

RESEARCH ARTICLE

Genetic Diversity, Variability and Correlation Studies in Bitter Gourd (*Momordica charantia* L.)

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Thirty one genotypes of bitter gourd (*Momordica charantia* L.) were evaluated for 10 quantitative traits during August 2016. Significant differences among bitter gourd genotypes indicated the presence of wide variation for all the traits. All the 10 traits showed significant and positive association with yield. Genotype IHR-147-4 took the shortest time to first female flower appearance (26.57 days after planting). A close proximity in the phenotypic and genotypic coefficients of variability was observed for peduncle length, fruit length, fruit girth, number of fruits, fruit weight and fruit yield indicating little influence of environment for the expression of these traits. High heritability was recorded for peduncle length, fruit length, fruit girth and fruit weight. Number of fruits followed by fruit weight, fruit length and fruit girth exhibited maximum positive direct effect on fruit yield. Principal component analysis revealed that first three principal components (PC1, PC2 and PC3) accounted for 72.28% of the total variation with the proportionate contribution values of 40.83, 17.43, and 14.01 respectively. The genotypes were grouped in to four different clusters based on the genetic distance. The divergence value for cluster analysis indicated that the genotypes from clusters I and II had the highest inter-cluster distance and were expected to provide high heterosis if crossed and to show wide variability in genetic architecture.

Key Words: Bitter gourd, Variability, Heritability, Genetic advance, Principle component, D² analysis

Introduction

Bitter gourd (*Momordica charantia* L.; $2n=2x=22$), also known as bitter melon, bitter cucumber, bitter squash, balsam pear, karela, cassilla and maiden apple (Morton, 1967), is an important fast growing warm seasonal climbing annual cucurbit vegetable grown in tropics and subtropics. It is widely cultivated in India, China, Malaysia, Africa, and South America (Minraj *et al.*, 1993; Singh, 1990). It is mainly valued for its nutritional and medicinal properties. It has been used for centuries in the ancient traditional medicine of India, China, Africa, and Latin America. Bitter gourd fruits also possess anti-oxidant, anti-microbial, anti-viral, anti-diabetic activities (Welihinda *et al.*, 1986; Raman and Lau, 1996). The immature fruits are used as fried, stuffed, dried and pickled (Morton, 1967). Among the cucurbits, bitter gourd is considered a prized vegetable because of its high nutritive values in respect of ascorbic acid and iron (Behera, 2004) besides, its immense medicinal values, mainly, for its hypoglycemic properties. The

ripe fruits are rich in vitamin A. Fruit also contains two major alkaloids viz., momordicin and cucurbitacin; momordicin is the momordicoside glycoside of tetracyclic triterpenoides with cucurbitane skeleton (Vandana and Chandra, 1990). Lee *et al.* (1995) has identified a protein MAP-30, in both seeds and fruits of bitter gourd, which inhibits human immunodeficiency virus (HIV).

In India, the genetic analysis based on quantitative traits has been made in this crop by Mishra *et al.* (1998), Ram *et al.* (2000), Dalamu *et al.* (2012) and Resmi and Sreelathakumary (2012). Success in any plant breeding programme solely depends upon the existence of genetic variability present in the population. It is proved that larger the variability, greater is the scope for selection and improvement. It is the genotypic variability and more specifically the additive variances, which is most important for a plant breeder as, it determines the genetic gain through selection. Yield is a complex entity which is associated with a number of component characters. Before aiming at an improvement in yield, it is necessary

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to have information on genetic variability and heritability, in respect of important characters associated with yield. Genotypic and phenotypic coefficients of variation are useful in detecting the amount of variability present in the available genotypes. The main purpose of estimating heritability and the genetic parameters that compose the heritability estimate is to compare the expected gains from selection based on alternative selection strategies (Holland *et al.*, 2003). The efficiency of selection depends on the direction and magnitude of association between yield and its component characters. The correlation coefficients indicate association between two characters and form a basis for selecting desirable plant type and path coefficient analysis splits the correlation coefficients into direct and indirect effects to measure the relative importance of each character. Information on character association and direct and indirect effects of component traits on yield would greatly help in formulating the selection criteria and using them effectively in crop improvement programme (Sharma and Bhutani 2001, Bhavne 2003, Singh *et al.*, 2008, Islam 2009).

Improvement in yield is normally attained through exploitation of the genetically diverse parents in hybrid breeding programmes. Since, the crossing programme involving genetically diverse parents is likely to produce high heterotic effects and also more variability could be expected in the segregating generations. Genetic diversity between genotypes indicates the differences in gene frequencies. For identifying such diverse parents for crossing, multivariate analysis using Mahalanobis D^2 statistic (1936) has been used in several crops. This is a valuable tool to study genetic divergence at inter varietal and sub-species level in classifying the crop plants.

Considering the availability of genetic variability, its scope of yield improvement, the present investigation was undertaken to study the character association and direct and indirect effects of component characters on yield and genetic divergence among 31 genotypes of bitter melon to locate suitable parental groups likely to provide superior segregants on hybridization.

Materials and Methods

The experimental materials comprised of 31 genotypes of bitter melon and advanced breeding lines maintained at Division of Vegetable Crops, ICAR- IHR, Bengaluru. The experiment was laid out in a randomized complete block design (RCBD) with three replications at the

experimental farm, Division of Vegetable Crops, ICAR- IHR, Bengaluru, during August 2016. Seeds were sown in 98-cell plug-trays, using cocopeat as a growing medium. The seedlings were ready for transplanting 15 days after germination (two true- leaf stage) and transplanted in the main field in raised beds, covered by white polythene mulch, at spacing of 150 cm between beds and 50 cm between plants. Treatments were allotted at random in rows of each replication. All the recommended cultural practices were followed to raise a healthy crop.

Thus ten plants per genotype were maintained in each row. The fruits were harvested at marketable stage. Five plants were selected at random from each experimental plot (5 m X 1.5 m) for recording observations on 10 quantitative traits viz., days to first male flower, node to first male flower, days to first female flower, node to first female flower, peduncle length (cm), fruit length (cm), fruit girth (cm), number of fruits per plot, individual fruit weight (g) and total fruit yield per hectare (kg). Means across three replications were calculated for each character.

The data were subjected to analysis of variance according to Panse and Sukhatme (1967). The genotypic and phenotypic coefficients of variation were computed according to Burton and Devane (1953). The broad sense heritability was computed according to Falconer and Mackay (1996). Genetic advance over mean was worked out according to Johnson *et al.* (1955). Path coefficient analysis provides an effective means of partitioning correlation coefficients into unidirectional and alternative pathways thus permitting a critical examination of specific factors that produce a given correlation, which can be successfully employed in formulating an effective selection programme (Salahuddin *et al.* 2010). The genetic diversity was analyzed by Mahalanobis D^2 analysis (Mahalanobis 1936) and clustering of genotypes was done according to Tocher's method as described by Rao (1952). The programming codes were developed using statistical analysis system (SAS) package available at ICAR- IHR, Bangalore, India (SAS V 9.3).

Results and Discussion

The analysis of variance for 10 quantitative characters exhibited significant differences for all the characters under study which indicated considerable amount of variation among the genotypes. Mean performance of the 31 genotypes for different traits studied was presented

in Table 1. Maximum variability was recorded for fruit yield per hectare followed by fruit weight, number of fruits per plot and fruit length (Table 2).

Table 1. Analysis of variance for different quantitative traits in bitter gourd

Character	Source of variation		
	Replication	Treatment	Error
Df	2	30	60
Days to first male flower	3.00	13.21**	6.93
Node to first male flower	0.72	7.61**	3.88
Days to first female flower	4.74	10.26**	7.67
Node to first female flower	0.20	10.35**	9.85
Peduncle length	19.02	29.60**	2.99
Fruit length	0.59	61.23**	4.09
Fruit girth	1.53	10.31**	1.24
Number of fruits / plot	8782.26	3365.22**	836.42
Fruit weight	461.54	2845.48**	377.41
Fruit yield	99734160	30789504**	7055594

** Significant at P<0.01 level

The higher degree of variation was observed in phenotypic and genotypic variance among the characters studied. Maximum variation was observed by fruit weight followed by fruit yield per hectare. Low variance was observed for days to first male flower and days to first female flower. Characters such as peduncle length, fruit length, fruit girth showed narrow differences between the values of GCV and PCV (Table 2) indicating variability due to genetic constitution indicating better scope of selection through these traits for improvement. High heritability was recorded for peduncle length, fruit length, fruit girth and fruit weight indicating low environmental influence for the expression of these traits (Table 2). The rest of the traits showed low to moderate level of heritability. The higher estimates of heritability coupled with higher genetic advance observed for fruit weight, whereas moderate heritability with high genetic advance for number of fruits per plot indicated that heritability of these traits is mainly owing to additive effects.

The genotypic correlation were higher than their corresponding phenotypic correlation for all the traits studied suggesting strong inherent association between these traits at genotypic level (Table 3), which was in agreement with the results obtained by Srivastva and Srivastva (1976), Singh *et al.* (1977), Indresh (1982), Lawande and Patil (1989), Panthi *et al.* (1995) and Singh *et al.* (2013). Yield per hectare showed significant and

positive association with all the 10 traits studied. Fruit weight has significant and positive correlation with days to first male flower, node to first male flower, days to first female flower, node to first female flower, peduncle length, fruit length and fruit girth and significant negative correlation with number of fruits per plot. Fruit girth had a positive significant correlation with days to first female flower, node to first female flower, peduncle length. Fruit length showed significant positive association with node to first male flower, days to first female flower, node to first female flower, peduncle length.

It was observed from path analysis that number of fruit followed by fruit weight, fruit length and fruit girth exhibited maximum positive direct effect (Table 4). Node to first female flower exhibited negative direct effect on fruit yield and its positive and significant association with fruit yield was due to its high indirect positive effect through days to first female flowering. Islam *et al.* (2009), Sundaram (2010), Sharma and Bhutani (2001) Dalamu and Behera (2013) also reported maximum direct contribution of number of fruits per plant in bitter gourd. Through present path analysis study, it may be concluded that improvement in yield could be bought by selection for component character like number of fruits followed by fruit weight, fruit length and fruit girth.

The residual factor determines how best the causal factors account for the variability of the dependent factor. The residue obtained was 0.214 indicating that selected characters contributed the remaining 79 percent. Similar observations were made by earlier workers (Mahesh *et al.*, 2014).

Principle component analysis and clustering of genotypes help in selection of suitable genotypes to be used in breeding for improvement in desired characters (Cheema *et al.*, 2011). Eigen values of 10 principal component axes and percentage of variation accounting for them obtained from the principal component analysis revealed that the first axis largely accounted for the variation among the genotypes (40.83 %) (Table 5). Two dimensional ordinations of 31 bitter gourd genotypes on PC axis 1 and 2 revealed scattered diagram of genotypic distribution pattern on axis. Three principle components had eigen values > 1 and explained most of the total variation with PC1, PC2 and PC3 contributions and accounts for 72.28 per cent of total variation amongst bitter gourd genotypes. This finding was in agreement with that of Kundu *et al.* (2012) and Singh *et al.* (2014) in bitter gourd. Moreover, the first

6 principal components contributed 90.57 per cent of the total variation with proportionate contribution values of 40.83, 17.43, 14.01, 7.71, 5.56 and 5.00 per cent respectively. The first PC has positive association with all the 10 traits. The second PC has positive association with days to first male flower, node to first male flower, number of fruits and fruit yield per plot, while negative

association with days to first female flower, node to first female flower, peduncle length, fruit length, fruit girth and fruit weight. The third PC has positive association with days to first male flower, node to first male flower, days to first female flower, node to first female flower, while negative association with peduncle length, fruit length, fruit girth, number of fruits per plot and yield

Table 2. Mean performance of 31 bitter gourd genotypes for yield and yield attributes

Sl. No.	Genotype	Days to first male flower	Node to first male flower	Days to first female flower	Node to first female flower	Peduncle length (cm)	Fruit length (cm)	Fruit girth (cm)	Number of fruits / plot	Individual fruit weight (g)	Fruit yield (Kg/ Ha)
1	Arka Harit	29.71	6.43	29.86	10.75	7.25	8.19	9.99	37.00	58.08	2040
2	IIHR-144-1	32.58	9.31	30.25	11.2	3.56	5.93	7.64	137.33	11.56	5560
3	IIHR-80-1-2	33.00	8.00	33.00	10.00	1.12	4.64	7.78	79.33	6.48	2453.33
4	Pusa Vishesh	25.68	5.35	29.67	12.00	7.50	15.67	12.08	51.33	67.78	5453.33
5	Pusa Do Mausami -5	28.67	7.13	30.85	12.83	9.44	18.30	11.46	104.00	69.60	9533.33
6	Phule Ujwala	29.32	8.78	31.58	12.73	11.61	15.50	12.40	91.67	95.98	8546.66
7	IIHR -30-4	30.81	10.56	31.85	12.83	8.63	11.40	14.60	105.67	97.00	11160
8	IIHR -49-34-5	28.26	7.53	30.64	12.36	11.50	13.80	12.25	169.67	47.40	8613.33
9	IIHR -46-1	31.11	9.50	30.4	13.00	10.40	16.20	12.74	75.67	89.34	10106.67
10	NDBI-09-7	31.29	9.57	31.00	13.00	10.00	16.10	12.7	60.00	73.575	6480
11	NDBT-7-9	26.67	6.78	29.63	17.00	4.58	16.58	11.02	87.33	67.92	8853.33
12	CO-1-2	31.25	7.00	32.4	14.25	9.56	17.20	12.34	59.67	132.00	7266.66
13	IIHR -38-2	31.10	9.15	30.11	12.22	13.64	19.50	14.66	90.00	62.76	9960
14	IIHR -151-2	29.52	6.94	30.54	11.36	7.75	10.37	11.45	65.00	36.60	4053.33
15	IIHR -40-1	31.70	10.50	35.29	14.00	11.20	16.20	12.46	112.33	83.22	13786.67
16	IIHR -148-7	37.33	12.00	31.65	15.08	12.58	16.28	13.78	153.33	80.48	13826.67
17	IIHR -101-1-7	28.67	8.84	33.14	14.62	11.90	9.10	11.30	61.33	34.62	3373.33
18	IIHR -17-1	29.8	10.50	30	15.8	10.53	12.00	12.56	56.00	91.30	5760
19	IIHR -8-2	31.46	10.15	30.67	15.75	11.92	12.10	11.32	116.33	108.48	10786.67
20	IIHR -86-11-6	29.35	8.59	30.62	14.14	11.40	10.30	12.96	107.67	30.375	6066.66
21	IIHR -147-4	29.89	8.11	26.57	9.89	8.85	8.24	12.84	172.33	27.28	9093.33
22	IIHR -12-6	29.61	9.33	29.4	12.60	13.14	20.14	10.79	132.67	44.16	10760
23	IIHR -80-1-3	27.33	9.50	26.33	11.00	1.60	4.57	8.30	83.00	5.22	1306.66
24	Preethi-1	29.53	8.83	28.91	11.4	8.83	17.50	11.68	122.67	81.00	10360
25	IIHR- 44-2	31.44	8.41	33.25	14.71	9.06	15.89	14.55	118.00	89.82	12093.33
26	NABG-1-5	30.78	9.00	32.00	14.14	8.50	14.14	12.28	85.00	40.86	7293.33
27	IIHR- Sel-5-8	28.62	6.26	28.79	11.33	8.31	11.67	13.09	88.67	61.26	6200
28	IIHR- 145	30.90	10.53	33.20	13.20	11.38	23.50	11.62	74.33	104.58	7093.33
29	Hirkani- 6	28.85	6.06	30.6	10.64	6.80	11.10	13.80	80.67	65.48	6213.33
30	Meghana- 1	31.29	8.12	31.00	11.29	11.2	14.40	14.30	107.00	55.48	9106.66
31	IIHR -14-4	29.89	7.88	28.94	9.86	5.75	12.50	14.38	89.33	70.12	7720
	Mean	30.13	8.49	30.74	12.72	9.01	13.55	12.11	95.94	64.17	7771.71
	CD 5 %	4.21	3.15	4.43	5.02	2.76	3.23	1.78	46.28	31.08	4250.86
	SEm ±	0.07	0.05	0.07	0.09	0.04	0.05	0.03	0.83	0.56	76.67

Table 3. Estimate of genetic parameters for morphological traits in bitter gourd

Character	Range	CV	PVAR	GVAR	PCV	GCV	h ²	GA	GAM
Days to first male flower	25.68 - 37.33	8.739	9.027	2.093	9.972	4.803	23.195	1.437	4.771
Node to first male flower	5.35 - 12.00	23.209	5.131	1.244	26.666	13.130	24.246	1.131	13.338
Days to first female flower	26.33 - 35.29	9.011	8.536	0.861	9.504	3.019	10.093	0.608	1.979
Node to first female flower	9.86 - 17.00	24.685	10.025	0.165	24.892	3.202	1.655	0.108	0.849
Peduncle length (cm)	1.12 - 13.64	19.203	11.863	8.870	38.230	33.057	74.768	5.312	58.968
Fruit length (cm)	4.57 - 23.50	14.932	23.143	19.047	35.494	32.200	82.302	8.168	60.264
fruit girth (cm)	7.64 - 14.66	9.201	4.268	3.025	17.049	14.353	70.874	3.020	24.927
Number of fruits	37 - 172.33	30.142	1679.358	842.933	42.711	30.260	50.194	42.373	44.227
Fruit weight (g)	5.22 - 132.00	30.271	1200.103	822.688	53.979	44.693	68.552	48.921	76.338
Fruit yield (Kg/ Ha)	1306.667 - 13826.67	34.178	14966897	7911303	49.779	36.192	52.859	4218.72	54.283

CV: coefficient of variation, PVR: phenotypic variance, GVR: genotypic variance, PCV: Phenotypic coefficient of variation, GCV: genotypic coefficient of variation, h² heritability (broad sense), GA: genetic advance, GAM: genetic advance over mean

Table 4. Correlation coefficient at genotypic (above diagonal) and phenotypic (below diagonal) level in bitter gourd genotypes

	Days to first male flower	Node to first male flower	Days to first female flower	Node to first female flower	Peduncle length (cm)	Fruit length (cm)	Fruit girth (cm)	Number of fruits / plot	Individual fruit weight (g)	Fruit yield (Kg/ Ha)
Days to first male flower	0.000	1.162**	1.107**	0.741**	0.246*	0.115 ^{NS}	0.050 ^{NS}	0.530**	0.136 ^{NS}	0.782**
Node to first male flower	0.398**	0.000	1.038**	2.483**	0.464**	0.227*	-0.003 ^{NS}	0.447**	0.253*	0.668**
Days to first female flower	0.250*	0.086 ^{NS}	0.000	2.403**	0.736**	0.682**	0.332**	-0.411**	0.788**	0.475**
Node to first female flower	0.062 ^{NS}	0.171 ^{NS}	0.279**	0.000	1.810**	1.927**	0.830**	-0.265*	2.831**	2.046**
Peduncle length (cm)	0.179 ^{NS}	0.276**	0.156 ^{NS}	0.249*	0.000	0.696**	0.661**	0.210*	0.522**	0.652**
Fruit length (cm)	0.017 ^{NS}	0.147 ^{NS}	0.158 ^{NS}	0.191 ^{NS}	0.556**	0.000	0.515**	0.050 ^{NS}	0.693**	0.729**
fruit girth (cm)	0.096 ^{NS}	0.074 ^{NS}	0.097 ^{NS}	0.050 ^{NS}	0.463**	0.371**	0.000	0.095 ^{NS}	0.580**	0.642**
Number of fruits	0.151 ^{NS}	0.165 ^{NS}	0.003 ^{NS}	-0.018 ^{NS}	0.190 ^{NS}	0.030 ^{NS}	0.104 ^{NS}	0.000	-0.228*	0.529**
Fruit weight (g)	0.167 ^{NS}	0.165 ^{NS}	0.193 ^{NS}	0.127 ^{NS}	0.425**	0.566**	0.416**	-0.108 ^{NS}	0.000	0.638**
Fruit yield (Kg/ Ha)	0.136 ^{NS}	0.259*	0.239*	0.157 ^{NS}	0.470**	0.496**	0.453**	0.656**	0.410**	0.000

Table 5. Path coefficient analysis of yield contributing characters in bitter gourd genotypes

	Days to first male flower	Node to first male flower	Days to first female flower	Node to first female flower	Peduncle length (cm)	Fruit length (cm)	Fruit girth (cm)	Number of fruits / plot	Individual fruit weight (g)	Fruit yield (Kg/ Ha)
Days to first male flower	0.109	0.0265	0.2820	-0.0241	-0.076	0.0390	0.016	0.354	0.056	0.782**
Node to first male flower	0.126	0.023	0.265	-0.081	-0.143	0.077	-0.009	0.298	0.103	0.668**
Days to first female flower	0.120	0.024	0.255	-0.079	-0.227	0.232	0.102	-0.274	0.321	0.475**
Node to first female flower	0.081	0.057	0.613	-0.033	-0.557	0.655	0.256	-0.177	1.152	2.046**
Peduncle length (cm)	0.028	0.011	0.188	-0.059	-0.307	0.237	0.204	0.140	0.213	0.652**
Fruit length (cm)	0.013	0.005	0.174	-0.063	-0.214	0.340	0.159	0.034	0.282	0.729**
fruit girth (cm)	0.005	-0.001	0.085	-0.028	-0.204	0.176	0.308	0.063	0.236	0.642**
Number of fruits	0.058	0.010	-0.105	0.009	-0.065	0.018	0.029	0.668	-0.097	0.529**
Fruit weight (g)	0.015	0.006	0.201	-0.092	-0.065	0.236	0.179	-0.152	0.407	0.638**

per hectare. Similar findings were also reported by Singh *et al.* (2014) in bitter gourd. The fourth PC had positive association with days to first male flower, days to first female flower, fruit girth and fruit weight, while negative association with node to first male flower, node to first female flower, peduncle length, fruit length, number of fruits per plot and fruit yield. The fifth component has positive association with days to first female flower, node to first female flower, fruit length, number of fruits per plot and fruit yield, while negative association with days to first male flower, node to first male flower, peduncle length, fruit girth and fruit weight. The sixth PC has positive association with days to first female flower, node to first female flower, peduncle length, fruit girth and number of fruits per plot, while negative association with days to first male flower, node to first male flower, fruit length, fruit weight and fruit yield. The traits having positive association with PCs have major role in genetic diversity analysis and explaining total genetic variation in bitter gourd and which is in agreement with findings of Kundu *et al.* (2012) and Singh *et al.* (2014).

Cluster analysis helps group individuals with the same description (Hair *et al.* (1995). Genotypes in a cluster exhibit a high degree of homogeneity (Cheema *et al.*, 2011). Cluster analysis grouped 31 genotypes into four clusters (Table 6). Cluster 1 had six genotypes, cluster 2 had five genotypes, cluster 3 had three genotypes, and cluster 4 had 17 genotypes accommodating more than 50 per cent of total genotypes. Average inter-cluster distance was found maximum (10590.56) between cluster I and cluster II followed by cluster I and cluster III (7094.97) (Table 7). Therefore, hybridization between the genotypes from cluster I and cluster II and cluster I and cluster III are likely to be fruitful for developing divergent heterotic cross combinations which may be potentially exploited in bitter gourd breeding programmes. Cluster IV exhibited highest cluster mean values for most of the traits viz., days to first male flower, node to first male flower, days to first female flower, node to first female flower, peduncle length, fruit girth, fruit weight and fruit yield per hectare (Table 8). Cluster II represented highest cluster mean value for fruit length and number of fruits per plot. Lowest mean value for days to first female flower was observed in cluster II whereas the least cluster mean for node to first female flower was recorded in cluster III.

Table 6. Principle component analysis of various traits in bitter gourd

Parameter	PC 1	PC 2	PC 3	PC 4
Eigen value (Root)	4.08	1.74	1.40	0.77
Percent	40.83	17.43	14.01	7.71
Cumulative percent	40.83	58.27	72.28	80.00
Traits	Eigen vectors			
Days to first male flower	0.23	0.49	0.27	0.43
Node to first male flower	0.27	0.44	0.24	-0.22
Days to first female flower	0.25	-0.01	0.53	0.31
Node to first female flower	0.29	-0.12	0.32	-0.65
Peduncle length (cm)	0.39	-0.08	-0.14	-0.07
Fruit length (cm)	0.36	-0.28	-0.12	-0.08
Fruit girth (cm)	0.31	-0.21	-0.34	0.41
Number of fruits	0.13	0.52	-0.47	-0.18
Fruit weight (g)	0.36	-0.33	0.08	0.11
Fruit yield (Kg/ Ha)	0.42	0.15	-0.28	-0.02

Table 7. Clustering pattern of bitter gourd genotypes

Cluster	Number of genotypes	Genotypes
Cluster I	6	Arka Harit, IIHR- 151-2, Pusa Vishesh, IIHR Sel 5-8, Hirkani- 6, IIHR- 14-4
Cluster II	5	PDM- 5, Preeti- 1, IIHR- 12-6, IIHR- 49-34-5, IIHR- 147-4
Cluster III	3	IIHR- 144-1, IIHR-80-1-2, IIHR-80-1-3
Cluster IV	17	Phule Ujala, IIHR- 46-1, NDBI- 9-7, IIHR-38-2, Megana-1, Co-1-2, IIHR- 145, IIHR- 17-1, IIHR-8, NDBT- 7-9, IIHR- 101- 1- 7, IIHR- 86- 11-6, NABG- 1-5, IIHR- MC- 84-4, Preeti (rkvv), IIHR- 40-1, IIHR- 148-7

Table 8. Average Intra- (diagonal) and inter-cluster distances (D²) for studied traits in bitter gourd genotypes

Cluster	1	2	3	4
1	0.00			
2	10590.56	0.00		
3	7094.97	3495.61	0.00	
4	3819.15	6771.49	3275.93	0.00

The knowledge of the characters contributing to divergence is an important factor and this study helps in identifying the diversity in different proportion which ultimately helps in deciding the utilization of genetic material for the improvement of specific character (Table

Table 9. Cluster means for different characters in bitter gourd

Cluster	Days to first male flower	Node to first male flower	Days to first female flower	Node to first female flower	Peduncle length (cm)	Fruit length (cm)	Fruit girth (cm)	Number of fruits / plot	Individual fruit weight (g)	Fruit yield (Kg/ Ha)
Cluster I	28.71	6.48	29.73	10.99	7.22	11.58	12.46	68.66	59.88	5280
Cluster II	29.19	8.18	29.27	11.81	10.35	15.59	11.80	140.26	53.88	9672
Cluster III	30.97	8.93	29.86	10.73	2.09	5.04	7.90	99.88	7.75	3106.66
Cluster IV	31.21	9.38	31.54	14.09	10.54	14.65	12.93	96.49	77.27	9311.37

Table 10. Relative contribution of various traits towards genetic divergence in bitter gourd genotypes

Sl. No.	Character	Percent contribution
1	Days to first male flower	10 %
2	Node to first male flower	9 %
3	Days to first female flower	18 %
4	Node to first female flower	12%
5	Peduncle length	9 %
6	Fruit length	6 %
7	fruit girth	12 %
8	Number of fruits	10 %
9	Fruit weight	10 %
10	Fruit yield	4 %

9). The maximum contribution to genetic divergence was by days to first female flower followed by node to first female flower, fruit girth, fruit weight and days to first male flower. Therefore necessary attention is required to be focused on these characters. In contrary to this result, Singh *et al.* (2014) has reported maximum contribution of fruit weight and fruit length to the diversity of bitter gourd. There is always difference of opinion in specifying the trait that is contributing high or low towards the genetic diversity. The contribution mainly depends upon the genotypes included in the study and the environmental influence over the character.

For future experiment, traits contributing maximum to genetic diversity should be given priority as selection parameters and the diverse genetic material of the present study may be utilized for attempting heterotic cross combination and developing hybrid varieties for Comment [DRK13]: Not required. May be deleted. improvement of bitter gourd yield. Based on the findings of present study, it is concluded that for selection of superior genotypes, primary emphasis should be given on fruit length, fruit width, fruit weight and number of fruits. Hybridization between the genotypes from cluster I and cluster II and cluster I and cluster III and selection in segregating population, based on fruit

length, fruit width and fruit weight for yield components, should result in improvement of fruit yield and quality of bitter gourd.

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