Indian J. Hort. 71(1), March 2014: 55-60

Assessment of genetic diversity based on cluster and principal component analyses for yield and its contributing characters in bitter gourd

H.K. Singh[*], V.B. Singh[**], Randhir Kumar, D.K. Baranwal[***] and P.K. Ray
Department of Horticulture (Veg. & Flori.), Bihar Agricultural University, Sabour 813210, Bhagalpur

ABSTRACT

An experiment was carried out to analyze multivariate analysis based on cluster and principal component (PC) for yield and its eleven contributing traits in 32 bitter gourd genotypes including two checks, *i.e.* Pusa Do Mausami and Kalyanpur Sona during summer of 2011 & 2012. The cluster analysis categorized all 32 bitter gourd genotypes into 6 major clusters. Extreme genetic divergence was estimated among clusters. Average inter-cluster distance was found maximum (717.86) between cluster V (NDBT-12) and cluster VI (NDBT-76). The proportionate contribution of fruit weight and fruit length towards genetic divergence was 74 and 13%, respectively. Highest cluster mean values for fruits/ plant, fruit weight (g) and fruit yield/plant (kg) was found in cluster V followed by cluster II. Principal component analysis revealed that first six principal components (PC1, PC2, PC3, PC4, PC5 and PC 6) accounted for 83.19% of the total variations with the proportionate contribution values of 23.88, 16.81, 13.28, 11.23, 9.38 and 8.61%, respectively. The first PC has positive association with node No. to anthesis of first staminate flower and days to first fruit harvest, while negative association with fruit weight (g), fruits/ plant and fruit yield/ plant (kg). Promising diverse parents identified based on cluster and PC analyses were selected for future hybridization programme.

Key words: Bitter gourd, cluster, dendrogram, principal component

INTRODUCTION

Bitter gourd (*Momordica charantia* L.) is a widely consumed cucurbit belong to family Cucurbitaceae and used as a supplementary food for curing diabetes patients. It is native to tropical Asia and mainly confined to Indo-Myanmar centre of origin. Bitter gourd is widely cultivated and distributed in Malaysia, China, India, tropical Africa and North and South America. The 100 g edible fruit part constitutes 2.1 g protein, 1.8 mg iron, 20 mg calcium, 88 mg vitamin C, 55 mg phosphorus and 210 I.U. vitamin A (Laxuman, 5). For consumption, green/ immature fruits are boiled, curried, stuffed or sliced and fried. The fruits and seeds of bitter gourd possess cooling, appetitising, stomachic, antipyretic, carminative, antiheliminthic, aphrodisiac and vermifuge properties (Grover and Yadav, 2). Besides, it was found to have tremendous application in antiviral therapy especially against HIV infection and act as acytostatic in certain cancers (Thakur *et al*., 9).

Multivariate analysis of elite germplasm collections is a prerequisite for choosing promising genetically diverse lines for desirable traits (Mladenovic *et al.*, 6). Based on the genetic divergence the genotypes are assigned to specific heterotic groups to create segregating progenies with maximum genetic variability for further breeding purposes. Genetic diversity analysis is well exploited for transferring desirable genes from diverse genetic stock available in the gene pool for broadening the genetic base in crops with narrow genetic base (Haussmann *et al*., 3). Cluster analysis and PC (principal component) analysis are the important genetic diversity measuring tools employed for exhibiting relative genetic differences among the genotype collection of various crop species. However, despite the potential medicinal and economic values, there are only few reports of multivariate analysis in Indian bitter gourd genotypes (Singh *et al*., 8; Dey *et al*., 1; Shankar *et al*., 7). In view of this, the present study was conducted to classify a set of bitter gourd genotypes based on multivariate analysis that may be used for generating more heterotic cross combinations and finally superior useful hybrids.

MATERIALS AND METHODS

The current study was performed to assess multivariate analysis during summer 2011 & 2012 to evaluate 32 bitter gourd genotypes including two checks, *i.e.* Pusa Do Mausami and Kalyanpur Sona at Main Experimental Station of Narendra Dev University of Agriculture & Technology (NDUA&T), Kumarganj, Faizabad (India) which is located in between 24.47° and 26.56° N latitude and 82.12° and 83.98° E longitude having elevation of 113 m above the mean

---

[*] Corresponding author's E-mail: shemant237@yahoo.com
[**] Deptt. of Hort. (Veg. Sci.), N.D.U.A. & T., Kumarganj, Faizabad (U.P.)
[***] Deptt. of Plant Breeding & Genetics, Bihar Agril. Univ., Sabour

sea level in the Gangetic alluvial plains of eastern Uttar Pradesh that falls under humid sub-tropical climate (Table 1). The soil type of experimental site was sandy loam. The genotypes under present study were collected from the Department of Horticulture (Vegetable Science), NDUA&T, Faizabad. The experiment was conducted in randomized complete block design with three replications to assess the performance of 32 bitter gourd genotypes. The crop was planted in 2.5 m long row, spaced 2.0 m apart, whereas 50 cm plant to plant spacing was maintained. All the recommended agronomic package and practices and protective measures were followed to raise a good crop. Data were recorded for yield and its ten contributing traits in bitter gourd, *viz*. node number to anthesis of first staminate flower, node number to anthesis of first pistillate flower, days to anthesis of first staminate flower, days to anthesis of first pistillate flower, days to first fruit harvest, vine length (m), fruit length (cm), fruit diameter (cm), number of fruits per plant, average fruit weight (g) and fruit yield per plant (kg).

Data of five plants from each genotype was averaged replication wise and mean data was used for statistical analysis. Cluster and PC analysis of 32 bitter gourd genotypes based on yield and its ten component traits to assess the magnitude of genetic variation was performed by using statistical software Windostat version 8.6 from Indostat services. Clustering pattern among 32 bitter gourd genotypes exhibiting dendrogram was assessed by using Tocher's method (Fig. 1). Average intra- (diagonal) and inter-cluster distance was estimated by using Tocher's method representing Euclidean^2 distances considering yield and its ten contributing traits in bitter gourd genotypes (Table 2; Fig. 2). Cluster mean value and its deviation from grand mean value for each corresponding contributing traits has been represented in Table 3.

RESULTS AND DISCUSSION

The 32 bitter gourd genotypes were categorized into six distinct clusters using Tocher's method (Fig. 1) and their Euclidean^2 distance using D^2 - statistics depicted in Fig. 2. Twenty genotypes were classified in first cluster accounting 60 per cent of total genotypes followed by eight genotypes categorized in second cluster. Besides these two clusters, remaining four clusters have one genotype in each cluster (Table 1). Average inter-cluster distance was found maximum (717.86) between cluster V (NDBT-12) and cluster VI (NDBT-76).

Table 1. Clustering pattern of genotypes based on dendrogram by Tocher's method.

Cluster No.	No. of genotype (s)	Genotype (s)
I	20	NDBT-66, NDBT-70, NDBT-69, NDBT-4, NDBT-63, NDBT-72, NDBT-9, NDBT-5, NDBT-62, NDBT-77, NDBT-54, NDBT-67, NDBT-53, NDBT-67, NDBT-2, NDBT-71, NDBT-74, NDBT-7, Kalyanpur Sona and NDBT-73
II	8	NDBT-65, Pusa Do Mausami, NDBT-83, NDBT-10, NDBT-15, NDBT-19, NDBT-57 and NDBT-1
III	1	NDBT-61
IV	1	NDBT-58
V	1	NDBT-12
VI	1	NDBT-76

Table 2. Average Intra- (diagonal) and inter-cluster distances (D^2) for studied traits in bitter gourd genotypes using Tocher's method.

Cluster	I	II	III	IV	V	VI
I	23.89	75.92	44.28	70.25	235.75	155.10
II		15.94	176.92	224.17	64.50	386.20
III			0.00	12.27	405.62	54.59
IV				0.00	473.28	51.48
V					0.00	717.86
VI						0.00

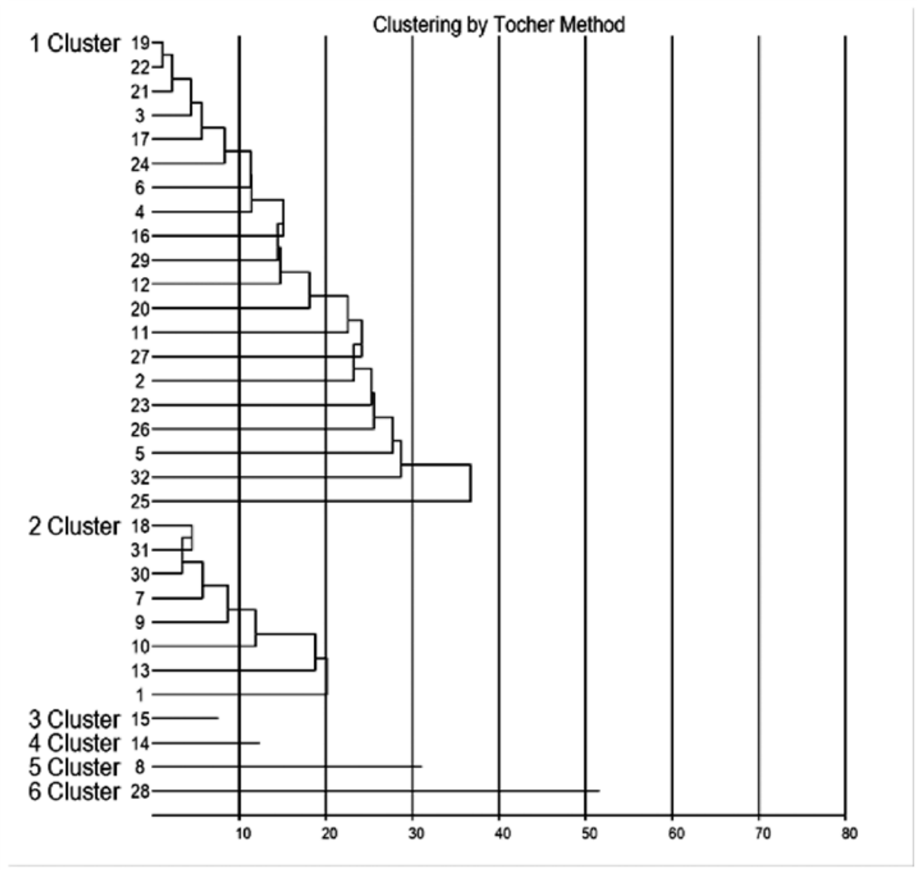

Fig. 1. Dendrogram (Tocher's method) showing clustering pattern among 32 bitter gourd genotypes for different traits.

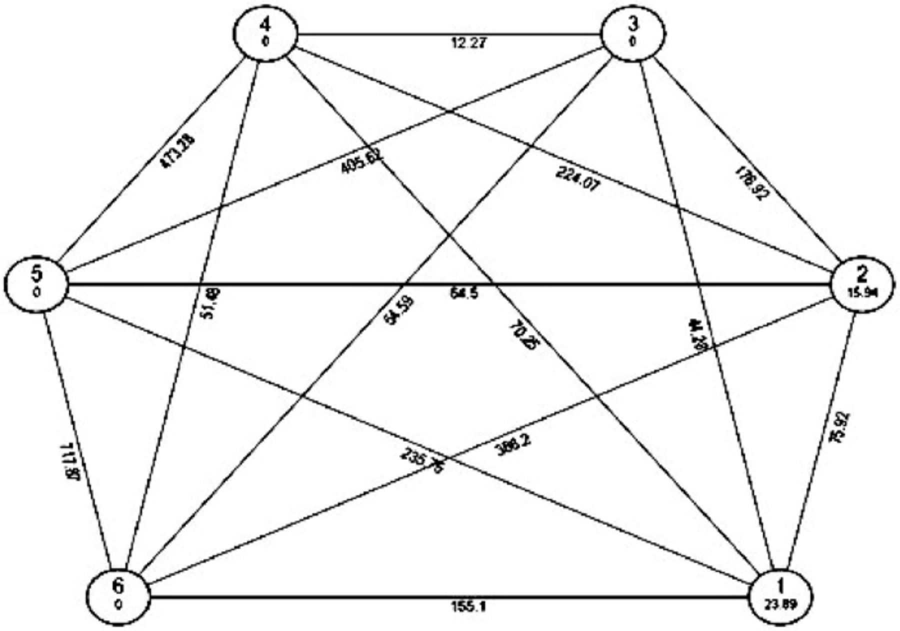

Fig. 2. Clustering formed by Tocher's method representing average distances within and between the clusters based on Euclidean^2 distance.

Therefore, hybridization between NDBT-12 and NDBT-76 is likely to be fruitful for developing extreme divergent heterotic cross combination and may be potentially exploited in bitter gourd breeding programmes. Similarly, lowest inter-cluster distance was found between clusters III and IV (12.27), which exhibit more genetic similarity (Table 2). The highest intra-cluster distance was observed in the cluster I (23.89) indicating genotype belonging to this cluster were far diverged from cluster II.

The present study found that out of the eleven yield and its contributing traits, seven major traits contributed 100 per cent towards genetic divergence. Out of seven major traits, proportionate contribution of fruit weight (g) and fruit length (cm) towards genetic divergence were found 74 and 13 per cent respectively (Fig. 3). Previous studies (Singh *et al.*, 8; Laxuman, 5) have also reported maximum contribution of fruit weight to genetic divergence in bitter gourd genotypes. Therefore, fruit weight would be the important parameter for selecting divergent genotypes. Cluster V exhibited highest cluster mean values for most of the studied traits. Highest cluster mean values for fruits/ plant, fruit weight (g) and fruit yield/ plant (kg) was found in Cluster V followed by cluster II (Table 3). Cluster VI represented highest cluster mean value for node No. to anthesis of first staminate flower, days to first fruit harvest and fruit length (cm).

The PCA of the eleven traits in 32 bitter gourd genotypes is shown in Table 4. The first five PCs having Eigen values greater than one accounted for 74.58% (Table 4) of total variation amongst bitter gourd genotypes. This finding was in agreement with that of Kundu *et al.* (4) on bitter gourd. Moreover, the first 6 principal components contributed 83.19 percent of the total variation with proportionate contribution values of 23.88, 16.81, 13.28, 11.23, 9.38 and 8.61% respectively. Two dimensional ordinations of 32 bitter gourd genotypes on PC axis 1 and 2 are represented in Fig. 4, which revealed scattered diagram of genotypic distribution pattern on axis. Interestingly, distribution of genotypes along the two axes in the PCA plot was consistent with the grouping of these genotypes obtained using cluster analysis. The first PC has positive association with node no. to anthesis of first staminate flower and days to first fruit harvest, while negative association with fruit weight, fruits/plant and fruit yield/plant. The second PC has positive association with days to anthesis of first staminate flower and node No. to anthesis of first staminate flower, while negative association with vine length (m) and days to anthesis of first pistillate flower. The third PC has positive association with days to first fruit harvest, fruit length and fruit yield/plant, while negative association with fruit diameter and days to anthesis of first staminate flower. The fourth PC has positive association with node no. to anthesis of first pistillate flower and fruits/ plant, while negative association with fruit length (cm) and days to anthesis of first staminate flower. The fifth component has negative association with fruit diameter. The traits of bitter gourd that demonstrated positive association with PCs have major role in

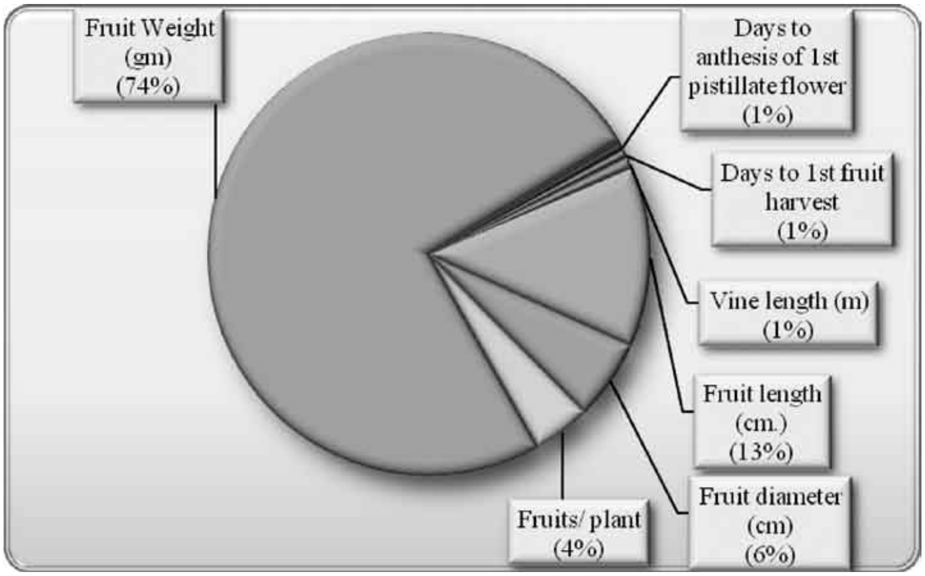

Fig. 3. Graphical representation of proportionate contribution of studied major traits (in parentheses value) towards genetic divergence.

Table 3. Average of studied traits for each cluster and the difference between each cluster mean with total mean.

Cluster No.	Node No. to anthesis of first staminate flower	Node No. to anthesis of first pistillate flower	Days to anthesis of first staminate flower	Days to anthesis of first pistillate flower	Days to first fruit harvest	Vine length (m)	Fruit length (cm)	Fruit diameter (cm)	Fruits/ plant	Fruit wt. (g)	Fruit yield/ plant (kg)
Cluster I	10.12	13.12	47.87	50.77	62.67	2.18	17.01	4.54	15.53	68.03	0.92
	0.18	0.09	0.21	-0.12	-0.06	0.02	0.24	-0.01	-1.10	-0.42	-0.07
Cluster II	9.38	12.29	47.17	51.63	62.92	2.15	16.68	4.50	19.89	73.35	1.22
	-0.56	-0.74	-0.49	0.74	0.19	-0.01	-0.09	-0.05	3.26	4.90	0.23
Cluster III	10.00	14.33	46.33	48.33	61.00	2.02	16.29	5.16	13.53	61.07	0.75
	0.06	1.30	-1.33	-2.56	-1.73	-0.14	-0.48	0.61	-3.10	-7.38	-0.24
Cluster IV	8.67	12.33	47.67	50.00	62.33	2.11	12.33	4.38	13.4	56.3	0.65
	-1.27	-0.70	0.01	-0.89	-0.40	-0.05	-4.44	-0.17	-3.23	-12.15	-0.34
Cluster V	10.67	15.00	49.33	51.67	62.67	2.15	15.60	4.75	23.83	77.40	1.55
	0.73	1.97	1.67	0.78	-0.06	-0.01	-1.17	0.20	7.20	8.95	0.56
Cluster IV	11.67	14.67	47.33	50.33	65.00	2.13	18.99	4.62	11.93	48.50	0.62
	1.73	1.64	-0.33	-0.56	2.27	-0.03	2.22	0.07	-4.70	-19.95	-0.37

Table 4. Principal component analysis for eleven traits in 32 bitter gourd genotypes.

Parameter	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6
Eigen value (Root)	2.63	1.85	1.46	1.23	1.03	0.95
Cumulative Eigen value	2.63	4.48	5.94	7.17	8.20	9.15
Explained variation (%)	23.88	16.81	13.28	11.23	9.38	8.61
Cumulative explained variation (%)	23.88	40.69	53.97	65.20	74.58	83.19
Trait			Eigen vectors			
Node No. to anthesis of first staminate flower	0.34	0.18	0.22	0.05	0.04	0.39
Node No. to anthesis of first pistillate flower	0.06	-0.05	0.09	0.65	-0.36	0.47
Days to anthesis of 1st staminate flower	-0.06	0.42	-0.26	-0.45	0.21	0.34
Days to anthesis of 1st pistilate flower	-0.26	-0.48	-0.13	-0.03	0.18	0.02
Days to first fruit harvest	0.17	-0.23	0.57	-0.09	-0.03	-0.42
Vine length (m)	-0.07	-0.60	-0.13	-0.02	0.24	0.29
Fruit length (cm)	-0.09	-0.26	0.36	-0.49	-0.24	0.48
Fruit diameter (cm)	-0.09	-0.14	-0.53	-0.08	-0.59	-0.14
Fruits/ plant	-0.52	0.16	0.22	0.21	0.18	0.03
Fruit wt. (g)	-0.56	0.07	0.06	0.19	0.19	0.03
Fruit yield/ plant (kg)	-0.42	0.16	0.25	-0.19	-0.50	-0.05

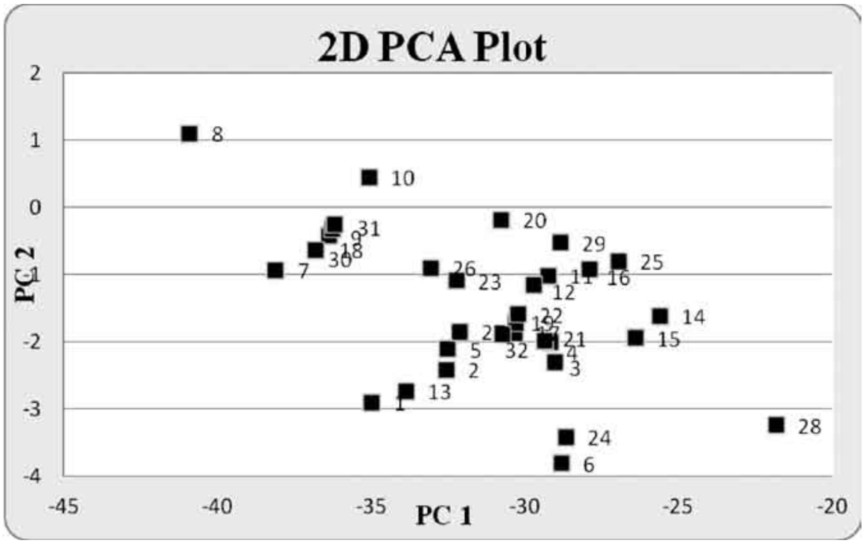

Fig. 4. Scattered diagram: Two dimensional ordination of 32 bitter gourd genotypes based on PC (Principal component) axis 1 and 2.

genetic diversity analysis and explaining total genetic variation are in agreement with findings of Kundu *et al.* (4).

For future experiment, traits contributing maximum to genetic diversity such as fruit weight and length should be given top priority as selection parameters and diverse genotypes identified in the present study may be utilized for attempting heterotic cross combination and developing hybrid varieties.

ACKNOWLEDGEMENT

Authors express their gratitude to Department of Horticulture (Vegetable Science), NDUA&T, Kumarganj, Faizabad for providing facility and bitter gourd genotypes.

REFERENCES

1. Dey, S.S., Behera, T.K., Munshi, A.D. and Sirohi, P.S. 2007. Studies on genetic divergence in bitter gourd (*Momordica charantia* L.). *Indian J. Hort.* **64**: 53-57.

2. Grover, J.K. and Yadav, S.P. 2004. Pharmacological actions and potential uses of *Momordica charantia*: A review. *J. Ethnopharmacol.* **93**: 123-32

3. Haussmann, B.I.G., Parzies, H.K., Presterl, T. Susic, Z. and Miedaner, T. 2004. Plant genetic resources in crop improvement. *Plant Genet. Resour.* **2**: 3-21.

4. Kundu, B.C., Hossain, M.M., Khaleque Mian, M.A. and Mian, I.H. 2012. Multivariate analysis in bitter gourd (*Momordica charantia* L.). *J. Asiatic Soc. Bangladesh* Sci. **38**: 125-34.

5. Laxuman, 2005. Studies on diversity, heterosis and combining ability in bitter gourd (*Momordica charantia*). M.Sc. thesis submitted to University of Agricultural Sciences, Dharwad.

6. Mladenovic, E., Berenji, J., Kraljevic-Balalic, M., Cukanovic, J. and Blagojevic, I. 2012. Multivariate analysis of species from Cucurbitaceae family. *Genetika,* **44**: 227-34.

7. Shankar, R., Bagle, B.G. and More, T.A. 2009. Diversity analysis of bitter gourd (*Momordica charantia* L.) germplasm from tribal belts of India. *Asian Australasian J. Plant Sci. Biotech.* **3**: 21-25.

8. Singh, B., Singh, A.K. and Kumar, S. 2013. Genetic divergence studies in bitter gourd (*Momordica charantia* L.). *Acad. J. Plant Sci.* **6**: 89-91.

9. Thakur, J.C., Khattra, A.S. and Brar, K.S. 1994. Genetic variability and heritability for quantitative traits and fruit fly infestation in bitter gourd. *J. Res. PAU*, **31**: 161-66.

Received: November, 2013; Revised: January, 2014;
Accepted: February, 2014