Tracking of Diversity among a Wide Local Collection of Bitter Gourd (*Momordica charantia L.*) Landraces in Bangladesh

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Abstract— *Genetic diversity of twenty bitter gourd genotypes based on ten characters was measured through multivariate analysis. The 20 genotypes fell into five distant clusters. The cluster IV comprised the maximum number (6) of genotypes followed by same in cluster II and cluster III (5). The cluster I and V comprised 3 and 1genotypes respectively. The highest inter-cluster distance (64.53) was observed between the cluster III and V. The lowest inter-cluster distance (7.05) was observed between the cluster II and III. The inter-cluster distances were larger than the intra-cluster distances. The intra-cluster distance in the entire five clusters was more or less low indicating that the genotypes within the same cluster were closely related. Fruit diameter and fruits per plant were the important component characters having higher contribution to the genetic divergence. Path co-efficient analysis revealed that branch per vine, fruits length, and fruit diameter had positive direct effect on fruit yield. Wide genetic diversity was observed in 20 genotypes of bitter gourd, which were grouped into five clusters. The genotypes of clusters III were more diverse from the genotypes of cluster V.Fruit diameter and fruits per plant were found responsible for the maximum diversity. Hybridization between the genotypes of cluster III and cluster V will manifest the wide genetic variability. Considering group distance and the agronomic performance, the inter genotypic crosses between G16 and G1; G16 and G17; G16 and G10; G16 and G4; G16 and G13 might be suitable choice for future hybridization programme.*

Keywords— Diversity, Path co-efficient, Bitter Gourd (Momordica charantia L.), Landraces, Agronomic performance and Hybridization.

I. INTRODUCTION

Bitter gourd *(Momordica charantia* L.), is an important monoecious and cross- pollinated vegetable crop of the family Cucurbitaceae grown in Bangladesh. It is locally known as karala/uchha.It is extensively cultivated throughout the country under two situations *i.e.* rainy season (July to August) and summer season (February to March). According to Chakravatry (1959), bitter gourd is believed to have originated in the tropics of the old world and is widely distributed in China, Malaya, India, tropical Africa and certain other countries. In terms of nutritive value, bitter gourd ranks first among cucurbits, the most important nutritional contribution being vitamins and minerals especially iron, phosphorus and ascorbic acid. Fruit also contains two alkaloids *viz.*, momordicin and cucurbitacin, momordicin is the momordicosidesglycosides of tetracyclic triterpinoides with cucurbitaneskeleton (Chandra Vadana and Subhash Chandra, 1990).Bitter gourd contains a reasonable amount of different nutrients such as proteins, carbohydrates, fats, minerals and vitamins A, B2, and C etc. Rajasekaran and Shanmugavalu (1984), reported very high amount of vit. C (95 mg/100g) and protein (16.5%) found in some Indian bitter gourd variety. The fruits are bitter to taste due to the presence of substance called cucurbitacin. Bitter gourd is also reported to use against diseases like paralysis, indigestion and vomiting pain and diabetes (Mier and Yaniv, 1985). Fruits and other part of bitter gourd are reported to have cooling, stomachic, appetitising, carminative, antipyrietic, antihelminthic, aphrodisiac and vermifuge properties (Blatter *et al.,* 1935). Various medicinal uses with clinical properties of insulin have been isolated from this species (Baldwa *et al.,* 1977). Among the traditional vegetables bitter gourd occupied important position in export trade. The fruits are used as fried, stuffed, dried and pickled (Morton, 1967). However, inspite of its importance, adoptability and export potential, research priority given to this crop is quite meagre especially on genetic improvement. Among the cucurbits, it is considered a prized vegetable because of its high nutritive values especially ascorbic acid and iron (Behera, 2004). A compound known as charatin present in the bitter gourd is used in the treatment of diabetes to lower blood sugar levels (Shetty *et al.,* 2005). During, 2011-2012 bitter gourds were grown over an area of 9311.74 hectares and its annual production was 46000 Mt (BBS, 2012). During 2013, bitter gourds were grown over an area of 24000

acres, it's per acre yield 2177 kg and annual production was 52000 ton. In Bangladesh, vegetable production is not evenly distributed throughout the year and most of the vegetable are produced during winter (Quasem, 2003; BARI, 2006). Hence there is a severe deficiency of vegetables during summer season due to adverse climatic conditions (Chowdhury, 1993; Ali *et al*., 1993 and Rashid, 1999). The bitter gourd production can meet up the crisis. It grows more or less in every areas of Bangladesh. Young shoots and leaves are extensively used as vegetable in the Philippines where the plants are found in the wild in waste places. The juice of the leaves and fruits of bitter gourd has been used as an anthelmintie, and is applied externally for malignant ulcers (Oliver, 1960). According to Ayensu (1984), the leaves are also used traditionally in the treatment of breast cancer. Bitter gourd may contribute to the nutritional shortage of the people of Bangladesh. Particularly, it can provide added proteins, minerals and vitamins to the diet. Although bitter gourd is an important vegetable crop, there is no recommended variety in Bangladesh and very little is known about its improvement practice. The considerable increases in bitter gourd production is no doubt remarkable, but the fact remains that the bitter gourd growers are surrounded with a number of problems, like the pests and diseases, high labour charge etc. Very few research works relating to diversity of bitter gourd have been conducted in Bangladesh. So, intensive research efforts are needed in several areas, particularly, selection of superior genotypes. There are a lot of variabilities among the existing bitter gourd germplasm of Bangladesh. An understanding of the nature and magnitude of the variability among the genetic stocks of bitter gourd is of prime importance for the breeder. A good knowledge of genetic wealth might also help in identifying desirable cultivars for commercial production. Because of its nature of high cross pollination, hardly any genetically pure strain is available to the growers. Among the local cultivated varieties, a wide range of genetic variability exists in this crop which can be exploited for its improvement. The basic key to a breeder is to develop high yielding varieties through selection, either from the genotypes or from the segregates of a crop. Expression of different plant character is controlled by genetic and environmental factors. In a hybridization program knowledge of interrelationship among and between yield and yield components is necessary. Path analysis partitions the components of correlation co-efficient into direct and indirect and visualizes the relationship in more meaningful way (Bhatt, 1973). Estimation of genetic diversity is considered as an important factor, which is also essential prerequisite for hybridization program for developing high yielding variety. Multivariate analysis is a useful tool in quantifying the degree of divergence between biological populations at genotypic level. Based on the information, the present study was undertaken to know the yield potentiality of genotypes and to know the genetic diversity among the genotypes for future hybridization program.

II. MATERIALS AND METHODS

This chapter deals with the major information regarding materials and methods that were used in conducting the experiment. It consists of a short description of locations of the experimental site, characteristics of soil, climate, materials, layout and design of the experiment, land preparation, manuring and fertilizing, transplanting of seedlings, intercultural operations, harvesting, data recording procedure, economic and statistical analysis etc. The research work relating to determine the genetic diversity of bitter gourds was conducted at the A field experiment was conducted with 20 genotypes of bitter gourd (Momordica charantia L.) at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, to study the genetic diversity among the genotypes for yield and yield contributing characters, estimate genetic parameters, association among the characters and their contribution to yield during April 2015 to September 2015. Soil of the experimental site belongs to the general soil type, Shallow Red Brown Terrace Soils under Tejgaon Series. Top soils were clay loam in texture, olive-gray with common fine to medium distinct dark yellowish brown mottles. Soil pH ranged from 6.0- 6.6 and had organic matter 0.84%. Experimental area was flat having available irrigation and drainage system and above flood level. Twenty genotypes of bitter gourd were used for the present research work. The purity and germination percentage were leveled as around 100 and 80, respectively. The genetically pure and physically healthy seeds of these genotypes were collected from Plant Siddiq Bazar, Gulistan, Dhaka, Narayanganj local market, Dhaka, Agargaon local market, Agargaon, Dhaka, Kawran bazar, Dhaka. The name and origin of these genotypes are presented in (Table 1). The experiment was laid out Randomized Complete Block Design (RCBD) with three replications. The genotypes were distributed into the every plot of each block of the prepared layout of the experiment. The individual plot was 3 m × 1 m in size. The twenty genotypes of the experiment were assigned at random into plots of each replication. The distance maintained spacing row to row 50 cm and plant to plant 2 m. The distance maintained between two blocks was 1 m. After final land preparation, pits of 50 cm × 50 cm × 45 cm were prepared in each plot with a spacing of a spacing of 3 m × 1 m. Pits were kept open in the sun for 7 days to kill harmful insect and microorganisms. To control field cricket 5 mg Furadan was also mixed with the soils of each pit before making it ready for dibbling. The following doses of manure and fertilizers were applied to the plots for ridge gourd cultivation (Anonymous, 1991). Total cowdung, half of TSP and one third MOP were applied in the field during final land preparation. Remaining TSP and one third MOP and whole gypsum and zinc oxide and one third of urea were applied in pit one week

prior to transplantation. Remaining urea and MoP were applied as top dressing in four installments at 20, 40, 60 and 75 days after transplanting. Several weeding and mulching were done as per requirement. At the very first stage weeding was done for ease of aeration and less competition seedling growth and mulch was provided after an irrigation to prevent crust formation and facilitate good aeration.

At the seedling stage red pumpkin beetle attacked tender leaves and also after the initial stage they attacked plants several times for this Marathon and Ripcord was sprayed in the field. In mature stage fruit fly caused severe damage to the fruit. For protection from fruit fly, MSGT (Mashed Sweet Gourd Trap) and Pheromone baitwas used along with ripcord, sevin powder. Fruits were picked on the basis of horticultural maturity, size, colour and age being determined for the purpose of consumption as the fruit grew rapidly and soon get beyond the marketable stage, frequent picking was done throughout the harvesting period. Data were recorded on Days to first male flowering, Days to first female flowering, Vine length (m), Number of nodes per vine, Branches per vine, Fruit length (cm), Fruit diameter (cm), Number of fruit per plant, Weight per fruit (g), Yield per plant (kg) parameters from the studied plants during the experiment. The details of data recording are given below on individual plant basis.

TABLE 1
NAME AND ORIGIN OF TWENTY BITTER GOURD GENOTYPES USED IN THE PRESENT STUDY

Sl. No.	Genotypes No.	Location
1	G_1	Agargaon local market, Agargaon, Dhaka
2	G_2	Siddiq Bazar, Gulistan, Dhaka
3	G_3	Narayanganj local market
4	G_4	Agargaon local market, Agargaon, Dhaka
5	G_5	Siddiq Bazar, Gulistan, Dhaka
6	G_6	Agargaon local market, Agargaon, Dhaka
7	G_7	Siddiq Bazar, Gulistan, Dhaka,
8	G_8	Siddiq Bazar, Gulistan, Dhaka,
9	G_9	Narayanganj local market
10	G_{10}	Narayanganj local market
11	G_{11}	Kawran bazar,Dhaka
12	G_{12}	Narayanganj local market
13	G_{13}	Agargaon local market, Agargaon, Dhaka
14	G_{14}	Siddiq Bazar, Gulistan, Dhaka,
15	G_{15}	Kawran bazar,Dhaka
16	G_{16}	Agargaon local market, Agargaon, Dhaka
17	G_{17}	Narayanganj local market
18	G_{18}	Siddiq Bazar, Gulistan, Dhaka,
19	G_{19}	Narayanganj local market
20	G_{20}	Kawran bazar,Dhaka

2.1 Statistical analysis

Mean data of the characters were subjected to multivariate analysis. Univariate analysis of the individual character was done for all characters under study using the mean values (Singh and Chaudhury, 1985) and was estimated using MSTAT-C computer programme. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV %) were also estimated using MSTAT-C. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2007 software through four techniques viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA).

2.2 Path co-efficient analysis

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985), using simple correlation values. In path analysis, correlation co-efficient is partitioned into direct and

indirect independent variables on the dependent variable. In order to estimate direct & indirect effect of the correlated characters, say x1, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

ryxl =Pyxl + Pyx2rxlx2+ Pyx3rxlx3

ryx2= Pyxl rxlx2 + Pyx2 + Pyx3r x2x3

ryx3=Pyxlrxlx3 + Pyx2rx2x3 +Pyx3

Where, r's denotes simple correlation co-efficient and P's denote path co-efficient (Unknown). P's in the above equations may be conveniently solved by arranging them in matrix form. Total correlation, say between x1 and y is thus partitioned as follows:

Pyx1 = The direct effect of x1 on y.

Pyx2rx1x2 = The indirect effect of x1 via x2 on y

Pyx3rx1x3 = The indirect effect of x1via x3 on y

After calculating the direct and indirect effect of the characters, residual effect (R) was calculated by using the formula given below (Singh and Chaudhary, 1985):

$$P2RY = 1 - \sum P_{iy} .riy$$

Where, P2RY = (R2); and hence residual effect, R= (P2RY) ½

Piy = Direct effect of the character on yield

riy = Correlation of the character with yield

2.3 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance (D^2) statistic and its auxiliary analyses. The parents selection in hybridization programme based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) suggested that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a hybridization programme. Multivariate analysis viz. Principal Component analysis, Principal Coordinate analysis, Cluster analysis and Canonical Vector analysis (CVA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

2.4 Principal Component analysis (PCA)

Principal Component analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, Principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity.Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

2.5 Principal Coordinate analysis (PCO)

Principal Coordinate analysis is equivalent to PCA but it is used to calculate inter unit distances. Through the use of all dimension of p it gives the minimum distance between each pair of the n points using similarity matrix (Digby*et al.*, 1989).

2.6 Cluster analysis (CA)

Cluster analysis divides the genotypes of a data set into some number of mutually exclusive groups. Clustering was done using non-hierarchical classification. In Genstat, the algorithm is used to search for optimal values of chosen criterion proceeds as follows. Starting from some initial classification of the genotypes into required number of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion.

When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

2.7 Canonical Vector analysis (CVA)

Canonical vector analysis (CVA) finds linear combination of original variabilities that maximize the ratio of between group to within group variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing of the ratio of among groups to the within group variations. The canonical vector are based upon the roots and vectors of WB, where W is the pooled within groups covariance matrix and B is the among groups covariance matrix.

2.8 Calculation of D^2 values

The Mahalanobis's distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952), and Singh and Chaudhury (1985). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statistic is defined by the formula

$$D^2 = \sum_{i}^{x} d_i^2 = \sum_{i}^{x} (Y_i^j - Y_j^k) \quad (j \neq k)$$

Where,

Y = Uncorrelated variable (character) which varies from i = 1 ------to x

x = Number of characters.

Superscript j and k to Y = A pair of any two genotypes.

2.9 Computation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

$$\text{Average intra-cluster distance} = \frac{\sum D_i^2}{n}$$

Where,

D_i^2 = the sum of distances between all possible combinations (n) of genotypes included in a cluster

n= Number of all possible combinations between the populationsin cluster

2.10 Computation of average inter-cluster distances

Average inter-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

$$\text{Average inter-cluster distance} = \frac{\sum D_{ij}^2}{n_i \times n_j}$$

Where,

$\sum D_{ij}^2$ = The sum of distances between all possible

Combinations of the populations in cluster i and j

n_i= Number of populations in cluster i

n_j= Number of populations in cluster j

2.11 Cluster diagram

Using the values of intra and inter-cluster distances ($D = \sqrt{D^2}$), a cluster diagram was drawn as suggested by Singh and Chuadhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

III. RESULT AND DISCUSSION

This chapter comprises the presentation and discussion of the findings obtained from the study. The data pertaining to 20 bitter gourd genotypes as well as yield and its contributing characters were computed and statistically analyzed and the results thus obtained are discussed below under the following heads:

3.1 Analysis of variance

The analysis of variance indicated significantly higher amount of variability among the genotypes for all the characters studied *viz*., vine length, branch per vine, nodes per vine, days to first male flowering, days to first female flowering, fruit length, fruit diameter, fruit weight, fruits per plant and fruits yield per plant (Table 2). The variation due to replication was non-significant for all the characters studied.

3.2 Path coefficient analysis

Though correlation analysis indicates the association pattern of components traits with yield, they simply represent the overall influence of a particular trait on yield rather than providing cause and effect relationship. The technique of path coefficient analysis developed by Wright (1921) and demonstrated by Dewey and Lu (1959), facilitates the portioning of correlation coefficients into direct and indirect contribution of various characters on yield. It is standardized partial regression coefficient analysis. As such, it measures the direct influence of one variable upon other. Such information would be of great value in enabling the breeder to specifically identify the important component traits of yield and utilize the genetic stock for improvement in a planned way.

In path coefficient analysis the direct effect of a trait on fruit yield per plant and its indirect effect through other characters were computed and the results are presented in Table 3.

3.3 Direct effect

Three out of nine characters had positive direct effect on fruit yield per plant. The characters which had positive direct effect were branches per vine (0.88), fruit length (3.15) and fruit diameter (1.62). However, character *viz.,* vine length (-0.26), nodes per vine (-1.25), days to first male flowering (-0.03), days to first female flowering (-0.54), fruit weight (-3.00) and fruits per plant (-0.13) had negative direct effect on fruit yield (Table 3). Path coefficient analysis revealed that fruit yield per plant was directly influenced by branches per vine, fruit length and fruit diameter. Hence, selection for any of these independent traits leads to improving the genotypes for fruit yield per plant.

3.4 Indirect effects

Days to fist male flowering had negative indirect effect through vine length (-0.01), branches per vine (-0.21), nodes per vine (-0.51), days to first female flowering (-0.31) and fruit diameter (-0.19) (Table 3). However, its indirect effects through fruit length (0.77), fruit weight (0.18) and fruits per plant (0.08). The effect of days to first female flowering to fruit yield per plant through fruit diameter (0.25), fruit weight (0.79) and fruits per plant (0.05) was remarkable, its contribution through other traits was low. Vine length influenced the fruit yield per plant indirectly through fruit length (0.43) and fruit diameter (0.51) (Table 3). The indirect and positive effect on fruit yield per plant was exhibited by nodes per vine via fruit length (0.62), fruit diameter (0.14), fruit weight (0.18) and fruits per plant (0.03) Whereas, through other traits it had also negative indirect effects. Branches per vine showed positive indirect effect to fruit yield per plant via vine length (0.01), nods per vine (0.19), days to first male flowering (0.01), days to first female flowering (0.09) (Table 3). It had a negative indirect effect through fruit length (-0.47) and fruit diameter (-0.29).Fruit length showed indirect effect on fruit yield per plant had positive through days to first female flowering (0.08) (Table 3).Fruits per plant had positive indirect effect through branches per vine (0.21), nodes per vine (0.31), days to first female flowering (0.20) and fruit diameter (0.26) to fruit yield per plant (Table 3). This trait showed negative indirect effect via fruit length (-0.11) and fruit weight (-0.37) (Table 3).Fruit weight showed indirect positive effects on fruit yield per plant by nodes per vine (0.07), days to first female flowering (0.14), fruit length (2.60) and fruit diameter (0.36) (Table 3). It showed indirect negative effect on fruit yield per plant through vine length (-0.05) and fruits per plant (-0.02) (Table 3).From the present path analysis study in bitter gourd, it may be concluded that improvement in fruit yield per plant could be brought by selection for component characters like branches per vine, fruit length, fruits per plant and fruit diameter.

TABLE 2

ANALYSIS OF VARIANCE OF DIFFERENT CHARACTERS IN BITTER GOURD

Source	Df	Mean sum of square									
		DFMF	DFFF	VL	NPV	BPV	FL	FD	FPP	FW	FYP
Rep	2	44.60	56.12	0.01	44.82	0.47	0.91	1.52	64.12	538.02	0.970
Treatment	19	19.55**	28.89**	0.18**	16.71**	43.42**	27.49**	2.85**	21.39**	1731.10**	0.361**
Error	38	6.39	7.71	0.01	2.76	2.13	2.72	1.36	2.77	121.51	0.058

***** Correlation is significant at the 0.01 level.***

DFMF = Days to first male flowering, DFFF = Days to first female flowering, VL = Vine length (M), BPV = Branches per vine, NPV = Nodes per vine, FL = Fruit length (cm), FD = Fruit diameter (cm), FPP = Fruits per plant, FW = Fruit weight (g), FYP = Fruits yield per plant (Kg).

TABLE 3

PATH COEFFICIENT ANALYSIS SHOWING DIRECT AND INDIRECT EFFECTS OF DIFFERENT CHARACTERS ON YIELD OF BITTER GOURD

	Direct effect	Indirect effect									Genotypic correlation with yield
		DFMF	DFFF	VL	NPV	BPV	FL	FD	FPP	FW	
DFMF	-0.03	-	-0.31	-0.01	-0.51	-0.21	0.77	-0.19	0.08	0.18	-0.232
DFFF	-0.54	-0.02	-	-0.04	-0.42	-0.15	-0.45	0.25	0.05	0.79	-0.539**
VL	-0.26	0.00	-0.08	-	-0.02	-0.02	0.43	0.51	-0.02	-0.51	0.026
NPV	-1.25	-0.01	-0.18	0.00	-	-0.14	0.62	0.14	0.03	0.18	-0.620**
BPV	0.88	0.01	0.09	0.01	0.19	-	-0.47	-0.29	-0.03	0.00	0.378**
FL	3.15	-0.01	0.08	-0.04	-0.24	-0.13	-	-0.38	0.00	-2.48	-0.062
FD	1.62	0.00	-0.08	-0.08	-0.10	-0.16	-0.75	-	-0.02	-0.66	-0.231
FPP	-0.13	0.02	0.20	-0.04	0.31	0.21	-0.11	0.26	-	-0.37	0.346**
FW	-3.00	0.00	0.14	-0.05	0.07	0.00	2.60	0.36	-0.02	-	0.117

Residual effect: **0.342**

** = Significant at 1%, * = Significant at 5%.

DFMF = Days to first male flowering, DFFF = Days to first female flowering, VL = Vine length (M), BPV = Branches per vine, NPV = Nodes per vine, FL = Fruit length (cm), FD = Fruit diameter(cm), FPP = Fruits per plant, FW = Fruit weight (g), FYP = Fruits yield per plant (Kg).

TABLE 4

DISTRIBUTION OF TWENTY GENOTYPES IN DIFFERENT CLUSTERS

Cluster no.	No. of Genotypes	No. of populations	Name of genotypes
I	3, 7, 12	3	G3, G7, G12
II	8, 9, 14, 15, 20	5	G8, G9, G14, G15, G20
III	1, 4, 10, 13, 17	5	G1, G4, G10, G13, G17
IV	2, 5, 6, 11, 18, 19	6	G2, G5, G6, G11, G18, G19
V	16	1	G16
Total	20		

3.5 Genetic diversity

The knowledge of available genetic diversity is an important factor for any heritable improvement and its nature and degree is useful for selecting desirable parents from a germplasm for the successful breeding programme. There is still much scope for improving of genetic architecture desirable for hybrid through heterosis breeding. Its magnitude in desirable direction is preferable. The success of hybridization depends upon the selection of suitable parental genotypes and performance of their cross combinations.

3.6 Nonhierarchical clustering

With the application of covariance matrix for nonhierarchical clustering, 20 Bitter gourd genotypes were grouped into five different clusters. It is stated that the highest 30% genotypes were included in cluster IV and it was followed by 25% in both cluster II and III, 15% genotypes in cluster I, and the remaining 5% genotypes were in cluster V. The composition of clusters with different genotypes is presented in (Table 4).Cluster IV had the maximum 6 genotypes (G2, G5, G6, G11, G18, G19) followed by cluster II which had 5 genotypes (G8, G9, G14, G15, G20), cluster III also had 5 genotypes (G1, G4, G10, G13, G17) and cluster I had 3 genotypes (G3, G7, G12). Cluster V comprised with one genotype (G16) (Table 4).

3.7 Principal component analysis (PCA)

Eigen values of principal component axis, percent of total variation and cumulative variation accounted for them obtained from principal component analysis are presented in (Table 5). The results showed that the first principal axis, vile length (m) largely accounted for the variation among the genotypes which alone contributed 24.96% of the total variation among the genotypes. The first seven characters of the principal component axes with eigen values above unity accounted for 91.24% of the total variation among the ten characters. The rest three characters contributed remaining 8.76% of total variation. Based on principal component scores I and II obtained from the principal component analysis, a two-dimensional scatter diagram (Z_1-Z_2) using component score 1 as X axis and component score 2 as Y axis was constructed, which has been presented in (Figure 1 and Table 11).

TABLE 5

EIGEN VALUES AND PERCENTAGE OF VARIATION FOR CORRESPONDING 10 COMPONENT CHARACTERS IN 20 GENOTYPES OF BITTER GOURD

Principal component axes	Eigen values	Percent variation	Cumulative % of Percent variation
I	2.496	24.96	24.96
II	1.945	19.45	44.41
III	1.374	13.74	58.15
IV	0.995	9.95	68.10
V	0.927	9.27	77.37
VI	0.770	7.70	85.07
VII	0.617	6.17	91.24
VIII	0.456	4.56	95.80
IX	0.380	3.80	99.60
X	0.041	0.40	100.00

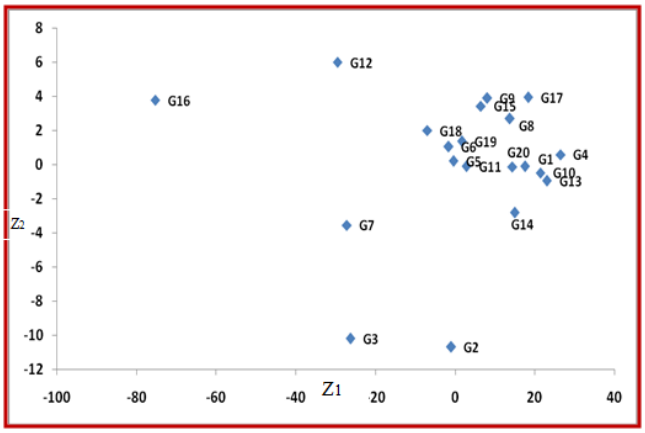

FIGURE 1. SCATTER PATTERN OF BITTER GOURD GENOTYPES OF BASED ON THEIR PRINCIPAL COMPONENT SCORES

3.8 Inter cluster distance

The inter cluster D^2 values are given in (Table 6) and the nearest and farthest cluster from each cluster based on D^2 value is given in (Table 7). The inter cluster D^2 values were maximum (64.53) between the cluster III and cluster V, followed by II and V (57.96) and IV and V (48.98). The higher inter-cluster distances between these clusters indicate to obtain wide spectrum variability of population. However, the highest inter cluster distance was observed between clusters III and V indicated the genotypes in these clusters were diverse than those clusters. Cluster V was the most diverse as many other clusters showed the maximum inter cluster distance with it (Table 7). The minimum distance observed between clusters II and III (7.05) indicated close relationship among the genotypes included.

3.9 Intra cluster distance

The intra cluster D^2 values were given in (Table 6). The intra cluster distance was observed in the clusters I, II, III and IV. The intra cluster distance was higher in cluster I (0.330) followed by cluster IV (0.240) and The lowest in cluster II (0.067). No intra cluster distance was observed for cluster V because of one genotype included in this cluster. The intra cluster distances in all the five clusters were lower than the inter cluster distances and which indicated that genotypes within the same cluster were closely related. The inter cluster distances were larger than the intra cluster distances which indicated wider genetic diversity among the genotypes of different groups.

3.10 Cluster diagram

The positions of the genotypes in the scatter diagram were apparently distributed into five groups, which indicated that considerable diversity existed among the genotypes (Figure 2).

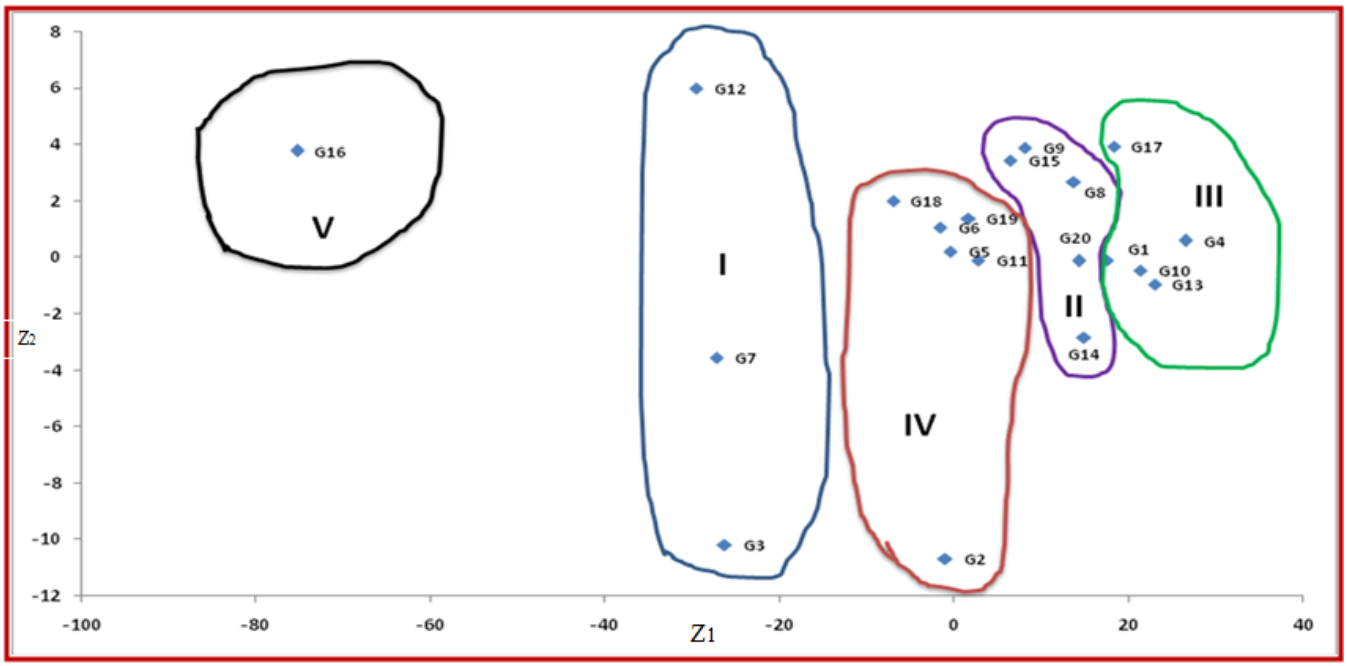

FIGURE 2. SCATTER DIAGRAM OF BITTER GOURD GENOTYPES OF BASED ON THEIR PRINCIPAL COMPONENT SCORE

TABLE 6
INTRA (BOLD) AND INTER CLUSTER DISTANCES (D^2) FOR 20 GENOTYPES OF BITTER GOURD

Cluster	I	II	III	IV	V
I	**0.330**	29.82	36.58	20.86	28.61
II		**0.067**	7.05	9.72	57.96
III			**0.165**	16.44	64.53
IV				**0.240**	48.98
V					**0.00**

TABLE 7
THE NEAREST AND FARTHEST CLUSTERS FROM EACH CLUSTER BETWEEN D^2 VALUES OF BITTER GOURD

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	**I**	**IV (**20.86)	**III (**36.58)
2	**II**	**III (**7.05)	**V (**57.96)
3	**III**	**II (**7.05)	**V(**64.53)
4	**IV**	**II (**9.72)	**V (**48.98)
5	**V**	**I (**28.61)	**III (**64.53)

TABLE 8
CLUSTER MEAN VALUES OF 10 DIFFERENT CHARACTERS OF 20 GENOTYPES OF BITTER GOURD

Characters	I	II	III	IV	V
Vine length (m)	4.52	4.32	4.20	4.17	4.25
Branches per vine	36.00	38.53	40.07	35.39	43.00
Nodes per vine	84.22	83.67	83.07	81.39	81.00
Days to first male flowering	55.44	53.00	54.33	53.89	51.67
Days to first female flowering	60.78	61.33	63.60	59.89	61.33
Fruit length (cm)	24.88	18.55	17.96	19.60	25.90
Fruit diameter (cm)	13.14	13.19	12.81	13.63	13.50
Fruit weight (g)	135.55	96.80	87.07	109.17	183.33
Fruits per plant	22.89	23.20	20.80	21.33	22.00
Fruit yield per plant (Kg)	2.18	2.33	2.12	2.39	2.47

3.11 Cluster mean analysis

The cluster means of 10 different characters (Table 8) were compared and indicated considerable differences between clusters for all the characters studied. The maximum vine length was observed in cluster I (4.52), whereas the minimum vine length was observed in cluster IV (4.17). The maximum (43.00) and the minimum (35.39) branches per vine were observed in cluster V and IV respectively. Genotypes in cluster V showed the lowest nodes per vine (81.00) and that in cluster I had the highest mean (84.22) nodes per vine. The maximum (55.44) and the minimum (51.67) days to first male flowering were observed in cluster I and V respectively. The maximum days to first female flowering were observed in cluster III (63.60), whereas the minimum days to first flowering were observed in cluster IV (59.89). Cluster V had the maximum fruit length (25.90), cluster III had the minimum fruit length (17.96). The maximum fruit diameter (13.63) was observed in the cluster IV, whereas the minimum fruit diameter (12.81) was observed in cluster III. Fruit weight was the highest in cluster V with a mean value of (183.33) and it was least in genotypes belongs to the cluster III (87.07). The highest fruits per plant were recorded by the cluster II (23.20) while cluster III (20.80) showed the least fruits per plant. The maximum fruit yield per plant was observed in cluster V (2.47), whereas the minimum fruit yield per plant was observed in cluster III (2.12).

3.12 Contribution of characters towards divergence

Contribution of characters towards the divergence obtained from canonical varieties analysis is presented in (Table 9). The character, which gave high absolute magnitude for vector 1, was considered to be responsible for primary differentiation. Likewise, the characters, which gave higher absolute magnitude for vector 2 was considered to be responsible for secondary differentiation. If the same character given equal magnitude for both the vectors than the character was considered responsible for primary as well as secondary differentiation.

TABLE 9

RELATIVE CONTRIBUTIONS OF THE THIRTEEN CHARACTERS OF 20 VARIETIES TO THE TOTAL DIVERGENCE

Characters	Principal Component	
	Vector-1	Vector-2
Vine length (m)	-4.1397	-1.4697
Branch per vine	0.2165	-0.3741
Nodes per vine	0.3173	-0.1575
Days to first male flowering	-0.0466	0.1198
Days to first female flowering	-0.0009	-0.3257
Fruit length (cm)	-0.8297	0.3994
Fruit diameter(cm)	0.4920	1.3151
Fruit weight (g)	-0.6014	-0.0662
Fruits per plant	0.0992	0.0280
Fruits yield per plant (Kg)	-1.0496	2.5485

TABLE 10

SALIENT FEATURES OF GENOTYPES IN FIVE DIFFERENT CLUSTERS

Cluster	Salient features
I	Long vine, More nodes per vine
II	More fruits per plan, Medium nodes
III	Moderate branches per vine, Late female flowering
IV	Early female flowering, Higher fruit diameter
V	Highest branches per vine, Early male flowering, Highest fruit length, More fruit weight, Highest fruit yield per plant

TABLE 11

PRINCIPAL COMPONENT SCORE 1 & 2.

Genotypes	Z_1	Z_2
1	17.506	-0.107
2	-1.006	-10.665
3	-26.288	-10.196
4	26.485	0.596
5	-0.425	0.208
6	-1.662	1.056
7	-27.2	-3.541
8	13.715	2.692
9	8.066	3.889
10	21.343	-0.472
11	2.769	-0.101
12	-29.551	6.004
13	23.009	-0.938
14	14.871	-2.822
15	6.45	3.434
16	-75.309	3.78
17	18.3	3.937
18	-7.017	2.002
19	1.645	1.371
20	14.299	-0.128

In vector (Z_1) obtained from PCA, the important characters responsible for genetic divergence in the axis of differentiation were days to first male flowering (0.119), fruit length (0.3994), fruit diameter (1.3151), fruits per plant (0.0280) and fruit yield per plant (2.5485) were important because all these characters had positive signs (Table 9).

On the other hand, vine length, days to first male flowering, days to first female flowering, branches per vine, nodes per vine, days to first female flowering, possessed the negative sign in the first axis of differentiation and vine length, branches per vine, nodes per vine, days to first female flowering and fruit weight possessed negative signs in the second axis of differentiation that means it had minor role in the genetic diverse. Fruit diameter and fruits per plant had positive signs in both the vectors, which indicated they were the important component characters having higher contribution to the genetic divergence among the materials studied.

3.13 Salient feature cluster`s genotype

The genotypes of cluster I was the best in terms of long vine and more nodes per vine (Table 10). The genotypes of cluster II produced more fruits per plant and medium nodes per vine. The genotype of cluster III possessed moderate branches per vine and late female flowering. The genotypes of cluster IV produced early female flowering and the highest fruit diameter and the cluster V possessed the highest branches per vine, early male flowering, the highest fruit length, more fruit weight, the highest fruit yield per plant**.**

IV. CONCLUSION

Path co-efficient analysis revealed that branch per vine, fruits length, and fruit diameter had positive direct effect on fruit yield. Wide genetic diversity was observed in 20 genotypes of bitter gourd, which were grouped into five clusters. The genotypes of clusters III were more diverse from the genotypes of cluster V.Fruit diameter and fruits per plant were found responsible for the maximum diversity. Hybridization between the genotypes of cluster III and cluster V will manifest the maximum heterosis and create wide genetic variability. The highest heterosis would be manifest in cross combination involving the genotypes belonging to divergent clusters. Considering group distance and the agronomic performance, the inter genotypic crosses between G16 and G1; G16 and G17; G16 and G10; G16 and G4; G16 and G13 might be suitable choice for future hybridization programme.

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