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Studies on genetic diversity for quantitative and quality traits in wild/semi domesticated small bitter gourd genotypes

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Abstract

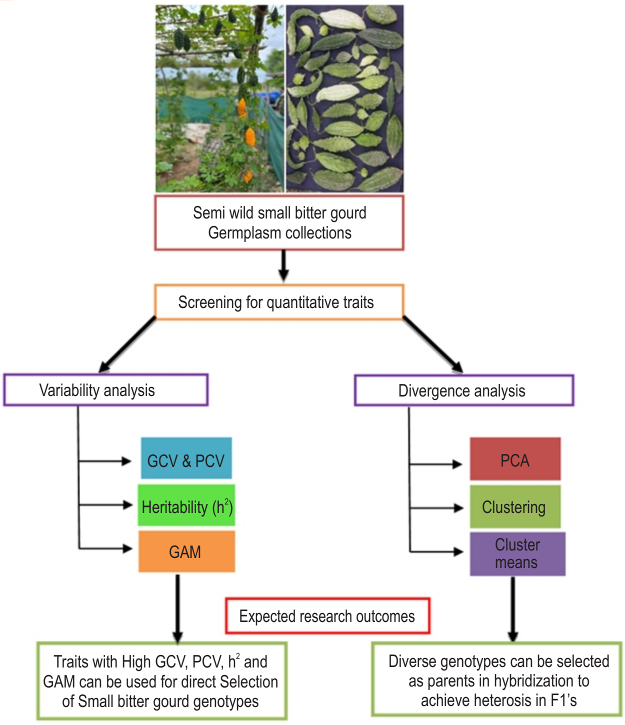
Aim: To evaluate genetic divergence for quantitative traits *viz.* growth, yield and quality characters among twenty small bitter gourd genotypes (*Momordica charantia* L var muricata) under Cauvery delta region.

Methodology: A field experiment was laid out in a Randomized Block Design with 3 replications. Genetic divergence among 20 genotypes was estimated using Principal component analysis and Cluster analysis. The data analysis was done using statistical tools *viz.,* SPSS, GRAPES and TNAUSTAT.

Results: GCV and PCV were found to be high for all the traits under investigation with the exception of days to the first and final fruit harvest, total phenol, vitamin C, and antioxidant FRAP activity, which had moderate values. The principal components (PCA) found five independent components accounting 85.78% of the total variance among 20 genotypes. Hierarchical cluster analysis grouped twenty genotypes into four distinct clusters.

Interpretation: High GCV and PCV indicate that the phenotype is resultant of genetic constitution and not due to environmental effect. The traits with high heritability and genetic advance responded well for direct selection. Heterosis can be exploited through hybridization between the genotypes placed in different clusters and are likely to produce superior F1 hybrids.

Key words: Genetic diversity, Heritability, *Momordica charantia,* Small bitter gourd



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Introduction

Bitter gourd (*Momordica charantia* L.) is available in two forms: the large-fruited form, botanically known as *M. charantia* var. charantia and the small-fruited wild form, known as *M. charantia* var. muricata which is considered as progenitor of commercially grown large-fruited bitter gourd. Both types offer nutritious veggies and medicinally significant components that are utilized to treat liver, spleen, diabetes, rheumatism, and gout (Bharathi *et al.,* 2012; Bano *et al.,* 2019). However, several reports claim that small bitter gourd (SBG) types or wild forms are more nutritious and richer in metabolites compared to large types and they have a characteristics flavour and taste along with the therapeutic properties (Behera *et al.,* 2007). SBG is not cultivated, it is often collected wild or grown only in backyards in kitchen gardens in certain pockets of Tamil Nadu, Kerala (Priyanka *et al.,* 2018), West Bengal and Andaman Islands (John and Antony, 2009).

Small bitter gourd is considered as a valuable germplasm resource in the bitter gourd breeding program as these wild forms are resistant to several pest and diseases. Considerable morphological and biochemical differences exist within the small bitter gourd genotypes necessitating further exploration. Suma *et al.* (2023) opined that with proper and systematic exploitation of genetic variation among muricata types may give this variant an individual crop status. But unfortunately, most of the previous researchers focused on studying genetic diversity of large fruited bitter gourd genotypes having only few or no muricata types included in the study. In these studies, it is clearly noted that the muricata types are largely ignored, which is evident from the previous studies by Jatav *et al.* (2022), Looregipoor *et al.* (2023), Mallikarjuna *et al.* (2024) and Bhardwaj *et al.* (2024) where the main focus was given to large bitter gourd genotypes. Limited studies have been conducted to study the genetic variability and diversity present exclusively among the small bitter gourd genotypes collected from different parts of India.

John and Antony (2009) collected and evaluated 14 SBG germplasms for leaf and fruit characteristics, where only the mean values for each trait were represented and it lacked the variability, heritability and diversity information. Asna *et al.* (2024) characterized small bitter gourd genotypes, and found that four genotypes namely AC-16/1, AC-16/16, IC 467681 and JJNS-15/65 were superior for yield, nutritional value and disease resistance. However, the above work lacks in analyzing genetic diversity using cluster analysis. Despite its nutritional, therapeutic and breeding values, the wild bitter gourd is facing the verge of extinction in Tamil Nadu and rest of Southern peninsular India. Hence, there is an urgent need for this crop to be scientifically evaluated and documented for useful traits to identify promising lines with commercial value, adaptability to adverse growing conditions and further conservation. Under these circumstances, the current investigation was taken up, to showcase the genetic diversity of small bitter gourd to identify promising elite types either for cultivation or further breeding programs.

Materials and Methods

Study area: The experiment was carried out during kharif season from June to October during the year 2023 and 2024. The experimental field (Fig. 1) falls under the Cauvery Delta agroclimatic zone of Tamil Nadu, located at Horticulture farm of Department of Horticulture, Central University of Tamil Nadu situated at Neelakudi, Thiruvarur. The study area experiences tropical climate and was found to have fertile alluvial soils which is very deep, very heavy, black to brown in colour,clayey in texture with 40 to 45 percent clay fraction, which has good adsorption and water retention capacity. The average temperature varied 28°C to 35°C, with annual rainfall of around 1,200 mm.

Experimental study: The experiment was designed under Randomized Complete Block design (RCBD), with three replications. Twenty diverse genotypes *viz.,* IC639012, IC636486, IC639010, IC638996, IC636495, Ic636489, IC639020, IC639000, IC639016, MCM-1 (Lalgudi, Tiruchirapalli, TN), MCM-2 (Attur, Salem, TN), MCM-3 (Chengalpattu, TN), MCM-4 (Ariyalur TN), MCM-5 (Karunagaranalur, Koradacherry, Thiruvarur, TN), MCM-6 (Nagakudi, Nannilam, Thiruvarur, TN), MCM-7 (Thirunallar, Karaikkal district, Puducherry), MCM-8 (Vaduvur, Thiruvarur, TN), MCM-9 (Needamangalam, Thiruvarur, TN), MCM-10 (Pattukottai, Thanjavur, TN) and MCM-11 (Manakkal, Koradacherry, Thiruvarur, TN) were selected for study. Among which 9 genotypes (IC series) were collected from NBPGR, Regional Station, Thrissur, Kerala and others (MCM series) were local collections. The selected genotypes represented a diverse range of wild, semi-domesticated and landrace forms. The genotypes were classified based on their morphology and local cultivation practices.

Cultural practice: The bitter gourd cultivation aspects and plant protection measures were carried out according to the recommendations given by Tamil Nadu Agricultural University and Directorate of Horticulture and Plantation Crops (2020).

Data collection: Five randomly selected and labelled plants were used to record the observations on growth, yield and quality traits such as vine length (m), days to first staminate flower emergence, days to first pistillate flower emergence, node of first staminate flower, node of first pistillate flower, length of fruit (cm), girth of fruit (cm), individual fruit weight (g), thickness of fruit (mm), pulp to seed ratio, number of fruits per plant, days till the first fruit harvest, days till the final fruit harvest, yield per plant (kg), total phenol (mg GAE g f.wt^{-1}) was estimated by the Folin-Ciocalteu method, as suggested by Singleton and Rossi (1965), total flavonoid content (mg QE g f.wt^{-1}) was determined by the method outlined by Zhishen *et al*. (1999), vitamin C (mg 100 g^{-1}) (AOAC 1995), antioxidant FRAP (mg m l^{-1}) assay was performed as suggested by Benzie and Strain (1996).

Statistical analysis: The replication mean values were used for statistical analysis in the software. TNAUSTAT statistical package developed by Manivannan (2014) was used for variability analysis

Fig. 1: Experimental field view of small bitter gourd established to screen twenty small bitter gourd genotypes for variations in growth, yield, and quality traits.

like GCV, PCV and heritability. Principal Component Analysis was carried out using the correlation matrix method in KAU- GRAPES 1.0.0., an online R-based tool (Gopinath *et al.,* 2020). Cluster analysis employed Ward method (Ward, 1963) and squared Euclidean distance. It was carried out by IBM SPSS STATISTICS version 20.

Results and Discussion

The phenotypic coefficients of variation (PCV) and genotypic (GCV) coefficients of variation were categorized as moderate (10–20%), high (above 20%) and low (less than 10%) as suggested by Sivasubramanian and Madhava Menon (1973). In the present study, the GCV and PCV were found high for most of the characters (Table 1) *viz.,* yield per plant (65.21 % and 65.98 %), individual fruit weight (54.93 % and 55.59 %), number of fruits per plant (39.21 % and 39.68 %), node of first staminate flower (35.88 % and 36.31 %), vine length (32.04 % and 32.43 %), thickness of fruit (31.96 % and 32.35 %), pulp to seed ratio (29.80 % and 30.16 %),node of first pistillate flower (26.32 % and 26.64 %), total flavonoid (24.95 % and 25.25 %), fruit length (23.40 % and 23.68 %), days to first pistillate flower emergence (23.35 % and 23.62 %), days to first staminate flower emergence (22.27 % and 22.54 %), girth of fruit (21.29 % and 21.55 %) respectively.

The highest GCV and PCV values showed the presence of high variability in these traits whereas GCV and PCV were moderate for total phenol (18.92 % and 19.15 %), antioxidant FRAP (17.02 % and 17.23 %), days to first fruit harvest (14.68 % and 14.86 %) and Vitamin C (13.99 % and 14.16 %), while the least was recorded for days till the final fruit harvest (9.44 % and 9.56 %) respectively, indicating less variability for these traits, significantly influenced by the environment. The findings of this study, corroborate with the reports of Agalya *et al.* (2023) and Mallikarjuna *et al.* (2024), where the growth and yield traits like fruit yield per vine, fruit weight, fruit length, vine length, fruit girth, node of first female flower inflorescence, number of fruits per vine, number of seeds per fruit recorded high PCV and GCV indicating the trait importance in selection program. The same findings were also reported by Aftab *et al.* (2024), Kumanan *et al.* (2024) in bitter gourd and Das *et al.* (2024) in bottle gourd. For every variable under study, considerable genotype-to-genotype variations were noted, suggesting the presence of high degree of variability among the genotypes. Phenotype is the result of both genetic makeup of plant and the influence of surrounding environment. In the present study, the presence of higher GCV was noticed, suggesting strong correlation of genetic constitution in exhibiting phenotype with less environmental influence. This parameter offers greater scope in direct selection of genotypes for further crop breeding in small bitter gourd.

The heritability in broad sense (Table 1) was recorded high for yield per plant (99.37 %), individual fruit weight (99.36 %), number of fruits per plant (99.25 %), node of first staminate flower (99.24 %), fruit length (99.20 %), thickness of fruit (99.14 %), pulp to seed ratio (99.02 %), node of first pistillate flower (98.39 %), total flavonoid (98.14 %), vine length (98.11 %), days to first pistillate flower emergence (97.46 %), days to first staminate flower emergence (95.46 %), girth of fruit (77.18 %), total phenol (73.72 %), whereas moderate heritability were recorded for antioxidant FRAP (62.57 %), Vitamin C (62.37 %), days till first fruit harvest (58.76 %) and final fruit harvest (57.47 %). The findings in this study are in accordance with Yadav *et al.* (2025) who reported moderate heritability with low genetic advance for the trait, days to first fruit harvest indicating a complex interplay between genetic potential and environmental conditions in cherry tomato. Similarly, Zhu *et al.*(2025) studied genetic tendency of antioxidant activity in leaves and flowers of loquat and found that FRAP activity exhibited a trend of small inheritance in the F1 generation, indicating moderate genetic transmission ability. Heritability is a good index of transmission of characters from

Table 1: Estimates of phenotypic and genotypic coefficients of variation, heritability, genetic advance as per cent over mean for different traits of small bitter gourd genotypes

Characters	Mean	Range (Min-max)	Coefficients of Variation		Heritability (%)	GA as % of mean
			GCV (%)	PCV (%)		
Vine length (m)	2.97	1.38 - 4.78	32.04	32.43	98.11	65.24
Days to first staminate flower emergence	32.35	22 – 45	22.27	22.54	95.46	45.34
Days to first pistillate flower emergence	49.30	32 – 69	23.35	23.62	97.46	47.53
Node of first staminate flower	10.40	4 – 17	35.88	36.31	99.24	73.05
Node of first pistillate flower	15.40	8 – 21	26.32	26.64	98.39	53.59
Length of fruit (cm)	6.57	4.17 - 10.60	23.40	23.68	99.20	47.64
Girth of fruit (cm)	8.31	5.10 - 11.10	21.29	21.55	77.18	43.35
Individual fruit weight(g)	12.85	3.57 - 31.83	54.93	55.59	99.36	111.84
Thickness of fruit (mm)	3.69	1.34 - 6.00	31.96	32.35	99.14	65.08
pulp to seed ratio	3.86	1.95 - 6.53	29.80	30.16	99.02	60.67
Number of fruits per plant	40.51	16.00 - 74.00	39.21	39.68	99.25	79.83
Days till the first fruit harvest	66.70	52.00 - 84.00	14.68	14.86	57.47	29.90
Days till the final fruit harvest	126.25	108.00 - 150.00	9.44	9.56	58.76	19.23
Yield per plant (kg)	0.55	0.16 - 1.46	65.21	65.98	99.37	132.75
Total Phenol (mg GAE g f.wt^{-1})	60.64	40.63 - 79.57	18.92	19.15	73.72	38.52
Total Flavonoid (mg QE g f.wt^{-1})	49.30	30.91 - 67.55	24.95	25.25	98.14	50.80
Vitamin C (mg 100 gm^{-1})	97.71	77.50 - 123.50	13.99	14.16	62.37	28.49
Antioxidant FRAP (mg ml^{-1})	34.30	25.17 - 44.62	17.02	17.23	62.57	34.66

Table 2: Clustering pattern of 20 genotypes of bitter gourd on the basis of genetic divergence

Cluster	No. of genotype	Members
I	3	IC639012, IC639016, MCM-6
II	9	IC636486, IC639010, IC638996, IC636495, IC639000, MCM-1, MCM-2, MCM-3,MCM-5
III	6	IC636489, IC639020, MCM-7, MCM-8, MCM-9, MCM-10
IV	2	MCM-4, MCM-11

parents to its progeny. High heritability indicates lesser influence of traits by the environment (Bhardwaj *et al*., 2024). Genetic advance as percentage of mean (GAM) reported high for all the traits in the study and found moderate only for days to final fruit harvest (19.23 %). The findings of this study showed that all the yield and yield attributing traits exhibited high heritability coupled with high genetic advance as percent mean which is in conformity with the reports Terfa and Gurmu (2020) and Agalya *et al.* (2023). In the present study, the occurrence of high heritability coupled with high GAM for yield and yield related traits indicated the influence of additive gene action. This advocates direct selection of genotype based on phenotype in later generations by the plant breeders.

Principal component analysis (PCA) is a numerical method for classifying several subjects into significant uncorrelated variables. The multivariate numerical approach of considered genotypes for growth, yield and quality parameters conducted in the present study, illustrated that significant variation among the selected genotypes existed. Biplot possessed principal component of variances occupied by each accession and overall component response of the accessions on the characters (Fig. 2). The first five principal components showed an Eigenvalue greater than one, accounting 85.78% of the total variance among 20 genotypes.

Among five principal components (Pcs), PC1 recorded the maximum variability (39.10 %), subsequently PC2 (19.87 %) followed by PC3 (13.55 %), PC4 (7.42 %) and PC5 (5.81 %).The first principal component had high positive value in days till the first fruit harvest (0.917) followed by days to first staminate flower emergence (0.864) and days to first pistillate flower emergence (0.858), while no negative values were registered in PC1. The second principal component showed high positive values for total flavonoid (0.844) followed by vitamin C (0.830), while high negative readings recorded for individual fruit weight (-0.536) and fruit length (-0.435). The third principal component showed maximum positive result for fruit girth (0.721) and pulp to seed ratio (0.663), while negatively correlated with vine length (-0.449) and node of first staminate flower (-0.438). The fourth principal component had maximum positive value for number of fruits per plant (0.622) and yield per plant (0.548), while showing negative association with days to first staminate flower emergence (-0.320) and days to first pistillate flower emergence (-0.308). The

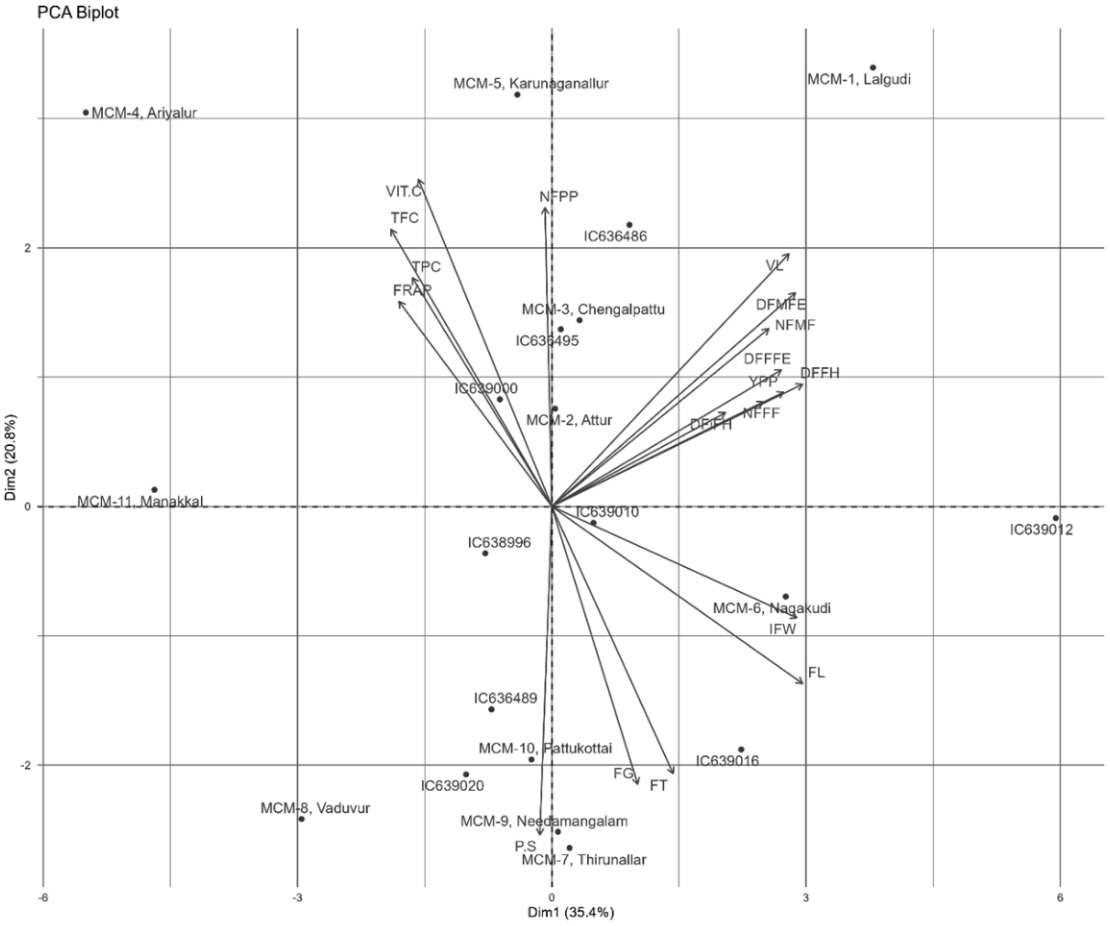

Fig. 2: PCA Biplot distribution of twenty small bitter gourd genotypes and characters representedon principal component axes PC1 and PC2.

fifth principal component exhibited high positive values for pulp to seed ratio (0.550) and node of first pistillate flower (0.520).

It is crucial to take into account how particular features (characters) tend to be connected with various principal components (PCs) while selecting traits for breeding program. These characteristics frequently exhibit a propensity to stick together. Therefore, concentrating on these factors during breeding process can result in quicker improvements in yield and its contributing traits. In simple terms, correlated characteristics can be enhanced in parallel to produce superior overall results in the desired traits. The first five PCs showed maximum variation in the growth, yield and quality considered for the study and as a result, these characteristics could be taken into consideration to improve small bitter gourd. Variables were represented as vectors in the biplot, and each vector's length represented the level of variations in that parameter. The highly diverse and least genotypes comparable with other types were at furthest distant from their place of origin. Assessment of genotypes, PC1 and PC2 showed that they were dispersed among the four quadrants, emphasizing the highest level of genetic variation (Fig. 2). Prasanth *et al.* (2020) reported that the maximum cumulative variance of 80% was contributed by first four PCs, in which the first PC consisted positive loadings for all the traits which is exactly correlating with our findings. PCA facilitates a plant breeder to go for easy selection of a promising genotype from the five PCs having majority variance percentage (85.78%) instead of depending on the whole enormous population. The comprehensive clustering diagrams for small bitter gourd was constructed on the basis of all the quantitative traits (Fig. 2).

To elucidate the phenotypic diversity among the SBG genotypes, a hierarchical cluster analysis was performed. The analysis utilized the Ward's minimum variance method with Squared Euclidean distance as the dissimilarity metric. This method effectively partitioned the twenty genotypes into four distinct clusters (Table 2), confirming substantial heterogeneity for the assessed growth, yield, and quality traits. The distinct clusters facilitate the identification of genetically divergent genotypes, which are critical for selecting complementary parental lines in hybridization programs. Cluster I had three genotypes (IC639012, IC639016, MCM-6), followed by Cluster II

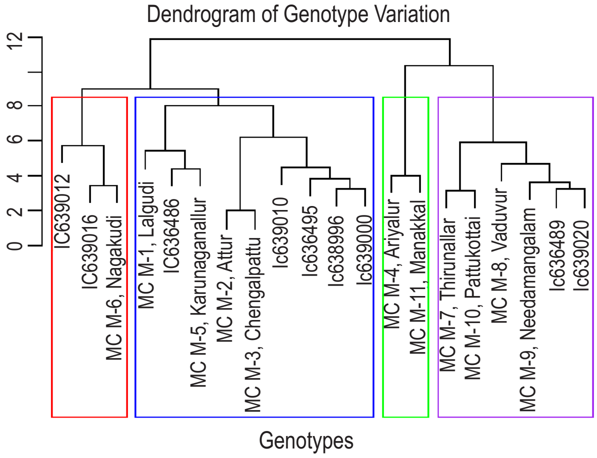

Fig. 3: Dendrogram showing cluster analysis of twenty small biter gourd genotypes.

Table 3: Cluster means for different characters in small bitter gourd

Observations	**Cluster 1**	**Cluster 2**	**Cluster 3**	**Cluster 4**
Vine length (m)	3.96	3.46	2.06	2.04
Days to first staminate flower emergence	39.33	36.22	26.50	22.00
Days to first pistillate flower emergence	57.33	52.00	46.33	34.00
Node of first staminate flower	12.33	13.00	7.67	4.00
Node of first pistillate flower	18.67	17.22	13.17	9.00
Length of fruit (cm)	8.40	6.14	7.11	4.20
Girth of fruit (cm)	8.15	7.90	10.06	5.19
Individual fruit weight (g)	22.34	11.65	12.75	4.35
Thickness of fruit (mm)	3.45	3.39	4.92	1.72
pulp to seed ratio	4.34	3.35	4.62	3.25
Number of fruits per plant	34.78	47.56	29.33	51.00
Days till the first fruit harvest	76.00	68.33	63.83	54.00
Days till the final fruit harvest	137.33	126.56	122.67	119.00
Yield per plant (kg)	0.85	0.65	0.38	0.23
Total Phenol (mg GAE g f.wt^{-1})	47.07	63.31	58.57	75.24
Total Flavonoid (mg QE g f.wt^{-1})	31.60	52.80	47.56	65.38
Vitamin C (mg 100 gm^{-1})	27.23	35.13	34.35	41.03
Antioxidant FRAP (mg ml^{-1})	80.52	103.79	92.01	113.25

with nine genotypes (IC636486, IC639010, IC638996, IC636495, IC639000, MCM-1, MCM-2, MCM-3, MCM-5), Cluster III with six genotypes (IC636489, IC639020, MCM-7, MCM-8, MCM-9, MCM-10) and Cluster IV with two genotypes (MCM-4, MCM-11). Cluster means for all eighteen characters showed considerable variability among the Clusters for each of them (Table 3). The present study revealed that the Cluster I showed the highest mean values for vine length, days to first staminate flower emergence, days to first pistillate flower emergence, node of first pistillate flower, length of fruit, individual fruit weight, days till first fruit harvest, days till final fruit harvest and yield per plant.

Therefore, emphasis should be laid on these traits while selecting genotypes from Cluster I. Cluster II was superior only for node of first staminate flower. Cluster III was superior for fruit the traits girth, fruit thickness and pulp to seed ratio. Cluster IV was superior for number of fruits per plant, total phenol, total flavonoid, vitamin C and antioxidant FRAP. Similar results with respect to clustering pattern and cluster means were reported by Selvam *et al.* (2020), who grouped 18 genotypes into five clusters among which two clusters had only 2 genotypes, which corroborates with the findings of this study. Similarly, Meghashree *et al.* (2024), grouped fifty bitter gourd accessions based on their nutritional diversity into four clusters, whose results are in agreement with our study.

Cluster analysis revealed that the selected populations were genetically diverse when placed in different clusters, whereas genotypes grouped under same cluster were genetically identical to each other. The results of cluster analysis vividly suggest the breeder to proceed for cross breeding (hybridization) using genotypes of different clusters, which would lead to the development of potential hybrid/hybrid derivatives as a result of hybridization program (Bhati *et al.,* 2023).

In conclusion, the study underscores significant genetic variability and heritability among small bitter gourd genotypes, suggesting substantial potential for selection and genetic improvement. The diversity revealed through PCA and cluster analysis highlights the importance of small bitter gourd types as reservoirs for further breeding programs. These results provide a strong basis for targeted crop improvement, germplasm conservation, and future hybridization. The study has significant implications for enhancing yield, quality and resilience in small bitter gourd cultivation.

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