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GENETIC DIVERGENCE STUDIES FOR YIELD AND YIELD ATTRIBUTES IN BITTER GOURD (*MOMORDICA CHARANTIA* L.)

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Abstract

The present experiment was conducted during *Rabi* season of 2017-18 to study genetic diversity for quantitative and qualitative traits in bitter gourd and twenty seven genotypes were grouped into eight clusters which indicate the presence of diversity for different traits. The cluster II had the highest number containing 12 genotypes followed by cluster I containing seven genotypes. The maximum intra-cluster distance (96.27) was recorded within cluster VIII and the maximum inter-cluster distance (1028.37) was between cluster VIII and I indicating the existence of wide genetic variability. The cluster VIII (329.15 cm) registered maximum vine length. The genotypes included in clusters VI were with high number of primary branches per vine, cluster III took less number of days (45.40) to first female flowering, cluster IV took less number of days (43.51) to first fruit harvest and cluster I took more number of days (143.19) to last harvest. The cluster VI registered high number (20.70) of fruits per vine and high fruit length (19.31 cm). The genotypes included in clusters VIII had maximum average fruit weight (41.90 g). Less fruit fly infestation (21.17%) and high number (20.20) of seeds per fruit were observed in cluster VI. The clusters with genotypes VIII registered high 100 seed weight (19.49 g) and total fruit yield per vine (6.58 kg) which can be utilised in breeding programme for enhancing their respective characters. Based on cluster mean analysis these genotypes can be used in crop improvement programme in bitter gourd for above-mentioned characters.

Introduction

Bitter gourd (*Momordica charantia* L) is an important commercial cucurbit belonging to Cucurbitaceae is native of India. It is a large genus with 7 species of annual and perennial climbers of which *Momordica charantia* L. is widely cultivated. The crop is highly cross pollinated as it is monoecious.

It is a valuable vegetable owing to its high nutritive and medicinal properties. The fruits are also pickled, canned and dehydrated. Every part of the plant is used medicinally. The fruits have cooling, digestive, laxative, antipyretic, antidiabetic properties and its administration is useful in bioliousness, blood diseases, rheumatism and asthama. The leaf is used as a laxative and as an ointment for sours. It is claimed that the fruit powder is used for healing wounds, leprous and malignant ulcers. It is reported for its usefulness in snakebites. The roots have abortifacient activity (Gayathry *et al.* 2022).

Commercial F_1 hybrids are quiet common in bitter gourd and selection of new parents for higher heterosis is a continuous process. Generally diverse plants are expected to give high hybrid vigour (Harrington 1940). Hence, it is important to study of genetic divergence among the germplasm collection for identification of parents for further breeding programme. The information on genetic divergence of various traits particularly of those that contribute to yield and

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quality would be of most useful in planning the breeding programme. D^2 statistics developed by Mahalanobis (1936) provides a measure of magnitude for divergence between two genotypes. Grouping of genotypes based on D^2 analysis will be useful in choosing suitable parental lines for heterosis breeding. This type of study is also useful in selection of parents for hybridization to recover superior transgressive segregants and it can further result into release of improved open pollinated varieties for commercial cultivation. Considering the above facts, the present experiment was undertaken to assess the extent of genetic diversity in the available germplasm based on 18 traits comprising of qualitative and quantitative traits.

Materials and Methods

The present investigation was carried out at Research Farm of the Department of Vegetable Science, College of Horticulture, Mojerla, Wanaparthy, India during the *Rabi* season of 2017-2018. The experimental materials comprised of 27 genotypes (Table 1) of bitter gourd collected from different sources. The experiment was laid out in a randomized block design with three replications. Seeds were sown at a spacing of 2.0 x 0.5 m. The genotypes studied are IC 256147, IC 541249, IC 336200, IC 256110, IC 324546, IC 598170, IC 467670, IC 598172, IC 598171, IC 467673, IC 510632, IC 068345, IC O68306, IC 599431, IC 599421, IC 264699, IC 085608, IC 264705, IC 599428, IC 470943, IC 599434, IC 256206, IC 398610, IC 599423, IC 599424 and two check varieties Aakash (VNR SEED), MBTH-102 (Mahyco).

All the recommended cultural practices were adopted for raising the crop successfully. The observation were recorded on five randomly selected plants per replication for each genotype on 18 characters: i) total vine length (cm), ii) number of primary branches per vine, iii) number of nodes per vine, iv) internodal length, v) number of days to first male flower appearance, vi) number of days to first female flower appearance, vii) nodes at which first male flower appears, viii) nodes at which first female flower appears, ix)days to first fruit harvest, x) days to last fruit harvest, xi) number of fruits per vine, xii) average fruit weight (cm), xiii) fruit length (cm), xiv) fruit diameter (cm), xv) fruit fly infestation (%), xvi) number of seeds per fruit, xvii) 100 seed weight (g), xviii) total fruit yield per vine (kg). Mean across three replications were calculated for each traits and the analysis of variation was carried out. Multivariate analysis was done utilizing Mahalanobis D^2 statistic. The inter and intra cluster distances were worked out as per method suggested by Singh and Chaudhary (1977) to find actual divergence within and between the clusters.

The genetic divergence between genotypes was estimated using Mahalanobis's D^2 statistics (1936). All the genotypes used were clustered into different groups following Tocher's method. The device suggested by this method was started with two closely associated populations and find a third population which had the smallest average of D^2 from the first two. Similarly, the fourth was chosen to have a smallest average D^2 value from the first three and so onIf at any stage increase in average D^2 value exceeded the average of already included, because of the addition of new genotypes, then that genotype was deleted. The genotypes that are included already in that group were considered as the first cluster. This procedure was repeated till D^2 values of the other genotypes were exhausted omitting those that were already included in the former cluster and grouping them into different cluster.

Based on D^2 values, average intra and inter cluster distances were calculated as per Euclidean method. The average intra and inter cluster distances were calculated by the formula given by Singh and Chaudhary (1977). The character contribution towards genetic divergence was computed using method given by Singh and Chaudhary (1977).

In all the combination, each character is ranked on the basis of di = $y_i^j - y_i^k$ values.

Where,

di = mean deviation

y_i^j = mean value of the j^{th} genotype for the i^{th} character and

y_i^k = mean value of the k^{th} genotype for the i^{th} character.

Rank 'I' is given to the highest mean difference and rank 'p' is given to the lowest mean difference. Where, P is the total number of characters.

Finally, number of times that each character appeared in the first rank is computed and per cent contribution of characters towards divergence was estimated.

Results and Discussion

Clustering of genotypes in the present study is presented in Fig. 1. Based on D^2 values, the 27 genotypes were grouped into eight highly divergent clusters (Table 3). Some of genotypes were so divergent in all the characters, hence each single genotype formed a separate cluster. Thus four clusters *viz.*, III (IC-256110), IV (IC-398610), VI (IC-599434), VII (IC-470943) were solitary with one genotype in each cluster. The cluster V (IC-085608, IC-256206) and cluster VIII (IC-264705, IC-599423) includes two genotypes each. The remaining two clusters were having maximum number of genotypes. Cluster II had the highest with 12 genotypes *viz*., (IC-510632, IC-599431, IC-599428, IC-541249, IC-598172, IC-599421, IC-467670, IC-598171, IC-599424, IC-264699, Aakash (C) and MBTH-102 (C) followed by cluster I with 7 genotypes *viz.*, (IC-068345, IC-068306, IC-467673, IC-324546, IC-256147, (IC-336200) and (IC-598170) (Table. 1). In clustering pattern there was no parallelism between geographical distribution of genotypes and genetic divergence. Therefore, geographical diversity could not be related to genetic diversity in the material investigated. The present results in agreement with the results reported by Dey *et al.* (2007), Resmi and Sreelathalumari (2012) and Singh *et al.* (2013).

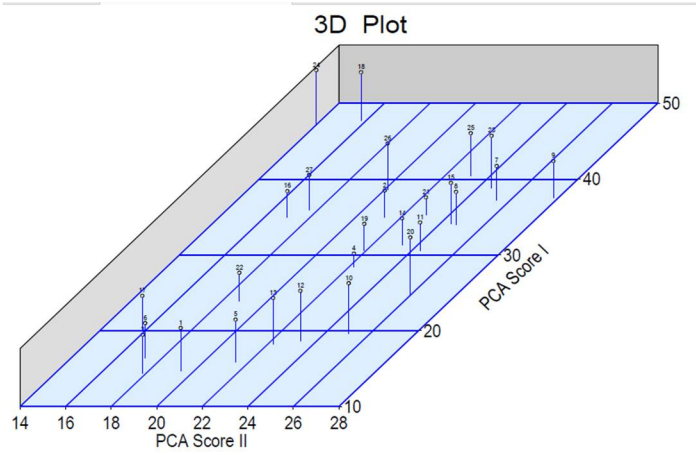

Fig. 1. Three dimensional plot showing clustering pattern for divergence of bitter gourd genotypes.

Results presented in the Table 2, showed that the intra-cluster distances indicates the divergence among the genotypes within the clusters and inter-cluster indicates diversity between clusters. The intra cluster D^2 values ranged from 0.00 (Cluster III, IV, VI and VII) to 96.27

(Cluster VIII). The cluster VIII had the maximum D^2 value (96.27) followed by Cluster II (84.55). The inter cluster distance was minimum between clusters V (54.64) indicating close relationship and similarity for most of the characters of the genotypes included in these clusters. The maximum inter cluster distance was observed between clusters VIII and I (1028.37) followed by between clusters VIII and V (748.37) indicating wider genetic diversity among the genotypes included in these groups. Cluster VII followed by the VI is the most diverse as all other clusters showed maximum inter cluster distance from it.

Table 1. Cluster classification of 27 genotypes of bitter gourd.

Cluster	No. of genotypes	Genotypes
I	7	IC-068345, IC-068306, IC-467673, IC-324546, IC-256147, IC-336200, IC-598170
II	12	IC-510632, IC-599431, IC-599428, IC-541249, IC-598172, IC-599421, IC-467670, IC-598171, IC-599424, Aakash, MBTH-102, IC-264699
III	1	IC-256110
IV	1	IC-398610
V	2	IC-085608, IC-256206
VI	1	IC-599434
VII	1	IC-470943
VIII	2	IC-264705, IC-599423

Table 2. Average intra (bold) and inter-cluster D^2 values for eight clusters in 27 genotypes of bitter gourd.

Clusters	I	II	III	IV	V	VI	VII	VIII
I	56.42	407.11	260.14	554.24	105.68	468.11	154.47	1028.37
II		84.55	139.57	114.51	259.37	118.27	228.16	317.31
III			0	291.59	138.53	112.34	234.67	596.26
IV				0	409.08	200.94	246.65	227.55
V					54.64	286.99	184.25	748.37
VI						0	348.55	379.94
VII							0	692.83
VIII								96.27

Cluster I displayed least intra cluster distance denoting the similarity of genotypes. While maximum intra cluster distance was recorded in cluster VIII and this might be due to limited gene exchange or selection practices among the genotypes for diverse characters. Therefore, hybridization programme between the genotypes belonging to cluster V and VIII may be undertaken for getting good segregants. Emphasis should be laid on characters contributing maximum D^2 values for choosing the cluster for the purpose of further selection and choice of parents for hybridization. Hence, selection for divergent parents based on the characters will be useful for heterosis breeding in bitter gourd. More or less Similar results were reported in bitter gourd by Kutty and Dharmatty (2005), Sanwal *et al.* (2007), Sundaram *et al.* (2008), Islam *et al.* (2009), Kundu *et al.* (2012), Muralidhara *et al.* (2014), Singh *et al.* (2015).

The per cent contribution of each character towards divergence presented in Table 4 showed that total fruit yield per vine contributed maximum (3504.27%) towards divergence followed by 100- seed weight (2421.65%), fruit length (1680.91%), number of seeds per fruit (797.72%), number of nodes per vine (740.74%), fruit diameter (256.41%), days to last fruit harvest, number of fruits per vine, fruit fly infestation percentage (142.45%), internodal length, nodes at which first male flower appears (56.98%) and number of days to first male flower appears, nodes at which first female flower appears (28.49%). The remaining characters *viz.*, vine length, number of

primary branches per vine, number of days to first female flower appears, days to first fruit harvest, average fruit weight did not contribute to the total divergence. The cluster mean for the 18 characters studied in bitter gourd genotypes revealed considerable differences among all the clusters (Table 3). From the Table 5, it is evident that vine length was highest in cluster VIII (329.15 cm) and lowest in cluster I (200.18 cm). Maximum number of primary branches per wine was recorded in cluster VIII (20.93). The cluster IV had the highest number of nodes per vine (66.10) followed by cluster VII (63.33). The cluster III had the highest internodal length (9.09 cm) followed by cluster VI (6.73 cm). The cluster III had showed the early number of days to first male flower appearance (36.77 days) followed by cluster VII (38.30 days). The maximum number of days required to appear first female flower in cluster III (45.40 days), nodes at which first male flower appears recorded in cluster VI (7.11), nodes at which first female flower appears recorded in cluster V (11.18) and days to first harvest in cluster IV (43.51). Maximum days required to last harvest was recorded in cluster I (143.19).

Table 3. **The nearest and farthest clusters from each cluster based on D^2 values in 27 genotypes of bitter gourd.**

Cluster No.	Nearest cluster with D^2 values	Farthest cluster with D^2 value
I	V (105.68)	VIII (1028.37)
II	IV (114.51)	I (407.11)
III	VI (112.34)	VIII (596.26)
IV	II (114.51)	I (554.24)
V	I (105.68)	VIII (748.37)
VI	III (112.34)	I (468.11)
VII	I (154.47)	VIII (692.83)
VIII	IV (227.55)	I (1028.37)

Table 4. Per cent contribution of different characters towards diversity in 27 bitter gourd genotypes.

S. No.	Characters	Times ranked 1st	Per cent contribution
1	Vine length (cm)	0.0	0.00
2	Number of primary branches per vine	0.0	0.00
3	Number of nodes per vine	26.0	740.74
4	Internodal length (cm)	2.0	56.98
5	Number of days to first male flower appearance	1.0	28.49
6	Number of days to first female flower appearance	0.0	0.00
7	Nodes at which 1st male flower appears	2.0	56.98
8	Nodes at which 1st female flower appears	1.0	28.49
9	Days to first fruit harvest	0.0	0.00
10	Days to last fruit harvest	5.0	142.45
11	Number of fruits per vine	5.0	142.45
12	Average fruit weight (g)	0.0	0.00
13	Fruit length (cm)	59.0	1680.91
14	Fruit diameter (cm)	9.0	256.41
15	Fruit fly infestation (%)	5.0	142.45
16	Number of seeds per fruit	28.0	797.72
17	100 - seed weight (g)	85.0	2421.65
18	Total fruit yield per vine (kg)	123.0	3504.27

The genotypes of cluster VI had maximum number of fruits per vine (20.70). The average fruit weight was highest in cluster VIII (41.90 g). The highest fruit length (19.31 cm) and fruit diameter (2.95 cm) was maximum in cluster VI. Fruit fly infestation percentage was maximum in

cluster IV (51.93). Number of seeds per fruit was highest in cluster VI (20.20) and lowest in cluster I (5.58) and the highest 100 seed weight was found in cluster VIII (19.49 g). The total fruit yield per vine also recorded highest (6.58 kg) in cluster number VIII (Table 5).

Table 5. Mean values of clusters for 18 characters in 27 bitter gourd genotypes.

Cluster	Vine length(cm)	Number of primary branches per vine	Number of nodes per vine	Internodal length (cm)	Number of days to first male flower appearance	Number of days to first female flower appearance	Nodes at which first male flower appears	Nodes at which first female flower appears	Days to first harvest	Days to last harvest	Number of fruits per vine	Average fruit weight (g)	Fruit length (cm)	Fruit diameter (cm)	Fruit fly infestation (%)	Number of seeds per fruit	100 Seed weight (g)	Total fruit yield per vine (kg)
I	200.18	14.87	39.54	5.41	41.51	49.56	10.40	14.35	63.33	143.19	15.36	13.02	7.40	2.25	26.23	5.58	9.23	0.66
II	313.05	16.36	48.50	6.48	40.34	48.04	10.61	13.94	62.69	138.85	16.56	27.42	13.95	2.92	25.91	15.23	18.08	2.57
III	275.50	12.97	30.30	9.09	36.77	45.40	9.63	14.27	61.43	119.87	15.54	24.23	14.31	2.29	33.17	15.77	16.80	1.68
IV	313.30	16.87	66.10	5.22	38.53	47.53	11.44	13.30	43.51	119.97	13.47	31.37	16.05	2.92	51.93	15.97	16.27	3.21
V	205.87	15.57	43.23	5.12	39.13	49.72	8.28	11.18	64.52	124.98	17.28	22.93	8.32	2.12	25.30	9.68	12.53	1.26
VI	254.40	21.63	37.73	6.73	41.43	52.30	7.11	11.20	63.20	126.17	20.70	21.87	19.31	2.95	21.17	20.20	15.93	2.32
VII	213.77	10.83	63.33	4.30	38.30	48.87	14.89	19.40	61.63	127.40	14.80	21.07	9.63	1.91	29.00	11.17	11.07	0.99
VIII	329.15	20.93	56.47	5.85	43.35	53.92	11.72	13.45	67.93	130.02	17.32	41.90	14.73	2.50	28.78	18.37	19.49	6.58

Many workers have observed more diverse parents within its overall limits of fitness, the greater are the chances of heterotic expression in F1's and a broad spectrum of variability in segregating generations. In choosing parents for hybridisation programme the clustering pattern could be employed that would likely to render the maximum possible variability for various economic characters. Moreover, it will be effective to intercross genotypes belonging to more diverse clusters like cluster VI and VIII, cluster I and VIII and cluster V and VIII to create wide spectrum of variability and to produce transgressive segregates for bitter gourd.

It is suggested that hybridization among the genotypes of above said clusters would produce segregants for more than one economic character. The potential lines are picked out from different clusters and used as parents in a hybridization programme. The choice should be based on genetic distance and depending upon the objective of the breeding programme.

Reference

Choudhary BR., Pandey S, Singh PK and Singh R 2011. Genetic divergence in hermaphrodite ridge gourd (*Luffa acutangula)*. Vegetable Sci. **38**(1): 68-72.

Dey SS, Behera TK, Munshi AD and Sirohi PS 2007. Studies on genetic divergence in bitter gourd (*Mormordica charantia* L.). Indian J. Hort. **64**(1): 53-57.

Gayathry KS, Kumar R and Krishnan S (2022). A comprehensive review on bitter gourd (*Momordica charantia*). Food Prod. Process. Nutr. **4**(1): 1-21.

Harrington JB (1940). Yielding capacity of wheat crosses as indicated by bulk hybrid tests. Can. J. Res, **18**(11): 578-584.

Islam MR, Hossain MS, Bhuiyan MSR, Husna A and Syed MA 2009. Genetic Variability and Path Co-efficient Analysis of Bitter Gourd (*Momordica charantia* L.). Int. J. Sustain. Agri. **1**(3): 53-57.

Kundu BC, Hossain MA, Mian K and Mian IH 2012. Genetic divergence in bitter gourd (*Momordica charantia* L.). J. Asiatic Soc. Bangladesh Sci. **38**(2): 125-134.

Kutty MS and Dharmatti PR 2005. Genetic Divergence in Bitter gourd. Karnataka J. Agri. Sci. **18**(3): 740-743.

Mahalanobis PC1936. On the generalized distance in statistics. Proceed. Nat. Ins. Sci. India. **12**: 49- 55.

Muralidhara MS, Gowda NCN and Narayanaswamy P 2014. Correlation and path analysis for different quantitative characters in pumpkin (*Cucurbita moschata* Duch ex. Poir), Indian Hort. J. **4**(2): 112-115.

Rao CR 1952. Advanced statistical methods in biometrical research. Jhon wiley and Sons, inc. New York pp: 357-363.

Resmi J and Sreelathakumary I 2012. Studies on genetic divergence in bitter gourd (*Momordica charantia* L.). J. Hort. Sci. **7**(2): 152-155.

Sanwal SK, Yadav RK, Rai N, Allav DSY and Singh PK 2007. Genetic diversity and interrelation analysis in sweet gourd *(Momordica cochinchinensis)* genotypes of northeast India. Vegetable Sci. **34**(11): 64-66.

Singh RK and Chaudhary BD 1977. Biometrical methods in quantitative genetic analysis (3rd ed.). New Delhi: Kalyani Publishers.

Singh B, Singh AK and Kumar S 2013. Genetic Divergence Studies in Bitter Gourd (*Momordica charantia* L.). Academic J. Plant Sci. **6**(2): 89-91.

Singh HK, Singh VB, Kumar R, Barnawal DK and Ray PK 2015. Character association, heritability and path analysis for yield and its contributing traits in bitter gourd (*Momordica charantia* L.). Prog. Agri. Sci. **15**(1): 41-47.

Sundaram V 2008. Genetic diversity studies for parental selection in bitter gourd (*Momordica charantia* L.). Asian J. Hort. **3**(2): 333-335.

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