GENETIC VARIABILITY AND DIVERSITY ANALYSIS FOR AGRO-MORPHOGENIC TRAITS OF BITTER GOURD (*Momordica charantia*L.) GENOTYPES

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BY

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CERTIFICATE

This is to certify that the thesis entitled, "GENETIC VARIABILITY AND DIVERSITY ANALYSIS FOR AGRO-MORPHOGENIC TRAITS OF BITTER GOURD (Momordica charantia L.) GENOTYPES" 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 bona fide research work carried out by MST. SANZIDA AFROJ, Registration No. 09-03314, 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 been duly acknowledged.

Dated: June, 2016
Place: Dhaka, Bangladesh

Prof. Dr. Naheed Zeba
Supervisor

Dedicated to
My
Beloved Parents

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SOME COMMONLY USED ABBREVIATIONS

Full word	Abbreviation
Accessions	ACC
Agro-Eco1ogical Zone	AEZ
And Others	*et al*.
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	$h^2 b$
Journal	J
Kilogram	Kg
Meter	M
Mean Sum Of Square	MSS
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

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MST. SANZIDA AFROJ

ABSTRACT

An experiment was conducted in the horticultural experimental field of Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh, during the period from March 2015 to September, to study the genetic variability in yield and yield contributing characters of bitter gourd with twelve genotypes of bitter gourd. G4 gave the best performance on vine length, branches per vine, early flowering and number of fruits per plant, the highest fruit length, fruit diameter, fruit weight and fruit yield per plant. The genotype G5 performed excellent for early flowering and G1 for the maximum number of fruits per plant. The fruit yield per plant showed the highest range of variation (3.69-12.74 Kg) with the mean value of 9.6 Kg. The significant positive correlation was found between yield and fruit length, fruit diameter and average fruit weight at genotypic and phenotypic level. Path co-efficient analysis indicated that branches per vine, fruit length, fruit weight and number of fruits per plant had direct positive effect on yield. Positive indirect effect was also found by vine length and days to flowering on yield of bitter gourd. All the genotypes show high heritability. The genotypes were also tested for genetic divergence utilizing the multivariate analysis. The genotypes were grouped into four clusters. The maximum inter-cluster distance (35.73) was presented between cluster I (contained one genotype) and cluster II (contain two genotypes). The minimum inter cluster distance (6.50) presented between cluster III (contained 3 genotypes) and cluster IV (contain 6 genotypes). The highest intra- cluster distance in cluster IV (4.454) and the lowest intra-cluster distance cluster I (0.0) was presented. Considering the magnitude of cluster mean and agronomic performance G3 (MC003), G4 (MC004), G5 (MC005), G6 (MC006) and G11 (MC1011) considered promising and might be recommended for future hybridization program.

CHAPTER I
INTRODUCTION

Bitter gourd (*Momordica charantia* L.) locally known as karala/uchha, is an important vegetable and belongs to the family Cucurbitaceae. Compared to other cucurbits, bitter gourd has relatively high nutritional value, in respect of iron and ascorbic acid contents. It is a good source 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 %) (Anonymous. 2010). Ripe fruits are rich in vitamin A, folates, Carotene-ß 190 µg, Carotene-a 185 µg, Lutein-zeaxanthin170 µg. Among all cucurbits vegetables bitter gourd contains the maximum amount of minerals and vitamins. Bitter melon notably contains phyto-nutrient, polypeptide-P, a plant insulin known to lower blood sugar levels. In addition, it composes hypoglycemic agent called charantin. Charantin increases glucose uptake and glycogen synthesis inside the cells of liver, muscle and adipose tissue. Together, these compounds may have been thought to be responsible for blood sugar levels reduction in the treatment of type-2 diabetes (Ooi *et al*., 2012). Bitter melon stimulates easy digestion and peristalsis of food through the bowel until it is excreted from the body. Thus, it helps in relieving indigestion and constipation problems. Early laboratory tests suggest that certain phyto-chemical compounds in bitter melon might be effective in the treatment of HIV infection (http://www.nutrition-and-you.com/bitter-gourd.html). It has great demand in Bangladesh throughout the year but it is available and cheaper during the kharif season. The average yield per acre is 10-12 tons in Bangladesh (Anonymous. 2010).

It has export potentiality because of its excellent keeping quality and grows round the year due to its photo insensitivity (Rashid, 1999). As a monoecious crop, bitter gourd is highly cross pollinated and thus, there exists a wide genetic variability in nature. But there is few released varieties of this popular vegetable as per its requirements. Genetic diversity is one of the important tools to quantify genetic variability in both cross and self-pollinated crops and

also important for crop improvement as well as variety development programme (Gaur *et al*., 1978; Anand *et al*., 1975; Marani and Avieli, 1973; Matzinger *et al*., 1962; Murty, 1965). Multivarite analysis by means of Mahalanobis D^2 statistics is an useful tool in quantifying the degree of genotypic divergence among biological populations and to assess the relative contribution of different components to the total divergence both at inter and intra-cluster levels (Das and Gupta, 1984; Jatasra and Paroda, 1978; Sachan and Sharma, 1971; Ram and Panwan, 1970; Murty and Arunachalam, 1966). Many researchers have adopted this D^2 technique for measuring divergence among genotypes of pumkin (Rashid, 2000; Masud *et al*., 1995), cucumber (Prasad *et al*., 1993) and snake gourd (Banik, 2003).

Very few research efforts related to estimate the variability in bitter gourd have been conducted in the country. An understanding of the nature and degree of variability among the germplasm is a prerequisite for its variety improvement. Therefore, the present study was undertaken to analyze the genetic variability of a number of bitter gourd genotypes for selecting parents of diverse group for further breeding program.

The present study was undertaken with the following objectives.

- To know the yield potentiality of the studied genotypes,
- To know the nature of association of traits, direct and indirect relation between yield contributing characters,
- To screen out the suitable parents group which are likely to provide superior segregants on hybridization and
- To assess the magnitude of genetic divergence in genotypes for identifying the genetically divergent parents to use them in future breeding program.

CHAPTER II
REVIEW OF LITERATURE

The need for the maintenance of wild species, local varieties and outdated genotypes in gene banks is obvious, which have become an important form of gene maintenance. However, in order to determine the extent of genetic diversity the genotypes in gene banks should be characterized and evaluated, which would permit the documentation of genotypes of interest in breeding program. Several research reports showed that there is a vast opportunity to work with bitter gourd. Literature related to the present study has been described below;

2.1 Origin and domestication of bitter gourd

Bitter gourd (*Momordica charantia* L.) is an important vegetable crop in tropical countries, including China and India. It is mainly valued for its nutritional and medicinal properties (Behra, 2004). The origin of this crop is probably India with secondary centre of diversity in China (Grubben, 1997). A wide range of genetic diversity exists in India with respect to fruit morphology (growth habit, maturity and various fruit characters including shape, size, colour and surface texture (Robinson and Decker-Walters, 1999). Morphological characters are the primary source of identification in most groups and for hypothesizing phylogenetic relationships.

In Indian Sanskrit Ayurvedic texts written in 2000 to 200 BCE by members of the Indian Aryan culture, describe Wild or small fruited cultivated forms of bitter gourd (Decker Walters, 1999). In China, the earliest reference of *M. charantia* was in 1370 CE (Yang and Walters, 1999).

Eastern India may be considered as primary center of origin based on both historical literature (Miniraj *et al*., 1993; Chakravarty, 1990; Walters and Decker Walters, 1988) and molecular analysis like amplified fragments length polymorphism (AFLP), random amplified polymorphic DNA (RAPD) (Dey *et*

al., 2006), inter simple sequence repeats (ISSR) (Gaikwad *et al*., 2008; Singh *et al*., 2007).

2.2 Variability and genetic parameter

The fundamental key to achieve the genetic improvement of a crop through a proper breeding program is to assess the amount and nature of variation of plant characters in breeding population. It helps the breeder for improving the selection efficiency. For this reason, many researchers studied variation in tomatillo and tomato. It has been suggested by Yi *et al.* (2008) that domestication and inbreeding dramatically reduced the genetic variation.

The success of any crop improvement program depends on the presence of genetic variability and the extent to which the desirable trait is heritable. Genetic variability can be estimated using both morphological and molecular markers. The presence of genetic variability in the breeding material has been emphasized by previous researchers (Reddy *et al*., 2013; Singh, 2009; Shuaib *et al*., 2007).

The assessment of variability present in any crop species is an essential prerequisite for formulating an effective breeding program, as the existing variability can be used to enhance the yield level of cultivars following appropriate breeding strategies (Patil *et al*., 2012). Sreelathakumary and Resmi (2015) observed that the characters of 33 bitter gourd genotype showed ample variation as the wide range obtained for days to seedling emergence, vine length and inter-nodal length. Days to first male and female flower plays an important role in deciding the earliness or lateness of the crop. The early and late female flower appearance helps in occurrence of early or late flush of the crop. Days to first male flower showed wide range of variations among the genotypes.

Parameters of genotypic phenotypic coefficients of variation (GCV and PCV) are useful in detecting the amount of variability present in the available genotypes. High phenotypic co-efficient of variation than the genotypic co-

efficient of variation indicates more influence of environment on the expression of genes controlling the trait. Therefore, it can be referred that selection based upon phenotypic expression of the particular character wouldn't be productive for the improvement of that crop (Bhuiyan, 2014). If the genotypic co-efficient of variation and phenotypic co-efficient of variation are close to each other, it suggests environmental influence is minor on the expression of the genes controlling the trait. So, selection based upon phenotypic expression of that character would be effective for the improvement of the specific crop.

Evaluation of 18 genotypes of ridge gourd for growth, earliness, and yield and fruit quality parameter showed that PCV was higher than GCV for most of the trait (Koppad *et al*., 2015). An experiment was conducted by Pathok *et.al*. (2014) to determine the variability among eight characters of bitter gourd hybrid. High genotypic (GCV) and phenotypic co-efficient of variation (PCV) was observed for number of fruits per plant, fruit weight and fruit length whereas, low GCV and PCV was observed for days to first male and female flower anthesis. In another study, genetic variability was estimated in fifty genotype of snake gourd. The phenotypic co-efficient of variation was found higher than the genotypic co-efficient of variation for most trait studied. The GCV obtained for various yield and yield attributing characters ranged from (5.08 to 47.15) (Devi and Mariappan, 2013).

From variability studied of bottle gourd germplasm with 13 quantitative traits showed continuous variation among accessions, primarily due to fruit and seed size and shape. A wide range of variation was also recorded in the quantitative traits for other fruit, leaf and seed characters plant height, fruit circumference handle length, leaf blade width and leaf blade length (Mladenovic *et al*., 2012). Guffar (2008) was conducted an experiment with 15 sponge gourd genotypes. Among the characters the highest GCV recorded for yield per plant followed by top fruit perimeter and average fruit weight.

Kabir (2007) conducted an experiment on variability and estimation of genetic parameter, 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-efficient of variation were recorded in the parameters, number of fruits per plant and second highest was recorded from yield of fruits per hectare. However, days require to first flowering, fruit length, fruit breadth, single fruit weight and weight of fruit per plant recorded moderate GCV and PCV.

Zaman *et al.* (2004) reported the performance of three sponge gourd lines. Two lines produced the highest number of fruits per plant and lower were recorded in Local. Maximum individual fruit weight was obtained form Local. 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). 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, number of primary branches, days to first male flowering, days to first female flowering, node number of first male flower, fruit length, seeds per fruit. Banik (2003) 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 (GCV and PCV 30.75 and 30.96, h^2b 98.64%), fruit length (GCV and PCV 29.92 and 30.04, h^2b 99.19%) and first

female flower node number (GCV and PCV 25.87 and 26.59, h^2b 94.63%) and number of fruits per plant (GCV and PCV 19.82 and 20.59; h^2b 92.67%).

Chowdhury and Sharma (2002) studied genetic variation, heritability, genetic advance 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 coefficient 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.

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. 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.

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. In case of seed germination there was a wide range of variation. Robinson and Decker-Walters (1997) reported that male flowering was earlier than female flowering in several genotypes of bottle gourd.

Mathew and Khader (1999) conducted an experiment on genetic studies in snake gourd (*Trichosanthes anguina*) and observed the genetic variability and

heritability of 12 traits in 34 *Trichosanthes 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.

Rumaran *et al.* (1997) 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. Walkers (1997) found variation in the duration of germination of cucumber seed. He 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.

Hossain (1996) conducted an experiment on floral biology of ridge gourd. 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 10^{th} to 21^{st} node. Saha *et al.* (1992) studied the variability of pumpkin , 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 3.03 5 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.

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 it 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 characters at phenotypic as well as genotypic level with a very wide range of values. It was observed by Rahman *et al.* (1990) in a study that 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.

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. Mongal *et al.* (1981) 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. 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.

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. 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. 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.

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 (3622 to 45.00 days) and days to first female flower opening (45.00 to 61.33 days). Nodes number for 1 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 19^{th}, 25^{th}, 14^{th} and 14^{th} days respectively. Node for first female flower in bottle gourd, sweet gourd, white gourd and water melon were 28^{th}, 34^{th}, 21^{th} and 19^{th} days respectively.

2.3 Correlation co-efficient and path analysis

To evaluate the relationships between the characters, correlation is the best estimate. It will help the breeder to decide about selection methods. Many of the cases, correlation between yield and yield contributing characters was

studied as yield is one of the basic targets to most of the breeders. Yield contributing characters are also interlinked. So, to plan effective breeding program for obtaining maximum yield, association of characters with yield and with its components is very much important.

Correlation analysis may vary due to agro-climatic variations from year to year and place to place. Higher heritability than yield shows that there is positive correlation between these, then there may be chance to increase in total yield by proper selection of that component. Negative correlation co-efficient among yield components indicate selection for any component might not bring change for yield improvement.

The homework of correlation does not offer an exact image of relative status of direct and indirect consequence of each of the component characters towards the preferred character. So, this can be overawed by ensuing path coefficient analysis. Path co-efficient analysis is a typical tool which measures the direct stimulus of one character upon another and permits the separation of correlation co-efficient into constituents of direct and indirect effects.

Path co-efficient analysis between yield and yield contributing characters provides a precise image of the comparative importance of direct and indirect effects of each component characters on fruit yield. It also offer valuable surplus information for refining fruit yield through selection for its yield attributes. Many researchers have studied correlation and path co-efficient analysis between yield and yield contributing characters. Some of the likely cases are described here.

From eighteen genotypes of ridge gourd characters showed that 90 days after sowing (DAS) (R=0.8659), average fruit weight (R=0.9298), tendril length (R=0.4955) had positive and significant correlation with yield but sex ratio (R=0.4606) and days to first male flowering (R=-0.512) had the negative significant association with the fruit yield per vine (Koppad *et al.*, 2015). In another study, among 20 bitter gourd hybrid characters correlation analysis

revealed that number of fruit per plant hand significant positive correlation for yield. Further, path co-efficient analysis partitioned the correlation into direct and indirect effects. Yield was found to be directly correlated with fruit weight, number of fruits per plant and fruit length (Pathok *et. al*., 2014).

Bottle gourd characters studied that a positive correlation between plant height and fruit length (R=0.33). The correlation between fruit weight and all other variables was positive (R=0.22-0.59). The correlation between fruit weight and all other variables was positive (R=0.22-0.59) (Mladenovic *et. al*., 2012).

Among the yield contributing characters days to male flower, days to female flower, fruit length, fruit diameter, average fruit weight and total number of fruits per plant were found to have highly significant and positive genotypic and phenotypic association with fruit yield per plant. Results indicated that these characters have major contribution towards the fruit yield per plant in snake gourd (Podder *et. al.,* 2010). In an experiment of Kabir (2007) 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.

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 with 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) carried out 98 hybrids of cucumber derived from crosses involving 14 male and 7 female parents 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. 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 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 found that general genotypic correlation co-efficient were higher than those related to phenotypic or environmental factors. However, both genotypic and phenotype 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. Mongal *et al.*(1981) 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 lenght, 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. In another study, 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. In a similar study, Chawdhury 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.

2.4 Genetic diversity

Genetic divergence has been considered as an essential parameter in crop improvement program to identify the most diverse parents. Highly heterotic F_1 generation can only be found from genetically diverse parents. Many researchers have studied genetic divergence based on Mahalanobis' D^2-statistics. Among them the most relevant current publications are reviewed below:

In a study, the principal component analysis was carried out with 17 genotypes of bitter gourd. PCA produce. Eigen values of principal component axes of coordination of genotypes with the first axes totally accounted for 88.12% variation, precise information about the extent of genetic divergence is crucial for an effective breeding programme (Ghosh *et. al*., 2015). To evaluate the nature and magnitude of genetic divergence in 30 bitter gourd genotypes results revealed the presence of wide genetic diversity. The genotypes were grouped into 6 clusters. Among the 12 quantitative characters studied, individual fruit weight constituted a maximum of 64.14% contribution to the divergence, followed by days to first female flower appearance intra-cluster mean performance are major contributors of genetic diversity (Singh *et al*., 2013).

Distance analysis classified parents in four well separated cluster DC_1, (298.173) was highly diverse class and DC_4 (209.090-278.047) was low diverse class while DC_2 (278.048-268.647) and DC_3 (268.648-209.089) were optimum divergence classes. Higher frequencies of heterotic hybrids were produced by parents with moderate diversity than the parents with high diversity (Laxuman *et. al*., 2012).

Genetic divergence of twenty bitter gourd genotypes was studied by D^2 and PCA. The genotypes fall into four clusters. Inter and intra cluster distances in were larger than intra cluster distances suggesting wider genetic diversity among the genotypes of different groups (Islam *et. al*., 2010). Quamruzzaman *et al.* (2008) 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 in cluster II (0.882) and the lowest in 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) assessed the genetic diversity among 64 pointed gourd genotypes through multivariate analysis from an experiment conducted. 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 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) 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 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/plant and average fruit weight had high direct effect towards the fruit yield/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.

Guffar (2007) conducted a research and found, 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), petiole length (13.28), days to first male flower (103.28), days to first female flower (107. 80) and other characters. 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 inter-cluster distance (45.9 between cluster II and V and minimum (10.3) between cluster II and IV.

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 IV (4) & Cluster III (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 Ito 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 using multivariate analysis and the genotypes were grouped into seven distinct cluster. 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 cluster analysis for yield and its components. The genotypes were grouped into 11 clusters irrespective of geographic and genetic diversity.. 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 cluster.

Dora *et al.* (2003) 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. In a different study, 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 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 for 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 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.

CHAPTER III

MATERIALS AND METHODS

This chapter clarifies information regarding methodology, used in implementation of the experiment. It describes a brief statement of experimental site, planting materials, climate and soil, seed bed preparation, design of the experiment, other operations done, data collection methods, statistical analysis procedure etc., which are presented as follows:

3.1. Experimental site

The experiment was conducted at Horticultural farm in the Sher-e-Bangla Agricultural University, Dhaka-1207, under AEZ-28 (Mudhupur tract). The experimental area was situated at 23°79'N latitude and 90°30'E longitude at an altitude of 8.6 meter above the sea level. The experimental site is indicated on the AEZ map of Bangladesh in (Appendix I).

3.2 Climate

Subtropical climate considered by high temperature, high relative humidity and heavy rainfall in Kharif season (April-September). High temperature, relative humidity, excessive rainfall and sunshine hours prevailed at the experimental site during the study period are presented in (Appendix II).

3.3 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 sandy loam texture. 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).

3.4 Design and layout of the experiment

The experiment was designed in RCBD. Number of genotypes were 12, replications were 3, spacing was 2m × 1m and plot size was 110 m^2.

3.5 Planting materials

Twelve genotypes of bitter gourd were used for the study. Seeds were collected from Department of Genetics and Plant Breeding, local market and personal collection from abroad. The experimental genotypes are presented in Table 1.

Table 1. Name of twelve bitter gourd genotypes used in the present study

Sl. No.	Genotypes No.	Identification No.	Source
01	G_1	MC-001	Dept. of Genetics and Plant Breeding
02	G_2	MC-002	,,
03	G_3	MC-003	,,
04	G_4	MC-004	,,
05	G_5	MC-005	,,
06	G_6	MC-006	,,
07	G_7	MC-007	,,
08	G_8	MC-008	,,
09	G_9	MC-009	,,
10	G_{10}	MC-010	,,
11	G_{11}	MC-011	,,
12	G_{12}	MC-012	,,

3.6 Seed treatment

To ensure better germination, seeds were soaked in water overnight.

3.7 Seed sowing in the pot and raising of seedlings

Seeds were sown in the transparent thin plastic pot. Three seeds were sown in each pot and germination of seeds were completed within ten days. Preparation of pots to raising of seedlings are chronologically illustrated in Plate 1.

3.8 Land preparation

The experimental plot was well prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to

Bring about good tilth in the first week of March, 2015. Weeds and other

Plate 1. Different steps of seed preparation, sowing and raising of seedlings. (A) Pot preparation for seed sowing (B) Leveling of pots (C) soaking of seed, (D) Sowing of seed, (E) seedlings for transplanting.

stables were removed carefully from the experimental plot and leveled properly (Plate 2A).

3.9 Pit preparation

After final land preparation, pits of 30 cm × 30 cm x 30 cm were prepared in each plot with a spacing of 2 m × 1m and filled with well decomposed manure. Pits were kept open in the sun for 6 days to kill harmful insect and microorganisms (Plate 2B).

3.10 Manure and fertilizers application

The manure and fertilizers were applied to the plots for bitter gourd cultivation according to the doses in Table 2. Total cow dung, half of TSP and one third MOP were applied in the field during final land preparation. Remaining TSP, one third MOP, whole gypsum, 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 shows doses of manure and fertilizers used in the study.

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

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

3.11 Transplanting of seedlings

Healthy and vigorous seedlings of one month old were selected for transplanting in the main land. The seedlings were removed carefully from the small plastic pots by avoiding any injuries and sown one seedling per pit in the

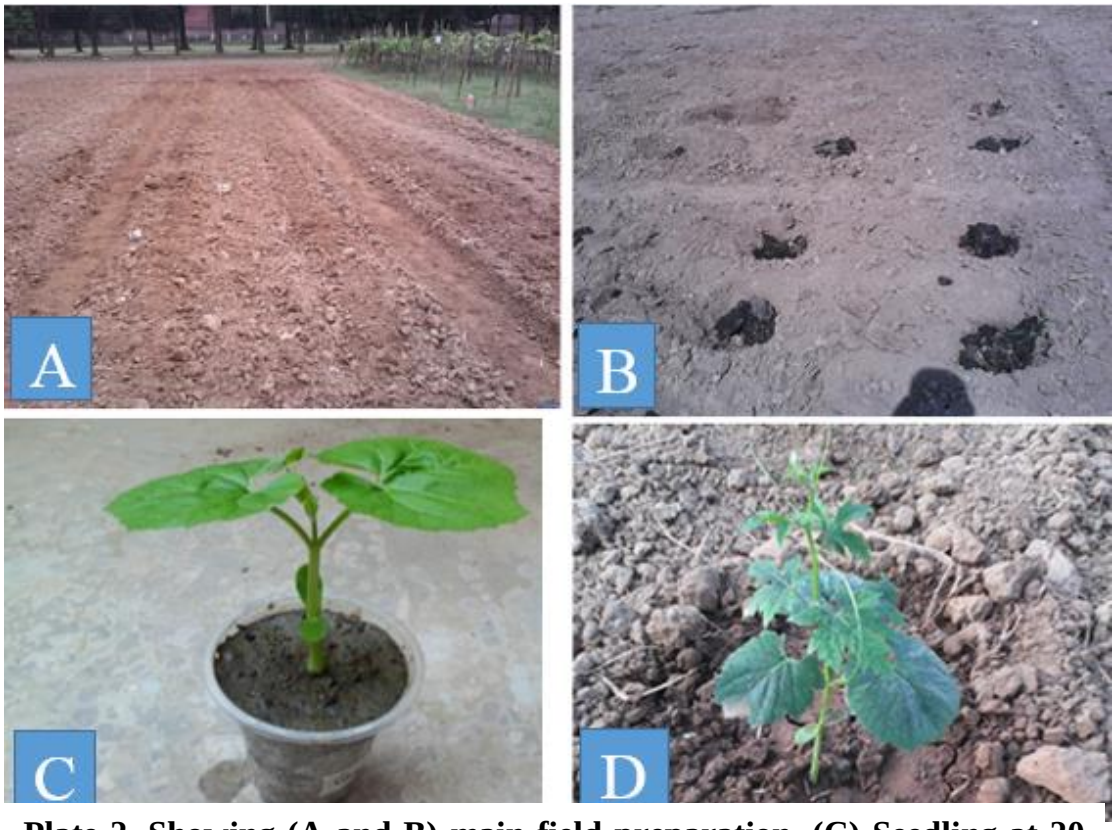

Plate 2. Showing (A and B) main field preparation, (C) Seedling at 20 DAS, (D) Transplanting of seedling in the main field

evening time. Slight watering was done after transplantation. Seedling size and transplanting of seedlings in the pit are presented in Plate 2(C and D).

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. Different intercultural operations provided.

3.12.1 Weeding

Several weeding 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.

3.12.2 Irrigation and after-care

In the early stage, irrigation was done twice daily by water cane. In mature stage flood irrigation was done whenever it was necessary.

3.12.3 Pesticide application

At the seedling stage red pumpkin beetle attacked tender leaves and gradually attacked the whole plant. Malathion 25 EC and Ripcord was sprayed in the field to control the infestation of insect pests. In mature stage fruit fly caused damage to the fruit. Ripcord, sevin powder were sprayed for controlling this insect. Poison bait was also applied and showed good performance to control fruit flies.

3.12.4 Stalking and tying

Mechanical support was provided to the growing plants by dhaincha sticks to keep them erect and support the plant before flowering. The vines were tied with thin rope with the dhaincha sticks. A bamboo macha was then prepared

and allowed the vine to creep on the macha. The bamboo macha was prepared using bamboo, plastic rope and metallic wire.

3.13 Harvesting

Fruits were picked on the basis of horticultural maturity, size, colour and age being determined for the purpose of consumption. Fruits were picked with sharp knife and care was taken to avoid injury of the vine.

3.14 Data recording

Data were recorded on the following parameters from the studied plants throughout their life cycle. The recorded data were on the individual plant basis. The data on different yield contributing characters are recorded as,

3.14.1 Days to first male flowering

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

3.14. 2 Days to first female flowering

The number of days required for first female 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 Branches per vine

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

3.14.5 Number of nodes per vine

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

3.14.6 Number of fruits per plant

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

3.14.7 Average fruit weight (g)

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

3.14.8 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.

3.14.9 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.

3.14.10 Yield per plant (kg)

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

3.15 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 Analysis (CVA).

3.15.1 Estimation of genotypic and phenotypic variances

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

a. **Genotypic variance,** $\delta^2 g = \frac{MSG - MSE}{r}$

Where, MSG = Mean sum of square for genotypes

MSE = Mean sum of square for error, and

r = Number of replication

b. Phenotypic variance, $\delta^2 p = \delta^2 g + \delta^2 e$

Where, $\delta^2 g$ = Genotypic variance,

$\delta^2 g$ = Environmental variance = Mean square of error

3.15.2 Estimation of genotypic and phenotypic co-efficient of variation

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

$$GCV = \frac{\delta_g \times 100}{\bar{x}}$$

$$PCV = \frac{\delta_p \times 100}{\bar{x}}$$

Where, GCV = Genotypic co-efficient of variation

PCV = Phenotypic co-efficient of variation

= Genotypic standard deviation

= Phenotypic standard deviation

= Population

3.15.3 Estimation of heritability

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

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

Where,

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.15.4 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. σ_p

Or Genetic advance, 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

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.15.5 Estimation of genetic advance at mean's percentage

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

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

3.15.6 Estimation of correlation co-efficient

Simple correlation co-efficient (r) was estimated with the following formula (Singh and Chaudhary, 1985; Clark, 1973).

$$r = \frac{\sum xy - \frac{\sum x \cdot \sum y}{N}}{\sqrt{[\{\sum x^2 - \frac{(\sum x)^2}{N}\}\{\sum y^2 - \frac{(\sum y)^2}{N}\}]}}$$

Where, $\sum$ = Summation

x and y are the two variables correlated

N = Number of observation

3.15.7 Path co-efficient analysis

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985) using simple correlation values. In path analysis, correlation co-efficient is partitioned into direct and indirect independent variables on the dependent variable. In order to estimate direct & indirect effect of the correlated characters, say x1, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

$$r_{yx1} = P_{yx1} + P_{yx2}r_{x1x2} + P_{yx3}r_{x1x3}$$

$$r_{yx2} = P_{yx1}r_{x1x2} + P_{yx2} + P_{yx3}r_{x2x3}$$

$$r_{yx3} = P_{yx1}r_{x1x3} + P_{yx2}r_{x2x3} + P_{yx3}$$

Where, r's denotes simple correlation co-efficient and P's denote path co-efficient (Unknown). P's in the above equations may be conveniently solved by arranging them in matrix from.

Total correlation, say between x1 and y is thus partitioned as follows:

P_{yx1} = The direct effect of x1 on y.

$P_{yx2}r_{x1x2}$ = The indirect effect of x1 via x2 on y.

$P_{yx3}r_{x1x3}$ = The indirect effect of x1 via x3 on y.

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

$$P^2_{RY} = 1 - \sum P_{iy} \cdot riy$$

Where, P^2_{RY} = (R^2); and hence residual effect, $R = (P^2_{RY})^{1/2}$

P_{iy} = Direct effect of the character on yield

Riy = Correlation of the character with yield.

3.15.8 Estimation of Genetic Diversity

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.

3.15.8.1 Principal Component Analysis (PCA)

Principal component analysis, one of the multivariate techniques, is used to examine the interrelationship among several characters and can be done from the sum of squares and product matrix for the characters. Therefore, principal component were computed from the correlation matrix and genotype scores obtained from the first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than the unity. Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.15.8.2 Principal Coordinate Analysis (PCO)

Principal coordinate analysis is equivalent to principal component analysis but it is used to calculate inter-unit distances. Through the use of all dimensions of P it gives the maximum distances between each pair of the n point using similarity matrix (Digby et al., 1989).

3.15.8.3 Cluster analysis

To divide the genotypes of the study into some number of mutually exclusive groups clustering were done using non-hierarchical classification. Starting from some initial classification of the genotypes into required groups, the algorithm repeatedly transfers genotypes from one group to another so long as such

transfers improve the criterion, the algorithm switches to a second stage which examine the effect of swapping two genotypes of different classes and so on.

The average intra-cluster distances for each cluster was calculated by taking possible D^2 values within the member of a cluster obtained from the Principal Coordinate Analysis (PCO). The formula used was D^2/n, where D^2 is the sum of distances between all possible combinations (n) of the genotype included in the cluster. The square root of the average D^2 values represents the distances (D) within cluster.

3.15.8.4 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. 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.

3.15.8.5 Selection of varieties for future hybridization program

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 (D2) express the maximum divergence among the genotypes included into these different clusters. Variety (s) or line(s) were selected for efficient hybridization program according to Singh and Chuadhury (1985). According to them the following points should be considered while selecting genotypes for hybridization program:

1 .Selection of cluster from which genotypes are selected for use as parent (s)

2 .Choice of particular genotype(s) from the selected cluster(s)

3. Relative influence of the characters to the total variabilities

4. Other important characters of the genotypes

CHAPTER IV

RESULTS AND DISCUSSION

The experiment was directed to perform the variability analysis of different genotypes of bitter gourd (*Momordica charantia* L.) using yield contributing characters. This chapter encompasses the findings obtained from the experiment. The data were collected from the seedling stage to after harvest stage. The gradual change of active vegetative growth, flowering, fruiting and harvesting is presented in Plate 3. The data pertaining to ten yield contributing characters have been presented and statistically analyzed with the possible interpretations are discussed below.

4.1 Genetic variability, heritability and genetic advance

Variability and estimation of genetic parameter in order to different plant characters are discussed below. The mean performance of different traits of 12 genotypes of bitter gourd is presented in Appendix IV.

4.1.1 Days to first male flowering

The variance due to days to first flowering showed that the genotypes differ significantly. The range of days to first male flowering varied from 36.0 days to 42.0 days with mean value 39.28 days (Appendix IV). The genotypic co-efficient of variation and phenotypic co-efficient of variation were 6.35 and 6.52 respectively (Table 3). The phenotypic variance and genotypic variance suggested minor influence of environment on the expression of genes controlling the trait. Therefore, selection based upon phenotypic expression of this character would be effective for the improvement of the crop. A similar finding was reported by Singh et al. (2002) in ridge gourd.

4.1.2 Days to first female flowering

Significant variation was found for days to female flowering and it ranged from 40 DAT in G5 to 47 DAT in G_{11} with the mean value 44.25 (Appendix IV). The genotypic and phenotypic variance was 5.55 and 6.21 respectively. The phenotypic variance and genotypic variance define low environmental

Plate 3. Some stages of experimental field (A) Established seedling in experimental field (B) First Flowering (C) Part of the experimental field at flowering stage of plant (D) Harvesting stage.

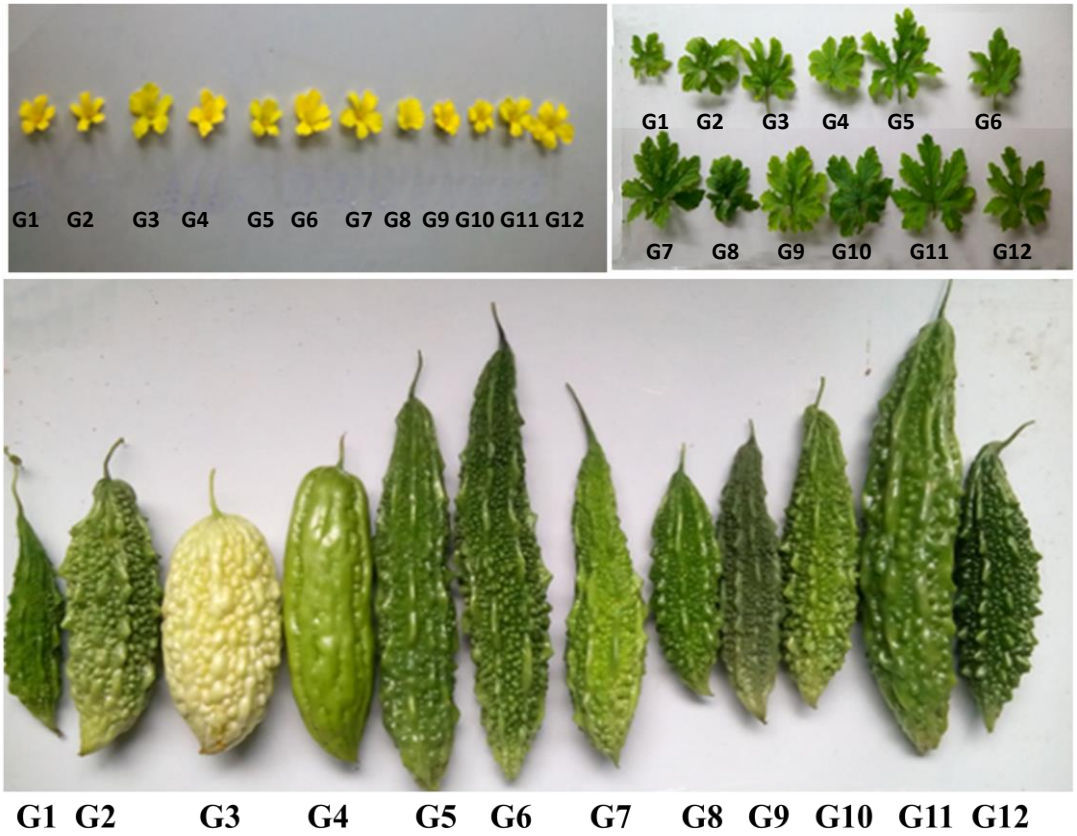

Plate 4. Comparison of the studied bitter gourd genotypes based on flower, leaf and fruit. A. Flower, B. Leaf and C. Fruit.

Table 3: Estimation of genetic parameters in ten characters of twelve genotypes in Bitter gourd

Traits	MS	o^2g	o^2e	o^2P	GCV	ECV	PCV	h^2b	GA (5%)	GA (% mean)	CV (%)
DFMF	12.78**	6.23	0.32	6.55	6.35	1.45	6.52	95.07	5.01	12.76	1.45
DFFF	13.58**	6.02	1.54	7.56	5.55	2.80	6.21	79.66	4.51	10.20	2.80
VL	1.38**	0.65	0.09	0.73	14.92	5.44	15.88	88.26	1.56	28.87	5.44
BPV	252.20**	124.33	3.54	127.87	24.54	4.14	24.88	97.24	22.65	49.84	4.14
NPV	144455.66**	71846.66	762.35	72609.01	37.93	3.91	38.13	98.95	549.26	77.73	3.91
NFPP	234.92**	107.77	19.37	127.14	16.90	7.16	18.35	84.77	19.69	32.05	7.16
AFW	7898.27**	3886.41	125.45	4011.86	38.32	6.89	38.94	96.87	126.40	77.70	6.89
FL	25.92**	12.82	0.27	13.09	16.34	2.36	16.51	97.95	7.30	33.30	2.36
FD	0.3881**	0.19	0.01	0.20	11.94	2.65	12.23	95.32	0.88	24.01	2.65
FYPP	15.874**	7.94	0.00	7.94	29.34	0.42	29.35	99.98	5.80	60.44	0.42

DFMF= Days to first male flowering, DFFF= Days to first female flowering, VL= Vine length, BPV= Branch per vine, NPV= Node per vine, NFPP= Number of fruits per plant, AFW= Average fruit weight (g), FL= Fruit length (cm), FD= Fruit Diameter (cm), FYPP= Fruit yield per plant (kg), MS = mean sum of square, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance, σ^2e = Environmental variance, PCV = Phenotypic Coefficient of Variation, GCV= Genotypic Coefficient of Variation and ECV= Environmental Coefficient of Variation, h^2_b = Heritability in broad sense, GA= Genetic advance * Significant at 5% level of probability, ** Significant at 1% level of probability

influence on the expression of genes governing days to female flowering. Many author also found similar result (Miah *et al*., 2000; Sharma *et al*., 2000). The heritability estimates was high (79.66%) with the low genetic advance (4.51%) and genetic advance in percent of mean 10.20%, indicating this character was governed by non-additive genes. Guffar (2008) support the findings.

4.1.3 Vine length

The twelve genotypes had adequate variation for this trait presented in (Table 3). There were significant differences in vine length among the genotypes. The maximum value of vine length (6.63 m) was recorded in G_4 (Appendix IV). The minimum value (4.47 m) of vine length was found in G_1. Robinson and Decker-walters (1997) also found similar significant variation for vine length. The phonotypic expression of plant characters depend on the interaction between genotypic characters and environment. The more environmental effect inhibits the expression of genetic characters. Vine length had high cotraits of genotypic and phenotypic variances (Table 3). The phenotypic co-efficient of variation was higher than genotypic one which indicated more influence of environment. Less difference between PCV (10.9%) and GCV (8.88%) took the advantage of vine length at final harvest. High values of heritability and low values of genetic advance and genetic advance in percent of mean have recorded for vine length, indicating that this character was controlled by non-additive gene effects. So, selection of this character wouldn't be effective. The result of Chowdhury and Sharma (2002) contradict with the present findings where the high heritability is coupled with high genetic advance for this character.

4.1.4 Branches per vine

The maximum number of branches was 63.33 showed in G_4 and the minimum number of branches was 33.33 in G_{10}. The mean value was 45.44 for number of branches (Appendix IV). There was minor environmental influence on the exposure to the character, because the difference between phenotypic (24.88) and genotypic (24.54) co-efficient of variation was very close to each other

(Table 6) described minor environmental influence on the expression of genes controlling this trait. So, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. High heritability (97.24) with low genetic advance (22.65) and moderate genetic advance in percent of mean (49.84) indicates non-additive gene action controlling this trait. Variation in branch per vine was also observed in snake gourd genotypes by Banik, (2003).

4.1.5 Nodes per vine

Significant differences in nodes per vine were found from 1150.30 to 427.70 among the genotypes (Table 3). The mean value was recorded 706.64 for nodes per vine. The maximum number of nodes per vine observed in genotype G4. The genotypic (37.93) and phenotypic (38.13) co-efficient of variation indicated that minor environmental impact on the expression of the character (Table 6). The heritability estimates for this trait was high (98.95), genetic advance was (54.93%) and genetic advance in percent of mean (77.73) were found high, this trait was governed by non-additive gene. High heritability and low genetic advance for this character was also observed by Banik (2003).

4.1.6. Number of fruits per plant

From the present study we observed that the highest number of fruit per plant was recorded 84.73 in genotype G_1 and the lowest number of fruit per plant 47.70 recorded in genotype G_4 (Appendix IV). Anonymous (2000) reported that number of fruits per plant varied significantly among the studied cucumber lines. The difference between the genotypic co-efficient of variance (16.90) and phenotypic co-efficient of variance (18.35) indicates less environmental influence (Table 3). The heritability estimates for this strait was high (84.77%), genetic advance (19.69%) and genetic advance in percent of mean (32.05%), revealed that this character was governed by additive gene and selection for this character would be effective (Table 3). Chowdhury and Sharma (2002) also reported similar findings in respect to average fruit weight in ridge gourd.

4.1.7 Fruit Length

The mean fruit length was noticed as 21.92 cm with a range of 13.77 cm to 25.23 cm. The genotype G4 showed the maximum fruit length and the genotype G1 showed the minimum fruit length (Appendix IV). The genotypic variance (12.82) and phenotypic variance (13.09) with the co-efficient of variation genotypic (16.34) and phenotypic (16.51) were closed to each other (Table 3), indicating minor environmental influence on this character that would be effective for improvement of this crop. High heritability estimates 97.95% with low genetic advance (7.30%) over percent of mean (33.30%) (Table 3) indicate that effective selection may be made for fruit length. Sharma *et al.* (2000), Krisna Prasad and Singh (1994), and Hormuzdi and More (1989) were reported the similar findings for bitter gourd.

4.1.8 Fruit Diameter

The mean fruit breadth was 3.65 cm with a range of 3.23 cm (in genotype G_{11}) to 4.27 cm (in genotype G_4) (Appendix IV). Sharma et al. (2000), Krisna Prasad and Singh (1994), Hormuzdi and More (1989) found similar results. Almost similar genotypic (0.19) and phenotypic variances (0.20) with GCV (11.94%) and PCV of (12.23%) values found (Table 3) which were closed to each other, indicating minor environmental influence on this character that would be effective for its improvement. High heritability estimates (95.32%) with low genetic advance (0.88%) over moderate percent of mean (24.01%) (Table 3) indicate that effective selection may be made for fruit breadth. High heritability coupled with low genetic gain for this character was observed by Saha *et al*., (1992).

4.1.9 Fruit weight

The highest single fruit weight was found as 268.17 g in genotype G_4, where the minimum fruit weight was recorded as 43.88 g in genotype G_1 with the mean value of 162.62 g (Appendix IV). Prasad and Singh (1992) found more variation among bitter gourd genotypes in case of fruit weight. The genotypic (3886.41) and phenotypic (4011.86) variance for fruit weight was high (Table

3). The estimation of GCV and PCV for this character were (38.32%) and (38.94%) respectively and closed to each other, indicating less environmental influence for the expression of this character (Table 3). Therefore, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. High heritability (96.87%) associated with high genetic advance in percent of mean (77.70%) and low genetic advance (12.64%) (Table 3) was observed indicating fruit weight governed by additive gene. Chowdhury and Sharma (2002) also reported similar findings in respect to average fruit weight in ridge gourd and pumpkin.

4.1.10. Fruit yield (kg) per plant

The fruit yield per plant was found as 12.74 kg in genotype G_4 which is highest and the lowest was recorded as 3.69 kg in genotype G_1 with the mean value 9.6 kg (Appendix IV). Similar genotypic variance (7.94) and phenotypic (7.94) variance (Table 3) suggested no influence of environment on the expression of the genes controlling this character which gives idea about selection. Estimation of high heritability (99.98%) with low genetic advance (5.80%) and high genetic advance of percent (60.44%) (Table 3) revealed that this character was governed by additive gene and provides opportunity for selecting high valued genotypes for breeding program. Abusaleha and Dutta (1990) found similar result for this character in bitter gourd.

4.2. Correlation studies

Determination of correlation co-efficient was provided the information how yield depends on different yield contributing characters. The correlation co-efficient, ‘r’ and the parameter correlated are shown in Table (4 and 5).

4.2.1 Days to first male flowering

Days to first male flowering had non-significant positive correlation with no. of fruit per plant (0.097 and 0.101) at both genotypic and phenotypic level. It showed significant negative relation with fruit diameter and fruit yield per plant (-0.647). It also showed insignificant negative relation with other characters (Table 4 and 5). Khan *et al*. (2008) reported similar result in pointed gourd.

Table 4. Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotypes of bitter gourd

	DFFF	VL	BPV	NPV	NFPP	AFW	FL	FD	FYPP
DFMF	1.000**	-0.303	-0.12	-0.016	0.097	-0.521	-0.259	-0.867**	-0.647*
DFFF		-0.182	-0.225	-0.092	0.165	-0.564	-0.267	-0.837**	-0.677*
VL			0.468	0.329	-0.577	0.647*	0.51	0.658*	0.559
BPV				0.576	-0.444	0.526	0.421	0.44	0.445
NPV					-0.672*	0.632*	0.635*	0.317	0.483
NFPP						-0.904**	-0.888**	-0.389	-0.823**
AFW							0.838**	0.735**	0.952**
FL								0.409	0.836**
FD									0.764**

* Significant at 5% level of probability

** Significant at 1% level of probability

DFMF= Days to first male flowering, DFFF= Days to first female flowering, VL= Vine length, BPV= Branch per vine, NPV= Node per vine, NFPP= Number of fruits per plant, AFW= Average fruit weight (g), FL= Fruit length (cm), FD= Fruit Diameter (cm), FYPP= Fruit yield per plant (kg)

Table 5. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotypes of bitter gourd

	DFFF	VL	BPV	NPV	NFPP	AFW	FL	FD	FYPP
DFMF	0.947**	-0.29	-0.115	-0.01	0.101	-0.51	-0.257	-0.843**	-0.639*
DFFF		-0.176	-0.203	-0.074	0.122	-0.512	-0.247	-0.776**	-0.637*
VL			0.455	0.319	-0.515	0.611*	0.493	0.641*	0.541
BPV				0.572	-0.426	0.519	0.418	0.433	0.442
NPV					-0.640*	0.626*	0.632*	0.315	0.482
NFPP						-0.888**	-0.860**	-0.357	-0.789**
AFW							0.829**	0.720**	0.945**
FL								0.401	0.832**
FD									0.756**

* Significant at 5% level of probability

** Significant at 1% level of probability

VL= Vine Length (m), BPV= Branch/Vine, NPV= Node/Vine, DFFM= Days to 1st flower (male), DFFF= Days to 1st Flower (Female), FL= Fruit Length (cm), FB= Fruit Breadth (cm), FW= Fruit Weight, NFPP= No. of Fruit/Plant and FYPP= Fruit/Plant(kg)

4.2.2. Days to first female flowering

Days to first female flowering had non-significant positive correlation with no. of fruit per plant (0.165 and 0.122) at both genotypic and phenotypic level. It showed significant negative relation with fruit diameter and fruit yield per plant. It also showed non-significant negative relation with other characters studied (Table 4 and 5). Khan *et al*. (2008) reported similar result in case of pointed gourd. Guffar (2008) also found similar result in case of bitter gourd.

4.2.3 Vine Length

Vine length had positive and significant effect on AFW (0.647 and 0.611) and FD (0.658 and 0.641), while non-significant and positive correlation with node per vine (0.329 and 0.319), fruits length (0.51 and 0.493), FYPP (0.559 and 0.541) at genotypic and phenotypic level (Table 4 and 5). This finding was supported by Abusaleha and Dutta (1988). Vine length of bitter gourd had non-significant and negative correlation with fruit per plant (-0.577 and -0.515) at genotypic and phenotypic level (Table 4 and 5).

4.2.4 Branches per vine

No. of branch per vine had non-significant positive relation with NPV(0.576), AFW(0.526), FL(0.421), FD(0.44) and FYPP(0.445) at both level while non-significant negative correlation with NFPP(-0.444) (Table 4 and 5).

4.2.5 Nodes per vine

Node per vine had significant positive relation with FL (0.635) and AFW (0.632) while significant negative relation with NFPP (-0.672) (Table 4 and 5).

4.2.6 Fruit length

Fruit length had significant positive relation (0.836 and 0.832) with fruit yield per plant while non-significant positive relation with fruit diameter (0.409 and 0.401) (Table 4 and 5).

4.2.7 Fruit diameter

Fruit diameter had significant positive relation (0.764 and 0.756) with fruit yield per plant (Table 4 and 5).

4.2.8 Fruit weight

Av. fruit wt. had significant positive relation with FL (0.838 and 0.829), FD (0.735 and 0.720) and FYPP (0.952 and 0.945) at both level (Table 4 and 5).

4.2.9 Number of Fruits/plant

No. of fruits per plant had significant negative relation with AFW (-0.904), FL (-0.888) and FYPP (-0.823) (Table 4 and 5) indicating that they had no effect on yield.

4.3. Path analysis

Path analysis showed that the cause and effect situation of dependent and independent variable. For example yield is considered as dependent variable and vine length, days to first flowering and fruit characters are independent variable. Path analysis gives the original pictures of inter relationship between yield and yield attributing characters. Path co-efficient analysis was showed direct and indirect effects of different characters on yield of bitter gourd in (Table 6).

4.3.1 Days to first male flowering

Days to first male flowering had direct negative effect on yield of bitter gourd (-0.167). It also had indirect negative effect on yield via DFFF (-0.167) and NFPP (0.016). Besides positive indirect effect with yield via VL (0.051), BPV (0.020), NPV (0.003), AFW (0.087) and FL (0.043) showed in(Table 6). Li et al. (1997) found negative effect of days to first male flowering with yield.

4.3.2 Days to first female flowering

Days to first female flowering had positive direct effect on yield of bitter gourd (0.237) which influence to genotypic correlation with fruits per plant (0.165). It also had indirect negative effect with all the characters except number of fruits per plant (Table 6). Rastogi et al. (1990) showed that days to female flowering had positive and direct effect on yield, which is supported by present findings.

Table 6. Path coefficient analysis showing direct and indirect effects of different characters on Fruit/Plant (kg) of bitter gourd

Characters	Direct effect	Indirect effect									Genotypic correlation with Yield
		DFMF	DFFF	VL	BPV	NPV	NFPP	AFW	FL	FD	
DFMF	-0.167	-	-0.167	0.051	0.020	0.003	-0.016	0.087	0.043	0.144	-0.648*
DFFF	0.237	0.237	-	-0.043	-0.053	-0.022	0.039	-0.134	-0.063	-0.199	-0.677*
VL	-0.108	0.033	0.019	-	-0.049	-0.036	0.062	-0.069	-0.055	-0.071	0.559
BPV	0.019	-0.002	-0.004	0.009	-	0.011	-0.009	0.011	0.008	0.008	0.444
NPV	-0.227	0.004	0.021	-0.075	-0.130	-	0.152	-0.143	-0.144	-0.072	0.483
NFPP	0.854	0.083	0.141	-0.493	-0.379	-0.574	-	-0.773	-0.759	-0.332	-0.823**
AFW	0.823	-0.950	-0.900	0.950	0.959	0.915	-0.911	-	0.955	0.933	0.952**
FL	0.402	-0.104	-0.107	0.205	0.169	0.255	-0.365	0.337	-	0.196	0.836**
FD	-0.252	0.219	0.221	-0.166	-0.110	-0.079	0.098	-0.185	-0.123	-	0.764**

Residual effect: 0.19

4.3.3 Vine length

Path co-efficient analysis (Table 6) indicated that vine length had direct and negative (-0.108) effect on yield. Vine length had indirect positive effect on DFMF (0.033), DFFF (0.019) and NFPP (0.062). Besides negatively indirect effect via other characters were estimated (Table 6). Shah and Kale (2002) reported similar result with the present study and they stated that vine length had positive direct effect on yield per plant.

4.3.4 Branches per vine

No. of branch per vine had direct positive effect (0.019) on yield while indirect positive effect via VL (0.009), NPV (0.011), FL (0.008) and AFW (0.011). It had indirect negative effect via DFMF (-0.002), DFFF (-0.004) and NFPP (-0.009) (Table 6).

4.3.5 Nodes per vine

Node per vine had direct negative effect (-0.227) and indirect positive effect via DFMF (0.004), DFFF (0.021) and NFPP (0.152) while negative indirect effect via others (Table 6).

4.3.6 Fruit length

Fruit length had direct positive effect on yield (0.402) while indirect positive effect via VL, BPV, NPV and AFW (Table 6).

4.3.7 Fruit diameter

Fruit diameter had direct negative effect (-0.025) while indirect positive effect via DFMF (0.219), DFFF (0.039), NFPP (0.083) and indirect negative via others (Table 6).

4.3.8 Fruit weight

Av. fruit wt. had direct positive effect (0.823) on yield while indirect positive effect via VL, BPV, NPV, FL and FD (Table 6).

4.3.9 Number of Fruits/plant

No. of fruits per plant had direct positive effect on yield while indirect positive

effect via DFMF and DFFF and indirect negative effect via other characters (Table 6).

4.4. Genetic divergence in bitter gourd

4.4.1. Cluster analysis

The experiment was conducted to investigate the genetic divergence of twelve genotypes of bitter gourd. The genotypes were divided into four cluster according to D^2 values (Table 7). The cluster IV had maximum number of genotypes (6) followed by cluster III which had 3 genotypes. Cluster II and I had two and one genotypes respectively. Remarkably cluster I had G_1 whereas cluster II had G_4 and G_{12}. Furthermore cluster III had G_6, G_8 and G_{11}, cluster IV showed 6 genotypes (G_2, G_3, G_5, G_7, G_9 and G_{10}). Clustering was done at random that indicate a broad genetic base of the genotypes. Genetic variability in bitter gourd was also found by Prasad *et al*. (2001).

4.4.2. Principal component analysis (PCA)

Proper idea about genetic divergence is an important tool for breeding program. The diversity analysis is useful to determine the magnitude of divergence among population (Murthy and Quadri, (1966)). Principal component analysis was studied with fifteen genotypes of bitter gourd. First three Eigen values for three principal co-ordination axes of genotypes accounted for 95.97% variation (Table 8). Based on principal component scores I and II obtained from the Principal component analysis (Table 9), a two-dimensional scatter diagram (Z1-Z2) using component score I as X axis and component score II as Y axis was Constructed, which has been presented in (Figure 1).

4.4.3. Principal coordination analysis (PCO)

Principal coordination analysis (PCO) indicated that there was moderate level of variation present among twelve genotypes of bitter gourd due to low inter genotypic distance. The maximum intra-cluster distance was presented in cluster IV (4.54) (Table 10) which had six genotypes. The minimum intra-cluster distance was recorded in cluster I (Table 10) which contained one genotype (G_1) (Table 10). Maximum inter cluster distances was found between

Table 7. Distribution of genotypes in different clusters

Cluster	Number of genotype	Genotype Number
I	1	G1
II	2	G4 and G12
III	3	G6, G8 and G11
IV	6	G2, G3, G5, G7, G9 and G10

Table 8. Eigen values and yield percent contribution of 10 characters of twelve genotypes of bitter gourd

Principle component axes	Eigen values	Percent variation	Cumulative % of Percent variation
I	4.6874	80.16	80.16
II	0.6207	10.62	90.77
III	0.3038	5.20	95.97
IV	0.0980	1.68	97.65
V	0.0834	1.43	99.07
VI	0.0387	0.66	99.73
VII	0.0126	0.22	99.95
VIII	0.0027	0.05	100.00
IX	0.0003	0.01	100.00
X	0.0000	0.00	100.00
XI	0.0000	0.00	100.00

Table 9. PC scores of twelve genotypes of bitter gourd

Genotype	PC1	PC2
G1	294.63	78.64
G2	174.82	-1.29
G3	82.41	-31.77
G4	-455.13	-37.93
G5	132.91	-63.18
G6	-101.72	-10.78
G7	75.39	-6.58
G8	-32.56	15.4
G9	114.75	-11.99
G10	130.34	-13.23
G11	-35.28	15.31
G12	-380.57	67.41

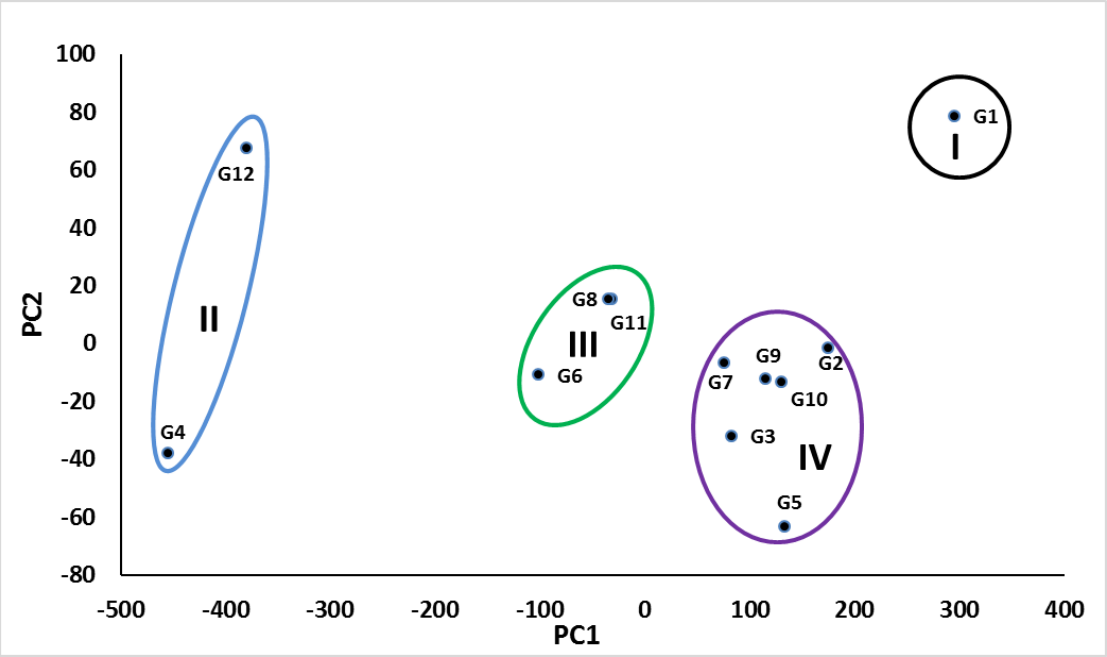

Figure1. Scatter distribution of twelve genotypes of bitter gourd based on their principal component scores super imposed with cluster

Table 10. Intra (Bold) and inter cluster distances (D^2)

Cluster	I	II	III	IV
I	**0.00**			
II	35.730	**1.796**		
III	15.870	19.850	**2.769**	
IV	14.960	23.020	6.500	**4.454**

cluster I and II while the minimum was observed between III and IV. Khan *et al.* (2008) reported twelve clusters in pointed gourd. Quaruzzaman et al. (2008) reported six clusters in ridge gourd.

4.4.4. Non-hierarchical clustering

Twelve *Momordica charantia* L. genotypes were divided into different groups. Cluster I contained one genotype, cluster II and IV contained two and three genotypes respectively, cluster III presented six genotypes of bitter gourd. From cluster mean (Table 11), cluster II had the maximum mean value for seven characters namely vine length (4.21 cm), Branch per vine (23.29) node per vine (83.28), fruit length (13.57), fruit breadth (4.21 cm), fruit weight (58.04 gm), Number of fruit per plant (83.61) and fruit yield per plant (1.96 kg). This cluster mean gives idea about the cluster II could be used for future hybridization program for vine length (m), branch per vine, node per vine, fruit length (cm), number of fruit per plant and fruit per plant (kg). Cluster III had required for days to first flower male (51.05) and days to first flower female (54.87). Cluster IV had highest mean value for fruit weight (101.57) and days to first flower required (56.39) days, cluster III and cluster IV had moderate mean value for all character. These genotypes of cluster could be used for future hybridization program. Singh *et al*. (2013) reported that contribution of the characters to the divergence in bitter gourd.

4.4.5. Conical variate analysis

Conical variate analysis (CVA) was done to calculate the inter-cluster distance. (Table 10) were presented intra and inter-cluster distance (D^2) values. In this study the inter-cluster distances were more than the intra-cluster distances. It proved that the wide range of genetic variability among genotypes of bitter gourd. Intra and inter-cluster distances were indicated in (Table 10). On the basis of intra and inter cluster (D^2) value, the close cluster of cluster I was cluster IV (14.96) and distant cluster was cluster II (35.73). Cluster II consists of nearest cluster with D^2 values was III (19.85) and distant cluster was cluster I (35.73) In case of cluster III the nearest cluster was IV (6.50) and the distant

Table 11. Cluster mean values of 10 different characters of 12 genotypes of bitter gourd

Traits	I	II	III	IV
Days to first male flowering	40.00	39.00	40.70	38.70
Days to first female flowering	45.00	43.50	46.00	43.50
Vine length	4.50	5.90	5.10	5.50
Branch per vine	37.00	57.70	41.00	45.00
Node per vine	427.70	1121.70	763.60	586.30
Number of fruits per plant	84.70	54.70	57.70	61.70
Average fruit weight(g)	43.90	211.10	164.70	165.30
Fruit length (cm)	13.80	24.60	22.30	22.20
Fruit Diameter (cm)	3.30	3.90	3.50	3.70
Fruit yield per plant (kg)	3.70	11.10	9.50	10.20

cluster was cluster II (19.85). The closest cluster of cluster IV was the cluster III (6.50) and farthest cluster was cluster II (23.02). With the help of D2 values within and between clusters, an arbitrary cluster diagram (Figure 2) was constructed, which showed the relationship between different genotypes. Diagram also showed the intra and inter cluster distance of twelve genotypes of bitter gourd. Shanmugam and Rangasamy (1982) stated that genotypes distributed in different clusters are sign of broad genetic base of diversity.

4.4.6 Selection of genotypes as parents for hybridization program

Genetically dissimilar parent selection is the fundamental work for hybridization program. Maximum heterosis could be obtained in offspring from the crosses between genetically diverse parents. On the basis of cluster mean and agronomic performance, the genotype G_4 for maximum vine length, branches per vine, fruit length, number of fruits and fruit weight and fruit yield per plants. G_3 and G_5 was found promising for early flowering. Therefore considering group distance and other agronomic performance, the genotypes G_3, G_4, G_{11} might be selected for future hybridization program.

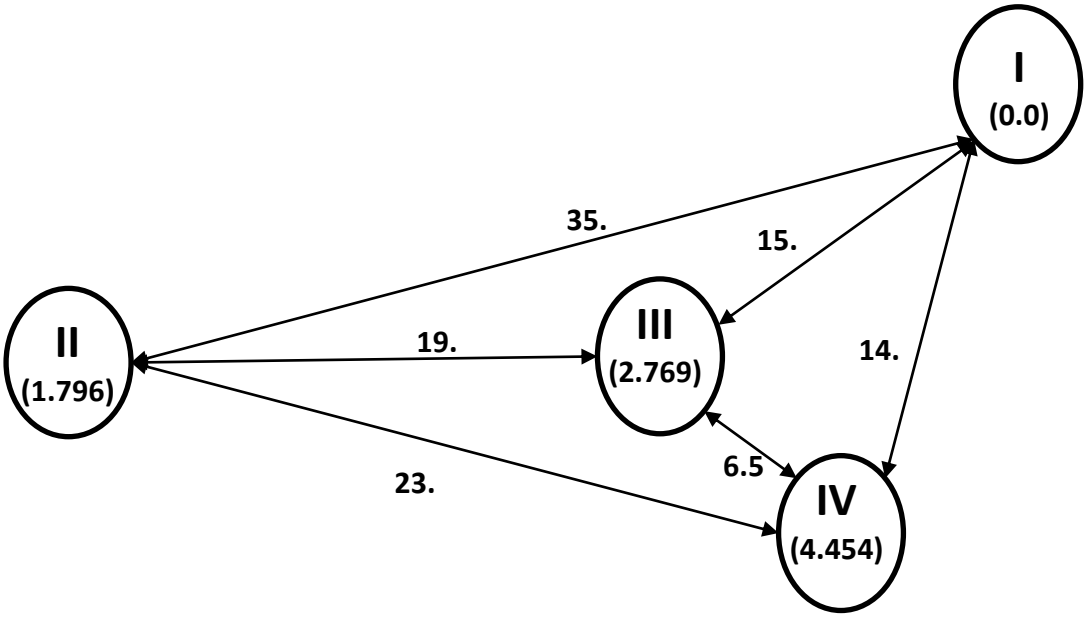

Figure 2. Diagram showing intra and inter cluster distance of twelve genotypes of bitter gourd

CHAPTER V

SUMMARY AND CONCLUSION

The experiment was executed in Horticultural farm, at Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh, with twelve genotypes of bitter gourd during March to September 2015. Seeds were sown in pots. The seedlings were transplanted in the main field in Randomized complete Block Design (RCBD) with three replications. In order to investigate yield potential, genetic variability, character association, genetic divergence of twelve genotypes, data were recorded on yield contributing parameter such as vine length, branches per vine, nodes per vine, days to first male flowering, days to first female flowering, fruit length, fruit diameter, fruit weight, number of fruits per plant, fruit yield per plant (kg).

The genotypic and phenotypic variance along with co-efficient of variation for both (genotypic and phenotypic), showed adequate variation present among genotypes for all characters. In case of vine length, fruit weight, number of fruits per plant, fruit yield per plant, environmental influence were found more for expression of the trait. On the other hand branches per vine, node per vine, fruit length, fruit breadth had minimum difference between genotypic and phenotypic variance suggesting additive gene action for the expression of the characters.

Correlation co-efficients among the characters were used to investigate the relationship between yield and yield attributing traits. Most of the character showed higher genotypic correlation co-efficient than phenotypic correlation co-efficient which gives idea about the relationship between the characters under study. The significant positive correlation was found between yield and fruit length, fruit diameter and average fruit weight at genotypic and phenotypic level. There was non- significant positive correlation between yield and vine length, branch per vine and node per vine at genotypic and phenotypic level. Significant negative correlation was found between yield and days to first

male flowering, days to first female flowering and number of fruits per plant at genotypic and phenotypic level.

Path co-efficient analysis indicated that DFFF, BPV, NFPP, AFW and FL had direct and positive effect on yield, while DFMF, VL, NPV and fruit diameter had negative and direct effect on yield. It was also found that average fruit weight had highest positive correlation (0.952) and contributed to yield through direct effect (0.823) with fruit yield per plant gives idea about selection will be more judicious for future breeding.

Genetic diversity among bitter gourd genotypes was executed through principal component analysis (PCA), cluster analysis, canonical variate analysis (CVA) using GENSTAT software. The first three principal component axes accounted for 95.97% variation towards the divergence. Among four clusters cluster IV had highest number of genotypes (6). In order to PCA, D^2 value and cluster analysis the genotypes were grouped into four different clusters obtained from principal component scores.

The maximum inter-cluster distance was found between cluster I and II (35.73) which indicated that the genotypes of two clusters if used in hybridization may produce a wide range of segregating generation. While the minimum inter-cluster distance was found between cluster III and IV (6.50). The highest intra-cluster distance was observed in cluster IV (4.454) which obtained six genotypes. The lowest intra-cluster distance was observed in cluster I (0.00) contained two genotypes.

Therefore, hybridization between genotypes belonging to cluster I with cluster II, cluster II with cluster III, Cluster III with cluster IV and cluster II with cluster IV will produce maximum heterosis in respect of yield, single fruit weight and maximum number of fruit per plant.

G_4 was found promising for maximum vine length, branches per vine, fruits length, number of fruit and fruit weight and fruit yield per plant. G_3 and G_5 was

found promising for early flowering. Therefore considering group distance and other agronomic performance, the inter-genotypic crosses between G_3, G_4, G_{11} and also other improved variety and might be suggested for future hybridization program. From the findings of the present study, the following recommendations could be provided.

(i) Selection should be applied for desired characters such as lowest days to first flowering and increased number of fruits per plant, fruit weight, fruit diameter and fruit length to develop high yielding varieties,

(ii) The genetic diversity exist among the bitter gourd genotypes could be used as a useful tool for future breeding program,

(iii) More importance should be given on G_3, G_4, G_5 and G_{11} for higher yield and attractive color.

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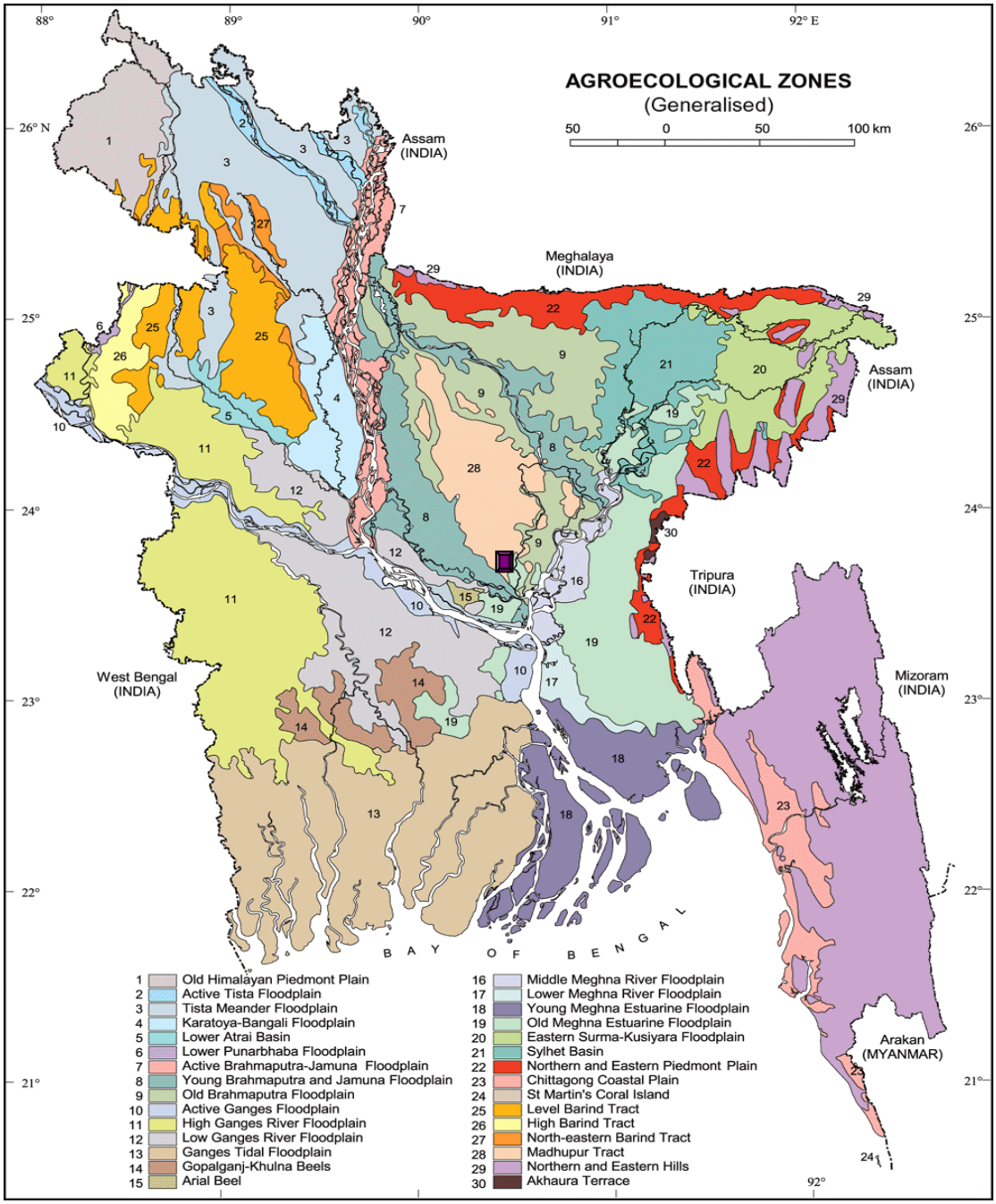
APPENDICES

Appendix I. Map showing the experimental site under the study



The experimental site under study

Appendix II. Monthly average Temperature, relative humidity and total rainfall of the experimental site during the period from March, 2015 to September, 2015.

Month	Monthly Average Air temperature (°C)		Avg. Relative humidity (%)	Total Rainfall (mm) (total)
	Maximum	Minimum		
March, 2015	30.0	20.6	52	4
April, 2015	31.0	23.3	68	166
May, 2015	32.9	25.4	71	185
June, 2015	32.7	26.6	77	375
July, 2015	33.2	26.0	81	623
August, 2015	32.2	26.9	79	395
September, 2015	33.0	26.0	78	346

Source: Agricultural Yearbook, 2015

Appendix III: Morphological, physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site

A. Physical composition of the soil

Soil separates	%
Sand	36.90
Silt	26.40
Clay	36.66
Texture class	Clay loam

B. Chemical composition of the soil

Sl. No.	Soil characteristics	Analytical data
1	Organic carbon (%)	0.82
2	Total N (kg/ha)	1790.00
3	Total S (ppm)	225.00
4	Total P (ppm)	840.00
5	Available N (kg/ha)	54.00
6	Available P (kg/ha)	69.00
7	Exchangeable K (kg/ha)	89.50
8	Available S (ppm)	16.00
9	pH (1:2.5 soil to water)	5.55
10	CEC	11.23

Source: Central library, Sher-e-Bangla Agricultural University, Dhaka

Appendix IV. Mean performance of various growth parameter and yield components of 12 genotypes of bitter gourd.

G	DFMF	DFFF	VL	BPV	NPV	NFPP	AFW	FL	FD	FYPP
G1	40	45	4.47	37.00	427.67	84.73	43.88	13.77	3.30	3.69
G2	40	46	6.33	45.33	533.67	66.63	137.49	21.13	3.77	9.10
G3	36	40	5.07	50.67	620.33	65.27	180.72	20.77	4.10	11.79
G4	38	43	6.63	63.33	1150.33	47.70	268.17	25.23	4.27	12.74
G5	36	40	5.60	44.00	565.67	59.53	203.82	23.58	4.10	12.08
G6	39	45	5.43	35.33	805.67	55.27	188.80	22.77	3.80	10.41
G7	39	45	6.00	51.67	631.00	60.37	157.02	23.72	3.60	9.45
G8	41	46	5.27	34.67	741.33	59.73	152.87	21.73	3.47	9.12
G9	42	46	5.47	45.00	591.33	56.00	156.65	20.55	3.27	8.77
G10	39	44	4.80	33.33	576.00	62.37	156.08	23.43	3.33	9.72
G11	42	47	4.50	53.00	743.67	57.97	152.47	22.33	3.23	8.84
G12	40	44	5.10	52.00	1093.00	61.67	154.12	24.05	3.50	9.50
Min	36.00	40.00	4.47	33.33	427.70	47.70	43.90	13.77	3.23	3.69
Max	42.00	47.00	6.63	63.33	1150.30	84.73	268.17	25.23	4.27	12.74
Mean	39.28	44.25	5.39	45.44	706.64	61.44	162.67	21.92	3.65	9.6
$LSD_{0.05}$	0.96	2.10	0.50	3.18	46.75	7.45	18.97	0.88	0.16	0.07
CV%	1.45	1.45	1.45	1.45	1.45	1.45	1.45	1.45	1.45	1.45