GENETIC DIVERSITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS IN SWEET GOURD (*Cucurbita moschata L.*)

শেরেবাংলা কৃষি বিশ্ববিদ্যালয় গ্রন্থাগার
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CERTIFICATE

*This to certify that thesis paper entitled, "**GENETIC DIVERSITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS IN SWEET GOURD** (Cucurbita moschata L.) submitted to the Faculty of Agriculture Sher-e- Bangla Agricultural University Dhaka, in partial fulfillment of the requirements for the degree of MASTER OF SCIENCE in GENETICS AND PLANT BREEDING, embodies the result of a piece of bonafide research work carried out by Shamima Sultana, Registration No.05-01641 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, has been availed of during the course of this investigation has duly been acknowledged.

Dated: June, 2011
Place: Dhaka, Bangladesh

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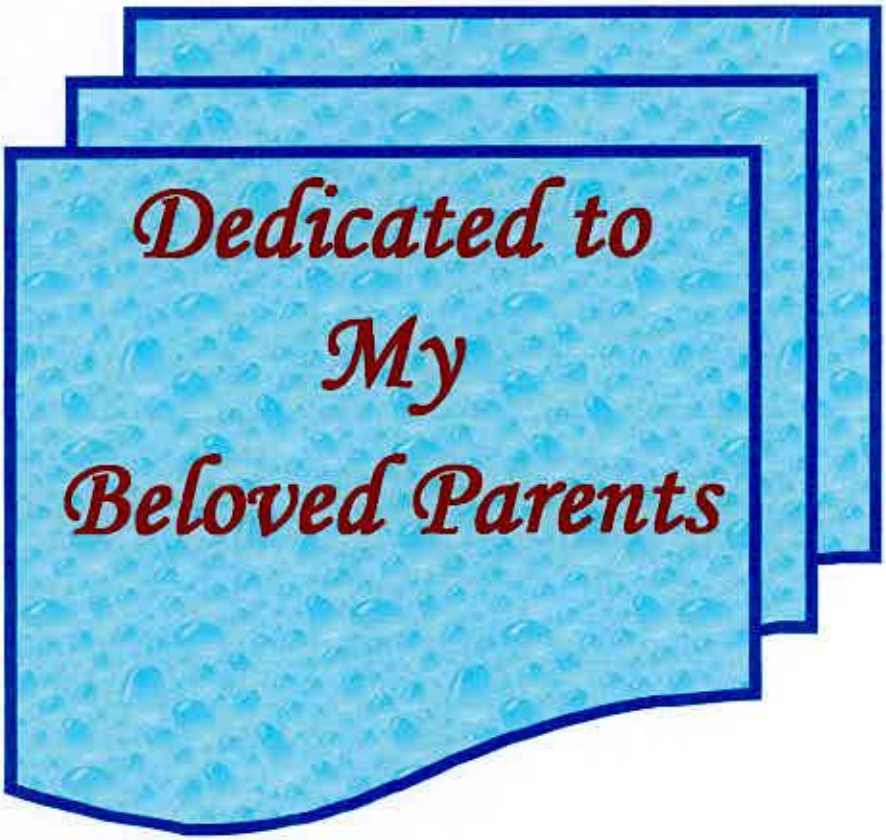
Dedicated to
My
Beloved Parents

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GENETIC DIVERSITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS IN SWEET GOURD (*Cucurbita moschata L.*)

BY
SHAMIMA SULTANA

ABSTRACT

Twenty seven genotypes of sweet gourd (*Cucurbita moschata L.*) were studied in a field experiment at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, during March 2010 to September 2010. Among them, six genotypes did not germinate. Sweet gourd is a nutrient powerhouse, low in fat and calories and rich in disease fighting nutrients such as α-carotene, β-carotene, fiber, vitamin-C & E, K, Mg, pantothenic acid. There are significant quantities of the carotinoids like lutien and zeaxanthin, both of which helps to maintain eye health. It's an important summer vegetable and very adaptive to climate change. Lack of high yielding, disease and pest tolerant varieties is the main constrains towards its production. Among the cultivated land races, a wide range of genetic variability exists in this crop that can be exploited for its improvement. The objectives of the study were to measure the variability among the genotypes for yield and yield contributing characters, estimate genetic parameters, association among the characters and their contribution to yield. This helps to choose desirable parents for establishing new breeding population. High genotypic co-efficient of variation (GCV) was observed for fruit yield per plant, number of male flower per plant and number of female flower per plant. Low genotypic co-efficient of variation (GCV) was observed for days to first female flowering, days to first male flowering and fruit length. In all cases phenotypic variances were higher than the genotypic variances. High heritability with high genetic advance in percent of mean was observed in yield per plant, number of male flower, pedicel length of female flower, and pedicel length of male flower indicated that these traits were under additive gene control and selection for genetic improvement for this trait would be effective. Correlation studies revealed that highly significant and positive association of yield per plant was found with number of female flower followed by fruit length, number of male flower, fruit breadth and fruit weight at both genotypic and phenotypic level. Path co-efficient analysis revealed that maximum direct contribution towards yield per plant with traits of number of female flower followed by number of male flower and days to first male flowering. The highest intra-cluster distance was found in cluster V, low in IV and no distance was found in cluster I. Among six clusters the highest inter cluster distance was observed between cluster II and cluster III and the lowest between cluster IV and cluster V. Considering all the characters the G_{21} (BD-2150), G_1 (BD-2151), G_{11} (BD 2229) and G_{13} (BD 266) genotypes were selected for future breeding programme.

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LIST OF ABBREVIATED TERMS

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

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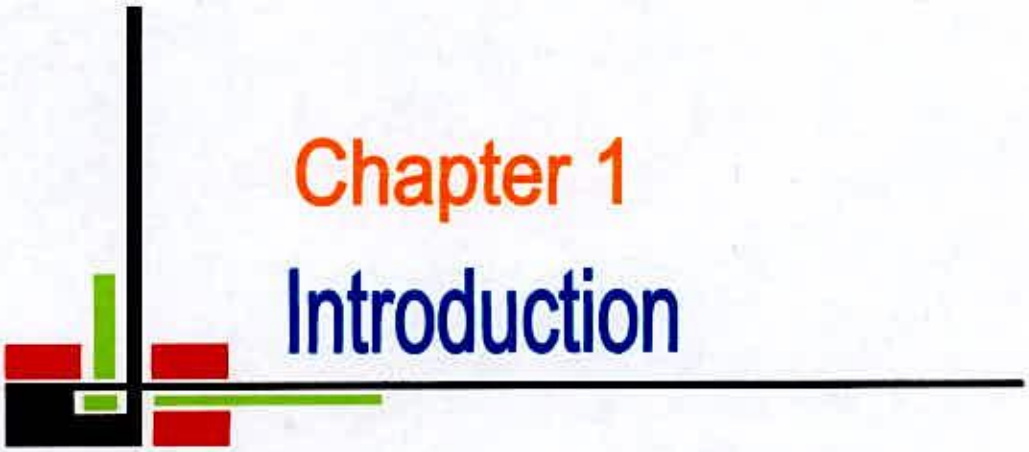

Chapter 1

Introduction

পোস্টবোলা কৃষি বিশ্ববিদ্যালয় গন্থাগার
সংযোজন নং 99
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CHAPTER I
INTRODUCTION

Sweet gourd (*Cucurbita moschata* duch. Ex Poir) is locally known as 'Misti kumra' or 'Misti lau' or 'Misti kadu' and is considered to have originated from Central and North America (Whitaker and Davis, 1962). It grows well throughout the entire tropical and sub tropical regions of the world and milder areas of the temperate zones of hemispheres. It is widely cultivated in many countries of the world like India, China, Malaysia, Taiwan and Bangladesh.

Sweet gourd belongs to the family Cucurbitaceae. There are 27 species under the genus *Cucurbita*, five of which are in cultivation. These are *C. moschata, C. maxima, C. ficifolia, C. pepo and C. mixta,* commonly known as Sweet gourd or Pumpkin. Pumpkin is highly cross pollinated crop having chromosome number 2n=40. *C. moschata* is probably the most widely grown species of Cucurbita and this species is cross compatible with *C. maxima*, *C. pepo* and *C. mixta*. It is insect pollinated and a 1000 m isolation distance is necessary to maintain purity of cultivars (Tindall, 1987). It is seed propagated, day- neutral, monoecious (male and female flowers in same plants) and vine crop. It is an annual crop having a climbing or trailing habit (Katyal and Chanda, 1985).

Pumpkin is relatively high in energy and carbohydrates and a good source of vitamins, especially high carotenoid pigments and minerals (Bose and Som, 1986). The nutrient per 100g edible portions of fruit is 90 ml water, 8g carbohydrate, 1g protein, 0.5 g fibers, 20 mg calcium, 0.8 mg iron, 210 µg β-carotene, 0.05 mg thiamine, 0.05 mg riboflavin, 0.5mg niacin and 15 mg ascorbic acid (Tindall, 1987). It may contribute to improve the nutritional status of the people, particularly the vulnerable groups in respect of vitamin A requirement.

The delicate shoots and leaves are used as delicious and nutritious vegetable. The fleshy large fruits can be consumed at mature and immature stages. It is one of the main vegetable in a wedding party or on other occasional party in northern India

(chauhan, 1989. The sweet pie and pumpkin haluwa are the delicious items prepared from mature fruit (shanmugavelu, 1989). Seeds are very nutritious (it contains 40-50% oil and 30% protein) and eaten in many countries of the world (Tindall, 1987).

Pumpkin is a very common vegetable in Bangladesh and particularly popular among the rural people. It is grown round the year in our country. It has the longest natural storability among all the cucurbits. The well-matured fruits (ripe fruits) can be stored for 2 to 4 months (Yawalkar, 1985). Due to its good taste and keeping quality, nutritional status, easier cooking quality, reasonable market price and year round availability, its demand is increasing day by day in the country.

It becomes available even in the lean period when other vegetables are scarce in Bangladesh. Among the non-traditional crops, Bangladesh has been earning a handsome amount of foreign currency by exporting pumpkin to the U.K., Pakistan and Middle East (Alamgir, 1998).

Vegetable production rate in Bangladesh is very low; yearly only 6.967 million M tones (BBS, 2007). Vegetable consumption rate is 104 g per day per adult, against the optimum amount of about 300 g per day per adult (Rashid, 2002). The total Production of pumpkin is 0.154 million M tones in a year in this country (BBS, 2007).

The Productivity of local genotypes ranged from 6.931 t/ha to 19.07 t/ha (Hamid *et al.*, 1991). On the other hand, there are many exotic genotypes, which have short life cycle but high yield potential. Some of these exotic genotypes bear deep green long fruits, which are attractive. Flower buds of the genotypes appear 20 to 25 days earlier than the local genotypes. The exotic genotypes do not need big trellis because of their medium climbing habits. However, the exotic types are rich in carotene and sugar content but more susceptible to different virus diseases then the local genotypes. These variabilities among the indigenous and exotic

genotypes are important genetic attributes, which can be combined though hybridization to develop short vine type varieties with high yield having high carotene and sugar, virus resistance and high number of female flowers with small fruit type. Night-blindness is a serious problem in Bangladesh. Encouraging the mass people to take more pumpkin as a source of vitamin-A easily be solved the problem. Being a cross-pollinated crop, it seems easy to transfer suitable traits by crossing appropriates genotypes of pumpkin.

A good knowledge of genetic resources might also help in identifying desirable cultivars for commercial cultivation. Because of its high cross-pollination, hardly any genetically pure strain is available to the growers. For this, inbred line should be developed through selfing and selection in the local and exotic germplasms. Lack of high yielding, disease and pest tolerant variety is the main constrains towards its production. Among the cultivated land races, a wide range of genetic variability exists in this crop that can be exploited for its improvement. Besides, information on quality aspects of fruits is very scanty in Bangladesh. Not much research has been done in this direction. It is the touchstone to a breeder to develop high yielding quality varieties through selection, either from the existing genotypes or from the segregates of a cross. Hence, information on variability, character association and path co-efficient analysis in respect of yield, its contributing characters and quality aspects required to be properly assessed for its improvement.

Therefore, considering the above facts the present investigation was carried out to achieve the following objectives;

1. To study the genetic variability among the pumpkin genotypes,
2. To find out the relationship among the genotypic traits and to estimate their direct and indirect effects towards yield improvement and
3. To screen out suitable parental groups with better performances for future breeding program.

Chapter 2
Review of literature

CHAPTER II

REVIEW OF LITERATURE

Sweet gourd *(Trichosanthes anguina L.)* is a member of the family Cucurbitaceae. It is an important summer vegetables in this country. Sweet gourd is an annual monoecious climbing type herbaceous crop. Actually a few works have been done for the improvement of this crop in Bangladesh and other countries in the world. However, research efforts on the genetic resources, diversity on genetic and molecular level, correlation, path co-efficinet analysis, heritabilily and genetic advance seem to be meager. However, information available in these aspects of sweet gourd and some other cucurbit crops have been reviewed and presented in this section.

2.1 Variability, Heritability and Genetic Advance:

Banik *et al.* (2003) conducted a field experiment to study the nature and extent of combining ability of parents and crosses and the mode of gene action in controlling the individual characters in 6x6 diallel including reciprocals in snake gourd. The significant mean sum of squares due to general and specific combining ability (GCA and SCA) for these characters indicated both additive and as well as non-additive type of gene actions were involved for the expression of these characters. The experiment was conducted at the experimental farm of Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Salna, Gazipur, Bangladesh during May 2001 to September 2002.

Rajkumar (2007) *et al.* conducted a field experiment in Tamil Nadu, India, from 2003 to 2005, to determine the genetic variation including the mean, genotypic (GCV) and phenotypic coefficients of variation (PCV), heritability and genetic advance with 30 genotypes of snake gourd (*Trichosanthes cucumerina*). Significant differences among genotype for all the characters were noted. All the characters exhibited less difference between GCV and PCV values. The characters flesh thickness, fruits per plant, days to fruit maturity and 100-seed

weight showed equal GCV and PCV values indicating less influence of environment in their expression. The heritability estimate was high for all the characters except days to first female flower. The maximum heritability was observed for ascorbic acid content of the fruit, followed by the crude fiber content and nodes for first female flower. The genetic advance as a percentage of mean was high for fruits per plant and fruit length. High heritability coupled with high genetic advance was observed for fruits per plant and fruit length. They are governed by additive genes and could be effectively improved through selection.

Narayanankutty *et al.* (2006) estimated genetical parameters of 36 snake gourd (*Trichosanthes cucumerina*) genotypes indicated a good amount of genetic variation in the germplasm collections. Characters such as fruit yield, fruit weight and seeds per fruit exhibited high values of heritability and genetic gain indicating additive gene effects are important in determining these characters. The character association analysis revealed that yield was strongly correlated with fruit weight, fruits per plant, fruit girth, fruit length, days to first harvest, flesh thickness and days to first female flower opening. Fruit weight and fruits per plant have the maximum positive direct effects on yield and the indirect contribution of other characters was mainly through days to first harvest, seeds per fruit and 100-seed weight.

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

length and first male flower node. The PCV was lowest for days to maturity, 100 seed weight and days to first male flower opening. The GCV along with heritability was high for the above characters. High heritability coupled with high genetic advance was noticed for fruit yield per plant (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%).

Mathew and Khader (1999) conducted an experiment on genetic studies in snake gourd *(Trichosanthen anguina)* and observed the genetic variability and heritability of 12 traits in *34 Trichosanthen anguina in* Kerela, India and reported that the genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) were almost equal for all characters. The highest GCV and PCV were recorded for mean fruit weight, seed per fruit, fruit yield per plant and fruit length. High heritability was observed for mean fruit weight, seeds per fruit, fruit length, days to first male flower and fruit yield per plant.

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

Chowdhury and Sarma (2002) studied genetic variation, heritability, genetic advance, and correlation for yield and yield components (vine length, number of nodes, node on which the first flower appeared, number of fruits per plant, fruit length, fruit girth, and fruit weight) were studied in 12 *Luffa acutangula* cultivars

(AAUJ-1, AAUJ-2, AAUJ-3, Mangaldoi, Tezpeu, Tihu, Mirza Short, Rangamati Long, Borpeta Long, Tiniali Long, Pusa Nazder, and HRS C-2) grown in Gwuahati, Assam, India. The genetic coefficient of variation (GCV) was higher than the phenotypic coefficient of variation (PCV) for all characters. High values of heritability, PCV, GCV, and genetic advance were recorded for vine length, yield per hectare, and fruit weight, indicating that these traits were characterized by additive gene effects. The correlation coefficients revealed that yield per hectare can be improved through selection for greater fruit number per plant, fruit length and girth, and individual fruit weight.

Quamruzzaman *et al.* (2009) studied heterosis in bottle gourd in a set of 13 F, with 26 parents. Results indicated highly significant differences for all the character among the materials studied. Heterosis was higher for yield per plant, number of fruits per plant and individual fruit weight, medium in fruit length and fruit diameter, and lower in days to 1st harvest. Hybrids F1 10 x 17 and 19 x 26 manifested highest heterosis over mid parent (73.1%) and better parent (61.8%), respectively, for yield per plant.

Narayan *et al.* (1996) studied genetic variability, heritability in broad sense, genetic advance in 25 diverse populations of bottle gourd. Wide range of variation was observed in most of the characters. The high value of GCV and heritability estimates associated with greater genetic advance was observed for number of primary branches per plant and yield per plant indicated that these two characters had additive gene effect and, therefore, they are more reliable for effective selection.

Bharathi *et al.* (2006) assessed genetic variability for 10 characters (days to flowering, vine length, number of nodes on which first flower appears, internode length, fruit length, girth, weight and volume, number of fruits, and yield per plant) in 32 genotypes of spine gourd (*Momordica dioica*) during 2003/04, in Bhubaneswar, Orissa, India. Analysis of variance revealed significant differences

among the genotypes studied. Phenotypic coefficient of variation (PCV) ranged from 15.26% for fruit girth to 34.28% for fruit weight, while genotypic coefficient of variation (GCV) ranged from 14.38% for fruit girth to 33.52% for fruit weight. High heritability coupled with high genetic advance were recorded for fruit weight, fruit volume and number of fruits per plant, indicating the preponderance of additive gene effects for these characters and their potential use in selection programmes to improve spine gourd productivity.

Masud *et al.* (2006) conducted a field experiment with seven inbred lines and their twenty-one hybrids of bottle gourd. Result showed significant variation in seven characters of the twenty eight populations. Variabilities were high in all seven characters indicating the possibilities of improvement through selection. Specific combining ability variance were significant for all characters while general combining estimates were significant for days to anthesis, fruit length, fruit diameter and yield per plant which indicated the presence of dominance for all the characters but additivity is for only few characters. Parent-two showed good GCA for earliness and fruit length, Parent-five showed good GCA for fruit length only and parent-seven showed good GCA for fruit diameter and fruit yield per plant. The cross involving parent-three and parent-five, which is the best for earliness, fruit length (53.5%) and; fruit yield per plant (106.8%).

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

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.

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 ten 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.

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

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.

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

Rumaran *et al.* (1997) conducted 30 pumpkin genotypes in a field trial and reported that genotypic co-efficient of variation was smaller than phenotypic coefficient 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.

2.1.1 Leaf Length (cm)

Asmaul Husna (2009) conducted an experiment with thirty one genotypes of bottle gourd in Sher-e Bangla Agricultural University. She found that the phenotypic variance (14.18) was appeared to be higher than the genotypic variance (14.14). The GCV (22.63) and PCV (22.67) were close to each other. Heritability (99.69%) estimates for this trait was very high, genetic advance (9.91) and genetic advance in percent of mean (59.65) were found moderately high indicating this trait was governed by the additive gene.

Gaffar (2008) conducted an experiment with fifteen genotypes of sponge gourd in Sher-e Bangla Agricultural University. He found that the genotypic and phenotypic variances of leaf length were 24.13 and 25.55, respectively. The GCV (20%) was slightly lower than PCV (20.58%). Heritability for this trait was 97% with moderate genetic advance (9.83) and genetic advance in percent of mean (40.03) was considerable for this trait indicating apparent variation was due to genotypes.

2.1.2 Leaf breadth

Asmaul Husna (2009) found GCV (22.87) was lower than PCV (23.04) for this character in bottle gourd.

Gaffar (2008) observed GCV (20.94%) was slightly lower than the PCV (23.31%) heritability in broad sense was high (94%) with moderate genetic advance (7.81) for this character in sponge gourd.

2.1.3 Days to first flowering

Rajkumar (2007) *et al.* found significant differences among genotype for all the characters in snake gourd. The heritable estimate was high for all the characters except days to first female flower. Banik et al. (2010) found in his experiment the parent P_4 was the best general combiner for fruits per plant, first male and female flower.

Quamruzzaman *et al.* (2008) conducted experiment the genetic divergence among thirty genotypes of ridge gourd *(Luffa acutangula)* at the farm of Olericulture Division, HRC and in different RARS, BAR] during the summer season of2005. The genotype RGN05, RGN06, RGN07, RGN08, RGN 13, RGN 17, RGN 18, RGN27, RGN29 recorded highest cluster mean values for days to 1 st male flower open (56.0 days) and single fruit weight (141.0 g) and RGN03, RGN 12 lowest mean values for days to 1st female flower open (27.0 days) and single fruit weight (85.0 g). The role of days to 1st male flower open, days to 1st female flower open, fruit diameter, single fruit weight and fruit number in PCA indicates their importance in genetic divergence. Sureshbabu (1989) studied 50 genotypes of pumpkin and observed considerable variability for days to first male flower anthesis (41.0-73.0 days) and days to first female flower opening (41.0-84.5 days). Lowest PCV was observed for days to first male flower anthesis (13 .08).

Rahman *et al.* (1991) reported that male flower were earlier than female flower in several genotypes of bottle gourd. Islam (1993) also reported that the male flowering was earlier than female flowering in several genotypes of bottle gourd. In Bitter gourd, Mannan (1992) recorded considerable variability among

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

2.1.4 Pedicel length of flower (cm)

Asmaul Husna (2009) found that in bottle gourd male flower pedicel length is 3.5-21 cm and in female flower pedicel length is 3.13-9 cm.

Rashid (1993) reported that in bottle gourd, male flower pedicel length is longer than female flower pedicel length. Grubben (2004) stated that male flowers have 7-31 cm long pedicel and female flowers have 2-10 cm long pedicel in bottle gourd.

2.1.5 Fruit length and breadth (cm)

Mathew and Khader (1999) recorded the highest GCV and PCV for fruit length in snake gourd.

Banik (2003) found high heritability coupled with high genetic advance for fruit length (GCV and PCV 29'.92, and 30.04; h^2b 99.19%) in snake gourd.

Asmaul Husna (2009) found GCV (16.49) and PCV (17.50) in male flower and GCV (15.84) and PCV (17.39) in female flower of bottle gourd plant.

Significant variation for fruit length and diameter were noticed in bitter gourd (Mangal *et al.,* 1981) sponge gourds (Arora *et al.,* 1983; Prosad and Singh, 1990), ribbed gourd and bottle gourd (Rahman *et al.,* 1991). Rahman *et al.* (1986) indicated high GCV and PCV for both length (31.73 and 33.75) and diameter (39.23 and 41.96) of fruits in bottle gourd. They also observed minimum difference between GCV and PCV. Characters having high GCV indicate high potentiality for effective selection (Burton and de Vane, 1953).

Saha *et al.* (1992) observed high GCV and PCV for fruit length (30.34 and 31.76) and low for fruit diameter (8.87 and 10.23) in pumpkin. They estimated high h^2 for both length (11.27 %) and diameter (75.07 %). They also found high genetic advance for fruit length (59.72) but low for fruit diameter (15.82).

2.1.6 Fruit weight (Kg)

Mathew and Khader (1999) recorded the highest GCV and PCV were for mean fruit weight. They observed high heritability for mean fruit weight in snake gourd.

High GCV and PCV were reported (39.55 and 41.00) by Saha *et al.* (1992); (30.2 and 36.4) by Doijode and Sulladmath (1986) for fruit weight in pumpkin. Rana *et al.* (1986) also obtained high value for this trait in pumpkin. Mannan (1992) reported narrow difference between GCV and PCV for this trait in bitter gourd indicating less environmental influence on this character. High h^2 coupled with genetic advance for average fruit weight was noticed in pumpkin (82.9% and 49.6) by Doijode and Sulladmath (1986); (93.03% and 78.58) by Saha *et al.* (1992). Prasad and Singh (1992) also obtained similar results for this trait in snake gourd and cucumber. On the other hand, low heritability (45.1%) and very high genetic advance (133.05) was recorded for this trait in ribbed gourd by thakur and Choudhury (1965). Vashistha *et al.* (1983) and Vijay (1987) noted low GCV and PCV for fruit weight in water melon (0.28 and 0.41) and musk melon (0.01 and 0.02), respectively, whereas Mangal *et al.* (1981) found high value (291.89 and 318.47) in bitter gourd.

2.1.7 Number of fruits per plant

Mathew and Khader (1999) recorded the highest GCV and PCV were for fruit yield per plant and fruit length. High heritability was observed for fruit yield per plant in their experiment.

Banik (2003) also found that significant differences in fruits per plant. The highest phenotypic co-efficient of variation was observed for fruit yield per plant. High heritability coupled with high genetic advance was noticed for number of fruits per plant (GCV and PCV 19.82 and 20.59; h^2b 92.67%).

Rahman *et al.* (1986) noted the value of genotypic and phenotypic variances for number of fruits per vine per plant in bottle gourd (1.43 and 3.10), whereas Prasad and Singh (1989), Abusaleha and Dutta (1990), Mangal *et al.* (1981) reported the value in ribbed gourd (202.26 and 475.98), muskmelon (1.71 and 1.90), cucumber (1.15 and 1.24) and bitter gourd (9.02 and 10.45).

2.1.8 Yield per plant (kg)

Banik (2003) also found that significant differences in 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.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%).

The variation for yield per plant was recorded in bottle gourd (Rahman *et al.*, 1991), water melon (chezhiyan, 1984), musk melon (Swamy *et al.*, 1984) and pumpkin (Rana *et al.*, 1986; Shaha *et al.*, 1992). Mangal *et al.* (1981) found high value (47759.63 and 55149.80) in bitter gourd while, low GCV and PCV were recorded for this character in water melon (0.44 and 1.15) and musk melon (0.04 and 0.07) by Vashistha *et al.* (1983) and Vijay (1987). Singh and Prasad (1989) and Saha *et al.* (1992) recorded high GCV and PCV for yield per plant in pointed gourd (46.50 and 64.10) and pumpkin (28.82 and 31.21). High h^2 associated with high genetic advance for yield per plant was reported by Saha *et al.* (1992).

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2.2 Correlation Co-efficient:

Kumaresan *et al.* (2006) conducted field experiments in Madurai, Tamil Nadu, India, during the 2000 rabi season, to determine correlations among different economic parameters and their direct and indirect effects on fruit yield in 6 snake gourd (*Trichosanthes cucumerina*) cultivars and their 30 hybrids. Yield per vine in snake gourd was positively associated with main vine length, number of fruits per vine, fruit weight, number of seeds per fruit, seed weight per fruit and ascorbic acid content of the fruits. However, negative association was observed with days to first female flower opening, days to first male flower opening, fruit length, fruit girth and acid content of the fruit. This indicates that the selection for the characters will simultaneously result in improving the yield per vine.

Kumar *et al.* (2007) conducted an experiment to study the correlation coefficient of 20 bottle gourd *(Lagenaria vulgaris)* genotypes. Fruit yield per vine in bottle gourd is the result of interaction of number of inter-related characters. Therefore, selection should be based on these components character after assessing their correlation with fruit yield per vine. The fruit yield per vine showed positive and significant correlation with number of branches per vine, vine length, nodes number of first male flower, nodes number of first female flower, length of edible fruits, number of fruits per vine, number of seeds per fruits and 100-seed weight at genotypic and phenotypic levels. This indicated that fruit yield can be improved by making selection on the basis of no. of branches per vive, vine length, nodes no. of first female flower, length of edible fruit and no. of fruit per vine.

Hazra *et al.* (2003) studied sixty-eight diverse female clones of T. dioica. These were grown at the Horticultural Research Station, Mondouri, West Bengal, India to evaluate growth, morphological, yield and quality characters and their relationship through correlation and path analysis. The magnitude of genotypic correlation coefficients was higher than phenotypic correlation coefficients for all the pairs of characters, and in most cases, a wide gap was recorded between the

two estimates of correlation coefficients, indicating the influence of environment on the correlated response of the pair of characters. Most of the character pairs showed negligible or insignificant correlation that might have resulted due to simultaneous vegetative and reproductive growth in the plant. Only fruit number per plant had significant positive correlation with yield, whereas fruit weight showed highest positive direct effect on yield. However, from the overall study, most of the fruit characters, viz. fruit weight, pulp content of fruit, fruit number per plant and fruit volume, and growth traits, such as leaves per plant and leaf length, were identified as important yield contributors.

Prasana *et al.* (2002) studied the correlation between the yield and yield components of ridge gourd (*Luffa acutangula*) in Bangalore, Karnataka, India, during the rabi of 1999. Fruit yield per hectare was positively associated with vine length at 90 days after sowing (DAS), number of leaves at 90 DAS, number of female flowers, total dry weight of plant, number of fruits, and fruit girth and weight.

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.

Narayan *et al.* (1996) studied correlation analysis in 25 diverse populations of bottle gourd. Correlation coefficient revealed that fruit yield per plant can be successfully improved by making selection or greater fruit number, higher fruit weight, greater number of primary branches and genotypes with lesser number of days to anthesis of first male flower.

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.

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

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

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.

Sarker *et al.* (1999) studied correlation and path co-efficient of 16 divergence types of pointed gourd indicated that fruit weight, fruit diameter and number of primary branches per plant were positively and significantly correlated with yield per plant at genotypic and phenotypic levels.

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.

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

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.

Mandal (1987) conducted a study on 30 diverse cucumber genotypes and found high positive correlation at the genotypic and phenotypic levels between yield per plant with number of fruits and female flowers per plant, fruit length and weight.

According to Singh *et al.* (1986) 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 in pointed gourd. Reddy and Rao (1984) observed negative and non-significant correlation between male flower pedicel length, female flower pedicel length traits (r =0 0.222) in ribbed gourd.

2.3 Path Co-efficient:

Kumaresan *et al.* (2006) conducted field experiments in Madurai, Tamil Nadu, India, during the 2000 rabi season, to determine correlations among different economic parameters and their direct and indirect effects on fruit yield in 6 snake gourd (Trichosanthes cucumerina) cultivars and their 30 hybrids. Path coefficient

analysis revealed that it would be highly rewarding to lay emphasis on the number of fruits per vine and fruit weight to increase the yield per vine directly.

Kumar *et al.* (2007) conducted an experiment to study the path coefficient of 20 bottle gourd *(Lagenaria vulgaris)* genotypes. Path analysis revealed that number of branches per vine, vine length, nodes number of first female flower and number of fruit per vine had positive direct effect on fruit yield per vine. Narayan *et al.* (1996) studied path-coefficient analysis in 25 diverse populations of bottle gourd. Path coefficient analysis revealed that maximum weight age should be given primarily to days to first harvest followed by average weight of edible fruit, number of fruits per plant and days to anthesis of first female flower while formulating selection indices for improvement of yield in bottle gourd.

Rahman *et al.* (1986) studied Variability, correlation and path coefficients in four lines of bottle gourd. Path coefficient analysis revealed that fruit diameter and fruit length had high positive direct effect on fruit weight per plant. Number of fruits per plant also had considerable positive direct effect on fruit weight per plant. Singh *et al.* (2002) were carried out 98 hybrids of cucumber derived from crosses involving fourteen male and seven female parents. Path coefficient analysis indicated that fruit weight had the highest direct effect on 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 fiuit, fruits per plant or vine, fruit per branch and length of the vine of ridge gourd.

Miah *et al.* (2000) conducted an experiment on bitter gourd for correlation and path coefficient analysis. 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 path co-efficient of 16 divergence types of pointed gourd. The path analysis revealed that fruit volume followed by fruit weight and fruit diameter had maximum positive direct effects on yield. Li *et al.* (1997) conducted an experiment on cucumber genotypes. From path analysis, they concluded that fruits per plant and average fruit weight affected the yield directly.

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

Kumaran *et al.* (1998) carried out an experiment on correlation and path analysis studies in pumpkin. They found that number of fruit per plant exhibited the highest direct effect on yield. High positive indirect effects were exerted by number of fruit per plant and mean fruit weight.

Abusaleha and Dutta (1989) carried out an experiment on correlation and path analysis studies in cucumber. Path coefficient analysis revealed that f,uuits per vine and fruit length had the greatest direct effects on yield.

Chaudhury and Mandal (1987) conducted a study on 30 diverse cucumber genotypes and Path co-efficient analysis revealed that the number of fruits, female flowers per plant, fruit length, fruit weight and fruit diameter were the most important characters determining yield.

Parhi *et al.* (1995) studied correlation and path co-efficient of thirteen genotypes of bitter gourd. Path analysis revealed that fruit breadth, days to

opening of first male and female flower, vine length and number of seeds per fruit had the maximum positive direct effect on yield in bitter gourd. The characters like fruit weight and fruit length though have significant positive correlation with yield, exhibited low direct effect. Besides direct selection for yield, indirect selection through number of seeds per fruit and fruit weight would prove worth for further improvement in yield of bitter gourd.

Prasanna *et al.* (2002) studied the correlation between the yield and yield components of ridge gourd *[Luffa acutangula]* in Bangalore, Karnataka, India, during the rabi of 1999. Fruit yield per hectare was positively associated with vine length at 90 days after sowing (DAS), number of leaves at 90 DAS, number of female flowers, total dry weight of plant, number of fruits, and fruit girth and weight. Path coefficient analysis showed that vine length at 90 DAS, number of female flowers per vine, number of branches per vine, number of fruits per vine, fruit girth, and fruit weight had direct positive effects on fruit yield, whereas the number of leaves at 90 DAS, total dry weight of the plant, and fruit length had negative direct effects on fruit yield. The fruit yield of ridge gourd can be enhanced through the improvement of vine length at 90 DAS, number of female flowers, number of branches, number of fruits per vine, fruit girth, and fruit weight.

Umamaheswarappa *et al.* (2004) conducted an experiment on the effect of various rates of nitrogen (0, 60 and 120 kg/ha), phosphorus (0, 50 and 100 kg/ha) and potassium (0, 30 and 60 kg/ha) on bottle gourd (*Lagenaria siceraria*), conducted in Bangalore, Karnataka, India, in 1999 showed that fruit yield/ha had strong positive association with vine length, number of leaves per vine, number of female flowers per vine, number of branches per vine, vine girth, total chlorophyll content in leaf, total dry weight of plant, number of fruits per vine, fruit weight, fruit length and fruit girth. Path coefficient analysis revealed that number of fruits per vine had maximum direct effect on fruit yield followed by fruit weight.

2.4 Genetic Diversity:

Genetic diversity is one of the important tools to quantify variability in both self and cross-pollinated crops (Griffing and Lidstorm, 1954; Murty and Arunachalam, 1966: Guar *et al.* 1978).

The quantification of genetic diversity through biometrical procedure made it possible to choose genetically diverse plants for a successful hybridization programme (Rao, 1952). D^2 analysis (originally outlined by Mahalanobis, 1936 and extended by Rao, 1952) is one of potential methods of estimating the degree of genetic diversity. The wide diversity of genotypes can be shown by cluster analysis from the same geographical regions. To understand the usable variability, grouping or classification of genotypes based on suitable scale. Multivariate analysis formulated by Mahalanobis (1936) is a powerful tool in quantifying the degree of divergence among biological population based on multiple characters. Studies on genetic diversity in bottle gourd carried out so far are presented as follows:

Khatun *et al.* (2010) conducted at the field and laboratory of the Department of Horticulture, Bangladesh Agricultural University, Mymensingh during the period from April 2004 to September 2004 to study the nature and magnitude of genetic diversity of 38 snake gourd genotypes collected from different regions of the country. Based on D2 analysis, the genotypes were grouped into four different clusters, where the cluster I possessed maximum number (21) of genotypes followed by the cluster 11(8), III (7), and IV (2). Clustering pattern revealed that geographical diversity was not associated with genetic diversity i.e., genotypes collected from same location were grouped into different clusters. The maximum inter-cluster distance was observed between the clusters III and IV and that of minimum in between the clusters I and II. In case of intra-cluster distance, the maximum distance was observed in the cluster IV and that of minimum was observed in the cluster III. Considering cluster mean, the genotypes of cluster IV could be selected for yield per plant and other yield contributing characters.

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

BARI annual report 2008-09 revealed that Genetic divergence among 30 snake gourd genotypes was estimated using Mahalanobis's D^2 staistic. Cluster V contained the highest number of genotypes (13) and cluster III &IV contained the lowest (3). The highest intra- cluster distance was observed in cluster III (1.665) and the lowest in cluster V (0.430). The highest inter- cluster distance was observed between cluster I and III (26.954) and the lowest in cluster II and IV (5.693).

Islam *et al.* (2010) studied genetic divergence of twenty bitter gourd genotypes through Moahalanobis's D^2 and principal component analysis in Pakistan. The genotypes under study fall into four clusters. The cluster I contained the highest number of genotypes and it was 10. Cluster IV contained the lowest number of genotypes. Cluster II produced the highest mean value for weight per fruit. The inter cluster distances were much higher than the intra cluster distances. Cluster I exhibit the highest intra cluster distance while the lowest distance was observed in cluster III. The highest inter cluster distance was observed between I and II while the lowest distance was observed between the cluster II and IV. The highest intra cluster means for weight per fruit and five important yield contributing characters were obtained from cluster II. Therefore, more emphasis should be given on the cluster for selecting genotypes as parents for crossing with the genotypes of cluster II which may produce new recombination with desired traits. Considering all the characters the G1 (Shaparan), G5, (Rampali gaj), G9 (Nabil), G12

(Nandita) G14 (Eureca), G16 (Tia) and G19 (Maharaj) were selected for future breeding programme.

Preeti *et al.* (2010) observed wide range of genetic diversity among twenty three germplasm lines of ash gourd collected from different parts of U.P. and Uttarakhand. Genotypes PAG-50, Pant Petha-1, PAG-64, PAG-12, PAG-14 and PAG-09 were high yielding lines while considering both the season's summer and kharif 2006. Based on Mahalanobis D2 analysis all germplasm lines were grouped into 5 clusters. The clustering pattern indicated that geographical distribution need not necessarily be related to the genetic diversity. Cluster I was very large containing 14 genotypes (summer) and 10 genotypes (kharif) season. The commercially released cultivar Pant Petha-1 was grouped in cluster II along with other genotypes in both the seasons. The inter-cluster distance was found maximum between cluster III and cluster IV (summer) and cluster II and cluster V in (kharif) seasons. The genotypes in these clusters may possibly be utilized in hybrid breeding programme for successful exploitation of hybrid vigour in ash gourd.

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 for the cluster 11 (0.882) and the lowest for the cluster III (0.220). The highest inter-cluster distance was observed between cluster I and II (15.045) where as the lowest was observed between cluster IV and V (3.402).

Gaffar (2008) conducted an experiment with 15 sponge gourd genotypes at the experimental farm of Sher-e-Bangla Agricultural University, during April 2007 to October 2007. The genotypes were grouped into five clusters. The highest intra cluster distance was noticed for the cluster Iii (0.999) and the lowest for the cluster IV (0.439). The highest inter-cluster distance was observed

between cluster IV and V (7.163) where as the lowest was observed between cluster I and IV (2.258).

Khan *et al.* (2008) assessed the genetic diversity among 64 pointed gourd genotypes through multivariate analysis from an experiment conducted in Regional Agricultural Research Station, Ishurdi, Pabna during the growing season 2002-2003. The genotypes were grouped into twelve clusters. The cluster V consisted of highest number of genotypes and it was nine, the cluster VI and cluster VIII contained the lowest number of genotypes and it was two in each. The clustering pattern of the genotypes under this study revealed that the genotypes collected from the same location were grouped into different clusters. The genotypes of Jessore were distributed in different clusters. The highest inter genotype distance as 366.3 observed between the genotypes P0022 and P0007 and the lowest 2.6 as observed between the genotypes P0043 and P0044. Cluster V had the highest cluster mean value for internodes length, fruit weight per plant and yield the highest inter-cluster distance was noticed between cluster III and 11 (45.71) and the lowest between cluster VII acid Y 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.

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 11 (4) & Cluster IV (3).The highest intra cluster distance was computed for cluster IV (35.80) followed by cluster I (28.12) and Cluster V (26.63). The minimum intra cluster distance was found in III (18.87).

Bharathi *et al.* (2005) The genetic divergence among 32 genotypes of spine gourd (*Momordica dioica*) for 12 traits (vine length, number of days to flowering, node on which the first flower appeared, internode length, mature leaf size, pedicel length, petiole length, fruit weight, fruit length, fruit girth, number of fruits per plant, and yield per plant) was evaluated in Orissa, India. The analysis of variance revealed significant variation among the genotypes for all traits. The genotypes were grouped into 7 clusters based on D2 values. Cluster III had the highest number of genotypes (11), followed by clusters IV (9) and VI (4). The intracluster distance ranged from 30.34 (cluster I) to 371.56 (cluster III). The intercluster distance was greatest between clusters VI and VII (864.75). Genotypes included in cluster II were characterized by early flowering, and presence of the longest vines and internodes. Cluster VI recorded the greatest number of fruits, pedicel length and yield. Cluster VII was superior with regard to the node on which the first flower appeared. Cluster III had the greatest fruit weight, fruit length and fruit girth. Yield per plant, number of fruits, fruit weight, internode length, fruit length and pedicel length accounted for 93.55% of the diversity. Thus, selection for divergent parents based on these traits is recommended.

Genetic divergence using Mahalanobis D^2 statistics was studied for seven quantitative characters including yield per vine in a collection of twenty diverse cultivars of bottle gourd by Badade *et al.* (2001). The cultivars differed significantly for almost all of the characters and were grouped into 10 clusters based on the similarities of D^2 value. Considerable diversity within and between clusters was noted and it was observed for the characters viz. vine -length, number of branches, fruit per vine, length and diameter of fruit and yield per vine.

Karuppaiah *et al.* (2005) evaluated genetic divergence in 12 genotypes of bitter gourd *(Momordica charantia)* grown in Annamalai, Tamil Nadu, India, during June-July 2001. Using Mahalanobis D^2 technique, the genotypes were grouped into clusters I (4 genotypes), II (one genotype), III (3 genotypes) and IV (four genotypes). Among the four clusters, cluster IV (LA-7, LA-9, LA-10 and LA-

12) registered the highest mean values for vine length (6.2 m), number of male flowers per plant (79.3), number of female flowers per plant (23.2), yield per plant (5.2 kg), single fruit weight (242.2 g), fruit length (29.4 cm), number of fruits per plant (24.1), number of seeds per fruit (52.3), fruit size index (173.2). and 100-seed weight (18.6 g). Hence, it is desirable to involve LA-7, LA-9, La-10 and LA- 12 of cluster IV in breeding programmes.

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

Islam (2004) estimated genetic divergence among 42 bottle gourd (L. siceraria) accessions from Bangladesh was estimated in Japan during 2000 using D2 and canonical analysis. The accessions were grouped into five clusters. No clear relationship was observed between geographic origin and genetic diversity. The maximum intercluster distance was between cluster I and cluster II, and the minimum was between cluster III and cluster IV. Primary branches per plant, fruit length and weight, number of fruits and yield per plant contributed the most to the total genetic divergence. The results obtained by D2 analysis were also confirmed by canonical analysis. The accessions included in the most divergent clusters I and II, are promising parents for a hybridization programme for obtaining high heterosis and thus, better segregants in bottle gourd.

Dora (2001) studied eleven genotypes of *Trihosanthes dioica* and the genotypes were grouped into four clusters based on Mahalanobis's D^2 statistics and found that intercluster 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.

Masud *et al. (1995)* carried out an experiment to study the genetic divergence among 27 genotypes of pumpkin *(Cucurbita moschata)* collected from eight districts of Bangladesh was group into seven cluster. No relationship was found between genetic divergence and geographic distribution of the genotypes. Maximum inter cluster distance was observed between cluster II and VII and was minimum between V and VI. Number of fruits per plant and yield per plant showed maximum contribution to the total divergence. The results obtained by D^2 analysis were confirmed by principal component analysis.

Chapter 3

Materials and Methods

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CHAPTER III

MATERIALS AND METHODS

The investigation was carried out at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh during the period from March 2010 to August 2010 to study on the genetic diversity, correlation and path analysis in sweet gourd. A brief description about the locations of the experimental site, characteristics of soil, climate, materials, layout and design of the experiment, land preparation, manuring and fertilizing, transplanting of seedlings, intercultural operations, harvesting, data recording procedure, economic and statistical analysis etc., which are presented as follows:

3.1. Experimental site

The research work was conducted at the Sher-e-Bangla Agricultural University Farm, Dhaka-1207 during March 2010 to August 2010.

3.2 Geographical Location

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

3.3 Climate

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

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

3.4 Characteristics of soil

Soil of the experimental site belongs to the general soil type, Shallow Red Brown Terrace Soils under Tejgaon Series. Top soils were clay loam in texture, olive-gray with common fine to medium distinct dark yellowish brown mottles. Soil pH ranged from 6.0- 6.6 and had organic matter 0.84%. Experimental area was flat having available irrigation and drainage system and above flood level. Soil samples from 0-15 cm depths were collected from experimental field. The analyses were done by Soil Resource and Development Institute (SRDI), Dhaka. Physicochemical properties of the soil are presented in (Appendix III).

3.5 Planting materials

Twenty one genotypes of sweet gourd were used for the present research work. The purity and germination percentage were leveled as around 100 and 80, respectively. The genetically pure and physically healthy seeds of these genotypes were collected from Plant Genetic Resources Centre (PGRC) of Bangladesh Agricultural Research Institute (BARI) Gazipur. The name and origin of these genotypes are presented in (Table 1).

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

SL No.	Genotype No.	BARI ACC Number	Origin
1	G1	BD-2151	PGRC,BARI
2	G2	BD-2153	PGRC, BARI
3	G3	BD-2174	PGRC, BARI
4	G4	BD-2177	PGRC, BARI
5	G5	BD-264	PGRC, BARI
6	G6	BD-2196	PGRC, BARI
7	G7	BD-2203	PGRC, BARI
8	G8	BD-2212	PGRC, BARI
9	G9	BD-2214	PGRC, BARI
10	G10	BD-2222	PGRC, BARI
11	G11	BD-2229	PGRC, BARI
12	G12	BD-4590	PGRC, BARI
13	G13	BD-266	PGRC, BARI
14	G14	BD-9489	PGRC, BARI
15	G15	BD-9490	PGRC, BARI
16	G16	BD-9491	PGRC, BARI
17	G17	BD-9493	PGRC, BARI
18	G18	BD-9494	PGRC, BARI
19	G19	BARI mistikumra-1	PGRC, BARI
20	G20	BARI mistikumra-2	PGRC, BARI
21	G21	BD-2150	PGRC, BARI

Here, PGRC = Plant Genetic Resources Centre, BARI = Bangladesh Agricultural Research Institute

3.6 Design and layout of the experiment

The experiment was laid out Randomized Complete Block Design (RCBD) with three replications. The genotypes were distributed into the pit of each block of the prepared layout of the experiment. The twenty one genotypes of the experiment were assigned at random into pits of each replication. The distance maintained spacing pit to pit 3 m. The distance maintained between two blocks was 3 m.

3.7 Poly bag preparation and raising seedling

Due to uncertain rainfall during the period of the study, the seeds were dibbled in poly bag for higher germination percentage and to get healthy seedlings and when the seedlings become 20 days old; those were transplanted in the main field in the pit. Seeds were sown 10 March, 2010 before sowing seeds were treated with Bavistin for 5 minutes.

3.8 Land preparation

The experiment plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about good tilth in the first week of March, 2010. Weeds and other stables were removed carefully from the experimental plot and leveled properly.

3.9 Pit preparation

After final land preparation, pits of 55 cm x 55 cm x 50 cm were prepared in each block with spacing of 3 m x 3 m. Pits were kept open in the sun for 7 days to kill harmful insect and microorganisms. To control field cricket 5 mg Furadan was also mixed with the soils of each pit before making it ready for dibbling.

3.10 Application of manure and fertilizers

Total cowdung, half of TSP and one third MOP were applied in the field during final land preparation. Remaining TSP and one third MOP and whole gypsum and zinc oxide and one third of urea were applied in pit one week prior to transplantation. Remaining urea and MOP were applied as top dressing in four installments at 20, 40, 60 and 75 days after transplanting. Doses of manure and fertilizers used in the study are shown in table 2.

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

SL No.	Fertilizer/Manure	Dose
1.	Cowdung	10 ton/ha
2.	Urea	125 kg/ha
3.	TSP	125 kg/ha
4.	MOP	150 kg/ha
5.	Gypsum	75 kg/ha
6.	Zinc Oxide	10 kg/ha

3.11 Transplanting of seedlings

Within 12 days germination of seeds was completed and the seedlings of different accessions were planted in the pit on 2 April, 2010. In each pit two seedlings were planted and the soil around the plant was firmly pressed by hand.

3.12 Intercultural operations

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

3.12.1 Thinning and gap filling

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

3.12.2 Weeding and mulching

Several weeding and mulching were done as per requirement. At the very first stage, weeding was done for ease of aeration and less competition seedling growth and mulch was provided after an irrigation to prevent crust formation and facilitate good aeration.

3.12.3 Irrigation and after-care

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

3.12.4 Pesticide application

At the seedling stage red pumpkin beetle attacked tender leaves for this Malathion and Ripcord was sprayed in the field. In mature stage cucurbit fruit fly caused severe damage to the fruit. For a protection from fruit fly, MSGT,(Mashed Sweet Gourd Trap) and Pheromone bait was used along with ripcord, sevin powders.

3.13 Harvesting

The fruit takes about 7-10 days from setting to reach marketable stage. Fruits were picked on the basis of horticultural maturity, size, color and age being determined for the purpose of consumption as the fruit grew rapidly and soon get beyond the marketable stage, frequent picking was done throughout the harvesting period. Fruits were picked with sharp knife and care was taken to avoid injury of the vine.

3.14 Data recording

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

3.14.1 Plant characteristics

3.14.1.1 Leaf length (cm)

Leaf length was measured in three to five leaves in each germplasm in cm and average data ware recorded.

3.14.1.2 Leaf breadth (cm)

Leaf breath was measured in three to five leaves in each germplasm in cm and average data ware recorded.

3.14.1.3 Internodes distance (cm)

Internodes distance was measured in three to five Internodes in each germplasm in cm and average data ware recorded.

3.14.2 Inflorescences characteristics

3.14.2.1 Days to first male flowering

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

3.14.2.2 Days to first female flowering

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

3.14.2.3 Pedicel length of male flower (cm)

Pedicel length of male flower was measured in three to five flowers in each germplasm in cm and average data ware recorded.

3.14.2.4 Pedicel length of female flower (cm)

Pedicel length of female flower was measured in three to five flowers in each germplasm in cm and average data ware recorded.

3.14.3 Fruit characteristics

3.14.3.1 Fruit length (cm)

Fruit length was measured in three to five fruits in each germplasm in cm and average data was recorded during fruit harvest for vegetable use.

3.14.3.2 Fruit breadth (cm)

Fruit diameter was measured in three to five fruits in each germplasm in cm, then the data was divided by two and average data was recorded during fruit harvest for vegetable use.

3.14.3.3 Fruit weight (Kg)

Weight of three to five fruits in each germplasm during harvest for vegetable use was measured in kilogram.

3.14.3.4 Fruit yield per plant (Kg)

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

3.15.1 Statistical analysis

Mean data of the characters were subjected to multivariate analysis. Univariate analysis of the individual character was done for all characters under study using the mean values (Singh and Chaudhury, 1985) and was estimated using MSTAT-C computer program. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV %) were also estimated using MSTAT-C. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2000 software through four techniques viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA).

3.15.1.1 Estimation of genotypic and phenotypic variances

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

$$\textbf{Genotypic variance } (\sigma^2 g) = \frac{\textbf{GMS-EMS}}{\textbf{r}}$$

Where,

GMS = Genotypic mean sum of squares

EMS = Error mean sum of square

r = number of replications

$$\text{Phenotypic variance } (\sigma^2 p) = \sigma^2_g + \text{EMS}$$

Where,

σ^2_g = Genotypic variance

EMS = Error mean sum of square

3.15.1.2 Estimation of genotypic and phenotypic correlation co-efficient

For calculating the genotypic and phenotypic correlation co-efficient for all possible combinations the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956) were adopted. The genotypic co-variance component between two traits and have the phenotypic covariance component were derived in the same way as for the corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows:

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

Where,

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

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

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

Phenotypic correlation (r_{pxy}) =

$$\frac{\sigma_{pxy}}{\sqrt{\sigma^2_{px}\ \sigma^2_{py}}}$$

Where,

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

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

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

3.15.1.3 Estimation of genotypic and phenotypic co-efficient of variation

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

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

Where,

σ^2_g = Genotypic variance

$\overline{x}$ = Population mean similarly,

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

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

Where,

σ^2_{ph} = Phenotypic variance

$\overline{x}$ = Population mean

3.15.1.4 Estimation of heritability

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

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

Where,

h^2 b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.15.1.5 Estimation of genetic advance

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

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

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

Where,

K = Selection intensity, the value which is 2.06 at 5% selection intensity

σ_{ph} = Phenotypic standard deviation

h^2 b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.15.1.6 Estimation of genetic advance mean's percentage

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

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

3.15.1.7 Estimation of path co-efficient

Path coefficient analysis was done according to the procedure employed by Dewey and Lu (1959) quoted in Singh and Chaudhary (1985), using phenotypic correlation coefficient value. In path analysis, correlation coefficients between yield and yield contributing characters were partitioned into direct and indirect effects of yield contributing characters on grain yield per hectare. In order to estimate direct and indirect effects of the correlated characters, i. e. 1, 2, 3.....and 13 on yield y, a set of simultaneous equations (eight equations in this example) is required to be formulated as shown in below:

$r_{1.y} = P_{1.y} + r_{1.2} P_{2.y} + r_{1.3} P_{3.y} + r_{1.4} P_{4.y} + r_{1.5} P_{5.y} + r_{1.6} P_{6.y} + r_{1.7} P_{7.y} + r_{1.8} P_{8.y}+ r_{1.9}P_{9.y} + r_{1.10} P_{10.y} + r_{1.11} P_{11.y} + r_{1.12} P_{12.y}$

$r_{2.y} = r_{1.2} P_{1.y} + P_{2.y} + r_{2.3} P_{3.y} + r_{2.4} P_{4.y} + r_{2.5} P_{5.y} + r_{2.6} P_{6.y} + r_{2.7} P_{7.y} + r_{2.8} P_{8.y}+ r_{2.9}P_{9.y} + r_{2.10} P_{10.y} + r_{2.11} P_{11.y} + r_{2.12} P_{12.y}$

$r_{3.y} = r_{1.3} P_{1.y} + r_{2.3} P_{2.y} + P_{3.y} + r_{3.4} P_{4.y} + r_{3.5} P_{5.y} + r_{3.6} P_{6.y} + r_{3.7} P_{7.y} + r_{3.8} P_{8.y}+ r_{3.9}P_{9.y} + r_{3.10} P_{10.y} + r_{3.11} P_{11.y} + r_{3.12} P_{12.y}$

$r_{4.y} = r_{1.4} P_{1.y} + r_{2.4} P_{2.y} + r_{3.4} P_{3.y} + P_{4.y} + r4_{1.5} P_{5.y} + r_{4.6} P_{6.y} + r_{4.7} P_{7.y} + r_{4.8} P_{8.y}+ r_{4.9} P_{9.y} + r_{4.10} P_{10.y} + r_{4.11} P_{11.y} + r_{4.12} P_{12.y}$

$r_{5.y} = r_{1.5} P_{1.y} + r_{2.5} P_{2.y} + r_{3.5} P_{3.y} + r_{4.5} P_{4.y} + P_{5.y} + r_{5.6} P_{6.y} + r_{5.7} P_{7.y} + r_{5.8} P_{8.y}+ r_{5.9} P_{9.y} + r_{5.10} P_{10.y} + r_{5.11} P_{11.y} + r_{5.12} P_{12.y}$

$r_{6.y} = r_{1.6} P_{1.y} + r_{2.6} P_{2.y} + r_{3.6} P_{3.y} + r_{4.6} P_{4.y} + r_{5.6} P_{5.y} + P_{6.y} + r_{6.7} P_{7.y} + r_{6.8} P_{8.y}+ r_{6.9} P_{9.y} + r_{6.10} P_{10.y} + r_{6.11} P_{11.y} + r_{6.12} P_{12.y}$

$r_{7.y} = r_{1.7} P1.y + r_{2.7} P_{2.y} + r_{3.7} P_{3.y} + r_{4.7} P_{4.y} + r_{5.7} P_{5.y} + r_{6.7} P_{6.y} + P_{7.y} + r_{7.8} P_{8.y}+ r_{7.9} P_{9.y} + r_{7.10} P_{10.y} + r_{7.11} P_{11.y} + r_{7.12} P_{12.y}$

$r_{8.y} = r_{1.8} P_{1.y} + r_{2.8} P_{2.y} + r_{3.8} P_{3.y} + r_{4.8} P_{4.y} + r_{5.8} P_{5.y} + r_{6.8} P_{6.y} + r_{7.8} P_{7.y} + P_{8.y}+ r_{8.9} P_{9.y} + r_{8.10} P_{10.y} + r_{8.11} P_{11.y} + r_{8.12} P_{12.y}$

$r_{9.y} = r_{1.9} P_{1.y} + r_{2.9} P_{2.y} + r_{3.9} P_{3.y} + r_{4.9} P_{4.y} + r_{5.9} P_{5.y} + r_{6.9} P_{6.y} + r_{7.9} P_{7.y} + r_{8.9} P_{8.y} + P_{9.y} + r_{9.10} P_{10.y} + r_{9.11} P_{11.y} + r_{9.12} P_{12.y}$

$r_{10.y} = r_{1.10} P_{1.y} + r_{2.10} P_{2.y} + r_{3.10} P_{3.y} + r_{4.10} P_{4.y} + r_{5.10} P_{5.y} + r_{6.10} P_{6.y} + r_{7.10} P_{7.y} + r_{8.10} P_{8.y} + r_{9.10} P_{9.y} + P_{10.y} + r_{10.11} P_{11.y} + r_{10.12} P_{12.y}$

$r_{11.y} = r_{1.11} P_{1.y} + r_{2.11} P_{2.y} + r_{3.11} P_{3.y} + r_{4.11} P_{4.y} + r_{5.11} P_{5.y} + r_{6.11} P_{6.y} + r_{7.11} P_{7.y} + r_{8.11} P_{8.y} + r_{9.11} P_{9.y} + r_{10.11} P_{10.y} + P_{11.y} + r_{11.12} P_{12.y}$

$r_{12.y} = r_{1.12} P_{1.y} + r_{2.12} P_{2.y} + r_{3.12} P_{3.y} + r_{4.12} P_{4.y} + r_{5.12} P_{5.y} + r_{6.12} P_{6.y} + r_{7.12} P_{7.y} + r_{8.12} P_{8.y} + r_{9.12} P_{9.y} + r_{10.12} P_{10.y} + r_{11.12} P_{11.y} + P_{12.y}$

Where,

r_{1y} = Genotypic correlation coefficients between y and I th character (y = Grain yield)

P_{iy} = Path coefficient due to i th character (i= 1, 2, 3,……,13)

1 = Days to first male flowering

2 = Days to first female flowering

3 = Leaf length (cm)

4 = Leaf breadth (cm)

5 = Internode distance (cm)

6 = Pedicel length of male flower (cm)

7 = Pedicel length of female flower (cm)

8 = Number of male flower per plant

9 = Number of female flower per plant

10 = Fruit weight (kg)

11 = Fruit length (cm)

12 = Fruit breadth (cm)

Total correlation, say between 1 and y i. e., r_{1y} is thus partitioned as follows:

$P_{1.y}$ = the direct effect of 1 on y

$r_{1.2} P_{2.y}$ = indirect effect of 1 via 2 on y

$r_{1.3} P_{3.y}$ = indirect effect of 1 via 3 on y

$r_{1.4} P_{4.y}$ = indirect effect of 1 via 4 on y

$r_{1.5} P_{5.y}$ = indirect effect of 1 via 5 on y

$r_{1.6} P_{6.y}$ = indirect effect of 1 via 6 on y

$r_{1.7} P_{7.y}$ = indirect effect of 1 via 7 on y

$r_{1.8} P_{8.y}$ = indirect effect of 1 via 8 on y

$r_{1.9} P_{9.y}$ = indirect effect of 1 via 9 on y

$r_{1.10} P_{10.y}$ = indirect effect of 1 via 10 on y

$r_{1.11} P_{11.y}$ = indirect effect of 1 via 11 on y

$r_{1.12} P_{12.y}$ = indirect effect of 1 via 12 on y

Where,

$P_{1.y}$, $P_{2.y}$, $P_{3.y}$,..... $P_{8.y}$ = Path coefficient of the independent variables 1, 2, 3,.....,12 on the dependent variable y, respectively.

$r_{1.y}$, $r_{2.y}$, $r_{3.y}$, ..., $r_{12.y}$ = Correlation coefficient of 1, 2, 3, ..., 12 with y, respectively.

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)

$P^2_{RY} = 1 - (r_{1.y}P_{1.y} + r_{2.y}P_{2.y} + ... + r_{12.y}P_{12.y})$

Where,

$P^2_{RY} = R^2$

Hence residual effect, $R = (P^2_{RY})^{1/2}$

$P_{1.y}$ = Direct effect of the 1st character on yield y.

$r_{1.y}$ = Correlation of the 1st character with yield y.

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3.15.2 Multivariate analysis

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

3.15.2.1 Principal component analysis (PCA)

Principal component analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done

from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity. Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.15.2.2 Principal coordinate analysis (PCO)

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

3.15.2.3 Cluster analysis (CA)

Cluster analysis divides the genotypes of a data set into some number of mutually exclusive groups. Clustering was done using non-hierarchical classification. In Genstat, the algorithm is used to search for optimal values of chosen criterion proceeds as follows. Starting from some initial classification of the genotypes into required number of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

3.15.2.4 Canonical vector analysis (CVA)

Canonical vector analysis (CVA) finds linear combination of original variabilities that maximize the ratio of between group to within group variation, thereby

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

3.15.2.5 Calculation of D^2 values

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

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

Where,

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

x = Number of characters.

3.15.2.6 Computation of average intra-cluster distances

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

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

Where,

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

n = Number of all possible combinations between the populations in cluster.

3.15.2.7 Computation of average inter-cluster distances

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

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

Where,

$\sum D_{ij}^2$= The sum of distances between all possible combinations of the populations in cluster i and j.

n_i= Number of populations in cluster i.

n_j = Number of populations in cluster j.

3.15.2.8 Cluster diagram

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

3.15.2.9 Selection of varieties for future hybridization programme

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

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

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

iii. Relative contribution of the characters to the total divergence

iv. Other important characters of the genotypes performance

Chapter 4

Results and Discussion

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CHAPTER IV

RESULTS AND DISCUSSION

The results obtained from the study are presented and discussed in this chapter. The data pertaining to sweet gourd genotypes as well as yield and its contributing characters were computed and statistically analyzed and the results thus obtained are discussed below under the following heads:

1. Genetic parameters
2. Correlation co-efficient
3. Path co-efficient analysis
4. Multivariate analysis

4.1 GENETIC PARAMETERS

The analysis of variances indicated that the existence of highly significant variation among the genotypes studied. The mean sum of square, mean, range, variance components, genotypic and phenotypic coefficients of variations, heritability, genetic advance and genetic advance in percent of mean (GAPM) are presented in (Table 3).

The results are discussed character wise as follows:

4.1.1 Leaf length (cm)

Mean sum of square for leaf length was 24.51 which was highly significant due to genotypes in sweet gourd (Table 3) indicating existence of considerable difference for this trait. The maximum leaf length was found 21.60 in BD-2212 and the minimum was recorded 11.33 in BARI mistikumra-2 with mean value 17.20 (Appendix IV). The phenotypic variance (8.71) appeared to be slightly higher than the genotypic variance (7.90) suggested less influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation (16.34) and phenotypic co-efficient of variation (17.16) were close to each other. This character showed high heritability (90.70) estimation together with moderately high genetic advance

in percent of mean (32.03) indicating the trait was governed by the additive gene. Therefore selection based on this character would be effective. Asmaul Husna (2009) found that the genotypic variance (14.18) was appeared to be higher than the genotypic variance (14.14) in bottle gourd. The GCV (22.63) and PCV (22.67) were close to each other. Heritability (99.69%) estimates for this trait was very high, genetic advance (9.91) and genetic advance in percent of mean (59.65) were found moderately high indicating this trait was governed by the additive gene. Gaffar (2008) found high heritability and moderate genetic advance for this trait in sponge gourd. Photograph showing variation of leaf length among different genotypes of wax gourd in Plate 1a and 1b.

4.1.2 Leaf breadth (cm)

Significant mean sum of square for leaf breadth (38.32) indicated considerable difference among the genotype studied (Table 3). The maximum leaf breadth was found 30.67 in BD-9490 and the minimum was recorded 15.20 in BARI mistikumra-2 with mean value 23.39 (Appendix IV). The phenotypic variance (8.71) appeared to be slightly higher than the genotypic variance (7.90) suggested less influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 15.04 and 15.76 respectively. Heritability (91.12%) estimates for this trait was very high, genotypic advance (6.92) and genotypic advance in percent of mean (29.59) was found moderately high, indicated that this character was governed by additive gene. Husna (2009) found GCV (22.87) was lower than PCV (23.04) for this character in bottle gourd. Gaffar (2008) observed heritability in broad sense was high (94%) with moderate genetic advance (7.81) for this character in sponge gourd and also found the similar GCV (20.95%) and PCV (23.31%) in sponge gourd. Photograph showing variation of leaf breadth among different genotypes of sweet gourd in Plate 1a and 1 b.

Table 3 Estimation of genetic parameters in thirteen characters of 27 genotypes in sweet gourds

Parameters	Range	Mean	MS_G	$\sigma^2 p$	$\sigma^2 g$	$\sigma^2 e$
Leaf length without petiole (cm)	**11.33-21.60**	17.20	24.51**	8.71	7.90	0.81
Leaf breadth (cm)	**15.20-30.67**	23.39	38.32**	13.58	12.37	1.21
Internode distance	**10.00-20.00**	14.17	29.12**	12.61	8.25	4.36
Days to first male flowering	**60.00-86.33**	70.38	150.44**	62.30	44.07	18.23
Days to first female flowering	**65.67-87.00**	75.17	135.82**	55.90	39.96	15.93
Pedicel length of male flower (cm)	**8.07-26.47**	16.67	105.05**	35.86	34.60	1.26
Pedicel length of female flower (cm)	**2.07-8.63**	4.45	9.94**	3.41	3.27	0.14
Number of male flower per plant	**1.00-15.33**	6.77	40.94**	17.31	11.82	5.49
Number of female flower per plant	**1.00-7.00**	3.53	11.34**	6.10	2.62	3.48
Fruit length (cm)	**39.60-74.40**	53.34	201.36**	85.62	57.87	27.75
Fruit breadth (cm)	**17.33-35.00**	27.59	65.34**	26.90	19.23	7.67
Fruit weight (kg)	**0.80-3.58**	2.09	1.77**	0.67	0.55	0.13
Fruit yield per plant (kg)	**0.80-9.92**	4.01	21.00**	8.73	6.14	2.60

** Variation is significant at the 0.01 level.

MS = mean sum of square, $\sigma^2 p$ = Phenotypic variance, $\sigma^2 g$ = Genotypic variance and $\sigma^2 e$ = Environmental variance.

Table 3 Continued.

Parameters	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)	CV (%)
Leaf length without petiole (cm)	17.16	16.34	5.23	90.70	5.51	32.03	5.23
Leaf breadth (cm)	15.76	15.04	4.70	91.12	6.92	29.59	4.70
Internodes distance	25.06	20.27	14.73	65.43	4.79	33.80	14.73
Days to first male flowering	11.21	9.43	6.07	70.74	11.50	16.34	6.07
Days to first female flowering	9.95	8.41	5.31	71.50	11.01	14.65	5.31
Pedicel length of male flower (cm)	35.91	35.28	6.73	96.49	11.90	71.39	6.73
Pedicel length of female flower (cm)	41.42	40.57	8.35	95.94	3.65	82.02	8.35
Number of male flower per plant	61.38	50.72	34.57	68.28	5.85	86.41	34.57
Number of female flower per plant	69.78	45.76	52.68	43.00	2.19	62.04	52.68
Fruit length (cm)	17.35	14.26	9.87	67.59	12.88	24.15	9.87
Fruit breadth (cm)	18.79	15.89	10.04	71.47	7.64	27.69	10.04
Fruit weight (kg)	39.26	35.38	17.02	81.20	1.37	65.55	17.02
Fruit yield per plant (kg)	73.53	61.64	40.09	70.27	4.28	106.73	40.09

PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation, CV(%) = Coefficient of variation in percent.

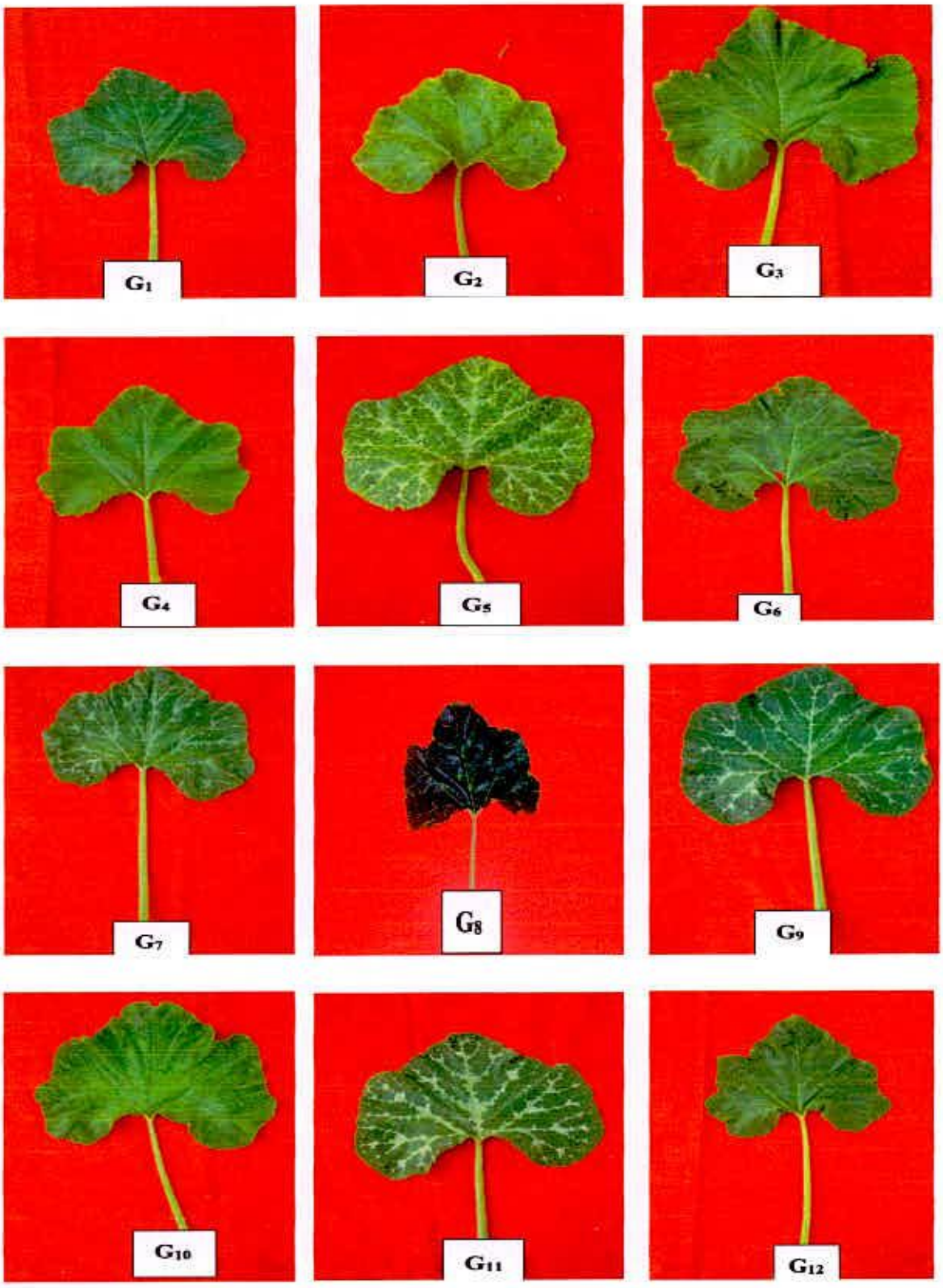

Plate 1a. Showing variation in leaf among different sweet gourd genotypes (G_1-G_{12})

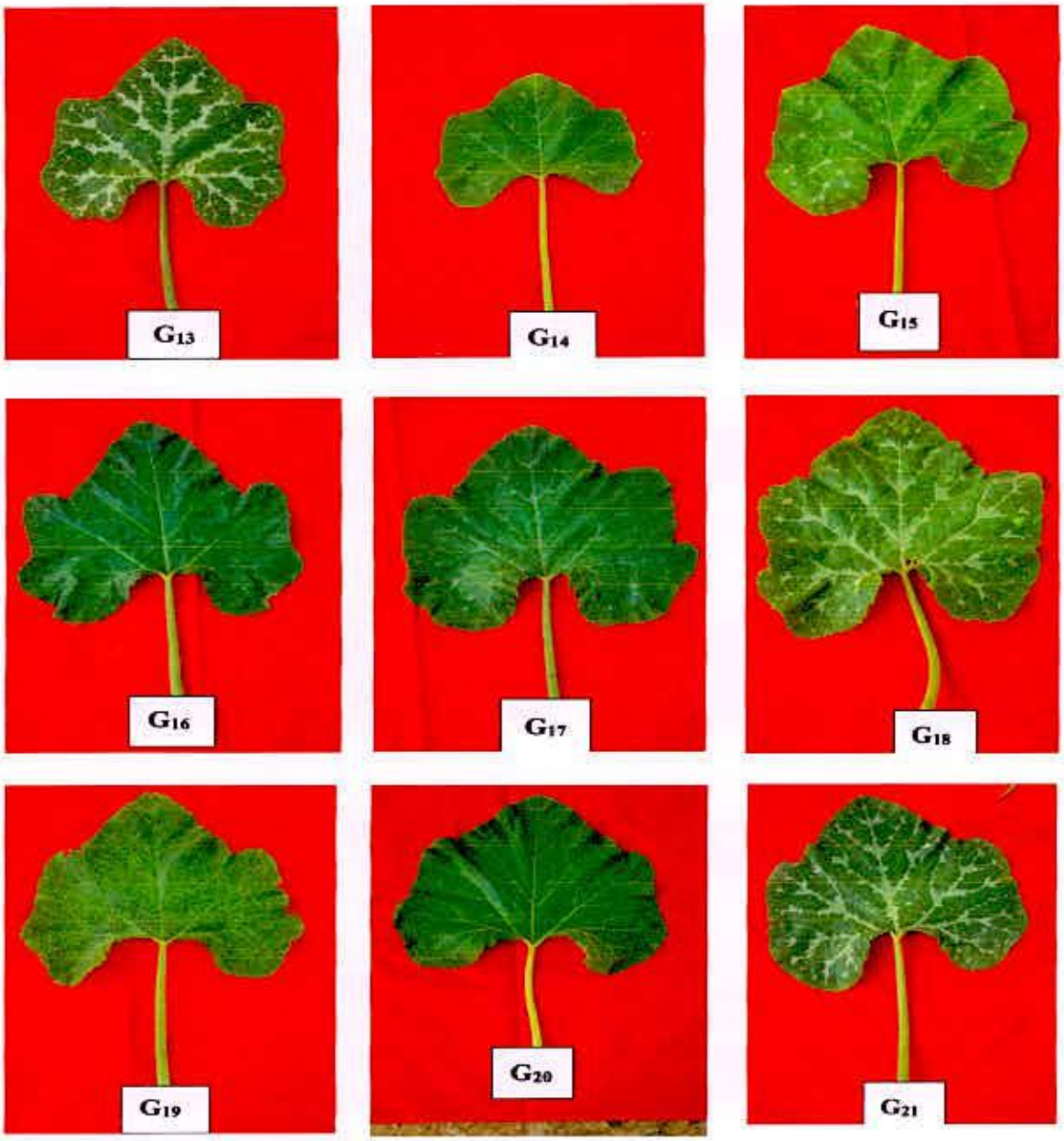

Plate 1b. Showing variation in leaf among different sweet gourd genotypes (G_{13}-G_{21})

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4.1.3 Internodes distance (cm)

Mean sum of square for internodes distance was significant (29.12) due to genotypes in sweet gourd (Table 3) indicating existence of considerable differences for this trait. The maximum internodes distance was found 20 in BD-2151 and the minimum was recorded 10 in BD-2229 with mean value 14.17 (Appendix IV). The differences in magnitudes in between genotypic (1.06) and phenotypic (1.51) variances was relatively high for the internodes distance indicating large environmental influence on these characters. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 25.06 and 20.27 respectively. Heritability (65.43%) estimates for this trait was high, genotypic advance (4.79) and genotypic advance in percent of mean (33.80) were found moderately high, revealed that character was controlled by additive gene. Gaffar (2008) found high heritability (94%) and genetic advance for this trait in sponge gourd. Photograph showing variation of twig among different genotypes of sweet gourd in plate 1c.

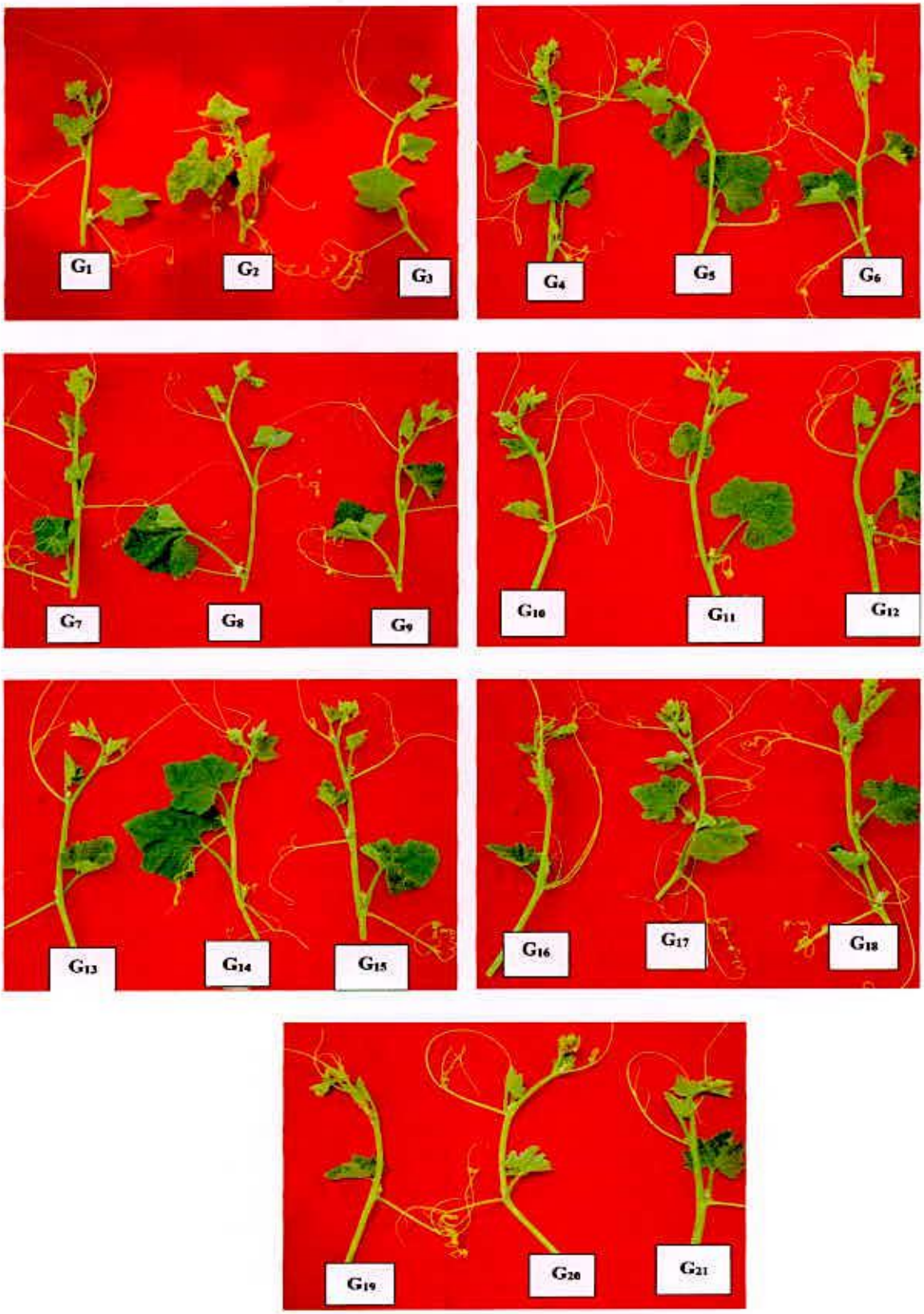

Plate 1c. Showing variation in twig among different sweet gourd genotypes

4.1.4 Days to first male flowering

Significant differences was observed among all genotypes (150.44) studied for this character (Table 3). The mean performance of days to first male flowering indicated that the maximum duration (86.33) to first flowering was produced by BARI mistikumra-2 and that of minimum (60.00) by BD-266 with mean value 70.38 (Appendix IV). Genotypic and phenotypic variance ware observed 62.30 and 44.07 respectively for days to first male flowering with large environmental influence and difference between the genotypic co-efficient of variation (9.43) and phenotypic co-efficient of variation (11.21) indicating existence of less variation among the genotypes. This character showed moderately high heritability (70.74%) estimation together with low genetic advance in percent of mean (16.34) indicated that the non-additive gene effect. Therefore selection based upon phenotypic expression of this character would not be effective for the improvement of this crop. Mathew and Khader (1999) also observed high heritability for this trait in snake gourd. Singh and Lal (2005a) in their study reported similar results. Samsun Nahar (2009) estimated heritability for this trait was high (84.54%) and genetic advance in percent of mean (12.29) were found low revealed that the character is governed by non-additive gene.

4.1.5 Days to first female flowering

Days to first female flowering showed significant variation among genotype mean square (135.82). The maximum duration (87.00) to first flowering was produced by BARI mistikumra-1 and that of minimum (65.67) by BD-2153 with mean value 75.17 (Appendix IV). The genotypic variance and phenotypic variance for this trait were 39.96 and 55.90 respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait. The phenotypic co-efficient of variation (9.95) was slightly higher than the genotypic co-efficient of variation (8.41) for this character (Table 3).Days to first female flower showed moderate heritability

(71.50%) with low genetic advance in percent of mean ((14.65). Therefore selection based upon phenotypic expression of this character would not be effective. These results were confirmed with the finding of Singh and Lal (2005a).

4.1.6 Male flower pedicel length (cm)

Significant mean sum of square for male flower pedicel length was significant due to genotypes in sweet gourd (Table 3) indicating existence of considerable difference for this trait. The maximum male flowers pedicel length was found 26.47 in BD-2203 and the minimum was recorded 8.07 in BARI mistikumra-1 with mean value 16.67 (Appendix IV). The genotypic variance was 34.60 and phenotypic variance was 35.86.). The phenotypic variance appeared to be slightly higher than the genotypic variance suggested less influence of environment on the expression of the genes controlling this trait.. The difference between genotypic co-efficient of variation (35.28) and phenotypic co-efficient of variation (35.91) was minimum. Heritability (96.49%) estimates for this trait was very high, genotypic advance (11.90) and genotypic advance in percent of mean (71.39) was found very high. Indicating, this character was governed by additive gene effects. Therefore, selection would be effective. Asmaul Husna (2009) found high heritability (99.55%) and genetic advance for this trait in bottle gourd. Photograph showing variation of male and female flower among some genotypes of sweet gourd in Plate 2a & 2b.

4.1.7 Female flower pedicel length (cm)

Mean sum of square for female flower pedicel length was significant (9.94) due to genotypes in sweet gourd (Table 3) indicating the existence of considerable difference for this trait. The maximum female flowers pedicel length was found 8.63 in BD-2214 and the minimum was recorded 2.07 in BARI mistikumra-1 with mean value 4.45 (Appendix IV). The genotypic variance and phenotypic variance for this trait were 3.27 and 3.41

respectively. The phenotypic variance appeared to be slightly higher than the genotypic variance suggested less influence of environment on the expression of the genes controlling this character. The difference between phenotypic co-efficient of variation (41.42) and genotypic co-efficient of variation (40.57) was minimum in case of female flowers pedicel length. Heritability (95.94%) estimates for this trait was high, genotypic advance (3.65) was low and genotypic advance in percent of mean (82.02) was found high, indicated that this character was controlled by additive gene effects. Therefore selection would be effective. Asmaul Husna (2009) found that female flower pedicel length is 3.13-9 cm in bottle gourd.

Plate 2a. Showing phenotypic variation in male and female flower among different genotypes of sweet gourd

Plate 2b. Showing phenotypic variation in male and female flower among different genotypes of sweet gourd

4.1.8 No. of male flower

Significant mean sum of square (40.94) for no. of male flower indicated considerable difference among the genotypes studied (Table 3). The maximum no. of male flower was found (15.33) in BD-9491 and the minimum was recorded (1.00) in BARI mistikumra-1 & BARI mistikumra-2 with mean value 6.78 (Appendix IV). The phenotypic variance (17.31) appeared to be higher than the genotypic variance (11.82) suggested considerable influence of environment on the expression of the genes controlling this character. The genotypic co-efficient of variation was 50.72 and phenotypic co-efficient of variation was 61.38. Heritability (68.28%) estimates for this trait was moderately high, genotypic advance (5.85) was moderately high and genotypic advance in percent of mean (86.41) was found high, indicated that the trait was governed by additive gene. Singh *et al.* (2002) also estimated high GCV and PCV for male flowers per plant in ridge gourd. Asmaul Husna (2009) found genotypic co-efficient of variation was 31.86 and phenotypic co-efficient of variation was 31.95. Heritability (99.40%) estimates for this trait was very high, genotypic advance (4.47) was moderately high and genotypic advance in percent of mean (83.86) was found high in bottle gourd.

4.1.9 No. of female flower

Mean sum of square for no. of female flower was significant (11.34) due to genotypes in sweet gourd (Table 3) indicating existence of considerable difference for this trait. The maximum no. of female flower was found 7.00 in BD-266 and the minimum was recorded 1.00 in BARI mistikumra-1 & BARI mistikumra-2 with mean value 3.54 (Appendix IV). The differences in magnitudes in between genotypic (2.62) and phenotypic (6.10) variances was relatively high for this trait indicating large environmental influence on these characters. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 45.76 and 69.78 respectively. Heritability (43.00%) estimates for this trait was low, genotypic advance (2.19) was low and genotypic advance in percent of mean (62.04) was found high, revealed that the trait

was controlled by additive gene. Asmaul Husna (2009) also found the differences in magnitudes in between genotypic (13.41) and phenotypic (15.74) variances was relatively high for this trait in bottle gourd and the GCV and PCV were 35.14 and 38.08 respectively. She also found heritability (85.15%) high, genotypic advance (8.92) was moderately high and genotypic advance in percent of mean (85.60) was found high and also additive gene effect in bottle gourd.

4.1.10 Fruit length (cm)

Significant mean sum of square for fruit length (201.36) indicated considerable difference among the genotypes studied (Table 3). The maximum fruit length was found 74.40 in BD-2150 and the minimum was recorded 39.60 in BARI mistikumra-2 with mean value 53.34 (Appendix IV). The highest genotypic and phenotypic variance was observed 57.87 and 85.62 respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this character. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 14.26 and 17.35 respectively. Heritability (67.59%) estimates for this trait moderately high, genetic advance (12.88) was high and genotypic advance in percent of mean (24.15) was found moderately high, indicated that the trait was governed by additive gene and selection for this character would be effective. Banik (2003) found the highest phenotypic co-efficient of variation for fruit length. Mathew and Khader (1999) also reported high heritability for fruit length in snake gourd. Rahman *et al.* (1986) indicated minimum differences between GCV and PCV in bottle gourd for fruit length. Photograph showing variation of fruit length among some genotypes of sweet gourd in Plate 3a and 3b.

4.1.11 Fruit breadth (cm)

Mean sum of square fruit breadth was significant (65.34) due to genotypes in sweet gourd (Table 3) indicating existence of considerable variation for this trait. The maximum fruit breadth was found 35.00 in BD-2150 and the minimum was recorded 17.33 in BARI mistikumra-1 with mean value 27.59 (Appendix IV). The genotypic variance and phenotypic variance were 19.23 and 26.90 respectively. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 15.89 and 18.79 respectively. Heritability (71.47%) along with genetic advance (7.64) and genetic advance in percent of mean (27.69) estimates for this trait was moderately high indicated that this character was controlled by additive gene effects. Asmaul Husna (2009) reported the GCV and PCV were 15.84 and 17.39 respectively in bottle gourd and heritability (82.93%) estimates for this trait was high along with moderately high genetic advance (8.76) and genetic advance in percent of mean (38.08) indicated that this character was controlled by additive gene effects. Photograph showing variation of fruit breadth among some genotypes of sweet gourd in Plate 3a and 3b.

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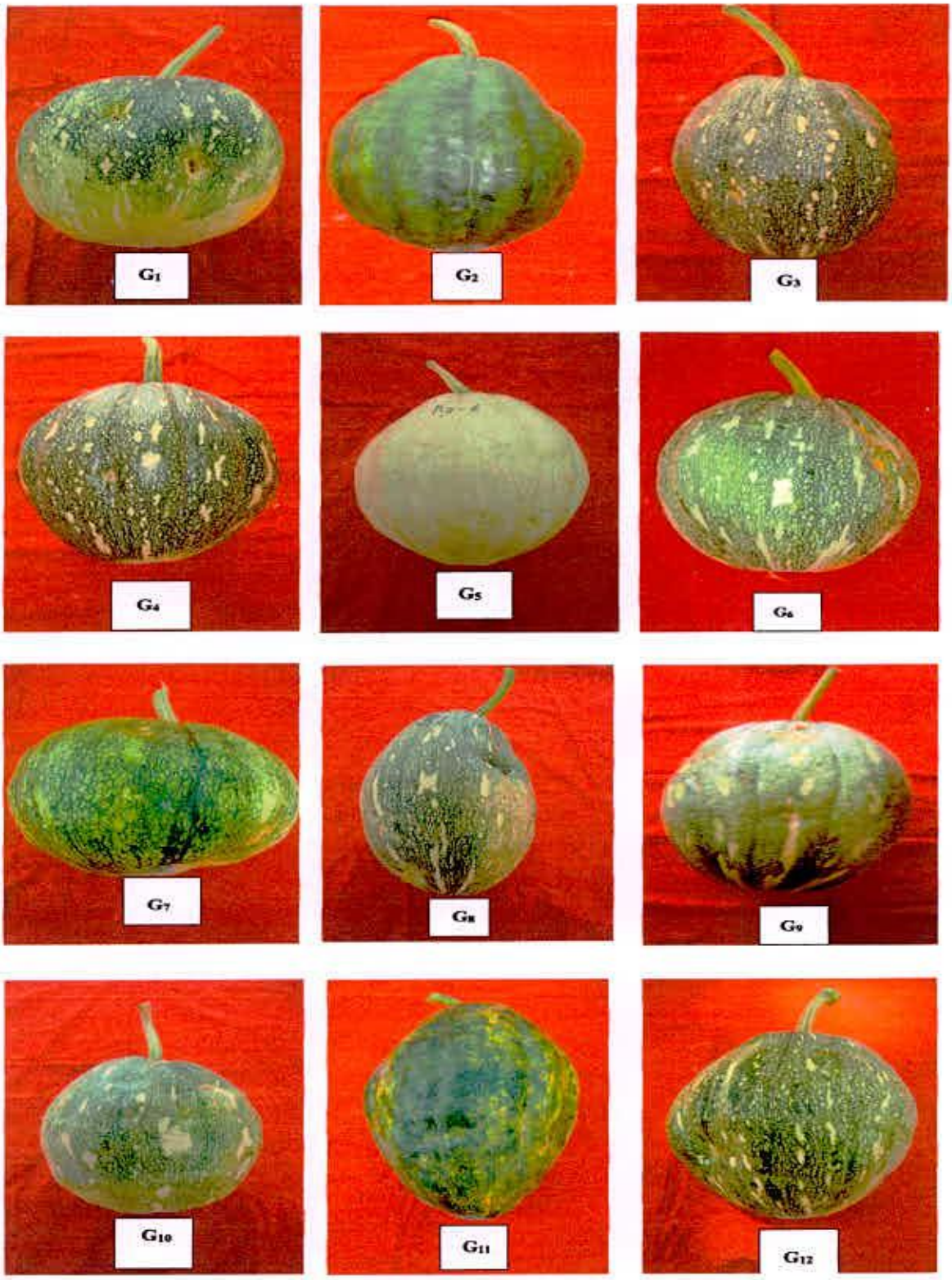

Plate 3a. Showing phenotypic variation in fruits among different genotypes of sweet gourd

Plate 3b. Showing phenotypic variation in fruits among different genotypes of sweet gourd

4.1.12 Fruit weight (kg)

Mean sum of square for fruit weight was significant (1.77) in sweet gourd (Table 3) indicating existence of considerable difference for this trait. The maximum weight per fruit was found 3.58 kg in BD-2150 and the minimum was recorded 0.8 kg in BARI mistikumra-1 with mean value 2.09 (Appendix IV). The differences in magnitudes in between genotypic (0.55) and phenotypic (0.67) variances was minimum for this trait indicating less environmental influence on these characters. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 35.38 and 39.26 respectively for fruit weight which indicating that significant variation exists among different genotypes. Heritability (81.20%) estimates for this trait was high together with considerable low genetic advance (1.37) and high genetic advance in percent of mean (65.55) indicated that selection for this character would be effective for increasing yield per plant. Saha *et al.* (1992) found similar GCV (39.55) and PCV (41.00) for the fruit weight in pumpkin. Kumaran *et al.* (1997) reported similar types of result which confirmed the present findings. This result is in consonance with the findings of Chowdhury and Sharma (2002) in ridge gourd and Rumaran *et al.* (1997) pumpkin. Rahman *et al.* (1986) also found the similar result in bottle gourd.

4.1.13 Yield per plant (kg)

The genotypes differed significantly for yield per plant. The highly significant genotypic difference indicated that there was a wide range of variation among the varieties for yield per plant (Table 3). The highest yield per plant was found 9.92 kg in BD-2229 followed by BD-2151 (9.41kg), BD-266 (8.14) and BD-2150 (7.15) and the minimum was recorded 0.80 kg in BARI mistikumra-1 with mean value 4.01 kg (Appendix IV). The differences in magnitudes in between genotypic (6.14) and phenotypic (8.73) variances for this trait indicating environmental influence on these characters. The genotypic coefficient of variation and phenotypic co-efficient of variation were 61.64 and 73.53 respectively for yield per plant which indicating that significant variation exists among different

genotypes. The heritability value (70.27%) as well as genetic advance (4.28) and genetic advance in percent of mean (106.73) were observed very high. High heritability with high genetic advance in percent of mean provided opportunity for selecting high valued genotypes for breeding programme. Narayanankutty *et al.* (2006) fruit yield exhibited high values of heritability and genetic gain indicating additive gene effects are important in determining the character. Pandey *et al.* (2002) observed high degree of variability for yield per plant and higher estimate of heritability and genetic advance was observed for yield per plant.

4. CORRELATION CO-EFFICIENT

Yield is a complex product being influenced by several interdependent quantitative characters. Selection for yield may not be effective unless the directly or indirectly influences of other yield components are taken into consideration. When selection pressure is exercised for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated traits. Hence knowledge regarding association of character with yield and among themselves provides guideline to the plant breeder for making improvement through selection provide a clear understanding about the contribution in respect of establishing the association by genetic and non genetic factors. Higher genotypic correlations than phenotypic one might be due to modifying or masking effect of environment in the expression of the character under study (Nandpuri *et al.,* 1973). Results of genotypic and phenotypic correlation co-efficient of thirteen yield and its contributing traits of sweet gourd were estimated separately as vegetative character and reproductive character with yield and shown in Table 4 which discussed character wise as bellows:

Table 4. Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of sweet gourd

Charac.		LB	ID	DFMF	DFFF	PLMF	PLFF	NMF	NFF	FL	FB	FW	FYP
LLWP	r_g	0.713**	0.324**	-0.779**	-0.575**	0.121	0.125	0.338**	0.540**	0.346**	0.335**	0.252	0.316*
	r_p	0.652**	0.240	-0.633**	-0.484**	0.007	0.112	0.248	0.326**	0.244	0.272*	0.212	0.245
LB	r_g		0.485**	-0.594**	-0.405**	-0.093	0.044	0.065	0.334**	0.419**	0.259	0.307*	0.133
	r_p		0.367**	-0.493**	-0.329**	-0.101	0.042	0.065	0.062	0.312*	0.168	0.220	0.103
ID	r_g			-0.266	-0.270*	-0.107	-0.102	-0.011	0.451**	0.090	-0.131	0.075	0.270*
	r_p			-0.230	-0.258	-0.086	-0.086	-0.004	0.276*	0.126	-0.103	0.028	0.171
DFMF	r_g				0.914**	-0.515**	-0.335**	-0.597**	-0.881**	-0.559**	-0.498**	-0.386**	-0.723**
	r_p				0.878**	-0.442**	-0.295*	-0.410**	-0.537**	-0.383**	-0.307*	-0.269*	-0.550**
DFFF	r_g					-0.590**	-0.286*	-0.443**	-0.775**	-0.461**	-0.245	-0.183	-0.689**
	r_p					-0.508**	-0.243	-0.329*	-0.529**	-0.327**	-0.167	-0.159	-0.543**
PLMF	r_g						0.244	0.373**	0.416**	0.341**	0.251	0.170	0.566**
	r_p						0.240	0.296*	0.268	0.276*	0.214	0.163	0.459**
PLFF	r_g							0.028	0.034	0.376**	0.487**	0.449**	0.167
	r_p							0.001	0.011	0.297*	0.416**	0.390**	0.130
NMF	r_g								0.852**	0.435**	0.572**	0.316*	0.687**
	r_p								0.769**	0.307*	0.409**	0.269*	0.638**
NFF	r_g									0.576**	0.407**	0.317	0.918**
	r_p									0.369**	0.260	0.224	0.839**
FL	r_g										0.793**	0.861**	0.691**
	r_p										0.682**	0.734**	0.520**
FB	r_g											0.968**	0.518**
	r_p											0.827**	0.420**
FW	r_g												0.492**
	r_p												0.431**

** Correlation is significant at the 0.01 level. * Correlation is significant at the 0.05 level.

LLWP = Leaf length without petiole (cm), LB = Leaf breadth (cm), ID = Internode distance (cm), DFMF = Days to first male flowering, DFFF = Days to first female flowering, PLMF = Pedicel length of male flower (cm), PLFF = Pedicel length of female flower (cm), NMF = Number of male flower per plant, NFF = Number of female flower per plant , FL = Fruit length (cm), FB = Fruit breadth (cm), FW = Fruit weight (g) and FYP = Fruit yield per plant (kg).

4.2.1 Leaf length without petiole (cm)

Highly significant positive relationships were found in leaf length and leaf breadth at both genotypic and phenotypic levels (Table 4). Highly significant positive association of leaf length with internodes distance, number of male flower per plant, number of female flower per plant, fruit length and fruit breadth was found at both genotypic and phenotypic levels indicating that these traits are governed by same gene and simultaneous improvement would be effective. But this character showed significant but negative correlation at both genotypic and phenotypic level between this trait and other characters like days to first male flowering and days to first female flowering. But this character showed insignificant and positive correlation with pedicel length of male flower, pedicel length of female flower and fruit weight. Significant and positive relationship was found with fruit yield per plant. This feature indicated that if the length of leaves become increase, it shortens days to first male and female flowering and increase fruit yield per plant. Asmaul Husna (2009) also reported leaf length is significantly and positively correlated with leaf breadth petiole length at both genotypic and phenotypic level.

4.2.2 Leaf breadth (cm)

Leaf breadth showed highly significant and positive correlation with internodes distance at both genotypic and phenotypic level but in case of number of female flower and fruit length highly significant at genotypic level but significant at phenotypic level (Table 4) indicated that if the leaf breadth is increased, all these parameters also increased. On the other hand, this character produced insignificant but positive correlation with pedicel length of female flower, number of male flower, fruit breath and yield per plant indicated that the association among these traits is largely influenced by environmental factors. This trait shows significant but negative association with days to first female flowering and insignificant but negative association with pedicel length of male flower. Asmaul Husna (2009) also reported same correlation of leaf breadth with yield. Li et al. (1997) also found similar result in cucumber for this trait.

4.2.3 Internodes distances (cm)

The character showed highly significant and positive relationship with no. of female flowers at genotypic levels but significant at phenotypic levels (Table 4) indicated that if internodes distance is increased, then no. of female flowers also increased. Positive and insignificant correlation between yield and internodes distance showed that selection of genotypes with higher internodes distance are expected to yield better. The character showed insignificant and positive relationship with fruit length and fruit weight at both genotypic and phenotypic level. On the other hand, this character possessed insignificant but negative correlation with days to first male flowering, pedicel length of male flower, pedicel length of female flower, number of male flower and fruit breadth indicated that the association between these traits largely influenced by environmental factors.

4.2.4 Days to first male flowering

Here the character showed highly significant and positive correlation with days to first female flowering at both genotypic and phenotypic level indicated that the traits are governed by same gene and simultaneous improvement would be effective (Table 4). This character produced highly significant and negative correlation with pedicel length of male flower, pedicel length of female flower, number of male flower, number of female flower, fruit length, fruit breadth, fruit weight and fruit yield per plant at both genotypic and phenotypic level except pedicel length of female flower, fruit breadth and fruit weight, which are significant at phenotypic level. This result shows, if days to first male flowering decrease all of these negatively associated parameters increase as well as yield increase. Kumaresan *et al.* (2006) found negative association of yield per vine with days to first male flower opening; Badade *et al.* (2001) reported yield is significantly and negatively correlated with days to first male appearance.

4.2.5 Days to first female flowering

Similar trends of correlation of days to first female flowering between other characters also observed. Here the character showed highly significant and negative correlation at both genotypic and phenotypic level (Table 5) with pedicel length of male flower, number of male flower, number of female flower, fruit length and yield per plant. This indicated that delayed to first female flower emergence decreased the pedicel length of male and female flower, number of female flower, fruit length and yield. This character showed insignificant and negative correlation with fruit breadth and fruit weight.

4.2.6 Pedicel length of male flower (cm)

Male flower pedicel length showed positive and highly significant correlation with number of male flower, number of female flower and fruit length at genotypic level significant at phenotypic level. It shows positive but insignificant relationship with pedicel length of female flower, fruit breadth and fruit weight indicated that the association among these traits is largely influenced by environmental factors. Yield per plant had highly significant positive relationship with this trait. This feature shows if the pedicel length of male flower is increased, yield also increased.

4.2.7 Pedicel length of female flower (cm)

Female flower pedicel length showed insignificant positive relationship with number of male flower, number of female flower and fruit yield per plant at both genotypic and phenotypic level (Table 4). But this character produces highly significant positive relationship with fruit length, breadth and weight at both genotypic and phenotypic level indicating if female flower pedicel length is increased, fruit length, fruit breadth and fruit weight also increased.

4.2.8 Number of male flowers per plant

Number of male flowers per plant had highly significant positive correlation with number of female flower, fruit length, fruit breadth and fruit yield per plant at both genotypic and phenotypic level expect fruit length which is significant at phenotypic level (Table 4). This character also shows significant positive relationship with fruit weight at both levels. This feature indicated that increased number of male flower per plant would increase number of female flower per plant, fruit length, fruit breadth, fruit weight and yield. These findings also supported Chawdhury and Mandal's (1987) findings in cucumber and Asmaul Husna (2009) in bottle gourd.

4.2.9 Number of female flowers per plant

This trait showed highly significant positive relationship with fruit length, fruit breadth, and fruit yield per plant (Table 4). This feature indicated that increased number of female flowers per plant would lead to increase number of fruits per plant. Therefore yield could be improved through the production of a good number of female flowers per plant by appropriate agronomic management practice. Mohanty (2001) reported similar trend of relationship.

4.2.10 Fruit length (cm)

Fruit length showed highly significant positive relationship with fruit breadth, fruit weight and fruit yield per plant at both genotypic and phenotypic level (Table 4). Narayanankutty *et al.* (2006) reported that yield is strongly correlated with fruit length in snake gourd. Chowdhury and Sarma (2002) studied *Luffa acutangula* and found that yield per hectare can be improved through selection for fruit length.

4.2.11 Fruit Breadth (cm)

Positive and Highly significant correlation fruit breadth was found with fruit weight and yield per plant at both genotypic and phenotypic level (Table 4) revealed that any increase in this trait should bring about an enhancement in the yield. Narayanankutty *et al.* (2006) reported that yield is strongly correlated with

fruit breadth in snake gourd. Chowdhury and Kumaresan *et al.* (2006) negative association was observed in yield with fruit girth in snake gourd. Prasana *et al.* (2002) studied the correlation between the yield and yield components of ridge gourd (*Luffa acutangula*) . Fruit yield per hectare was positively associated with fruit girth and weight.

4.2.12 Fruit weight (kg)

Fruit weight showed highly significant and positive correlation with number of fruit per plant and yield per plant at both genotypic and phenotypic level (Table 4) indicated that if the fruit weight is increased, then the number of fruit per plant and yield per plant is increased. Narayanankutty *et al.* (2006) reported strongly correlated with fruit weight in snake gourd. Chowdhury and Sarma (2002) studied *Luffa acutangula* cultivars and observed that yield per hectare can be improved through selection individual fruit weight. Kumaresan *et al.* (2006) Yield per vine in snake gourd was positively associated with fruit weight. Prasana *et al.* (2002) found in ridge gourd (*Luffa acutangula*) fruit yield per hectare was positively associated with fruit weight.

4.3 PATH CO-EFFICIENT ANALYSIS

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

4.3.1 Leaf length without petiole (cm)

Leaf length without petiole showed negatively direct effect (-0.041) on yield (Table 5). This character, however, showed positive indirect effect through number of female flower (0.278), days to first male flowering (0.136), fruit weight (0.049), pedicel length of male flower (0.082), fruit length (0.016) and fruit breadth (0.007).). The negative indirect effect via leaf breadth (-0.119) followed by number of male flower (-0.051), days to first female flowering (-0.037), pedicel length of female flower (-0.009) and internodes distance (-0.005) which

were contributed to result insignificant positive genotypic correlation with yield per plant (0.244). Li et al. (1997) also found similar result in cucumber for their trait.

4.3.2 Leaf breadth (cm)

Leaf breadth showed a negative direct effect (-0.184) on yield (Table 5). This character, however showed also positive indirect effect through number of female flower (0.194) followed by days to first male flowering (0.104), fruit weight (0.051), fruit length (0.020) and fruit breadth (0.005).The negative indirect effects were also observed via leaf length without petiole (-0.027) followed by days to first female flowering (-0.025), pedicel length male flower (0.0180, number of male flower (-0.013), internodes distance (-0.008) and pedicel length of female flower (-0.003).

4.3.3 Internodes distance (cm)

It was found that internodes distance showed the negative direct effect (-0.023) on yield (Table 5).This character also showed the highest positive indirect effect through number of female flower (0..235) followed by days to first male flowering (0.048), fruit length (0.009), pedicel length of female flower (0.007), fruit weight (0.006) and number of male flower (0.000). The negative indirect effects of this character on yield were also observed via leaf breadth (-0.068), days to first female flowering (-0.019), pedicel length of male flower (-0.015), leaf length without petiole(-0.010) and fruit breadth (-0.003) which finally made insignificant positive correlation between internodes distance and yield per plant (0.168).

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Table 5. Path coefficient analysis showing direct and indirect effects of different characters on yield of sweet gourd

Characters	Direct effect	Indirect effects												Pearson correlation with yield
		LLWP	LB	ID	DFMF	DFFF	PLMF	PLFF	NMF	NFF	FL	FB	FW	
LLWP	-0.041	-	-0.119	-0.005	0.136	-0.037	0.021	-0.009	-0.051	0.278	0.016	0.007	0.049	0.244
LB	-0.184	-0.027	-	-0.008	0.104	-0.025	-0.018	-0.003	-0.013	0.194	0.020	0.005	0.051	0.096
ID	-0.023	-0.010	-0.068	-	0.048	-0.019	-0.015	0.007	0.000	0.235	0.009	-0.003	0.006	0.168
DFMF	-0.214	0.026	0.090	0.005	-	0.067	-0.076	0.022	0.083	-0.455	-0.024	-0.008	-0.062	-0.547**
DFFF	0.076	0.020	0.059	0.006	-0.188	-	-0.088	0.018	0.066	-0.447	-0.021	-0.004	-0.037	-0.539**
PLMF	0.176	-0.005	0.019	0.002	0.093	-0.038	-	-0.018	-0.061	0.231	0.018	0.006	0.037	0.458**
PLFF	-0.076	-0.005	-0.008	0.002	0.063	-0.018	0.042	-	0.000	0.009	0.019	0.011	0.089	0.130
NMF	-0.207	-0.010	-0.012	0.000	0.086	-0.024	0.052	0.000	-	0.660	0.020	0.011	0.061	0.637**
NFF	0.858	-0.013	-0.042	-0.006	0.113	-0.040	0.047	-0.001	-0.159	-	0.024	0.007	0.050	0.839**
FL	0.066	-0.010	-0.057	-0.003	0.079	-0.024	0.049	-0.022	-0.064	0.317	-	0.018	0.166	0.516**
FB	0.027	-0.011	-0.032	0.002	0.064	-0.012	0.038	-0.031	-0.084	0.219	0.045	-	0.189	0.413**
FW	0.230	-0.009	-0.041	-0.001	0.058	-0.012	0.028	-0.030	-0.055	0.188	0.048	0.022	-	0.426**

Residual effect: 0.391, ** Correlation is significant at the 0.01 level. * Correlation is significant at the 0.05 level.

LLWP = Leaf length without petiole (cm), LB = Leaf breadth (cm), ID = Internodes distance (cm), DFMF = Days to first male flowering, DFFF = Days to first female flowering, PLMF = Pedicel length of male flower (cm), PLFF = Pedicel length of female flower (cm), NMF = Number of male flower per plant, NFF = Number of female flower per plant , FL = Fruit length (cm), FB = Fruit breadth (cm), FW = Fruit weight (g) and FYP = Fruit yield per plant (kg).

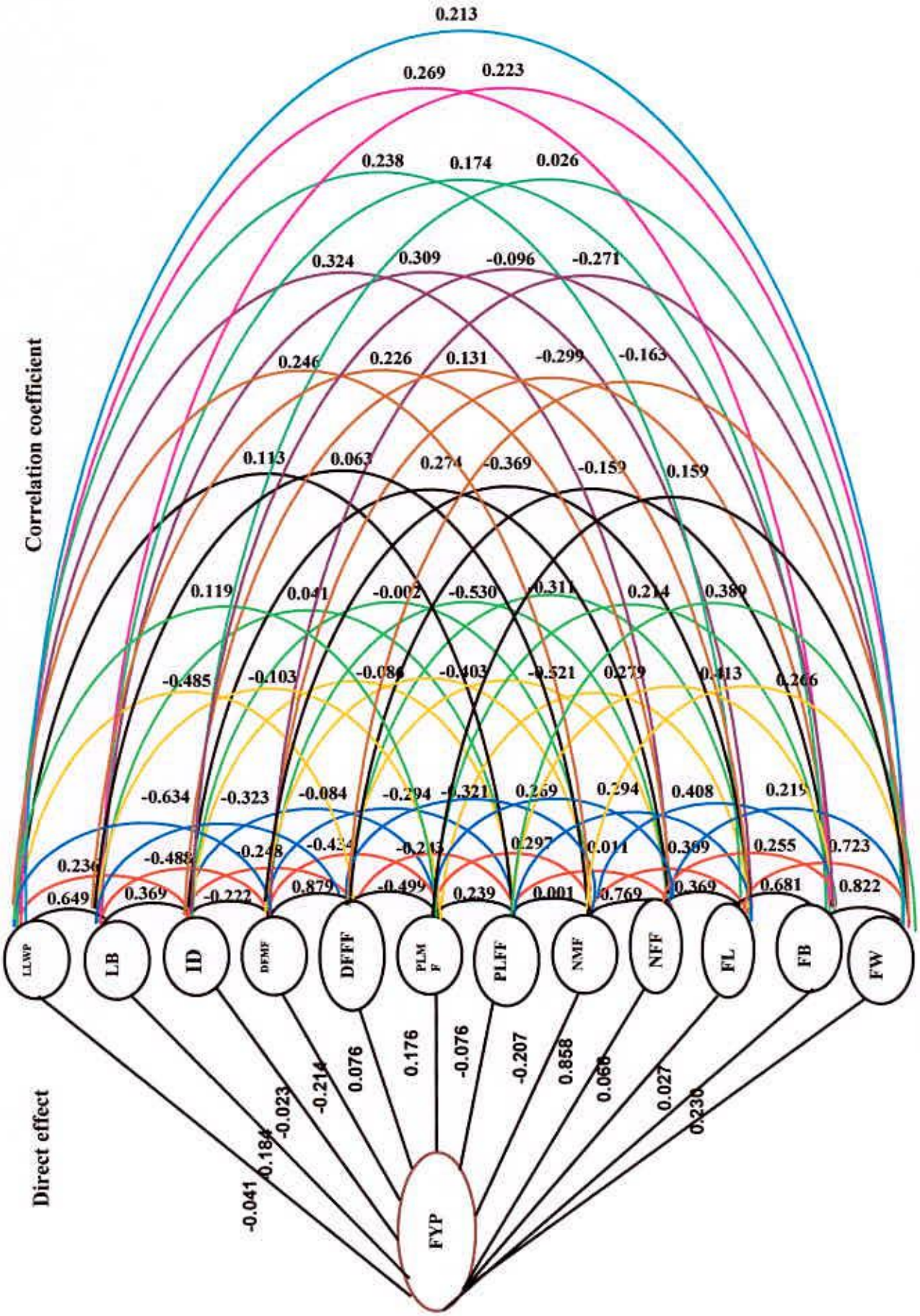

Figure 1. Diagrammatic representation of direct effects and correlation coefficients of variables on dependent variable in pumpkin genotypes

4.3.4 Days to first male flowering

Days to first male flowering showed the negative direct effect (-0.214) on yield (Table 5). The character also showed the maximum positive indirect effect through leaf breadth (0.090) followed by number of male flower (0.083), days to first female flowering (0.067), leaf length (0.026), pedicel length of female flower (0.022) and internodes distance (0.005). The negative indirect effect of this character on yield via number of female flower (-0.455) was the highest followed by pedicel length of male flower (-0.076), fruit weight (-0.062), fruit length (-0.024) and fruit breadth (0.008) which finally made highly significant negative correlation between days to first male flowering and yield per plant (-0.547**).

4.3.5 Days to first female flowering

Days to first female flowering showed a positive direct effect (0.076) on yield (Table 5). This character, also showed the highest positive indirect effect through number of male flower (0.066) followed by leaf breadth (0.059), leaf length (0.020), pedicel length of female flower (0.018) and internodes distance (0.006) on yield. The character also produced negative indirect effect on yield via no. of female flower (-0.447), days to first male flowering (-0.188), pedicel length of male flower (-0.088), fruit weight (-0.037), fruit length (-0.021) and fruit breadth (-0.004). The cumulative effects produced a highly significant negative genotypic correlation on yield (-0.539**).

4.3.6 Pedicel length of male flower (cm)

Male flower pedicel length showed a positive direct effect (0.176) on yield (Table 5). This character also showed the highest positive indirect effect through number of female flower (0.231) followed by days to first male flowering (0.093), fruit weight (0.037), leaf breadth (0.019), pedicel length of female flower (0.018) fruit breadth (0.006) and internodes distance (0.002). The character also produced the negative indirect effect on yield via number of male flower (-0.061), days to first female flowering (-0.038), fruit length (-0.018) and leaf length (-0.005). The cumulative effects of these characters produced a highly significant negative

genotypic correlation on yield (-0.539). Figure 1 showing Path diagram of yield and its contributing traits in twenty one genotypes of sweet gourd.

4.3.7 Pedicel length of female flower (cm)

Female flower pedicel length showed a negative direct effect (-0.076) on yield (Table 5). This character also showed the highest positive indirect effect through fruit weight (0.089), days to first male flowering (0.063), pedicel length of male flower (0.042), fruit length (0.019), fruit breadth (0.011), number of female flower (0.009) and internodes distance (0.002). The character also produced the negative indirect effect on yield via days to first female flowering (-0.018), leaf breadth (-0.008), and leaf length (-0.005). The cumulative effects of these characters produced a positive genotypic correlation on yield (0.130). Asmaul Husna (2009) found negative correlation with fruit yield per plant regarding this character in bottle gourd.

4.3.8 Number of male flower

Number of male flower showed a positive direct effect (-0.207) on yield (Table 5). This character also showed the highest positive indirect effect through number of female flower (0.660), days to first male flowering (0.086), fruit weight (0.061) pedicel length of male flower (0.052), fruit length (0.020) and fruit breadth (0.011). This character, however, showed negative indirect effect through days to first female flowering (-0.024), leaf breadth (-0.012) and leaf length (-0.010) which were contributed to result significant positive genotypic correlation with yield per plant (0.637**). This finding also supported Chadhury and Mandal (1987) findings in cucumber.

4.3.9 Number of female flower

Number of female flower produced a positive direct effect (0.858) on yield (Table 5). The character, however, showed also some positive indirect effect through days to first male flowering (0.113), fruit weight (0.050), pedicel length of male flower (0.047), fruit length (0.024) and fruit breadth (0.007). The negative indirect

effects were also observed via number of male flower (-0.159) followed by leaf breadth (-0.042), days to first female flowering (-0.040), leaf length (-0.013) internodes distance (-0.006), and pedicel length of female flower (-0.001) which were contributed to result significant positive genotypic correlation with yield per plant (0.516**). Figure 1 showing Path diagram of yield and its contributing traits in twenty one genotypes of sweet gourd.

4.3.10 Fruit length (cm)

Fruit length showed positive direct effect (0.066) on yield (Table 5). This character, however, showed positive indirect effect through number of female flower (0.317) followed by fruit weight (0.166), days to first male flowering (0.079), pedicel length of male flower (0.049) and fruit breadth (0.018). The negative indirect effects were also observed via number of male flower (-0.064), leaf breadth (-0.057), days to first female flowering (-0.024), pedicel length of female flower (-0.022), leaf length (-0.010) and internodes distance (-0.003) which were together contributed to result significant positive genotypic correlation with yield per plant (0.516**).

4.3.11 Fruit breadth (cm)

Fruit breadth showed positively direct effect (0.027) on yield (Table 5). This character, however, showed positive indirect effect through number of female flower (0.219), fruit weight (0.189), days to first male flowering (0.064), fruit length (0.045), pedicel length of male flower (0.038) and internodes distance (0.002). The negative indirect effects were also found number of male flower (-0.084), leaf breadth (-0.032), pedicel length of female flower (-0.031), days to first female flowering (-0.012), and leaf length (-0.011) which were contributed to result significant positive genotypic correlation with yield per plant (0.413**). The result is in also agreement with those of Asmaul Husna (2009) in bottle gourd, Rahman *et al.* (1986) in bottle gourd and Parhi *et al.* (1995) in bitter gourd. Chadhury and Mandal (1987) and Mondal *et al.* (1989) also found similar result for fruit breadth in cucumber and water melon respectively.

4.3.12 Fruit weight (kg)

Weight per fruit had the positive direct effect (0.230) on yield (Table 5). This character also showed positive effect indirect effect through number of female flower (0.188), days to first male flowering (0.058), fruit length (0.048), pedicel length of male flower (0.028) and fruit breadth (0.022). But negative indirect effect through number of male flower (-0.055), leaf breadth (-0.041), pedicel length of female flower (-0.030), days to first female flowering (-0.012), leaf length (-0.009) and internodes distance (-0.001). However, all these effects contributed to result significant positive genotypic correlation with fruit yield per plant (0.426**). Significant genotypic correlation between fruit weight and yield further strengthened their reliability in the process of selection for higher yield. Kumaresan et al. (2006) conducted an experiment in snake gourd and Path coefficient analysis revealed that it would be highly rewarding to lay emphasis on the number of fruits per vine and fruit weight to increase the yield per vine directly. The result is in consonance with the finding of Asmaul Husna (2009) in bottle gourd, Kumararn *et al.* (1998) in pumpkin for this trait.

Residual effect

The residual effect was found (0.391) which indicated that there were other contributors responsible for yield but not taken into consideration in the present investigation. According to Sengupta and Kataria (1971), residual effects towards yield might also be due to environmental factors and sampling errors.

Path analysis indicated that number of female flower per plant was the most important character that had the highest contribution to yield per plant as it exhibited the highest direct effect on yield followed by single fruit weight, pedicel length of male flower, days to first female flowering and fruit length.

4.4 MULTI VARIATE ANALYSIS

4.4.1 Principal component analysis (PCA)

Principal component analysis was carried out with twenty one genotypes of sweet gourd. First three Eigen values for three principal coordination axes of genotypes accounted for 72.96% variation (Table 6). A two dimensional scattered diagram (Fig. 2) was developed on the basis of the principal component score; Z_1 and Z_2 score (Appendices V).

4.4.2 Principal coordinates analysis (PCO)

The results obtained from principal coordinate analysis showed that the highest inter genotypic distance was observed between genotypes G20 and G21 (47.46) followed by G1 and G20 (46.39) and the lowest distance was observed (0.75) between genotypes G3 and G14 followed by the distance (1.42) between genotypes G4 and G9 (Table 7). The difference between the highest and the lowest inter genotypic distance indicated the highest variability among the 21 genotypes of sweet gourd. The highest intra-cluster distance was recorded in cluster V (0.261) having five genotypes viz. BD-264, BD-2203, BD-2212, BD-9493, BD-4590. The lowest intra-cluster distance was observed in cluster I (0.000) which is BD-2150. It favored to decide that intra-group diversity was the highest in cluster V and the lowest in cluster I. Cluster III having six genotypes BD-266, BD-2214, BD-2151, BD-2153, BD-2229 and BD-2222 and had an intra-cluster distance 0.177. Cluster IV consisted BD-2174, BD-2177, BD-2196, BD-9489, BD-9494, BD-9491, BD-9490 and had an intra-cluster distance 0.109. Cluster II having two genotypes BARI mistikumra- 1 and BARI mistikumra -2 and had an intra-cluster distance 0.01. (Table 8 and 10).

4.4.3 Non-hierarchical clustering

The computations from covariance matrix gave non-hierarchical clustering among twenty one genotypes of sweet gourd and grouped them into five clusters. Khatun *et al.* (2010) conducted an experiment in 38 snake gourd genotypes and the

genotypes were grouped into four different clusters. Banik (2003) studied 26 genotypes of snake gourd and the genotypes were grouped into seven distinct clusters. Asmaul Husna (2009) reported five clusters in bottle gourd. Gaffar (2008) reported similar number of clustering in 15 sponge gourd genotypes. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. So the results obtained through PCA were confirmed by non-hierarchical clustering. Table 8 represents the clusters occupied by 21 genotypes of sweet gourd. It explains that cluster IV contained the highest number of genotypes seven, cluster III constitute by six genotypes, cluster V constitute by five genotypes and cluster II constitute by two genotypes and cluster I having only one genotype. Cluster IV having seven genotypes BD-2174, BD-2177, BD-2196, BD-9489, BD-9494, BD-9491, BD-9490. The cluster IV genotypes are collected from Plant Genetic Resource Centre, BARI, Gazipur. Cluster mean for 13 traits are presented in (Table 9). From the table 9, it was observed that the mean value of cluster IV ranked first for leaf breadth (25.77) and internodes distance (15.19). Cluster II having two genotypes viz. BARI mistikumra-1, BARI mistikumra-2 and cluster V having five genotypes viz. BD-264, BD-2203, BD-2212, BD-9493 and BD-4590. They were collected from Plant Genetic Resource Centre, BARI, Gazipur. These clusters were unable to lead in respect of the highest cluster mean value for maximum characters. Among 13 characters cluster I produced the maximum cluster mean for the six characters viz. pedicel length of male flower (22.60), No. of male flowers per plant (9.33), fruit length (74.40), fruit breadth (35.00), fruit weight (3.58) and fruit yield per plant (7.15). Similarly cluster III ranked first for leaf length without petiole (18.40), days to first male flowering (67.78), pedicel length of female flower (5.52) and number of female flowers per plant (4.78) and had six genotypes viz. BD-266, BD-2214, BD-2151, BD-2153, BD-2229, BD-2222. All the genotypes were collected from Plant Genetic Resource Centre, BARI, Gazipur.

Table 6. Eigen values and yield percent contribution of 13 characters of twenty one germplasm of sweet gourd.

Characters	Eigen values	Percent variation	Cumulative % of Percent variation
Leaf length without petiole (cm)	5.735	44.12	44.12
Leaf breadth (cm)	2.066	15.89	60.12
Internode distance (cm)	1.684	12.95	72.96
Days to first male flowering	1.176	9.05	82.01
Days to first female flowering	0.812	6.24	88.25
Pedicel length of male flower (cm)	0.558	4.29	92.54
Pedicel length of female flower (cm)	0.328	2.53	95.07
Number of male flower per plant	0.233	1.80	96.87
Number of female flower per plant	0.185	1.42	98.29
Fruit length (cm)	0.137	1.06	99.35
Fruit breadth (cm)	0.035	0.27	99.62
Fruit weight (g)	0.033	0.25	99.88
Fruit yield per plant (kg)	0.018	0.13	100.00

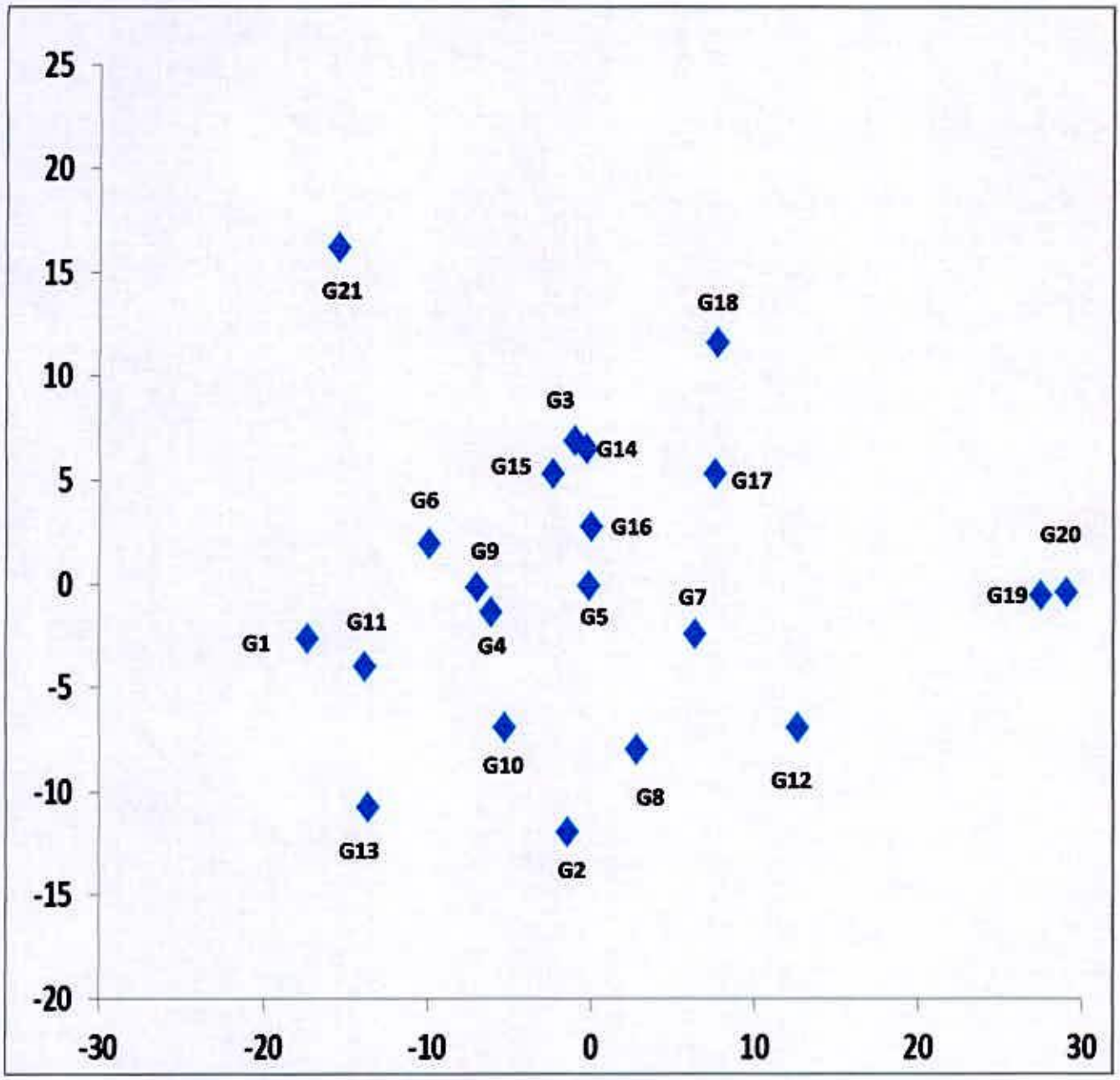

Figure 2. Scattered diagram of twenty one sweet gourd genotypes

Table 7.Ten highest and ten lowest inter genotypic distance among the 21 sweet gourd genotypes

Highest distance				Lowest distance			
Sl No.	Genotype		Distance	Sl No.	Genotype		Distance
01	G20	G21	47.46	01	G3	G14	0.75
02	G1	G20	46.39	02	G4	G9	1.42
03	G19	G21	46.04	03	G19	G20	1.57
04	G1	G19	44.82	04	G14	G15	2.13
05	G13	G20	43.86	05	G3	G15	2.41
06	G11	G20	43.04	06	G5	G16	2.92
07	G13	G19	42.30	07	G15	G16	3.45
08	G11	G19	41.46	08	G6	G9	3.60
09	G6	G20	38.98	09	G1	G11	3.71
10	G6	G19	37.42	10	G3	G16	3.74

Table 8. Distribution of genotypes in different clusters

Cluster no.	No. of Genotypes	No. of population	varieties
I	G21	1	BD-2150
II	G19, G20	2	BARI mistikumra-1, BARI mistikumra-2
III	G1, G2, G9, G10, G11, G13	6	BD-266, BD-2214, BD-2151, BD-2153, BD-2229, BD-2222
IV	G3, G4, G6, G14, G15, G16, G18	7	BD-2174, BD-2177, BD-2196, BD-9489, BD-9494, BD-9491, BD-9490
V	G5, G7, G8, G12, G17	5	BD-264, BD-2203, BD-2212, BD-9493, BD-4590

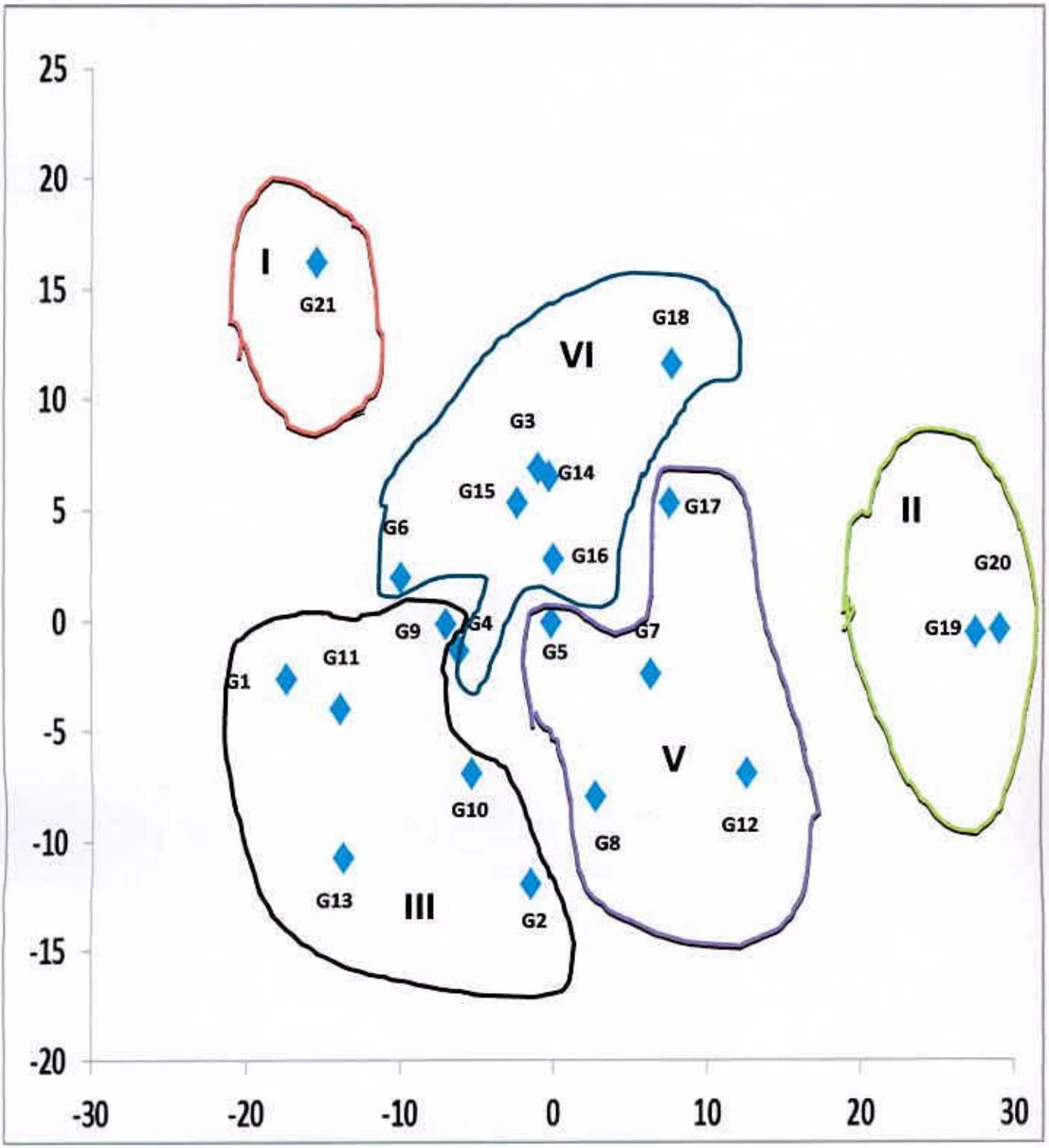

Figure 3. Scattered diagram of twenty one sweet gourd genotypes superimpose cluster

Table 9. Cluster mean values of 13 different characters of 21 genotypes

Characters	I	II	III	IV	V
Leaf length without petiole (cm)	17.67	12.83	18.40	17.83	16.53
Leaf breadth (cm)	21.87	18.33	23.47	25.77	22.29
Internode distance (cm)	11.33	13.00	14.33	15.19	13.60
Days to first male flowering	70.67	85.83	63.06	69.91	73.60
Days to first female flowering	74.33	86.83	67.78	76.19	78.13
Pedicel length of male flower (cm)	22.60	8.23	20.86	12.47	19.71
Pedicel length of female flower (cm)	5.10	2.09	5.52	4.65	3.72
Number of male flower per plant	9.33	1.00	7.72	7.05	7.07
Number of female flower per plant	4.67	1.00	4.78	3.67	2.67
Fruit length (cm)	74.40	40.06	54.18	57.27	47.95
Fruit breadth (cm)	35.00	18.03	27.65	30.11	26.35
Fruit weight (g)	3.58	0.85	2.05	2.54	1.71
Fruit yield per plant (kg)	7.15	0.85	6.10	3.63	2.70

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Table 10. Intra (Bold) and inter cluster distances (D^2) for 21genotypes

Cluster	I	II	III	IV	V
I	**00.00**	15.472	11.858	6.825	10.326
II		**00.01**	17.922	14.444	10.447
III			**0.177**	7.284	9.274
IV				**0.109**	6.450
V					**0.261**

Table 11. Relative contributions of the thirteen characters of 21 varieties to the total divergence

Characters	Vector-1	Vector-2
Leaf length without petiole (cm)	0.5349	-0.1190
Leaf breadth (cm)	0.1333	0.0045
Internodes distance (cm)	-0.1342	0.1140
Days to first male flowering	0.9228	-0.3450
Days to first female flowering	-0.0185	0.1123
Pedicel length of male flower (cm)	0.1329	0.0509
Pedicel length of female flower (cm)	-0.5019	0.2415
Number of male flower per plant	0.1079	0.2099
Number of female flower per plant	0.3500	-1.9159
Fruit length (cm)	-0.0214	-0.2980
Fruit breadth (cm)	-0.4121	-0.1813
Fruit weight (g)	1.3447	-1.4068
Fruit yield per plant (kg)	0.0004	1.4252

4.4.4 Canonical variate analysis

The highest inter-cluster distance was observed (Table 10) between cluster II and cluster III (17.922) followed by between cluster I and cluster II (15.472) and cluster I and cluster V (14.444). Similarly, the lowest inter-cluster distance was observed between the cluster II and cluster IV (6.16). Moderate or intermediate distance was found between cluster I and cluster III (11.858). On the other, the highest intra-cluster distance was found in cluster V (0.261) followed by cluster III (0.177). The lowest intra-cluster distance was observed between in cluster I (00.00). The inter cluster distances were found much higher than the intra cluster distances suggesting wider genetic diversity existed among the genotype of different groups. Result of different multivariate analysis were superimposed in figure 2 from which it may be concluded from the above results that different multivariate techniques supplemented and confirmed one another.

As per scatter diagram the genotypes were apparently distributed into five clusters. It was also revealed that the genotypes of cluster I were more diverse from the genotypes of cluster II. Islam *et al.* (2004) also observed the similar result. It is assumed that maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. However, for a practical plant breeding the objective is not only high heterosis but also to achieve high-level production. In the present study the maximum distance existence between cluster II and cluster III. But considering the yield and duration crosses involving cluster I and II may exhibit high heterosis for yield. Main and Bahl (1989) reported that the parents separated by D^2 values of moderate magnitude generally showed higher heterosis.

4.4.5 Contribution of characters towards divergence of the genotypes

The values of Vector I and Vector II are presented in Table 11. Vector I obtained from PCA expressed that leaf length without petiole (0.5349), leaf breadth (0.1333), days to first male flowering (0.9228), pedicel length of male flower (0.1329), number of male flower per plant (0.1079), fruit yield per plant (0.3500), fruit weight (1.3447) and number of female flower per plant (0.0004) were major characters that contribute to the genetic divergence. It was the reflection of first axis of differentiation. In vector II leaf breadth (0.0045), internodes distance (0.1140), days to first female flowering (0.1123), fruit yield per plant (0.0509), pedicel length of female flower (0.2415), number of male flower per plant (0.2099), pedicel length of male flower (1.4252) showed their important role toward genetic divergence. Negative values in both vectors fruit length and fruit breadth had lower contribution towards the divergence.

4.4.6 Selection of genotypes as parent for future hybridization programme

Selection of genetically diverse parents is an important step for hybridization program. So the genotypes were to be selected on the basis of specific objectives. A high heterosis could be produced from the crosses between genetically distant parents (Falconer, 1960; Moll *et al.* 1962; Ramanujam *et al.* 1974; Ohaderi *et al.* 1984)

Considering the magnitude of cluster mean and agronomic performance the genotype G_1 (BD-2151) for minimum days of first female flowering and maximum internodes distance from cluster III, G_{21} (BD-2150) for maximum fruit length, fruit breadth and fruit weight from cluster I, G_{11} (BD 2229) for maximum yield per plant from cluster III and G_{13} (BD 266) for maximum number of female flower and minimum days of first male flowering from cluster III. Therefore considering group distance and other agronomic performance the inter genotypic crosses between G_1 (BD-2151) and G_{21} (BD-2150); G_{11} (BD 2229) and G_{13} (BD 266) may be suggested for future hybridization program.

Chapter 5

Summary and Conclusion

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CHAPTER V

SUMMARY AND CONCLUSION

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

The field experiment was laid out in Randomized Complete Block Design (RCBD) with three (3) replications. Data on different characters were recorded and analyzed statistically. The analysis of variance of all the traits was computed and significant differences were found among the accessions in respect of different characters studied. The maximum value in respect of days to first male flowering (86.33days) was observed in G_{20} (BARI mistikumra-2) and minimum days (60.00days) to first male bud were recorded in G_{13} (BD-266). Genotype number G_{19} (BARI mistikumra-1) recorded the maximum value (87.00days) for days to first female flowering and lowest days to first female flowering (65.67days) was recorded in G_1 (BD-2151). Genotype no. G_8 (BD-2212) is the highest leaf length (21.60cm) and genotype no. G_{20} (BARI mistikumra-2) is the lowest leaf length (11.33cm) was counted. In case of leaf breadth, the highest value (30.67cm) was recorded in G_{15} (BD-9490) and the lowest value was (15.20 cm) recorded in G_{20} (BARI mistikumra-2). The maximum male flowers pedicel length was found in BD-2203 and the minimum was recorded in BARI mistikumra-1.In genotype no. G_7 (BD-2203), the highest male flower pedicel length (26.47 cm) and in genotype no. G_{19} (BARI mistikumra-1), the lowest male flower pedicel length (8.07cm) were counted. In genotype no G_9 (BD-2214), the highest female flower pedicel length (8.63cm) and in genotype no. G_{19} (BARI mistikumra-1), the lowest female flower pedicel length (2.07 cm) were counted. In case of no. of male flower, the highest value (16.00) was observed in G_{16} (BD-9491) and the lowest value (1.00) was observed in G_{19} (BARI mistikumra-1). In case of no. of female flower, the highest value (7.00) was observed in G_{13} (BD-

266) and the lowest value (1.00) was observed in G_{19} (BARI mistikumra-1) and G_{20} (BARI mistikumra-2). In respect of fruit length, longest fruit (74.40cm) was observed in G_{21} (BD-2150) and the genotype no. G_{20} (BARI mistikumra-2) had the smallest length of (39.60cm). In case of fruit breadth, the highest value (35.00cm) was observed in G_{21} (BD-2150) and the lowest value (17.33cm) was observed in G_{19} (BARI mistikumra-1). In case of average weight per fruit, the highest value (3.58 kg) was observed in G_{21} (BD-2150) and the lowest value (0.80 kg) was observed in G_{19} (BARI mistikumra-1). Genotype no G_{11} (BD-2229) is the highest average yield per plant (9.92) and genotype no. G_{19} (BARI mistikumra-1) is the lowest no. of fruit per plant (0.80) was counted.

The phenotypic variance was higher than the corresponding genotypic variance in all the characters, indicating greater influence of environment on the expression of these characters. The maximum differences between phenotypic and genotypic coefficient of variation were 69.78% and 45.76% respectively, which indicated that number of female flower mostly depended on environmental effect. The highest estimated heritability among thirteen yield contributing characters 96.49%, 95.94%, 91.12%, 90.70%, 81.20% was in pedicel length of male flower, pedicel length of female flower, leaf breadth, leaf length and fruit weight respectively. The lowest heritability was 43.00% in no. of female flower.

The maximum genetic advance was observed in respect of fruit length (12.88) and followed by maximum value was 11.90 in advance for pedicel length of male flower among thirteen characters of sweet gourd genotypes. The maximum genetic advance in percent of mean (GAMP) was obtained for fruit yield per plant (106.73%) and the lowest was for days to first female flowering (14.65%).

The genotypic correlation coefficient was generally higher than the corresponding phenotypic correlation coefficient which indicated that the apparent association might be due to genetic reason. Yield per plant was significantly and positively correlated with pedicel length of male flower, number of male flower, number of

female flower, fruit length, fruit breadth and fruit weight both at genotypic and phenotypic levels. Therefore, correlation study revealed that selection based on these characters would be effective for increasing yield per plant.

The results of path coefficient analysis revealed that number of female flower had the highest positive direct (0.858) effect on yield per plant followed by fruit weight (0.230), pedicel length of male flower (0.176), days to first female flowering (0.076), fruit length (0.066) and fruit breadth (0.027). Such results indicated that direct selection based on these characters would be effective for yield improvement in pumpkin. On the other hand, days to first male flowering (-0.214), number of male flower (-0.207), leaf breadth (-0.184), pedicel length of female flower (-0.076) and leaf breadth without petiole (-0.041) showed negative direct effect on yield per plant. So, direct selection based on these characters would not be effective. Number of male flower had considerable positive indirect (0.660) effect via number of female flowers per plant. The highest negative indirect effect was displayed by days to first female flowering (-0.447) via number of female flowers per plant. The indirect effect of days to first female flowering via number of female flower (-0.447) and days to first male flower (-0.188) and number of female flower via number of male flower (-0.159) were also considerable high in negative direction.

The residual effect was 0.391, which indicated that some more other characters were responsible for contribution to yield per plant but not taken into consideration in the present investigation.

Multivariate analysis carried out through principal component analysis (PCA), principal coordinate analysis (PCO), cluster analysis, and canonical vector analysis (CVA) using Genstat 5.13 software programme. The first three principal characters with Eigen values were contributed 72.96% variation toward divergence. As per as PCA, D2 and cluster analysis using the genotypes were

grouped into five different clusters. Cluster I, II, III, IV and V comprised one, two, six, seven and five genotypes respectively.

The highest inter-cluster distance was observed (Table 12 or Figure 4) between cluster II and cluster III (17.922) followed by between cluster I and cluster II (15.472), between cluster II and cluster IV (14.444). Similarly, the lowest inter-cluster distance was observed between the cluster IV and cluster V (6.450). On the other, the highest intra-cluster distance was found in cluster V (0.261) followed by cluster IV (0.177). The lowest intra-cluster distance was observed between in cluster I (00.00) .

The highest inter-genotypic distance was observed between genotypes G_{20} and G_{21} (47.46) followed by G_1 and G_{20} (46.39) and the lowest distance was observed (0.75) between genotypes G_3 and G_{14} followed by the distance (1.42) between genotypes G_4 and G_9. Cluster I ranked first for pedicel length of male flower (22.60), number of male flower per plant (9.33), fruit length (74.40), fruit breadth (35.00), fruit weight (3.58) and fruit yield per plant (7.15). Cluster III ranked first for leaf length without petiole (18.40), days to first male flowering (63.06), days to first female flowering (67.78), pedicel length of female flower (5.52), number of female flower per plant (4.78). Cluster V ranked first for leaf breadth (25.77) and internodes distance (15.19).

Findings of the present study indicated significant variation among the genotypes for all the characters studied. Considering diversity pattern and other field performances, the genotypes G_1 (BD-2151) from cluster III, G_{21} (BD-2150) from cluster I; G_{11} (BD 2229) from cluster III and G_{13} (BD 266) from cluster III could be best choice as suitable parents for efficient hybridization program. Therefore considering group distance and other agronomic performance the inter genotypic crosses between G_1 (BD-2151) and G_{21} (BD-2150); G_1 (BD-2151) and G_{11} (BD 2229), G_1 (BD-2151) and G_{13} (BD 266), G_{21} (BD-2150)and G_{11} (BD 2229), G_{21}

(BD-2150)) and G_{13} (BD 266), G_{13} (BD 266) and G_{11} (BD 2229) may be suggested for future hybridization programme.

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

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

ii. Selection procedure would be applied for desired characters such as leaf length, fruit breadth, fruit weight, number of fruit per plant, days to first male flower, days to first female flowering, pedicel length of male flower, female flower pedicel length to develop high yielding varieties.

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

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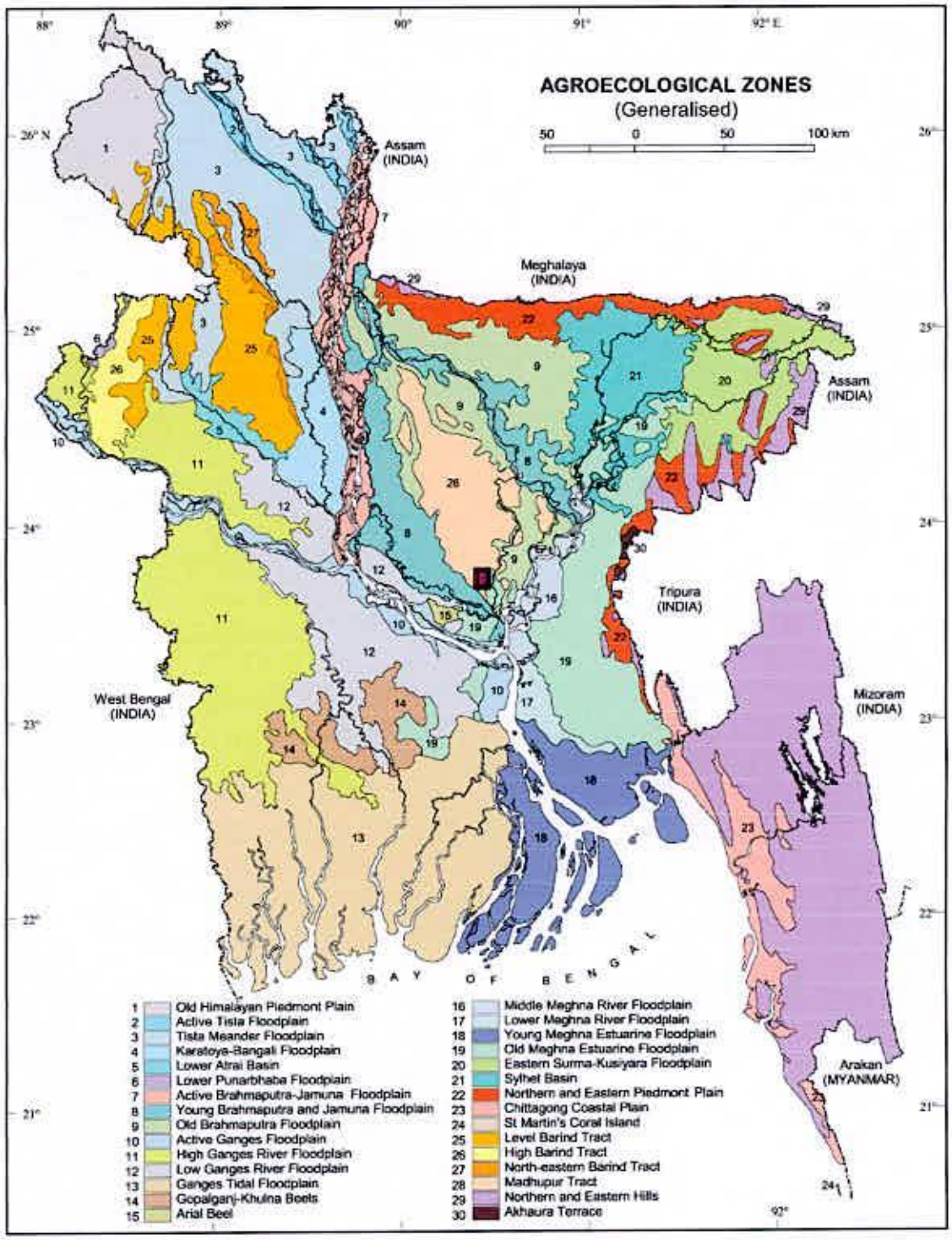
Appendices

Appendix 1. Location of experimental field



Appendix II. Monthly average temperature, relative humidity and total rainfall of the experimental site during the period from March 2009 to August 2009

Month	Air temperature (°c)		Relative Humidity (%) (total)	Rainfall (mm)	Sunshine (hr)
	Maximum	Minimum			
March, 2010	34.6	16.5	67	45	7.3
April, 2010	35.8	20.3	65	88	8.3
May, 2010	36.7	20.3	70	205	7.7
June, 2010	35.4	22.5	80	577	4.2
July, 2010	34	24.6	83	563	3.1
August, 2010	36	23.6	81	319	4.0

Source: Bangladesh Metrological Department (Climate and Weather division), Agargaon, Dhaka- 1212.

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	%	Methods employed
Sand	36.90	Hydrometer method (Day, 1915)
Silt	26.40	Do
Clay	36.66	Do
Texture class	Clay loam	Do

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B. Chemical composition of the soil

Sl. No.	Soil characteristics	Analytical data	Methods employed
1	Organic carbon (%)	0.82	Walkley and Black, 1947
2	Total N (kg/ha)	1790.00	Bremner and Mulvaney, 1965
3	Total S (ppm)	225.00	Bardsley and Lanester,1965
4	Total P (ppm)	840.00	Olsen and Sommers, 1982
5	Available N (kg/ha)	54.00	Bremner, 1965
6	Available P (kg/ha)	.69.00	Olsen and Dean, 1965
7	Exchangeable K (kg/ha)	89.50	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	pH (1 : 2.5 soil to water)	5.55	Jackson, 1958
10	CEC	11.23	Chapman, 1965

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

Appendix IV. Mean performance of different parameter of 21 genotypes of sweet gourd

Genotypes	LLWP	LB	ID	DFMF	DFFF	PLMF	PLFF	NMF	NFF	FL	FB	FW	FYP
BD-2151	18.37	27.00	20.00	61.67	65.67	21.50	5.20	8.67	6.33	62.17	27.30	2.35	9.41
BD-2153	18.27	23.07	16.00	64.33	65.67	12.50	4.60	5.67	3.33	45.62	24.90	1.67	2.52
BD-2174	17.43	23.13	13.00	71.67	75.00	10.47	6.03	4.00	2.33	59.87	28.10	1.95	2.63
BD-2177	18.30	28.50	18.33	66.00	71.67	13.07	4.10	9.67	7.00	56.10	26.13	2.08	5.36
BD-264	17.37	22.03	18.00	73.33	75.33	21.43	5.17	7.33	3.67	53.57	27.47	2.31	4.53
BD-2196	19.83	30.50	16.33	65.67	69.33	13.97	2.20	6.33	3.67	61.20	28.87	2.40	3.30
BD-2203	12.40	20.37	13.00	76.33	77.67	26.47	5.17	5.00	1.33	48.83	25.73	1.40	1.40
BD-2212	21.60	24.37	11.33	69.33	74.00	19.53	3.07	6.33	2.33	43.97	28.00	1.85	2.62
BD-2214	17.20	23.40	10.00	64.33	73.33	20.83	8.63	5.33	2.67	55.53	31.43	2.86	4.34
BD-2222	20.50	25.03	11.00	64.67	70.00	21.13	6.93	4.67	2.67	52.00	25.43	1.41	2.28
BD-2229	14.87	20.70	10.00	63.33	66.00	24.50	3.53	11.67	6.67	56.97	30.33	2.18	9.92
BD-4590	15.03	24.33	14.67	74.33	79.00	15.83	3.13	4.00	2.00	43.00	20.00	1.00	1.00
BD-266	21.17	21.63	19.00	60.00	66.00	24.73	4.23	10.33	7.00	52.77	26.53	1.85	8.14
BD-9489	14.27	21.43	13.00	72.67	77.33	18.90	4.20	5.67	2.00	59.00	31.00	3.20	3.20
BD-9490	21.47	30.67	17.33	66.67	79.67	11.20	3.07	5.00	3.33	57.50	30.37	2.63	3.37
BD-9491	17.90	22.63	12.33	69.67	77.00	10.93	5.70	15.33	5.33	52.37	31.33	2.15	4.18
BD-9493	16.23	20.33	11.00	74.67	84.67	15.30	2.07	12.67	4.00	50.37	30.57	1.98	3.95
BD-9494	15.63	23.50	16.00	77.00	83.33	8.77	7.27	3.33	2.00	54.83	34.97	3.40	3.40
BARI mistikumra-1	14.33	21.47	12.00	85.33	87.00	8.07	2.07	1.00	1.00	40.53	17.33	0.80	0.80
BARI mistikumra-2	11.33	15.20	14.00	86.33	86.67	8.40	2.10	1.00	1.00	39.60	18.74	0.90	0.90
BD-2150	17.67	21.87	11.33	70.67	74.33	22.60	5.10	9.33	4.67	74.40	35.00	3.58	7.15
Mean	17.20	23.39	14.17	70.38	75.17	16.67	4.46	6.78	3.54	53.34	27.60	2.09	4.02
Min	11.33	15.20	10.00	60.00	65.67	8.07	2.07	1.00	1.00	39.60	17.33	0.80	0.80
Max	21.60	30.67	20.00	86.33	87.00	26.47	8.63	15.33	7.00	74.40	35.00	3.58	9.92

LLWP = Leaf length without petiole (cm), LB = Leaf breadth (cm), ID = Internodes distance (cm), DFMF = Days to first male flowering, DFFF = Days to first female flowering, PLMF = Pedicel length of male flower (cm), PLFF = Pedicel length of female flower (cm), NMF = Number of male flower per plant, NFF = Number of female flower per plant , FL = Fruit length (cm), FB = Fruit breadth (cm), FW = Fruit weight (g) and FYP = Fruit yield per plant (kg).

Appendix V. Principal component score of 21 genotypes of sweet gourd

Genotypes	Z_1	Z_2
1	-17.309	-2.663
2	-1.428	-11.94
3	-0.302	6.515
4	-6.115	-1.363
5	-0.113	-0.135
6	-9.879	1.903
7	6.354	-2.422
8	2.785	-8.012
9	-6.951	-0.203
10	-5.275	-6.936
11	-13.856	-4.045
12	12.604	-6.9
13	-13.586	-10.804
14	-0.961	6.88
15	-2.37	5.271
16	0.037	2.787
17	7.604	5.304
18	7.695	11.597
19	27.463	-0.566
20	29.035	-0.432
21	-15.431	16.163

শেরেবাংলা কৃষি বিশ্ববিদ্যালয় গ্রন্থাগার
সংযোজন নং 29/38920 3.3.15
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