Vegetable Science (2024) 51(2): 275-282
doi: 10.61180/vegsci.2024.v51.i2.11
ISSN- 0970-6585 (Print), ISSN- 2455-7552 (Online)
www.isvsvegsci.in

RESEARCH ARTICLE

Genetic divergence studies using multivariate analysis in bitter gourd (*Momordica charantia* L.)

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Abstract

The genetic divergence of 70 bitter gourd genotypes was studied for eight different morpho horticultural traits by adopting the Mahalanobis D^2 statistics (SAS software program) using Tocher's method. The genotypes were divided into seven clusters using squared Euclidean distance. The results revealed the presence of considerable genetic diversity. The first three principal components contributed 79.20% and 76.50% of total variability during the summer season and *kharif* season, respectively. The clustering pattern of genotypes revealed that genetic diversity was independent of geographical diversity. In summer, among the 7 clusters, the maximum number of genotypes were found in cluster IV, while it was cluster I for *kharif*. Among the eight quantitative characters studied, fruit width contributed a maximum of 17.75% genetic divergence, followed by 1st female flower emergence on a node in the summer, while for *kharif*, 1st female node constituted a maximum of 17.95% contribution to the divergence, followed by fruit width. Together, PC1's eigenvalue of 3.84, PC2's eigenvalue of 1.27, and PC3's eigenvalue of 1.22 account for 48, 16, and 15.3% of the total variability, respectively, in the summer season. The ranking of genotypes based on intra-cluster mean performance for these characters, which are major contributors to genetic diversity, revealed its usefulness as a means of selecting parents for heterosis breeding. Genotypes VRBTG-29, VRBTG-47, VRBTG-10, VRBTG- 31, VRBTG- 47-3 and VRBTG- 28 stood out for earliness, number of fruits/plant and total yield and were found to be more diverse for important horticultural traits. The maximum inter-cluster distance was observed between clusters VI and VII during the summer season and between clusters VII and cluster II during *kharif* season. The intra-cluster distance was maximum for cluster VI and cluster VIII during the summer and *kharif* seasons, respectively. Selecting genotypes from the clusters having high inter-cluster distance for crossing gives better transgressive segregants.

Keywords: Bitter gourd, Genetic diversity, Clusters, Euclidean distance, D^2 analysis, Principal component analysis.

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Citation: Bhardwaj, D.R., Pandey, J., Singh, A., Kumar, S., & Gautam, K. (2024). Genetic divergence studies using multivariate analysis in bitter gourd (*Momordica charantia* L.). Vegetable Science, 51(2), 275-282.

Source of support: Nil

Conflict of interest: None.

Received: 30/04/2024 **Revised:** 28/09/2024 **Accepted:** 30/09/2024

Introduction

Bitter gourd (*Momordica charantia* L., 2n = 2x = 22), is a monoecious cucurbit crop known as 'karela', bitter cucumber, bitter melon and balsam pear. This is widely grown in India, China, Malaysia, Africa, and South America (Behera et al., 2023). Tropical Asia, specifically Eastern India (which encompasses the states of Odisha, West Bengal, Assam, Kerala, Jharkhand, and Bihar), and Southern China, often known as the Indo-Burma region, are its main centers of origin (Zeven and Zhukovsky, 1975). The total acreage of bitter gourd in India is 115.4 thousand ha, with a production of 1439.5 thousand MT in 2022-23 (NHB, 2023). The crop needs a minimum temperature of 18°C for early growth, although the ideal range is between 24 to 27°C (Palada et al. 2003). Bitter gourd cultivation has recently gained popularity because of consumer awareness of its nutritional and antidiabetic properties. Among cucurbits, bitter gourd

is rich in vitamins (A & C) and minerals (Mg, Fe, Mn, P and Zn) as well as in medicinal properties (Behera et al., 2023; Bharathi et al., 2012).

Vegetable breeders' efforts have resulted in a noticeable increase in yield as well as the development of many new varieties and hybrids possessing specific quality traits. To expand the genetic base, a high-level genetically diverse population serves as an important reserve for any breeding program (Matsumura et al., 2020). This crop still lacks adequate information on genetic makeup and divergence, although having relatively broad phenotypic species variation for several morphological traits. To exploit the potential of heterosis, the choice of parents that are diverse and capable of producing productive hybrids depends on the type and extent of genetic divergence. Utilizing genetically diverse parents in breeding is key to improving yield and quality in any breeding program. As it outcrosses nature, it has a broad spectrum of genetic diversity, and the crop anticipates having plenty of scopes to improve through a heterosis breeding program. Understanding gene activity and combining ability accountable for significant characteristics is also crucial (Singh et al. 2020). To generate potential transgressive segregants and new gene recombination in the gene pool, genetic divergence is considered an essential factor in selecting genetically diverse parents for effective and successful hybridization. Hence, it is essential to conserve, characterize, and utilize genetic resources, and conduct baseline studies such as multivariate analysis (Singh et al. 2014). It is highly acceptable, as D^2 statistics (Mahalanobis, 1936) measure the degree of divergence between the two genotypes being compared. The D^2 analysis-based genotype grouping will help to select appropriate parental lines for hybridization.

In any effective plant breeding program, the breeder requires a fundamental understanding of nature and the degree of genetic diversity and variability in the germplasm lines, as well as the link between various traits (Behera et al., 2023). It provides information on how various traits are inherited and helps in selecting plants with desirable qualities, enabling the breeding of new cultivars for commercial production. The ability to promote genetic diversity through traditional breeding methods largely depends on the presence of a wide range of germplasm and significant genetic variability. Assigning genotypes to heterotic groups and categorizing accessions according to their genetic variability to produce segregated progenies with the greatest genetic diversity for future breeding purposes. To strengthen the ongoing improvement programme, the current study was undertaken to select suitable parents among genotypes through a cluster approach.

Materials and Methods

Plant material

The experimental materials comprised 71 indigenous genotypes of bitter gourd, including some of the commercially released varieties collected from different research organizations. The experiment was laid out in a randomized complete block design (RCBD) with three replications in two different seasons, *viz*, summer and *kharif* and carried out at the ICAR-Indian Institute of Vegetable Research, Varanasi (U.P.) during 2020-21. The spacing used in the experiment was row-to-row 250 cm and plant-to-plant 60 cm. The recommended doses of fertilizers and cultural practices, along with plant protection measures, were followed to raise a good crop. Five plants were randomly selected and labeled in each replication. Observations were recorded for eight morpho-horticultural traits, i.e.,1st emergence of female flower on node number, fruit length (cm), fruit circumference (cm), fruit width (cm), fruit weight (g), number of fruits per plant, vine length (cm) and fruit yield/ plant (kg). The data were subjected to multivariate analysis of genetic divergence following Mahalanobis D^2 statistics. Grouping of entries was done by using Tocher's method (Rao, 1952).

Statistical analysis

To determine the level of significance among the genotypes for various traits, the mean values were subjected to analysis of variance according to Federer (1956 & 1961).

Cluster analysis

The clustering of genotypes into different groups was carried out using the average linkage method. The appropriate number of clusters was determined from Pseudo F and Pseudo T2 statistics values using the SAS computer software (version 9.2) to group sets of genotypes into similar clusters (SAS, 2008). The genetic difference between groups was determined using the Mahalanobis (D^2) statistics (Mahalanobis, 1936). The D^2 analysis was performed based on the mean values of all traits by using the SAS software program.

Principal component analysis (PCA)

The principal component analysis was computed by using the PRINCOMP procedure (9.2 version) of the statistical analysis system (SAS, 2008). The investigation of a suitable multivariate technique for analyzing data for all the characters is considered. The following formula was computed scores on the first component which was extracted by a principal component analysis.

$$PC1=b11(X1) +b12+\cdots b1p=(Xp)$$

Where PC1= the subject's score on principal component 1 (the first component extracted), b1p = the regression

coefficient (or weight) for observed variable p, as used in creating principal component 1 and Xp = the subject's score on observed variable p.

Results and Discussion

Analysis of variance

The existence of Significant ($P \leq 0.01$) variation was observed in traits including 1st female bearing node, fruit length, fruit circumference, fruit width, fruit weight, number of fruits per plant, vine length and fruit yield per plant (Table 1). Genotypes BT-3 and BT-2 stood out significantly for most of the traits in the summer and *kharif* seasons, respectively. CLO-1 showed high mean values for 1st female bearing node in both seasons. Genotypes VRBTG-29, VRBTG-47 for summer and VRBTG-10 for *kharif* contributed high values for yield per plant, whereas VRBTG-31, VRBTG-28 and VRBTG-4-7-3 posed high values for a number of fruits per plant in both seasons.

Cluster analysis

Seventy-one bitter gourd genotypes were divided into seven clusters according to the dendrogram generated by the cluster analysis (Figure 1). The seven grouping patterns of the 71 bitter gourd genotypes are presented in Table 2. It would be more fruitful to select suitable diverse parents based on genetic divergence analyses than to do so based solely on proximity to one another. The number of genotypes present in the clusters, the number of clusters generated, and the superposition of the genotypes inside the clusters all suggested the prospect of genetic improvement for yield and yield components. The largest group of the seven clusters for the summer season was cluster IV, which had fifteen genotypes, followed by cluster V, which had thirteen genotypes. Cluster I has twelve genotypes, cluster II has eleven, cluster VII has ten, cluster III has six and cluster VI has four genotypes. In *kharif*, the number of genotypes in cluster I was the largest, followed by clusters V, VI, III and IV, having 19, 15, 11, 10 and 6 genotypes, respectively. Cluster II and cluster VII consisted of 5 genotypes each.

While considering the overall impact of the eight characters, the genotypes within the same cluster showed minimal genetic divergence from each other. In contrast, a greater genetic diversity was noticed among genotypes from different clusters. This conclusion is based on the estimated average intra-cluster and inter-cluster distances across seven clusters. (Table 3). For the summer season, the high inter-cluster distance was found between cluster VI and cluster II (7.405), followed by I and VI (5.274), III and VI (5.037) in the current analysis. Similarly, cluster V maintained a high-class inter-cluster distance from cluster II (4.531), cluster III (2.977), and cluster I (2.689). Cluster IV recorded high-order inter-cluster distance from cluster II (3.501) and III (2.633). In the *kharif* season, the investigation revealed the high inter-cluster distance between cluster VII and cluster II (7.081), cluster II and IV (5.15), cluster IV and cluster VII (4.930), cluster II and V (4.842), cluster I and VII (4.536) and cluster VI and VII (4.037). To create high-yielding bitter gourd genotypes, a cross between the genotypes belonging to the aforementioned cluster pairs is advised (Dey et al., 2007).

The smallest inter-cluster distances were observed between cluster I and IV (1.941), followed by cluster IV and VII (2.321), cluster I and VII (2.480) for the summer season while it was lowest between cluster III and V (1.796), cluster V and I (2.373), cluster V and VI (2.531) in *kharif* season data (Table 3). This showed that due to the minimal genetic diversity among the genotypes of the top three cluster pairs,

Table 1: Analysis of variance in genotypes

Summer season									
Source of variation	*DF*	*1st female bearing node*	*Fruit length (cm)*	*Fruit circum. (cm)*	*Fruit width (cm)*	*Fruit weight (g)*	*No. of fruits/ plant*	*Vine length (cm)*	*Yield/ plant (kg)*
Replication	2	2.07	6.70	1.39	0.58	343.06	2.26	1169.02	0.010
Treatment	70	15.15**	29.32**	19.35**	1.96**	1574.87**	97.14**	4870.49**	1.270**
Error	140	2.72	2.12	0.44	0.07	72.01	4.99	483.04	0.029
Total	212	6.82	11.14	6.69	0.70	570.80	35.39	1938.20	0.439
Kharif season									
Source of variation	*DF*	*1st female bearing node*	*Fruit length (cm)*	*Fruit circum. (cm)*	*Fruit width (cm)*	*Fruit weight (g)*	*No. of fruits/ plant*	*Vine length (cm)*	*Yield/ plant (kg)*
Replication	2	5.77	4.92	2.82	0.33	432.51	20.48	61.41	0.196
Treatment	70	12.24**	71.03**	18.08**	1.83**	2323.43**	138.83**	13458.96**	1.568**
Error	140	1.86	0.23	0.16	0.02	23.09	7.33	64.96	0.019
Total	212	5.32	23.65	6.10	0.62	786.50	50.88	4487.47	0.532

*, ** significant at 5% and 1% level, respectively

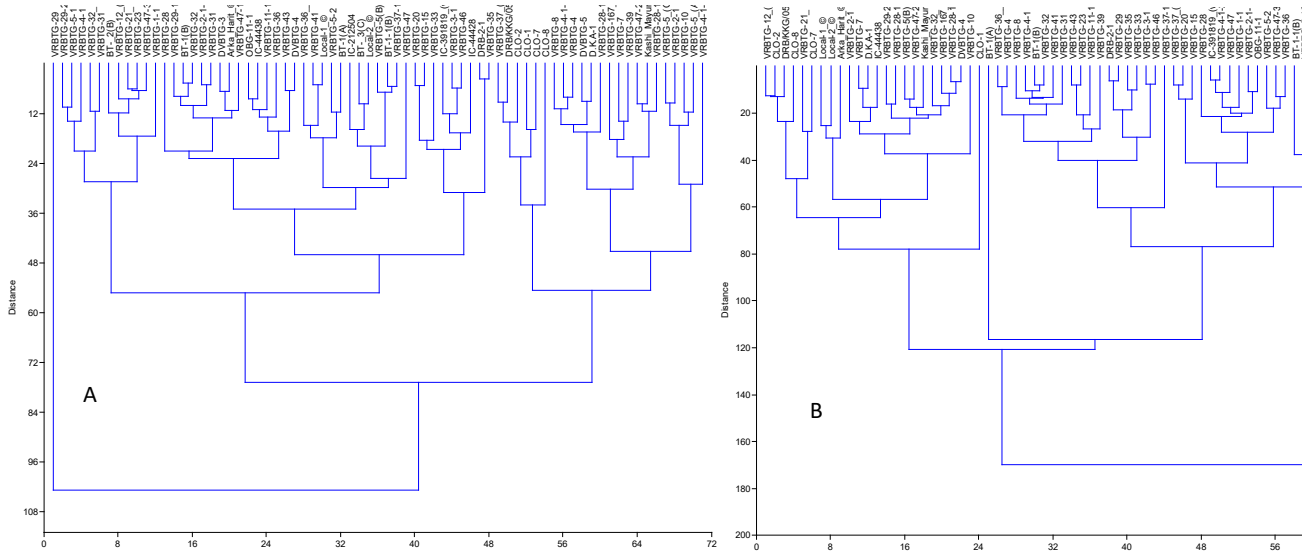

Figure 1: Grouping patterns of bitter gourd genotypes as per cluster analysis A) Summer B) *Kharif*

hybridization between them could not be profitable. These findings are similar to those of Ram et al. (2011), Moharana et al., (2018) and Kundu et al. (2012).

In order to achieve maximum heterosis in crossing and to be used in the hybridization program to produce a wide spectrum of variation among the plants, the selection of genotypes from distant clusters is anticipated. Among the clusters, cluster VI showed the highest intra-cluster distance (2.213), followed by cluster V (1.770), cluster I (1.689) and cluster IV (1.610), whereas cluster VII (1.531) represented the lowest in summer. Furthermore, the maximum number of genotypes fell in cluster IV followed by clusters V, I and II. In the *kharif* season, cluster VII had the maximum intra-cluster distance (2.627) followed by cluster IV (2.187), cluster VI (1.721), and cluster III (1.591), while cluster II exhibited the minimum intra-cluster distance (1.372). There seems to be greater genetic variation among the genotypes across different clusters, as indicated by the average inter-cluster distances being greater than the average intra-cluster distances. This suggests significant genetic variation among the genotypes, highlighting their distinct identities. This conclusion is supported by the larger inter-cluster distances compared to the intra-cluster distances (Debata et al. 2017).

In the summer, the cluster means for various traits were intuited through seven clusters. Cluster I revealed the higher value for the number of fruits per plant, first female flower emergence on a node, fruit length. Cluster II showed the highest mean for a node to female flower emergence whereas a maximum number of lowest means, i.e., for fruit length, fruit width and fruit weight. Cluster III exhibited the highest means for fruit length and vine length. Cluster IV shows the second-highest values for the first female flower emergence node and vine length. The number of fruits per plant and fruit width showed the highest cluster mean in clusters V and VI, respectively. Cluster VII exhibited the second highest cluster mean for fruit width while lowest for the first female flower emergence node. The clustering patterns were in accordance with Devmore et al. (2007) and Silveira et al. (2022).

For the *kharif,* the cluster means for each of the eight characters for seven clusters revealed that cluster I showed higher values for the first female flower emergence node, fruit width and yield per plant while it exhibits the lowest values for fruit length and vine length. Cluster II exhibits the highest mean for the first female flower emergence node and second highest for vine length, as well as the lowest means for fruit circumference, fruit width and fruit weight. Cluster III had the highest mean value for vine length and the lowest value for the first female flower emergence node. Cluster IV showed the highest mean for fruit length and second highest values for the first female flower emergence node, yield/plant and number of fruits/plant. The second-highest values for fruit circumference and fruit width were obtained in cluster V. The Highest cluster mean for the number of fruits/ plant and yield per plant was shown in cluster VI while the maximum number of highest mean values was obtained in cluster VII for fruit circumference, fruit width and fruit weight (Table 4). These findings are very similar to the results of Tyagi et al. (2017). The contribution of each trait to total divergence is presented in Table 4. The highest contribution towards the divergence was recorded for fruit width (17.75) followed by node at the first female bearing node (15.30) in summer, whereas in *kharif* highest contribution was observed in a first female bearing node (17.95) followed by fruit width (16.34).

Table 2: Number of genotypes assigned to each cluster

Summer season		
Clusters	*No. of genotypes*	*Genotypes*
I	12	VRBTG-29-2, IC-391819 (white), IC-044428, VRBTG-2-1-1, OBG-11-1, BT-1(B), VRBTG-43, BT-1(A), VRBTG-3-1, VRBTG-47-1, VRBTG-31, VRBTG-5-1
II	11	VRBTG-37 (white), VRBTG-20, VRBTG-15, DRB-2-1, DRB/KKG/05, VRBTG-35, VRBTG-46, CLO-1, CLO-2, CLO-8, CLO-7
III	6	Kashi Mayuri, VRBTG-5 (A), VRBTG-5 (C), VRBTG-2-1, VRBTG-8, VRBTG-10
IV	15	VRBTG-5(B), BT-1-1(B), VRBTG-167(C), VRBTG-29-1, VRBTG-4-1-1, VRBTG-7, VRBTG-4, DVBTG-3, VRBTG-4-1-2, VRBTG-32, VRBTG-28-1-1, VRBTG-41, DVBTG-5, IC-044438, VRBTG-403 (©)
V	13	VRBTG-28, VRBTG-36, IC-212504, VRBTG-32, VRBTG-31, VRBTG-47-2, VRBTG-5-2, VRBTG-28-1, VRBTG-4-1, VRBTG-39, VRBTG-33, VRBTG-36, VRBTG-11-1
VI	4	BT-3(C), VRBTG-1-1, VRBTG-29, VRBTG-47
VII	10	BT-2(B), VRBTG-37-1 (white), VRBTG-12, VRBTG-21, VRBTG-47-3, DVBTG-4, VRBTG-23, D.K.A-1, VRBTG-401(©), VRBTG-402
Kharif season		
Clusters	*No. of genotypes*	*Genotypes*
I	19	VRBTG-37 (white), VRBTG-36, VRBTG-20, VRBTG-15, DRB-2-1, VRBTG-4, IC-391819 (white), VRBTG-2-1-1, VRBTG-21, BT-1(B), VRBTG-43, VRBTG-35, VRBTG-3-1, VRBTG-4-1-2, VRBTG-29, VRBTG-33, VRBTG-31, VRBTG-23, VRBTG-46
II	5	DRB/KKG/05, CLO-1, CLO-2, CLO-8, CLO-7
III	10	VRBTG-2-1, VRBTG-7, VRBTG-31, VRBTG-12, VRBTG-28-1-1, IC-044438, D.K.A-1, VRBTG-401, VRBTG-402, VRBTG-403
IV	6	VRBTG-5 (A), VRBTG-8, VRBTG-10, BT-1(A), VRBTG-41, VRBTG-5-1
V	15	VRBTG-5 (C), BT- 3 (C), VRBTG-32, VRBTG-167 (C), VRBTG-4-1-1, IC-044428, VRBTG-28-1, VRBTG-4-1, OBG-11-1, VRBTG-1-1, DVBTG-3, DVBTG-4, VRBTG-32, VRBTG-47, DVBTG-5
VI	11	Kashi Mayuri ©, VRBTG-5(B), VRBTG-28, VRBTG-29-2, VRBTG-47-2,VRBTG-5-2, VRBTG-47-3, VRBTG-47-1, VRBTG-39, VRBTG-36, VRBTG-11-1
VII	5	IC-212504, BT-1-1(B), BT- (B), VRBTG-37-1 (white), VRBTG-29-1

Table 3: Estimate of average intra and inter-cluster distances for seven clusters

Summer season							
Clusters	*I*	*II*	*III*	*IV*	*V*	*VI*	*VII*
I	1.689						
II	2.980	1.578					
III	3.150	4.840	1.582				
IV	1.941	3.501	2.633	1.610			
V	2.689	4.531	2.977	2.621	1.770		
VI	5.274	7.405	5.037	4.358	3.745	2.213	
VII	2.480	5.010	3.769	2.321	2.687	3.292	1.531
Kharif season							
Clusters	*I*	*II*	*III*	*IV*	*V*	*VI*	*VII*
I	1.533						
II	3.736	1.372					
III	2.690	4.616	1.591				
IV	3.634	5.150	3.581	2.187			
V	2.373	4.842	1.796	3.349	1.445		
VI	3.757	5.879	3.090	2.844	2.531	1.721	
VII	4.536	7.081	3.432	4.930	2.566	4.037	2.627

Table 4: Cluster means for yield components based on D^2 analysis

Summer season								
Clusters	*1st female bearing node*	*Fruit length (cm)*	*Fruit circum. (cm)*	*Fruit width (cm)*	*Fruit weight (g)*	*No. of fruits/ plant*	*Vine length (cm)*	*Yield/ plant (kg)*
I	11.67	12.96	10.41	3.32	57.14	18.25	157.69	0.96
II	14.52	7.41	8.45	2.72	26.88	17.70	190.85	0.47
III	13.00	16.94	10.24	3.26	80.56	23.22	237.94	1.92
IV	14.07	12.95	12.51	3.98	65.71	18.09	198.18	1.18
V	11.59	11.94	12.36	3.94	65.90	29.05	167.51	1.91
VI	12.92	13.73	17.38	5.54	105.42	24.00	138.92	2.64
VII	10.60	13.28	14.14	4.50	80.67	16.93	147.13	1.38
% Contribution	15.30	12.45	8.14	17.75	12.14	11.40	13.21	9.61
Kharif season								
Clusters	*1st female bearing node*	*Fruit length (cm)*	*Fruit circum. (cm)*	*Fruit width (cm)*	*Fruit weight (g)*	*No. of fruits/ plant*	*Vine length (cm)*	*Yield/ plant (kg)*
I	12.63	10.96	10.99	3.50	43.16	18.74	291.68	0.81
II	15.93	6.45	6.97	2.22	24.67	17.53	430.33	0.42
III	11.30	14.71	12.27	3.91	65.90	19.43	433.93	1.31
IV	14.67	23.74	9.57	3.06	75.28	25.39	323.50	1.87
V	13.78	13.80	13.56	4.32	70.91	19.31	363.69	1.38
VI	13.73	16.26	12.89	4.11	76.06	32.27	350.55	2.48
VII	13.07	16.61	16.41	5.23	114.33	12.67	363.87	1.50
% Contribution	17.95	7.31	9.53	16.34	13.61	15.15	7.98	12.14

Principal component analysis

According to principal component analysis, the most significant contributor to the total variance at each axis for differentiation is significant (Sharma et al., 1998). Determining eight quantitative characters, the principal component analysis of the 71 bitter gourd genotypes produced positive results (Table 5). The outcome revealed that eight PCs in total had been retrieved. However, 79.20% and 76.50% of the overall variability were supplied by the first three principal components in the summer and *kharif* seasons, respectively, all of which had eigenvalues greater than one. Together, PC1's eigenvalue of 3.84, PC2's eigenvalue of 1.27, and PC3's eigenvalue of 1.22 account for 48%, 16%, and 15.3 percent of the total variability, respectively, in the summer season. However, for the *kharif* season, the eigenvalues of PC1 (3.31), PC2 (1.78) and PC3 (1.02) accounted for 41.4, 22.3, and 12.8% of the total variability. Silveira et al. (2022) found a similar result and used it to explain 72.8 and 70% of the overall variability in bitter melon genotypes. The contribution of each trait to total divergence is presented in Table 6. The highest contribution towards the divergence was recorded for fruit weight in both seasons, indicating the stability of trait expression across the seasons.

For both seasons, fruit circumference (0.446–0.444) and fruit width (0.443–0.498) were significant variables in the PC1, while in addition, the first female flower emergence node (0.355) and fruit length (0.442) were also significant in the case of *kharif*. Hence, both vegetative and reproductive characters contributed to the component. The second PC has a positive association with the first female flower emergence node, number of fruits/plant, vine length and yield/plant while a negative association with fruit circumference and fruit width in both seasons, which is weighed by phenological and yield-contributing variables. In the third PC, first female flower emergence node, and fruit length, fruit weight and vine length showed a positive association and the number of fruits per plant, yield/plant, fruit circumference and fruit width showed a negative association for summer while in *kharif* most of the traits were negatively related *viz*., first female flower emergence node, fruit length, fruit circumference, fruit weight and vine length. The results are in close conformity with the findings of Singh et al. (2014), Jatav et al., (2022) and Singh & Kandasamy (2020). The traits of bitter gourd that demonstrated a positive association with PCs have a major role in variance contribution by the respective principal component (PC).

Table 5: Eigen values and percentage proportion of eight PCs

	Summer season			*Kharif season*		
	Eigen values	*Proportion*	*Cumulative proportion*	*Eigen values*	*Proportion*	*Cumulative proportion*
PC1	3.841	0.48	0.48	3.313	0.414	0.414
PC2	1.278	0.16	0.64	1.786	0.223	0.637
PC3	1.22	0.153	0.792	1.02	0.128	0.765
PC4	0.839	0.105	0.897	0.849	0.106	0.871
PC5	0.603	0.075	0.973	0.807	0.101	0.972
PC6	0.193	0.024	0.997	0.205	0.026	0.998
PC7	0.025	0.003	1	0.019	0.002	1
PC8	0.001	0	1	0	0	1

Table 6: Vector loadings of explained variation by the first three PCs

	Summer season			*Kharif season*		
	PC1	*PC2*	*PC3*	*PC1*	*PC2*	*PC3*
1st female bearing node	-0.237	0.012	0.363	0.355	0.271	-0.06
Fruit length (cm)	0.312	0.152	0.489	0.442	-0.376	-0.033
Fruit circum.(cm)	0.446	-0.308	-0.023	0.444	-0.374	-0.033
Fruit width (cm)	0.443	-0.314	-0.022	0.498	-0.018	0.141
Fruit weight (g)	0.459	-0.018	0.278	0.135	0.585	-0.325
No. of fruits/ Plant	0.162	0.71	-0.402	0.114	0.121	0.858
Vine length (cm)	-0.161	0.332	0.623	0.444	0.403	-0.107
Yield/plant (kg)	0.434	0.411	-0.021	-0.075	0.355	0.348

Conclusion

Genotypes BT-3 and BT-2 stood out as significant for most of the traits in both summer and *kharif* seasons, respectively. Genotypes such as VRBTG-29, VRBTG-47, VRBTG-10. VRBTG-31, VRBTG-47-3 and VRBTG-28 are suggested for inclusion in bitter melon breeding programs concerning fruit yield per plant and number of fruits per plant. The results of this study imply that various principal components, which contribute to both vegetative and reproductive traits, could be used to group the significant characters responsible for variation in the bitter gourd genotypes. Clusters showed a lot of difference that was statistically significant. This demonstrated the potential for genotype improvement through hybridization between two clusters. This increases the chances of obtaining desirable recombinants. However, crossing closely related genotypes within the same cluster is unlikely to produce good segregants, as their low variation limits the potential for suitable outcomes. To increase the possibility of isolating good segregants in the segregating generations, it would be reasonable to look for crossings between the various genotypes that belong to clusters that are separated from one another by large inter-cluster distances. Clusters VI and VII displayed the highest intra-cluster distance for the summer and *kharif* seasons, respectively. Additionally, cluster IV for genotypes from the *kharif* season and cluster VI for genotypes from the summer season both displayed the highest cluster means for various characteristics. The cluster with the highest mean yield values may be chosen for yield in isolation.

Acknowledgment

The authors are thankful to the Director, ICAR-IIVR, Varanasi, for providing the necessary facilities.

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सारांश

करेले के 70 प्रक्षेत्रों की आनुवंशिक विविधता का अध्ययन आठ विभिन्न लक्षणों के लिए महालनोबिस डी वर्ग सांख्यिकी (एस.ए.एस. सॉफ्टवेयर प्रोग्राम) का उपयोग करके टॉचर के तरीके से किया गया। प्रभेदों युक्लिडियन दूरी का उपयोग करके सात समूहों में विभाजित किया गया। परिणामों ने महत्वपूर्ण आनुवंशिक विविधता की उपस्थिति को स्पष्ट किया। पहले तीन प्रमुख घटकों ने क्रमशः गर्मी (एस-1) और खरीफ (एस-2) मौसम में कुल भिन्नता का 79.20 प्रतिशत और 76.50 प्रतिशत योगदान दिया । प्रभेदों का समूह-विन्यास दर्शाता है कि आनुवंशिक विविधता भौगोलिक विविधता से स्वतंत्र थी। एस-1 में सात समूहों में से, समूह पांच में सबसे अधिक संख्या में प्रभेद पाए गए, जबकि एस-2 के लिए समूह था अध्ययन किए गए आठ मात्रात्मक लक्षणों में, फल की चौड़ाई ने 17.75 प्रतिशत आनुवंशिक विभाजन में अधिकतम योगदान दिया, इसके बाद एस-1 में पहले मादा फूल का प्रकट होना था, जबकि एस-2 में प्रथम मादा पार्श्व गांठ ने विभाजन में 17.95 प्रतिशत का अधिकतम योगदान दिया, इसके बाद फल की चौड़ाई थी। इसी प्रकार, पीसी-1 का ईजेनवैल्यू 3.84 , पीसी-2 का ईजेनवैल्यू 1.27 और पीसी-3 का ईजेनवैल्यू 1.22, एस-1 मौसम में क्रमशः 48 प्रतिशत, 16 प्रतिशत और 15.3 प्रतिशत कुल भिन्नता की व्याख्या करते हैं। इन लक्षणों के लिए अंतर-समूह औसत प्रदर्शन के आधार पर प्रभेदों की रैंकिग, जो आनुवंशिक विविधता में सबसे महत्वपूर्ण योगदान करने वाले थे, यह दर्शाती है कि ओज प्रजनन के लिए नर-मादा का चयन करने का एक प्रभावी तरीका है। प्रभेदों वी.आर.बी.टी.जी.-29, वी.आर.बी.टी.जी.-47, वी.आर.बी.टी.जी.-10, वी.आर.बी.टी.जी.-31, वी.आर.बी.टी.जी.-47-3 और वी.आर.बी.टी.जी.-28 अगेतीपन, फल/पौधे की संख्या और कुल उपज के लिए उल्लेखनीय थे और महत्वपूर्ण बागवानी लक्षणों में अधिक विविधता पाई गई। एस-2 मौसम में समूह सात और समूह 2 के बीच। एस-1 और एस-2 मौसम के दौरान, समूह छः और समूह आठ के लिए अंदरूनी समूह दूरी अधिकतम थी। उच्च अंतर-समूह दूरी वाले समूहों से प्रभेदों का चयन संकरण के लिए बेहतर ट्रांसग्रेसिव विभाजन परिणाम देता हैं।