

Original Research Paper

Genetic divergence study in bitter gourd (*Momordica charantia* L.)

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ABSTRACT

The genetic divergence of forty bitter gourd genotypes was studied for sixteen different parameters by adopting Mahalanobis D² statistics using Tocher's method. The genotypes were grouped into six clusters irrespective of geographic divergence, indicating no parallelism between geographic and genetic diversity. A maximum of 32 genotypes entered in cluster I, followed by 4 genotypes in cluster II. The cluster III, IV, V and VI had single genotypes each. Maximum inter cluster distance observed between cluster II and cluster IV followed by cluster IV and cluster V and cluster II and V. This indicates, the genotypes belonging to cluster II (GYB-3-1-2, Bit-3-1-2-1, Bit-3-1-1-1, ArkaHarit), cluster IV (IC-68238) and cluster V (Bit-18-1-1) are more diverse and hence, hybridization between genotypes of respective cluster may improve the yield and quality of bitter gourd.

Keywords: Bitter gourd, clusters, D² analysis and genetic divergence

INTRODUCTION

Bitter gourd (*Momordica charantia* L.) is considered as a valuable vegetable crop for its nutritional and medicinal properties, but it is neglected in terms of genetic and molecular breeding. Even though bitter gourd has a relatively broad phenotypic species variation due to diverse morphological traits, the studies on multi variate analysis is limited (Singh *et al.*, 2013). Genetic divergence has been considered as an important factor in discriminating the genetically diverse parents for efficient and successful hybridization programme in order to get potential transgressive segregants and also provide new recombination of genes in the gene pool.

D² statistics (Mahalanobis, 1936) is highly acceptable as it provides a measure of magnitude for divergence between two genotypes under comparison. Grouping of genotypes based on D² analysis will be useful in choosing suitable parental lines for hybridization. Therefore, the present study was conducted to identify suitable parents out of 40 bitter gourd genotypes to initiate a breeding programme by identifying the clusters that are diverse and contain genotypes with good performance.

MATERIALS AND METHODS

The present investigation was carried out at the Department of Vegetable Science, College of Horticulture, Yelachenahalli, Mysuru district, Karnataka during 2017-18. The experimental materials comprised of 40 indigenous genotypes of bitter gourd including some of the commercially released varieties from different institutes of India as listed in Table 1. The experiment was laid out in a randomized complete block design (RCBD) with two replications. The spacing used in this experiment was 120×90 cm. The recommended NPK fertilizer doses and cultural practices along with plant protection measures were followed to raise a commercial crop (Choudhary *et al.*, 2003). Five randomly chosen plants in each replication of each entry were labelled and used for recording the observations. The mean of five plants was taken for analysis. Observations were recorded for 16 parameters like Vine length (m), Number of branches per vine, Duration of crop (days), Node at which first female flower appears, Days to first female flower opening, Days to 50 per cent flowering, Days to first fruit picking, Fruit length (cm), Fruit diameter (cm), Average fruit weight (g), Number of fruits per vine, Fruit yield per vine (kg), Fruit yield per hectare (t), Number of seeds per fruit, Flesh thickness (mm)



and Ascorbic acid (mg/100g). The data were subjected to multivariate analysis of genetic divergence using

Mahalanobis D² statistic. Grouping of entries was done by Tocher's method (Rao, 1952).

Table 1. List of genotypes and their sources of collection

Sl. No.	Genotypes	Source	Sl. No.	Genotypes	Source
1	Preethi	KAU, Vellanikkara	21	Bit-10-1-1	COH, Kolar, Karnataka
2	Yellapur Local-2	Yellapur, Karnataka	22	West Bengal Local-2	West Bengal
3	Bit-25-2-1	COH, Kolar, Karnataka	23	Kotla Local-1	Rajasthan
4	Meghnaa-2	Masood seeds, Bangladesh	24	Bit-10-1-2	COH, Kolar, Karnataka
5	Jhalawar Local-3	Jalawar, Rajasthan	25	Bit-5-1-4-1	COH, Kolar, Karnataka
6	CO-1	TNAU, Coimbatore	26	Contai Bolder	Barasat Agri Hybrid seeds, West Bengal
7	Bit-22-1-1-3	COH, Kolar, Karnataka	27	Bit-1-2-2-4	COH, Kolar, Karnataka
8	Bit-9-2-4-1	Maharashtra	28	Bit-18-1-1	Varanasi, Uttar pradesh
9	GYB-3-1-2	Tamil Nadu	29	Jhalawar Local-1	Jalawar, Rajasthan
10	Bit-1-2-3	COH, Kolar, Karnataka	30	Bit-3-1-1-1	Tamil Nadu
11	Yellapur Local-1	Yellapur, Karnataka	31	GYB-5-1-5-2	COH, Kolar, Karnataka
12	Bit-37-2-1	COH, Kolar, Karnataka	32	Bit-22-1-1-1	COH, Kolar, Karnataka
13	DEB-505	Debgiri Pvt Ltd. Kolkatta	33	Bit-9-2-1-2	Maharashtra
14	Bit-3-1-2-1	Tamil Nadu	34	GYL-2	COH, Kolar, Karnataka
15	Bit-9-3-2-3	Maharashtra	35	GYB-2-2	COH, Kolar, Karnataka
16	Bit-5-1-2-1	COH, Kolar, Karnataka	36	Katahi	Hyderabad
17	West Bengal Local-1	West Bengal	37	Bit-35-1-1	Odisha
18	Jhalawar Local-2	Jalawar, Rajasthan	38	Bit-31-2-2	COH, Kolar, Karnataka
19	Super Green	Super Seeds, Odissa	39	ArkaHarit	IIHR, Bengaluru
20	IC-68238	NBPGR, New Delhi	40	Bit-9-1-4-1	Maharashtra

RESULTS AND DISCUSSION

The results from the analysis of variance for 16 characters indicated significantly high differences among 40 genotypes of bitter gourd under study. These 40 genotypes were grouped into six clusters. The distribution of genotypes into 6 clusters were presented in Table 2. Cluster I is the largest cluster having 32 genotypes followed by cluster II with four genotypes (GYB-3-1-2, Bit-3-1-2-1, Bit-3-1-1-1 and ArkaHarit). Cluster III (Yellapur Local-2), cluster IV (IC-68238), cluster V (Bit-18-1-1) and cluster VI (Jhalawar Local-2) had one genotype each. The genotypes collected from different geographical regions were present in same clusters indicating that there was no association

between geographical distribution and genetic diversity as reported earlier by Bhagwat *et al.* (2013) in bitter gourd.

The intra and inter-cluster D² and D values among 6 clusters are furnished in the Table 3. and illustrated in Figure 1. Intra-cluster average D² values ranged from 0 to 104.02. Among the clusters, cluster II had the maximum intra-cluster distance (104.02) followed by cluster I (96.08). The clusters like III, IV, V and cluster VI had no inter cluster distance (zero) as they were represented by single genotypes. The maximum inter cluster D² value was found between cluster II and VI (1620.05) followed by cluster IV and VI (1262.95), cluster II and V (1098.44), cluster II and cluster III

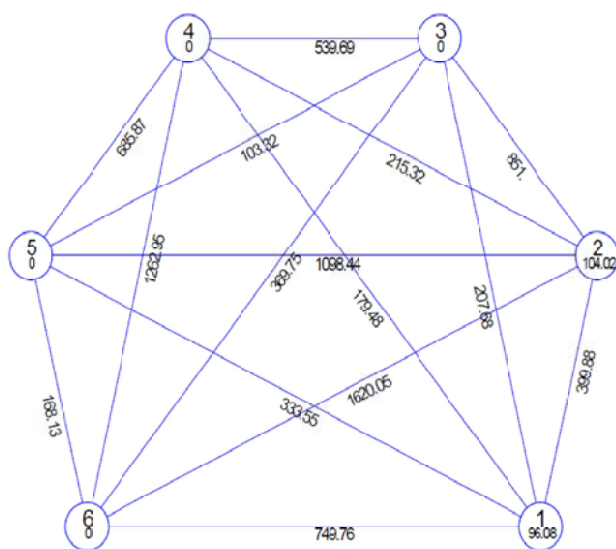
Table 2. Cluster composition based on D² statistics in bitter gourd

Cluster	Number of genotypes	Genotypes included in the cluster
I	32	Preethi, Bit-25-2-1, Meghnaa-2, Jhalawar Local-3, CO1, Bit-22-1-1-3, Bit-9-2-4-1, Bit-1-2-3, YellapurLocal-1, Bit-37-2-1, DEB-505, Bit-9-3-2-3, Bit-5-1-2-1, West Bengal Local-1, Super Green, Bit-10-1-1, West Bengal Local-2, Kotla Local-1, Bit-10-1-2, Bit-5-1-4-1, Contai Bolder, Bit-1-2-2-4, Jhalawar Local-1, GYB-5-1-5-2, Bit-22-1-1-1, Bit-9-2-1-2, GYL-2, GYB-2-2, Katahi, Bit-35-1-1, Bit-31-2-2, Bit-9-1-4-1
II	4	GYB-3-1-2, Bit-3-1-2-1, Bit-3-1-1-1, ArkaHarit
III	1	YellapurLocal-2
IV	1	IC-68238
V	1	Bit-18-1-1
VI	1	Jhalawar Local-2

Table 3. Intra-cluster (diagonal) and inter-cluster D² and D values in bitter gourd genotypes

	I	II	III	IV	V	VI
I	96.08 (9.80)	399.88 (19.20)	207.68 (14.41)	179.48 (13.34)	333.55 (18.26)	749.76 (27.38)
II		104.02 (10.12)	851.00 (29.17)	215.32 (14.67)	1098.44 (33.14)	1620.05 (40.25)
III			0.00(0.00)	539.69 (23.23)	103.32 (10.16)	369.75 (19.23)
IV				0.00 (0.00)	685.87 (26.19)	1262.95 (35.54)
V					0.00 (0.00)	168.13 (12.96)
VI						0.00 (0.00)

Figures in parenthesis denotes corresponding D values

**Mahalanobis Euclidean Distance (Not to the scale)****Fig1. Intra-cluster and inter-cluster distance of bitter gourd genotypes (Trocher's method)**

Highest inter cluster distance was found in cluster II and VI, suggesting that hybridisation between the genotypes from these clusters may lead to high heterotic effects and better segregants (Rabbani *et al.*, 2012). Similarly, lowest inter cluster distance was observed in cluster III and V indicating that, genotypes exhibited higher genetic similarity (Tyagi *et al.*, 2017).

The Per cent contribution of sixteen characters towards total divergence in bitter gourd genotypes is shown in Table 4. Among all the characters, ascorbic acid contributed the maximum (37.31%) to the diversity by taking first rank in 291 times out of 780 combinations, followed by fruit length (15.64% with 122 times ranked first), fruit diameter (14.36% with 112 times ranked first), flesh thickness (11.92% with 93 times ranked first), number of seeds per fruit (9.49% with 74 times ranked first), days to first female flower opening (6.92% with 54 times ranked first), average fruit weight (1.28% with 10 times ranked first). While, there was little and negligible

Table 4. Per cent contribution of sixteen characters towards total divergence in bitter gourd genotypes

Sl. No.	Characters	No. of times ranked first	Per cent germplasm contribution
1	Vine length (m)	4	0.51
2	Number of branches per vine	7	0.90
3	Duration of crop (days)	0	0.00
4	Node at which first female flower appears	1	0.13
5	Days to first female flower opening	54	6.92
6	Days to 50 per cent flowering	0	0.00
7	Days to first fruit picking	0	0.00
8	Fruit length (cm)	122	15.64
9	Fruit diameter (cm)	112	14.36
10	Average fruit weight (g)	10	1.28
11	Number of fruits per vine	6	0.77
12	Fruit yield per vine (kg)	6	0.77
13	Fruit yield per hectare (t)	0	0.00
14	Number of seeds per fruit	74	9.49
15	Flesh thickness (mm)	93	11.92
16	Ascorbic acid (mg/100g)	291	37.31
	Total	780	100.00

contribution from number of branches per vine (0.90%), number of fruits per vine (0.77%), fruit yield per vine (0.77%), vine length (0.51%) and node at which first female flower appears (0.13%). Similar results were reported by Sidhu and Pathak, 2016 in bitter gourd. However, the duration of crop, days to 50 per cent flowering, days to first fruit picking and fruit yield per hectare had no contribution towards genetic divergence. Similar findings were also observed by Sundaram (2008) and Bhagwat *et al.* (2013). Apart from the divergence, the performance of genotypes and the character with maximum contribution towards divergence should also be given due consideration which appear as desirable for improvement of bitter gourd (Deepa and Mariyappan, 2013).

Cluster means of forty genotypes showed that mean values of cluster varied for all the sixteen characters studied. Cluster II, V and VI performed better for the biometric parameters studied. Among the clusters, cluster VI was generally poor and cluster I as well as cluster III were intermediate in number of fruits per vine and fruit yield (Table 5.). Cluster II with four genotypes showed early flowering, flowering at lower

node and early fruit picking. Cluster II had smaller fruits but the number of fruits per vine was highest. Cluster VI with one genotype had longer fruits (30 cm), lower fruit diameter with high average fruit weight and higher ascorbic acid content (112.43). Higher number of branches, longer duration of crop and higher fruit yield was noticed in cluster V with one genotype (Bit-18-1-1). Highest vine length was observed in the cluster III (3.67 m). Cluster I with maximum number of genotypes showed intermediate performance for almost all the characters observed. The best cluster with yield and yield components studied was cluster V followed by cluster III and cluster I. By using these elite germplasms, there is a scope for varietal improvement in bitter gourd.

Inter-crossing of genotypes based on the mean performance for their characters would be effective for further crop improvement. To develop early varieties with small fruits and higher number of fruits per vine, cluster II would be effective as it showed early flowering. Selection from cluster I would be useful in breeding moderately early flowering, intermediate yield with longer crop duration. Cluster VI can be used in breeding for longer fruits with greater average fruit

Table 5. The cluster mean of sixteen characters for six clusters in bitter gourd genotypes

Sl. No.	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
1	Vine length (m)	2.71	1.91	3.67	1.84	2.58	2.33
2	Number of branches per vine	10.54	8.15	10.60	8.50	11.00	9.40
3	Duration of crop (days)	95.79	85.56	92.13	86.50	98.50	94.00
4	Node at which first female flower appears	15.39	11.33	15.50	14.10	14.30	16.50
5	Days to first female flower opening	41.46	35.69	37.60	42.55	41.35	44.50
6	Days to 50 per cent flowering	44.10	37.88	41.50	44.75	47.50	44.77
7	Days to first fruit picking	58.74	50.59	56.00	58.00	61.50	59.50
8	Fruit length (cm)	16.94	7.05	22.43	13.49	29.05	30.00
9	Fruit diameter (cm)	4.82	4.46	4.48	5.48	5.04	2.85
10	Average fruit weight (g)	84.68	36.91	85.60	79.00	88.70	91.85
11	Number of fruits per vine	12.87	14.76	13.10	12.10	14.60	8.85
12	Fruit yield per vine (kg)	1.11	0.53	1.14	0.96	1.28	0.69
13	Fruit yield per hectare (t)	10.24	4.92	10.55	8.87	11.82	6.38
14	Number of seeds per fruit	18.06	8.75	23.50	10.50	20.50	18.25
15	Flesh thickness (mm)	6.09	4.63	4.94	9.41	6.69	4.11
16	Ascorbic acid (mg/100g)	94.56	101.45	84.10	100.50	102.42	112.43

weight and higher ascorbic acid content, as the demand is increasing in our country. To breed varieties with higher yield and late flowering, selection from cluster V would be useful.

CONCLUSION

Genetic divergence has been considered as an important factor in discriminating the genetically diverse parents for efficient and successful hybridization programme in order to get potential

transgressive segregants and also provide new recombination of genes in the gene pool. Maximum inter cluster distance observed between cluster II and cluster IV followed by cluster IV and cluster V and cluster II and V. This indicates, the genotypes belonging to cluster II (GYB-3-1-2, Bit-3-1-2-1, Bit-3-1-1-1, ArkaHarit), cluster IV (IC-68238) and cluster V (Bit-18-1-1) are more diverse and hence, hybridization between genotypes of respective cluster may improve the yield and quality of bitter gourd.

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