GENETIC VARIABILITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS OF SOME YIELD AND YIELD CONTRIBUTING CHARACTERS IN BITTER GOURD
(*Momordica charantia L.*)

BY

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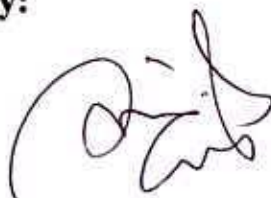for the degree of

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This is to certify that thesis entitled, "*Genetic variability, correlation and path co-efficient analysis of some yield and yield contributing characters in Bitter gourd (Momordica charantia L.)*" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE** in **GENETICS AND PLANT BREEDING**, embodies the result of a piece of bonafide research work carried out by **Md. Rafiqul Islam**, Registration No. **07-02643** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

I further certify that such help or source of information, as has been availed of during the course of this investigation has duly been acknowledged.

Dated: June, 2009
Place: Dhaka, Bangladesh

(Dr. Md. Sarowar Hossain)
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Dedicated to
My
Beloved Parents

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ABSTRACT

Twenty genotypes of bitter gourd (*Momordica charantia L.*) were studied in a field experiment conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, during April 2008 to September 2008. The objectives of the study were to measure the variability among the genotypes for yield and yield contributing characters, estimate genetic parameters, association among the characters and their contribution to yield. There was a great deal of significant variation for all the characters among the genotypes. Considering genetic parameters high genotypic co-efficient of variation (GCV) was observed for branches per vine, yield per plant and number of fruit per plant whereas low genotypic co-efficient of variation (GCV) was observed days to first male and female flowering. In all cases, phenotypic variances were higher than the genotypic variance. Differences between genotypic and phenotypic coefficients revealed that the major portion of the phenotypic variance was genetic in nature. High heritability with low genetic advance in percent of mean was observed in days to first female flowering which indicated that non-additive gene effects were involved for the expression of this character and selection for such trait might not be rewarding. High heritability with high genetic advance in percent of mean was observed for yield per plant and vine length indicated that this trait was under additive gene control and selection for genetic improvement for this trait would be effective. The results obtained, showed that yield per plant had high positive and high significant relation with number of nodes per vine. Correlation studies revealed that highest significant association of yield per plant with fruit diameter and number of fruit per plant at genotypic level. Path co-efficient analysis revealed maximum direct contribution towards yield per plant with maximum number of fruit per plant followed by vine length. Considering all the characters the G_1 (Shaparan), G_5 (Rampali gaj), G_9 (Nabil), G_{12} (Nandita), G_{14} (Eureca), G_{16} (Tia) and G_{19} (Maharaj) were selected for future breeding programme.

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LIST OF ABBREVIATED TERMS

FULL WORD	ABBREVIATION
Agro-Ecological Zone	AEZ
And others	*et al.*
Accessions	ACC
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Centimeter	cm
Co-efficient of Variation	CV
Etcetera	etc.
Figure	Fig.
Genotype	G
Genetic Advance	GA
Genotypic Co-efficient of Variation	GCV
Genotypic Variance	$\delta^2{}_g$
Gram	g
Heritability in broad sense	h^2b
Journal	j.
Kilogram	Kg
Meter	m
Mean Sum of Square	MSS
Millimeter	mm
Muriate of Potash	MP
Number	No.
Percent	%
Phenotypic Co-efficient of Variation	PCV
Phenotypic variance	$\delta^2{}_p$
Randomized Complete Block Design	RCBD
Replication	R
Research	Res.
Sher-e-Bangla Agricultural University	SAU
Standard Error	SE
Square meter	m^2
Triple Super Phosphate	TSP

Chapter I
Introduction

CHAPTER I

INTRODUCTION

Bitter gourd (*Momordica charantia* L.), locally known as karala/uchha, is an important home garden vegetable. It is a fast growing warm seasonal climbing annual, native to South Asia. Bitter gourd is a tropical and subtropical vine of the Cucurbitaceae family. It is widely grown for edible fruit, which is among the most bitter of all vegetables. The original home of the species is not known, other than it is a native of the tropics. It is widely grown in South and Southeast Asia, China, and Africa. The herbaceous tendril-bearing vine grows to 5 m. It bears simple; alternate leaves 4-12 cm across, with 3-7 deeply separated lobes. Each plant bears separate yellow male and female flowers (Rashid, 2004). From nutritional point of view, bitter gourd can be considered as nutrition rich fruit vegetable. It contains considerable amount of water (83-92%), carbohydrates (4.0-10.5%), protein (1.5-2.0%), fat (0.2-1.0%), minerals (0.5-1.0%) and fiber (0.8-1.7 %) (Gopalan *et. al.* 1982). Ripe fruits are rich in vitamin- A. Among all cucurbit vegetables, bitter gourd contains the maximum amount of minerals and vitamins.

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. The fruit pulp of Balsam Pear contains "momordicin", which is mixed with oil and used externally as a balsam (Oliver, 1960). Its leaves are used to clean metals and wash hands and body since they form a slightly soapy solution in water (Dalziel, 1984).

Due to high keeping quality (Banerjee and Mangal, 1986), it has also export potentiality. The fruit has a distinct warty looking exterior and an oblong shape. It is hollow in cross-section, with a relatively thin layer of flesh surrounding a central seed cavity filled with large flat seeds and pith. Seeds and pith appear white in unripe fruits, ripening to red; they are not intensely bitter and can be removed before cooking. However, the pith will become sweet when the fruit is fully ripened, and the pith's color will turn red. The pith can be eaten uncooked in this state, but the flesh of the gourd will be far too tough to be eaten anymore. Red and sweet bitter gourd pith is a popular ingredient in some special South East Asian style *salad.* Bitter gourd comes in a variety of shapes and sizes. The typical Chinese phenotype is 20 to 30 cm long, oblong with bluntly tapering ends and pale green in color, with a gently undulating, warty surface.

The bitter gourd more typical of India has a narrower shape with pointed ends, and a surface covered with jagged, triangular "teeth" and ridges. Coloration is green or white. Between these two extremes are any numbers of intermediate forms. Some bear miniature fruit of only 6 - 10 cm in length, which may be served individually as stuffed vegetables. These miniature fruit are popular in Southeast Asia as well as India. Bitter gourds are seldom mixed with other vegetables due to the strong bitter taste, although this can be moderated to some extent by salting and then washing the cut gourd before use. In Bangladesh, vegetables are grown in 0.2 million hectares of land which is about 1% of the cultivated. Winter vegetables are usually grown in 58.96% of the total land area while 41.04% area is covered by summer vegetables (BBS, 2005).

Vegetables become rare during summer season. Besides, there are lean periods at the end of winter and summer seasons when there is always a scarcity of vegetables in this country. The nutritional problems and vegetable scarcity in Bangladesh during that gap period can be

reduced to some extent through improvement of production technology of cucurbitaceous crops like bitter gourd.

Yet no comprehensive systematic research has been done in this crop in Bangladesh. Present harvestable yield of bitter gourd is very low (3.72 t/ha, BBS, 2003) due to unavailability of high yielding varieties. Bitter gourd is monoecious and highly cross-pollinated in nature. Such pollination mechanism can be exploited for hybrid seed production commercially. Moreover, there is a great scope of development of open pollinated varieties utilizing the existing variability. As a minor vegetable, bitter gourd did not get proper attention for its genetic improvement in the past. Considering the availability of genetic variability, its scope of yield improvement and export potential, the present investigation was undertaken with the following objectives:.

> To know the yield potentiality of genotypes

> To know the association of traits with yield and its contributing traits

> To study the genetic diversity among the genotypes

> To screen out the suitable parental groups which are likely to provide superior segregates on hybridization

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Chapter II
Review of literature

CHAPTER II

REVIEW OF LITERATURE

Bitter gourd (*Momordica charantia* L.) is a member of the family Cucurbitaceous. It is an important vegetable in this country. A few works have been done for the improvement of this crop in Bangladesh and other countries in the world. Research effort on the variability of its genetic resources and diversity on genetic seems to be meager. However, information available in these aspects of bitter gourd and some other Cucurbitaceous crops have been reviewed and presented in this section.

2.1 Variability, Heritability and Genetic Advance

Rahman *et al.* (1990) in a study observed significant variation for days to first flowering among the genotypes of bitter gourd, ribbed gourd and sweet gourd. Rahman *et al.* (1990, 1991) also concluded that days to male flowering was earlier than days to female flowering in several genotypes of ribbed gourd, bitter gourd, bottle gourd and sweet gourd. They also reported that bitter gourd, sweet gourd, ribbed gourd and bottle gourd genotypes differed significantly for fruit breadth and weight per fruit.

Miah *et al.* (2000) studied 30 genotypes of bitter gourd and observed the highest genotypic as well as phenotypic co-efficient of variation were found for fruit length followed by days to female flowering, fruit yield per plant, fruit weight and nodes per vine

Guffar (2008) was conducted an experiment with 15 sponge gourd genotypes at the experimental farm of Sher-e-Bangla Agricultural University, during April 2007 to October 2007. Among the characters the highest GCV recorded for yield per plant (63.90) followed by top fruit perimeter (46.60) and average fruit weight (39.52). Genotypes included in cluster I were suitable for yield per plant (6.55), cluster III for having the highest mean value for inter node length (17.62), cluster V for leaf length (30.43), leaf breadth (24.65),

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petiole length (13.28), days to first male flower (103.28), days to first female flower (107.80) and other characters.

Zaman *et al.* (2004) reported the performance of three sponge gourd lines at the farm of Olericulture Division, HRC and in different RARS, BARI during the summer season of 2004. The line Sg 6-3-2-2-10-10 and Sg 6-3-1-2-1-6 produced the highest number of fruits per plant (34) and lower was recorded in Local (26). Maximum individual fruit weight was obtained form Local (189 g). The line Sg 6-3-2-2-10-10 gave the highest yield (20.0 t/ha) closely followed by Sg 6-3-1-2-1-6 (19.4 t/ha).

Singh *et al.* (2002) conducted an experiment on 80 ridge gourd genotypes to determine variability and heritability of nineteen yield contributing characters. High PCV and GCV were observed for node number for appearance of 1st male flower, male flowers per plant, sex ratio main axis and branches, fruit per plant, fruit weight, seeds per fruit, and yield per plant. The GCV and PCV values were almost equal for most of the characters studied. The broad sense heritability estimates were high for all the characters.

Hossain (1996) was conducted an experiment on floral biology of ridge gourd at the experimental farm of IPSA (Institute of Post Graduate Studies). Male, female and hermaphrodite flower buds appeared 29-38 days after seeding. The male flower buds developed earlier and in lower nodes than the female and hermaphrodite ones. The first male, female/hermaphrodite flowers were produced an average in the 10th to 21st node.

Rahman *et al.* (1991) reported that male flower were earlier than female flower in several genotypes of bottle gourd, ribbed gourd and sweet gourd. They reported significant variations for that character among the genotypes of bitter gourd, sweet gourd, ribbed gourd and bottle gourd. Significant variation for fruit length and diameter were also observed.

Abusaleha and Dutta (1990) carried out a study with 65 genetic stocks to assess the genetic variation and heritability in ridge gourd. Significant variability was observed for all the

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characters at phenotypic as well as genotypic level with a very wide range of values. Swamy *et al.* (1984) also conducted an experiment on muskmelon and reported a wide range of variability among the genotypes for number of seeds per fruit.

Chowdhury and Sharma (2002) were studied genetic variation, heritability, genetic advance and correlation for yield and yield components (vine length, number of nodes, node on which the first flower appeared, number of fruits per plant, fruit length, fruit girth and fruit weight) in 12 *Luffa acutangula* cultivars. The genetic co-efficient of variation (GCV) was higher than the phenotypic co-efficient variation (PCV) for all the characters. High values of variability, PCV, GCV and genetic advance have recorded for vine length, yield per hectare and fruit weight indicating that these characters were controlled by additive gene effects. The correlation co-efficient revealed that yield per hectare could be improved through selection for higher fruit number per plant, fruit length and girth and individual fruit weight.

Banik (2003) conducted an experiment on variability and genetic advance of 26 genotypes of snake gourd with respect of 15 quantitative yield contributing characters and found significant difference among the characters like vine length at harvest (2.197 to 3.87 m), number of primary branches (5.23 to 11.88), days to first male flowering (41.67 to 68.67 days), days to first female flowering (48.67 to 71.33 days), node number of first male flower (6.33 to 17.67 days), fruit length (20.67 to 71.17 cm), seeds per fruit (39.03 to 69.50). Banik also found that significant differences in first female flower, node number (mean value 19.28) and fruits per plant. The highest phenotypic co-efficient of variation was observed for fruiting node on main vine, fruit yield per plant, fruit length and first male flower node. The PCV was lowest for days to maturity, 100 seed weight and days to first male flower opening. The GCV along with heritability was high for the above characters. High heritability coupled with high genetic advance was noticed for fruit yield per plant

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(GCV and PCV 30.75 and 30.96; h^{2}b 98.64%), fruit length (GCV and PCV 29.92 and 30.04; h^{2}b 99.19%) and first female flower node number (GCV and PCV 25.87 and 26.59; h^{2}b 94.63%) and number of fruits per plant (GCV and PCV 19.82 and 20.59; h^{2}b 92.67%).

Kabir (2007) conducted an experiment on variability and estimation of genetic parameter, correlation, path analysis and genetic diversity of 24 accessions of pointed gourd with respect of different parameter such as days to flower, fruit length, fruit breadth, single fruit weight, pulp seed ratio, and number of fruits per plant, weight of fruit per plant and yield of fruit. The accession PG020 showed the highest performance in weight of fruits per plant, single fruit weight and yield. The highest genotypic and phenotypic co-efficients were recorded in the parameter number of fruits per plant (5415.55% and 5623.67%) and second highest was recorded from yield of fruits ton per hectare (410.30% and 410.98%). However, days require to first flowering (49.86% and 52.41%), fruit length (7.4% and 7.42%), fruit breadth (23.56% and 26.79%), single fruit weight (172.27% and 173.28%), and weight of fruit per plant (161.87% and 162.85%) recorded moderate GCV and PCV. Correlation coefficient indicated that fruit yield per plant was highly significant and there was a positive association with weight of fruit per plant, number of fruits per plant and single fruit weight. Path analysis indicates fruit breadth, number of fruits per plant and weight of fruits per plant directly contributed to the yield of pointed gourd accessions.

Sharma *et al.* (2000) evaluated 10 cucumber lines and testers under different environmental conditions and reported that day to first female flower, nodal position of fruits per plant, marketable yield per plant, fruit length and fruit diameter had wide range of variation.

Mathew and Khader (1999) conducted an experiment on genetic studies in snake gourd (*Trichosanthen anguina*) and observed the genetic variability and heritability of 12 traits in 34 *Trichosanthen anguina* in Kerela, India and reported that the genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) were almost equal for all

characters. The highest GCV and PCV were recorded for mean fruit weight, seed per fruit, fruit yield per plant and fruit length. High heritability was observed for mean fruit weight, seeds per fruit, fruit length, days to first male flower and fruit yield per plant.

In case of seed germination there was a wide range of variation. Robinson and Decker-Walkers (1997) reported that cucumber germinated from two days to two weeks. Rahman (1988) noted that in pointed gourd it took two to three weeks for sprouting and three months for flowering or fruiting after planting of vine or roots.

Rumaran *et al.* (1997) was conducted 30 pumpkin genotypes in a field trial and reported that genotypic co-efficient of variation was smaller than phenotypic co-efficient of variation for most of the traits studied. However, GCV was high for mean fruit weight, number of fruits per plant, number of seeds per fruit, yield per plant and fruit, total soluble solids content. High heritability coupled with high genetic advance were observed for vine length, mean fruit weight, number of fruits per plant, number of seeds per fruit, fruit yield per plant and total soluble solids content of fruits. Islam (1993) reported that male flowering was earlier than female flowering in several genotypes of bottle gourd.

Saha *et al.* (1992) studied the variability, character association and path analysis of pumpkin and reported that phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV). High genotypic variance and phenotypic variance were found for fruit length (30.34 and 31.76), fruit weight (39.55 and 41.00) and low for fruit diameter (8.87 and 10.23) among the pumpkin genotypes. They also reported high heritability estimate, for both length (91.27) and diameter (75.07) of fruits indicating effectiveness of selection based on good phenotypic performances in pumpkin.

Varghese (1991) reported an experiment on the variability among 48 snake gourd genotypes in respect of different yield contributing characters and found significant differences among the characters. Main vine length varied from 3.035 to 7.85 m with high heritability (97.0%).

In case of number of branches per vine, heritability was 91.0%. Moderate GCV and PCV in fruit length and breadth (32.15 and 32.51; 20.26 and 21.23) was also observed in snake gourd germplasms. Narrow differences between GCV and PCV in fruit weight with high heritability (h^2b) were also observed. GCV and PCV for yield per plant were 30.0 and 31.33 respectively. 100 seed weight varied from 20.0 to 41.0 g with high heritability 97.8% in snake gourd.

Mangal *et al.* (1981) noticed that in bitter gourd significant variation for fruit length and diameter present and high heritability in bitter gourd for vine length.

Sharma and Dhankar (1990) reported that almost similar estimates of GCV and PCV (13.54 and 14.00) for days to first female flower opening in bottle gourd. They also observed high heritability (93.47%) with considerably high genetic advance for days to flowering in bitter gourd. In watermelon days to first female flower opening regard from 37.17 to 61.72 days and the PCV and GCV were 19.10 and 19.91 respectively (Rajendran, 1985).

Mondal *et al.* (1989) studied the genetic variability of 31 watermelon genotypes and observed a wide range of variability for days to first fruit harvest, fruit length, fruit diameter, number of fruits per plant and fruit yield per plant.

Rahman *et al.* (1986) reported high GCV and PCV for both length (31.73 and 33.75) and diameter (39.23 and 41.96) of fruits in bottle gourd. They also observed minimum difference between GCV and PCV. The variability for yield per plants and significant variations were also recorded for fruit length and diameter in bottle gourd Rahman *et al.* (1991).

Doijode and Sulladmath (1988) found high GCV and PCV (30.2 and 36.4), high heritability (h^2b) with high genetic advance for average fruit in pumpkin. Narrow difference between GCV and PCV observed for fruit weight in bitter gourd indicating less environmental

influence on this character. Significant difference was also found among bitter gourd genotypes for seeds per fruit (Mannan, 1992).

Bose and Som (1986) stated that the sex ratio in cucurbits varied from 5:1 to 25-30:1, the ratio of male: female flower was changed by the climate and environmental factors.

Joseph (1978) conducted an experiment on variability among 25 lines of snake gourd and found that main vine length varied from 4.01 to 6.17 m. Days to first male flower anthesis (36.22 to 45.00 days) and days to first female flower opening (45.00 to 61.33 days). Nodes number for 1st female flowering was recorded to be 15.11 to 23.44.

Haque (1971) stated that petiole length for bottle gourd, sweet gourd; white gourd and watermelon were 13.84 cm, 14.53 cm and 12.14 cm, respectively. He also noted that node for first male flower in bottle gourd, sweet gourd; white gourd and melon were 19th, 25th, 14th and 14th, respectively. Node for first female flower in bottle gourd, sweet gourd, white gourd and water melon were 28th, 34th, 21st and 19th, respectively.

2.1.1 Days to first flowering

In Bitter gourd, Mannan (1992) recorded considerable variability among eight lines for days to first male flower (66.7-81.6 days) and female flower (72.80-85.67 days) opening. Ramchandran and Gopalkrishnan (1979) also reported significant variability among 25 diverse genotypes of bitter gourd.

Rahman et al. (1990) found significant differences for days to flowering among the different entries of ribbed gourd, bitter gourd, bottle gourd and sweet gourd. High genotypic and phenotypic variances for days to flowering in bitter gourd were also reported by Cruz and Villareal (1970) and Pal et al. (1983).

Sharma and Dhankhar (1990) reported almost similar estimates of GCV and PCV (13.54 and 14.00) for days to first female flower opening in bottle gourd. They also observed high heritability (93.47%) along with considerably high genetic advance (26.99) for days to

flowering in bitter gourd. Banik (2003) observed the wide variation among the 26 genotypes of snake gourd. Deshpande *et al.* (1978) noticed the first male and female flowers in bitter gourd after 34 and 40 days of planting seedling, respectively. Days to flower was observed to be markedly influenced by the environment as was indicated by much higher environmental variance compared to the low genetic variance (Srivastava and Srivastava 1976, Singh *et al.* 1977). Both low and high values for h_b^2 have been reported for this character.

Abdel *et al.* (1982) studied heritability of yield components in watermelon and reported that h^2 for number of days to flowering was 94%. Singh *et al.* (1977) studied twenty varieties of bitter gourd and reported least genetic co-efficient of variation (4%), low h^2 (22%) and very low genetic advance (4%).

Sureshbabu (1989) studied 50 genotypes of pumpkin and observed considerable variability for days to first male flower anthesis (41.0-73.0 days) and days to first female flower opening (41.0-84.5 days). Lowest PCV was observed for days to first male flower anthesis (13.08). Vahab (1989) found significant differences among 50 genotypes of bitter gourd for all the 18 characters studied. The PCV was low for days to first female flower opening (3.38).

Quamruzzaman *et al.* (2008) were conducted experiment the genetic divergence among thirty genotypes of ridge gourd (*Luffa acutangula*) at the farm of Olericulture Division, HRC and in different RARS, BARI during the summer season of 2005. The genotype RGN05, RGN06, RGN07, RGN08, RGN13, RGN17, RGN18, RGN27, RGN29 recorded highest cluster mean values for days to 1st. male flower open (56.0 days) and single fruit weight (141.0 g) and RGN03, RGN12 lowest mean values for days to 1st female flower open (27.0 days) and single fruit weight (85.0 g). The highest fruit length (23 cm), fruit number per plant (26) and yield per plant (9.7 kg) obtained from RGN16 and RGN20. The

role of days to 1st male flower open, days to 1st. female flower open, fruit diameter, single fruit weight and fruit number in PCA indicates their importance in genetic divergence.

2.1.2 Vine length (m)

Vahab (1989) found significant difference among 50 genotypes of bitter gourd for vine length. Mangal *et al.* (1981) noted high h^2 values in bitter gourd for vine length. Chaudhury (1987) reported that the genetic advance in bitter gourd was very high for vine length (151.53). Wide variations for this trait were reported in sponge gourd (Prosad and Singh, 1990). In snake gourd, Joseph (1978) found variability among 25 lines. The main vine length varied from 4.01 to 6.17 m. Arora *et al.* (1983) found significant varietal difference for the characters in sponge gourd genotype HS-3 with maximum vine length (275.1 cm). Prasad and Singh (1989) in ridge gourd noticed low h^2 for vine length (5.0%).

2.1.3 Branches and number of nodes per vine

Rahman *et al.* (1991) reported significant differences for number of branches per vine in bitter gourd and ribbed evaluating 25 diverse lines of bitter gourd, Ramachandran (1978) observed considerable variability for several vegetative and reproductive characters. The primary branches per plant in different bitter gourd genotypes ranged from 18.00 to 35.89 with a general mean of 27.12. The estimated phenotypic, genotypic and environmental variances (VP = 2.64, Vg = 20.81, VE = 0.83) showed a predominant influence of genetic component in relation to the environmental effects on this character. Mangal *et al.* (1981) noted high h^2 for branches per vine in bitter gourd. Rahman *et al.* (1990) reported that number of nodes per vine varies from 52.2 to 62.2 among the 12 genotypes of bitter gourd.

2.1.4 Number of fruits per plant

Prasad and Singh (1989) noted high value of genotypic and phenotypic variances for number of fruits per vine per plant in ribbed gourd (202.26 and 475.98) whereas Rahman *et al.* (1986), Abusaleha and Dutta (1990), Mangal *et al.* (1981) reported low value in

muskmelon (1.71 and 1.90), bottle gourd (1.43 and 3.10), cucumber (1.15 and 1.24) and bitter gourd (9.02 and 10.45). High GCV and PCV were observed for fruits per plant by Reddy and Rao (1984) in ribbed gourd (75.40 and 109.38). Characters having high GCV indicate high potentiality for effective selection (Burton and de Vane, 1953). High heritability along with high genetic advance and moderately high h^2 along with considerably high GA was noticed by Vijay (1987) in muskmelon (90.16% and 165.21).

2.1.5 Fruit length and diameter (cm)

Significant variation for fruit length and diameter were noticed in bitter gourd (Srivastava and Srivastava, 1976; Mangal *et al.*, 1981) other gourds (Arora *et al.*, 1983; Prosad and Singh, 1990, Rahman *et al.*, 1991). Rahman *et al.* (1986) indicated high GCV and PCV for both length (31.73 and 33.75) and diameter (39.23 and 41.96) of fruits in bottle gourd. They also observed minimum difference between GCV and PCV. Saha *et al.* (1992) observed high GCV and PCV for fruit length (30.34 and 31.76) and low for fruit diameter (8.87 and 10.23) in pumpkin. They estimated high h^2 for both length (11.27 %) and diameter (75.07 %). They also found high genetic advance for fruit length (59.72) but low for fruit diameter (15.82). Chaudhari *et al.* (1991) reported that fruit flesh thickness ranges 2.75-9.56 cm with 24.19% PCV and 18.05 GCV and moderate heritability with least genetic advance (1.73).

2.1.6 Yield per plant (kg)

Mangal *et al.* (1981) found high value (47759.63 and 55149.80) in bitter gourd while, low GCV and PCV were recorded for this character in water melon (0.44 and 1.15) and musk melon (0.04 and 0.07) by Vashistha *et al.* (1983) and Vijay (1987). The variability for yield per plant was also recorded in bottle gourd (Rahman *et al.*, 1991) and pumpkin (Rana *et al.*, 1986). Singh and Prasad (1989) and Saha *et al.* (1992) recorded high GCV and PCV for yield per plant in pointed gourd (46.50 and 64.10) and pumpkin (28.82 and 31.21). High h^2 associated with high genetic advance for yield per plant was reported by Saha *et al.* (1992).

2.2 Correlation, co-efficient and path analysis

Singh and Ram (2003) conducted an experiment on 28 musk melon genotypes to determine the correlation among fruit characters. The simple correlation among fruit traits showed that polar diameter, latitudinal diameter, flesh thickness and seed cavity size were positively correlated with fruit weight.

Eleven pointed gourd (*T. dioica*) selections were assessed to estimate genetic variability and correlation for yield and its attributes. High genetic co-efficient of variation (GCV) estimate was observed for the characters such as node at which first female flower appeared, length of vine, number of nodes per plant and number of fruits per plant. The heritability estimate was high for all the characters. The character having high GCV also exhibited high genetic advance. Yield per plant had significant positive correlation with number of fruits per plant (Dora *et al.*, 2003).

Shah and Kale (2002) conducted an experiment on correlation co-efficient analysis of yield components of 55 genotypes of ridge gourd. The fruit weight per vine was positively and significantly correlated with number of fruits per vine, average fruit weight, number of female flower per vine and vine length, indicating the close association and dependency of yield these characters. The fruit length was negatively correlated with fruit diameter and fruit number per vine, while it was positively correlated with average fruit weight.

Singh *et al.* (2002) were carried out 98 hybrids of cucumber derived from crosses involving 14 male and 7 female parents and found that fruit weight, fruit girth and fruit length had high correlations with fruit yield. Genotypic correlation co-efficient were higher than phenotypic co-efficient which indicated strong association among these traits. Path coefficient analysis also indicated that fruit weight had the highest direct effect on fruit yield.

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Badade *et al.* (2001) conducted an experiment to study the correlation of 20 bottle gourd (*Lagenaria vulgaris*) genotypes. Yield was found significantly and positively correlated with number of branch per vine, number of fruits per vine and significantly and negatively correlated with days to first male and female flower appearance and weight of deformed fruits per vine at both phenotypic and genotypic levels. Fruit length showed positive but non significant correlation with fruit yield.

Rao *et al.* (2000) conducted an experiment on the segregating population of ridge gourd for correlation and path coefficient analysis. Path analysis revealed that yield improvement could be achieved by direct selection for days to 50% flowering, girth of fruit, fruits per plant or vine, fruit per branch and length of the vine of ridge gourd.

Miah *et al.* (2000) noted that fruit yield in bitter gourd showed significant positive association with average fruit weight, fruit breadth and number of nodes per vine in genotypic and phenotypic correlation with days to male flowering. Path analysis revealed that average fruit weight, number of fruits per plant, days to male flowering and fruit length had positive direct effect on fruit yield.

Sarker *et al.* (1999) studied correlation and path co-efficient of 16 divergence types of pointed gourd indicated that fruit weight, fruit diameter and number of primary branches per plant were positively and significantly correlated with yield per plant at genotypic and phenotypic levels. The path analysis revealed that fruit volume followed by fruit weight and fruit diameter had maximum positive direct effects on yield.

Li *et al.* (1997) noted that number of fruits per plant, average fruit per plant, average fruit weight, fruiting rate and leaf area of cucumber genotypes were positively correlated to yield. Days to flowering and vine length were negatively correlated. From path analysis, they also concluded that fruits per plant and average fruit weight affected the yield directly.

Ananthan and Pappoah (1997) reported that fruit number per vine and seed number per fruit were positively correlated with total yield while days to first female flowering, days to first male flowering, sex ratio, fruit girth, pulp thickness and total soluble solids content were negatively correlated with total yield in cucumber.

Abusaleha and Dutta (1990) carried out a study with 65 genetic stocks to assess the genetic variation and heritability in ridge gourd. Significant variability was observed for all the characters at phenotypic as well as genotypic level with a very wide range of values.

Sych (1990) conducted path co-efficient analysis in 150 genotypes of watermelon and found that fruit weight and number of fruits per plant had considerable direct effects on yield.

Rastogi *et al.* (1990) conducted an experiment with 25 diverse cucumber cultivars and found that general genotypic correlation co-efficient were higher than those related to phenotypic or environmental; factors. However, both genotypic and phenotypic co-efficient for fruits per plant gave positive and significant association with number of primary branches, number of female flower, fruit weight and number of fruits per plant. Female flower per plant showed highly significant positive correlations with number of primary branches, fruit yield and fruit per plant. Longer vine length increased the number of male flowers and produced heavier fruits.

Mondal *et al.* (1989) studied path co-efficient in 31 genotypes of watermelon and observed that the number of fruits per plant and fruit diameter affected fruit yield directly. Path co-efficient analysis revealed that for increasing fruit yield selection should be based on plant having more number of fruits with larger diameter.

Kumaran *et al.* (1998) carried out an experiment on correlation and path analysis studies in pumpkin. They found that positive and significant correlation of vine length, mean fruit weight, number of fruit per plant and number of seeds per fruit with fruit yield per plant. They also found that number of fruit per plant exhibited the highest direct effect on yield.

High positive indirect effects were exerted by number of fruit per plant and mean fruit weight.

Abusaleha and Dutta (1989) found that the yield of cucumber is positively correlated with vine length (r = 0.35), branches per vine (r = 0.29), fruits per vine (r = 0.48), fruit length (r = 0.60) and fruit girth (r = 0.43). Days to first male and female flowering, nodal position female flower, percentage of misshapen fruits and non-marketable yield were negatively correlated with yield. Path coefficient analysis revealed that fruits per vine and fruit length had the greatest direct effects on yield.

Prasad *et al.* (1988) in a study found that phenotypic and genotypic co-efficient of variation of water melon were high for fruit per plant, average fruit weight, seed per fruit, 100 seed weight and fruit yield per plant. They also reported that fruit yield was correlated with vine length (r = 0.47), branches per plant (r = 0.75), fruit weight (r = 0.88), length (r = 0.63) and girth (r = 0.61).

Vijay (1987) worked with nine agronomic characters of 95 diverse musk melon stocks and found that fruits per vine, flesh thickness and yield per vine showed the greatest genotypic co-efficient of variation. Heritability and genetic advance were high for fruit per vine, total soluble solids content, flesh thickness and yield per vine. Fruits per vine and fruit weight were positively correlated with yield.

Chadhury and Mandal (1987) conducted a study on 30 diverse cucumber genotypes and found high positive correlations at the genotypic and phenotypic levels between yield per plant with number of fruits and female flowers per plant, fruit length and weight. Path co-efficient analysis revealed that the above characters and fruit diameter were the most important characters determining yield.

According to Singh *et al.* (1986) fruits per plant, fruit length and yield showed high heritability and genetic advance in pointed gourd. According them, yield was positively and

significantly correlated with fruits per plant (r = 0.60) and days to flowering, days to fruit set and days to ripeness were negatively correlated with all the other characters with the exception of a positive correlation between days to flowering and fruit weight.

Reddy and Rao (1984) observed negative and non-significant correlation between these traits (r =0 0.222) in ribbed gourd. Patil (1988) reported that main vine length had positive and significant correlation with yield in cucumber.

2.3 Genetic diversity

Many workers stressed importance of genetic divergence in selection of parents for hybridization. According to Singh and Gupta (1968) the more diverse the parents, within a reasonable range the more would be the chance of improving the characters in question.

Ramachandran *et al.*, (1981) grouped 25 bitter gourd germplasm into 10 clusters based on their D^2 values. The inter-cluster distance value observed was maximum between cluster VI and VIII (8569.31) and the minimum was between cluster II and III (393.62). The co-efficient of variation estimated for different characters among the 10 clusters showed greater role for yield per plant (38.84), fruits per plant (25.68), female flowers per plant (19.82) and fruit length (19.05) in determining the inter-cluster distance. It was further observed that the character yield per plant, fruits per plant, female flowers per plant and fruit length contributed predominantly to divergence.

Karuppaiah *et al.* (2005) were evaluated genetic divergence in 12 genotypes of bitter gourd (*Momordica charantia*) grown in Annamalai, Tamil Nadu, India, during June-July 2001. Using Mahalanobis D^2 technique, the genotypes were grouped into clusters I (4 genotypes), II (one genotype), III (3 genotypes) and IV (four genotypes). Among the four clusters, cluster IV (LA-7, LA-9, LA-10 and LA-12) registered the highest mean values for vine length (6.2 m), number of male flowers per plant (79.3), number of female flowers per plant (23.2), yield per plant (5.2 kg), single fruit weight (242.2 g), fruit length (29.4 cm), number

of fruits per plant (24.1), number of seeds per fruit (52.3), fruit size index (173.2), and 100-seed weight (18.6 g). Hence, it is desirable to involve LA-7, LA-9, La-10 and LA-12 of cluster IV in breeding programmes.

Kadam and Kale (1987) observed highly significant difference between cultivars suggesting considerable divergence among 30 ridge gourd cultivars. The 30 cultivars were grouped into 20 clusters based on their D^2 values. Cluster A having two cultivars had the lowest intra-cluster D^2 values (8.22) while clusters I which has two cultivars had the highest intra-cluster value of 18.59. The highest inter-cluster distance was observed between clusters E and M (387.11) and it was minimum between cluster D and G (19.79).

Mathew *et al.* (1986) studied the genetic distance among five botanical varieties of *Couches melee*, viz., Couches melee. Variety cognomen (oriental pickling melon), *Cucumis melo* variety inodorus (musk melon), *Cucumis melo* var. flexusus (snake melon), *Cucumis melo* var. utilisimus (long melon) and *C. melo* var. momordica snap melon. The genetic distance was calculated considering four quantitative characters, node to first male flower, fruit weight, seeds per fruit and fruits per plant. Maximum genetic distance of 12.49 was observed between musk melon and snake melon. Long melon and snap melon were the closest ($D^2 = 0.38$). Musk melon and long melon were also placed distantly ($D^2 = 9.16$) followed by muskmelon and snap melon ($D^2 = 8.79$). Fruits per plant contributed maximum to total diversity (80.0%). Seeds per fruit did not contribute to total diversity. They found that selection of botanical varieties based on fruits per plant would be logical in selection of divergent parents.

Prasad *et al.* (1993) reported grouping of the lowest number of fruits per plant in one cluster having lower yield in cucumber. Based on the multivariate analysis the 26 genotypes of snake gourd were grouped into seven distinct clusters. No relationship was found between genetic divergence and geographic distribution of the genotypes (Banik, 2003).

Quamruzzaman *et al.* (2008) were studied the genetic divergence among thirty genotypes of ridge gourd (*Luffa acutangula*) using D^2 and principal component analysis. The genotypes were grouped into six clusters. The highest intra cluster distance was noticed for the cluster II (0.882) and the lowest for the cluster III (0.220). The highest inter-cluster distance was observed between cluster I and II (15.045) where as the lowest was observed between cluster IV and V (3.402).

Khan *et al.* (2008) were assessed the genetic diversity among 64 pointed gourd *genotypes* through multivariate analysis from an experiment conducted in Regional Agricultural Research Station, Ishurdi, Pabna during the growing season 2002-2003. The genotypes were grouped into twelve clusters. The cluster V consisted of highest number of genotypes and it was nine, the cluster VI and cluster VIII contained the lowest number of genotypes and it was two in each. The clustering pattern of the genotypes under this study revealed that the genotypes collected from the same location were grouped into different clusters. The genotypes of Jessore were distributed in different clusters. The highest inter genotype distance as 366.3 observed between the genotypes P0022 and P0007 and the lowest 2.6 as observed between the genotypes P0043 and P0044. Cluster V had the highest cluster mean value for internode length, fruit weight per plant and yield the highest inter-cluster distance was noticed between cluster III and II (45.71) and the lowest between cluster VII and VI (3.33). The highest intra cluster distance was computed for cluster III and that was lowest for the cluster II. The first five axes accounted for 77.65% of the total variation among the 13 characters describing 64 pointed gourd genotypes. Fruit weight, seeds per fruit and fruit weight per plant contributed maximum to the total divergence.

Sanwal *et al.* (2008) were evaluated thirty eight indigenous collections of chow-chow for eight quantitative and quality traits. High values of genotypic coefficient of variance along with high heritability and genetic advance were recorded for number of fruits/plant, fruit

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yield per plant, TSS, acidity and ascorbic acid. Number of fruits per plant and average fruit weight showed positive and significant correlation with fruit yield per plant. The number of fruit per plant and average fruit weight had high direct effect towards the fruit yield per plant. Hence, these characters should be given more emphasis while making selection for high yielding genotypes. On the basis of genetic divergence, relative magnitude of D^2 values thirty-eight genotypes were grouped into seven clusters. The maximum genetic divergence was observed between cluster III and VII followed by cluster II and VI. The cluster V and VI displayed lowest degree of divergence. The minimum intra-cluster distance was exhibited for cluster VI followed by cluster V. However, it was highest for cluster III. The mean values were higher in cluster I and IV for two characters i.e. fruit length and average fruit weight, while cluster II had high mean values for number of fruits/plant.

Masud *et al.* (2001) studied genetic divergence in 19 genotypes of sponge gourd (*Luffa cylindrica*) collected from local and exotic resources. The genotypes were grouped into five clusters. The genetic divergence of the genotypes did not follow their geographical distribution and was fairly at random. There was no evidence of close relationship between geographical distribution and genetic divergence as estimated by D^2 statistics. Maximum intercluster distance (45.9) was observed between cluster II and V and minimum (10.3) between cluster II and IV. Fruit length and diameter were significant contributors to genetic divergence.

Kabir (2007) reported that genetic divergence studied 24 accessions of pointed gourd. The accessions were grouped into five clusters. The cluster I and III had the highest number of accessions (6) followed by cluster V (5), cluster II (4) & Cluster IV (3). The highest intra cluster distance was computed for cluster IV (35.80) followed by cluster I (28.12) and Cluster V (26.63). The minimum intra cluster distance was found in III (18.87).

Hazra *et al.* (2003) reported that genetic divergence studied on 167 accessions of pointed gourd and grouped in eight non-overlapping clusters, with cluster IV comprising of the highest number of accessions (37 accessions) and cluster VI comprising of the lowest number of genotypes (6 accessions). Inter cluster distance ranged from 1.25 in cluster I to 1.65 in cluster VII. Cluster VIII and V were the most diverse as indicated by the maximum inter cluster distance between them (6.04).

Banik (2003) studied 26 genotypes of snake gourd were tested using multivariate analysis and the genotypes were grouped into seven distinct cluster. No relationship was found between genetic divergence and geographical distribution of genotypes. The highest inter genotypes distance was observed between genotypes SG 026 and SG 010 (1.897). The inter cluster distance was maximum between cluster II and IV (17.74). Main vine length, first female flower node number, nodes on main vine, fruit length and number of seeds per fruit had the highest contribution towards the divergence.

Harshawardhan and Ram (2003) conducted an experiment on severity germplasms of musk melon lines to elucidate genetic divergence using a non-hierarchical Euciden cluster analysis for yield and its components. The genotypes were grouped into 11 clusters irrespective of geographic and genetic diversity. Group VIII contained the largest number of 11 genotypes. The maximum genetic distance occurred between cluster II and X.

Dora *et al.* (2003) conducted an experiment on eleven genotypes of pointed gourd to find out genetic divergence following Mahalanobis's D^2 statistics. The eleven genotypes were grouped into four clusters. Cluster I and II comprised of four genotypes each, cluster III comprised of two genotypes and cluster IV comprised of only single genotype. Genetic draft and natural selection in different environment can cause high diversity among genotypes that is geographical isolation (Updhaya and Mutry, 1970).

Raseed *et al.* (2002) studied the genetic divergence of 47 pumpkin genotypes collected from different parts of Bangladesh using Mahalanobis's D^2 and principal component analyses. The genotypes were grouped into seven clusters. Cluster III had the maximum (11) and cluster IV and VII had the minimum number (4) of genotypes. The characters like fruit weight yield per plant contributed maximum towards total divergence.

More and Seshadri (2002) studied the genetic divergence in muskmelon. After evaluation, based on statistical analysis they classified 98 genotypes into 12 clusters. The crosses involving parent belonging to medium divergent cluster may also exhibit significant and positive heterosis (Miah and Bhal, 1989).

Dora *et al.* (2001) studied eleven genotypes of *Trihosanthes dioica* and the genotypes were grouped into four clusters based on Mahalanobis's D^2 statistics and found that inter cluster distances were greater than intra cluster distances, indicating considerable genetic diversity among genotypes. The highest D^2 value (984.3) was recorded between cluster II and IV.

Ram *et al.* (2001) performed cluster analysis in 167 pointed gourd genotypes (*Trihosanthes dioica*) collected from different ecogeographic region of India. On the basis of different yield contributing agro morphological traits, the genotypes were grouped into eight clusters which were non-overlapping. Cluster IV comprising the most number of genotypes (37 accessions) and cluster VI comprising the lowest number of genotypes (6 accessions). Intra cluster distance ranged from 1.258 in cluster I and 1.655 in cluster VII. Cluster VIII and V were the most diverse as indicated by maximum inter cluster distance between them (6.049). The results indicated the potential for wide scope of varietal improvement through hybridization and selection due to the wide genetic diversity present in the accession studied.

Principal component and grouping analyze of data on 31 plant morphological traits were used to estimate genetic divergence in 15 accessions of *Cucurbita* by Choer *et al.* (2000). It

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was observed that the accessions dispersed in a bidirectional space way, forming three groups, each on having two subgroups. Grouping analysis by the Ward method showed similar results to those obtained from principal component analysis. The traits that mostly contributed to genetic divergence were presence of thorns on the petiole internode number of the main vine up to the first female flower, fruit shape, fruit diameter, skin texture, predominant skin colour and number of days to the first male flower on the main vine.

Ramos *et al.* (2000) were evaluated the genetic diversity of 40 squash accessions collected from distinct areas of the Northeast region of Brazil. The data were analyzed using canonic variable and Tocher cluster analysis adopting Mahalanobis D^2 general distance. It was observed that 65% of the accessions were clustered in a group. The disperse results based on the first four canonic variables (71% of total variability) did not permit a correlation between genetic diversity and eco-geographical origin.

Rashid (2000) found that no relationship between geographic distribution and genetic diversity in pumpkin. The result suggested that geographic isolation is not the only factor causing genetic diversity and this point should be considered in selecting parents for hybridization. Varalaksmi *et al.* (1994) conducted an experiment with 48 genotypes of ridge gourd collected from different regions of India to analyze genetic divergence. Nineteen (19) quantitative characters were selected to study genetic divergence using Mahalanobis D^2 statistics and Tocher method to form cluster. The 58 genotypes were grouped into five clusters but, in general there was no association between geographical distance and genetic divergence. There was substantial variation in cluster means for whole plant sex ratio, fruit number per plant, fruit weight and yield per plant. The inter cluster D^2 value indicated that cluster III was most divergent from the other clusters.

Prasad *et al.* (1993) were evaluated 32 genotypes landraces of cucumber for 14 characters. Mahalanobis's D^2 analysis indicated considerable diversity among the genotypes that were grouped into 8 clusters independently of their geographical distribution.

Mathew *et al.* (1986) studied genetic distance among five botanical varieties of *Cucumis melo*. The genetic distance was calculated for nodes to first female flower, fruit weight, seeds per fruit and fruits per plant. Total D^2 was estimated according to Mahalanobis (1963). The magnitude of D^2 indicated closeness among the varieties. The character fruits per plant contributed maximum to total divergence (80%). Seeds per fruit did not contribute to the total divergence and concluded that selection of botanical varieties based on fruits per plant would be a logical step in the selection of divergence parents in crop improvement programme.

Sidhu and Gautam (1985) obtained higher inter cluster distance than cluster distance in watermelon and reported the low intra cluster and high inter cluster distance indicated that the population grouped were homozygous within and heterozygous between clusters.

Digby *et al.* (1989) reported that the coordinates obtained from the Principal Component Analysis (PCA) to calculate distances among the points. PCA is used for the graphical representation of the points while PCO is used to calculate the minimum distance straight line between each pair of points.

Chapter III
Materials and Methods

CHAPTER III

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., which are presented as follows:

3.1. Experimental site

The research work relating to determine the genetic diversity of bitter gourds was conducted at the Sher-e-Bangla Agricultural University Farm, Dhaka-1207 during April 2008 to September 2008.

3.2 Geographical Location

The experimental area was situated at 23°77'N latitude and 90°33'E longitude at an altitude of 8.6 meter above the sea level (Anon., 2004). The experimental field belongs to the Agro-ecological zone of "The Modhupur Tract", AEZ-28 (Anon., 1988a). This was a region of complex relief and soils developed over the Modhupur clay, where floodplain sediments buried the dissected edges of the Modhupur Tract leaving small hillocks of red soils as 'islands' surrounded by floodplain (Anon., 1988b). The experimental site was shown in the map of AEZ of Bangladesh in (Appendix I).

3.3 Climate

Area has subtropical climate, characterized by high temperature, high relative humidity and heavy rainfall in Kharif season (April-September) and scanty rainfall associated with moderately low temperature during the Rabi season (October-March). Meteorological

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information regarding temperature, relative humidity, rainfall and sunshine hours prevailed at the experimental site during the study period was presented in Appendix II.

3.4 Characteristics of soil

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. Soil samples from 0-15 cm depths were collected from experimental field. The analyses were done by Soil Resource and Development Institute (SRDI), Dhaka. Physicochemical properties of the soil are presented in (Appendix III).

3.5 Planting materials

Twenty genotypes of bitter gourd were used for the 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 Genetic Resources Centre (PGRC) of Bangladesh Agricultural Research Institute (BARI). Gazipur, Parar Bond of Meghna, Comilla, Siddiq Bazar, Dhaka (some are collected from Thailand), Agargaon local market, Agargaon, Dhaka. The name and origin of these genotypes are presented in (Table 1).

3.6 Design and layout of the experiment

The experiment was laid out Randomized Complete Block Design (RCBD) with three replications figure1. 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. Fig. 1 showing layout of the experimental plot.

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Table 1. Name and origin of twenty Bitter gourd genotypes used in the present study

Sl. No.	Genotypes No.	BARI ACC Number/Genotypes	Origin
1	G_1	Shaparan	Siddiq Bazar, Dhaka
2	G_2	TB/qt 01-05× 03-01	PGRC, BARI
3	G_3	Deshi	Parar Bond, Meghna, Comilla
4	G_4	TB (Q) 07-01× 08-03	PGRC, BARI
5	G_5	Rampali gaj	Siddiq Bazar, Dhaka
6	G_6	Bt (N) 04-07	PGRC, BARI
7	G_7	BARRI Karla-I	HRC, BARI
8	G_8	Sagarica	Siddiq Bazar, Dhaka, Collected from (Thailand)
9	G_9	Nabil	Siddiq Bazar, Dhaka
10	G_{10}	Bt (N) 05-11	PGRC, BARI
11	G_{11}	Bt (N) 05-10	PGRC, BARI
12	G_{12}	Nandita	Siddiq Bazar, Dhaka, Collected from (Thailand)
13	G_{13}	Bt (N) 04-12	PGRC, BARI
14	G_{14}	Eureka	Siddiq Bazar, Dhaka, Collected from (Thailand)
15	G_{15}	Bt (N) 05	PGRC, BARI
16	G_{16}	Tia	Agargaon local market, Agargaon, Dhaka
17	G_{17}	Hirak	Siddiq Bazar, Dhaka
18	G_{18}	TB (Q) 06-01× 07-02	PGRC, BARI
19	G_{19}	Maharaj	Agargaon local market, Agargaon, Dhaka
20	G_{20}	BT/qt 01-04×02-02	PGRC, BARI

Here, PGRC = Plant Genetic Resources Centre, BARI = Bangladesh Agricultural Research Institute, HRC = Horticultural Research Centre
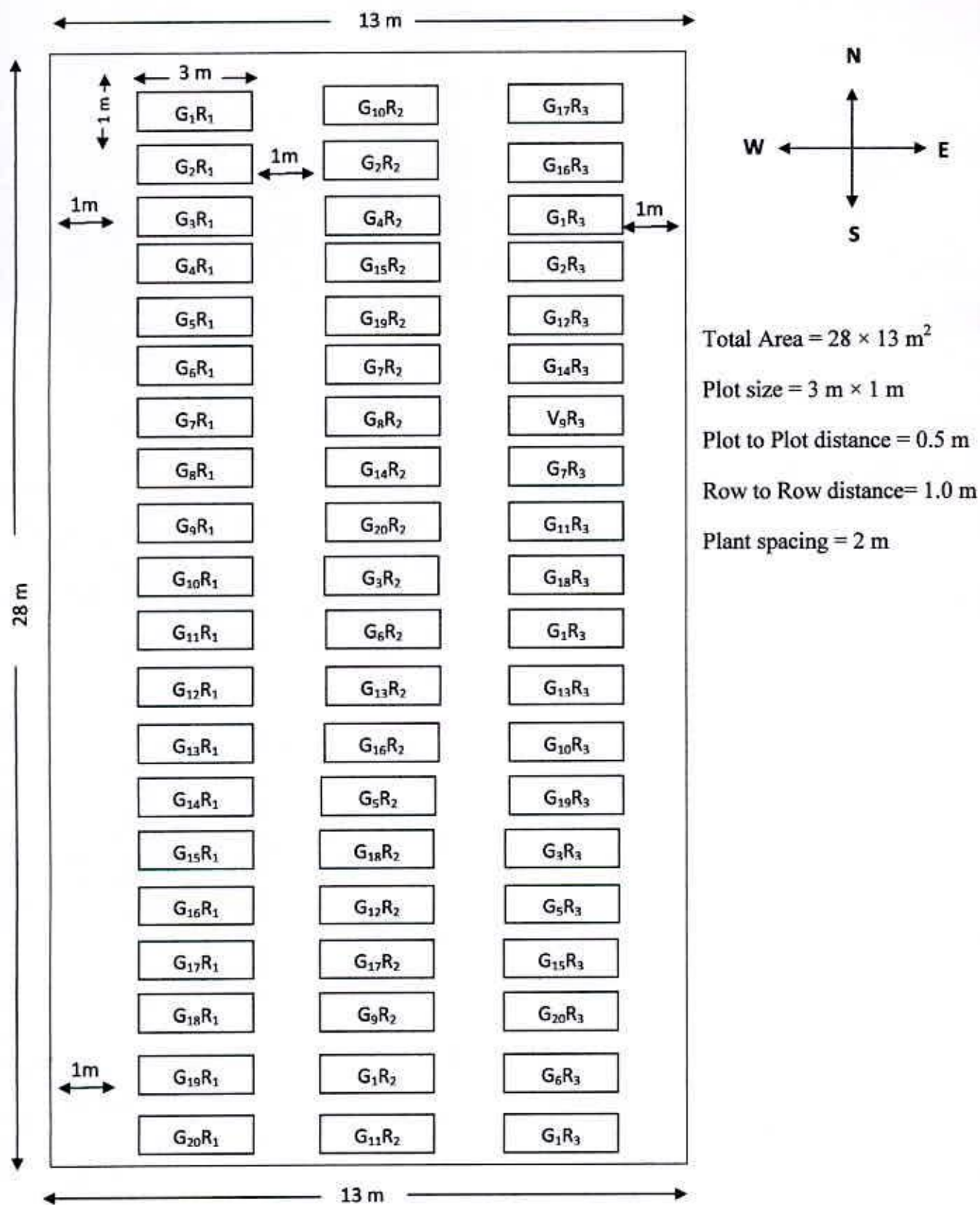
Fig.1. Layout of the experimental plot

3.7 Poly bag preparation and raising seedling

Due to uncertain rainfall during the period of the study, the seeds were dibbled in Poly bag for higher germination percentage and to get healthy seedlings and when the seedlings the seedlings become 25 days old; those were transplanted in the main field in the pit. Seeds were sown 17th. March, 2008, before sowing seeds were soaked in water for 24 hours and treated with Bavistin for 5 minutes.

3.8 Land preparation

The experiment plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about good tilth in the middle week of February 2008. Weeds and other stables were removed carefully from the experimental plot and leveled properly.

3.9 Pit preparation

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 × 1.25 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.

3.10 Manure and fertilizers application

The following doses of manure and fertilizers were applied to the plots for bitter 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. (Table 2) showing dose of manure and fertilizers used in the study.

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Table 2. Dose of manure and fertilizers used in the study

Sl. No.	Fertilizer/Manure	Dose
1.	Cowdung	10 ton/ha
2.	Urea	150 kg/ha
3.	TSP	100 kg/ha
4.	MOP	150 kg/ha
5.	Gypsum	80 kg/ha
6.	Zinc Oxide	8 kg/ha

3.11 Transplanting of seedlings

Germination of seeds was completed within 12 days and the seedlings of different accessions were planted in the pit on 12th. April, 2008. In each pit two seedlings were planted and the soil around the plant was firmly pressed by hand.

3.12 Intercultural operations

The following intercultural operations were done from time to time throughout the cropping season for proper growth and development of the plants.

3.12.1 Thinning and gap filling

Only one healthy seedling was kept per pit for the proper development and avoid crowd environment. For this whatever its need thinning and gap filling was done.

3.12.2 Weeding and mulching

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.

3.12.3 Irrigation and after-care

In the early stage irrigation was done twice daily by water cane. In mature stage flood irrigation was done when ever it's necessary.

Plate 1a: Field view of the experiment

Plate 1b: Field view of the experiment
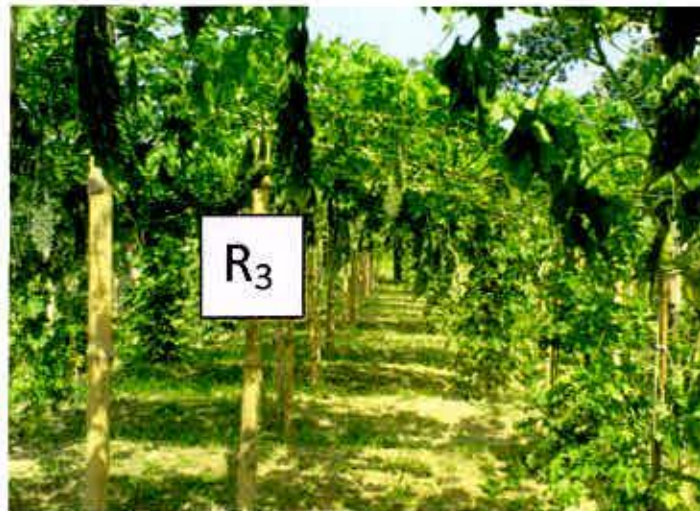
Plate 1c: Field view of the experiment

3.12.4 Pesticide application

At the seedling stage red pumpkin beetle attacked tender leaves and also after the initial stage they attacked plants several times for this Malathion 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 bait was used along with ripcord, sevin powder. The field view of the experiment shown in Plate 1a, Plate 1b and 1c.

3.13 Harvesting

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. Fruits were picked with sharp knife and care was taken to avoid injury of the vine.

3.14 Data recording

Data were recorded on following parameters from the studied plants during the experiment. The details of data recording are given below on individual plant basis.

3.14.1 Days to first male flowering

The number of days required for first male flower flowering was counted for three replication separately and average data was recorded.

3.14.2 Days to first female flowering

The number of days required for first female flower flowering was recorded for three replication separately and average data was recorded.

3.14.3 Vine length (m)

Vine length measured in meter in main vine and average data was recorded.

3.14.4 Number of nodes per vine

The number of nodes per vine was counted and average data was recorded.

3.14.5 Branches per vine

Branches per vine per vine were counted and average data was recorded.

3.14.6 Fruit length (cm)

Fruit length was measured in 3-5 fruits of different plants in cm and average data was recorded during fruit harvest for vegetable use.

3.14.7 Fruit diameter (cm)

Fruit diameter was measured in 3-5 fruits of different plants in cm and average data was recorded during fruit harvest for vegetable use.

3.14.8 Number of fruit per plant

The number of fruit per plant was counted and average data was recorded.

3.14.9 Weight per fruit (g)

Weight of 3-5 fruits of different plants during harvest for vegetable use was measured in gram (g).

3.14.10 Yield per plant (kg)

Weight of edible fruit fruits of selected plants from each accession was weighted in kilogram (kg).

3.15.1 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 2000 software through four techniques viz.,

Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA).

3.15.1.1 Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.* (1955).

Genotypic variance (σ^2_g) $= \dfrac{GMS - EMS}{r}$

Where,

GMS = Genotypic mean sum of squares

EMS = Error mean sum of square

r = number of replications

Phenotypic variance (σ^2_{ph}) $= \sigma^2_g + EMS$

Where,

σ^2_g = Genotypic variance

EMS = Error mean sum of square

3.15.1.2 Estimation of genotypic and phenotypic correlation co-efficient

For calculating the genotypic and phenotypic correlation co-efficient for all possible combinations the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956) were adopted.

The genotypic co-variance component between two traits and have the phenotypic co-variance component were derived in the same way as for the corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows:

Genotypic correlation (r_{gxy}) $= \dfrac{\sigma_{gxy}}{\sqrt{(\sigma^2_{gx} \cdot \sigma^2_{gy})}}$

Where,

σ_{gxy} = Genotypic co-variance between the traits x and y

σ^2_{gx} = Genotypic variance of the trait x

σ^2_{gy} = Genotypic variance of the trait y

Phenotypic correlation (r_{pxy}) = $\dfrac{\sigma_{pxy}}{\sqrt{(\sigma^2_{px} \cdot \sigma^2_{py})}}$

Where,

σ_{pxy} = Phenotypic covariance between the traits x and y

σ^2_{px} = Phenotypic variance of the trait x

σ^2_{py} = Phenotypic variance of the trait y

3.15.1.3 Estimation of genotypic and phenotypic co-efficient of variation

Genotypic and phenotypic co-efficient of variation were calculated by the formula suggested by Burton (1952)

Genotypic co-efficient of variation (GCV %) = $\sqrt{\dfrac{\sigma^2_g}{x}} \times 100$

Where,

σ^2_g = Genotypic variance

$\bar{x}$ = Population mean

Similarly,

The phenotypic co-efficient of variation was calculated from the following formula.

Phenotypic co-efficient variation (PCV) = $\sqrt{\dfrac{\sigma^2_{ph}}{x}} \times 100$

Where,

σ^2_{ph} = Phenotypic variance

$\bar{x}$ = Population mean

3.15.1.4 Estimation of heritability

Broad sense heritability was estimated (Lush, 1943) by the following formula, suggested by Johnson *et al.* (1955).

$$h^2{}_b\% = \frac{\sigma^2{}_g}{\sigma^2{}_{ph}} \times 100$$

Where,

$h^2{}_b$ = Heritability in broad sense

$\sigma^2{}_g$ = Genotypic variance

$\sigma^2{}_{ph}$ = Phenotypic variance

3.15.1.5 Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1943) and Johnson *et al.* (1955).

Genetic advance (GA) = K. $h^2{}_b$. σ_{ph}

$$GA = K. \frac{\sigma^2{}_g}{\sigma^2{}_{ph}}. \sigma_{ph}$$

Where,

K = Selection intensity, the value which

is 2.06 at 5% selection intensity

σ_{ph} = Phenotypic standard deviation

$h^2{}_b$ = Heritability in broad sense

$\sigma^2{}_g$ = Genotypic variance

$\sigma^2{}_{ph}$ = Phenotypic variance

3.15.1.6 Estimation of genetic advance mean's percentage

Genetic advance as percentage of mean was calculated from the following formula as proposed by Comstock and Robinson (1952):

$$\text{Genetic advance (\% of mean)} = \frac{\text{Genetic Advance (GA)}}{\text{Population mean } (\bar{x})} \times 100$$

3.15.2 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:

3.15.2.1 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.

3.15.2.2 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).

3.15.2.3 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.

3.15.2.4 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.

3.15.2.5 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

$$D^2 = \sum_i^x d_i^2 = \sum_i^x (Y_i^j - Y_j^k) \qquad (j \neq k)$$

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.

3.15.2.6 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 populations in cluster.

3.15.2.7 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 ombinations of the populations in cluster i and j.

n_i = Number of populations in cluster i.

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$$n_j = \text{Number of populations in cluster } j.$$

3.15.2.8 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.

3.15.2.9 Selection of varieties for future hybridization programme

Divergence analysis is usually performed to identify the diverse genotypes for hybridization purposes. The genotypes grouped together are less divergent among themselves than those, which fall into different clusters. Clusters separated by largest statistical distance (D^2) express the maximum divergence among the genotypes included into these different clusters. Variety (s) or line(s) were selected for efficient hybridization programme according to Singh and Chuadhury (1985). According to them the following points should be considered while selecting genotypes for hybridization programme:

i.   Choice of cluster from which genotypes are selected for use as parent (s)

ii. Selection of particular genotype(s) from the selected cluster(s)

iii. Relative contribution of the characters to the total divergence

iv. Other important characters of the genotypes performance

Chapter IV
Results and Discussion

CHAPTER IV

RESULTS 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:

1. Genetic parameters

2. Correlation co-efficient

3. Path co-efficient analysis

4. Multivariate analysis

4.1 GENETIC PARAMETERS

The analysis of variance indicated the existence of highly significant variability for all the characters studied. The mean sum of square, mean, range, variance components, coefficients of genotypic and phenotypic variations, heritability estimates, genetic advance and genetic advance in percent of mean (GAPM) are presented in (Table 3). The results are discussed character wise as follows:

4.1.1 Days to first male flowering

Mean sum of square for days to first male flowering was highly significant (Table 3) indicating existence of considerable difference for this trait. The maximum days to first male flowering was found 57.33 and the minimum was recorded 48.67 with mean value 52.00 (Appendix IV). The genotypic variance (28.190), phenotypic variance (29.518), genotypic co-efficient of variation (3.910) and phenotypic co-efficient of variation (4.001) were close to each other indicating less environmental influence in case of days

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Table 3. Estimation of genetic parameters of 20 Bitter gourd genotypes

Genetic Parameters→	MSG	MSE	Grand mean	σ^2g	σ^2p	GCV	PCV	ECV	h^2_b	GA	GAPM	mspg	mspe	CV%
Days to first male flowering	13.26**	2.48	52.00	28.190	29.518	3.910	4.001	3.026	95.503	7.871	15.137	58.16	1.01	3.03
Days to first female flowering	21.04**	3.49	61.00	27.333	29.756	3.163	3.300	3.033	91.858	6.245	10.138	-190.04	1.48	3.03
Vine length (m)	0.54**	0.08	3.78	225.17	250.01	11.89	12.53	7.396	90.065	23.245	615.59	-6.91	0.86	7.39
No. of nodes/vine	52.67**	2.86	84.91	36.291	66.832	11.66	15.82	1.990	54.303	17.696	20.841	-44.39	2.44	1.99
Branches/vine	24.40**	2.88	40.01	30.287	58.046	17.41	24.11	4.243	52.178	25.912	64.764	-20.90	0.13	4.24
Fruit length (cm)	20.93**	0.490	18.51	5.012	7.039	8.629	10.23	3.782	71.196	14.999	81.032	-7.97	-0.47	3.78
Fruit diameter (cm)	1.27**	0.43	10.00	2.795	3.592	16.46	18.66	6.197	77.828	29.911	281.383	-4.89	-0.39	6.20
No. of fruit/plant	591.91**	25.80	34.48	2.499	3.216	16.10	18.26	14.732	77.708	29.231	80.777	-74.10	-0.20	14.73
Weight/fruit (g)	1337.81**	2.57	103.60	118.26	376.73	9.616	17.16	1.548	31.390	11.099	10.713	1.60	-0.04	1.55
Yield/plant (Kg)	3.72**	0.02	2.72	0.152	0.180	16.53	17.98	1.334	84.503	31.296	1149.32	0.04	0.02	4.66

Here, ** indicates significant at 1% level of significance, MSG = Mean sum of squares due to genotypes, MSE = Mean sum of squares due to error, σ^2e = Environmental variance, σ^2g = Genotypic variance, σ^2p = Phenotypic variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, ECV = Environmental coefficient of variation, h^2_b = Heritability, GA = Genetic advance, GAPM = Genetic Advance in Percentage of Mean, mspg = Mean sum of product due to genotype, mspe = Mean sum of porduct due to error

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to first male flowering (Table 3). Heritability estimates for this trait was very high (95.503) but genetic advance (7.871) and genetic advance in percent of mean (15.137) was found low, indicated that selection for this character would be less effective. Singh et al. (2002) also found phenotypic co-efficient of variation higher than genotypic co-efficient of variation in respect to days to first male flower opening. Emaduddin (2008) found similar results in case of days to first male flowering.

4.1.2 Days to first female flowering

Mean sum of square for days to first female flowering was highly significant (Table 3) indicating existence of considerable difference for this trait. The maximum days to first female flowering was found 66.00 and the minimum was recorded 56.67 with mean value 61.60 (Appendix IV). The genotypic variance (27.333), phenotypic variance (29.756), genotypic co-efficient of variation (3.163) and phenotypic co-efficient of variation (3.300) were close to each other indicating less environmental influence in case of days to first female flowering. Heritability (91.858) estimates for this trait was very high but genetic advance (6.245) was found low and genetic advance in percent of mean (10.138) was found moderately low, indicated that selection for this character would be less effective. The results significant with the findings of Guffar (2008).

4.1.3 Vine length (m)

Mean sum of square for vine length (m) was highly significant (Table 3) indicating existence of considerable difference for this trait. The maximum vine length (m) was found 4.500 and the minimum was recorded 3.13 with mean value 3.776 (Appendix IV). The genotypic variance (225.174), phenotypic variance (250.013), genotypic co-efficient of variation (11.890) and phenotypic co-efficient of variation (12.529) were close to each other indicating less environmental influence in case of vine length. Heritability (90.065) estimates for this trait were moderate together with considerable moderate genetic

advance 23.245) and moderately high genetic advance in percent of mean (615.59) indicated that selection for this character would be more effective. Banik (2003) also found significant difference in snake gourd.

4.1.4 Number of nodes per vine

Mean sum of square for number of nodes per vine was highly significant (Table 3) indicating existence of considerable variability for this trait. The maximum number of nodes per vine was found 92.20 and the minimum was recorded 72.03 with mean value 84.91 (Appendix IV). The genotypic variance (36.291), phenotypic variance (66.832), genotypic co-efficient of variation (11.657) and phenotypic co-efficient of variation (15.891) were close to each other indicating less environmental influence in case of number of nodes per vine. Heritability (54.303) estimates for this trait was very high genetic advance (17.696) and genetic advance in percent mean (20.841) was also found high, indicated that selection for this character would be more effective. Mathew and Khader (1999) reported high heritability (98.24%) for number of seeds per fruit in snake gourd. Plate 2a and Plate 2b showing twig, male flower, female flower and fruit of different bitter gourd genotypes $(G_1 - G_{20})$.

4.1.5 Branches per vine

Mean sum of square for branches per vine was highly significant (Table 3) indicating existence of considerable difference for this trait. The maximum branches per vine were found 45.47 and the minimum was recorded 36.27 with mean value 40.10 (Appendix IV). The genotypic variance (30.287), phenotypic variance (58.046), genotypic co-efficient of variation (17.413) and phenotypic co-efficient of variation (24.107) were close to each other indicating less environmental influence in case of branches per vine. Heritability (52.178) estimates for this trait was moderate together with considerable moderate genetic
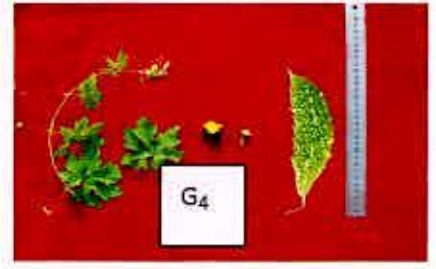
Plate 2a. Showing twig, male and female flower, fruit of different Bitter gourd genotypes (G₁-G₁₀)

Plate 2b. Showing twig, male and female flower, fruit of different Bitter gourd genotypes (G_{11}- G_{20})

advance (25.912) and genetic advance in percent of mean (64.764) indicated that selection for this character would be effective. Banik (2003) also found significant difference in snake gourd.

4.1.6 Fruit length (cm)

Mean sum of square for fruit length was highly significant due to genotypes in Bitter gourd (Table 3) indicating existence of considerable difference for this trait. The maximum fruit length was found 23.12 and the minimum was recorded 13.58 with mean value 18.51 (Appendix IV). The genotypic variance (5.012), phenotypic variance (7.039), genotypic co-efficient of variation (8.629) and phenotypic co-efficient of variation (10.227) were close to each other indicating less environmental influence in case of fruit length. Heritability (71.196) estimates for this trait was moderately high, genotypic advance (14.99) and genotypic advance in percent of mean (81.032) was found moderately high, indicated that selection for this character would be effective. Roy *et al.* (1993) found similar results in bitter gourd. Miah *et al.* (2000) reported the highest genotypic as well as phenotypic co-efficient of variations for fruit length in bitter gourd. Photograph showing variation of fruits among different genotypes of Bitter gourd in Plate 3a and Plate 3b.

4.1.7 Fruit diameter (cm)

Mean sum of square fruit diameter was highly significant due to genotypes in Bitter gourd (Table 3) indicating existence of considerable variation for this trait. The maximum fruit diameter was found 11.48 and the minimum was recorded 8.97 with mean value 10.63 (Appendix IV). The genotypic variance (2.795), phenotypic variance (3.592), the genotypic co-efficient of variation (16.459) and phenotypic co-efficient of variation (18.657) were close to each other indicating less environmental influence in case of fruit diameter. Heritability (77.828) estimates for this trait was high, genetic advance (29.911) was found moderately high and genetic advance in percent of mean (281.383) was found
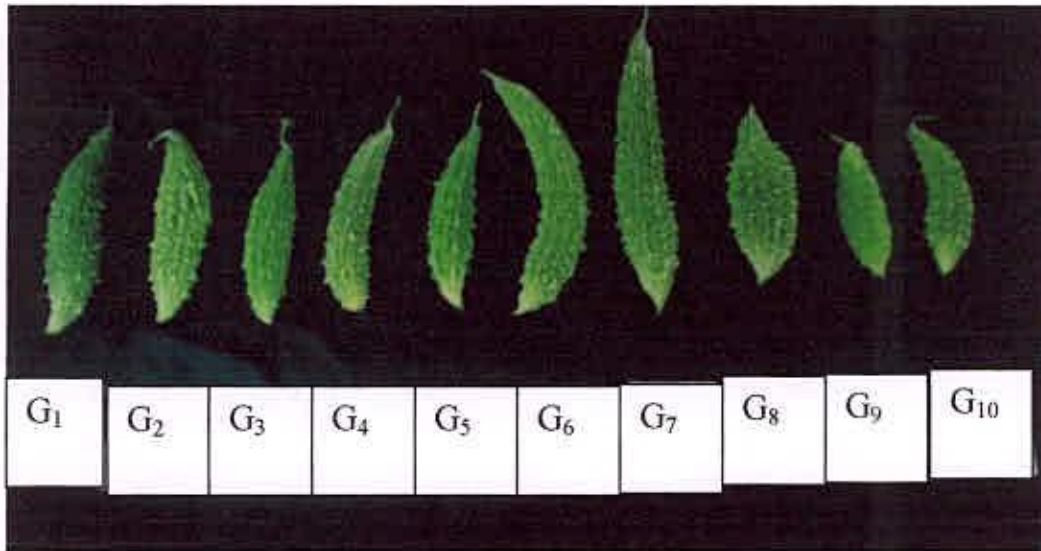
Plate 3a. Photograph showing variation in fruits among different genotypes of Bitter gourd
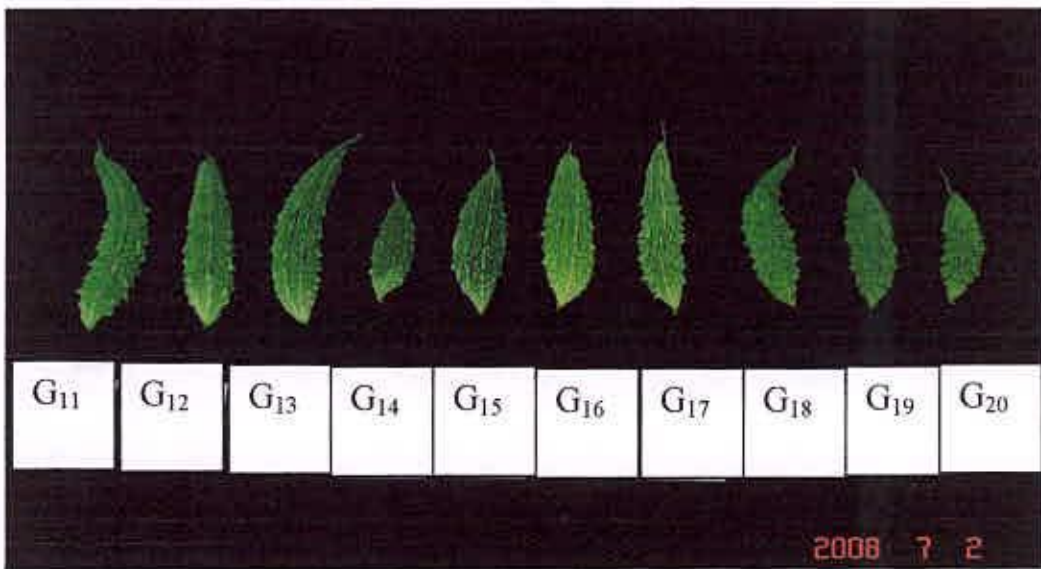
Plate 3b. Photograph showing variation in fruits among different genotypes of Bitter gourd

very high, indicated that selection for this character would be more effective.

4.1.8 Number of fruit per plant

Mean sum of square for number of fruit per plant was highly significant in Bitter gourd (Table 3) indicating existence of considerable variability for this trait. The maximum number of fruit per plant was found 62.33 and the minimum was recorded 14.00 with mean value 34.48 (Appendix IV). The genotypic variance (2.499), phenotypic variance (3.216), genotypic co-efficient of variation (16.097) and phenotypic co-efficient of variation (18.260) were close to each other indicating less environmental influence in case of no. of fruit per plant. Heritability (77.708) estimates for this trait was high, genetic advance (29.231) was found moderate and genetic advance in percent of mean (80.777) was found moderately high, indicated that selection for this character would be effective. Roy et al. (1993) found similar results in bitter gourd. Sanwal et al. (2008), Prasad et al. (1988) also reported in related to number of fruits per plant in chow-chow and water melon respectively.

4.1.9 Weight per fruit (g)

Mean sum of square for weight per fruit was highly significant in Bitter gourd (Table 3) indicating existence of considerable difference for this trait. The maximum weight per fruit was found 141.1 and the minimum was recorded 67.5 with mean value (Appendix IV). 103.6. The genotypic variance (118.258), phenotypic variance (376.734), genotypic co-efficient of variation (9.616) and phenotypic co-efficient of variation (17.163) were close to each other indicating less environmental influence in case of weight per fruit. Heritability (31.390) estimates for this trait was low together with considerable high, genetic advance (11.099) and genetic advance in percent of mean (10.713) indicated that selection for this character would be less effective. Chowdhury and Sharma (2002), Rumaran et al. (1997) also reported in respect to average fruit weight in ridge gourd and pumpkin, respectively.

4.1.10 Yield per plant (kg)

Mean sum of square for yield per plant (kg) was highly significant in Bitter gourd (Table 3) indicating existence of considerable difference for this trait. The maximum yield per plant was found 5.160 kg and the minimum was recorded 1.310 kg with mean value 2.723 kg (Appendix IV). The genotypic variance (0.152), phenotypic variance (0.180), genotypic co-efficient of variation (16.526) and phenotypic co-efficient of variation (17.978) were close to each other indicating less environmental influence in case of yield per plant. The heritability value (84.503) as well as genetic advance (31.296) and genetic advance in percent of mean (1149.321) were observed very high. The very high heritability with moderate genetic advance in percentage of mean provided opportunity for selecting high valued genotypes for breeding programme. This finding also supported Abusaleha and Dutta (1990) findings in cucumber.

4.2 CORRELATION CO-EFFICIENT

Yield is a complex product being influenced by several interdependent quantitative characters. Selection for yield may not be effective unless the other yield components influencing it directly or indirectly are taken into consideration. When selection pressure is exercised for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated traits. Hence knowledge regarding association of character with yield and among themselves provides guideline to the plant breeder for making improvement through selection provide a clear understanding about the contribution in respect of establishing the association by genetic and non genetic factors. Higher genotypic correlations than phenotypic one might be due to modifying or masking effect of environment in the expression of the character under study (Nandpuri *et al.* 1973). The results are discussed under the following heads:

Results of genotypic and phenotypic correlation co-efficient of different genotypes yield and its contributing traits of bitter gourd are shown in Table 4 and discussed characterwise as follows:

4.2.1 Days to first male flowering

Days to first male flowering found to display highly significant positive relationships with days to first female flowering and branches per vine at genotypic level and highly significant positive relationships with days to first female flowering at phenotypic level (Table 4). Highly significant positive association between days to first male flowering and days to first female flowering indicates that the traits are governed by same gene, pleiotropic effect and simultaneous improvement would be effective. The character reflected highly significant negative association with vine length and fruit length both at genotypic and phenotypic level and highly significant negative association with weight per fruit at phenotypic level. It appeared from the results that increasing days to first male flowering caused the plant to produce lesser vine length and fruit length. This character also showed insignificant positive correlation with yield per plant both levels. It also showed insignificant negative correlation with no. of nodes per vine, fruit diameter and no. of fruit per plant both at genotypic and phenotypic level and branches per vine and weight per fruit at phenotypic level. Khan *et al.* (2008) reported almost similar result in 64 genotypes of pointed gourd.

4.2.2 Days to first female flowering

The character reflected highly significant positive relationship with no. of nodes per vine and branches per vine at genotypic level. Highly significant positive association between days to first female flowering and branches per vine indicates that the traits are governed by same gene by pleiotropic effect and simultaneous improvement would be effective (Table 4). The character reflected highly significant negative association with fruit length and

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Table 4. Genotypic and phenotypic correlation co-efficient among ten characters

Parameters		Days to first female flowering	Vine length (m)	No. of nodes/vine	Branches /vine	Fruit length (cm)	Fruit diameter (cm)	No. of fruit/plant	Weight/fruit (g)	Yield/plant (Kg)
Days to first male flowering	G_v	0.686**	-0.801**	-0.081	0.534**	-0.590**	-0.282	-0.179	-0.427**	0.264
	P_v	0.677**	-0.726**	-0.039	-0.318	-0.477**	-0.288	-0.194	-0.235	0.220
Days to first female flowering	G_v		-0.181	0.219**	0.526**	-0.613**	-0.230	-0.164	-0.805**	0.006
	P_v		-0.158	0.134	-0.344*	-0.472**	-0.203	-0.153	-0.475**	-0.019
Vine length (m)	G_v			0.603**	0.015	0.401**	0.027	-0.093	-0.182	-0.084
	P_v			0.364*	0.114	0.333	0.029	-0.041	-0.044	-0.111
No. of nodes per vine	G_v				-0.559**	0.503**	-0.848**	-0.875**	-0.017	0.854**
	P_v				-0.251	0.367*	-0.640**	-0.692**	0.091	0.588**
Branches per vine	G_v					0.225	0.224	0.208	0.724**	-0.293
	P_v					0.343*	0.213	0.236	0.463**	-0.251
Fruit length (cm)	G_v						-0.258	-0.292	0.660**	0.496**
	P_v						-0.157	-0.162	0.597**	0.495**
Fruit diameter(cm)	G_v							0.987**	-0.540**	0.930**
	P_v							0.968**	-0.172	-0.764**
No. of fruit per plant	G_v								-0.620**	0.877**
	P_v								-0.162	-0.713**
Weight/fruit (g)	I_G									0.374*
	P_v									0.383

* indicates significant at 5% level of significance, ** indicates significant at 1% level of significance, I_G = genotypic variance, P_v – phenotypic variance

weight per fruit at both levels and significant negative association with branches per vine at phenotypic level. It appeared from the results that increasing days to first female flowering caused the plants to produce highest fruit length and higher weight per fruit. The character reflected significant positive association with no. of nodes per vine at phenotypic level and yield per plant at genotypic level. It also showed insignificant negative correlation with vine length, fruit length and no. of nodes per vine both at genotypic and phenotypic level and insignificant negative association with yield per plant at phenotypic level. Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Islam (1993) in bottle gourd, Rahman *et al.* (1990, 1991) also found significant variation for days to first flowering. Plate 4 showing phenotypic variation in flower (female) among different genotypes of Bitter gourd.

4.2.3 Vine length (m)

The character showed highly significant positive relationship with no. of nodes per vine and fruit length at genotypic level and significant positive correlation with no. of nodes per vine at phenotypic level (Table 4). It appeared from the results that increasing vine length caused the plants to increase number of nodes per vine and fruit length. The character showed insignificant positive relationships with branches per vine and fruit diameter at both levels and fruit length at phenotypic level. It also showed insignificant negative correlation number of fruit per plant, weight per fruit and yield per plant both at genotypic and phenotypic level. Insignificant association of these traits indicated that the association among these traits is largely influenced by environmental factors.

4.2.4 Number of nodes per vine

Number of nodes per vine showed highly significant positive correlation with fruit length at genotypic level and yield per plant at both the levels and significant at phenotypic level for fruit length (Table 4). This result revealed that with increasing the number of nodes per

Plate 4. Showing phenotypic variation in flower (female) among different genotypes of bitter gourd

vine fruit length and yield per plant. This character also showed highly significant negative association with fruit diameter and no. of fruit per plant both at genotypic and phenotypic level. This character showed insignificant positive correlation with weight per fruit at phenotypic level and insignificant negative association with branches per vine at phenotypic level and weight per fruit at genotypic level. This result implies that the interrelationship between these traits was governed by environment. Guffar (2008) also found significant result for number of nodes per vine.

4.2.5 Branches per vine

The character, showed highly significant positive correlation with weight per fruit both at genotypic and phenotypic level and significant positive correlation with fruit length at phenotypic level (Table 4). Highly significant positive association between branches per vine and weight per fruit indicates that the traits are governed by additive gene effect and simultaneous improvement would be effective. It also showed insignificant positive correlation with fruit diameter and no. of fruit per plant both at genotypic and phenotypic level and fruit length at genotypic level insignificant negative correlation with yield per plant both at genotypic and phenotypic level. Emaduddin (2008) reported similar result for branches per vine in ridge gourd.

4.2.6 Fruit length (cm)

Fruit length showed highly significant positive correlation with weight per fruit and yield per plant both at genotypic and phenotypic level (Table 4). Highly significant positive association between fruit length and yield per plant indicates that the traits are governed by same gene by pleiotropic effect and simultaneous improvement would be effective. This result revealed that with increase fruit length would have increase yield per plant. It also showed insignificant negative correlation with fruit diameter and no. of fruit per plant both at genotypic and phenotypic level. Insignificant association indicated that the association

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between these traits is largely influenced by environmental factors. Miah *et al.* (2000) reported the highest genotypic as well as phenotypic coefficient of variations for fruit length in bitter gourd.

. 4.2.7 Fruit diameter (cm)

Fruit diameter showed highly significant positive association with no. of fruit per plant at both levels. This result revealed that with increase fruit diameter would have increase no. of fruit per plant (Table 4). It also showed highly significant negative correlation with weight per fruit at genotypic level and yield per plant at phenotypic level. Insignificant negative correlation was observed weight per fruit at phenotypic level. Insignificant association indicated that the association between these traits is largely influenced by environmental factors.

4.2.8 Number of fruit per plant

Number of fruit per plant showed highly significant positive correlation with yield per plant at genotypic level (Table 4). This result revealed that with more number of fruit per plant would have increase yield per plant. It also showed that highly significant negative correlation with weight per fruit at genotypic level and yield per plant at phenotypic level. It also showed that insignificant negative correlation with weight per fruit at phenotypic level.

4.2.9 Weight per fruit (g)

The trait, weight per fruit showed significant positive correlation with yield per plant at genotypic level and insignificant positive association with yield per plant at phenotypic level indicated that the association between these two traits is largely influenced by environmental factors (Table 4). Chowdhury and Sharma (2002), Rumaran *et al.* (1997) also reported in respect to average fruit weight in ridge gourd and pumpkin respectively.

4.3 PATH CO-EFFICIENT ANALYSIS

Partitioning of genotypic correlation of different genotype, yield and its contributing traits in bitter gourd are shown in Table 5 and discussed characterwise as follows:

4.3.1 Days to first male flowering

Days to first male flowering showed the positive direct effect on yield (0.044) (Table 5). Days to first male flowering showed maximum positive indirect effect through fruit length (1.042) followed by branches per vine (0.133), fruit diameter (0.039), weight per fruit (0.015) and yield per plant (0.264). The negative indirect effect of this character on yield via days to first female flowering, (-0.778) was the highest followed by no. of nodes per vine (-0.047) and no. of fruit per plant which finally made insignificant positive correlation between days to first male flowering and yield per plant (0.264).

4.3.2 Days to first female flowering

Days to first female flowering showed negative direct effect on yield (-1.134) (Table 5). This character, however, showed positive indirect effect through days to first female flowering, (0.030), no. of nodes per vine (0.128), branches per vine (0.131), fruit length (1.084), fruit diameter (0.265), weight per fruit (0.029) and yield per plant (0.006). This character also showed negative indirect effect via vine length (-0.205), and number of fruit per plant (-0.294) was contributed to result totally insignificant positive genotypic correlation with yield per plant. This discrepancy with present finding might be due to environmental variation.

4.3.3 Vine length (m)

Vine length showed positively direct effect on yield (1.134) (Table 5). This character, however, showed positive indirect effect through days to first female flowering (0.205), number of nodes per vine (0.351) and weight per fruit (0.006). The negative indirect effect via days to first male flowering (-0.035) followed by branches per vine (-0.004), fruit

Table 5. Direct (bold) and indirect effect of 20 Bitter gourd genotypes

Parameters	Days to first male flowering	Days to first female flowering	Vine length (m)	No. of nodes/ vine	Branches per vine	Fruit length (cm)	Fruit diameter (cm)	No. of fruit per plant	Weight per fruit (g)	Yield per plant (Kg)
Days to first male flowering	**0.044**	-0.778	-0.909	-0.047	0.133	1.042	0.326	-0.320	0.015	0.264
Days to first female flowering	0.030	**-1.134**	-0.205	0.128	0.131	1.084	0.265	-0.294	0.029	0.006
Vine length (m)	-0.035	0.205	**1.134**	0.351	-0.004	-0.708	-0.031	-0.166	0.006	-0.084
No. of nodes/vine	-0.004	-0.248	0.683	**0.583**	0.139	-0.890	0.980	-1.566	0.001	0.854**
Branches/vine	-0.024	0.597	0.017	-0.326	**-0.249**	-0.398	-0.259	0.372	-0.026	-0.293
Fruit length (cm)	-0.026	0.695	0.455	0.294	-0.056	**-1.767**	0.299	-0.522	-0.023	0.496**
Fruit diameter (cm)	-0.012	0.260	0.030	-0.494	-0.056	0.457	**-1.156**	1.766	0.019	-0.930**
No. of fruit/plant	-0.008	0.186	-0.105	-0.510	-0.052	0.516	-1.141	**1.789**	0.022	-0.877**
Weight/fruit (g)	-0.019	0.912	-0.206	-0.010	-0.180	-1.166	0.624	-1.109	**-0.035**	0.374*

* indicates significant at 5% level of significance, ** indicates significant at 1% level of significance, Residual effect, R = 0.5952

length (-0.708), fruit diameter (-0.031) and no of fruit per plant (-0.166) was contributed to result insignificant negative genotypic correlation with yield per plant (-0.084).

4.3.4 Number of nodes per vine

A positive direct effect was observed for vine length on yield (0.583) (Table 5). The indirect effect via vine length (0.683), branches per vine (0.139), fruit diameter (0.980) and weight per fruit (0.001) was found to be positive. The negative high indirect effect via days to first male flowering (-0.004) followed by days to first female flowering (-0.248), fruit length (-0.890) and no. of fruit per plant (-1.566) was contributed to result totally highly significant positive genotypic correlation with yield per plant (0.854). Figure 2 showing Path diagram of yield and its contributing traits in different genotypes of Bitter gourd.

4.3.5 Branches per vine

Branches per vine showed the negative direct effect on yield (-0.249) (Table 5). This character showed positive indirect effect through days to first female flowering (0.597) followed by vine length (0.017) and no. of fruit per plant (0.372). But the negative indirect effect through days to first male flowering (-0.024), no. of nodes per vine (-0.326), fruit length (-0.398) fruit diameter (0.259) and weight per fruit (-0.026) finally made insignificant negative correlation between branches per vine and yield per plant (-0.293).

4.3.6 Fruit length (cm)

Fruit length showed negatively direct effect on yield (-1.767) (Table 5). This character, however, showed positive indirect effect through days to first female flowering (0.695), vine length (0.455), fruit diameter (0.299) and no. of nodes per vine (0.294). The negative indirect effect via days to first male flowering (-0.026) followed by branches per vine (-0.056), number of fruit per plant (-0.522) and weight per fruit (-0.023) was contributed to result highly significant positive genotypic correlation with yield per plant (0.496).

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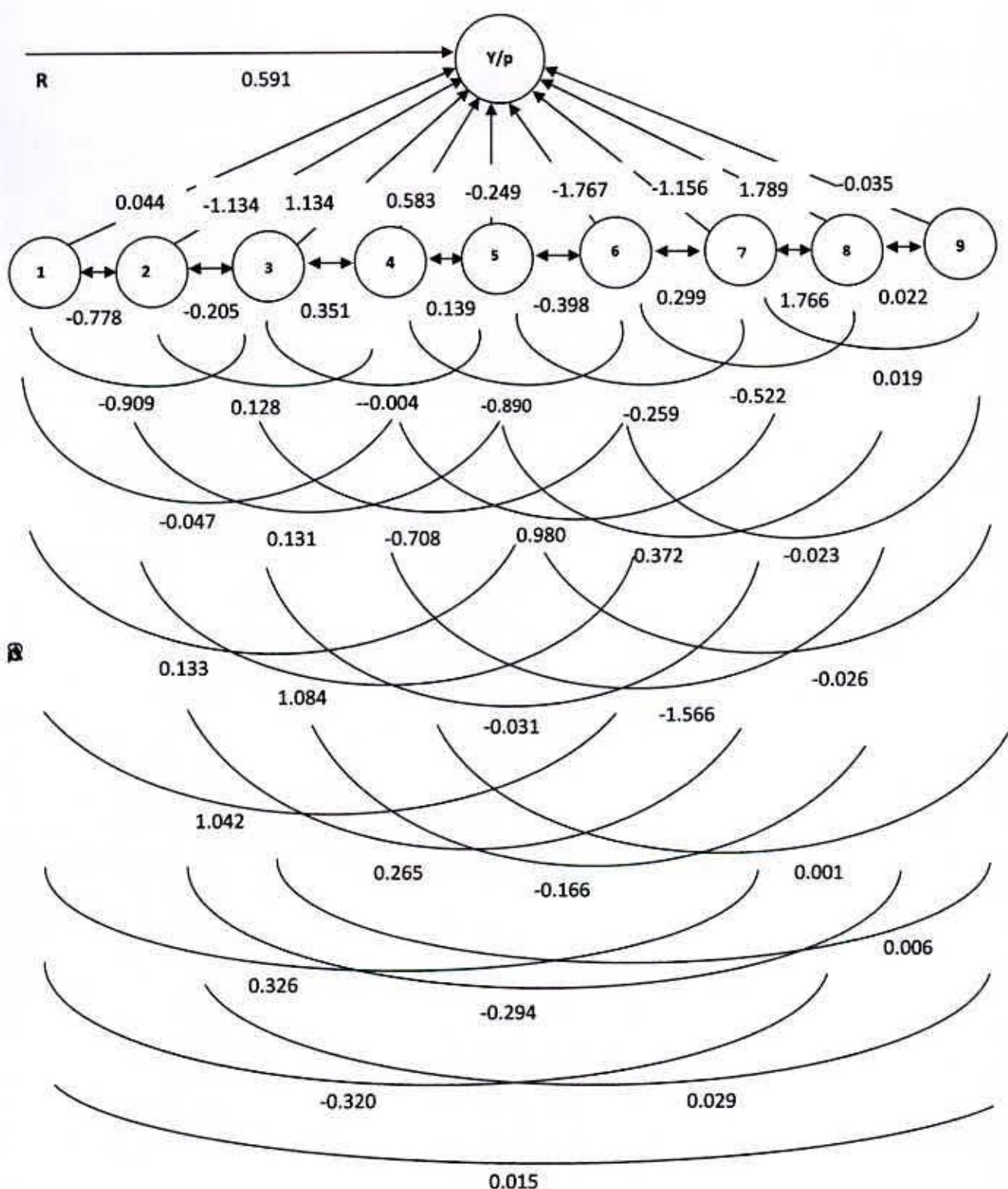
Fig. 2 Path diagram of yield and yield contributing characters in different genotypes of Bitter gourd

1= Days to first male flowering, 2 = Days to first female flowering, 3 = Vine length, 4 = No. of nodes per vine, 5 = Branches per vine, 6 = Fruit length, 7 = Fruit diameter, 8 = No. of fruit per plant, 9 = Weight per fruit, Y/p = Yield per plant. R = Residual effect=0.591

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4.3.7 Fruit diameter (cm)

Fruit diameter showed negatively direct effect on yield (-1.156) (Table 5). This character, however, showed positive indirect effect through days to first female flowering (0.260), vine length (0.030), fruit length (0.457), no. of fruit per plant (1.766) and weight per fruit (0.019). The negative indirect effect via days to first male flowering (-0.012) followed by no. of nodes per vine (-0.494) and branches per vine (-0.056) was contributed to result highly significant negative genotypic correlation with yield per plant (-0.930).

4.3.8 Number of fruit per plant

No. of fruit per plant had the highest positive direct effect on yield (1.789) (Table 5). The indirect effect via days to first male flowering (-0.008) followed by vine length (-0.510), branches per vine (-0.052), and fruit diameter (-1.141) was observed to be negative. But the direct effect of this trait and the positive indirect effect via days to first female flowering (0.186) followed by fruit length (0.516) and weight per fruit (0.022). The balanced total association negative and highly significant with yield per plant (-0.877). So direct selection based on this traits would be effective to increase the yield of this crop.

4.3.9 Weight per fruit (g)

Weight per fruit had the negative direct effect on yield (-0.035) (Table 5). This character also showed negative indirect effect through days to first male flowering (-0.019), vine length (-0.206 m), number of nodes per vine (-0.010), branches per vine (-0.180), fruit length (-1.166) and no. of fruit per plant (-1.109). But positive indirect effect through days to first female flowering (0.912), and fruit diameter (0.624) contributed to result significant positive genotypic correlation with grain yield per plant (0.374). Yield per plant would be significantly increased by direct selection of genotypes based on these traits.

4.4 MULTIVARIATE ANALYSIS

4.4.1 Principal component analysis (PCA)

Principal component analysis was carried out with 20 genotypes of bitter gourd. First 3 Eigen values for 3 principal coordination axes of genotypes accounted for 74.92% variation (Table 6). A two dimensional scattered diagram Fig. 3 was developed on the basis of the principal component score, Z_1 and Z_2 score (Appendices V) of two principal coordinates axes I and II Fig. 4.

4.4.2 Principal coordinates analysis (PCO)

The results obtained from principal coordinate analysis showed that the highest inter genotypic distance was observed between genotypes Bt (N) 05-11and Maharaj (1.7760) followed by Nabil and Bt (N) 05-11 (1.7442) and the lowest distance was observed (0.2238) between genotypes Bt (N) 04-07and Nabil followed by the distance (0.2332) between genotypes Nabil and Maharaj (Table 7). The difference between the highest and the lowest inter genotypic distance indicated the moderate variability among the 20 genotypes of bitter gourd. The highest intra-cluster distance was recorded in cluster I (0.490) containing three genotypes {TB/qt 01-05× 03-01, TB (Q) 07-01× 08-03, BARRI Karla-I, Sagarica, Bt (N) 05-11, Bt (N) 05-10, Bt (N) 05, Hirak, TB (Q) 06-01× 07-02 and BT/qt 01-04×02-02} The lowest intra-cluster distance was observed in cluster III (0.265) having one genotype viz. {Deshi, Bt (N) 04-07, Nandita and Bt (N) 04-12}. It favored to decide that intra-group diversity was the highest in cluster I and the lowest in cluster III. Cluster II having four genotypes viz. Rampali gaj, Nabil, Eureca and Maharaj and had an intra-cluster distance 0.337. Cluster IV having two genotypes viz. Shaparan and Tia and had an intra-cluster distance 0.312 (Table 8 and 10).

Table 6. Eigen values and percentage of variation for corresponding 10 component characters in 20 genotypes of Bitter gourd

Principal component axis	Eigen values	% of total variation accounted for	Cumulative percent
Days to First Flowering male	4.0645	36.95	36.95
Days to First Flowering female	2.2906	20.82	57.77
Vine length (m)	1.8866	17.15	74.92
No. of nodes/vine	0.9229	8.39	83.31
Branches/vine	0.5816	5.29	88.6
Fruit length (cm)	0.5315	4.83	93.43
Fruit diameter (cm)	0.3032	2.76	96.19
No. of fruit/ plant	0.2153	1.96	98.15
Weight/fruit (gm)	0.1401	1.27	99.42
Yield/ plant (kg)	0.0455	0.41	99.83

Table 7. Ten highest and ten lowest inter genotypic distance among the 20 genotypes of Bitter gourd

Sl. No.	Genotypic combination	Distances
A. 10 highest inter genotypic distance		
01.	G_{10} - G_{19}	1.7760
02.	G_9 - G_{10}	1.7442
03.	G_5 - G_{10}	1.6190
04.	G_{10} - G_{14}	1.4368
05.	G_4 – G_9	1.4299
06.	G_9 - G_{17}	1.4293
07.	G_1 - G_{10}	1.4281
08.	G_{17} - G_{19}	1.4247
09.	G_4 - G_{19}	1.3712
10.	G_8 – G_9	1.3613
B. 10 lowest inter genotypic distance		
01.	G_6 - G_{13}	0.2238
02.	G_9 - G_{19}	0.2332
03.	G_{12} - G_{13}	0.2365
04.	G_7 – G_{20}	0.2386
05.	G_6 - G_{12}	0.2422
06.	G_6 - G_{19}	0.2486
07.	G_{17} – G_{18}	0.2609
08.	G_{18} – G_{20}	0.2659
09.	G_{15} – G_{17}	0.2782
10.	G_3 - G_{13}	0.2958

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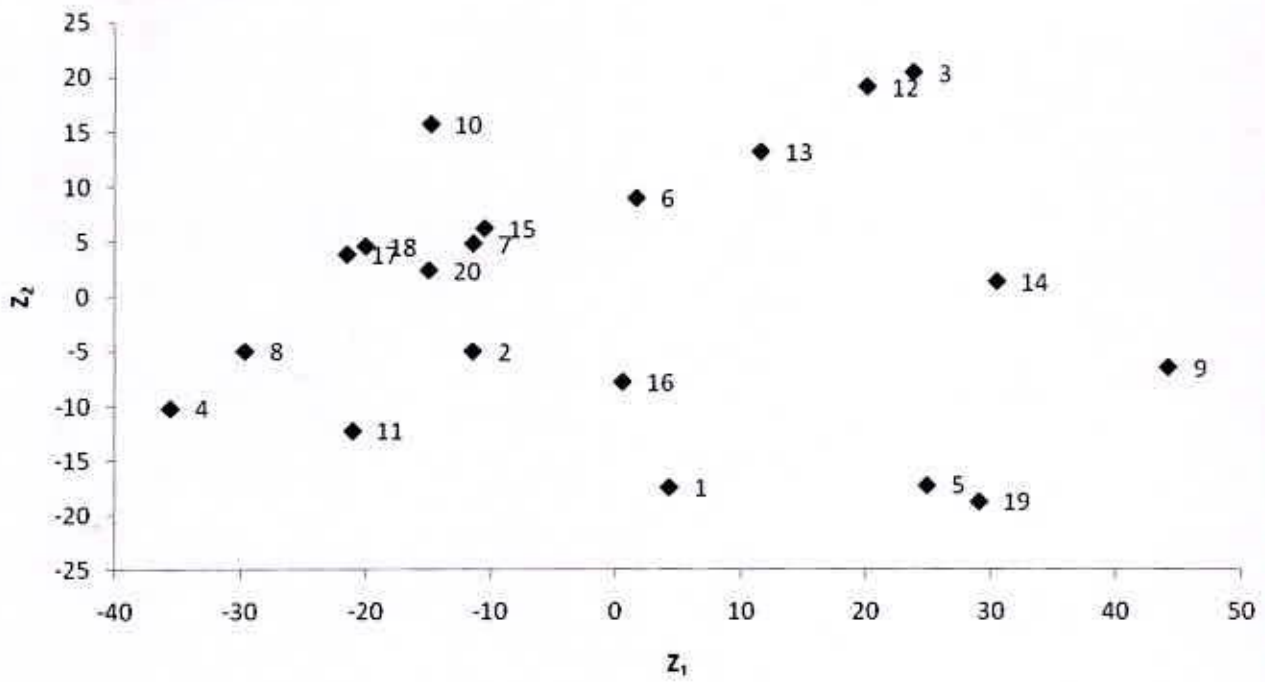
Fig. 3 Scatter diagram of 20 genotypes of bitter gourd based on their principal component scores
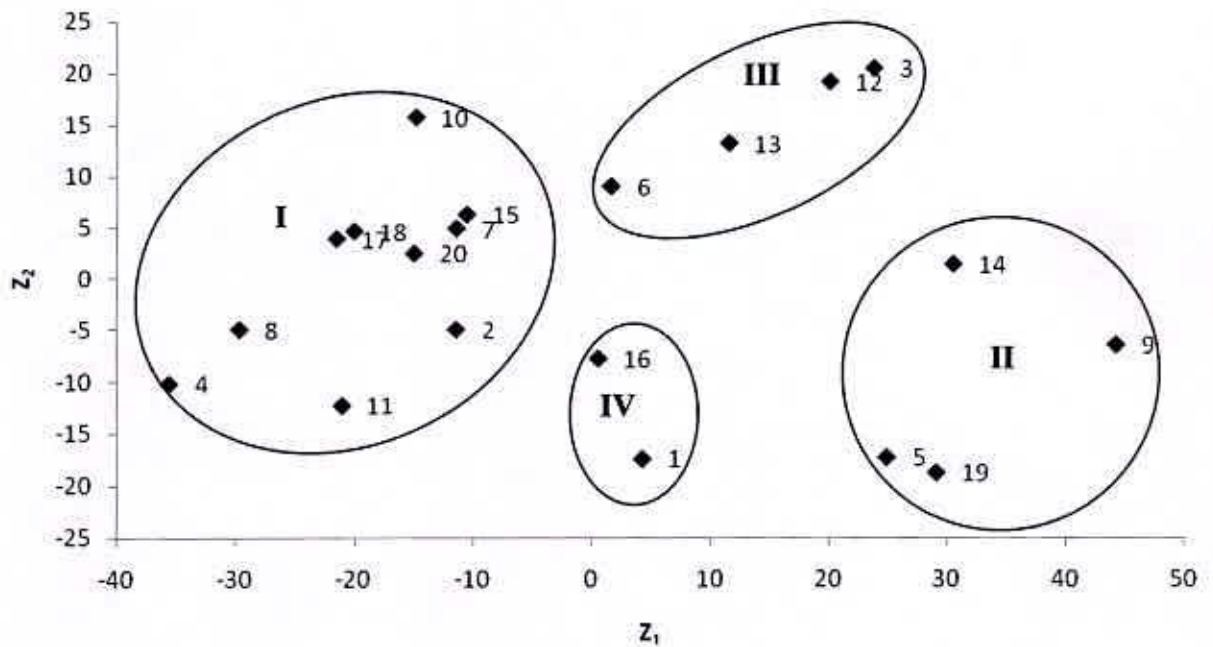
Fig. 4 Scatter distribution of 20 genotypes of bitter gourd based on their principal component scores superimposed with clusters

4.4.3 Non-hierarchical clustering

The computations from covariance matrix gave non-hierarchical clustering among 20 genotypes of bitter gourd and grouped them into four clusters. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. So the results obtained through PCA were confirmed by non-hierarchical clustering. Table 8 represents the clusters occupied by 20 genotypes of bitter gourd. It explains that's cluster I contained the highest number of genotypes ten, cluster IV constitute by two genotypes, cluster II constitute by four genotypes and cluster III constitute by four genotype. Cluster I was composed of {TB/qt 01-05× 03-01, TB (Q) 07-01× 08-03, BARI Karla-I, Sagarica, Bt (N) 05-11, Bt (N) 05-10, Bt (N) 05, Hirak, TB (Q) 06-01× 07-02 and BT/qt 01-04×02-02}. Among the genotypes of cluster I {TB/qt 01-05× 03-01, TB (Q) 07-01× 08-03, Bt (N) 05-11, Bt (N) 05-10, Bt (N) 05, TB (Q) 06-01× 07-02 and BT/qt 01-04×02-02} are collected from Plant Genetic Resource Centre, BARI, Gazipur. Cluster mean for 10 traits are presented in (Table 9). Cluster II was formed by four genotypes viz. Rampali gaj, Nabil, Eureca and Maharaj. Among them Rampali gaj and Nabil were collected from Siddiq Bazar, Gulistan, Dhaka, and Eureca was collected from Siddiq Bazar, Dhaka, (Collected from Thailand) and Maharaj was collected from Agargaon local market, Agargaon, Dhaka. These clusters were able to lead in respect of the highest cluster mean value for maximum characters. Among 10 characters this cluster stood first for six characters viz. vine length (4.35 m), no. of nodes per vine (89.58) , branches per vine (43.26) , no. of fruit per plant (56.17), weight per fruit (128.87 gm) and yield per plant (4.61 kg). Genotypes Deshi, Bt (N) 04-07, Nandita and Bt (N) 04-12 established cluster III. Among them Deshi genotype of this cluster are collected from Parar Bond, Meghna, Comilla and Bt (N) 04-07 and Bt (N) 04-12 are collected from Plant Genetic Resources Centre, Bangladesh Agricultural Research

Table 8. Distribution of 20 bitter gourd genotypes in four clusters

Cluster	Number of members	Bitter gourd genotypes
I	10	TB/qt 01-05× 03-01, TB (Q) 07-01× 08-03, BARRI Karla-I, Sagarica, Bt (N) 05-11, Bt (N) 05-10, Bt (N) 05, Hirak, TB (Q) 06-01× 07-02, BT/qt 01-04×02-02
II	4	Rampali gaj, Nabil, Eureca, Maharaj
III	4	Deshi, Bt (N) 04-07, Nandita, Bt (N) 04-12
IV	2	Shaparan, Tia

Table 9. Cluster mean for 10 characters of 20 Bitter gourd genotypes

Parameters	I	II	III	IV
Days to first male flowering	51.37	51.67	52.92	54
Days to first female flowering	60.93	61.17	62.5	64
Vine length (m)	3.56	4.35	3.56	4.15
No. of nodes per vine	85.24	89.58	80.74	82.25
Branches per vine	39.26	43.26	39.67	37.94
Fruit length (cm)	16.79	20.59	20.73	18.51
Fruit diameter (cm)	10.45	10.68	11.19	10.32
No. of fruit per plant	26.2	56.17	26.83	47.84
Weight per fruit (g)	86.5	128.87	122.64	100.5
Yield per plant (kg)	2	4.61	2.4	3.21

Table 10. Average intra (bold) and inter cluster distances (D^2) for 20 Bitter gourd genotypes

Cluster	I	II	III	IV
I	**0.490**			
II	11.413	**0.337**		
III	6.517	10.719	**0.265**	
IV	7.101	4.510	8.354	**0.312**

Institute, Gazipur and Nandita was collected from Siddiq Bazar, Dhaka, (Collected from Thailand). The highest cluster mean value was achieved for two characters viz. fruit length (20.73) and fruit diameter (11.19). Cluster IV had two genotypes named Shaparan and Tia between them Shaparan was collected from Siddiq Bazar, Dhaka and Tia was collected from Agargaon local market, Agargaon, Dhaka. The highest cluster mean value was achieved for two characters viz. days to first male flowering (54) and days to first female flowering (64).

4.4.4 Canonical variate analysis

The highest inter-cluster distance was observed (Table 10 or Figure 5) between cluster I and II (11.413). The intra cluster distance was the highest (0. 490) in cluster I. The lowest inter-cluster distance was observed between cluster II and IV (4.510) followed by cluster I and III (6.517). Moderate or intermediate distance was found between cluster II and III (10.719), cluster III and IV (8.354). The inter cluster distances were higher than the intra cluster distances suggesting wider genetic diversity among the genotype of different groups.

No parallel relationship was found between genetic and geographic divergence, which may be due to continuous exchange of germplasm from one place to another. Differently originated genotypes found in same cluster or genotypes from same origin were dispersed in different clusters. It was observed that group I formed with ten genotypes originated in Bangladesh and Bangladesh and group II occupied by four genotypes originated from Bangladesh and Thailand origin and group III occupied by four genotypes originated from Bangladesh and Thailand origin group IV occupied by two genotypes originated from Bangladesh origin. Genotypes from Thailand and Bangladesh being in different clusters, indicating the broad genetic variability. There was evidence from Shanmugam and Rangasamy (1982) showed that materials from same origin distributed in different clusters are an indication of broad genetic base of the genotypes belonging to that origin.
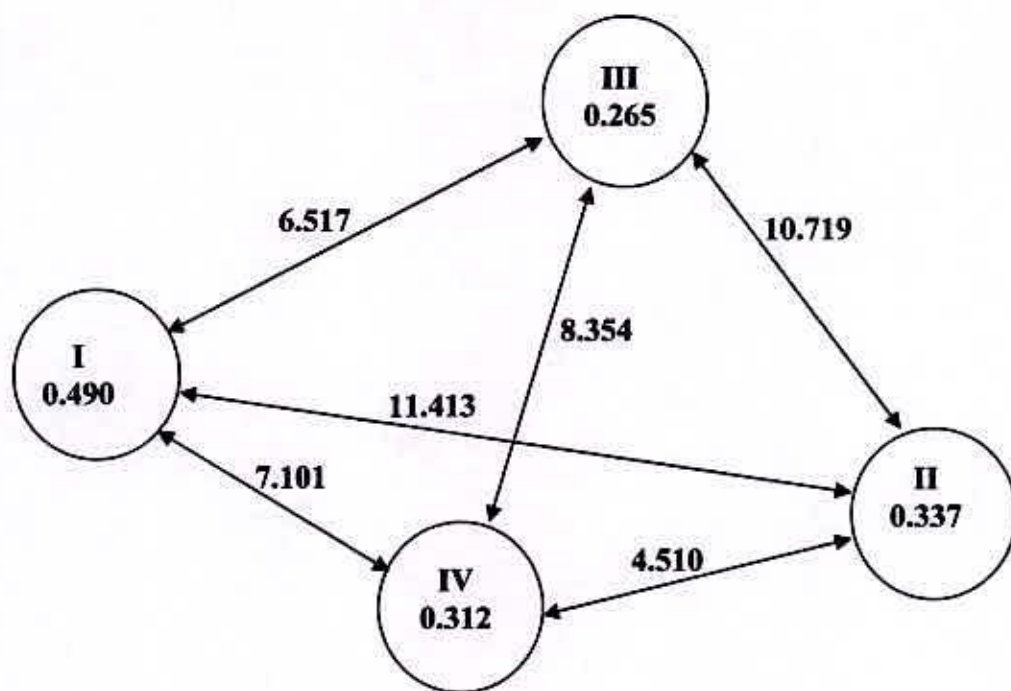
Fig. 5 Diagram showing intra and inter-cluster distances of 20 genotypes of Bitter gourd

4.4.5 Contribution of characters towards divergence of the genotypes

The values of Vector I and Vector II are presented in Table 11. Vector I obtained from PCA expressed that days to first male flowering (0.451), branches per vine (0.509), no. of fruit per plant (0.271) and yield per plant (1.568) were major characters that contribute to the genetic divergence. It was the reflection of first axis of differentiation. In vector II days to first male flowering (0.932) vine length (5.857), no. of nodes per vine (0.143), fruit length (0.407) and no. of fruit per plant (0.199) showed their important role toward genetic divergence. Vector I shows positive value for days to first male flowering, branches per vine and yield per plant and incase of Vector II vine length and no. of nodes per vine, fruit length and no. of fruits per plant. Negative values in both vectors for days to first female flowering, fruit diameter and weight per fruit had lower contribution towards the divergence.

Table 11. Latent vectors for 10 principal component characters of 20 genotypes of Bitter gourd

Characters	Vector1	Vector2
Days to first male flowering	0.451	-0.932
Days to first female flowering	-0.045	-0.275
Vine length (m)	-5.009	5.857
No. of nodes/vine	-0.268	0.143
Branches/vine	0.509	-0.430
Fruit length (cm)	-0.211	0.407
Fruit diameter (cm)	-0.717	-0.461
No. of fruit/ plant	-0.271	0.199
Weight/fruit (gm)	-0.080	-0.155
Yield/ plant (kg)	1.568	-1.942

4.4.6 Selection of genotypes as parent for hybridization programme.

Among the inter cluster distance, distance between I and II (11.413) were the highest and other clusters were more or less intermediate distance. Inter mediate diverse parents have the more chance to contribute heterosis in the subsequent generations.

To select cluster to obtain more heterotic genotype four pairs of clusters to be considered for this purpose, they are I and II, II and III, III and IV, IV and I. Cluster II had the highest cluster mean for vine length, no. of nodes per vine, branches per vine, no. of fruit per plant, weight per fruit and yield per plant, but average to below average for days to first male and female flowering were most important yield contributing character. The cluster II comprised with the genotype Rampali gaj, Nabil, Eureca and Maharaj. Hybridization between the genotypes of cluster II and cluster IV will manifest maximum heterosis and create wide genetic variability.

Genetically distant parents are usually able to produce higher heterosis. Considering magnitude of genetic distance, contribution of different characters towards the total divergence, magnitude of cluster means for different characters and field performance the genotypes G_{19}, G_9, G_{14} G_5 from cluster II and G_1, G_{16} from cluster IV would be suitable for highest yield per plant for future hybridization programme.

It assumed that highest heterosis would be manifest in cross combination involving the genotypes belonging to divergent clusters. However for a practical plant breeder, the objective was not only high heterosis but also to achieve high level of production. Therefore, considering group distance and the agronomic performance, the inter genotypic crosses between G_1 & G_3; G_1 & G_5; G_1 & G_9; G_1 & G_{14}; G_9 & G_{14}; G_9 & G_{16}; G_9 & G_{19}; G_{14} & G_{19}; G_{14} & G_{16} and G_{16} & G_{19} might be suitable choice for future hybridization programme.

Chapter V
Summary and Conclusion

CHAPTER V

SUMMARY AND CONCLUSION

The present experiment was carried out in the Farm of Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka-1207, Bangladesh to evaluate the field performance, variability, character association, genetic divergence and characterization of twenty bitter gourd genotypes using morphological characters.

The field experiment was laid out in Randomized Complete Block Design (RCBD) with three (3) replications. Data on different characters were recorded and analyzed statistically. The analysis of variance of all the traits was computed and significant differences were found among the accessions in respect of different characters studied. The maximum value in respect of days to first male flowering (57.33 days) was observed in G_1 and minimum days (48.67 days) to first male bud were recorded in G_{15}. Genotype number G_1 recorded the maximum value (66 days) days to first female flowering and lowest days to first female flowering (56.67 days) was recorded in G_{20}. In respect of vine length, genotype no. G_9 recorded the highest value (4.500) and genotype no. G_{15} counted the lowest value (3.130). Genotype no. G_5 is the highest number of nodes per (92.20) vine and genotype no. G_3 is the lowest number of nodes per (72.03) vines were counted. In case of branches per vine, the highest value (45.47cm) was recorded in G_5 and the lowest value was (36.27cm) recorded in G_{13}. In respect of fruit length, longest fruit (23.12 cm) was observed in G_9 and the genotype no. G_4 had the smallest length of (13.54 cm). In case of fruit diameter, the highest value (11.48 cm) was observed in G_{15} and the lowest value (8.97) was observed in G_2. Genotype no. G_{19} is the highest number of fruit per plant (62.33) and genotype no. G_{10} is the lowest number of nodes per (14.00) vines were counted. In case of average weight per

fruit, the highest value (141.1 gm) was observed in G_9 and the lowest value (67.5 gm) was observed in G_4. The highest average yield per plant (5.160 kg) was in G_{19} and the lowest yield per plant (1.31 kg) was recorded in G_{10}.

The phenotypic variance was higher than the corresponding genotypic variance in all the characters, indicating greater influence of environment on the expression of these characters. The maximum differences between phenotypic and genotypic coefficient of variation were 24.107% and 17.413% respectively which indicated that the average branches per vine mostly depended on environmental effect. The highest estimated heritability among ten yield contributing characters 95.503%, 91.858%, 90.065% and 84.503% was in days to first male flowering, days to first female flowering, vine length and yield per plant. The lowest heritability was 31.390% in weight per fruit.

The maximum genetic advance was observed in respect of yield per plant (31.296) and followed by maximum value was 29.911 in respect of genetic advance for average fruit diameter among ten characters of bitter gourd genotypes. The maximum genetic advance in percent of mean (GAMP) was obtained for yield per plant (1149.321%) and the lowest was for days to first female flowering (10.138%).

Multivariate analysis was carried out through principal component analysis (PCA), principal coordinate analysis (PCO), cluster analysis, and canonical vector analysis (CVA) using Genstat 5.13 software programme. As per as PCA, D^2 and cluster analysis using the genotypes were grouped into four different clusters. Cluster I, II, III and IV comprised 10, 4, 4, and 2 genotypes, respectively.

The maximum cluster distance was observed between cluster I and II (11.413) followed by the distance between clusters II and III (10.719), III and IV (8.354), I and IV (7.101). The

lowest inter-cluster distance was observed between cluster II and IV (4.510) followed by I and III (6.517).

The highest intra-cluster distance was identified in cluster I (0.490) and the lowest intra-cluster distance was observed in cluster III (0.265). Genotypes included in cluster III were suitable for fruit length (20.73 cm) and fruit diameter (11.19 cm), both in cluster I & II and II & III. Cluster IV had the highest mean for days to first male flowering (54 days) and days to first female flowering (64 days).

Findings of the present study indicated significant variation among the genotypes for all the character studied. Considering diversity pattern and other field performances, the genotypes G_5, G_9, G_{14}, and G_{19} from cluster II and cluster III comprises of G_{12} and G_1 and G_{16} from cluster IV could be best choice as suitable parents for efficient hybridization programme. The inter genotypic crosses between G_1 & G_3; G_1 & G_5; G_1 & G_9; G_1 & G_{14}; G_9 & G_{14}; G_9 & G_{16}; G_9 & G_{19}; G_{14} & G_{19}; G_{14} & G_{16} and G_{16} & G_{19} might be suitable choice for future hybridization programme.

The result of the present study revealed that a wide variability exists among the collected bitter gourd genotypes. In addition, there was also genotypic variability of different yield contributing characters with yield of bitter gourd. From the findings of the present study, the following conclusions could be drawn:

i.   Wide range of genetic diversity existed among the bitter gourd genotypes. That variability could be used for future breeding programme of bitter gourd in Bangladesh.

ii. Selection procedure would be applied for desired characters such as days to first male flower, first female flower and increase fruit length, fruit diameter, number of fruits per plant to develop high yielding varieties.

iii. Relatively higher value and lower differences between genotypic co-efficient of variation and phenotypic coefficient of variation of different yield contributing characters like average fruit weight, number of fruits per plant, yield per plant were observed which indicates high potentiality to select these traits in future which were less affected by environmental influence.

iv. Further collection of bitter gourd germplasm would be continued for getting more variability and desired traits in bitter gourd.

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Appendices

APPENDICES

Appendix I. Map showing the experimental site under the study

AGROECOLOGICAL ZONES
(Generalised)

1 Old Himalayan Piedmont Plain	16 Middle Meghna River Floodplain
2 Active Tista Floodplain	17 Lower Meghna River Floodplain
3 Tista Meander Floodplain	18 Young Meghna Estuarine Floodplain
4 Karatoya-Bangali Floodplain	19 Old Meghna Estuarine Floodplain
5 Lower Atrai Basin	20 Eastern Surma-Kusiyara Floodplain
6 Lower Punarbhaba Floodplain	21 Sylhet Basin
7 Active Brahmaputra-Jamuna Floodplain	22 Northern and Eastern Piedmont Plain
8 Young Brahmaputra and Jamuna Floodplain	23 Chittagong Coastal Plain
9 Old Brahmaputra Floodplain	24 St Martin's Coral Island
10 Active Ganges Floodplain	25 Level Barind Tract
11 High Ganges River Floodplain	26 High Barind Tract
12 Low Ganges River Floodplain	27 North-eastern Barind Tract
13 Ganges Tidal Floodplain	28 Madhupur Tract
14 Gopalganj-Khulna Beels	29 Northern and Eastern Hills
15 Arial Beel	30 Akhaura Terrace

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Appendix II. Monthly average record of air temperature, rainfall, relative humidity, soil temperature and Sunshine of the experimental site during the period from April 2008 to April 2009

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
April, 2008	36.9	19.6	64	91	8.5
May, 2008	36.7	20.3	70	205	7.7
June, 2008	35.4	22.5	80	577	4.2
July, 2008	34.0	24.6	83	563	3.1
August, 2008	36.0	23.6	81	319	4.0
September, 2008	34.8	24.4	81	279	4.4
October, 2008	34.8	18.0	77	227	5.8
November, 2008	32.3	16.3	69	0	7.9
December, 2008	29.0	13.0	79	0	3.9
January, 2009	28.1	11.1	72	1	5.7
February, 2009	33.9	12.2	55	1	8.7
March, 2009	34.6	16.5	67	45	7.3
April, 2009	35.8	20.3	65	88	8.3

Source: Bangladesh Meteorological Department (Climate & Weather Division) Agargoan, Dhaka - 1212

Appendix III. Physical characteristics and chemical composition of soil of the experimental plot

Soil characteristics	Analytical results
Agrological Zone	Madhupur Tract
P^H	6.00 – 6.63
Organic matter	0.84
Total N (%)	0.46
Available phosphorous	21 ppm
Exchangeable K	0.41 meq / 100 g soil

Source: Soil Resource and Development Institute (SRDI), Dhaka

Appendix IV: Mean performance of different parameters of 20 Bitter gourd genotypes

Parameters	Minimum	Mean	Maximum
Days to first male flowering	48.67	52.00	57.33
Days to first flowering	56.67	61.60	66.00
Vine length (m)	3.130	3.776	4.500
No. of nodes/vine	72.03	84.91	92.20
Branches/vine	36.27	40.01	45.47
Fruit length (cm)	13.54	18.51	23.12
Fruit diameter (cm)	8.97	10.63	11.48
No. of fruit/plant	14.00	34.48	62.33
Weight/fruit (g)	67.5	103.6	141.1
Yield/plant (Kg)	1.310	2.723	5.160

Appendix V. Principal component score 20 genotypes of Bitter gourd

Sl. No.	Genotype	Z1	Z2
01.	Shaparan	4.28	-17.43
02.	TB/qt 01-05× 03-01	-11.44	-5.01
03.	Deshi	23.86	20.35
04.	TB (Q) 07-01× 08-03	-35.61	-10.20
05.	Rampali gaj	24.91	-17.27
06.	Bt (N) 04-07	1.66	8.93
07.	BARRI Karla-I	-11.41	4.82
08.	Sagarica	-29.68	-4.99
09.	Nabil	44.27	-6.51
10.	Bt (N) 05-11	-14.77	15.65
11.	Bt (N) 05-10	-21.04	-12.29
12.	Nandita	20.13	19.05
13.	Bt (N) 04-12	11.62	13.11
14.	Eureca	30.54	1.34
15.	Bt (N) 05	-10.50	6.19
16.	Tia	0.56	-7.80
17.	Hirak	-21.51	3.84
18.	TB(Q) 06-01× 07-02	-20.02	4.57
19.	Maharaj	29.11	-18.73
20.	BT/qt 01-04×02-02	-14.96	2.40