J. Hortic. Sci.
Vol. 19(2), 2024

https://doi.org/10.24154/jhs.v19i2.1845

Original Research Paper

Cluster analysis by using D^2 statistics among the various bitter gourd (*Momordica charantia* L.) genotypes under Northern hilly regions of Kashmir

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ABSTRACT

Thirty-three bitter gourd genotypes were evaluated to estimate the *per* se performance, genetic variability and cluster analysis for growth and yield traits. *Per se* performance demonstrated that the genotypes *viz*., Phule Green Goal, B.G. Kantedar and NDBG-3 are high yielders, whereas, NDBG-5 and Pant Karela-1 were earlier in flowering. The higher magnitude of coefficient of variation at phenotypic as well as genotypic levels were observed for fruit yield per plant, total chlorophyll content and node number to anthesis of first pistillate flower. The presence of high heritability in broad sense (h^2_{bs}) along with high genetic advance in per cent of mean were observed for total chlorophyll content, node number to anthesis of first female flower and vine length. Estimates of cluster analysis revealed that 33 genotypes were grouped into six distinct clusters. Maximum inter-cluster distances were observed between clusters IV and VI, cluster III and VI, cluster II and VI and cluster IV and V, whereas, maximum intra-cluster distance was observed in cluster I. The crosses between the genotypes of cluster IV with VI and Cluster III with VI are likely to exhibit high hybrid vigour and could produce recombinants with desired traits in segregating generations.

Keywords: Bitter gourd, GCV, intra and inter cluster distances, PCV, *per se* performance

INTRODUCTION

Bitter gourd (*Momordica charantia* L.; $2n=2x=22$), family Cucurbitaceae, is one of the most nutritive and commercially important vegetable crops among the cucurbits grown throughout the country, from plain to an altitude of 1500 m in some parts of world. The crop has originated Indo-Burma region. It is a monoecious and highly cross-pollinated crop in which a large number of variations has been observed for most of the economically important traits. In India, the area under bitter gourd cultivation is 1.01 lakh ha with an annual production of 12 lakh tonnes and productivity of 12.16 MT/ha. Chhattisgarh, Telangana, Andhra Pradesh, Orissa, Madhya Pradesh, Uttar Pradesh and Bihar are the major bitter gourd producing states in the country (NHB database, 2022).

Research on cucurbitaceous vegetables, and especially bitter gourd in India, aims to increase yield potential and quality attributes, while, promoting sustainable productivity through the development of hybrids and varieties resistant to biotic and abiotic stress. A speedy crop and product improvement can be brought about in bitter gourd by assessing the genetic variability and diversity. Mahalanobis D^2 statistics (1936) recognized as very effective method for the assessment of genetic divergence. The selection of parental materials for hybridization programme, simply based on geographic diversity may not be successful experience. The choice of suitable diverse parent selected on the basis of genetic divergence analysis would be more rewarding than the choice made on the basis of geographic diversity.

MATERIAL AND METHODS

The present investigation was undertaken at vegetable Experimental Farm of Division of Vegetable Science, Sher-e-Kashmir University of Agricultural Sciences and Technology, Kashmir, Shalimar during summer, 2020. Shalimar comes under temperate zone, characterized by mild summers. Thirty-three diverse genotypes of bitter gourd were planted at 1 m x 1 m meter and evaluated in randomized complete block design with three replications, for various yield and yield attributing traits. The standard cultural and plant protection practices were followed to raise a healthy crop. The methodology described by Panse & Sukhatme (1967) was used to conduct the analysis of variance for the experimental design. Mahalanobis (1936) generalized distance (D^2) was used to determine the degree of divergence and the genotypes were grouped into clusters following Tocher's method (Rao et al., 1952).

Table 1 : Bitter gourd genotypes used in the study

Genotype	Source
Pant Karela-1	GBPUA&T, Pantnagar
PBTH-52	GBPUA&T, Pantnagar
P-14	MPKV, Rahuri
Phule Green Goal	MPKV, Rahuri
Phule Ujwala	MPKV, Rahuri
IIVR-B.G.-1	IIVR, Varanasi
IIVR-B.G.-2	IIVR, Varanasi
IIVR-B.G.-3	IIVR, Varanasi
IIVR-B.G.-4	IIVR, Varanasi
Kashi Urvashi	IIVR, Varanasi
Hirkunt	IIVR, Varanasi
HABH-21	IIVR, Varanasi
MC-84	IIVR, Varanasi
K.B.M.	IIVR, Varanasi
B.G. Kantedar	IGKV, Raipur
B.G. Sagar	IGKV, Raipur
NDBG-1	NDUA&T, Faizabad
NDBG-2	NDUA&T, Faizabad
NDBG-3	NDUA&T, Faizabad
NDBG-4	NDUA&T, Faizabad
NDBG-5	NDUA&T, Faizabad
NDBG-6	NDUA&T, Faizabad
NDBG-7	NDUA&T, Faizabad
NDBG-10	NDUA&T, Faizabad
NDBG-11	NDUA&T, Faizabad
NDBG-12	NDUA&T, Faizabad
NDBG-13	NDUA&T, Faizabad
NDBG-14	NDUA&T, Faizabad
NDBG-15	NDUA&T, Faizabad
NDBG-16	NDUA&T, Faizabad
NDBG-17	NDUA&T, Faizabad
Narendra Baramasi	NDUA&T, Faizabad
Local B.G. (Check)	SKUAST-Kashmir

RESULTS AND DISCUSSION

Per se performance

Mean performance of genotypes have been presented in Table 2a and 2b. Days to anthesis of first staminate flower ranged from 44.00 days (NDBG-4) to 67.66 days (Phule Green Goal). Three genotypes, Kashi Urvashi (46.00), K.B.M (46.33) and PBTH-52 (47.00), were significantly earlier in days to first staminate flower anthesis in order or merit as compared to general mean (54.71). Three genotypes *viz*., HABH-21 (52.66), P-14 (55.00) and Phule Green Goal (55.33) were significantly earlier in days to first pistillate flower anthesis. Node number to anthesis of first staminate flower were lowest in NDBG-2 followed by Pant Karela-1, HABH-21 (5.33), where the staminate flower appears at the earlier node which give the sufficient pollen for pistillate flower. Node number to anthesis of first pistillate flower appears on earlier node in NDBG-5 followed by Pant Karela-1 (5.66), P-14, IIVR-B.G.-3 (6.00). Thus, the genotypes identified for first staminate flower anthesis as early and late may be selected based on objective of programme and could be exploited in suitable breeding programme. Similar results obtained by Saho (2015) and Sagar et al. (2022) in bitter gourd.

Hirkunt, recorded longest vine length (2.37 m) followed by HABH-21 (2.36 m), IIVR-B.G-3 (2.34 m). Promising genotypes identified for fruit length were NDBG-10 (18.50 cm), followed by B.G. Sagar (18.00 cm), NDBG-4 (17.00 cm). The highest and lowest fruit diameter was recorded in Kashi Urvashi (2.46 cm) and IIVR-B.G.-4 (4.50 cm), respectively. In bitter gourd medium and low fruit diameter had more consumer preference for cooking purpose. The above results are in similar with the findings of Rani et al. (2014), Saho (2015) and Talukdar et al. (2018).

Most promising genotypes for number of fruits per plant were Phule Green Goal (19.33), Phule Ujwala (18.00) and IIVR-BG-2 (16.66). Highest mean performance for average fruit weight was recorded in (NDBG-6) (77.76 g) followed by NDBG-17 (75.63 g) and NDBG-11 (75.29 g). Similar results were obtained by Talukder et al. (2018) and Sagar et al. (2022). Minimum days for first fruit harvest

Table 2a : *Per se* performance of genotypes for growth and yield traits in bitter gourd

Genotype	Days to anthesis of first male flower	Days to anthesis of first female flower	Node number to anthesis of first male flower	Node number to anthesis of first female flower	Vine length (m)
Pant Karela-1	53.00	59.00	5.33	5.66	2.01
PBTH-52	47.00	72.33	8.00	11.33	1.71
P-14	66.00	55.00	5.66	6.00	2.20
Phule Green Goal	67.66	55.33	6.00	7.66	1.57
Phule Ujwala	64.33	72.33	7.33	9.66	1.99
IIVR-B.G.-1	54.00	66.66	7.33	9.00	1.59
IIVR-B.G.-2	61.66	61.00	7.00	13.00	2.23
IIVR-B.G.-3	54.00	55.33	5.66	6.00	2.34
IIVR-B.G.-4	58.33	67.66	7.33	11.00	2.20
Kashi Urvashi	46.00	72.33	8.33	11.33	1.27
Hirkunt	57.33	56.66	5.66	6.66	2.37
HABH-21	57.00	52.66	5.33	6.66	2.36
MC-84	57.33	70.00	6.66	13.00	2.14
K.B.M.	46.33	57.00	6.66	6.00	1.74
B.G. Kantedar	66.00	55.66	6.00	6.00	1.59
B.G. Sagar	57.33	61.66	7.33	12.00	2.21
NDBG-1	52.00	74.33	7.33	12.33	2.23
NDBG-2	48.66	55.33	5.00	5.33	1.82
NDBG-3	47.00	51.66	6.66	12.33	2.32
NDBG-4	44.00	61.00	5.66	11.33	2.07
NDBG-5	52.33	67.33	6.66	5.00	2.17
NDBG-6	54.66	55.33	6.66	13.00	2.25
NDBG-7	54.66	62.66	6.33	11.00	1.35
NDBG-10	48.00	66.66	7.66	10.66	2.14
NDBG-11	67.00	56.00	6.33	6.33	2.17
NDBG-12	47.00	64.33	6.00	11.66	2.20
NDBG-13	51.66	70.33	6.33	12.00	2.23
NDBG-14	52.00	67.66	7.66	6.00	1.65
NDBG-15	47.00	69.38	6.66	12.00	2.23
NDBG-16	54.00	74.66	7.66	12.33	2.23
NDBG-17	67.00	59.38	6.66	6.33	2.19
Narendra Baramasi	52.66	74.33	6.00	12.33	2.33
Local B.G.	53.33	65.66	6.33	7.66	1.64
Mean	54.71	62.95	6.60	9.41	1.98
C.V.	2.95	2.85	12.13	9.39	6.05
C.D. 5	2.63	2.93	1.30	1.44	0.21
C.D. 1%	3.51	3.90	1.74	1.92	0.28

Table 2b : *Per se* performance of various genotypes for growth and yield traits in bitter gourd

Genotype	Fruit diameter (cm)	Fruit length (cm)	No. of fruits/ plant	Average fruit weight (g)	Days to first fruit harvest	Fruit yield (kg)
Pant Karela-1	4.33	12.46	11.66	62.60	71.33	1.17
PBTH-52	4.31	14.00	12.66	67.50	79.00	0.80
P-14	3.49	12.53	16.00	73.00	87.66	1.54
Phule Green Goal	3.53	8.33	19.33	74.87	75.33	1.52
Phule Ujwala	4.10	12.50	18.00	61.53	88.00	0.68
IIVR-B.G.-1	4.33	12.33	15.66	62.40	73.33	0.64
IIVR-B.G.-2	3.18	11.50	16.66	62.37	97.33	0.81
IIVR-B.G.-3	3.24	11.76	13.66	60.09	77.33	0.60
IIVR-B.G.-4	4.50	11.66	13.00	69.39	74.00	1.48
Kashi Urvashi	2.46	10.83	14.66	66.86	67.33	0.70
Hirkunt	2.66	14.17	10.00	64.33	80.33	0.50
HABH-21	3.56	11.55	9.33	61.71	81.33	1.28
MC-84	3.96	13.50	7.00	69.72	75.33	1.05
K.B.M.	3.83	12.60	11.00	66.86	84.33	0.85
B.G. Kantedar	3.63	15.00	11.00	61.44	87.66	1.51
B.G. Sagar	3.19	18.00	7.66	72.43	77.66	1.26
NDBG-1	3.95	12.66	15.00	71.43	67.00	0.62
NDBG-2	3.46	13.90	12.66	70.78	76.33	0.57
NDBG-3	4.03	16.43	13.66	69.41	73.33	1.48
NDBG-4	4.33	17.00	11.66	73.06	74.33	0.75
NDBG-5	4.16	14.43	13.66	73.11	74.66	1.10
NDBG-6	3.36	14.66	14.66	77.76	86.33	0.76
NDBG-7	3.36	11.83	8.66	54.70	82.00	0.72
NDBG-10	2.60	18.50	12.00	74.00	81.33	0.69
NDBG-11	3.80	16.50	12.33	75.29	81.66	0.57
NDBG-12	3.96	15.30	7.00	52.96	76.00	0.66
NDBG-13	4.33	12.66	7.33	74.83	78.00	1.10
NDBG-14	3.20	16.00	8.00	54.87	66.00	0.71
NDBG-15	4.02	11.82	8.33	65.63	82.32	0.51
NDBG-16	3.95	12.66	15.33	71.43	82.33	1.17
NDBG-17	3.92	16.62	12.33	75.63	82.33	0.80
Narendra Baramasi	4.03	14.16	12.66	74.03	83.66	1.18
Local B.G.	2.67	11.32	7.03	61.43	81.33	0.48
Mean	3.73	12.80	12.38	67.46	78.45	0.97
C.V.	6.40	4.91	6.62	3.74	1.77	13.34
C.D. 5	0.39	1.05	1.34	4.41	2.28	0.21
C.D. 1%	0.52	1.39	1.78	5.87	3.03	0.281

Table 3 : Estimates of mean, phenotypic and genotypic coefficients of variation, heritability (bs) and genetic advance (as% of mean) for growth and yield traits in bitter gourd

Character	Mean	GCV	PCV	Heritability (bs) (%)	Genetic advance (% of mean)
Days to anthesis of first male flower	54.71	12.18	12.54	94.40	31.27
Days to anthesis of first female flower	62.95	11.36	11.71	94.00	29.09
Node number to anthesis of first male flower	6.60	11.52	16.73	47.40	20.95
Node number to anthesis of first female flower	9.41	30.29	31.71	91.20	76.38
Vine length (m)	1.98	29.12	29.74	95.80	75.27
Fruit diameter (cm)	3.73	15.02	16.33	84.60	36.49
Fruit length (cm)	12.80	22.93	23.45	95.60	59.19
No. of fruits plant^{-1}	12.38	26.32	26.95	93.90	68.87
Average fruit weight (g)	67.46	11.13	11.74	89.80	66.87
Days to first fruit harvest	78.45	8.75	8.93	96.04	27.86
Fruit yield plant^{-1} (kg)	0.97	42.40	44.45	90.90	9.510

GCV: genotypic coefficient of variation; PCV: phenotypic coefficient of variation

recorded in NDBG-14 (66.00) followed by NDBG-1 (67.00), Kashi Urvashi (67.33). These genotypes seem to be early in days to first marketable fruit harvest and may be considered promising genotype for early harvest of fruits. Among the high yielding genotypes five most promising genotypes identified in order of merit were Phule Green Goal, B.G. Kantedar and NDBG-3 exhibited average mean performance for number of fruit per plant also.

Genetic variability, heritability (bs) and genetic advance

The estimates of genotypic as well as phenotypic coefficient of variability were observed higher for fruit yield per plant (42.40%) followed by total chlorophyll content (36.83%) and node number to anthesis of first pistillate flower (30.29%) (Table 3). All the traits recorded high phenotypic variances compared to genotypic variances, which is indication of strong influences of environmental factors for their expression. The estimates of heritability in broad sense (h^2bs) ranged from 47.40% (node number to anthesis of first staminate flower) to 98.76% (total chlorophyll content). Highest estimates of heritability (>70%) were observed for all the character except for node number to anthesis of first staminate flower. Total chlorophyll content, node number to anthesis of first female flower, vine length, number of fruits per plant, and fruit weight all showed high heritability along with high genetic advance in per cent of mean, indicating that these characters may also offer good response to selection due to their high transmissibility and variability along

Table 4 : Distribution of bitter gourd genotypes in different clusters

Cluster	Genotype	Genotype
I	6	P-14, Phule Ujwala, IIVR-B.G-3, HABH-21, MC-84, B.G. Sagar
II	5	Kashi Urvashi, NDBG-6, NDBG-7, NDBG-10, NDBG-12
III	11	Pant Karela-1, Phule Green Goal, IIVR-B.G-1, IIVR-B.G-2, IIVR-B.G-4 B.G. Kantedar, NDBG-3, Narendra Baramasi, NDBG-16, NDBG-17, Local B.G. (Check)
IV	7	PBTH-52, K.B.M, NDBG-1, NDBG-4, NDBG-5, NDBG-13, NDBG-14
V	1	NDBG-11
VI	3	Hirkunt, NDBG-2, NDBG-15

Table 5 : Average intra cluster (diagonal) and inter cluster (above diagonal) distance values in bitter gourd

Cluster	I	II	III	IV	V	VI
I	**85.74**	119.48	165.48	145.90	193.33	194.65
II		**45.48**	55.47	101.49	197.46	209.25
III			**53.34**	153.25	193.08	273.26
IV				**60.27**	206.17	303.37
V					**0.00**	181.67
VI						**64.23**

with genetic advance showing additive gene effect. Studies have also found similar results in bitter gourd (Yadagiri et al., 2017; Triveni et al., 2021).

D^2 analysis (Clustering pattern)

The studies of genetic divergence among 33 genotypes of bitter gourd were carried out by using Mahalanobis D^2 statistics. All 33 genotypes were grouped into 6 different non-overlapping clusters (Table 5). Cluster III had highest number of genotypes (11), followed by cluster IV (7), I (6), II (5), VI (3), whereas, cluster V had only one genotype (Table 4). This indicated presence of considerable genetic diversity in the germplasm collections evaluated in the present study.

Average inter and intra-cluster distances

The minimum intra-cluster distance was found in cluster V (0.00) and maximum was recorded in cluster I (85.74) (Table 5). The maximum inter-cluster distance was observed between cluster IV and cluster VI (303.37), which suggested that members of these two clusters are genetically very diverse to each other. The inter cluster values between cluster III and cluster VI (273.26), cluster II and cluster VI (209.25), cluster IV and cluster V (206.17), cluster II and cluster V (197.46) and cluster I and cluster VI (194.65) were very high. Accordingly, the above-discussed crossing of genotypes from cluster pairings that are separated by a very high inter-cluster distance may produce desired transgressive segregates. The results are in agreement with the findings of Resmi & Srilathakumary (2012) and Singh & Kandasamy (2020) in bitter gourd.

Cluster means

Cluster IV showed maximum mean values for days to anthesis of first staminate flower (66.83), average fruit weight (78.94 g) and fruit yield (1.84 kg) (Table 6). Cluster II showed maximum values for days to anthesis of first pistillate flower (72.33), fruit diameter (4.11 cm) and number of fruits per plant (18.00). Cluster VI showed maximum values for node number to anthesis of first staminate flower (7.67) and fruit length (18.50 cm). Cluster III showed maximum values for node number to anthesis of first pistillate flower (5.16) and days to first fruit harvest (97.33). Cluster V showed maximum value for vine length

Table 6 : Clusters means for various quantitative characters in bitter gourd (*Momordica charantia*) genotypes

Cluster	Days to anthesis of first staminate flower	Days to anthesis of first pistillate flower	Node number to anthesis of first staminate flower	Node number to anthesis of first pistillate flower	Vine length (m)	Fruit diameter (cm)	Fruit length (cm)	No. of fruits/ plant	Average fruit weight (g)	Days to first fruit harvest	Fruit yield/ plant (kg)
I	53.18	63.40	6.61	9.53	2.00	3.83	13.31	11.65	72.81	76.82	0.93
II	64.33	72.33	7.33	9.67	2.00	4.11	12.50	18.00	61.54	88.00	0.68
III	61.67	61.00	7.00	13.00	2.23	3.18	9.50	16.67	62.37	97.33	1.60
IV	66.83	55.17	5.83	6.83	1.89	3.53	12.43	17.67	78.94	81.50	1.84
V	57.33	56.67	5.67	6.67	4.18	3.42	13.67	10.00	64.33	80.33	0.28
VI	48.00	66.67	7.67	10.67	4.17	2.60	18.50	12.00	74.00	81.33	0.58

(4.18 m). Therefore, crosses between members of clusters having high cluster means for important characters coupled with high inter cluster distances between them, are likely to be more useful. Tyagi et al. (2018) and Singh & Kandasamy (2020) also reported similar results in bitter gourd.

CONCLUSION

It is inferred that the most promising genotypes regarding yield were Phule Green Goal, B.G. Kantedar, NDBG-3 and B.G. Sagar. Additive gene action controls traits with high phenotypic and genotypic coefficients of variation, high heritability when combined with strong genetic advance. As this implies, these characters could offer positive response to the selection. The very high inter cluster value was observed between cluster IV and VI, cluster III and cluster VI and cluster II and cluster VI. Maximum cluster mean for fruit yield per plant was observed in cluster IV followed by cluster III. Therefore, crosses between members of clusters having high cluster means for important characters coupled with high inter cluster distances between them, are likely to be more useful.

ACKNOWLEDGEMENT

Authors are highly thankful to the Division of Vegetable Science, Division of Plant Breeding and Genetics, Sher-e-Kashmir University of Agricultural Sciences & Technology, Shalimar, Srinagar for providing the facilities for conducting this research.

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(***Received : 21.1.2023; Revised : 22.7.2024; Accepted : 25.7.2024)***