GENETIC DIVERSITY AND CHARACTER ASSOCIATION IN YIELD AND YIELD CONTRIBUTING TRAITS OF PUMPKIN (*Cucurbita moschata* Duchesne ex Poir.)

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CERTIFICATE

This is to certify that thesis entitled, "**GENETIC DIVERSITY AND CHARACTERS ASSOCIATION IN YIELD AND YIELD CONTRIBUTING CHARACTERS OF PUMPKIN** (*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 bona fide research work carried out by **Samsun Naher**, Registration No:**09-03596** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: December, 2014
Place: Dhaka, Bangladesh

Supervisor
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DEDICATED TO

MY

BELOVED PARENTS

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ABSTRACT

The experiment was conducted with twenty genotypes of pumpkin (*Cucurbita moschata* Duchesne ex Poir.) at the experimental field of Sher-e-Bangla Agricultural University during April 2014 to September 2014. Vegetables play a vital role in the overall economic performance of Bangladesh. Pumpkin is a very popular and one of the most important vegetable crops grown extensively throughout the tropical and subtropical countries. Due to its high nutritional content and lucrative market price, pumpkin may be considered as a high value crop. Pumpkins are rich in carbohydrate and minerals and cheaper source of vitamins, especially carotenoid pigments, which have a major role in nutrition in the form of pro-vitamin-A, antioxidants, when used at ripening stage. Thus, this vegetable can contribute to improve nutritional status of the people of Bangladesh, particularly the vulnerable group in respect of vitamin-A requirement. Lack of high yielding, disease and pest tolerant varieties are the main constrains towards its production. The objective of the study was to measure the variability among the genotypes for yield and yield contributing characters of pumpkin. This helps to choose desirable parents for establishing new breeding population. High genotypic coefficient of variation (GCV) was observed in fruit yield per plant, pedicel length of male flower, number of male flower per plant. Low GCV was observed in days to first male flowering and days to first female flowering. High heritability with high genetic advance in percent of mean was observed in yield per plant, pedicel length of male and female flower and fruit weight indicated these traits would be effective. Highly significant positive correlation was found between fruit length and fruit weight. Path co efficient analysis revealed that maximum direct contribution toward yield per plant was found fruit length followed by fruit weight. The highest intra cluster distance was found in cluster IV and the lowest was found in cluster I. Among five clusters the highest inter cluster distance was observed between cluster II and cluster V and the lowest between cluster I and cluster II. Considering all the characters G_{14} (BD 246) and G_6 (BD 309) G_{12} (9492) and G_{11} (BD 9494) may be selected for future breeding program.

List of Abbreviations of Technical Symbols and Terms

FULL NAME	ABBREVIATION
Agro-Ecological Zone	AEZ
And others	*et. al.*
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Centimeter	cm
Co-efficient of variation	CV
Days after sowing	DAS
Degree celsius	^{o}C
Degrees of freedom	d.f
Etcetera	etc.
Food and Agriculture Organization	FAO
Figure	Fig.
Genetic advance	GA
Genotypic co-efficient of variation	GCV
Genotypic variance	δ^2_g
Gram	g
Hectare	ha
Heritability in broad sense	h^2b
Journal	j.
Kilogram	Kg
Meter	m
Mean sum of square	MSS
Millimeter	mm
Murate of potash	MP
Number	No.
Percent	%
Phenotypic co-efficient of variation	PCV
Phenotypic variance	δ^2_p
Randomized complete block design	RCBD
Sher-e-Bangla Agricultural University	SAU
Standard error	SE
Square meter	m^2
Triple super phosphate	TSP
Unites Nations Development Program	UNDP

TABLE OF CONTENTS

CONTENTS (Continued)

CONTENTS (Continued)

CONTENTS (Continued)

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

CHAPTER I
INTRODUCTION

Pumpkin (*Cucurbita moschata* Duchesne ex Poir.) or sweet gourd is a very popular and common vegetable in Bangladesh. It is grown widely from homestead to commercial field and marketed all over the country. It is very nutritious due to high content of vitamin A and can play a vital role in meeting the vegetable shortage and nutritional problem.

Cucurbita moschata is medium-sized and widely grown in the tropics and subtropics, its fruit color is most often dark green, light yellow, or pale orange (Paris, 2010). Pumpkin grows well throughout the entire tropical and subtropical region of the world. It is well grown in Mediterranean countries, Turkey, Italy and Egypt which meet one-third of world production of pumpkin (Paris, 1996).

The genus *Cucurbita* originates from Central and South America. The wild ancestor of *Cucurbita moschata* is still unknown, but recent investigations of the phylogenetic relationships among wild and domesticated *Cucurbita* taxa, mainly based on DNA data, suggest that it will probably be found in lowland northern South America. Archaeological evidence for the association of cultivated *Cucurbita* with man dates back to 5000 years BC. After the discovery of the new world, the cultivated cucurbits were introduced into the old world (Grubben, 2004).

The Cucurbitaceae family comprises about 120 genera and 800 species. Pumpkin belongs to the cucurbitaceae family. All species of *Cucurbita* have 20 pairs of chromosomes (Rhodes *et al.*1968). Pumpkin also contains 20 pairs of chromosome (2n=40).

There are male (staminate) and female (pistillate) flowers (unisexual flowers) on a single plant (monoecious), and these grow singly, appearing from the leaf axils. Flowers have five fused yellow to orange petals (the corolla) and a green bell-shaped calyx. Male flowers in Cucurbitaceae generally have five stamens, but in Cucurbita there are only three, and their anthers are joined together so that there appears to be one (Mabberley,2008).Female flowers have thick pedicels, and an inferior ovary with 3–5 stigmas that each have two lobes (Lu and Jeffery, 2015). The calyx of *Cucurbita moschata* male flowers is comparatively short (Saade *et al.,* 2013).

Pumpkin is a storehouse of many anti-oxidant vitamins such as vitamin-A, vitamin-C and vitamin-E. It is rich in dietary fiber, anti-oxidants, minerals, vitamins. It is one of the very low calorie vegetables. 100 g fruit provides just 26 calories and contains no saturated fats or cholesterol. Every 100 gram edible portion of matured fruits contain 1.4g protein, 100mg calcium, 30mg phosphorus, 50 micro gm beta carotene and 2g vitamin C. This vegetable is one of the food items recommended by dieticians in cholesterol controlling and weight reduction programs. It is also an excellent source of many natural poly-phenolic flavonoid compounds such as, ß carotenes, crypto xanthin, lutein and zea-xanthin. The fruit is a good source of B-complex group of vitamins like folates, niacin, vitamin B-6 (pyridoxine), thiamin and pantothenic acid. It is also rich source of minerals like copper, calcium, potassium and phosphorus. Pumpkin seeds indeed are an excellent source of dietary fiber and mono-unsaturated fatty acids, which are good for heart health.

Pumpkins have anti-diabetic, antioxidant, anti-carcinogenic , and inflammatory pharmacological properties (Yadav *et al* 2010). Pumpkin seeds have high levels of crude protein, calcium, iron, potassium, phosphorus, magnesium, zinc, (Mansour *et al* 1993) and beta-carotene.

Pumpkin can be used in variety of delicious recipes either baked, stew- fried; however, it is eaten best after steam-cooking in order to get maximum

nutrients. In China, young tender pumpkin leaves consumed as cooked greens or in soups. In the Indian subcontinent where it is popular as *"kaddu or sitaphal"*, pumpkin is used in the preparation of "sabzee", sweet dishes (halwa), desserts, soups, curries etc. The fruit is used in the preparations of pies, pancakes, custard, ravioli. etc in Europe and USA. Golden nugget pumpkins are used to make wonderful, stuffing, soups etc. Roasted Pumpkin seeds (Pepita) can be eaten as snacks.

Vegetable production rate in Bangladesh is very low to meet the demand of people but there is considerable potential of growing vegetables in Bangladesh. Farmers who are engaged in the production of vegetables often earn higher incomes than those engaged in the production of cereal crops alone (Weinberger and Lumpkin, 2005). Vegetables like eggplant, radish, cabbage, cauliflower, and pumpkin gave returns at least three times higher than rice (Ateng, 1998). Vegetable production like pumpkin can be an economical agribusiness for Bangladesh.

Pumpkins are a perfect crop for production because they are extremely nutritious, last for up to a year and fetch good money at market. It can be grown all year round. It has the longest natural storability among all cucurbits. The well matured fruits can be stored for 2 to 4 months (Yawalkar, 1985).

In Bangladesh many pumpkin genotypes having diverse characteristics are grown in different parts of the country. Genotypes available in the market do not have uniformity or standardization in nomenclature. Moreover, no information on morphological and agronomical characteristics is available which can be used as delineating and standardizing different accessions. A good knowledge of genetic resources may help in identifying desirable cultivars for commercial cultivation.

Therefore, the present research was under taken with the following objectives:

- To study the genetic variability among the pumpkin plants,
- To assess the heritability of yield contributing characters of different genotypes,
- To study the interrelationships of yield contributing characters among themselves and with seed yield; and their direct and indirect effects,
- To assess the contribution of different traits towards divergence, and
- . To screen out suitable parental groups with better performances for future breeding program and to select promising genotypes considering high yield.

CHAPTER II
REVIEW OF LITERATURE

Sweet gourd 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-efficient analysis, heritability 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:

Naik *et al.* (2012) conducted a field experiment to study of genetic variability, heritability and genetic advance for fruit quality characters in Teasle gourd. Higher phenotypic coefficients of variation were observed for all the characters except fruit length at marketable stage. Total in mesocarp, total sugar in exocarp, reducing sugar in mesocarp, ascorbic acid in exocarp, ascorbic acid in mesocarp, total soluble solids (TSS) in exocarp, β-carotene in exocarp, acidity in mesocarp, β-carotene in mesocarp, TSS in mesocarp, acidity in exocarp showed high heritability coupled with high genetic advance indicating that these traits were under the additive gene control and simple selection can be used for further improvement in these traits of teasle gourd. The experiment were carried out at the research field of All India Coordinated Project on Vegetable Crops situated at C Block farm, Bidhan Chandra Krishi Viswa vidyalaya, Nadia duriing 2007 to 2008.

Banik (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 6×6 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 coefficients of variation (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 genetic 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 coefficient 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 F_1 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*) 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 3176), 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)

Ahamed *et al.* (2011) conducted an experiment to assess morphological and yield attributes of pumpkin **(***Cucurbita moschata*) in northern area of Bangladesh during kharif season. The range of variability was distinct for leaf length ranged from 30.6-47.2 cm in different genotypes.

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 (20.5 8%). 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

Ahamed *et al.* (2011) found the range of first flowering among twenty genotypes of pumpkin was at 52.0-73.7 days.

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 P4 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 of 2005. The genotype RGNO5, RGNO6, RGNO7, RGNO8, RGN 13, RGN 17, RGN 18, RGN27, RGN29 recorded highest cluster mean values for days to 1st male flower open (56.0 days) and single fruit weight (141.0 g) and RGNO3, 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 l 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).

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 Gopal krishnan (1979) also reported significant variability among 25 diverse genotypes of bitter gourd.

2.1.4 Number of male and female flowers per plant

Akter *et al* (2013) conducted experiment the genetic divergence among thirty accessions of pumpkin at the Research Farm of the Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Salna, Gazipur, during the growing season 2011-12. High genotypic coefficient of variation (GCV)

and high heritability coupled with high genetic advance in percent of mean were observed for beta-carotene followed by non-reducing sugar, number of male flowers per plant and number of female flowers per plant which indicated that these characters were under additive gene control and selection for genetic improvement for these traits might be effective.

2.1.5 Pedicel length of flower (cm)

Asmaul Husna (2009) found that in bottle gourd male flower pedicel length is 3.5-2 1 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.

2.1.6 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; h2b 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 at.,* 1983; Prosad and Singh, 1990), ribbed gourd and bottle gourd (Rahman *et al.,* 1991). Rahman *et at.* (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^2b 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).

2.1.7 Fruit weight (Kg)

Correlation studies revealed that highest significant association of yield per plant with reproductive characters number of fruit per plant followed by fruit weight at genotypic and phenotypic level. Path co-efficient analysis revealed maximum direct contribution towards yield per plant with of number of fruit per plant followed by fruit weight.

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 (028 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.

2.1.8 Number of fruits per plant

Akter *et al.* found that (2013) Correlation co-efficient between yield per plant with number of fruits per plant and single fruit weight was positive and highly significant. Path coefficient analysis revealed that the maximum direct contribution towards yield was obtained through number of fruits per plant followed by days to first female flower and single fruit weight indicated that these traits should be considered as primary components of yield.

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).

2.1.9 Yield per plant (kg)

Husna *et al.* (2012) studied Variability, correlation and path analysis among different characters of thirty one bottle gourd genotype. High genotypic co-efficient of variation (GCV) was observed for yield per plant, fruit weight whereas low genotypic co-efficient of variation was observed fruit breadth. Path co-efficient analysis resulted maximum direct contribution towards yield per plant with number of fruit per plant followed by fruit weight.

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; h2b 98.64%). The variation for yield per plant was recorded in bottle gourd (Rahman *et at.* 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 h2 associated with high genetic advance for yield per plant was reported by Saha *et al.* (1992).

2.2 Correlation Co-efficient:

Khule *et al* (2011) conducted field experiments to determine correlation and path coefficient analysis in sponge gourd *Luffa cylindrica* (Linn.) at Vegetable Research Station Jagudan, (Gujarat) with thirty sponge gourd genotypes. He found genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients suggesting that the environmental influence reduces the relationship between yield and yield contributing characters of sponge gourd. Path coefficient analysis showed that number of fruits per plant, days to appear first female flower, fruit length, fruit diameter, and number of seeds per fruit had direct positive effects on marketable fruit yield per plant which indicates that this character was the major contributor to fruit yield.

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 indicated that the selection for the characters would 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 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 pointed gourd (*Trichosanthes 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 season 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 insignificant 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 =00.222) 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 yiel4 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 fruit, 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 fruits 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 arc 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 SO 026 and SO 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^2staistic. Cluster V contained the highest number of genotypes (13) and cluster Ill &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 I (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 H 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 01 (Shaparan), G_5, (Rampaligaj), G_9 (Nabil), G_{12} (Nandita) G_{14} (Eureca), G_{16} (Tia) and G_{19} (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 D^2 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 II (0.882) and the lowest for the cluster III (0.220). The highest inter-cluster distance was observed between cluster I and II (15.045) whereas 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 (0.43 9). The highest inter-cluster distance was observed between cluster IV and V (7.163) whereas 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 II (45.71) and the lowest between cluster VII and VI (3.33). The highest intra cluster distance was computed for cluster III and that was lowest for the cluster II. The first five axes accounted for 77.65% of the total variation among the 13 characters describing 64 pointed gourd genotypes. Fruit weight, seeds per fruit and fruit weight per plant contributed maximum to the total divergence.

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 intra cluster distance ranged from 30.34 (cluster I) to 371.56 (cluster III). The inter cluster 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 93.5 5% 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 inter cluster 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 D^2 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 inter cluster distances were greater than intra cluster distances, indicating considerable genetic diversity among genotypes. The highest D^2 value (984.3) was recorded between cluster II and IV.

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 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 April 2014 to September, 2014 to study on Genetic diversity and characters association in yield and yield contributing characters of pumpkin. A brief description about the locations of the experimental site, characteristics of soil, climate, materials, layout and design of the experiment are given. Land preparation, manuring and fertilizing, transplanting of seedlings, intercultural operations, harvesting, data recording procedure, economic and statistical analysis etc. are presented as follows:

3.1. Experimental site

The present experiment was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka-1207, during the period from April 2014 to September 2014.

3.2 Geographical Location

The experimental area was situated at 23°74'N latitude and 90°35'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 ModhupurTract, AEZ-28. 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. The experimental site was shown in the map of AEZ of Bangladesh in (Appendix I).

3.3 Climate

Area has subtropical climate, characterized by high temperature, high relative humidity and heavy rainfall in Kharif season (April-September) and scanty

rainfall associated with moderately low temperature during the Kharif season (April-September). 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 5.47 to 5.63, organic matter 0.82%. Experimental area was flat having available irrigation and drainage system and above flood level. Soil samples from 0-15 cm depths were collected from experimental field. The analyses were done by Soil Resource and Development Institute (SRDI), Dhaka. Physicochemical properties of the soil are presented in (Appendix III).

3.5 Planting materials

Twenty genotypes of pumpkin 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).

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 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 3 m.

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

Sl. No.	Genotype	BARI ACC Number	Origin
1	G_1	(BD 4587)	PGRC,BARI
2	G_2	(BD 2203)	PGRC,BARI
3	G_3	(BD 2174)	PGRC,BARI
4	G_4	(BD 264)	PGRC,BARI
5	G_5	(BD 2212)	PGRC,BARI
6	G_6	(BD 309)	PGRC,BARI
7	G_7	(BD 306)	PGRC,BARI
8	G_8	(BD 204)	PGRC,BARI
9	G_9	(BD 249)	PGRC,BARI
10	G_{10}	(BD 245)	PGRC,BARI
11	G_{11}	(BD 9494)	PGRC,BARI
12	G_{12}	(BD 9492)	PGRC,BARI
13	G_{13}	(BD 258)	PGRC,BARI
14	G_{14}	(BD 246)	PGRC,BARI
15	G_{15}	(BD 2236)	PGRC,BARI
16	G_{16}	(BD 2205)	PGRC,BARI
17	G_{17}	(BD 4592)	PGRC,BARI
18	G_{18}	(BD 223)	PGRC,BARI
19	G_{19}	(BD 242)	PGRC,BARI
20	G_{20}	(BD 251)	PGRC,BARI

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

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. When the seedlings become 18 days old those were transplanted in the main field in the pit. Seeds were sown 13th May, 2014 before sowing seeds were treated with Bavistin for minutes. Plate 1 showing raising of seedling in polybag.

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 May, 2014. 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 instalments at 20, 40, 60 and 75 days after transplanting Doses of manure and 11 fertilizers used in the study are shown in Table 2.

Plate 1. Raising of seedling in polybag

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

SL No.	Fertilizers/Manures	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 10 days germination of seeds was completed and the seedlings of different accessions were planted in the pit on 25 April, 2014. In each pit two seedlings were planted and the soil around the plant was firmly pressed by hand. Field view of plants after transplanting of seedling is presented in plate 2.

3.12.1 Thinning and gap filling

Only one healthy seedling was kept per pit for the proper development and for avoiding crowd environment. For this whenever 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

Plate 2. Field view of plants after transplanting of seedlings

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 was 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 was 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 was 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 was 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 was 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 was 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 was 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.

114.3.2 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 (Singli 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 V techniques viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA).

3.15.1.1 Estimation of genotypic and phenotypic variances

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

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

Where,

GMS = Genotypic mean sum of squares

EMS = Error mean sum of square

r = number of replications

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

Where,

σ^2_g = Genotypic variance

EMS = Error mean sum of square

3. 15.1.2 Estimation of genotypic and phenotypic correlation co-efficient

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

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

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

$\bar{x}$ = 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

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).

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

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}

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

Where,

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

selection intensity

σ_{ph} = Phenotypic standard deviation

h^2b = 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):

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

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:

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

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

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

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

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

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

$$r_{7.y} = r_{1.7}\,P_{1.y} + r_{2.7}\,P_{2.y} + r_{3.7}\,P_{3.y} + r_{4.7}\,P_{4.y} + r_{5.7}\,P_{5.y} + r_{6.7}\,P_{6.y} + P_{7.y} + r_{7.8}\,P_{8.y} + r_{7.9}\,P_{9.y} + r_{7.10}\,P_{10.y} + r_{7.11}\,P_{11.y} + r_{7.12}\,P_{12.y}$$

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

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

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

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

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

Where,

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

P_{iy}= Path coefficient due to ith 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 1. e., r1 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 I 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 I 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 I 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 1via 11on 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)

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

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.

3.15.2 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobisr'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 Component 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 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.

3.15.2.3 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.

3.15.2.4 Calculation of D^2 values

The Mahalanobls'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

$$D^2 = \sum_1^x d_1^2 = \sum_1^x (Y_i^j - Y_j^k)^2 \qquad (j \neq k)$$

Where,

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

x = Number of characters.

3.15.2.5 Computation of average intra-cluster distances

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

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.

3.15.2.6 Computation of average inter-cluster distances

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

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 clusterj.

3.15.2.7 Cluster diagram

Using the values of intra and inter-cluster distances ($D = \sqrt{D^z}$), 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.

3.1 5.2.8 Selection of varieties for future hybridization programme

Divergence analysis is usually performed to identi1' 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

Chaudhury (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-IV
RESULTS AND DISCUSSION

The experiment was conducted to study the genetic variability, correlation, path coefficient analysis and genetic diversity of 20 sweet gourd accessions. The data on different yield and yield contributing characters of pumpkin were computed and statistically analysed. The results of the present study have been presented and discussed in this chapter under the following heading.

- Genetic variability
- Correlation coefficient analysis
- Path coefficient analysis
- Genetic diversity analysis

4.1. Genetic variability

The analysis of variance indicated that the existence of highly significant variation among the genotype studied. The mean, range, mean sum of square, variance components, genotypic and phenotypic co efficient of variance, heritability, genetic advance, genetic advance in percent of mean are presented in Table 3.

4.1.1. Leaf length without petiole (cm)

Considerable variations were observed among 20 genotypes of pumpkin for leaf length. Significant Mean sum of square for leaf length (16.882) indicated considerable variation was presesnt among genotype studied (Table 3). The maximum leaf length was observed 21.17 in G_{14} (BD 246) and minimum was 12.50 recorded in G_1 (BD 4587) with mean value 16.59 (Appendix V). The phenotypic variance (5.80) appeared to be slightly higher than genotypic variance (5.54) suggested that less influence of environment on the expression of this gene controlling this trait. The genotypic co-efficient of variation

Table 3. Estimation of genetic variability for yield contributing characters related to yield of pumpkin

SL No.	Characters	Range	Mean	Mean sum of square (MS)	Phenotypic variance (δ^2p)	Genotypic variance (δ^2g)	PCV (%)	GCV (%)	Heritability (%)	GA	GA (%)
1	Leaf length without petiole (cm)	12.50-21.17	16.59	16.882**	5.80	5.54	14.52	14.20	95.65	4.74	28.60
2	Leaf breadth (cm)	16.33-23.17	19.75	14.696**	5.18	4.76	11.52	11.04	91.94	4.31	21.82
3	Internode distance	10.23-18.70	13.80	17.863**	6.14	5.86	17.95	17.55	95.58	4.88	35.34
4	Days to first male flowering	64.33-75.67	69.37	29.961**	12.74	8.61	5.14	4.23	67.63	4.97	7.17
5	Days to first female flowering	68.00-83.00	75.22	64.571**	25.71	19.43	6.74	5.86	75.56	7.89	10.49
6	Pedicel length of male flower (cm)	7.17-23.57	15.17	69.979**	24.32	22.83	32.51	31.50	93.89	9.54	62.87
7	Pedicel Length of female flower (cm)	2.63-7.33	4.56	4.437**	1.53	1.45	27.12	26.46	95.16	2.42	53.16
8	Number of male flower per plant	4.67-13.67	9.28	23.483**	8.52	7.48	31.43	29.47	87.89	5.28	56.91
9	Number of female flower per plant	3.67-10.67	6.23	10.460**	3.84	3.31	31.42	29.20	86.32	3.48	55.88
10	Fruit length (cm)	22.67-41.67	30.56	85.082**	32.70	26.19	18.71	16.75	80.11	9.44	30.88
11	Fruit Breadth (cm)	39.68-74.67	59.52	289.82**	104.65	92.59	17.19	16.17	88.48	18.64	31.33
12	Fruit weight (kg)	1.71-3.67	2.72	1.043**	0.36	0.34	22.14	21.49	94.19	1.17	42.97
13	Fruit Yield per plant(kg)	2.27-18.33	9.11	57.729**	19.51	19.11	48.49	47.99	97.96	8.91	97.85

(14.20%) and phenotypic co-efficient of variation (14.52%) were close to each other. Asmaul Husna(2009) found 14.14 genotypic variance in bottle gourd. The GCV 22.63 and PCV 22.67 were close to each other respectively. This character showed high heritability (95.65) and moderate genetic advance in percent of mean (28.60) which indicated that the character is controlled by additive genes and that selection based on this character would be effective. Gaffar (2008) found high heritability and moderate genetic advance in sponge gourd. Fayeun *et al.* (2012) also found high heritability and moderate genetic advance in fluted pumpkin. Phenotypic variations among leaf length of different genotypes is presented in plate 3a and 3b.

4.1.2 Leaf breadth (cm)

Significant mean sum of square for leaf breadth (14.696) indicated considerable variation presented among genotypes studied (Table 3). The maximum leaf breadth was observed 23.17 in G_7 (BD 306) and minimum was 16.33 which was recorded in G_1 (BD 4587) with mean value 19.75 (Appendix V). The phenotypic variance (5.18) appeared to be slightly higher than genotypic variance (4.76) suggested that less influence of environment on the expression of this gene controlling this trait. The genotypic co-efficient of variation (11.04%) and phenotypic co-efficient of variation (11.52%) were close to each other. Husna (2009) found GCV (22.87) was lower than PCV (23.04) for this character in bottle gourd.

This character showed high heritability (91.94) and moderate genetic advance (4.31) and genetic advance in percent of mean (21.82) which indicated character was controlled by additive genes. Therefore the selection based on this character would be effective. Gaffar (2008) observed in broad sense heritability was high (94%) with moderate genetic advance (7.81) for this character in sponge gourd. Phenotypic variations among leaf breadth of different pumpkin genotypes is presented in 3a and 3b.

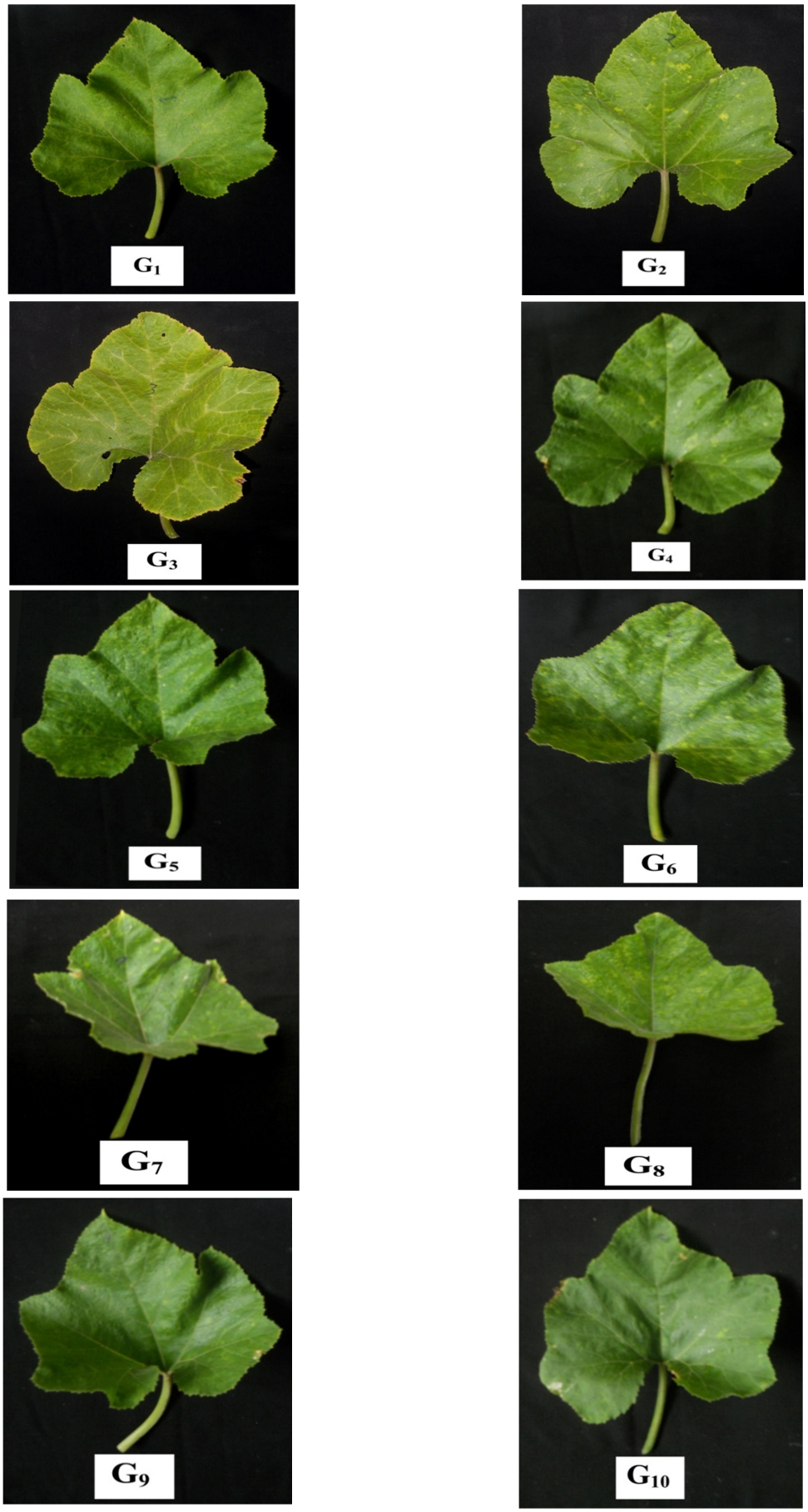

Plate 3a. Showing morphological variation in leaf among different pumpkin genotypes (G_1-G_{10})

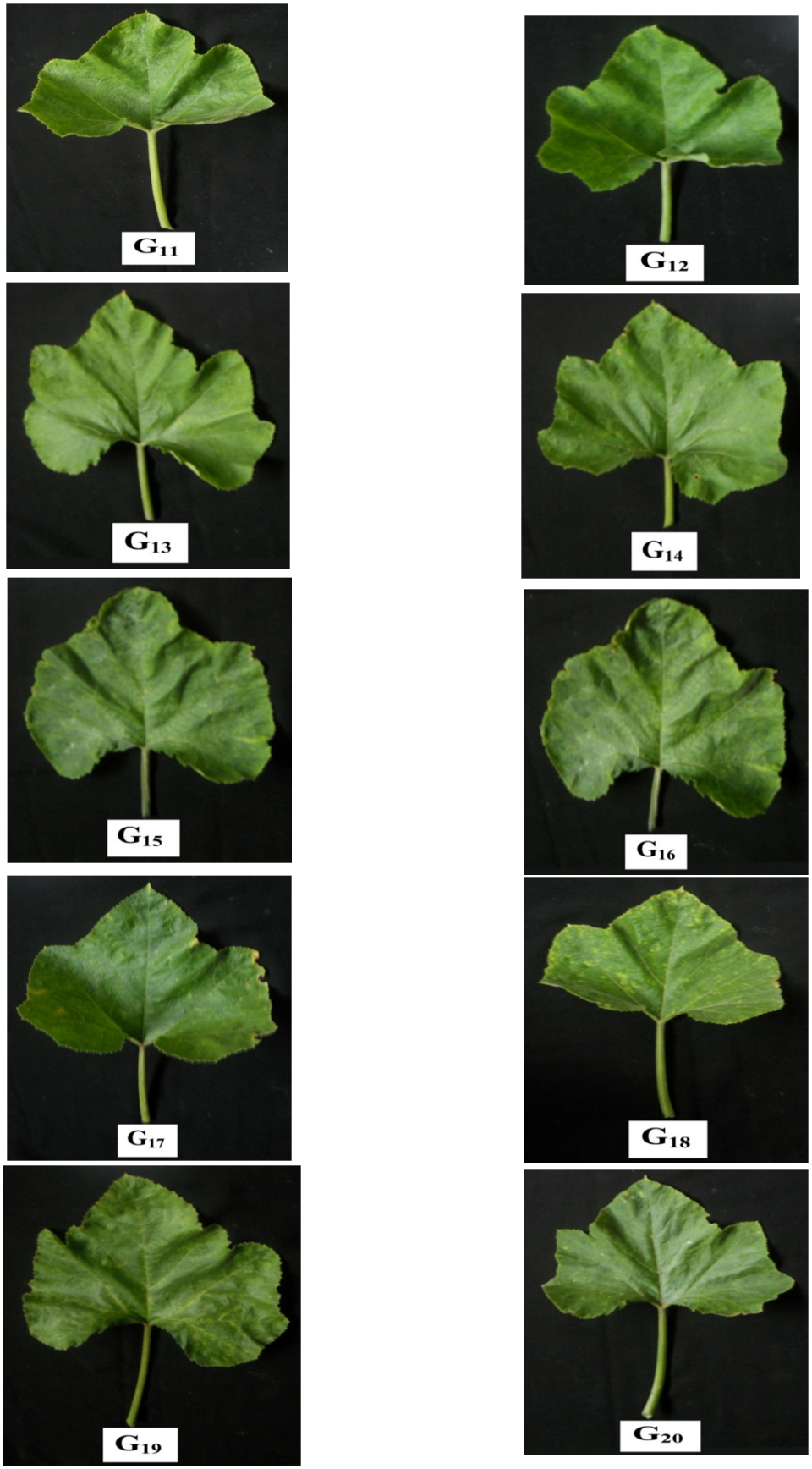

Plate 3b. Showing morphological variation in leaf among different pumpkin genotypes (G_{11}-G_{20})

4.1.3 Internode distance (cm)

Significant difference for internode distance observed among the pumpkin genotype studied (Table 3). Mean sum of square was significant (17.863). The maximum internode distance was observed 18.70cm in G_{14} (BD 258) and minimum was 10.23cm which was recorded in G_1 (BD 4587) with mean value 13.80 (appendix V). The difference between phenotypic variance (6.14) and genotypic variance (5.86) was slightly higher indicating less influence of environment on this character. The genotypic co-efficient of variation was 17.55%, and phenotypic co-efficient of variation was 17.95% respectively (Table 3).

Heritability showed high (95.58) and moderate genetic advance (4.88) and genetic advance in percent of mean (35.34) revealed that character was controlled by additive genes the selection based on this character would be effective. Fayeun *et al.* (2012) also found high heritability and moderate genetic advance in percent of mean. Plate 4a and 4b showing variation of twig among different genotypes of pumpkin.

4.1.4 Days to first male flowering

Days to first male flowering showed significant vaiation among genotype mean square (29.961). The maximum duration was observed 75.67 in G_7 (BD 306) and the minimum duration was 64.33 in G_1 (BD 4567) with mean value 69.37 (Table 3). The difference between phenotypic variance (12.74) and genotypic variance (8.61) was with large environmental influence (Table 3). The genotypic co-efficient of variation (4.23%) and phenotypic co-efficient of variation (5.14%) respectively. Singh and Lal (2005) in their study reported similar result.

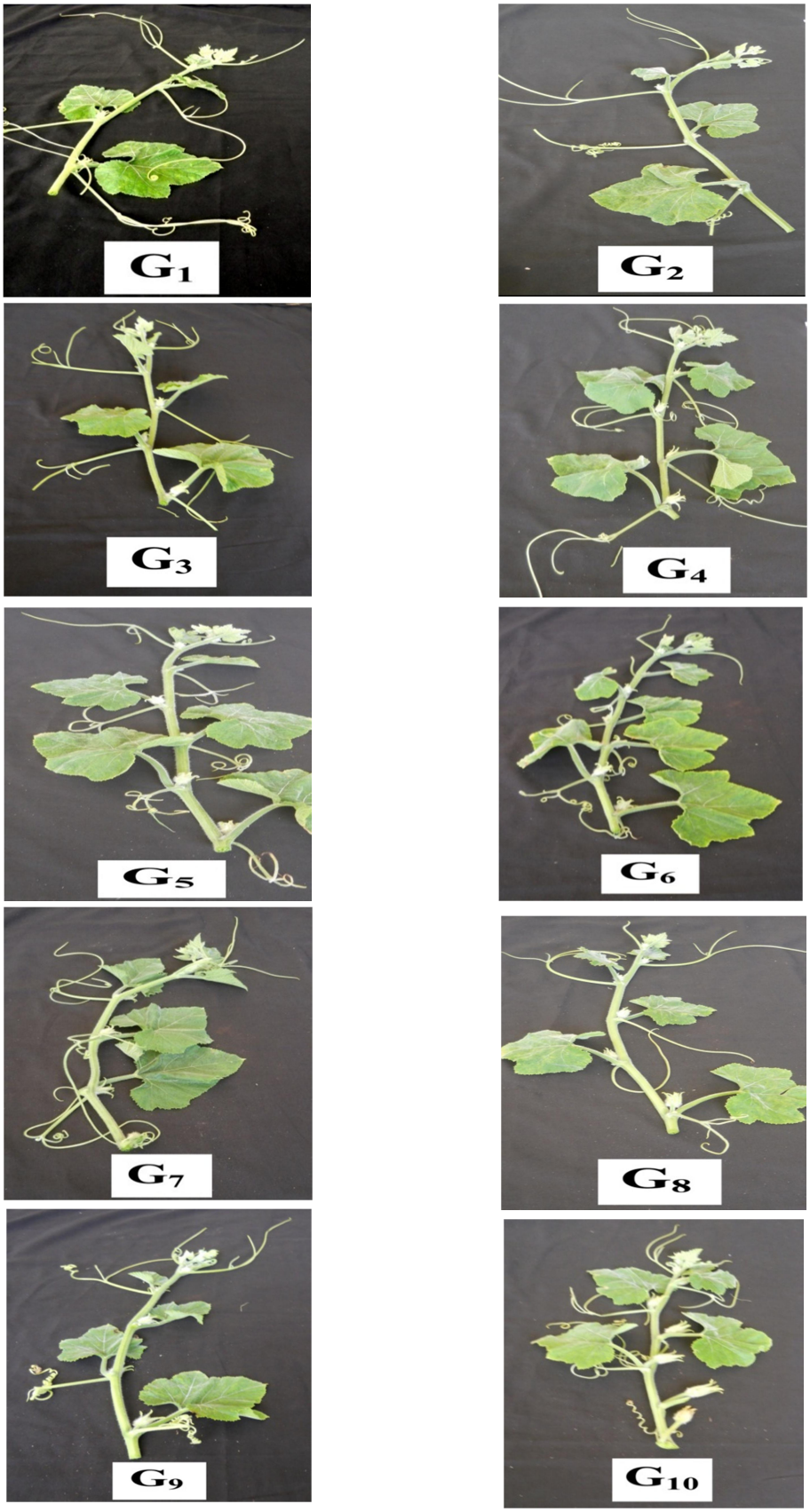

Plate 4a. Showing morphological variation in twig among different pumpkin genotypes (G1-G10)

Plate 4b. Showing morphological variation in twig among different pumpkin genotypes (G_{11}-G_{20})

Heritability showed high (67.63) with low genetic advance in percent of mean (7.17) revealed that which indicated character was controlled by non additive genes the selection based on this character would not be effective. Samsun Nahar (2009) estimated heritability for this trait was high (84.54%) and genetic advance in percent of mean (12.29) revealed that the character was governed by non additive gene.

4.1.5 Days to first female flowering

Significant difference was observed among days to first female flowering in pumpkin genotypes studied (Table 3). Mean sum of square was significant (64.571). The maximum duration was observed 83.00 in G_7 (BD 306) and the minimum duration was 68.00 in G_6 (BD 309) with mean value 75.22. The difference between phenotypic variance (25.71) and genotypic variance (19.43) was with large environmental influence. The genotypic co-efficient of variation and phenotypic co-efficient of variation was 5.86% and 6.74% respectively (Table 3).

Heritability showed high (75.56) with low genetic advance in percent of mean (10.49) revealed that character was controlled by non additive gene so the selection based on this character would not be effective. Singh and Lal (2005) also found similar result in their study.

4.1.6 Pedicel length of male flower (cm)

Mean sum of square for pedicel length was significant (69.979) in genotypes of pumpkin (Table 3). The maximum pedicel length was observed 23.57 in G_{15} (BD 245) and minimum was 7.17 recorded in G_{10} (BD 245) with mean value 15.17 (Appendix V). The phenotypic variance (24.32) appeared to be slightly higher than genotypic variance (22.83) suggested that less influence of environment on the expression of this gene controlling this trait. The genotypic co-efficient of variation (31.50%) and phenotypic co-efficient of variation (32.51%) were close to each other (Table 3).

Heritability showed high (93.89) and moderate genetic advance (9.54) and genetic advance in percent of mean (62.87) revealed that character was controlled by additive gene and the selection based on this character would be effective. Asmaul Husna (2009) also found high heritability (99.55%) and genetic advance for this trait in bottle gourd. Plate 5a and 5b showing variation of male and female flower among twenty genotypes of pumpkin.

4.1.7 Pedicel length of female flower

Mean sum of square for pedicel length was significant (4.437) in genotypes of pumpkin. The maximum pedicel length was observed 7.33 in G_2 (BD 2203) and minimum was 2.63 recorded in G_5 (BD 2212) with mean value 4.56(Appendix V). The phenotypic variance (1.53) appeared to be slightly higher than genotypic variance (1.45) suggested that less influence of environment on the expression of this gene controlling this trait. The genotypic co-efficient of variation (26.46%) and phenotypic co-efficient of variation (27.12%) were close to each other (Table 3). Asmaul Husna (2009) found similar result in bottle gourd.

Heritability showed high (95.16%) and high genetic advance in percent of mean (53.15) revealed that character is controlled by additive genes and the selection based on this character would be effective. Variation of male and female flower among twenty genotypes of sweet gourd shown in plate 5a and plate 5b.

4.1.8 Number of male flowers per plant

Significant difference observed among number of male flowering in pumpkin genotypes studied (Table 3). Mean sum of square was significant (23.483). The maximum number of male flower was 13.67 observed in G_{14} (BD 246) and the minimum number was 4.67 in G_3 (BD 2174) with mean value 9.28. The phenotypic variance (8.52) appeared to be slightly higher than genotypic

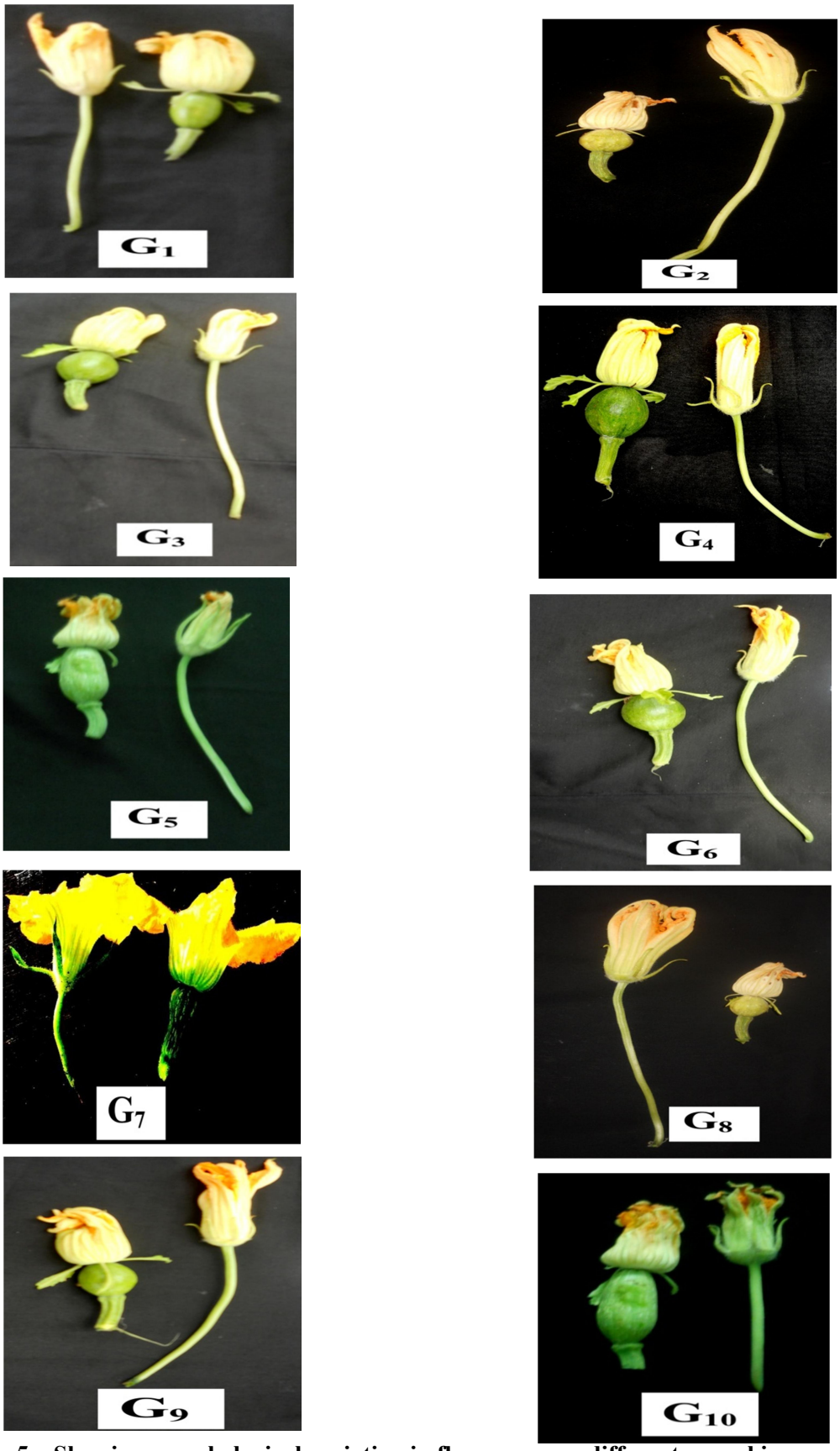

Plate 5a. Showing morphological variation in flower among different pumpkin genotypes (G_1-G_{10})

Plate 5b. Showing morphological variation in flower among different pumpkin genotypes (G_{11}-G_{20})

variance (7.48) suggested that less influence of environment on the expression of this gene controlling this trait. The genotypic co-efficient of variation was 29.47% and phenotypic co-efficient of variation was 31.43%, respectively. Husna *et al* (2011) found GCV 31.86 % and PCV 31.95% which was similar to the present study.

Heritability showed high (87.89) and with high genetic advance in percent of mean (56.69) revealed that character was controlled by additive gene so the selection based on this character would be effective.

4.1.9 Number of female flowers per plant

Significant difference was observed among number of female flowering in pumpkin genotypes studied (Table 3). Mean sum of square was significant (10.460). The maximum number of female flower was 10.67observed in G_{14} (BD 246) and the minimum number was 3.67 in G_2 (BD 2203) with mean value 6.23. The phenotypic variance (3.84) appeared to be slightly higher than genotypic variance (3.31) suggested that less influence of environment acted on the expression of this gene controlling this trait. The genotypic co-efficient of variation was 29.20% and phenotypic co-efficient of variation was 31.42%, respectively. Husna *et al* (2011) found GCV 35.14% and PCV 38.08% which was similar to the present study.

High heritabilty showed (86.32) with genetic advance in percent of mean (55.88) revealed that character was controlled by additive gene so the selection based on the character would be effective. Husna *et al.* (2011) also found high heritability (88.15) with high genetic advance in percent of mean (85.6).

4.1.10 Fruit Length (cm)

Mean sum of square of fruit length was significant (85.082). The maximum fruit length was found 41.67 in G_7 (BD 306) and the minimum number was 22.67 in G_6 (BD 309) with mean value 30.56. The phenotypic variance (32.70) appeared to be moderately higher than genotypic variance (26.19) suggested that moderate influence of environment acted on the expression of this gene controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were observed 16.75% and 18.71%, respectively. 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* indicated minimum differences between GCV and PCV in bottle gourd for fruit length.

High heritability found (80.11) with moderately high genetic advance in percent of mean (30.88) revealed that character was controlled by additive gene so the selection based on this character would be effective**.** Devi and Mariappan (2013) found high heritability (99.99) with high genetic advance (97.13) which also revealed that the character was controlled by additive gene. Photographs showed variation in fruit length of sweet gourds. Variation of fruit length among twenty genotypes of pumpkin is presented in plate 6a and 6b.

4.1.11 Fruit breadth (cm)

Significant mean sum of square of fruit breadth was found (289.82). The maximum fruit breadth was found 74.67 in G_{11} (BD 9494) and the minimum number was 39.68 in G_{16} (BD 2205) with mean value 59.5. The phenotypic variance (104.65) appeared to be higher than genotypic variance (92.59) suggested that influence of environment acted on the expression of this gene controlling this trait. The genotypic co-efficient of variation was16.17% and phenotypic co-efficient of variation was 17.19% respectively. Devi and Mariappan (2013) found GCV Phenotypic co efficient of variation 24.67 was slightly higher than genotypic co efficient of variation 24.66.

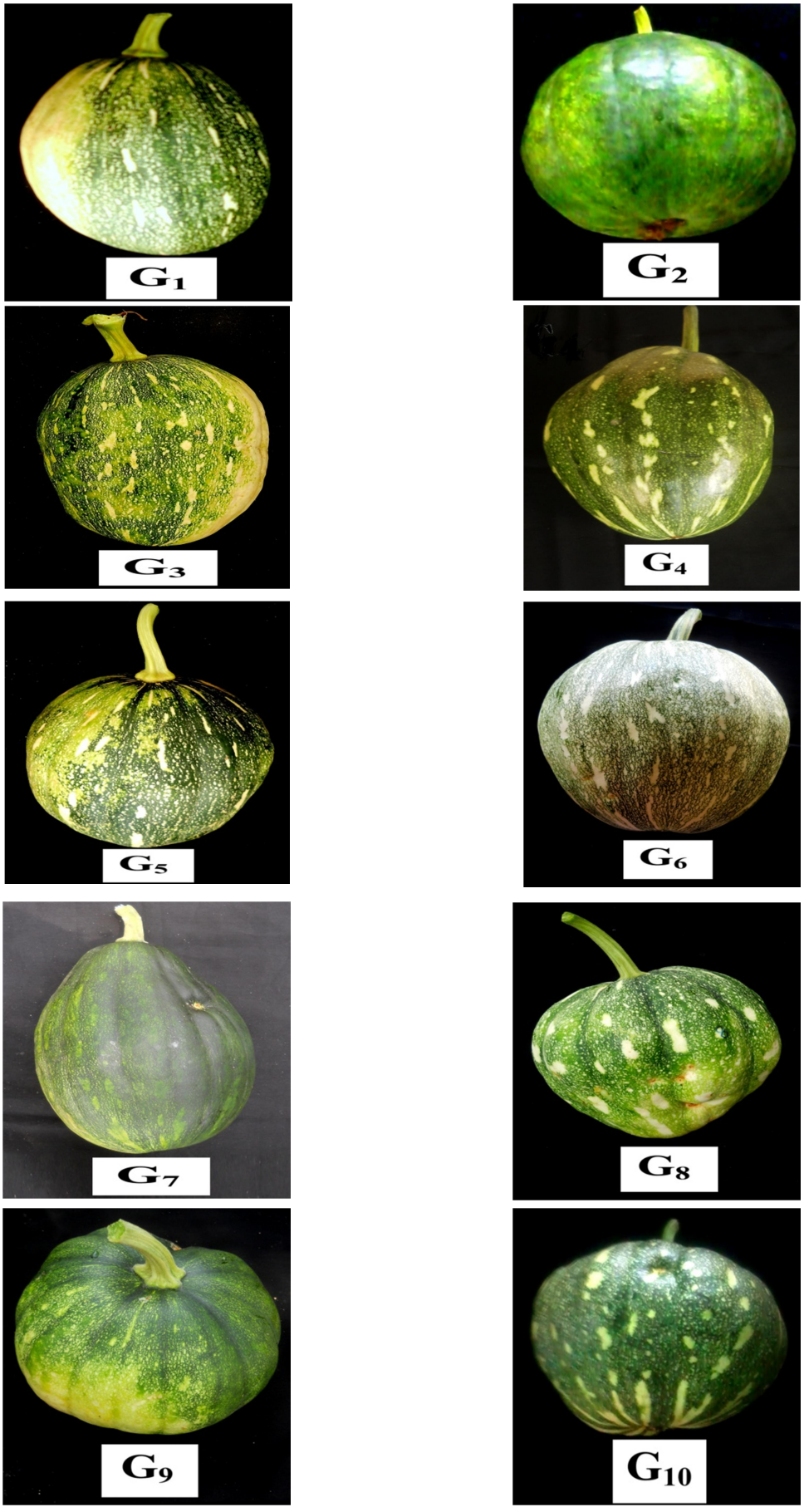

Plate 6a. Showing morphological variation in fruit among different pumpkin genotypes (G_1-G_{10})

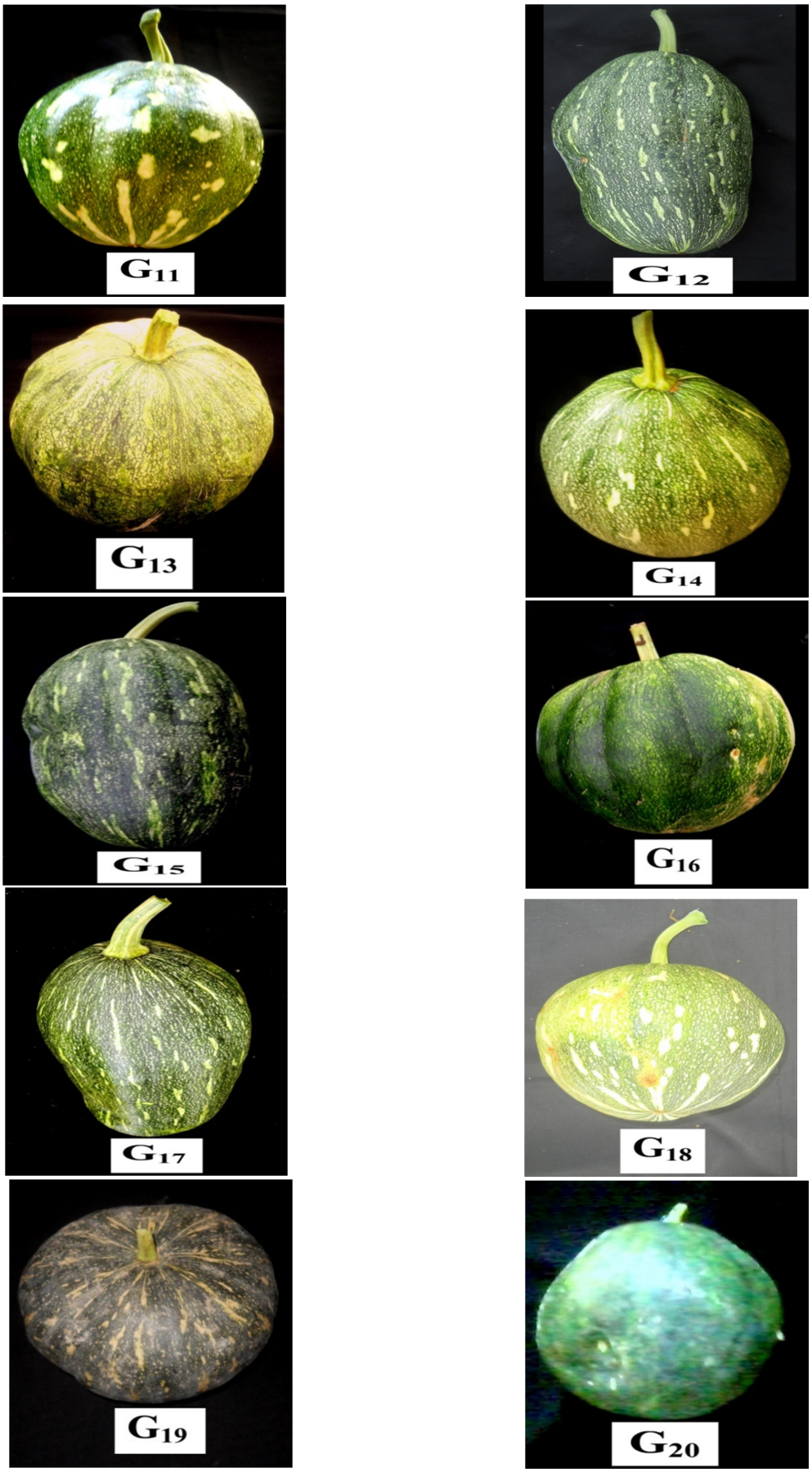

Plate 6b. Showing morphological variation in fruit among different pumpkin genotypes (G_{11}-G_{20})

Heritability found high (88.48) with moderately high genetic advance in percent of mean (31.33) revealed that character is controlled by additive gene so the selection based on this character would be effective. Asmaul Husna (2009) reported 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 in percent of mean (38.08). Plate 6a and 6b showing variation of fruit breadth among twenty genotypes of pumpkin.

4.1.12 Fruit weight (kg)

Significant mean sum of square of fruit weight was found (1.043). The maximum fruit weight found 3.67 kg in G_{12} (BD 9492) and the minimum fruit weight was 1.71 kg found in G_{18} (BD 223) with mean value 2.72. The phenotypic variance (0.36) appeared to be slightly higher than genotypic variance (0.34) suggested that less influence of environment acted on the expression of this gene controlling this trait. The genotypic co-efficient of variation was 21.49% and phenotypic co-efficient of variation was 22.14%, respectively. Saha *et al* (1992) found similar GCV and PCV for the fruit weight in pumpkin. Kumaran *et al* (1997) reported similar types of result which confirmed the present findings.

Heritability found high (94.19) with moderately high genetic advance in percent of mean (42.97) revealed that the character was controlled by additive gene so the selection based on this character would be effective. Rahman *et al.* (1986) also found the similar result in bottle gourd.

4.1.13 Fruit yield per plant (kg)

Mean sum of square of fruit weight was found was significant (57.729). The maximum fruit yield per plant found 18.33 kg in G_{14} (BD 246) and the minimum fruit yield per plant was 2.27 kg found in G_6 (BD 309) with mean value 9.11. The phenotypic variance (19.51) appeared to be slightly higher than genotypic variance (19.11) suggested that less influence of environment acted on the expression of this gene controlling this trait. The genotypic co-efficient of variation was observed 47.99% and phenotypic co-efficient of variation was observed 48.49% respectively. Husna *et al* (2011) found GCV (52.02 %) and PCV (54.35) which confirmed the result of present study.

High heritability (97.96) with very high genetic advance in percent of mean (97.85) revealed that character was controlled by additive gene so the selection based on this character would be highly effective. Narayankutty *et al.* (2006) fruit yield exhibited high values of heritability and genetic gain indicating additive gene effects are important in determining the character.

4.2. Correlation co-efficient

Yield is a complex product being influenced by several inter-dependable quantitative characters. Thus selection for yield may not be effective unless the other yield components influence it directly or indirectly are taken in to consideration. When selection pressure is exercised for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated characters. 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 (Dewey and Lu 1959). Result of genotypic and phenotypic correlation co-efficient analysis of thirteen yield and yield contributing characters of pumpkin were estimated separately as vegetative character and reproductive character with yield shown in Table 4 which discussed character wise below:

4.2.1 Leaf length without petiole (cm)

Leaf length showed highly significant positive correlation with leaf breadth and internode distance at both genotypic and phenotypic level indicated that if leaf length increased these parameters will also be increased (Table 4). Insignificant and negative correlation was found with pedicel length of male flower, pedicel length of female flower and fruit breadth. Positive but insignificant correlation was found in days to first male flowering, days to first female flowering, number of male flower per plant, number of female flower per plant, fruit length and fruit weight and fruit yield per plant. Husna *et al*. (2014) also reported leaf length was positively insignificant correlated with fruit yield per plnat. Li *et al* (1997) also found similar result in cucumber for this trait.

4.2.2 Leaf breadth (cm)

Highly significant and positive correlation was found between leaf breadth and internode distance. (Table 4). Insignificant and negative correlation was found with pedicel length of male flower, pedicel length of female flower and fruit breadth at both genotypic and phenotypic level. . Positive but insignificant correlation was found in days to first male flowering, days to first female flowering, number of male flower per plant, number of female flower per plant, fruit length and fruit weight and fruit yield per plant. Husna *et al*. (2014) also found leaf breadth has positive insignificant correlation with fruit yield per plant.

4.2.3 Internode distance (cm)

Positive and insignificant correlation was found in days to first male flowering, days to first female flowering, number of male flower per plant, number of female flower per plant, fruit length and fruit weight and fruit yield per plant indicating that association among these traits is largely influenced by

Table 4. Coefficients of phenotypic and genotypic correlation among different yield components of twenty pumpkin genotypes.

Characters	correlation	Leaf breadth (cm)	Internode distance	Days to first male flowering	Days to first female flowering	Pedicel length of male flower (cm)	Pedicel Length of female flower (cm)	Number of male flower per plant	Number of female flower per plant	Fruit length (cm)	Fruit Breadth (cm)	Fruit weight (kg)	Fruit Yield per plant(kg)
Leaf length without petiole (cm)	r_p	0.841**	0.901**	0.353	0.383	-0.139	-0.281	0.150	0.275	0.222	-0.258	0.268	0.218
	r_g	0.842**	0.909**	0.373	0.396	-0.135	-0.283	0.155	0.274	0.233	-0.258	0.267	0.220
Leaf breadth (cm)	r_p		0.834**	0.211	0.291	0.015	-0.212	0.283	0.200	0.068	-0.180	0.120	0.153
	r_g		0.832**	0.175	0.266	0.017	-0.213	0.290	0.201	0.083	-0.178	0.119	0.157
Internode distance	r_p			0.122	0.138	-0.258	-0.217	0.135	0.171	0.067	-0.179	0.185	0.183
	r_g			0.091	0.109	-0.261	-0.220	0.137	0.179	0.070	-0.178	0.186	0.185
Days to first male flowering	r_p				0.913**	0.247	0.298	0.060	-0.135	0.615**	0.092	0.434	0.326
	r_g				0.853**	0.248	0.305	0.060	-0.146	0.654**	0.107	0.449*	0.342
Days to first female flowering	r_p					0.077	0.278	0.038	-0.127	0.671**	0.108	0.570**	0.403
	r_g					0.072	0.280	0.040	-0.129	0.697**	0.105	0.582**	0.418
Pedicel length of male flower (cm)	r_p						0.214	0.041	0.131	-0.075	-0.156	-0.481*	-0.245
	r_g						0.217	0.037	0.136	-0.071	-0.157	-0.479*	-0.246

Table 4. Continued

Characters	correlation	Leaf breadth (cm)	Internode distance	Days to first male flowering	Days to first female flowering	Pedicel length of male flower (cm)	Pedicel Length of female flower (cm)	Number of male flower per plant	Number of female flower per plant	Fruit length (cm)	Fruit Breadth (cm)	Fruit weight (kg)	Fruit Yield per plant(kg)
PedicelLength of female flower (cm)	r_p							-0.099	-0.358	0.143	0.141	0.105	0.161
	r_g							-0.098	-0.368	0.144	0.145	0.107	0.162
Number of male flower per plant	r_p								0.469*	-0.354	-0.440	-0.025	0.131
	r_g								0.462*	-0.351	-0.440	-0.022	0.134
Number of female flower per plant	r_p									-0.265	-0.757**	-0.172	0.180
	r_g									-0.270	-0.769**	-0.174	0.181
Fruit length (cm)	r_p										0.388	0.596**	0.577**
	r_g										0.350	0.614**	0.583**
Fruit Breadth (cm)	r_p											0.466*	0.130
	r_g											0.473*	0.131
Fruit weight (kg)	r_p												0.695**
	r_g												0.696**

* and ** indicate significant at 5% and 1% level of probability, respectively.

environment (Table 4). Insignificant and negative correlation was found with pedicel length of male flower, pedicel length of female flower and fruit breadth at both genotypic and phenotypic level. Positive and insignificant correlation between yield and internode distance showed the selection of genotypes with higher internode distance are expected to yield better.

4.2.4 Days to first male flowering

The character showed highly significant and positive correlation with days to first female flowering and fruit length at both genotypic and phenotypic level indicated that the traits were governed by same gene and simultaneous improvement would be effective (Table 4). Fruit weight was significant and positively correlated at genotypic level indicating correlation between days to first male flowering and fruit weight had less influence of environment. Negative correlation but insignificant was found with number of female flower per plant which suggest if days to first male flowering increases number of female flower decreased. Positive correlation was found with pedicel length of male flower, pedicel length of female flower, number of male flower per plant, fruit breadth, fruit weight and fruit yield per plant at genotypic level.

4.2.5 Days to first female flowering

Days to first female flowering showed highly significant and positive correlation with and fruit length and fruit breadth at both genotypic and phenotypic level indicated that if days to first female flowering increases fruit length and breadth would be highly increased (Table 4). Negative correlation was found with number of female flower per plant which suggested that delayed of first female flowering increases the number of male flower. Positive association was found with pedicel length of male flower, pedicel length of female flower, number of male flower per plant, fruit breadth, and fruit yield per plant. Khan *et al* (2009) reported the similar result.

4.2.6 Pedicel length of male flower (cm)

Pedicel length of male flower showed positive but insignicant correlation with pedicel length of female flower, number of male flower per plant, number of female flower per plant which indicated the traits were governed by same gene and improvement would be effective. Highly negative correlation was found with fruit weight indicates increased length of pedicel will be decreased the weight of fruit. Negative association was found with fruit length, fruit breadth and fruit yield per plant. Husna *et al*. (2014) also found that pedicel length of male flower negative but insignificant correlation with fruit yield per plant.

4.2.7 Pedicel length of female flower (cm)

The character showed negative but insignificant relation with number of male flower per plant and number of female flower per plant indicating decreased pedicel length would increase the number of male and female flower. Positive but insignificant relation was found with fruit length, fruit breadth, fruit weight and fruit yield per plant indicating if pedicel length increased fruit length, breadth, weight and yield would also be increased.

4.2.8 Number of male flowers per plant

Number of male flower per plant showed highly significant positive correlation with number of female flower per plant and positive but insignificant correlation with fruit yield per plant at both genotypic and phenotypic level. It indicated if number of male flower increased number of female flower would be highly increased and fruit yield would also be increased. The character found negative association with fruit length, fruit breadth and fruit weight indicating increased number of female flower would decrease fruit length, fruit breadth and fruit weight. Khan *et al* (2009) also found Number of male flower per plant has highly significant positive correlation with number of female flower per plant.

4.2.9 Number of female flowers per plant

This character showed highly significant negative correlation with fruit breadth and negative but insignicant correlation with length and fruit weight at both genotypic and phenotypic level indicating if number of female flower increased fruit breadth would be decreased highly and fruit length and weight would also be decreased. Number of female flower had positive correlation with fruit yield per plant indicating that if the number of female flower increased number of fruit also increasesd. Mohanty (2001) reported similar trend of relationship.

4.2. 10 Fruit length (cm)

Fruit length showed positive but insignificant correlation with fruit breadth at both genotypic and phenotypic level (Table 4). Fruit length was highly significant with fruit weight and fruit yield per plant at both genotypic and phenotypic level indicating if fruit length increased fruit weight and fruit yield per plant would be highly increased. Narayankutty *et al*. (2006) reported that yield is strongly correlated with fruit length in snake gourd. Chowdhury and Sarma (2002) studied *Luffa acutangula* cultivars and observed that yield per hectare can be imoproved through selection of fruit length.

4.2.11 Fruit breadth (cm)

Positive and highly significant correlation was found with fruit weight and fruit length at both genotypic and phenotypic level indicating if fruit breadth may increased fruit weight and fruit length may also increased. Narayankutty *et al.* (2006) reported that yield is strongly correlated with fruit breadth in snake gourd. Khan *et al* (2009) found fruit breadth is positively correlated with fruit weight.

4.2.12 Fruit weight (kg)

Fruit weight showed highly significant positive correlation with fruit yield per plant at both genotypic and phenotypic level (Table 4) indicated that if fruit weight increased, then the fruit yield and number of fruit also increased.

Narayankutty *et al.* (2006) reported that yield is strongly correlated with fruit weight in snake gourd. Khan *et al* (2009) also found fruit weight has positive high correlation with yield. Husna *et al*. (2014) also found similar result in bottle gourd. Chowdhury and Sarma (2002) studied *Luffa acutangula* cultivars and observed that yield per hectare can be imoproved through selection of individual fruit weight. Prasana *et al*.(2002) found in ridge gourd (*Luffa acutangula*) fruit yield per hectare was positively associated with fruit weight. Kumaresan *et al*. (2006) yield per vine in snake gourd was positively associated with fruit weight.

4.3 Path analysis

Association of character determined by correlation co-efficient may not provide an exact picture of the relative importance of direct and indirect influence of each of yield components. In order to find out a clear picture of the inter relationship between yield per plant and other yield attributes, direct and indirect effects were worked out using path analysis at phenotypic level which also measured the relative importance of each component. Estimation of direct and indirect effect of path co-efficient analysis for pumpkin presented in Table 5.

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

Characters	LLWP	LB	ID	DFMF	DFFF	PLMF	PLFF	NMF	NFF	FL	FB	FW	FY
LLWP	**-1.504**	0.631	0.546	0.363	-0.200	0.0233	-0.0124	-0.0544	0.1611	-0.0364	0.0501	0.254	0.220
LB	-1.266	**0.750**	0.5004	0.1690	-0.1354	-0.0029	-0.0093	-0.1019	0.1181	-0.0130	0.0348	0.1133	0.157
ID	-1.367	0.6242	**0.601**	0.0878	-0.0551	0.0451	-0.0096	-0.0481	0.1052	-0.0109	0.0348	0.1771	0.185
DFMF	-0.561	0.1313	0.0547	**0.965**	-0.4311	-0.0429	0.0133	-0.0211	-0.0870	-0.0867	-0.0209	0.4277	0.342
DFFF	-0.5956	0.2011	0.0655	0.8237	**-0.505**	-0.0124	0.0122	-0.0141	-0.0758	-0.0151	-0.0205	0.5543	0.418
PLMF	0.2030	0.0127	-0.1559	0.2395	-0.0363	**-0.173**	0.0095	-0.0130	0.0811	0.0111	0.0307	-0.4562	-0.246
PLFF	0.4256	-0.1598	-0.1323	0.2945	-0.1415	-0.0375	**0.0439**	0.0344	-0.2163	-0.0225	-0.0283	0.1019	0.162
NMF	-0.2331	0.2175	0.0824	0.0579	-0.0202	-0.0064	-0.0043	**-0.351**	0.2716	0.0549	0.086	-0.0209	0.134
NFF	-0.4121	0.1508	0.1076	-0.1429	0.0651	-0.0238	-0.0161	-0.1624	**0.587**	0.0422	0.1503	-0.1657	0.181
FL	-0.3504	0.0622	0.0421	0.5350	-0.0490	0.0122	0.0063	0.1234	-0.1587	**-0.156**	-0.0684	0.5848	0.583**
FB	0.3850	-0.1335	-0.1071	0.1033	-0.0531	0.0272	0.0064	0.1546	-0.4521	-0.0548	**-0.195**	0.4505	0.131
FW	-0.4015	0.0892	0.1118	0.4336	-0.2941	0.0829	0.0047	0.0077	-0.1022	-0.0961	-0.0925	**0.952**	0.696**

Residual effect =0.3274 **correlation is significant at the 0.01 level 8 correlation at the 0.05 level.

Diagonally bold figures indicate the direct effect

LLWP = Leaf length without petiole (cm), LB= Leaf breadth (cm), ID = Internode distance (cm), DFMF = Days after first male flowering, DFFF = Days after first female flowering, PLMF = Pedicel length of first male flowering, PLFF = Pedicel length of first female flowering, 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 (kg), FY = Fruit yield per plant (kg)

4.3.1 Leaf length without petiole (cm)

Leaf length without petiole showed negatively direct effect (- 1.504) on yield (Table 5) .This character showed highest positive indirect effect through leaf breadth (0.631) followed by internode distance (0.546),days to first male flowering (0.363), fruit weight (0.2543), number of female flower per plant (0.1611), fruit breadth (0.0501), and pedicel length of male flower (0.0233). The character also produced negative indirect effect on yield via days to first female flowering (-0.200), pedicel length of female flower (-0.0124), number of male flower per plant (-0.0544), fruit length (-0.0364) which were contributed to result insignificant positive genotypic correlation with yield per plant (0.220). Lie *et al*. (1997) also found similar result in cucumber for their trait. Shamima Sultana (2011) also found negative direct effect (-0.041) on yield.

4.3.2 Leaf breadth

Leaf breadth showed a positive direct effect (0.750) on yield (Table 5). This character showed highest positive indirect effect through internode distance (0.5004), days to first male flowering (0.1690), number of female flower per plant (0.1181), fruit weight (0.1133) and fruit breadth (0.0348). The character also produced negative indirect effect on yield via leaf length without petiole (-1.266), days to first female flowering (-0.1354), pedicel length of male flower (-0.0029), pedicel length of female flower (-0.00935), number of male flower per plant (-0.1019), and fruit length (-0.0130) which finally made insignificant positive correlation between leaf breadth and yield per plant (0.157).

4.3.3 Internode distance (cm)

Internode distance showed a positive direct effect (0.601) on yield (Table 5). This character showed highest positive indirect effect through leaf breadth (0.6242) followed by fruit weight (0.1771), number of female flower per plant

(0.1052), days to first male flowering (0.0878), pedicel length of male flower (0.0451), fruit breadth (0.0348). The character also produced negative indirect effect on yield via leaf length without petiole (-1.367), days to first male flowering (-0.0551), pedicel length of female flower (-0.0096), number of male flower per plant (-0.0481) and fruit length (-0.0109) which finally made insignificant positive correlation between internode distance and yield per plant (0.185).

4.3.4 Days to first male flowering

Days to first male flowering showed a positive direct effect (0.965) on yield (Table 5). This character showed highest positive indirect effect through fruit weight (0.4277), leaf breadth (0.1313), internode distance (0.0547), pedicel length of female flower (0.0133). The negative indirect characters via leaf length without petiole (-0.561), days to first female flowering (-0.4311), pedicel length of male flower (-0.0429), Number of male flower per plant (-0.0867), and Fruit breadth (-0.0209) which finally contributed to insignificant positive genotypic correlation with (0.342).

4.3.5 Days to first female flowering

The character showed a negative direct effect (-0.505) on yield (Table 5). Days to first female flowering showed highest positive indirect effect on days to first male flowering (0.8237) followed by fruit weight (0.5543), leaf breadth (0.2011), internode distance (0.0655), pedicel length of female flower (0.0122).The negative indirect character via leaf length without petiole (-0.5956), pedicel length of male flower (-0.0124), number of male flower per plant (-0.0141), number of female flower per plant (-0.0758), fruit length (-0.0151) and fruit breadth (-0.0205). The cumulative effect produced a positive insignificant correlation with yield (0.418).

4.3.6 Pedicel length of male flower (cm)

Male flower pedicel length showed a negative direct effect (-0.173) on yield (Table 5). The character showed highest positive indirect effect on days to first male flowering (0.2395), leaf length without petiole (0.2030) followed by number of female flower per plant (0.0811), fruit breadth (0.0307), fruit length (0.0111). The character also produced negative indirect effect on yield through internode distance (-0.1559), days to first female flowering (-0.0363), number of male flower per plant (-0.0130), and fruit weight (-0.4562) which finally produced negative insignificant correlation with yield (-0.246).

4.3.7 Pedicel length of female flower (cm)

Pedicel length of female flower showed a negative direct effect (-0.0439) on yield (Table 5). The character showed highest positive indirect effect leaf length without petiole (0.4256), followed by days to first male flowering (0.2945), fruit weight (0.1019), number of male flower plant (0.0344). The character also produced negative indirect effect on yield through leaf breadth (-0.1598), internode distance (-0.1323), days to first female flowering (-0.1415), pedicel length of male flower (-0.0375), number of female flower per plant (-0.2163), fruit length (-0.0225), and fruit breadth (-0.0283) which finally contributed positive insignificant correlation with yield (0.162). Asmaul Husna (2009) found negative correlation with fruit yield per plant regarding these characters.

4.3.8 Number of male flowers per plant

Number of male flower per plant showed negative direct effect (-0.351) on yield (Table 5). The character showed highest positive indirect effect via number of female flower per plant (0.2716) followed by leaf breadth (0.2175), internode distance (0.0824), days to first male flowering (0.0579), fruit length (0.0549) and fruit weight (0.086). The character also produced negative

indirect effect on yield through leaf length without petiole (-0.2331), days to first female flowering (-0.0202), pedicel length of male flower (-0.0064), pedicel length of female flower (-0.0043), fruit weight (-0.0209). The cumulative effect produced a positive insignificant correlation with yield (0.134). Husna *et al* (2011) also found negative direct effect of number of male flower on yield.

4.3.9 Number of female flowers per plant

Number of female flower per plant showed positive direct effect (0.587) on yield (Table 5). The character showed highest positive indirect effect via leaf breadth (0.1508), followed by fruit breadth (0.1503), internode distance (0.1076), days to first male flowering (0.0579), fruit length (0.0422). The character also produced negative indirect effect on yield through leaf length without petiole (-0.4121), days to first male flowering (-0.1429), pedicel length of male flower (-0.0238), pedicel length of female flower (-0.0161), number of male flower per plant (-0.1624) and fruit weight (-0234.1657) which finally produced a positive insignificant yield (0.181). Shamima Sultana (2011) found similar result in sweet gourd.

4.3.10 Fruit length (cm)

Fruit length showed negative direct effect (-0.156) on yield (Table 5). The character showed highest positive indirect effect via fruit weight (0.5848), followed by days to first male flowering (0.5350), number of male flower per plant (0.1234), leaf breadth (0.0622), internode distance (0.0421), pedicel length of male flower (0.0122), pedicel length of female flower (0.0063). The character also produced negative indirect effect on yield through leaf length without petiole (-0.3504), days to first female flowering (-0.0490), number of female flower per plant (-0.1587) and fruit breadth (-0.0684). The cumulative

effect produced a highly significant positive correlation with yield (0.583). Husna *et al* (2011) also found negative direct effect of fruit length on yield.

4.3.11 Fruit breadth (cm)

Fruit breadth showed negative direct effect (-0.195) on yield (Table 5). The character showed highest positive indirect effect through fruit weight (0.4505), leaf length without petiole (0.3850), number of male flower per plant (0.1546), days to first male flowering (0.1033), pedicel length of male flower (0.0272), pedicel length of female flower (0.0064). The character also produced negative indirect effect on yield through leaf breadth (-0.1335), internode distance (-0.1071), days to first female flowering (-0.0531), number of female flower per plant (-0.521) and fruit length (-0.0548) which finally produced a positive significant yield (0.131).

4.3.12 Fruit weight (kg)

Fruit weight showed positive direct effect (0.952) on yield (Table 5). The character showed highest positive indirect effect through days to first male flowering (0.4336), followed by internode distance (0.118), leaf breadth (0.08892), pedicel length of male flower (0.0829), number of male flower per plant (0.0077), pedicel length of female flower (0.0047). The character also produced negative indirect effect on yield through leaf length without petiole (-0.4015), days to first female flowering (-0.2941), number of female flower per plant (-0.1022), fruit length (-0.0961) and fruit breadth (-0.0925). The cumulative effect produced a highly significant positive correlation with yield (0.696). Husna *et al* (2011) also found negative direct effect of fruit weight on yield, and also found highly significant positive correlation with 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 fruit per vine and fruit weight to increase the yield per vine

directly. The result is similar with the findings of AsmaulHusna (2009) in bottle gourd.

4.4 Genetic Diversity Analysis

The genetic diversity of pumpkin advanced lines are presented in Table 6 to Table 10 and Figure 1 to 3.

4.4.1 Principal Component Analysis (PCA)

Principal component analysis was carried out with 20 genotypes of pumpkin. The computed eigen values for the 13 variables subjected to principal component analysis together with the corresponding proportion and cumulative explained variance are given in Table 6. Following the Proportion of Variance Criterion, three principal components were retained and these are the principal components whose cumulative explained variances were equal to or more than 99%. In summary, the principal component analysis resulted in the reduction of the 13 original variables to three independent linear combination, principal component of variables. The first principal component accounted for 30.27 % of the total variation while principal components two and three accounted for 24.69 % and 13.75 %, respectively (Table 6).

Table 6. Eigen value, % variance and cumulative (%) total variance of the principal components

Principal component axes	Eigen value	% Variance	Cumulative (%) total variance
I	3.94	30.27	30.27
II	3.21	24.69	54.97
III	1.79	13.75	68.72
IV	1.39	10.67	79.39
V	0.85	6.54	85.94
VI	0.67	5.14	91.07
VII	0.55	4.25	95.32
VIII	0.24	1.85	97.17
IX	0.16	1.19	98.36
X	0.10	0.75	99.12
XI	0.06	0.47	99.59
XII	0.03	0.23	99.82
XIII	0.02	0.18	100.00

4.4.2 Non-Hierarchical Clustering

Twenty pumpkin genotypes were grouped into five different clusters non-hierarchical clustering (Table 7). These results confirmed the clustering pattern of the genotypes obtained through principal component analysis. Kundu *et al*. (2012) studied 36 genotypes of bitter gourd and genotypes were grouped into six distinct clusters. Khatun *et al*. (2010) conducted an experiment in 38 snake gourd genotypes and the genotypes were grouped into four different clusters. Asmaul Husna (2009) reported five clusters in bottle gourd. Gaffar (2008) reported similar number of clustering in fifteen sponge gourd genotype. In this study cluster I had the highest number of genotypes six, cluster II and cluster III constitute four genotypes. Cluster IV and cluster V had 3 genotypes (Table 7).

Cluster I had G_1 (BD 4587), G_3 (BD 2174), G_8(BD 204), G_9(BD 249), G_{17}(BD 4592) and G_{19}(BD 242). Cluster II consisted G_2 (BD 2203), G_{12} (BD 9492), G_{15} (BD 2236), and G_{20} (BD 251). Cluster III consisted G_4 (BD 264), G_6 (BD 309), G_{13} (BD 258) and G_{18} (BD 223). Cluster IV consisted G_5 (BD 2212), G_7 (BD 306) and G_{11} (BD 9494). Cluster V constituted by G_{10} (BD 245), G_{14} (BD 246)and G_{16} (BD 2205).

Among the thirteen genotypes cluster V earned the highest cluster mean value for leaf length without petiole (19.41), internode distance (16.82), number of male flower per plant (12.44), number of female flower per plant (8.22), fruit weight (3.04) and fruit yield per plant (12.01). (Table 8).

The genotypes included in cluster IV were highest mean value for leaf breadth (22.82), fruit length (33.39), and fruit breadth (68.56) (Table 8). Cluster II produced maximum cluster mean for days to first male flowering (72.25), days to first female flowering (79.50), pedicel length of male flower (19.51), pedicel length of female flower (6.02).

Table 7. Distribution of genotypes in different clusters

Cluster number	Number of genotypes	Percent (%)	Name of genotypes
I	6	30.00	G1,G3, G8, G9, 17 and G19
II	4	20.00	G2, G12, G15 and G20
III	4	20.00	G4, G6, G13 and G18
IV	3	15.00	G5, G7 and G11
V	3	15.00	G10, G14 and G16

Table 8. Cluster mean for thirteen yield and yield characters of pumpkin genotypes

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Leaf length without petiole (cm)	15.02	15.93	15.54	19.13	19.41
Leaf breadth (cm)	17.88	18.93	19.36	22.82	22.06
Internode distance	12.40	12.44	12.91	16.58	16.82
Days to first male flowering	69.00	72.25	66.08	72.22	67.78
Days to first female flowering	74.83	79.50	69.08	78.89	74.78
Pedicel length of male flower (cm)	13.01	19.51	18.87	14.61	9.33
Pedicel Length of female flower (cm)	4.61	6.02	3.99	4.19	3.63
Number of male flowers per plant	6.50	10.75	9.33	9.67	12.44
Number of female flowers per plant	5.00	6.25	7.58	4.89	8.22
Fruit length (cm)	33.32	31.49	24.50	33.39	29.06
Fruit Breadth (cm)	67.22	56.85	51.54	68.56	49.28
Fruit weight (kg)	2.99	2.74	1.82	3.00	3.04
Fruit yield per plant (kg)	10.17	9.75	4.55	9.31	12.01

4.4.3 Canonical Variate Analysis (CVA)

Canonical variate analysis was done to compute the inter-cluster distances. The intra and inter-cluster distance (D^2) values were shown in Table 9. In this experiment, the inter-cluster distances were higher than the intra-cluster distances thus indicating broader genetic diversity among the genotypes of different groups.

The highest inter cluster distance was observed between clusters II and V (36.23), followed by between cluster I and V (32.94), cluster II and IV (32.05), cluster II and III (31.15), and between cluster III and V (30.15). (Figure 1). However, the maximum inter-cluster distance was observed between the Clusters II and V (36.23), indicating genotypes from these two clusters, if involved in hybridization may produce a wide spectrum of segregating population. On the other hand, the maximum intra-cluster distance was found in cluster IV (27.50), which contained of3 genotypes, while the minimum distance was found in cluster I (19.87) that comprises 6 genotypes. The different multivariate analysis was superimposed in Figure 2 from which it could be concluded that different multivariate techniques supplemented and confirmed one another.

According to scatter diagram all the genotypes were apparently distributed into five clusters. It is assumed that the maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. Furthermore, for a practical plant breeder, the objective is to achieve high-level production in addition to high heterosis. In the present study the maximum distance existence between cluster II and V.

Table 9. Intra (Bold) and inter cluster distances (D^2) for 20 genotypes

Characters	I	II	III	IV	V
I	**19.87**	22.10	27.62	30.11	32.94
II		**21.26**	31.15	32.05	36.23
III			**21.01**	29.54	30.15
IV				**27.50**	24.70
V					**22.55**

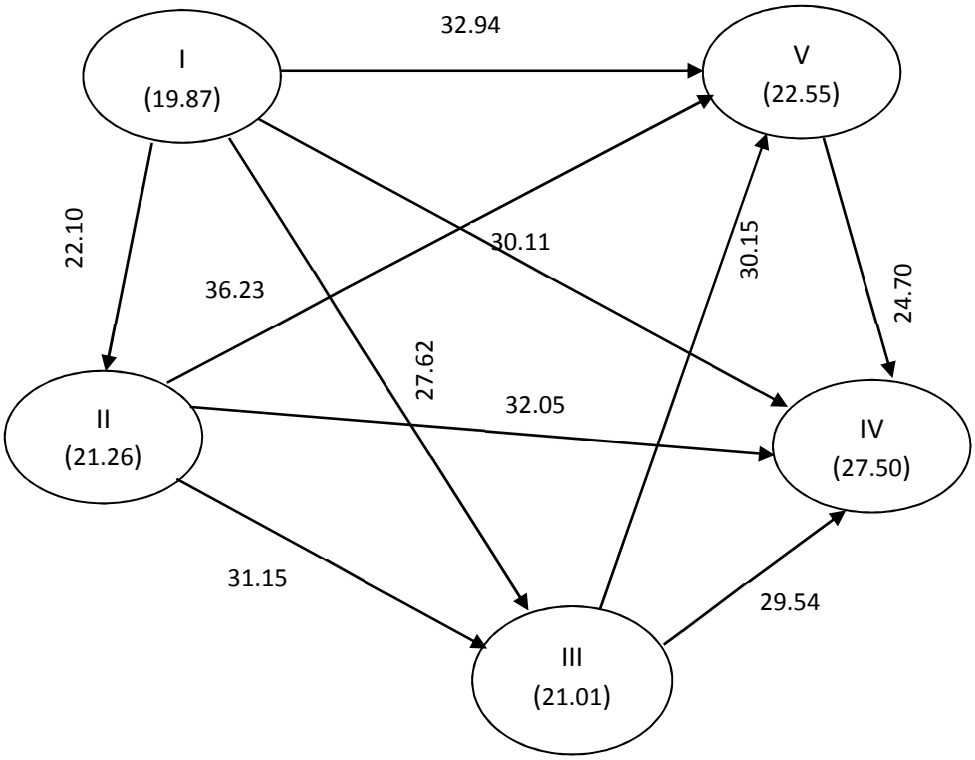

Fig 1. Cluster diagram showing the average intra and inter cluster distances (D= $\sqrt{D^2}$ Values) of 20 pumpkin genotypes.

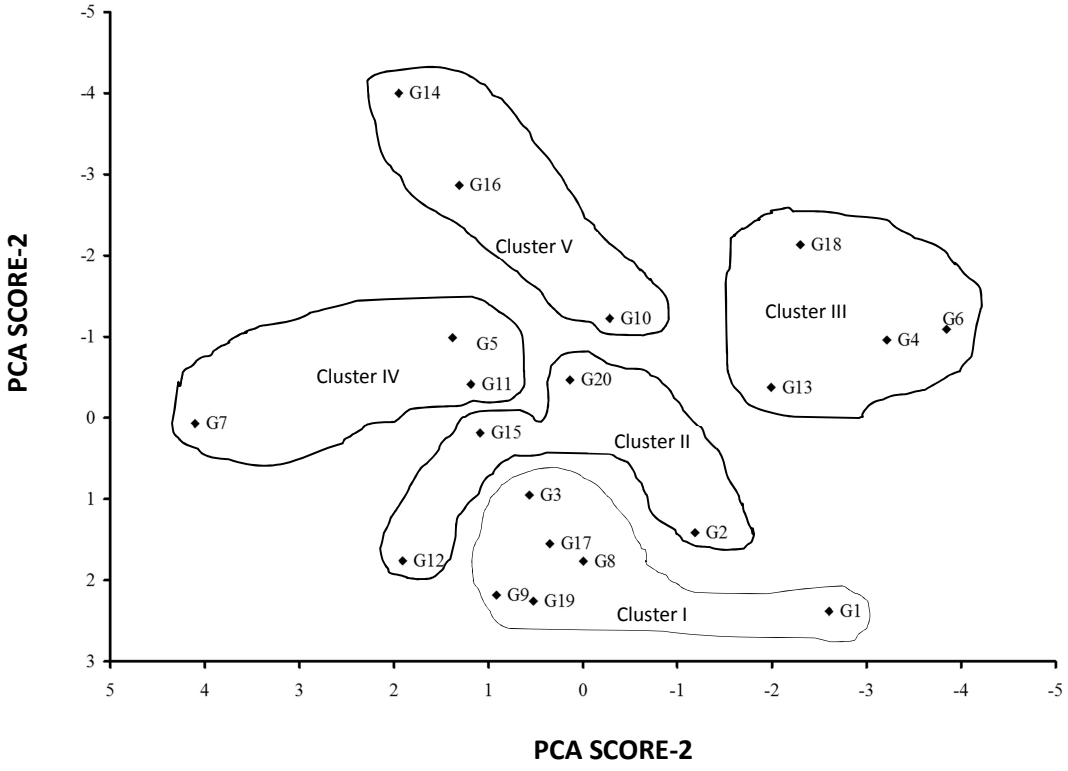

Fig 2. Scattered diagram of twenty pumpkin genotype

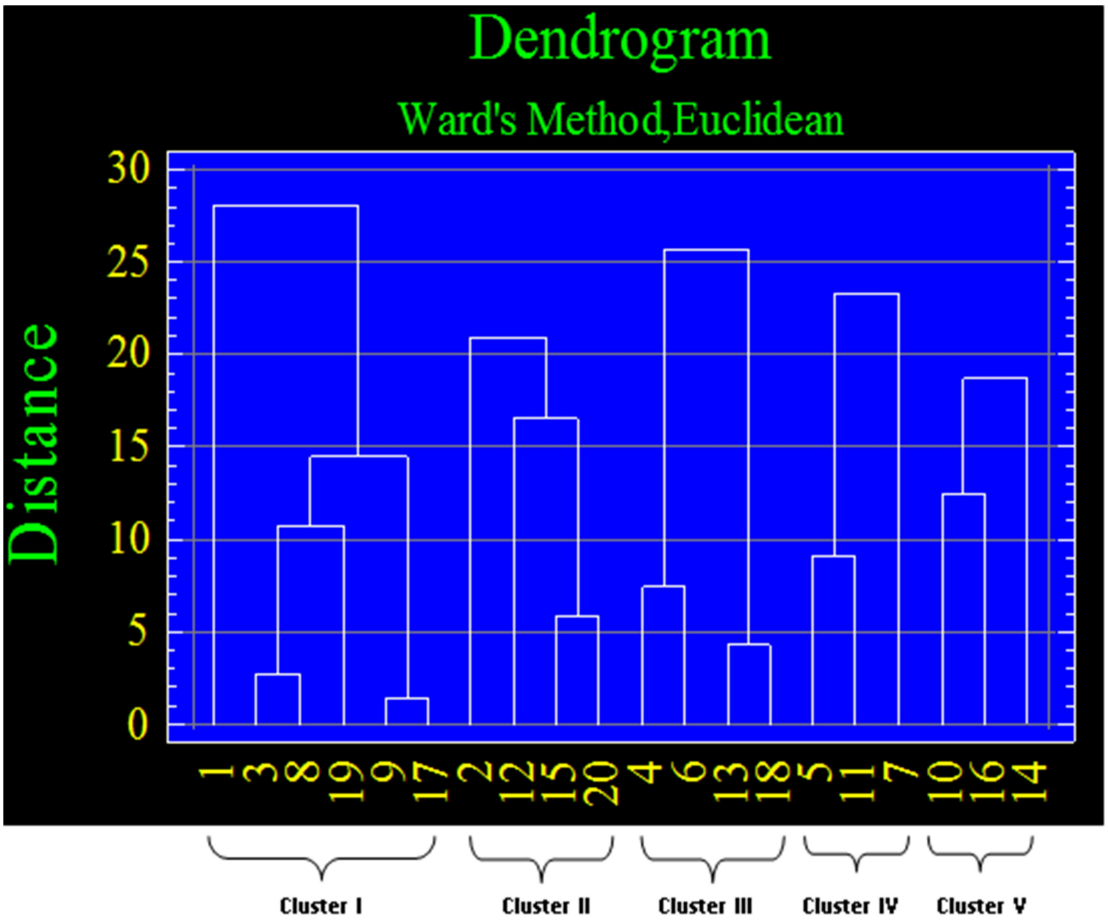

Fig 3. Dendrogram of twenty pumpkin genotype

4.4.4 Contribution of traits towards divergence of the genotypes

The latent vectors (Z_1 and Z_2) obtained from principal component analysis (PCA). The important characters responsible for genetic divergence in the axis of differentiation in vector I (Z_1) were days to first male flowering, days to first female flowering, pedicel length of male flower (cm), fruit length (cm), fruit Breadth (cm), fruit weight (kg), fruit Yield per plant(kg) (Table10). In the Vector II leaf length without petiole (cm), leaf breadth (cm), internode distance, days to first male flowering, days to first female flowering, pedicel length of male flower (cm), pedicel length of female flower (cm), number of male flower per plant, number of female flower per plant, fruit length (cm), fruit yield per plant (kg) showed their important role toward genetic divergence. The role of days to first male flowering, days to first female flowering, pedicel length of male flower (cm), fruit length (cm), fruit weight (kg), fruit yield per plant (kg) in both the vectors was important components for genetic divergence in these materials. Kundu *et al* (2012) found days to first male flowering and fruit yield per plant in both vectors is important components in genetic divergence of bitter gourd.

4.4.5 Selection of parents for future hybridization

Selection of genetically diverse parents is the prime task for any plant breeding activities. Therefore, considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotype G_6 (BD 309) for minimum days to first female flowering from cluster III, G_{14} (BD 246) for maximum number of fruit yield and for maximum number of female flowering from cluster V, G_{11} (BD 9494) for maximum fruit breadth from cluster IV, G_{12} (9492) for maximum fruit weight from cluster II. Therefore considering group distance and other agronomic performances the inter genotypic crosses between G_{14} (BD 246) and G_6 (BD 309); G_{12} (9492) and G_6 (BD 309); G_{14} (BD 246) and G_{11} (BD 9494) may be suggested for future hybridization program.

Table 10. Relative contribution of thirteen characters towards divergence of the genotypes

Characters	Vector 1	Vector 2
Leaf length without petiole (cm)	-0.0399	0.18393
Leaf breadth (cm)	-0.03201	0.12211
Internode distance	-0.0335	0.11187
Days to first male flowering	**0.07457**	**0.34996**
Days to first female flowering	**0.1249**	**0.54739**
Pedicel length of male flower (cm)	**0.02128**	**0.02538**
Pedicel length of female flower (cm)	-0.0868	0.03034
Number of male flower per plant	-0.12577	0.05518
Number of female flower per plant	-0.13194	0.05916
Fruit length (cm)	**0.29447**	**0.52623**
Fruit breadth (cm)	0.91269	-0.28795
Fruit weight (kg)	**0.03278**	**0.04081**
Fruit yield per plant (kg)	**0.11443**	**0.38344**

CHAPTER V
SUMMARY AND CONCLUSION

The present study was carried out at the Sher-e-Bangla Agricultural University Farm, Bangladesh during April 2014 to September 2014 to study on Genetic diversity and characters association in yield and yield contributing characters of pumpkin.

The field experiment was laid out in the main field in Randomized Complete Block Design (RCBD) with three replications. It was observed that significant variation exist among all the genotypes used for most of the characters studied. The maximum value in respect to days to first male flowering was observed as 75.67 in G_7 (BD 306) and the minimum duration was 64.33 in G_1 (BD 4567).

Gentotype G_7 (BD 306) recorded maximum duration of female flowering (83.00) and the minimum duration was 68.00 recorded in G_6 (BD 309). Genotype G_{14} (BD 246) recorded the highest leaf length 21.17 cm and minimum was 12.50 cm recorded in G_1 (BD 4587). In case of leaf breadth, G_7 (BD 306) recorded maximum (23.17 cm) leaf breath and minimum (16.33 cm) was recorded in G_1 (BD 4587). Genotype G_{14} (BD 258) recorded maximum internode distance (18.70) and G_1 (BD 4587) recorded minimum (10.23 cm).

Genotype G_{15} (BD 245) recorded maximum pedicel length (23.57 cm) of male flower and minimum was 7.17 cm recorded in G_{10} (BD 245). Genotype G_2 (BD 2203) recorded 7.33 cm maximum pedicel length of female flower and minimum was 2.63 cm recorded in G_5 (BD 2212). Genotype G_{14} (BD 246) recorded maximum number of male flower (13.67) and the minimum number was 4.67 in G_3 (BD 2174). The G_{14} (BD 246) recorded maximum number of female flower (10.67) and the minimum number was 4.67 in G_2 (BD 2203). Genotype G_7 (BD 306) recorded maximum fruit length (41.67 cm) and the minimum number was 22.67 cm in G_6 (BD 309).

Genotype G_{11} (BD 9494) recorded the maximum fruit breadth (74.67 cm) and the minimum number was 39.68 cm in G_{16} (BD 2205). In case of fruit weight G_{12} (BD 9492) was recorded maximum weight (3.67 kg) and the minimum fruit weight (1.7 kg) recorded in G_{18} (BD 223). Genotype number G_{14} (BD 246) recorded maximum average fruit yield (18.33 kg) per plant and the minimum fruit yield per plant was (2.27 kg) found in G_6 (BD 309).

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 difference between phenotypic and genotypic co efficient of variation were 31.42 % and 29.20%, which indicated that number of female flower mostly dependent on environmental effect. The highest heritability estimates among thirteen yield contributing characters were 97.96 %, 95.65%, 95.58%, 95.16%, 94.19 % in fruit yield per plant, leaf length without petiole, internode distance, pedicel length of female flower per plant and fruit weight.

The lowest heritability was 67.63% in days to first male flowering. The maximum genetic advance was observed in fruit breadth (18.64), followed by pedicel length of male flower (9.54) among thirteen character of sweet gourd genotypes. The maximum genetic advance in percent of mean was observed for fuit yield per plant (97.85 %) and the lowest was in days to first male flowering (7.17 %).

Correlation coefficients among the characters were studied to determine the association between yield and yield components. In general, most of the characters showed higher genotypic correlation co-efficient were higher than the corresponding phenotypic correlation co-efficient suggesting a strong inherent association between the characters under study and suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values.

In few cases, phenotypic correlation co-efficient were higher than their corresponding genotypic correlation co-efficient suggesting that both

environmental and genotypic correlation in these cases acted in the same direction and finally maximize their expression at phenotypic level. The significant positive correlation with fruit yield per plant were found in fruit length (G = 0.577, P =.583), and fruit weight (G = 0.695, P = 0.696).

Path co-efficient analysis revealed that days to first male flowering had highest positive direct effect (0.965) on yield per plant followed by fruit weight (0.952), leaf breadth (0.750), internode distance (0.601), number of female flower per plant (0.587). Such results indicated that direct selection based on these characters would be effective for yield improvement in pumpkin. On the other hand, leaf length without petiole (-1.504), days to first female flowering (-0.505), number of male flower per plant (-0.351), fruit breadth (-0.195), pedicel length of male flower ((-0.1730, fruit length (-0.156). So direct selection based on these characters would not be effective. Fruit weight via fruit yield per plant had highest positive indirect effect (0.696). The highest negative indirect effect (-1.367) was internode distance via leaf length without petiole.

Genetic diversity among pumpkin (*Cucurbita moschata)* genotypes was performed through Principal Component Analysis (PCA), Cluster Analysis, Canonical Variate Analysis (CVA) using GENSTAT computer program. According to PCA, D^2 and cluster analysis, the genotypes grouped into six divergent clusters using Z_1 and Z_2 values obtained from principal component scores. The highest inter-cluster distance was observed between clusters II and V (36.23), followed by between cluster I and V (32.94), cluster II and IV (32.05), cluster II and III (31.15), and between cluster III and V (30.15). On the other hand, the maximum intra-cluster distance was found in cluster IV (27.50), while the minimum distance was found in cluster I (19.87).

Considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotype G_6 (BD 309) for the minimum days to first female flowering from cluster III, G_{14} (BD 246) for the maximum number of fruit yield and for the

maximum number of female flowering from cluster V, G_{11} (BD 9494) for the maximum fruit breadth from cluster IV, G_{12} (9492) for the maximum fruit weight from cluster II. Therefore considering group distance and other agronomic performances inter genotypic crosses between G_{14} (BD 246) and G_6 (BD 309); G_{12} (9492) and G_6 (BD 309); G_{14} (BD 246) and G_{11} (BD 9494) may be suggested for future hybridization program.

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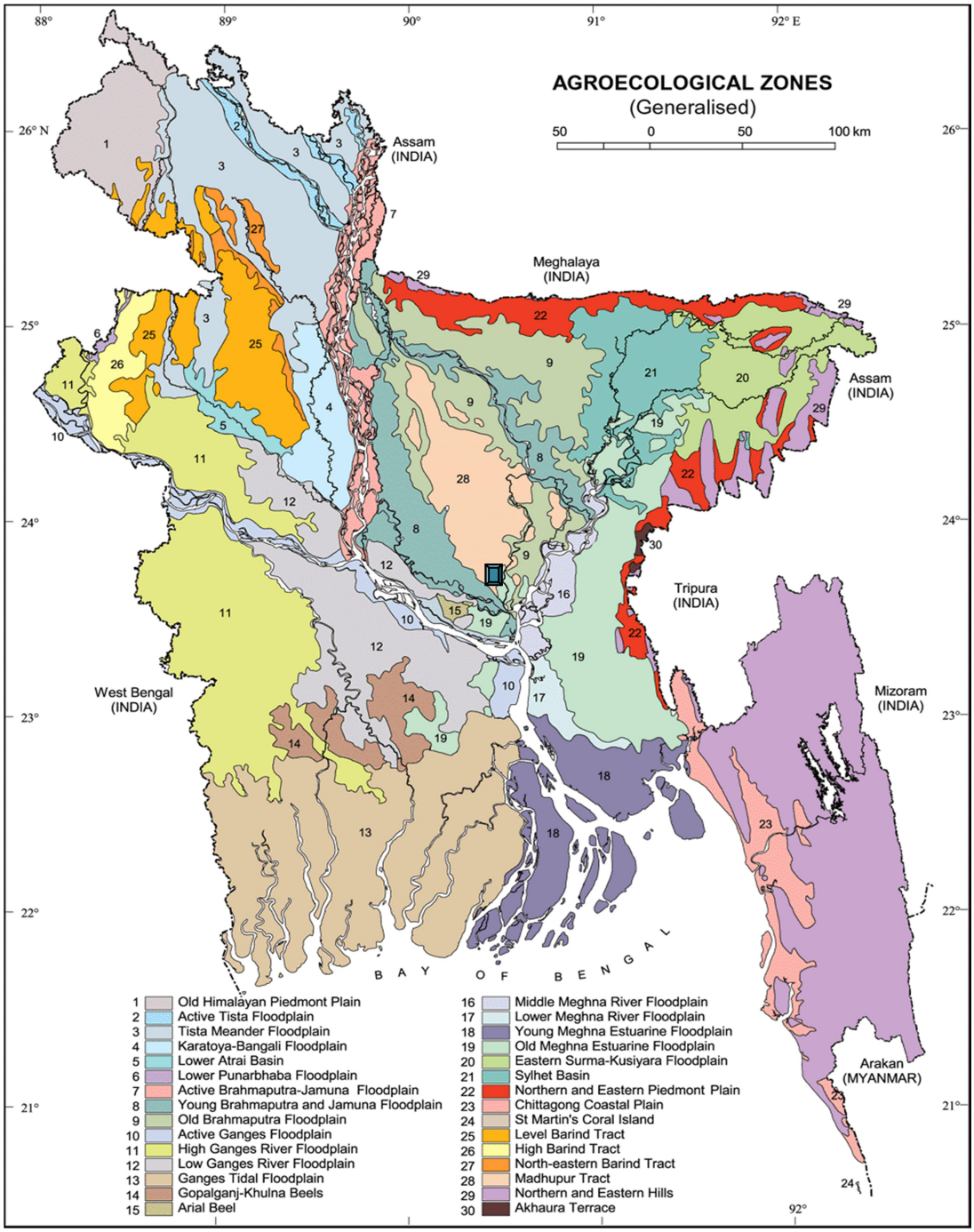
APPENDICES

Appendix I. Map showing the experimental site under the study



The experimental site under study

Appendix II. Monthly records of air temperature, relative humidity, rainfall and sunshine hours during the period from April 2014 to September 2014

Month	Year	Monthly average air temperature (^{o}C)		Average relative humidity (%)	Total rainfall (mm)	Total sunshine (hours)
		Maximum	Minimum			
April	2014	38.4	18.9	67	90	8.7
May	2014	35.8	21.6	70	205	7.7
June	2014	37.6	22.5	80	590	4.3
July	2014	34	23.3	85	614	3.2
August	2014	36	19.40	85	319	4.0
September	2014	33.2	18	78	210	4.15

Source: Bangladesh Meteorological Department (Climate division), Agargaon Dhaka-1212.

Appendix III. The mechanical and chemical characteristics of soil of the experimental site as observed prior to experimentation (0 - 15 cm depth).

Mechanical composition:

Particle size	constitution
Sand	40%
Silt	40%
Clay	20%
Texture	Loamy

Chemical composition:

Soil characters	**Value**
Organic matter	1.44 %
Potassium	0.15 meq/100 g soil
Calcium	3.60 meq/100 g soil
Magnesium	1.00 meq/100 g soil
Total nitrogen	0.072
Phosphorus	22.08 µg/g soil
Sulphur	25.98 µg/g soil
Boron	0.48 µg/g soil
Copper	3.54 µg/g soil
Iron	262.6 µg/g soil
Manganese	164 µg/g soil
Zinc	3.32 µg/g soil

Source: Soil Resources Development Institute (SRDI), Khamarbari, Dhaka

Appendix IV. Analysis of variance for different yield contributing characters of 20 pumpkin genotypes

Characters	d.f	Leaf length without petiole (cm)	Leaf breadth (cm)	Internoe distance (cm)	Days to first male flowering	Days to first female flowering	Pedicel length of male flower (cm)	Pedicel Length of female flower (cm)	Number of male flower per plant	Number of female flower per plant	Fruit length (cm)	Fruit Breadth (cm)	Fruit weight (kg)	Fruit Yield per plant (kg)
Replication	2	0.938	1.209	0.316	3.017	4.267	2.154	0.331	0.417	0.017	23.320	73.92	0.127	0.228
Genotypes	19	16.882**	14.696**	17.863**	29.961**	64.571**	69.979**	4.437**	23.483**	10.460**	85.082**	289.82**	1.043**	57.729**
Error	38	0.252	0.417	0.271	4.122	6.284	1.487	0.074	1.031	0.525	6.502	12.06	0.021	0.397

** indicates significant at 0.01 probability level.

Appendix V. Mean performance of 20 pumpkin genotypes based on different yield contributing characters of pumpkin

Genotypes	Leaf length without petiole (cm)	Leaf breadth (cm)	Internode distance	Days to first male flowering	Days to first female flowering	Pedicel length of male flower (cm)	Pedicel Length of female flower (cm)
G_1	12.50l	16.33 h	10.23 j	64.33 g	70.33 ghi	9.83 jk	4.33fg
G_2	14.50jk	18.33 efg	12.83 gh	70.00bcde	74.67 defg	18.67 bc	7.33a
G_3	16.83ef	19.00 def	14.17 ef	68.67 def	75.67 cdef	14.67 efgh	4.36 fg
G_4	13.17l	20.27 bc	11.20 i	64.33 g	69.33 hi	20.50 b	4.90 cde
G_5	18.13d	22.23 a	15.37 cd	71.67bcd	78.33abcd	14.83 efg	2.63 j
G_6	14.17k	17.17 gh	10.77 ij	67.33 efg	68.00 i	17.40 cd	3.06 ij
G_7	20.13b	23.17a	16.20bc	75.67a	83.00 a	15.67 def	5.20 cd
G_8	14.57ijk	19.17cde	12.27 h	70.67 bcde	76.00 cde	20.50 b	3.77 h
G_9	15.47ghi	18.30 efg	13.33 fg	68.33 def	73.67 defgh	11.17 ij	5.23 c
G_{10}	17.57de	20.50 b	15.27 d	65.00 fg	71.00 fghi	7.167 l	3.90 gh
G_{11}	19.13c	23.07 a	18.17a	69.33 cde	75.33 cdef	13.33 ghi	4.73 def
G_{12}	14.83hijk	18.50 ef	11.17 ij	72.67 abc	81.00 ab	19.50 bc	6.20 b
G_{13}	16.67f	19.83bcd	14.50de	65.33 fg	69.33 hi	14.00 fgh	4.47 ef
G_{14}	21.17a	22.83a	18.70 a	68.33 def	73.33 efgh	12.50 hi	3.17 i
G_{15}	18.17d	21.00b	12.33 h	73.33 ab	82.67a	23.53 a	5.23 c
G_{16}	19.50bc	22.83 a	16.50 b	70.00 bcde	80.00abc	8.33 kl	3.83 h
G_{17}	15.50gh	18.17 efg	13.50 fg	71.33 bcd	75.67cdef	12.57 hi	6.50 b
G_{18}	18.17d	20.17 bc	15.17 d	67.33 efg	69.67 hi	23.57a	3.53 hi
G_{19}	15.30hij	16.33 h	10.90 ij	70.67 bcde	77.67 bcde	9.33 jk	3.43 hi
G_{20}	16.23fg	17.87 fg	13.43 fg	73.00 abc	79.67 abc	16.33 de	5.33 c
$LSD_{(0.05)}$	0.829	1.06	0.860	3.35	4.14	2.01	0.449
SD	2.37	2.21	2.44	3.16	4.64	4.83	1.22
Minimum	12.50	16.33	10.23	64.33	68.00	7.17	2.63
Maximum	21.17	23.17	18.70	75.67	83.00	23.57	7.33
Mean	16.59	19.75	13.80	69.37	75.22	15.17	4.56
CV (%)	3.02	3.27	3.78	2.93	3.33	8.04	5.97

Genotypes with the different letter (s) are significantly different.

Appendix V. (Continued)

Genotypes	Number of male flower per plant	Number of female flower per plant	Fruit length (cm)	Fruit Breadth (cm)	Fruit weight (kg)	Fruit Yield per plant(kg)
G_1	7.667 def	4.333 hij	25.50 fgh	73.67ab	2.693 efg	7.237 f
G_2	11.00 b	3.667 j	28.20 efg	59.71 fg	2.033 h	6.833 f
G_3	4.667 h	5.667fgh	40.00 ab	58.62 fg	2.600 fg	9.533de
G_4	10.67 bc	9.000 b	23.33 h	51.83hi	1.833 hi	8.533de
G_5	12.00 ab	5.333ghi	30.17 def	66.33 cde	2.900 de	9.667 de
G_6	13.67a	7.333cde	22.67 h	48.33i	1.767i	2.267 h
G_7	8.667 d	5.333ghi	41.67 a	64.67 def	3.033cd	14.23 c
G_8	7.667 def	4.333hij	35.33 c	71.33 abc	2.620 fg	8.723de
G_9	5.333 gh	4.333hij	34.40 cd	68.17 bcde	3.363 b	16.82 b
G_{10}	12.00 ab	6.333 efg	29.00efg	57.83 gh	3.063 cd	9.190 de
G_{11}	8.333de	4.000ij	28.33 efg	74.67a	3.073cd	4.040 g
G_{12}	12.33ab	7.000 def	37.33abc	64.33 def	3.667a	15.83 b
G_{13}	6.333fgh	5.667gh	27.00efgh	58.33fg	1.967 hi	4.600 g
G_{14}	13.67 a	10.67 a	29.33efg	50.33 i	3.233 bc	18.33 a
G_{15}	9.000cd	6.000 fg	30.67de	57.33 gh	2.827 def	6.587 f
G_{16}	11.67 b	7.667 cd	28.83efg	39.68 j	2.837def	8.510 e
G_{17}	8.000 def	5.000ghij	28.17 efg	62.35efg	3.257bc	9.693 de
G_{18}	6.667efg	8.333 bc	25.00 gh	47.67 i	1.707 i	2.810 h
G_{19}	5.667gh	6.333efg	36.50 bc	69.17 abcd	3.410 b	9.009de
G_{20}	10.67bc	8.333 bc	29.77efg	46.03 i	2.433 g	9.733 d
$LSD_{(0.05)}$	1.67	1.19	4.21	5.74	0.239	1.04
SD	2.80	1.87	5.33	9.83	0.59	4.39
Minimum	4.67	3.67	22.67	39.68	1.71	2.27
Maximum	13.67	10.67	41.67	74.67	3.67	18.33
Mean	9.28	6.23	30.56	59.52	2.72	9.11
CV (%)	10.94	11.63	8.34	5.84	5.32	6.91

Genotypes with the different letter (s) are significantly different.