431**	0.416**	0.325*	0.231	-0.065	0.203	0.321*	0.470**	-0.390*	0.448**
4				1.000	0.614**	-0.560**	0.539**	-0.378*	0.526**	0.527**	0.525**	0.370*	0.201	-0.074	0.183	0.213	0.669	-0.242	0.571**
5					1.000	-0.390*	0.367*	-0.271	0.295	0.301	0.285	0.249	0.185	-0.077	0.318*	0.213	0.316*	-0.235	0.164
6						1.000	-0.815**	0.485**	-0.835**	-0.836**	-0.842**	-0.756**	-0.386*	-0.217	-0.488**	-0.179	-0.113	-0.123	-0.137
7							1.000	-0.509**	0.844**	0.853**	0.845**	0.688**	0.439**	0.142	0.453**	0.246	0.259	0.177	0.169
8								1.000	-0.546**	-0.544**	-0.548**	-0.418**	-0.115	-0.042	-0.106	-0.039	-0.112	-0.027	0.010
9									1.000	0.997**	0.991**	0.792**	0.374*	0.149	0.373*	0.238	0.191	0.198	0.159
10										1.000	0.988**	0.812**	0.379*	0.142	0.375*	0.236	0.190	0.192	0.165
11											1.000	0.772**	0.354*	0.169	0.356*	0.239	0.212	0.245	0.173
12												1.000	0.349*	0.164	0.427**	0.145	0.006	0.247	0.083
13													1.000	0.724**	0.884**	0.122	0.169	0.024	0.124
14														1.000	0.639**	0.024	-0.111	0.123	-0.132
15															1.000	0.075	0.029	0.105	0.035
16																1.000	0.083	0.114	0.232
17																	1.000	-0.079	0.781**
18																		1.000	-0.194
19																			1

1.Fruit Length (cm), 2.Fruit Breadth (cm), 3.Fruit thickness (cm), 4.Fruit weight (g), 5.Pulp (%), 6.Titrable Acidity (%), 7.pH, 8.Vitamin C (mg 100g -1) 9.Total sugar (%), 10.Non reducing sugar (%), 11.Reducing sugar (%), 12.TSS (oB),13.Leaf length (cm),14.Leaf width (cm),15.Petiole length (cm), 16.Inflorescence length (cm), 17.Stone length (cm), 18.Bisexual flower (%), 19.Stone weight (g)

Table 4. Composition of clusters based on D^2 analsysis

Cluster	Name of Genotypes
I	Dannalli Appe, Halasage, Nandgar Appe, Holekoppada Appe, Sadamidi, Dodderi Jeerige, Gurumurthy Appe, Kalakai, Shidadakke Appe, Huliappekai, Chanshi Appe, Mahabalagiri Appe, Adderi Jeerige, Gorana Appe, Anantha Bhatta Appe, Isagoor Appe, Jeerige, Kashimidi, Appemidi and Balekoppa Appe
II	Gaddalahalli Appe, Mani Bhatta Appe, Kovesara, Puttu, Kalwagudda, Kadikai, Kalkuni, Manipur, Thumbeebeedu, Muregeer, Hitalahalli Appe, Malange, Vattam, Tatamidi, Totapuri, Kangaramatha, Banganapalli and Dantimamidi
III	Kana Appe 1
IV	Dashehari
V	Aruna Gowda Appe
VI	Himsagar
VII	Alphonso

Table 5. Average intra and inter cluster D² and D values for 43 mango accessions

Cluster	I	II	III	IV	V	VI	VII
I	1626.11 (40.33)	6064.83 (77.88)	5848.58 (76.48)	12160.71 (110.28)	3641.04 (60.34)	14702.78 (121.26)	9201.99 (95.93)
II		1745.99 (41.79)	3210.02 (56.66)	3148.56 (56.11)	11513.29 (107.30)	4707.88 (68.61)	3382.47 (58.16)
III			0.00 (0.00)	5503.86 (74.19)	14062.89 (118.59)	10178.39 (100.89)	3723.81 (61.02)
IV				0.00 (0.00)	18291.48 (135.25)	2423.59 (49.23)	3762.96 (61.34)
V					0.00 (0.00)	18650.55 (136.57)	16458.58 (128.29)
VI						0.00 (0.00)	6152.21 (78.44)
VII							0.00 (0.00)

(Figures in parenthesis indicate D² values, Diagonal values are intra cluster values)

Table 6. Cluster means of D² cluster and contribution of characters towards divergence

Cluster/Character	I	II	III	IV	V	VI	VII	Number of times ranked first	Contributiontowards % divergence
Fruit length (cm)	7.90	9.03	4.05	10.50	10.50	10.30	8.80	1	0.11
Fruit breadth (cm)	5.64	6.88	3.03	6.40	5.90	7.40	7.40	2	0.22
Fruit thickness (cm)	4.94	6.13	2.75	5.60	5.30	5.60	7.30	1	0.11
Fruit weight (g)	116.29	246.98	22.60	170.50	150.00	322.50	246.20	8	0.89
Pulp (%)	60.18	66.59	46.46	62.30	58.25	67.00	66.90	1	0.11
Titrable acidity (%)	4.31	0.61	1.31	0.13	7.48	0.19	0.39	353	38.98
pH	3.02	4.32	3.86	5.61	3.05	4.81	4.31	102	11.19
Vit C (mg 100 g⁻¹)	75.06	40.02	60.00	18.29	89.90	12.80	23.80	63	6.98
Total sugar (%)	2.96	8.87	9.37	15.70	1.40	16.47	15.30	140	15.39
Non Reducing sugar (%)	1.74	5.26	5.68	9.23	0.86	9.87	8.37	1	0.11
Reducing sugar (%)	1.22	3.60	3.69	6.47	0.55	6.60	5.07	22	2.44
TSS ºB	10.13	17.00	20.60	19.00	10.30	23.13	19.10	42	4.65
Leaf length (cm)	13.80	15.70	14.87	14.30	13.44	15.92	17.18	1	0.11
Leaf width (cm)	3.69	3.90	3.77	3.30	3.14	3.40	3.80	4	0.44
Petiole length (cm)	1.91	2.58	3.00	1.60	1.64	2.50	3.00	1	0.11
Inflorescence length(cm)	24.70	26.71	21.00	28.30	28.00	32.50	29.00	8	0.89
Stone length (cm)	6.38	7.13	3.50	7.63	9.20	10.47	6.03	62	6.87
Bisexual flower (%)	7.59	8.45	25.47	18.78	6.94	12.32	1.59	1	0.11
Stone weight (g)	26.91	31.29	7.00	24.70	47.00	55.00	22.43	95	10.41

43 accessions, the presence of 38 accessions in two clusters (20 in cluster I and 18 in cluster II) indicated a low genetic base of these accessions. Except Appemidi, Balekoppa Appe and Chansi Appe all other members of the first cluster had less than 15° Brix and more acidity. In the second cluster, except Hittalahalli Appe and Malange, all members had more than 15° Brix and less acidity. Kana Appe1, which had the smallest fruit weight but the highest bisexual flower percentage, was grouped separately. Similarly, Dashehari, which had the highest total sugars; Aruna Gowda Appe, which exhibited the highest acidity; Himsagar, which possessed maximum stone weight and Alphonso, which differed from Dashehari in the percent of bisexual flowers, were grouped as mono clusters. Since, Mahanalobis distance analysis uses the covariance matrix for distance calculation, accessions with extreme values for important characters might have been separated from the rest as mono cluster. Based on cluster means, the study revealed that maximum fruit weight was observed for cluster VI (Himsagar), followed by cluster II and cluster VII (Alphonso). TSS was maximum in cluster IV (Himsagar) followed by III (Kana Appe-1) and VII (Alphonso) and acidity was maximum in cluster V (Aruna Gowda Appe). In highly heterozygous crops like mango, the low genetic base could be attributed to minor difference in the allelic pattern at different loci. Hence, minor differences between the varieties, like the acidity, can be explained. This probably is the basis for intervarietal differences. Even in the appemidi types, probably the present day cultivars would have a lineage in two different basic cultivars. Those varieties that have come from lesser acidic types have been grouped in one cluster and with high acidic types have been grouped in another cluster. Interestingly, the north Indian variety Dashehari, western region variety Alphonso, and eastern region variety Himsagar were identified as genetically distant from each other. This is in agreement with the earlier findings (Ravishankar *et al.*, 2000) stated that geographical diversity was closely associated with genetic diversity. On the contrary, it was opined (Karibasappa *et al.,* 1999 and Sulkeri *et al.*, 1994) that the geographic diversity may not necessarily be related to genetic diversity.

Conclusion

The genetic divergence study revealed high phenotypic and genotypic variance for fruit weight and vitamin 'C'. The values of heritability and GCV indicated that selection can be applied for improvement of fruit characteristics. The study also gives indication to the methodology to be adopted for improvement in mango, wherein there is scope for selection in F_1 generation progenies. In mango, where there is difficulty in raising large number of progenies by crossing going in for half-sib progenies gives a chance to select progenies with better characteristics.

REFERENCES

Burton, G. W. and De Vane, E. M. 1953. Estimating heritability in tall fescue from replicated clonal material. *Agron. J.,* 45: 478-481.

Falconer, D. S. 1989. Introduction to quantitative genetics, 3rd ed. Longman, New York.

Hanson, C. H., Robinson, H. F and Comstock, R. S. 1956. Biometrical studies of yield in segregating populations of Korean Lezpedeza. *Agron. J.*, 48: 268-272.

Karibasappa, G. S., Nalawadi, U. G., Sulikeri, G. S. and Hulmani, N. C. 1999.Characterization of mango germplasm in North Karnataka, India: 2 cluster analysis. *Indian. J Pl Genetic Res.*, 12(3): 341-347.

Panse, V. G., and Sukhatme, P. V. 1985. Statistical methods for Agricultural workers. Fourth Edition, ICAR, New Delhi.p. 347.

Rajan, S., Yadava, L. P., Kumar, R and Saxena, S. K. 2009. Genetic divergence in mango varieties and possible use in breeding. *Indian J. Hort.*, 66 (1): 7 – 12.

Rao, C. R. 1952. Advanced statistical methods in Biometrical Research. John Wiley and Sons, New York, P. 357-369.

Ravishankar, K. V., Anand, L. and Dinesh, M. R. 2000. Assessment of genetic relatedness among mango cultivars of India using RAPD markers. *Journal of Horticultural Science and Biotechnology* . 75: 198 – 201

Singh, B. D. 1991. Principles of plant breeding, Kalyani Publishers, Ludhiana, India.

Singh, R. K., and Chaudhury, B.D. 1977.Variance and covariance analysis. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi.

Sulikeri, G. S., Patil, V. K., Madalageri, M. B, and Hulmani, N. C. 1994. Performance of some introduced mango varieties and hybrids under Dharwad (Karnataka) conditions. *Lalbagh J.* 36: 29-32.

Yadav, 2003. Correlation studies among fruit characters of different clones of mango cv. Langra. *Environ. Ecol.*, 211(1) : 119 – 122.

****