

Genetic diversity studies for parental selection in bitter gourd (*Momordica charantia* L.)

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ABSTRACT

Nature and magnitude of genetic divergence assessed on twenty two bitter gourd genotypes assembled from different geographical locations showed the presence of wide genetic diversity. The genotypes were grouped into six clusters based on Mahalanobis D^2 statistics using Tocher's method. The clustering pattern of genotypes revealed that the genetic diversity was independent of the geographical diversity. Among the six clusters, maximum number of genotypes were found in cluster I and the clusters V and VI were found to be mono genotypic. Among the fourteen quantitative characters studied, individual fruit weight constituted a maximum of 26.83 per cent to the divergence, followed by yield of fruits per vine and length of fruit. Ranking of genotypes based on intra cluster mean performance for those characters which are major contributors of genetic diversity revealed its usefulness in selecting parents for heterosis breeding.

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Bitter gourd (*Momordica charantia* L.) is one of the most nutritive and commercially important cucurbitaceous vegetables grown throughout the country for its tubercled, fleshy, unripe fruits. Bitter gourd, a crop with moderate degree of saline tolerance is also found to perform well in summer rice fallow and thus offers great scope for development of varieties/hybrids for such a situation. The knowledge on genetic diversity is an important factor for heritable improvement in any crop and the information pertaining to nature and degree of divergence would be of immense use in selecting desirable parents from available germplasm for a successful breeding programme. The nature and magnitude of genetic distance between the genotypes serve as an indication for hybridisation to exploit high degree of heterosis. Genetic diversity is important to applied plant breeding as it reduces vulnerability to pests, besides it helps in the choice of parental combinations of the greatest promise. Hence, the present study was aimed at ascertaining the nature and magnitude of genetic diversity present in a set of twenty two bitter gourd genotypes.

MATERIALS AND METHODS

The present study was carried out during *rabi* 2004 at Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal of Union Territory of Pondicherry, located along the East Coast at the tail end of the river Cauvery. The experimental material consisted of twenty two bitter gourd genotypes collected from different geographical locations of the country. They were

evaluated in a Randomised Block Design with three replications. Observations were recorded on five randomly selected plants on fourteen important quantitative traits *viz.*, days to first male flower appearance, days to first female flower appearance, node of first male flower appearance, node of first female flower appearance, number of male flowers per vine, number of female flowers per vine, sex ratio (M/F), fruit length (cm), fruit girth (cm), individual fruit weight (g), vine length (m), number of primary branches per vine, number of fruits per vine and yield of fruits per vine (g). The D^2 analysis suggested by Mahalanobis (1936) was adopted to assess the genetic diversity among the twenty two genotypes and clustering of genotypes was performed using Tocher's method, as outlined by Rao (1952). The method suggested by Singh and Chaudhary (1977) was adopted for selection of genetically divergent parents from various clusters for use as parents to exploit high degree of heterosis.

RESULTS AND DISCUSSION

Clustering pattern of genotypes:

Mahalanobis's D^2 statistic, which measures the forces of differentiation at intra and inter cluster levels has been used as a powerful tool in quantifying the degree of divergence at genotypic level. The dispersion of these twenty two genotypes into six gene constellations indicated the presence of large amount of diversity in the population chosen for the study (Table 1). Two clusters *viz.*, cluster V and cluster VI were found to be mono genotypic, while the remaining clusters were found to constitute more than

Table 1 : Pattern of distribution of bittergourd genotypes to different clusters

Cluster	Genotype
I	CO 1, MDU 1, Arka Harit, Preethi, Green Long, White Long, IC 85636, IC 85638, IC 85643, IC 85645, NIC 13966, NIC 13980, NIC 14034 and NIC 14051
II	Bikaneer 1 and Bikaneer 2
III	Bikaneer 3 and Bikaneer 4
IV	ARBTH 1 and BGS 1
V	Vadipatti Local
VI	Paravai Local

one genotype. The clustering pattern of genotypes revealed that the geographical diversity need not be related to their genetic diversity as reported earlier by Wahab and Gopalakrishnan (1993) in bitter gourd and Dora *et al.* (2001) in pointed gourd.

Contribution of traits towards genetic divergence:

In addition to the knowledge on the degree of divergence, the contribution of different characters studied towards total genetic divergence also assumes significance in parental selection. In the present study

Table 2 : Contribution of different characters towards genetic divergence in bitter gourd

Character	Number of first rank	Percentage contribution
Days to first male flower appearance	1	0.4329
Days to first female flower appearance	0	0.0000
Node of first male flower appearance	20	8.6580
Node of first female flower appearance	0	0.0000
Number of male flowers per vine	13	5.6277
Number of female flowers per vine	20	8.6580
Sex ratio (M/F)	7	3.0303
Fruit length	29	12.5541
Fruit girth	11	4.7619
Number of primary branches per vine	7	3.0303
Vine length	8	3.4632
Individual fruit weight	62	26.8398
Number of fruits per vine	4	1.7316
Yield of fruits per vine	49	21.2121
Total	231	100.0000

the character, fruit weight was the maximum contributor for genetic divergence, followed by yield of fruits per vine and length of fruit (Table 2). The importance of fruit yield per plant in genetic divergence of bitter gourd was

Table 3 : Ranking of intracluster genotypes

Cluster	Genotype	Individual fruit weight (g)			Yield of fruits per vine (g)			Fruit length (cm)			Total Score
		Weight	Rank	Score	Yield	Rank	Score	Length	Rank	Score	
I	CO 1*	142.75	1	14	1543.62	8	7	25.76	2	13	34
	MDU 1*	111.06	4	11	2223.32	3	12	26.15	1	14	37
	Arka Harit	117.80	3	12	1513.97	10	5	14.22	13	2	19
	Preethi	107.70	6	9	1556.84	7	8	17.50	6	9	26
	Green Long	121.48	2	13	1479.05	12	3	22.18	3	12	28
	White Long	109.82	5	10	1540.53	9	6	20.99	4	11	27
	IC 85636	62.73	14	1	497.67	14	1	15.97	10	5	7
	IC 85638	96.90	8	7	2265.32	2	13	16.14	8	7	27
	IC 85643*	97.34	7	8	2335.98	1	14	16.39	7	8	30
	IC 85645	73.03	11	14	1809.88	5	10	16.00	9	6	20
	NIC 13966	95.21	9	6	2043.62	4	11	17.59	5	10	27
	NIC 13980	81.92	10	5	1284.25	13	2	15.52	11	4	11
	NIC 14034	66.68	13	2	1491.66	11	4	11.65	14	1	7
	NIC 14051	72.19	12	3	1805.88	6	9	14.97	12	3	15
II	Bikaneer1*	91.37	1	2	1298.97	2	1	17.56	1	2	5
	Bikaneer 2	80.17	2	1	1416.10	1	2	13.38	2	1	4
III	Bikaneer 3*	75.52	1	2	858.67	2	1	12.66	1	2	5
	Bikaneer 4	62.60	2	1	1037.89	1	2	12.34	2	1	4
IV	ARBTH 1	78.93	2	1	942.97	2	1	20.41	2	1	3
	BGS 1*	105.77	1	2	1553.52	1	2	22.42	1	2	6

* Genotypes with high score

reported earlier by Parhi *et al.* (1993) and the importance of length of fruit towards divergence was reported by Varalakshmi *et al.* (1994) in ridge gourd. The relative contribution of days to first female flower appearance and node of first female flower appearance for divergence among the genotypes were found nil, while the contribution of number of female flowers per vine and node of first male flower appearance were moderate. The contribution of other traits towards genetic divergence was observed to be very minimal. The study indicated that the characters such as individual fruit weight, yield of fruits per vine and fruit length should also be considered in parental selection as they are important contributors of genetic divergence.

Parental selection:

Selection of diverse parents from various clusters is considered to be an acceptable procedure in harnessing the heterosis. However, when the number of genotypes constituted by a cluster is more than one, an appropriate methodology needs to be adopted to select a parent or parents from within a cluster. To accomplish this, the intracluster genotypes are ranked based on a scoring technique suggested by Singh and Chaudhary (1977). The genotypes in each cluster should be ranked based on their mean performance with regard to the characters showing maximum contribution towards genetic diversity. Accordingly in the present study, the genotypes of cluster I, II, III and IV were ranked for individual fruit weight, yield of fruits per vine and length of fruit and a total score was assigned to each genotype as detailed in Table 3. The top ranking genotypes from each of these clusters based on their total score have been identified as parents.

In the present investigation, three top ranking genotypes from cluster I and one top ranking genotype each from the rest of the five clusters were identified as parents for use in the heterosis breeding programme (Table 4). From the above study, it may be concluded that the genetic diversity which is independent from

Table 4 : Parents identified from each cluster

Sr. No.	Cluster	Accession No.	Genotype
1.	I	2	MDU 1 (P1)
2.	I	1	CO 1 (P2)
3.	I	9	IC 85643 (P3)
4.	II	18	Bikaneer 1 (P4)
5.	III	20	Bikaneer 3 (P5)
6.	IV	22	BGS 1 (P6)
7.	V	15	Vadipatti Local (P7)
8.	VI	16	Paravai Local (P8)

geographical origin is the outcome of several factors and is likely to be more fruitful in selecting elite materials for future breeding programme to develop superior varieties.

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