# GENETIC VARIABILITY AND INTER RELATIONSHIP AMONG YIELD AND ITS CONTRIBUTING TRAITS OF SWEET GOURD (*Cucurbita maxima* L.)

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## *CERTIFICATE*

*This is to certify that thesis entitled,* ***"Genetic Variability and Inter Relationship Among Yield and Its Contributing Traits Of Sweet Gourd (Cucurbita Maxima L.)"*** *submitted to the faculty of Agriculture, Sher-e- Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of* ***MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING*** *embodies the result of a piece of bonafide research work carried out by* ***Kazi Mehedi Hasan****, Registration No.:* ***19- 10056*** *under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

***Dated:***

***Place: Dhaka, Bangladesh***

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# GENETIC VARIABILITY AND INTER RELATIONSHIP AMONG YIELD AND ITS CONTRIBUTING TRAITS OF SWEET GOURD (*Cucurbita maxima* L.)

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## ABSTRACT

A field experiment was conducted with 28 sweet gourd (*Cucurbita maxima* L.) genotypes at the experimental field of Sher-e-Bangla Agricultural University, Dhaka to determine the genetic variability, correlation and path coefficient for yield and its contributing traits during November' 2019 to March' 2020. Significant variation was present among all the genotypes for studied traits. Mean comparison table shows variation exist among all the fourteen characters. Phenotypic variance ($\delta^2p$) and phenotypic coefficient of variation (PCV) was higher than the genotypic variance ($\delta^2g$) and genotypic coefficient of variation (GCV) for all the traits under studied. High heritability coupled with high genetic advance in percent of mean was observed for pedicel length of male flower (98 cm and 46.38 cm), inter node distance (97 cm and 43.85 cm), leaf breadth (96 cm and 41.74 cm), pedicel length of female flower (94 cm and 23.36 cm),) respectively which indicated the effect of additive genes. The correlation coefficient revealed that fruit yield per plant had the highly significant positive correlation with fruit weight ($r_g$= 0.721, $r_p$= 0.807), fruit per plant ($r_g$ = 0.585, $r_p$ = 0.588), pericarp length ($r_g$ = 0.669, $r_p$ = 0.222), indicating those characters can be considered for phenotypic selection for future sweet gourd improvement program. The path coefficient had direct positive effects with fruit weight (0.802), fruit per plant (0.565), Pericarp length (0.670), number of male flower (0.036) which indicated that promising selection would be rewarding for those traits. The genotypes are grouped into five clusters, where cluster IV comprise maximum genotype (9) and cluster I had minimum genotypes (3). The highest intra cluster distance was observed in cluster I (3.352). Among five clusters the highest inter cluster distance was observed between cluster I and cluster III (3.735) and the lowest between cluster I and cluster IV (2.294). Considering genetic variation, leaf length without petiole (cm), fruit size (cm), fruit per plant, fruit weight (kg) cluster analysis, intra and inter cluster distance, agronomic performances BD-2150, BD-2175, BD-282 might be selected as promising parents for future hybridization program.

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## SOME COMMONLY USED ABBREVIATIONES

| FULL NAME | ABBREVIATION |
|---|---|
| Agro-Ecological Zone | AEZ |
| And others | *et. al.* |
| Bangladesh Agricultural Research Institute | BARI |
| Bangladesh Bureau of Statistics | BBS |
| Centimeter | $_{C}$m |
| 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 | $\delta^2_g$ |
| Heritability in broad sense | $h^2_b$ |
| Journal | *j.* |
| Kilogram | Kg |
| Meter | M |
| Mean sum of square | MSS |
| Millimeter | Mm |
| Murate of potash | MP |
| Percent | % |
| Phenotypic co-efficient of variation | PCV |
| 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 |

# CHAPTER I

## INTRODUCTION

Sweet gourd (*Cucurbita maxima* L.) is locally known as 'Misti kumra' or 'Misti lau' or 'Misti kadu' or winter squash. *C. maxima* comes from South America and has spread in the post-Columbian era around the world. The *C. maxima* is an annual plant belongs to the family Cucurbitaceae. In Bangladesh Sweet gourd is commonly grown vegetables, mostly because of their fruits' properties. This vegetable plant is a valuable source of dietary fiber and high carbon content. Flesh part of sweet gourd is high in carotenoids (mainly β-carotene and lutein), Starch, vitamin C and E.

Sweet gourd reduces the risk of coronary heart disease and hypertension as well as can lower serum cholesterol levels (Hussain *et al*., 2013). The seed, known to have high zinc content, was used to treat the early phases of the prostate problem. For this reason, the cultivation of this vegetable is increasing day by day. An increase in Cucurbita's popularity has encouraged the breeding of new variety (Pevicharova , 2017, Darrudi *et al.,* 2018, and Singh *et al.,* 2019).

Sweet gourd production percentage involves Asia (61.6%), Europe (16.3%), America (11.7%), Africa (8.9%) and Oceania (3.2%) and sweet gourd production worldwide (1.4 percent). In Bangladesh the sweet gourd production area 28394 acres and the production rate is 114407 M. ton (BBS, 2019)

Currently, *C. maxima* is one of the most important vegetable crops among 10 Cucurbitaceae species of worldwide, and together with *C. pepo* and *C. moschata*, it is one of the three most important Cucurbita species. (Loy *et al*., 2004, Parish *and Brown* 2005; Chomicki *et al.,* 2019). *C. maxima* is recognized as Cucurbitaceous most diverse species with great morphological variations and differences in size, shape and peel color (Ferriol *et al.,*2004) characterized by its fruit. The high levels of genetic diversity in *C.maxima* were confirmed by DNA studies (Ka´zmi *et al.,* 2017) It is an allotetraploid species, chromosome number 2n = 40 and an estimated 386.8 Mb genome size (Whitaker, T.W., 1930, Sun *et al.,* 2017). Seven large garden groups of *C. Maxima* cultivars were distinguished on the basis of their fruit characteristics (Goldman, 2004).

The selection target for Cucurbits is fruit morphology, flavor and nutritional features (Ferriol and Picos., 2008, Zhong *et al.,* 2017). Therefore, *C. maxima* main concerns are

fruit-associated traits and fruit yield properties (Pevicharova and velkov ., 2017 parish *and Brown .*, 2005)

sweet gourd is a nutritious crop, but overall production is low due to abiotic and biotic stresses, low level of crop management by farmers and the shortage of suitable varieties for varying geographical conditions (Singh *et al*. 2019). The present yield is not high enough to meet the demand of consumers and farmers because of its low yield potential, susceptibility to disease and pest. More food is required for its over growing population in Bangladesh. To meet up the high demand of food farmers are growing more cereal crops in decreasing agricultural land. So, at present the cultivation of vegetables has gone to marginal land because farmers are not interested to use their fertile land in vegetable cultivation.However genetic variability is essential for a successful breeding program of any crop species and a critical survey of genetic variability is necessary before initiating an improvement program aiming to develop high yielding varieties. The correlation co-efficient between yield components usually show a complex chain of interacting relationship. Path co-efficient analysis shows the components of correlation co-efficient into direct and indirect effects and visualize the relationship in more meaningful way. Multivariate statistics help the researcher to summarize data and reduce the number of variables (Anderson, 1972). The multivariate techniques, such as cluster analysis, vector analysis and principal component analysis may be an efficient tool in the quantitative estimation of genetic variation. To select germplasm in a more systemic and effective way, study of genetic diversity in genetic resources is a critical factor for breeders is necessary to better understand the evolutionary and genetic relationships among accessions (Lavanya et al. 2008). Multivariate technique also plays an important role in choice of divergent parents for hybridization to exploit maximum heterosis. Therefore, the present research was under taken with the following objective:

- **i.** To estimate the nature and magnitude of genetic variations among the sweet gourd genotypes in respect of different yield and yield contributing characters;
- **ii.** To estimate the extent of correlation between pairs of characters at genotypic and phenotypic level.
- **iii.** To assess the direct and indirect effect of different characters on yield of sweet gourd.
- **iv.** To identify the diversified parents among the genotypes for the utilization in future hybridization program.

# CHAPTER II
# REVIEW OF LITERATURE

The review of literatures contain report on the crop under study and other related crops studied by several researchers, which appears pertinent in understanding the problem which may help in the explanation and the interpretation of results of the present study. In this section, an attempt has been made to review the available information at home and aboard on direct and indirect genetic effects on the yield performance of different sweet gourd genotypes.

## 2.1 Variability, Heritability and Genetic Advance:

Narayan (2013) executed an experiment on 10 diverse genotype of sweet gourd and reported variability for fruit and seed characters viz., days to 50% germination, days to first male flower anthesis, days to first female flower anthesis, node number of first male flower, node number of first female flower, days to first fruit harvest, number of branches per vine, vine length, fruit length, number of fruits per vine, fruit yield per vine, number of seeds per fruit and 100 seed mass. Singh *et al*. (2019), conducted genetic variability in bottle gourd in both summer and rainy seasons and recorded the highest genotypic and phenotypic coefficients of variation for yield per vine.

Gayen and Hossain (2006), conducted genetic variability and heritability of bottle gourd and observed that magnitude of phenotypic coefficient of variation (PCV) was significantly higher than genotypic coefficient of variation (GCV) for all the characters, it reflected the effect of environment on expression of these traits. The estimation of heritability ranged from 60.60 to 95.45%. High genetic advance as percentage of mean was recorded for sex ratio, fruit length, fruit yield per plant and TSS. The sex ratio, fruit length, fruit yield per plant and TSS showed high heritability (above 80%) coupled with high genetic advance.

Singh and Kumar (2002), conducted genetic variability in bottle gourd and reported that the phenotypic coefficient of variation was higher than the genotypic coefficient of variation. High estimates of heritability were recorded for fruit yield per plant, vine length, number of days to first harvest, number of nodes to first male and female flowers, number of primary branches per plant, and fruit length, weight and diameter.

Naik *et al*. (2012) conducted a field experiment to study of genetic variability, heritability and genetic advance and other quality characters in teasle gourd. Higher phenotypic coefficients of variation were observed for all the characters except fruit length at marketable stage. In heritability and genetic advance, the traits are - 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, acidity in exocarp showed high heritability along 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 was 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.

Narayanankutty *et.al*. (2006) estimated genetic parameters of 36 snake gourd (*Trichosanthes cucumerina*) genotypes indicated a huge genetic variation in germplasm which is collected. Characters such as fruit yield, fruit yield per plant, weight of fruit and seeds per fruit have high heritability values and genetic gains, which indicating additive gene action.

Banik (2003) carried out an experiment on variability and genetic development of 26 snake gourd genotypes with a view to 15 quantitative yield contributing characteristics. Harvest length (2.197 to 3.87 m), primary branches number (5.23 to 11.88), first male flower opening (41.67 to 68.67 days), first female flower days (11.88), the first male flower node (48.67 to 71.33 days), length of fruit (20.67 to 71.17 cm), fruit seeds (39.03 to 69.50) also found that days of first female flower, fruits yield per plant was significantly high genetics effect. Days of first female flower opening, the PCV was lower than the first male flower opening and 100 seed weights. For all the other characters, the GCV and heritability were high. (GCV) was noted 30.96; $h^2$ PCV 30.75; length of fruit (GCV and PCV 29, 92%), and $h^2$ 30.04; the first female flower node (GCV and PCV 25.87); $h^2$ was 94.63% and fruit per plant number (GCV and PCV 19.82).

Dora *et al*. (2003) evaluated eleven characters of pointed gourds (*T. dioica*) in order to estimate genetic variability and yield contributing traits. The characteristics were estimated at high genetic coefficient of variance (GCV) in the first female flower opening, twig length, and number flower per plant and fruit number. The heritability was all the characters were high. GCV and PCV were also high in fruit per plant, fruit weight.

Chowdhury and Sarma (2002), experimented genetic modification, heritability, genetic advance, and the correlation of yield and yield contributing trait (twig length, number of flower, first flower opening, and number of fruit per plant).

In 12 *Luffa acutangulas*, fruit length, fruit wide and fruit weight have been studied. In all characters the genetic coefficient variation (GCV) was greater than the phenotypic variation coefficient (PCV). The heritability, PCV, GCV, and genetic advance values have been high. The length of the twig, yield per hectare, and fruit weight. The additive gene effects of these traits were characterized. The correlation coefficients have shown that selection on the character of yield per hectare increased number of fruit per plant, length of fruit and individual fruit weight.

Quamruzzaman *et al.* (2009) conducted an experiment and found that 13 $F_1$, 26 parents heterosis in bottle gourds was experimented the results showed very important distinctions between the materials studied for all characteristics. For fruit yield, heterosis is higher. Number of fruit per plant and weight of the single fruit, length of fruit and the diameter of the fruit is smaller in the early days. $F_l$ 10 x 17 and 19 hybrids 26 showed the highest heterosis in the parents and the better parents (73.1 percent), For yield per plant (61.8 percent).

Bharathi *et al.* (2006) assessed ten features (flowering days, twig-length, number of nodes at the first flowers, length of the internode, fruit length, weight and volume, fruit number and other features) in 32 genotypes of spine gourd (*Momordica dioica*) Bhubaneswar, Orissa, India. Analysis of the genotypic variance showed significant differences among phenotypic variance. The Phenotypic coefficient of variation (PCV) was 15.26% for fruit girth and 34.28% for fruit weight, and the genotypic coefficient variation (GCV) was between 14.38% for fruit girth and 12.75% fruit girth. Fruit weighs 33.52 percent. High ancestry and genetic prowess the weight, volume and number of fruits per plant were recorded for fruit, the prevalence of these characteristics of the additive gene effects and their potential use in spine gourd selection programs Productive performance.

Masud *et al.* (2006) carried out a field experiment with seven inbred lines and their 21 bottle gourd hybrids. The results showed considerable variations in the twenty-eight populations of seven characters. There was a lot of variation. Seven characters show the selection options for improvement. For all characters, the specific variation in combining capacity was significant. Days to anthesis, fruit length, and general combining ability were

all important. The fruit's diameter and fruit per plant demonstrate a dominance presence for all characters, but additive gene action is only seen for a few. Parent-two showed significant GCA, Parent-five proved good. Parent 7 fruit yielded per plant and fruit diameter showed significant. The cross that includes parents-3 and parents-5 is the best for fruit quality, fruit time (53.5%) and fruit yield per early age (106.8 percent).

### 2.1.1 Leaf Length (cm)

Ahamed *et al.* (2011) in the northern region of Bangladesh during the kharif season, conducted an experiment to evaluate the morphological and yield attributes in sweet gourd (*Cucurbita moschata*). The variability range for the leaf was different. In various genotypes, the length ranged from 30.6-47.2 cm.

Husna, A. (2009) A trial of 30 genotypes of bottle gourde at the Agricultural University of Sher-e-Bangla. The phenotypic variance (14.18) seemed to be higher than the genotypic variance variety (14.14). Close to each other were the GCV (22.63) and PCV (22.67). Heritability estimates (99.69 percent) for this feature were extremely high, genetic progress (9.91) and genetic progress was moderately found as a percentage of average (59.65) the additive gene was highly indicative of this feature.

Gaffar (2008) at Sher-e Bangla Agricultural University, conducted a fifteen-genotype study of sponge gourds. He found that the leaf length variances are genotypic and phenotypic 24.13 and 25.55, respectively. The GCV was slightly lower than PCV (20 percent) (20.5 8 percent). Patrimony for this feature was 97% with moderate genetic progress (9.83) and genetic progress was 95%. For this feature, medium (40.03) indicating obvious variation was considerable. It's been because of genotypes.

### 2.1.2 Leaf breadth

Husna, A. (2009) found GCV (23.04) bottle gourd to be lower than PCV (22.87). Gaffar (2008), observes that GCV (20.94%) is less than PCV's in a wider sense (23.3%). In sponge gourd, moderate genetic progress for this character (7. 81%) in leaf breadth.

Rajkumar *and* karuppaiah (2007) the genotype differences in all characters in snake gourd were significant in for all the characteristics except for the first female flower, the genotypic variance was high.

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 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. Also 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).

### 2.1.4 Number of male and female flowers per plant

Akter *et al*. (2013) conducted an experiment in genetic diversity between 30 pumpks in the Bangabandhu Sheik Mujibur Rahman Agricultural University (BSMRAU), Salnia, Gazipur Research Farm, was experimented by in the 2011-12 growth season. High genotype of variation coefficients (GCV) In addition, for beta carotene and non-reducing sugar, the number of male flowers per plant and the number of female flowers per plant were found to have high heritability and genetic progress in percent of the average. These characters are subject to genetic additive control and gene selection improvement could be effective for these characteristics.

### 2.1.5 Pedicel length of flower (cm)

Husna, A. (2009) found male flower pedicel in bottle size to be 3.5-2 1 cm long and 3.13-9 cm long in female flower pedicel size. Found male pedicel length in bottle gourd. Grubben (2004), said male flowers are about 7-31 cm long, and female's flower are about 2-10 cm long. Bottle gourd pedicel.

### 2.1.6 Fruit length and breadth (cm)

Husna, A. (2009) the highest GCV and PCV in snake gourd was recorded has found high heritability coupled with high fruit length genetics (GCV and PCV 29.92 and 30.04; h2b 99.19%) Gourd snake. GCV (16.49) and PCV (17.50) were detected by GCV (15.84) and PCV (17.39) male flower and in female bottle flowers the plant is gourd. Fruit length and diameter have changed significantly. Bitter Gourd, Sponge gourdes, ribbed gourds with bottle gourds. The length of both GCV and PCV was high (31.73 and PCV) 33.75) and bottle-gourd fruit diameter (39.23 and 41.96). They, as well, the minimal difference

between GCV and PCV has been observed. Characters with high character GCV show high selection potential

### 2.1.7 Fruit weight (Kg)

Akter *et al.* (2013) variability studies revealed that the most important combination of yield per plant with reproductive characters was the number of fruits per plant, followed by fruit weight at the genotypic and phenotypic levels. (30.2 And 36.4) were reported to have high GCV and PCV, (39.55 and 41.00) for weight of fruits with the sweet gourd. For this sweet gourd trait, reported a narrow difference between GCV and PCV in this trait indicates that this character has less environmental influence. Top $h^2$ sweet gourd was found to be associated with genetic progress in terms of average fruit weight. (82.9% and 49.6%); (93.03% and 78.58%). The results of were similar. In contrast, this trait in the ribbed gourd of Thakur and Choudhury was recorded with a low heritability (45.1 percent) and very high genetic advance (133.05%).

### 2.1.8 Number of fruits per plant

According to Akter *et al.* (2013) there is a positive and highly significant correlation between yields per plant and single fruit weight shows the maximum Contributions to yield were made by the number of fruits per plant. Days of first female flower and the weight of a single fruit. Such characteristics should be regarded as primary yield components also found that there are important fruit differences per plant. In the fruit yield per plant, the highest phenotypic coefficient variation (20.59) was observed than the genotypic variance GCV (19.82) on the character of number of fruit per plants.

### 2.1.9 Yield per plant (kg)

Husna *et al.* (2014) investigated variability, correlation and path analysis among thirty-one bottle-gourd characteristics. High genotypic of variation (GCV) on fruit weight per plant was observed, whereas the fruit width was observed to be low genotypic Co-efficient of variation. Path analysis resulted in maximum direct yield contribution by number of yield per plant, followed by the weight of fruit.

Banik (2003) also found that the fruits per plant are significantly different. For the fruit yield per plant, fruit length and the days of first male flower, the most important phenotypic coefficient variation has been observed on fruit length. The high genetic co-efficient of variation on fruit yield were noticed. Fruit yield per plant GCV (30.75), PCV (30.96); $h^2$b 98.64%.

## 2.2 Correlation Co-efficient:

Khule *et al*., (2011) Field experiments were conducted by in Vegetable Research Station Jagudan (Gujarat) with 30 sponge gourd genotypes to determine correlation and path coefficient of analysis in Sponge gourd (*Luffa cylindrica* L.). He found genotypic coefficients of variation were greater than the phenotypic coefficients of variation. The number of fruit per plant was shown high direct effect through the path coefficient analysis. On the other hand, first female flower, the length of fruit, the diameter of the fruit, and the number of male flower per plant shows direct positive impact on fruits weight.

Kumaresan *et al*. (2006) during the 20006 in rabi season in Madurai, Tamil Nadu, India, conducted experiments to determine correlations between different economic parameters, with direct and indirect impacts on fruit range in 6 countries. Cultivars with their 30 hybrids, Snake Gourd (*Trichosanthes cucumerina*). The main varietal length of the fruit per twig, the fruity weight per plant, the number of fruit per plant, and ascorbic acid content per fruit were positively associated per snake gourd. Negative combination indicated that the character selection would lead simultaneously to enhancing the fruit yield per plant.

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, and number of fruits per plant, 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 plant, vine length, nodes no. of first female flower, length of edible fruit and no. of fruit per vine.

Hazra *et al*. (2003) On 68 different genotypes of point gourd were researched by (*Trichosanthes dioica*). Their growth and morphology as well as their relationships through correlations in the Horticultural Research Station in Mondouri, western Bengal, India. The genotypic correlation coefficients for all characteristics was higher than the phenotypic correlation coefficients and a broad gap between two estimates of correlation

coefficients was generally identified, indicating environmental influence on the correlated response of the pair of characters.

Prasana *et al*. (2002) in Bangalore, Karnataka, India, studied the correlation between yield and yield components of the ridge gourd in the 1999 Rabi season. Fruit yield per hectare was positively linked at 90 days of sowing (DAS), 90 days leaves, number of female flowers, total plant dry weight, number of fruit and fruit circumference and weight.

Badade *et al*. (2001) conducted a study of 20 correlation genotypes of the bottles of gourds. The output has been found to be significant and the number of branches of each twig and the number of fruits of each twig are positive and male and female first days are significantly and negatively linked. The flower appearance and weight of deformed fruit per twig are at both phenotypic levels and the levels of genotypes. The length of the fruit was positive but negligible.

Shah and Kale (2002) The correlation coefficient experiment was carried out by Component yardstick analysis of 55 ridge gourd genotypes. The fruit weight per twig was positive and significantly linked to the amount of fruit per twig, the average weight of fruit, the number of female flowers per twig, and the length of wine. The fruit length was negative with the fruit diameter and fruit number per twig, while the fruit weight was positive.

**2.3 Path Co-efficient:**

Janaranjani and kantaswami (2015) evaluated path analysis with 18 different characters comprising of 36 hybrids of bottle gourd. The path analysis indicated that number of fruits per vine, days to first female flower opening (0.800), fruit cavity (0.380) and fruit weight (0.373) had positive direct effect on fruit yield, however fruit length (- 0.370) recorded high negative direct effect on fruit yield per vine. Number of primary branches (-0.189), days to first male flower opening (1.103), sex ratio (0.141) and number of pickings (-0.122) recorded negative low direct effect on fruit yield per vine.

Husna *et al*. (2011) conducted that the results of path coefficient analysis revealed the maximum direct contribution towards yield per plant with number of fruit per plant (0.680) followed by fruit weight (0.453) in 31 sweet gourd genotypes.

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 22 on the number of fruits per vine and fruit weight to increase the yield per plant directly.

Kumar *et al.* (2007) in a path coefficient study of 20 bottles of gourds (*Lagenaria vulgaris*), carried out an experiment. The experiment. Path analysis reveal that all factors must be taken into consideration are the number of branches per twig, length of the twig, and number of nodes at which the first female flower blooms. And the fruit per twig was directly positive in terms of fruit yield per twig. In 25 various sweet gourd populations, examined the path coefficient analysis. The analysis of the path coefficient showed this maximum The weight age should primarily be calculated on the number of days before first harvest followed by the average fruit weight per plant.

Prasanna *et al*. (2002) the study between yield and yield contributing character of ridge gourds (*Luffa acutangula*) in Bangalore, Karnataka, India, was studied by during the 2002 rabi. In the case of twigyards of 90 days after sowing of fruit yield per ha, number of leaves at 90 DAS, number of female flowers, total dry plant weight, number of fruits and weight of fruit yield was positive.

**2.4 Genetic Diversity:**

Khatun *and* Rahrnan (2010) conducted a field experiment of the nature and magnitude of genetic diversity of 38 snake gourd genotypes collected from various parts of the country in the field and laboratory of the Horticultural Department, Bangladesh Agricultural University, Mymensingh during the period between April 2004 and September 2004. $D^2$ analysis grouped the genotypes into four different clusters where cluster 1, which was followed by clusters 11 (8), III (7) and IV, was the maximum number (21) of genotypes (2). The pattern of clustering showed that geographical diversity is not linked with genetic diversity. i.e., from the same location genotypes collected were grouped into various clusters. Clusters III and IV were the largest inter cluster, while cluster I and Cluster I were the smallest ones observed. The maximum distance in cluster IV was observed at intra-cluster distance and the minimum in Cluster III was observed. Considering the means of clusters, cluster IV genotypes might be selected for plant yield and other characteristics contributing to yield.

Banik (2003) examined 26 snake gourd genotypes tested with multivariate analysis and grouped the genotypes in seven separate clusters. There was no relation between genetic

divergence and genotype geographic distribution. The maximum intergenotype distance between SO 026 and SO 010 was observed (1.897). The distance between Cluster II and Cluster IV was maximal (17.74). The most important contribution to the divergence were main twig length, first node of female flower, nodes on the main twig, fruit length, and the number of fruit per plant.

The 2008-09 Annual BARI Report shows that genetic differences among thirty snake gourd genotypes are estimated using the characteristic Cluster V. The highest genotype number (13) and the lowest Ill & IV cluster (3). Cluster III (1.665) and Cluster V were the highest intra-cluster distance observed (0.430). In Cluster I and III (26,954) and in Cluster I and II, the highest inter-cluster distance was observed (5.693).

Islam *et al.* (2010) studied the genetic divergence of 20 bitter gourd genotypes. The studied genotypes are divided into 4 clusters. The cluster I had the most genotypes and it was 10. The lowest number of genotypes was found in Cluster IV. The highest mean weight per fruit value is produced by Cluster II. The distances between the clusters were much higher than those within the clusters. The highest inter cluster distance was observed in Cluster I while the lowest in cluster III. The maximum inter cluster distance between I and II was observed while the minimum distance between the clusters was observed. Cluster II produced five significant yields and the highest intra-cluster weight per fruit. The selection cluster as parents for crossing cluster II genotypes which can produce new recombinances with desired features should therefore be emphasized. Taking all the characters 01 (Shaparan), G5, and G19 (Maharaj) into account, a further breeding program was selected for G9 (Nabil), G12 (Nandita), G14 (Eureca), G16 (Tia) and G19 (Maharaj).

Quamruzzaman *et al*. (2008) The genetic divergence in 30 genotypes (*Luffa acutangula*) of the ridge gourd was studied by $D^2$ and main component analysis by the genotypes have been grouped into six groups. Cluster II (0.882) and Cluster III (0.882) have the highest intra-cluster distance (0.220). Cluster I and II (15,045) were observed to have the highest intercluster inter-distance while Cluster IV and V were observed (3.402).

Gaffar (2008) conducted that the experimental in the field of the Sher-e-Bangla Agricultural University, from April 2007 to November 2007, with 15 sponge-gourd genotypes. The genotypes have been grouped into five groups. The Cluster III (0.999) and Cluster IV (0.999) have the highest inter cluster distance noted (0.43 9). Cluster IV to V

(7,163) had the highest intercluster distance, whereas Cluster I to IV had the smallest intercluster distance (2.258).

Khan *et al.*, (2008) examined 64 species genetic diversity through multivariate analysis of an experiment conducted in the 2002-2003 growing season of the Regional Agricultural Research Station, Ishurdi, Pabna. The genotypes were classified into 12 clusters. Cluster V consisted of the most genotypes and had nine genotypes. The lowest number of genotypes was included in cluster VI and cluster VIII, with each of two being two. The classification model of the genotypes in this study showed that the genotypes collected from the same location had been classified into various clusters. The Jessore genotypes have been distributed in various clusters. Between the genotypes, the highest inter genotype distance was 366.3. As observed between P0043 and P0044, P0022 and P0007 and the minimum 2.6 are respected. The internode length of Cluster V was the highest mean value between the clusters. Fruit weight per plant and output. Between Clusters III and II (45.71) and VII, the highest inter-cluster distance has been observed (3.33).

Kabir (2007) reported that 24 accessions of pointed gourd have been studied in genetic divergence. Five clusters grouped the accessions. The most accession numbers were presented in Clusters I and III (6), followed by Clusters V (5), 11 (4) and Cluster IV (3). Clusters IV (35.80), Cluster I (28.12) and Cluster V have been measured for the maximum intra-cluster distance (26.63). In III (18.87) we found the minimum intra-cluster distance.

The genetic difference of 32 spine gourd genotypes (*Momordica dioica*) for the following 12 characteristics were evaluated in Orissa, India (twig-length, number of days to bloom, first node of flowering, internode-length, mature leaf-size, pedicel-length, petiole weight, fruit-length, fruit-ground, fruit-plant number, yield per plant). The variance analysis revealed considerable variation in all genotypes. The genotypes were grouped into 7 $D^2$-based clusters. The most common genotypes (11), followed by clusters IV and V (9) and VI, were present in cluster III (4). The distance between the intra-cluster was 30.34 (cluster I) and 371.56. (Cluster III). The distance between the clusters VI and VII was greatest (864.75). Cluster II genotypes were characterized by early flower and the presence of the longest twigs and internodes. The most numerous fruit, pedicel length and yields were recorded in Cluster VI. The node at which the first flower appeared was superior in Cluster VII. The fruit weight, the fruit length and the fruit span of Cluster III were the highest.

Karuppaiah *et al*. (2005) the genetic divergence of in 12 bitter gourd genotypes (*Momordica. charantia*) was assessed during June-July 2001 in Annamalai, Tamil Nadu, and India. The genotypes were grouped using Mahalanobis D2 technology. I (four genotypes), II (one genotype), III (three genotypes), and IV (four genotypes). The highest average values for twig size (6.2 m), male numbers, were recorded among the four classes, Cluster IV (LA-7, LA-9, LA-10 and LA alternatively, 12). Plant flowers (79.3), number of plant female flowers (23.2), yield per Plant (5.2 kg), weight of single (242.2 g), length of fruit (29.4 cm) and number of fruits Plant fruits (24.1), number of fruit seeds (52.3).

Dora (2001) investigated 11 genotypes of (*Trihosanthes dioica)*, grouped into four clusters using the $D^2$ statistics of Mahalanobis and concluded that intra cluster distance are higher than inter cluster distance. The top $D^2$ between Cluster II and IV, value (984.3) has been recorded.

# CHAPTER III

# MATERIALS AND METHODS

The experimental field of study in the yield and yield character associations of sweet gourds was conducted in the Sher-e-Bangla Agricultural University, Dhaka, Bangladesh during the period of November 2019 to March 2020. A brief description of the test area, locations, soil characteristics, climatic characteristics, materials, layout and experimental design is provided. The following are presented: land production, manuring and fertilization, seed planting, intercultural transactions, harvesting, data recording, economic and statistical analyzes, etc.

## 3.1. Experimental site

During the period from November 2019 to March 2020, the present experiment took place at the Sher-e-Bangla Agricultural University, Dhaka-1207.

## 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 meters above the sea level. The experimental field belongs to the Agro-ecological zone of The Modhupur Tract, 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 low temperature, low relative Humidity and moderate rainfall in the winter season (November–March) and scanty rainfall associated with moderately low temperature during the winter season (November–March) 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

The soil of the experimental site is of Shallow Red Brown Terrace Soils, the general soil type under Tejgaon Series. Top floor was clay loam, olive-gray with common thin to medium distinct brown mottles of dark yellowish. The pH range of soil was from 5.47 to 5.63, organic matter 0.82%. The experimental area was flat, irrigated and drained, over flood level. Soil samples were collected from an experimental field from a depth of 0-15 cm. The Soil Resource and Development Institute (SRDI), Dhaka, carried out the analyses. Soil's physicochemical properties are shown (Appendix III).

### 3.5 Planting materials

For the current research work, 28 sweet gourd genotypes were used. The percentage of purity and germination was around 100 and 80 respectively. These genotypes have genetically pure and physically healthy seeds taken from the Bangladesh Agricultural Research Institute of (BARI Gazipur's) Plant Genetic Resource's Centre (PGRC). The genotypes' name and origin are given in (Table 1).

### 3.6 Design and layout of the experiment

The experiment was designed with three replications using the Randomized Comprehensive Block Design (RCBD). The genotypes were divided into the tank of each block of the experimental layout. The 28 genotypes of the experiments were allocated to each replication by random assignment. The distance between the cell and the cell was 3 m. The distance between two blocks remained 3 m.

### 3.7 Polybag preparation and raising seedling

The seeds have been dispersed into polybags for a higher germination percentage and healthy seedlings because of erratic precipitation during the period studied. When 22 days old, the seedlings will be transplanted in the pit into the main field. On 7 November 2019, seeds were planted before sowing for minutes with bavistin. (Rising of seedling in polybag Shown in plate 1.)

### 3.8 Land preparation

A number of snuffing and cross ploughing was used to prepare the plot for the experiment, followed by the loading and harrowing of a tractor and tiller in the second week of November 2019, weeds and other steel plots were carefully removed and properly lifted during a good month.

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

| Sl. No. | Genotype | BARI ACC Number | Origin |
|---|---|---|---|
| **1** | $G_1$ | BD- 232 | PGRC, BARI |
| **2** | $G_2$ | BD-264 | PGRC, BARI |
| **3** | $G_3$ | BD- 265 | PGRC, BARI |
| **4** | $G_4$ | BD- 266 | PGRC, BARI |
| **5** | $G_5$ | BD- 268 | PGRC, BARI |
| **6** | $G_6$ | BD- 269 | PGRC, BARI |
| **7** | $G_7$ | BD- 273 | PGRC, BARI |
| **8** | $G_8$ | BD- 274 | PGRC, BARI |
| **9** | $G_9$ | BD- 275 | PGRC, BARI |
| **10** | $G_{10}$ | BD- 277 | PGRC, BARI |
| **11** | $G_{11}$ | BD- 278 | PGRC, BARI |
| **12** | $G_{12}$ | BD- 279 | PGRC, BARI |
| **13** | $G_{13}$ | BD- 282 | PGRC, BARI |
| **14** | $G_{14}$ | BD- 288 | PGRC, BARI |
| **15** | $G_{15}$ | BD- 290 | PGRC, BARI |
| **16** | $G_{16}$ | BD- 306 | PGRC, BARI |
| **17** | $G_{17}$ | BD- 309 | PGRC, BARI |
| **18** | $G_{18}$ | BD- 2150 | PGRC, BARI |
| **19** | $G_{19}$ | BD- 2151 | PGRC, BARI |
| **20** | $G_{20}$ | BD- 2153 | PGRC, BARI |
| **21** | $G_{21}$ | BD- 2157 | PGRC, BARI |
| **22** | $G_{22}$ | BD-2174 | PGRC, BARI |
| **23** | $G_{23}$ | BD-2177 | PGRC, BARI |
| **24** | $G_{24}$ | BD-2196 | PGRC, BARI |
| **25** | $G_{25}$ | BD-2205 | PGRC, BARI |
| **26** | $G_{26}$ | BD-2212 | PGRC, BARI |
| **27** | $G_{27}$ | BARI-(v) 2 | PGRC, BARI |
| **28** | $G_{28}$ | BARI-(H) 1 | PGRC, BARI |

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

a)

(b)

(c)

(d)

(e)

(f)

**Plate1: Raising of seedling in polybag (a) seedling age 5 days (b) seedling age 6days (c) seedling age 7 days (d) seedling age 10 days (e) seedling age 15 days (f) seedling before transplanting day 21**

### 3.9 Pit preparation

The 55 cm x 55 cm x 50 cm pits were finally prepared in each block and spaced 3 m x 3 m. After final soil preparation. For 7 days in the sun, wells were kept open to kill harmful insects and micro-organisms. 5 mg cricket controller before preparing it for dibbling. Furadan was mixed with the soil in each pit.

### 3.10 Application of manure and fertilizers

During final preparation of the land, total cow dung, half of TSP and a third of MOP have been used on site. Applied in pit one week before transplant, remaining TSP and a third from MOP and whole gypsum and zinc oxide and one third of urea. Table 2 shows rest of urea and MOP in four installations at 20, 40 60- and 75-days following transplantation of the manure doses and 11 fertilizers used in the study.

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

| SL No. | Fertilizers/Manures | Dose |
|---|---|---|
| 1 | Cow dung | 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

The seed germination was completed within 10 days, and on 1 December 2020, the seedlings of various accessions were planted into a pit. Two seedlings were planted in each pot and the soil was firmly pressed by hand around the plant. On plate 2 A field view of plants and intercultural operations are shown in plate 2.

**(a)** **(b)** **(c)**

**(d)**

**Plate 2. Field view of plants after transplanting of seedlings (a) specific plant beside peat (b) seedling transplanting (c) mulching (d) field view after 21 days**

### 3.12 Intercultural Operation

#### 3.12.1 Thinning and gap filling

Just one healthy planting was maintained per pit, so it could be developed properly and crowded. For this, it was done whenever dilution and breakage filling is needed.

#### 3.12.2 Weeding and mulching

Several weeding and mulching tasks have been carried out as appropriate. At this stage, weeding has at the very first stage been performed to facilitate the aeration and reduce seedling growth and, following irrigation, mulch has been provided to prevent crust growth.

#### 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 whenever it's necessary.

#### 3.12.4 Pesticide application

During the planting process, tender leaves for the Malathion and Ripcord were attacked by a red sweet gourd beetle in the field. The fruit of the cucurbit is grown. Fly damaged the fruit seriously. MSGT and Pheromone bait were used in conjunction with seven ripcord powders for the protection of fruit flies.

### 3.13 Harvesting

The fruit takes about 7-10 days from the setting to the marketable stage. The result is that fruit has been harvested for the purposes of consumption based on horticultural maturity, size, colour, and age as the fruit grows quickly and is soon outdated in marketable terms. A sharp knife was taken on the fruits and care was taken to avoid twig injuries.

### 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 breadth was measured in three to five leaves in each germplasm in cm and average data was recorded.

#### 3.14.1.3 Internodes distance (cm)

Internode 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 character data have been analyzed multivariate. All study characters have been univariately analyzed for the individual character were used and the MSTAT-C program was estimated. The multiple range test (DMRT) was carried out by Duncan Conducted to test the differences between the mean genotypes for all characters. MSTAT-C has been also used to estimate the mean, scope and coefficient of variation (CV percent). Computers used multivariate analysis using software from GENSTAT 10.13 and Microsoft Excel2018 were used in four virtual techniques, namely Principal Component Analysis (PCA), Principal Coordination Analysis (PCO) and Cluster Analysis (CA) (CVA).

### 3.15.1.1 Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula

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

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,

$\sigma^2 g$ = Genotypic variance

EMS = Error mean sum of square

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

It used to calculate the genotypes and phenotypes for all possible combinations. The genotypic co-variance component between the two features was derived the same as the corresponding variance component with the phenotypic covariance component. The

components of covariance were used to calculate genotypic and phenotypic data. The relationship between the character pairs is the following:

Genotypic Correlation ($r_{gxy)} = \frac{\sigma^2 gxy}{\sqrt{\sigma^2 gx \sigma^2 gy}}$

Where,

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

$\sigma^2 gx$= Genotypic variance of the trait x

$\sigma^2 gy$ = Genotypic variance of the trait y

Phenotypic correlation ($r_{gxy}$) = $\frac{\sigma pxy}{\sqrt{\sigma^2 px \sigma^2 py}}$

Where,

$\sigma_{pxy}$= Phenotypic covariance between the traits and y

$\sigma^2 px$ = Phenotypic variance of the trait x

$\sigma^2_{py}$ = 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.

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

Where,

$\sigma^2 g$ = Genotypic variance

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

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

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

Where,

$\sigma^2 ph$ = Phenotypic variance

x = Population mean

**3. 15.1.4 Estimation of heritability**

Broad sense heritability was estimated by the following formula. $h^2_b\% = \frac{\sigma^2 g}{\sigma^2 ph}$

Where,

$h^2_b$= Heritability in broad sense

$\sigma^2 g$ = Genotypic Variance

$\sigma^2 ph$ = Phenotypic Variance

### 3.15.1.5 Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated using the formula.

Genetic advance (GA) = K. $h^2$ b. $\sigma_{ph}$

$$GA=K.\ \frac{\sigma^2 g}{\sigma^2 \sigma ph}\ .\ \sigma ph$$

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

$\sigma_{ph}$ = Phenotypic standard deviation

$h^2$b = Heritability in broad sense

$\sigma^2$= Genotypic variance

$\sigma^2 ph$ = Phenotypic variance

### 3.15.1.6 Estimation of genetic advance mean's percentage

Genetic advance as percentage of mean was calculated from the following formula

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

### 3.15.2 Multivariate analysis

General distance ($D^2$) and auxiliary analyzes assessed the genetic diversity of genotypes. The selection of parents from the Mahalanobis $D^2$ hybridization program is more reliable as necessary knowledge about a mass of features is available before the crossing. Biometric methods have enabled genetically diversified parents to be chosen as a parenting program by quantifying genetic diversity. The main component analysis, main component analysis and cluster analysis and Canonical Vector analysis (CVA), are efficient analysis of the components. Multivariate parameters 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)

One of the most important multivariable techniques is the analysis of the components used in order to examine interrelationships between several characters and to use the sum of squares and matrix of products for the characters. PCA therefore identifies linear combinations of a set of variables which maximize variation within them and shows a smaller number of dimensions to show the most original variability. The main components were therefore calculated from the correlation matrix and genotype ratings were obtained for the first components. (Which has the maximum variance accounting property) and subsequent latent roots components larger than unity. The contribution of different morphological characteristics to divergence from latent vectors of the first two main components is discussed.

### 3.15.2.2 Cluster analysis (CA)

Cluster analysis divides the genotypes in a set of mutually exclusive groups into several groups. A non-hierarchical classification was used for clustering. The algorithm is used in genstat to search for the optimal values of the selected criterion. Beginning with some initial grade 49 the algorithm divides the genotype into the number of groups required repeatedly. As long as that transfer improves the value of the criterion, genotypes are transferred from one group to another. If the criterion is not improved with a further transfer, the algorithm moves to a second stage, which examines the effect of swooping two different class genotype types etc.

### 3.15.2.3 Canonical vector analysis (CVA)

The linear combination of original variable canonical vector analysis (CVA) results in maximizing the relationship between group and group variation, giving original variables functions that can be used to discriminate between groups. Thus, a sequence of orthogonal transformations maximizes the ratio between group and group variations sequentially in this analysis. The canonical vectors are based on the roots and vectors of WB, where W is the covariance matrix of the groups and B the covariance matrix of the group.

### 3.15.2.4 Selection of varieties for future hybridization program

Divergence is typically used for the identification of different genotypes for purposes of hybridization. The combined genotypes are not so different from the genotypes in different groups. The most divergent genotypes of these different clusters are expressed by clusters that are separated by the largest statistical distance ($D^2$). For the efficient hybridization program Singh and Chaudhur varieties or lines have been selected (1985). In selecting genotypes for the hybridization program, the following points should be considered accordingly:

i. Choice of cluster from which genotypes are selected for use as parents

ii. Selection of particular genotypes from the selected clusters

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 28 sweet gourd accessions. The data on different yield and yield contributing characters of sweet gourd were computed and statistically analyzed. The results of the present study have been presented and discussed in this chapter under the following heading

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

## 4.1. Genetic variability and Heritability

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

### 4.1.1. Leaf length without petiole (cm

Leaf length without petiole showed significant variation among genotypes (AppendixV). The maximum leaf length was observed in G28 (21.17) and the minimum leaf length was observed in G1 (12.50) with mean value 14.873 (Appendix V). The difference between phenotypic variance (2.47) and genotypic variance (2.17) was low which shows less environmental influence. The genotypic coefficient of variation and phenotypic co-efficient of variation was observed 9.90% and 10.57% respectively. Heritability showed high (88%) with low genetic advance in percent of mean (19.10%) which indicate that this character was controlled by non-additive genes, the selection based on this character would not be effective (Table 3).

Fayeun *et al*. (2012) also found high heritability and moderate genetic advance in sweet gourd. The genotypic coefficient of variation (8.1%) and phenotypic coefficient of variation (9.51%).

Plate 3a and plate 3b plates showed morphological variation in leaf among different Sweet Gourd genotypes.

**Table 3. Estimation of genetic parameters for morphological and yield contributing characters related to yield**

| Yield attributing character | Environmental Variance | Genotypic Variance ($\delta^2g$) | Phenotypic Variance ($\delta^2p$) | Environmental Coefficient of Variation (ECV) | Genotypic Coefficient of Variation | Phenotypic Coefficient of Variation | Heritability (Broad Sense) | Genetic Advance | Genetic Advance as percentage at mean |
|---|---|---|---|---|---|---|---|---|---|
| LLWP | 0.30 | 2.17 | 2.47 | 3.70 | 9.90 | 10.57 | 88 | 2.84 | 19.10 |
| LB | 0.40 | 8.55 | 8.95 | 4.47 | 20.73 | 21.20 | 96 | 5.89 | 41.74 |
| ID | 0.09 | 2.60 | 2.69 | 4.06 | 21.66 | 22.03 | 97 | 3.26 | 43.85 |
| PLMF | 0.17 | 7.73 | 7.89 | 3.33 | 22.75 | 22.99 | 98 | 5.67 | 46.38 |
| PLFF | 0.13 | 1.90 | 2.03 | 3.03 | 11.71 | 12.10 | 94 | 2.75 | 23.36 |
| CP | 7.28 | 7.55 | 14.82 | 5.71 | 5.82 | 8.15 | 51 | 4.04 | 8.55 |
| NMF | 364.48 | 207.42 | 571.90 | 32.69 | 24.66 | 40.95 | 36 | 17.87 | 30.60 |
| NFF | 5.39 | 9.24 | 14.63 | 17.74 | 23.22 | 29.22 | 63 | 4.98 | 38.02 |
| FL | 0.64 | 1.72 | 2.36 | 11.00 | 18.06 | 21.14 | 73 | 2.31 | 31.77 |
| FB | 1.34 | 3.76 | 5.10 | 8.57 | 14.36 | 16.73 | 74 | 3.43 | 25.41 |
| PL | 0.04 | 0.15 | 0.19 | 6.49 | 12.53 | 14.12 | 79 | 0.70 | 22.93 |
| FPP | 0.61 | 0.45 | 1.07 | 23.94 | 20.58 | 31.57 | 43 | 0.91 | 27.64 |
| FW | 0.38 | 0.25 | 0.63 | 31.18 | 24.96 | 39.94 | 39 | 0.64 | 32.13 |
| FYPP | 8.79 | 4.27 | 13.07 | 45.05 | 31.40 | 54.92 | 33 | 2.43 | 36.99 |

** indicates significant at 0.01 probability level, * indicates significant at 0.05 probability level

LLWP=Leaf length without petiole (cm), LB= Leaf breadth (cm), ID= Internode distance (cm), PLMF =Pedicel length of male flower (cm), PLFF=Pedicel length of female flower (cm), CP=Chlorophyll percentage per plant, NMF= Number of male flower per plant, NFF= Number of female flower per plant, FL= Fruit length (cm), FB =Fruit Breadth (cm), PL =Pericarp length (cm), FPP= Fruit per plant (kg), FW =Fruit weight (kg), FYPP= Fruit Yield per plant (kg)

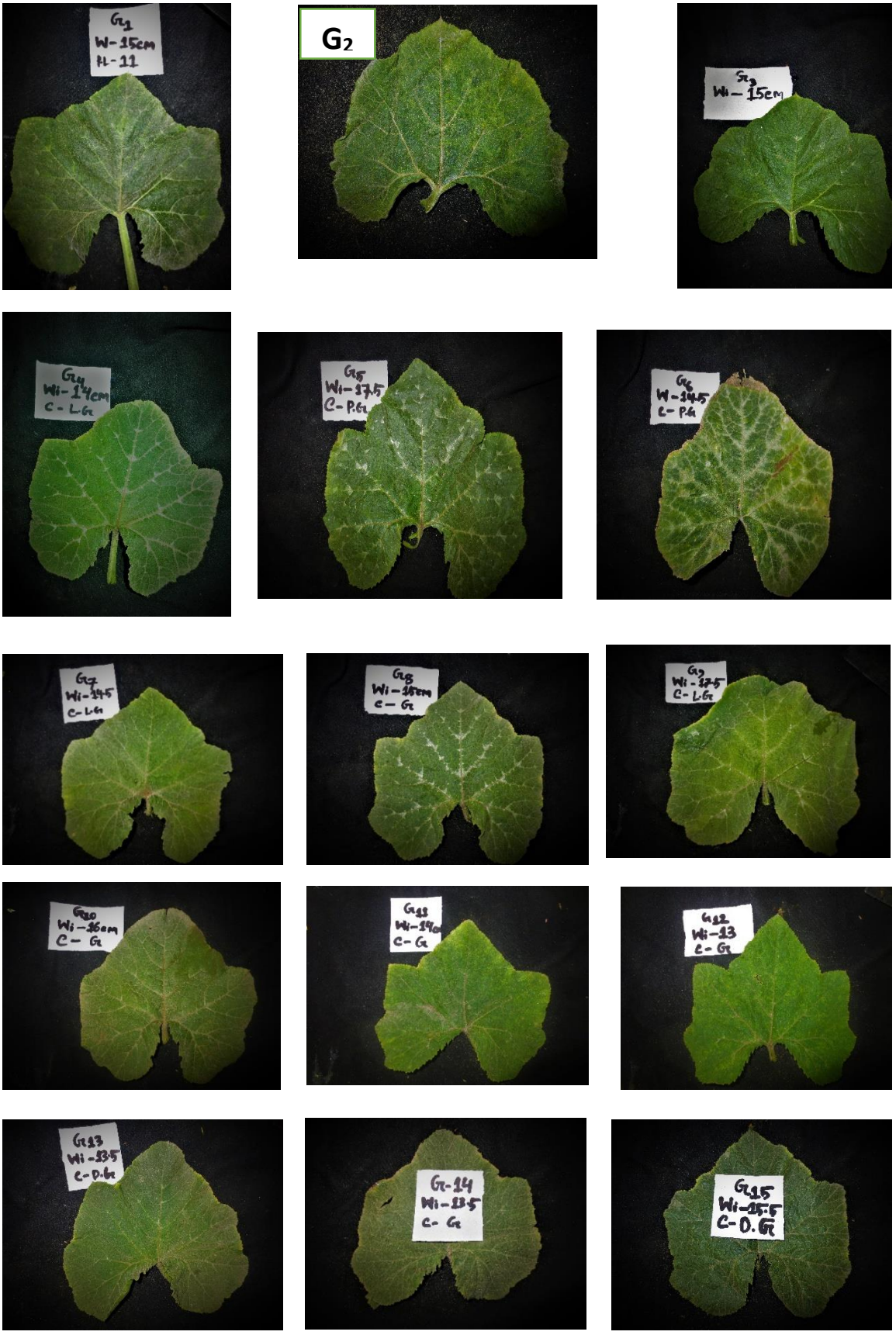


**Plate 3a. Showing morphological variation in leaf among different Sweet Gourd genotypes (G1-G15)**

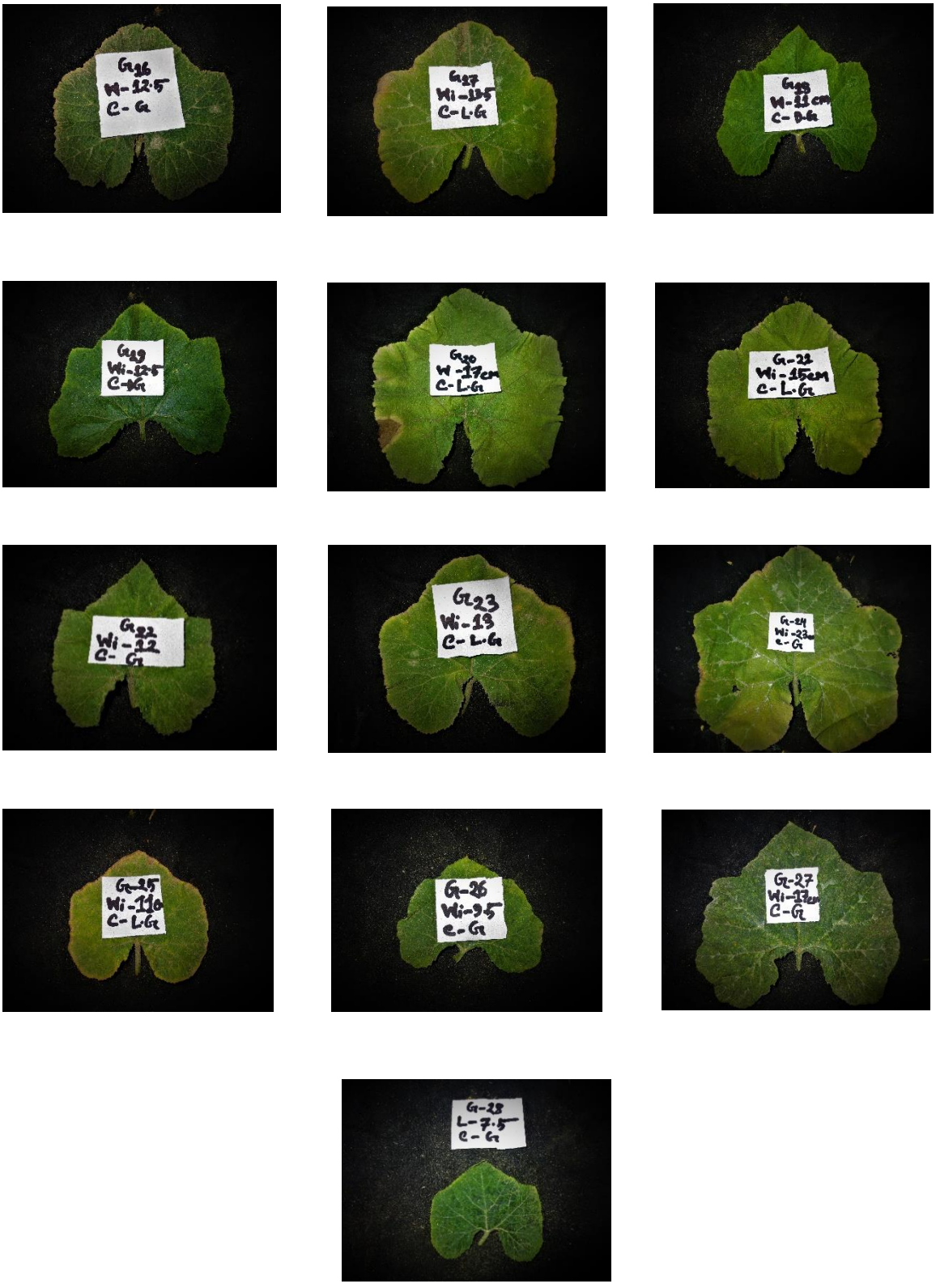


**Plate 3b. Showing morphological variation in leaf among different Sweet Gourd genotypes (G16-G28)**

### 4.1.2 Leaf breadth (cm)

Significant difference for leaf breadth observed among the bottle gourd genotype studied. (Appendix IV). The maximum leaf breadth was found (21.14) in G24 (BD-2196) and the minimum was recorded (5.44) in G2 (BD-264) with mean value 13.280 (Appendix V). The difference between phenotypic variance (8.95) and genotypic variance (8.55) showed low which indicate less environmental influence. The genotypic coefficient of variation and phenotypic co-efficient of variation was observed 20.73% and 21.20% respectively. Heritability showed high (96%) with high genetic advance in percent of mean (41.74) revealed that which indicated character was controlled by additive genes, the selection based on this character would be effective (Table 3).

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

Gaffar (2008) observed heritability in broad sense was high (94%) With high genetic advance (7.81) for this character in sponge gourd and also found the similar GCV (20.95%) and PCV (23.31%) in sponge gourd.

Plate 3a and plate 3b plates showed morphological variation in leaf among different Sweet Gourd genotypes.

### 4.1.3 Internode distance (cm)

Internode distance showed significant variation among genotype (Appendix IV). The maximum internodes distance was found 12.05 in G27 (BD 258) and the minimum was recorded 4.02 in G4 (BD 4587) with mean value 08.38 (Appendix V). The difference between phenotypic variance (2.69) and genotypic variance (4.06) was large which indicated high environmental influence. The genotypic coefficient of variation and phenotypic co-efficient of variation was observed 21.66% and 22.03% respectively. Heritability showed high (97%) with moderate genetic advance (3.26) and high genetic advance in percent of mean (43.85) revealed that character was controlled by additive genes the selection based on this character would be effective (Table 3).

Gaffar (2008) found high heritability (94%) and genetic advance in percentage of mean (40.45) for this trait in sponge gourd. Photograph showing variation of twig among different genotypes of sweet gourd. (Plate 4a & 4b)

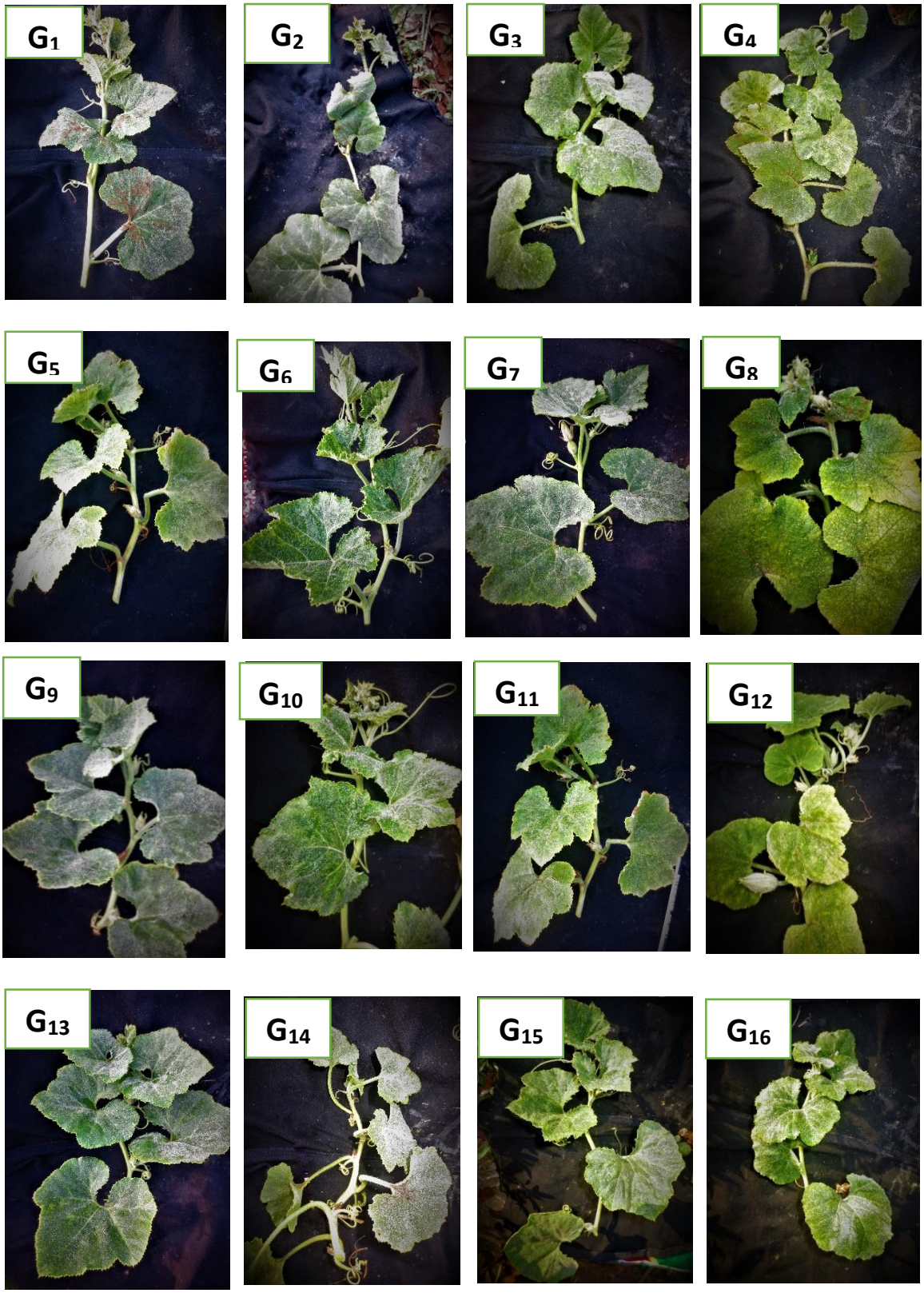


**Plate 4a. Showing morphological variation in twig among different Sweet Gourd genotypes (G1-G16)**

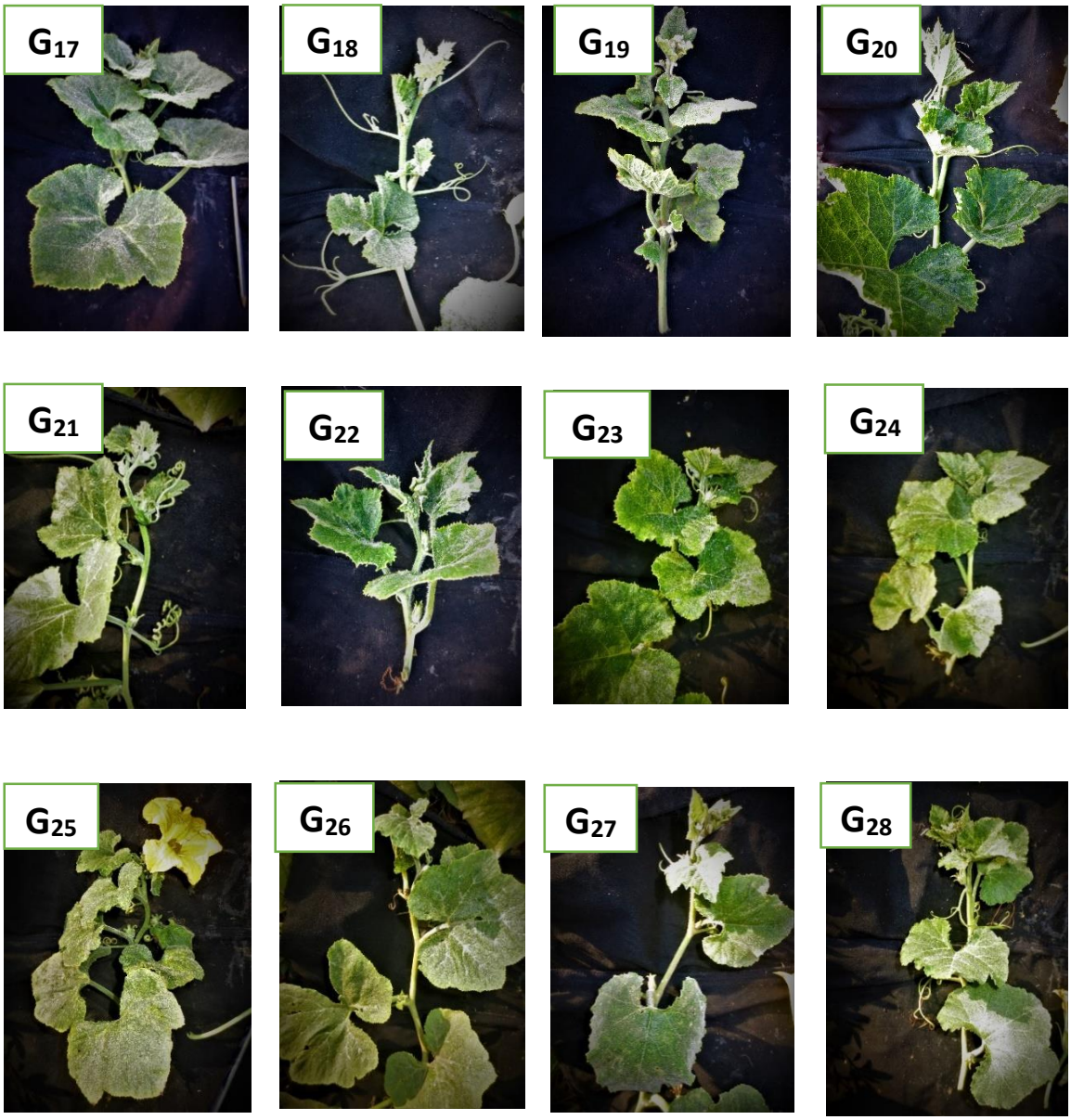


**Plate 4b. Showing morphological variation in twig among different sweet gourd genotypes (G17-G28)**

### 4.1.4 Pedicel length of male flower (cm)

Pedicel length of male flower showed significant variation among genotype (Appendix IV). The maximum pedicel length male flowers was found 16.87 in G24 and the minimum was recorded 6.27 in G1 (BD 288) with mean value 11.593 (Appendix V). The difference between phenotypic variance (7.89) and genotypic variance (7.73) showed low which indicate less environmental influence. The genotypic coefficient of variation and phenotypic co-efficient of variation was observed 22.75% and 22.99% respectively. Heritability showed highest (98%) with high genetic advance (5.67) and high genetic advance in percent of mean (46.38) revealed that character was controlled by additive genes the selection based on this character would be effective (Table 3).

Husna, A. (2009) found high heritability (99.55%) and genetic advance (4.25) for this trait in sweet gourd.

### 4.1.5 Pedicel length female flower (cm)

Pedicel length of female flower showed significant variation among genotypes (Appendix IV). The maximum female flowers pedicel length was found 8.63 in BD-2214 and the minimum was recorded 2.07 in BARI mistilmmra-l with mean value 4.45 (Appendix V). The difference between phenotypic variance (2.03) and genotypic variance (1.90) showed low which indicate less environmental influence. The genotypic coefficient of variation and phenotypic co-efficient of variation was observed 11.71% and 12.10% respectively. Heritability showed high (94%) with low genetic advance (2.75) and low genetic advance in percent of mean (23.36) revealed that character was controlled by non-additive genes the selection based on this character would not be effective (Table 3).

Husna,A. (2009) found that pedicel length of female flower shows low genetic advance (3.12) in sweet gourd.

Photograph showing variation of male and female flower among some genotypes of sweet gourd in Plate 5a and in plate 5b

### 4.1.6 Chlorophyll percentage

Chlorophyll percentage showed significant variation among genotypes (Appendix IV).The maximum Chlorophyll percentage was found 36.52 in G19 and the minimum was recorded

28.37 in G2 with mean value 33.326 (Appendix V). The difference between phenotypic variance (14.82) and genotypic variance (7.55) was high which indicate large environmental influence. The genotypic coefficient of variation and phenotypic co-efficient of variation was observed 5.82% and 8.15% respectively. Heritability showed high (51%) with high genetic advance (4.04) but low genetic advance in percent of mean (8.55) revealed that character was controlled by non-additive genes the selection based on this character would not be effective (Table 3).

### 4.1.7 Number of male flower

Number of male flower showed significant variation among genotype (Appendix IV). The maximum number of male flower was found G27 (70.25) and the minimum was recorded G12 (21.3) with mean value 42.45 (Appendix V). The difference between phenotypic variance (571.90) and genotypic variance (207.42) was high which indicate large environmental influence. The genotypic coefficient of variation and phenotypic co-efficient of variation was observed 24.66% and 40.95% respectively. Heritability showed low (36%) with high genetic advance (17.87) and low genetic advance in percent of mean (30.60) revealed that character was controlled by nonadditive genes the selection based on this character would not be effective (Table 3).

Husna, A. (2009) found that number of male flower showed low genetic advance (31.2) in sweet gourd.

The variation in flower morphology is shown in plate 5a and in 5b

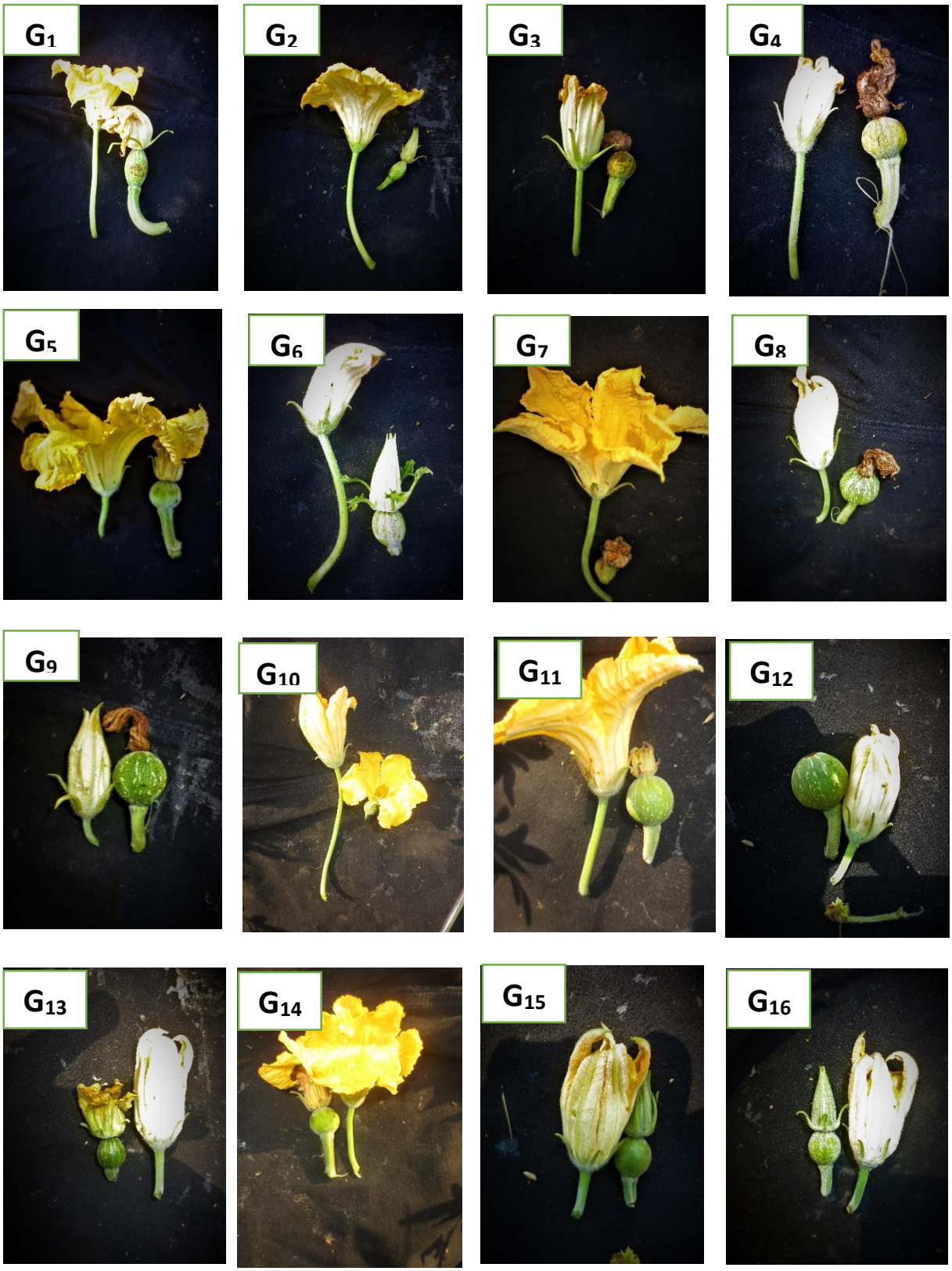


**Plate 5a. Showing morphological variation in flower among different Sweet Gourd genotypes ($G_1$-$G_{16}$)**


**Plate 5b. Showing morphological variation in flower among different sweet Gourd genotypes (G17-G28)**

### 4.1.8 Number of female flower

Number of female flower showed significant variation among genotype (Appendix IV). The maximum number of female flower was found 8.63 in G8 (17.12) and the minimum was recorded G1 (6.55) with mean value 12.302 (Appendix V). The difference between phenotypic variance (14.63) and genotypic variance (9.24) showed high which indicate large environmental influence. The genotypic coefficient of variation and phenotypic co-efficient of variation was observed 23.22% and 29.22% respectively. Heritability showed moderately high (63%) with high genetic advance (4.98) and moderately high genetic advance in percent of mean (38.02) revealed that character was controlled by additive genes the selection based on this character would be effective (Table 3).

Asmaul Husna (2009) found that number of female flower is 3.13-9 cm and low genetic advance (3.12) in sweet gourd.

### 4.1.9 Fruit length (cm)

Fruit length showed significant variation among genotype (Appendix IV). The maximum fruit length was found 10.47 in G28 and the minimum was recorded 4.56 in G6 with mean value 7.160 (Appendix V). The difference between phenotypic variance (2.36) and genotypic variance (1.72) showed low which indicate less environmental influence. The genotypic coefficient of variation and phenotypic co-efficient of variation was observed 18.06% and 21.14% respectively. Heritability was high (73%) with low genetic advance (2.31) and high genetic advance in percent of mean (31.77) revealed that character was controlled by additive genes the selection based on this character would be effective (Table 3).

Banik (2003) found the highest phenotypic co-cfficicnt of variation for fruit length. Mathew and Khader (1999) also reported high heritability for fruit length in snake gourd.

Photograph showing variation of fruit length among some genotypes of sweet gourd in Plate 6a and 6b.

### 4.1.10 Fruit Breadth (cm)

Fruit Breadth showed significant variation among genotype (Appendix IV). The maximum fruit breadth was found 10.47 in G28 and the minimum was recorded 4.56 in G23 with mean value 7.160 (Appendix V). The difference between phenotypic variance (5.10) and

genotypic variance (3.76) showed high which indicate large environmental influence. The genotypic coefficient of variation and phenotypic co-efficient of variation was observed 14.36% and 16.73% respectively. Heritability showed high (74%) with moderately high genetic advance (3.43) and moderately high genetic advance in percent of mean (25.41) revealed that character was controlled by additive genes the selection based on this character would be effective (Table 3).

Banik (2003) found the highest phenotypic co-cfficicnt of variation for fruit length. Mathew and Khader (1999) also reported high heritability for fruit length in snake gourd, Rahman *et al*. (1991) indicated minimum differences between GCV and pcv in sweet gourd for fruit breadth.

### 4.1.11 Pericarp length

Pericarp length showed significant variation among genotype (Appendix IV). The maximum Pericarp length was found 5.85 in G27 and the minimum was recorded 2.6 in G1 with mean value 3.07 (Appendix IV). The difference between phenotypic variance (0.19) and genotypic variance (0.15) showed low which indicate less environmental influence. The genotypic coefficient of variation and phenotypic co-efficient of variation was observed 12.53% and 14.12% respectively. Heritability showed high (79%) with low genetic advance (0.70) and moderately high genetic advance in percent of mean (22.93) revealed that character was controlled by additive genes the selection based on this character would be effective (Table 3).

### 4.1.12 Fruit per plant

Fruit Breadth showed significant variation among genotype (Appendix IV). The maximum fruit per plant was found 5.01 kg in BD-2150 and the minimum was recorded 1.67 kg in BARI mistikumra-1 with mean value 3.273 (Appendix IV). The difference between phenotypic variance (1.07) and genotypic variance (0.45) showed moderately high which indicate large environmental influence. The genotypic coefficient of variation and phenotypic co-efficient of variation was observed 20.58% and 31.57% respectively. Heritability showed high (43%) with moderately high genetic advance (0.91) and moderately high genetic advance in percent of mean (27.64) revealed that character was controlled by additive genes the selection based on this character would be effective (Table 3).

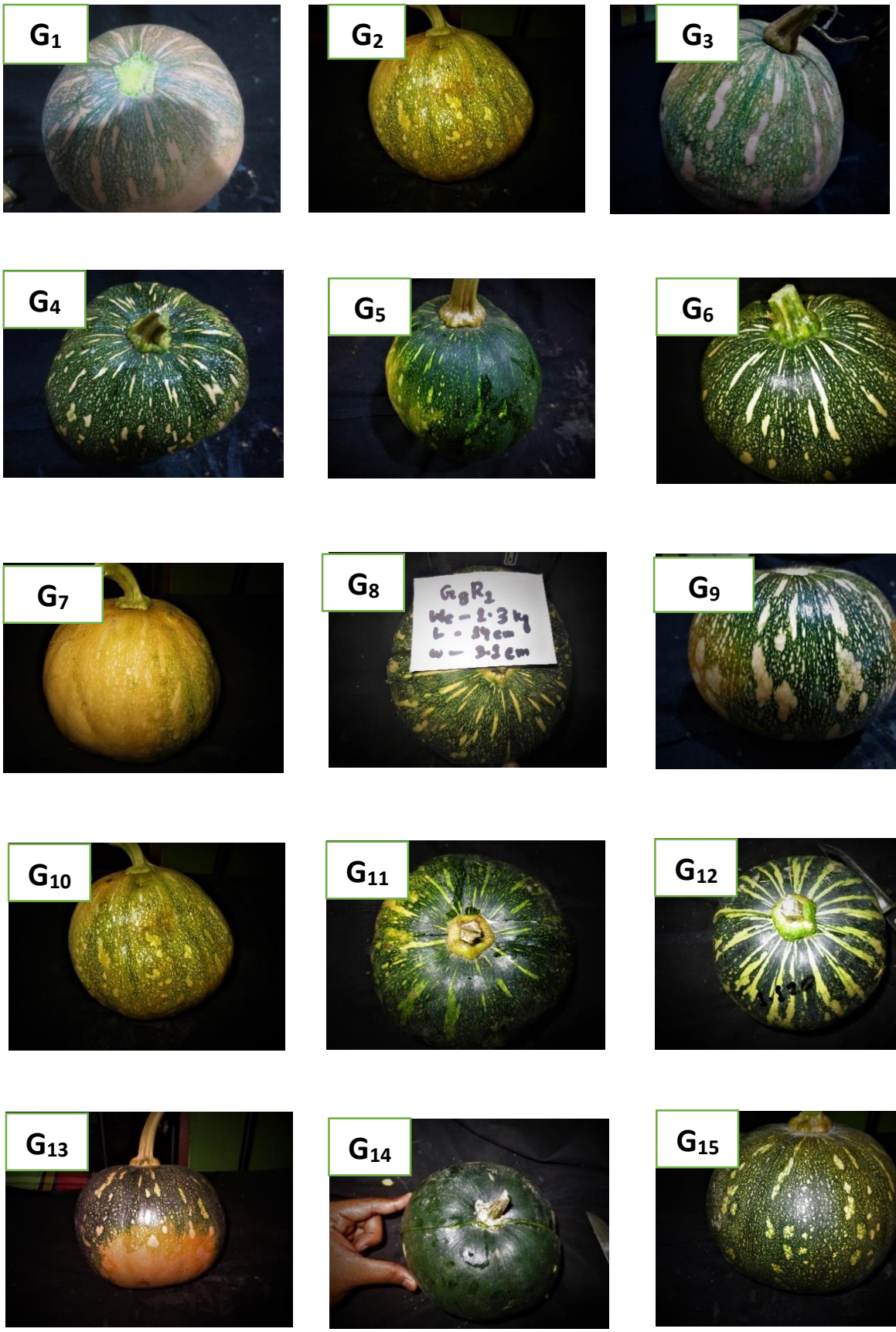


**Plate 6a. Showing morphological variation in fruit among different sweet gourd $G_1$-$G_{15}$**

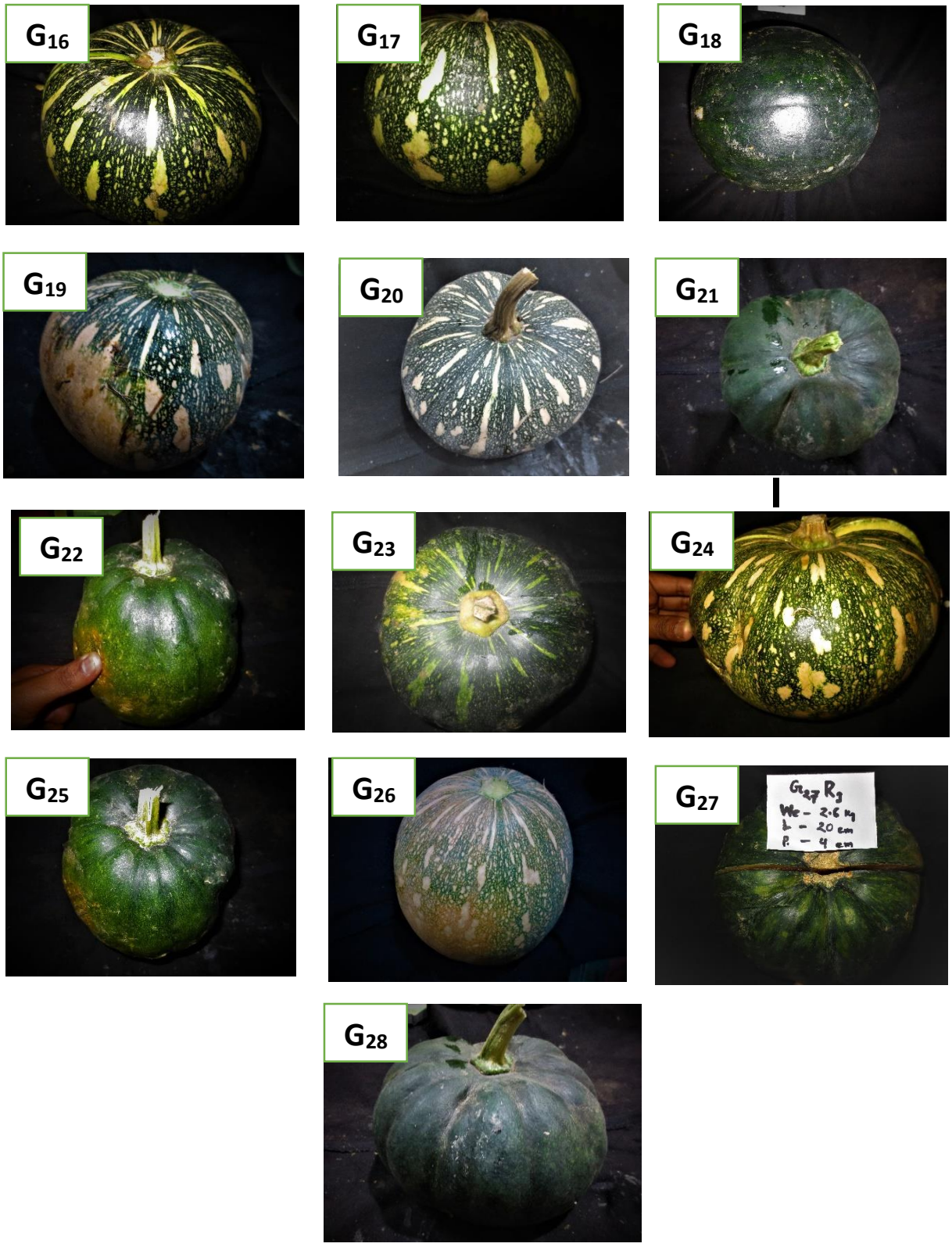


**Plate 6b. Showing morphological variation in fruit among different Sweet gourd $G_{16}$-$G_{28}$**

Kumaran et al. (1997) reported similar types of result which confirmed the present findings. This result is in consonance with the findings of Chowdhury and Sharma (2002) in ridge gourd and Rumaran et al. (1997) pumpkin. Rahman et al. (1986) also found the similar result in sweet gourd.

### 4.1.13 Fruit weight (kg)

Fruit weight showed significant variation among genotype (Appendix IV). The maximum weight per fruit was found 5.01 kg in G27 and the minimum was recorded 1.67 kg in G1 with mean value 3.33 (Appendix V). The difference between phenotypic variance (0.63) and genotypic variance (0.25) showed low which indicate less environmental influence. The genotypic coefficient of variation and phenotypic co-efficient of variation was observed 24.96% and 39.94% respectively. Heritability showed high (39%) with low genetic advance (0.64) and moderately high genetic advance in percent of mean (32.13) revealed that character was controlled by additive genes the selection based on this character would be effective (Table 3).

Saha *et al*. (1992) found similar GCV (39.55) and PCV (41.00) for the fruit weight in pumpkin.

Kumaran *et al*. (1997) reported similar types of result which confirmed the present findings.

### 4.1.14 Yield per plant (kg)

Yield per plant showed significant variation among genotype (Appendix IV) The highest yield per plant was found 16.321 kg in G12 followed by BD-2151 (9.41kg), BD-266 (8.14) and BD-2150 (7.15) and the minimum was recorded 3.16 kg in G15 with mean value 6.58 (Appendix V). The difference between phenotypic variance (13.07) and genotypic variance (4.27) showed high which indicate large environmental influence. The genotypic coefficient of variation and phenotypic co-efficient of variation was observed 31.40% and 54.92% respectively. Heritability showed high (33%) with low genetic advance (2.43) and high genetic advance in percent of mean (36.99) revealed that character was controlled by additive genes the selection based on this character would be effective (Table 3).

Narayanankutty *et al*. (2006) fruit yield exhibited high values of heritability and genetic gain indicating additive gene effects are important in determining the character.

Pandey et al. (2002) observed high degree of variability for yield per plant and higher estimate of heritability and genetic advance was observed for yield per plant.

### 4.2. 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. 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)

It observed that leaf length without petiole showed significant and positive correlation with pedicel length of female flower (g=0.609, p=0.584), number of female flower (g=0.374, p=0.308), number of male flower (g=0.442, p=0.237), pedicel length of male flower (p=0.349), leaf breadth (g=0.341, p=0.332), Pericarp length (p=0.217). It showed non-significant and positive correlation with internode distance (g=0.093, p=0.091), Pericarp length (g=0.301), pedicel length of male flower (g=0.369), fruit weight ( p=0.024), with number of leaf breath (g=0.341), fruit length ( g=0.062), fruit breadth (cm) (g=0.084, p=0.097), pedicel length of male flower (g=0.369), fruit per plant (g=0.209, p=0.081), fruit yield per plant (g=0.056, p=0.050), fruit weight (g=0.047), It found a non-significant but negative correlation with Chlorophyll percentage (p= -0.355, g= -0.134), fruit weight (g=-0.056) and fruit length (p=-0.007) (Table 4).

Husna *et al*. (2014) also reported leaf length without petiole was positively insignificant correlated with leaf breadth.

## Table 4. Coefficients of genotypic and phenotypic correlation among different yield components of 28 sweet gourd genotypes

| | | LLWP | LB | ID | PLMF | PLFF | CP | NMF | NFF | FL | FB | PL | FPP | FW |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| LB | Rg | **0.341** | | | | | | | | | | | | |
| | rp | **0.332 **** | | | | | | | | | | | | |
| ID | rg | **0.093** | **0.168** | | | | | | | | | | | |
| | rp | **0.091** | **0.163** | | | | | | | | | | | |
| PLMF | rg | **0.369** | **0.082** | **-0.116** | | | | | | | | | | |
| | rp | **0.349 **** | **0.076** | **-0.122** | | | | | | | | | | |
| PLFF | rg | **0.609 **** | **0.730**** | **0.28** | **0.651 **** | | | | | | | | | |
| | rp | **0.548 **** | **0.698 **** | **0.276 *** | **0.621 **** | | | | | | | | | |
| CP | rg | **-0.355** | **0.099** | **-0.107** | **-0.250** | **-0.093** | | | | | | | | |
| | rp | **-0.134** | **0.052** | **-0.054** | **-0.165** | **-0.088** | | | | | | | | |
| NMF | rg | **0.442 *** | **0.566 **** | **-0.234** | **0.256** | **0.461 *** | **-0.092** | | | | | | | |
| | rp | **0.237 *** | **0.378 **** | **-0.132** | **0.171** | **0.291 **** | **-0.216 *** | | | | | | | |
| NFF | rg | **0.374 *** | **0.029** | **0.038** | **0.233** | **0.234** | **-0.033** | **0.021** | | | | | | |
| | rp | **0.308 **** | **0.053** | **0.043** | **0.182** | **0.199** | **0.007** | **0.095** | | | | | | |
| FL | rg | **0.062** | **0.063** | **-0.244** | **0.002** | **-0.067** | **0.131** | **0.362** | **-0.382 *** | | | | | |
| | rp | **-0.007** | **0.026** | **-0.23 *** | **0.001** | **-0.017** | **-0.002** | **0.211** | **-0.272 *** | | | | | |
| FB | rg | **0.084** | **0.115** | **-0.015** | **0.174** | **0.163** | **-0.135** | **0.316** | **-0.243** | **0.297** | | | | |
| | rp | **0.097** | **0.127** | **-0.034** | **0.148** | **0.136** | **-0.013** | **0.075** | **-0.080** | **0.183** | | | | |
| PL | rg | **0.301** | **-0.162** | **0.029** | **0.304** | **0.149** | **-0.272** | **-0.08** | **0.139** | **0.136** | **0.457*** | | | |
| | rp | **0.217 *** | **-0.165** | **0.031** | **0.279 *** | **0.123** | **-0.149** | **0.020** | **0.102** | **0.108** | **0.380**** | | | |
| FPP | rg | **0.209** | **0.109** | **0.179** | **-0.164** | **0.150** | **-0.044** | **0.057** | **0.087** | **0.001** | **0.477 *** | **0.325** | | |
| | rp | **0.081** | **0.033** | **0.108** | **-0.115** | **0.114** | **-0.088** | **-0.03** | **-0.029** | **-0.006** | **0.209** | **0.209** | | |
| FW | rg | **-0.056** | **0.006** | **0.348** | **0.149** | **0.196** | **0.397 *** | **-0.312** | **-0.168** | **0.221** | **-0.062** | **0.509 **** | **-0.152** | |
| | rp | **0.024** | **0.010** | **0.192** | **0.075** | **0.092** | **0.089** | **-0.112** | **0.073** | **0.002** | **0.087** | **0.161** | **0.024** | |
| FYPP | rg | **0.056** | **0.049** | **0.391*** | **0.030** | **0.249** | **0.303** | **-0.233** | **-0.136** | **0.185** | **0.318** | **0.669**** | **0.585**** | **0.721**** |
| | rp | **0.050** | **0.086** | **0.196** | **-0.004** | **0.124** | **0.008** | **-0.094** | **0.036** | **-0.007** | **0.222*** | **0.253*** | **0.588 **** | **0.807 **** |

****. Correlation is significant at the 0.01 level (2-tailed).; *. Correlation is significant at the 0.05 level (2-tailed).**

LLWP= Leaf length without petiole (cm), LB= Leaf breadth (cm), D= Internode distance (cm), PLMF= Pedicel length of male flower (cm), PLFF= Pedicel length of female flower (cm), CP= Chlorophyll percentage per plant, NMF= Number of male flower per plant, NFF= Number of female flower per plant, FL= Fruit length (cm), FB= Fruit Breadth (cm), PL= Pericarp length (cm), FPP= Fruit per plant (kg), FW =Fruit weight (kg), FYPP= Fruit Yield per plant (kg)

### 4.2.2 Leaf breadth (cm)

It observed that leaf breath showed significant and positive correlation with pedicel length of female flower (g=0.730, p=0.0.698), number of female flower (g=0.374, p=0.308), number of male flower (g=0.566, p=0.378). It showed non-significant and positive correlation with internode distance (g=0.168, p=0.163), pedicel length of male flower(g=0.082, p=0.076) , Chlorophyll percentage per plant (g=0.099, p=0.052), number of female flower per plant (g=0.029, p=0.0.053), fruit length (g=0.063, p=0.026), fruit breadth (g=0.115, p=0.127), fruit per plant (g=0.109, p=0.033), fruit weigh (g=0.006, p=0.010), fruit yield per plant (g=0.049, p=0.086) It found a non-significant but negative correlation with pericarp length (g=0.168, p=0.163) (Table 4). Husna *et al*. (2014) also reported leaf breadth was positively insignificant correlated with fruit yield per plant.

### 4.2.3 Internode distance (cm)

It observed that internode distance showed significant and positive correlation with pedicel length of female flower (p=0.276), fruit yield per plant (g=0.391). It also observed a significant but negative correlation with fruit length (-0.231). It showed non-significant and positive correlation with number of female flower (g=0.038, p=0.043), internode distance (g=0.168, p=0.163), pedicel length of male flower(g=0.082, p=0.076), Pericarp length (g=0.029, p=0.031).pedicel length of female flower (g=0.283) , number of female flower per plant (g=0.029, p=0.0.053), fruit length (g=0.063, p=0.026), fruit per plant (g=0.179, p=0.108), fruit weigh (g=0.348, p=0.192), fruit yield per plant (p=0.196) It found a non-significant but negative correlation with Chlorophyll pedicel length of female flower (g= -0.116, p=0.-122), Chlorophyll percentage per plant (g= -0.107, p=0.-054), number of male flower (g= -0.234, p= -0.132), fruit breadth (g= -0.015, p= -0.034),fruit length (p= -0. 244)

Husna *et al*. (2014) also reported internode distance was positively insignificant correlated with internode distance.

### 4.2.4 Pedicel length of male flower (cm)

It observed that pedicel length of male flower showed significant and positive correlation with pedicel length of female flower (g=0.651, p=0.621), number of female flower (g=0.374, p=0.308), Pericarp length (p=0.279). It showed non-significant and positive

correlation with number of male flower (g=0.256, p=0.171), number of female flower per plant (g=0.233, p=0.182), fruit length (g=0.002, p=0.001), fruit breadth (g=0.174, p=0.148), Pericarp length (g=0.304, p=0.279), fruit weigh (g=0.149, p=0.075), fruit yield per plant (g=0.030), It found a non-significant but negative correlation with fruit per plant (g=-0.164, p=-0.115), Chlorophyll percentage per plant (g=-0.250, fruit yield per plant (p=-0.004) (Table 4). Husna *et al*. (2014) also reported pedicel length of male flower was positively insignificant correlated with fruit yield per plant.

### 4.2.5 Pedicel length of female flower (cm)

It observed that pedicel length of female flower showed significant and positive correlation with number of male flower (g=0.461, p=0.291), Pericarp length (p=0.279). It showed non-significant and positive correlation with number of male flower (g=0.256, p=0.171), number of female flower per plant (g=0.234, p=0.199), fruit breadth (g=0.163, p=0.136), Pericarp length (g=0.149, p=0.123), fruit per plant (g=0.150, p=0.114), fruit weigh (g=0.196, p=0.092), fruit yield per plant (g=0.249,p=0.124), It found a non-significant but negative correlation with, Chlorophyll percentage per plant (g=-0.093,p=-0.088), fruit length (g=-0.067, p=-0.017) (Table 4). Husna *et al*. (2014) also reported pedicel length of female flower was positively insignificant correlated with fruit yield per plant.

### 4.2.6 Chlorophyll percentage

It observed that Chlorophyll percentage showed significant and positive correlation with fruit weigh (g=0.196), It also observed a significant but negative correlation with number of male flower (p=-0.216), Pericarp length (p=0.279). It showed non-significant and positive correlation with number of male flower (g=0.256, p=0.171), number of female flower per plant (p=0.007), fruit length (g=0.131), fruit weigh (p=0.089), fruit yield per plant (g=0.303,p=0.008), It found a non-significant but negative correlation with, fruit breadth (g=-0.135, p=-0.013), Pericarp length (g=-0.272, p=-0.149), fruit per plant (g=-0.044, p=-0.088), number of male flower (p=-0.092), number of female flower per plant (g=-0.033), Chlorophyll percentage per plant (g=-0.093,p=-0.088), fruit length (p=-0.002) (Table 4).

Prasana *et al*. (2002) showed significant and positive correction between Chlorophyll percentage and yield per plant.

### 4.2.7 Number of male flower

It observed that number of male flower showed non-significant and positive correlation with number of female flower per plant (g=0.021, p=0.095), fruit breadth (g=0.316, p=0.075), fruit length (g=0.362, p=0.211), Pericarp length (p=0.020), fruit yield per plant (g=0.057), It found a non-significant but negative correlation with fruit weigh (p=-0.312, g=-0.112), fruit yield per plant (p=0.-094), Pericarp length (g=-0.082), fruit per plant (p=-0.032).

Husna *et al*. (2014) also reported number of male flower was negatively insignificant correlated with fruit yield per plant.

### 4.2.8 Number of female flower

It observed that number of female flower showed significant and negative correlation with fruit length (p=-0.382, g=-0.272) it also showed nonsignificant and positive correlation with Pericarp length (g=0.139, p=0.102), fruit per plant (g=0.087), fruit weight (p=0.073), fruit yield per plant (p=0.036) It found a non-significant but negative correlation with fruit breath (g=-0.243, p=-0.080) fruit per plant (p=-0.029), fruit weight (g=-0.168), fruit yield per plant (g=-0.136)

Narayankutty *et al*. (2006) have reported strong negative correlation between fruit yield and number of female flower snake gourd fruit length.

Chowdhury and Sarma (2002) showed negative correlation between number of female flower and fruit yield.

### 4.2.9 Fruit length (cm)

The fruit length shows non-significant but positive correlation with fruit breadth (p=0.297, g=0.183), Pericarp length (p=0.136, g=0.108), and fruit weight (p=0.001). fruit weight (p=0.221, g=0.002), fruit yield per plant (g=0.185). also found non-significant negative correlation with fruit yield per plant (p=-0.007), fruit per plant (p=-0.006)

Narayankutty *et al*. (2006) reported positive correlation (p=0.321, g=0.163) of yield with snake gourd's fruit length.

Khan *et al* (2009) found positive correlation with fruit weight.

### 4.2.10 Fruit breadth (cm)

This charecter showed significant positive correlation with the Pericarp length (p=0.457, g=0.380), fruit per plant (p=0.477), fruit yield per plant(p=0.222), also showed nonsignificant but positive correlation with fruit per plant (p=0.209) and fruit yield per plant(g=0.318), fruit weight (p=0.087). also found non-significant negative correlation with fruit weight (g=-0.062) (Table 4) Narayankutty *et al.* (2006), Khan *et al.* (2009),. found the weight of fruit to be positive for yield. Husna *et al.* (2014) Similar results were found in bottle gourd, too.

Chowdhury and Sarma (2002) studied cultivar *luffa acutangula* and noted the possibility to improve yield per hectare by selecting individual weights of the fruits. In ridge gourd (*Luffa acutangula*)

### 4.2.11 Pericarp length (cm)

The character was a highly positive significant positive correlation with the fruit weight (g=0.509) and fruit yield per plant (p=0.669, g=0.253), also shows non-significant but positive relationship with fruit per plant (p=0.325, g=0.209), fruit weight (p=0.161) indicates that by the increasing of Pericarp length increase the fruit weight, fruit per plant and fruit yield per plant (Table 4).

Kumaresan *et al*. (2006) showed positive correlation with the fruit weight on 20 genotypes of sweet gourd.

### 4.2.12 Fruit per plant (cm):

Fruit per plant showed significant positive correlation with fruit yield per plant (p=0.585, g=0.588) and positive but non-significant relationship with fruit weight (p=0.325,) and non-significant negative correlation with fruit weight (p=-0.152) (Table 4).

### 4.2.13 Fruit weight (kg)

Fruit weight shows significant positive correlation fruit yield per plant (p=0.721, g=0.807) at both phenotypic and genotypic level which indicated when increase the fruit weight obviously increase the fruit yield per plant (Table 4).

## 4.3 Path co- efficient analysis

Portioning of genotypic correlation of different genotype, yield and its contributing traits in sweet gourd are shown in Table 5 and discussed character wise as follows.

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)

### 4.3.1 Leaf length without petiole (cm)

Leaf length without petiole showed negative direct effect (- 0.011) on yield (Table 5). This character showed positive indirect effect on Pericarp length (- 1.930), fruit weight (0.024), fruit per plant (0.051), number of male flower (0.079), Chlorophyll percentage per plant (0.015), fruit breadth (0.029), fruit length (0.003).This character also shows negative indirect effect on yield via pedicel length of male flower (-2.067), leaf breadth (-0.044), pedicel length of female flower (-0.065), internode distance ( -0.011), number of female flower per plant (-0.031), which were contributed to result insignificant positively genotypic correlation with fruit yield per plant (0.050). 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 (cm)

Leaf breadth showed negatively direct effect (- 0.013) on yield (Table 5). it showed positive indirect effect followed by fruit weight (0.081), fruit per plant (0.023), number of male flower (0.013), fruit breadth (0.027), fruit breadth (0.035), and this traits also produced negative indirect effect on yield via length without petiole (-0.041), internode distance(-0.019), pedicel length of male flower (-4.725), pedicel length of female flower (-0.083), Chlorophyll percentage (-0.057), number of female flower per plant (-0.052), fruit length (-0.075), Pericarp length (-1.64), pedicel length of male flower (-5.907), Pericarp length ( - 0.025), Leaf length without petiole (- 0.011) which were contributed to result insignificant positively genotypic correlation with fruit yield per plant (0.086). Li *et al*. (1997) also found similar result in cucumber for their trait. Shamima Sultana (2011) also found negative direct effect (-0.034) on yield.

### 4.3.3 Internode distance (cm)

Internode distance showed negative direct effect (- 0.011) on yield (Table 5). It showed positive indirect effect through followed by pedicel length of male flower (6.498),

Chlorophyll percentage (0.045) fruit length (0.053), Pericarp length (9.632), fruit per plant (0.067), fruit weight (0.160), number of male flower (0.036), fruit breadth (0.027), fruit breadth (0.01), and. The character also produced negative indirect effect on yield via pedicel length of female flower (-0.034), leaf length without petiole (- 0.012), leaf breadth (-0.023) number of female flower per plant (-0.042), fruit breadth (-0.022) which were contributed to result insignificant positive genotypic correlation with fruit yield per plant (0.196). Lie *et al*. (1997) also found similar result in cucumber for their trait.

Sultana, S. (2011) also found negative direct effect (-0.041) on yield.

### 4.3.4 Pedicel length of male flower (cm)

Pedicel length of male flower showed highest negative direct effect (-5.907) on yield (Table 5). this character showed positive indirect effect through on internode distance (0.013), Chlorophyll percentage per plant (0.018), number of male flower per plant (0.057) fruit length (0.032), fruit breadth (0.039), Pericarp length (2.692), fruit weight (0.064) the character also produced negative indirect effect on yield via, Leaf length without petiole (- 0.041), Leaf breadth (-0.010), pedicel length of female flower (-0.074), number of female flower per plant (-0.019), fruit per plant (-0.062) which were contributed to result insignificant positive genotypic correlation with fruit yield per plant (-0.004). Lie *et al*. (1997) also found similar result in cucumber for their trait.

Sultana, S. (2011) also found negative direct effect (-3.041) on yield.

### 4.3.5 Pedicel length of female flower (cm)

Pedicel length of female flower showed negative direct effect (-0.012) on yield (Table 5). It shows positive indirect effect Chlorophyll percentage per plant (0.091), number of male flower per plant (0.011), fruit length (0.026), fruit breadth (0.040), Pericarp length (1.061), fruit per plant (0.067), fruit weight (0.080) and. The character also produced negative indirect effect on yield via, leaf length without petiole (-0.065), leaf breadth (-0.092), internode distance (-0.031), pedicel length of male flower (-3.662), number of female flower per plant (-0.021), pedicel length of male flower (-5.907), Pericarp length (- 0.025), Leaf breadth (-0.013) which were contributed to result insignificant positive genotypic correlation with fruit yield per plant (0.123). Lie *et al*. (1997) also found similar result in cucumber for their trait. Sultana, S. (2011) also found negative direct effect (-0.043) on yield.

### 4.3.6 Chlorophyll percentage

Chlorophyll Percentage per plant showed negative direct effect (-0.11) on yield (Table 5). It shows positive indirect effect on leaf length without petiole (0.015), internode distance (0.044),pedicel length of male flower (9.451), pedicel length of female flower (0.095), number of female flower per plant (0.256), fruit length (0.036), fruit breadth (0.025), fruit weight(0.072) Pericarp length (9.671) this character however showed highest positive indirect effect through followed by fruit weight (0.802), fruit per plant (0.565), number of male flower (0.036), fruit breadth (0.027), fruit breadth (0.01), and. The character also produced negative indirect effect on yield via, leaf breadth (-0.065), number of male flower per plant (-0.079), Pericarp length (-1.55), fruit per plant (-0.045), which were contributed to result insignificant positive genotypic correlation with fruit yield per plant (0.076). Lie *et al*. (1997) also found similar result in cucumber for their trait. Shamima, S., (2011) also found negative direct effect (-0.032) on yield.

### 4.3.7 Number of male flowers per plant

Number of male flower showed positive direct effect on yield (0.036) (Table 5). It shows positive indirect effect through followed by internode distance (0.016), Chlorophyll percentage per plant (0.024), fruit breadth (0.013), Pericarp length (0.3.871) this character also produced negative indirect effect on yield via, leaf length without petiole (-0.026), leaf breadth (-0.048), pedicel length of male flower (-9.451), Pedicel length of female flower (-0.034), Pericarp length (- 0.011), fruit length ( -0.051), fruit per plant (-0.028), fruit weight (-0.091) which were contributed to result insignificant positive genotypic correlation with fruit yield per plant (-0.094). Li *et al*. (1997) also found similar result in cucumber for their trait. Shamima, S., (2011) also found positive direct effect (0.052) on yield.

### 4.3.8 Number of female flowers per plant

Number of female flower showed negative direct effect on yield (-0.011) (Table 5). It shows positive indirect effect on Chlorophyll percentage per plant (0.034), number of male flower per plant (0.036), fruit length (0.068), Pericarp length (1.061), fruit weight (0.056) and. The character also produced negative indirect effect on yield via, leaf length without petiole (-0.036), leaf breadth (-0.066), internode distance (-0.044), pedicel length of male flower (-1.064), pedicel length of female flower (-0.024) fruit per plant (-0.016) fruit breadth (-0.024) which were contributed to result insignificant positive genotypic

correlation with fruit yield per plant (0.035). Li *et al.* (1997) also found similar result in cucumber for their trait. Shamima, S., (2011) also found negative direct effect (-0.0132) on yield.

### 4.3.9 Fruit length

Fruit length showed negative direct effect on yield (- 0.025) (Table 5). Fruit length shows positive indirect effect on leaf length without petiole (0.051) leaf breadth (0.051), internode distance (0.023), pedicel length of male flower (1.002), pedicel length of female flower (0.012), Chlorophyll percentage per plant (0.052), number of male flower per plant (0.072), number of female flower per plant(0.028), fruit breadth (0.051), Pericarp length (8.701), fruit per plant (0.013), fruit weight (0.009) The character also produced negative indirect effect on leaf breadth (-0.040) which were contributed to result insignificant positive genotypic correlation with fruit yield per plant (-0.071). Li *et al.* (1997) also found similar result in cucumber for their trait. Shamima, S., (2011) also found negative direct effect (-0.041) on yield.

### 4.3.10 Fruit breadth (cm)

Fruit breadth showed positive direct effect on yield (0.027) (Table 5). Fruit breadth shows positive indirect effect on internode distance (0.012), Chlorophyll percentage per plant (0.032), number of male flower per plant (0.018), number of female flower per plant (0.083), Pericarp length (3.391), fruit per plant (0.130), fruit weight (0.081). The character also produced negative indirect effect on yield via, pedicel length of male flower (-5.907), Pedicel length of male flower (-8.860), Pericarp length (- 0.025), Leaf breadth (-0.017) Leaf length without petiole (- 0.13), fruit length (-0.048) which were contributed to result significant positive genotypic correlation with fruit yield per plant (0.223). Li *et al*. (1997) also found similar result in cucumber for their trait. Shamima, S., (2011) also found positive direct effect (0.041) on yield.

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

| | LLWP | LB | ID | PLMF | PLFF | CP | NMF | NFF | FL | FB | PL | FPP | FW | FYPP(Phenotypic correlation ) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| LLWP | **-0.011** | -0.044 | -0.011 | -2.067 | -0.065 | 0.015 | 0.079 | -0.031 | 0.003 | 0.029 | 1.930 | 0.051 | 0.024 | 0.050 |
| LB | -0.041 | **-0.013** | -0.019 | -4.725 | -0.083 | -0.057 | 0.013 | -0.052 | -0.075 | 0.035 | -1.64 | 0.023 | 0.081 | 0.086 |
| ID | -0.012 | -0.023 | **-0.011** | 6.498 | -0.034 | 0.045 | -0.054 | -0.042 | 0.053 | -0.02 | 9.632 | 0.067 | 0.160 | 0.196 |
| PLMF | -0.041 | -0.010 | 0.013 | **-5.907** | -0.074 | 0.018 | 0.057 | -0.019 | 0.032 | 0.039 | 2.692 | -0.062 | 0.064 | -0.004 |
| PLFF | -0.065 | -0.092 | -0.031 | -3.662 | **-0.012** | 0.091 | 0.011 | -0.021 | 0.026 | 0.040 | 1.061 | 0.067 | 0.080 | 0.1238 |
| CP | 0.015 | -0.065 | 0.044 | 9.451 | 0.095 | **-0.011** | -0.079 | 0.256 | 0.036 | 0.025 | -1.55 | -0.045 | 0.072 | 0.076 |
| NMF | -0.026 | -0.048 | 0.016 | -9.451 | -0.034 | 0.024 | **0.036** | -0.011 | -0.051 | 0.013 | 3.871 | -0.028 | -0.09 | -0.094 |
| NFF | -0.036 | -0.066 | -0.044 | -1.064 | -0.024 | 0.034 | 0.036 | **-0.011** | 0.068 | -0.02 | 1.061 | -0.016 | 0.056 | 0.0355 |
| FL | 0.051 | -0.040 | 0.023 | 1.002 | 0.012 | 0.052 | 0.072 | 0.028 | **-0.025** | 0.051 | 8.701 | 0.013 | 0.009 | -0.071 |
| FB | -0.013 | -0.017 | 0.012 | -8.860 | -0.018 | 0.032 | 0.018 | 0.083 | -0.048 | **0.027** | 3.291 | 0.130 | 0.081 | 0.223* |
| PL | -0.024 | 0.022 | -0.012 | -1.595 | -0.014 | 0.018 | 0.015 | -0.012 | -0.023 | 0.091 | **9.670** | 0.102 | 0.121 | 0.253* |
| FPP | -0.011 | -0.053 | -0.014 | 6.497 | -0.015 | 0.091 | -0.018 | 0.031 | 0.066 | 0.061 | 1.741 | **0.565** | 0.024 | 0.588 ** |
| FW | -0.036 | -0.013 | -0.022 | -4.725 | -0.012 | -0.011 | -0.044 | -0.073 | -0.025 | 0.027 | 1.450 | 0.017 | **0.802** | 0.807** |

Residual effect= 0.144936

Diagonally bold figures indicate

The direct effect - LLWP=Leaf length without petiole (cm), LB= Leaf breadth (cm), ID= Internode distance (cm), PLMF =Pedicel length of male flower (cm), PLFF=Pedicel length of female flower (cm), CP=Chlorophyll percentage per plant, NMF= Number of male flower per plant, NFF= Number of female flower per plant, FL= Fruit length (cm), FB =Fruit Breadth (cm), PL =Pericarp length (cm), FPP= Fruit per plant (kg), FW =Fruit weight (kg), FYPP= Fruit Yield per plant (kg)

### 4.3.11 Pericarp length (cm)

Pericarp length showed positive direct effect on yield (9.670) (Table 5). Flash part length shows positive indirect effect on fruit weight (0.121), fruit per plant (0.102), fruit breadth (0.091), number of male flower per plant (0.015), Chlorophyll percentage per plant, (0.018), leaf breadth (0.022). The character also produced negative indirect effect on yield via, fruit length (-0.023), number of female flower per plant (-0.012), pedicel length of female flower (-0.014), pedicel length of male flower (-1.595), internode distance (-0.012), leaf length without petiole (-0.024). Which were contributed to result significant positive genotypic correlation with fruit yield per plant (0.253). Li *et al*. (1997) also found similar result in cucumber for their trait. Shamima, S., (2011) also found negative direct effect (5.045) on yield.

### 4.3.12 Fruit per plant

Fruit per plant showed positive direct effect on yield (0.565) (Table 5). Pedicel length of female flower shows highest positive indirect effect (6.497), also showed positive indirect effect on Chlorophyll percentage per plant (0.091), number of male flower per plant (0.031), fruit length (0.066), flash part length (1.741) Fruit Weight (0.024). showed negatively indirect effect indirect effect on flash part length (1.450), fruit per plant (0.017). The character also produced negative indirect effect on yield via, leaf length without petiole (-0.011), leaf breadth (-0.053), Pedicel length of female flower (-0.015), internode distance (-0.014), number of male flower per plant (-0.018) which were contributed to result highly significant positive genotypic correlation with fruit yield per plant (0.588).

Li *et al*. (1997) also found similar result in cucumber for their trait. Shamima, S., (2011) also found positive direct effect (0.061) on yield.

### 4.3.13 Fruit weight (kg)

Fruit Weight showed positive direct effect on yield (0.802) (Table 5). Fruit weight had a highest positive indirect effect on flash part length (1.450), fruit per plant (0.017). The character also produced negative indirect effect on yield via, Pedicel length of male flower (-4.725),leaf length without petiole (-0.036),leaf breadth (-0.013), internode distance (-0.022), pedicel length of female flower (-0.012), Chlorophyll percentage per plant (-0.011), number of male flower per plant (-0.044), number of female flower per plant (-0.073), fruit length (-0.025), which were contributed to result highly significant positive genotypic correlation with fruit yield per plant (0.807).

Li *et al*. (1997) also found similar result in cucumber for their trait. Shamima, S., (2011) also found positive direct effect (0.401) on yield.

### 4.4 Genetic diversity analysis of sweet gourd genotypes

Genetic divergence in sweet gourd was analyzed by using GENSTAT software program. Genetic diversity analysis involved several steps i.e., estimation of distance between the genotypes, clusters and analysis of inter-cluster distance. Therefore, more than one multivariate technique was required to represent the results more clearly and it was obvious from the results of many researchers. In the analysis of genetic diversity in sweet gourd multivariate techniques were used. The genetic diversity of sweet gourd advanced lines are presented in (Table 6 to Table 8 and Figure 1and 2.)

#### 4.4.1 Construction of scatter diagram

In multivariate analysis, cluster analysis refers to methods used to divide up objects into similar groups, or more precisely, groups whose members are all close to one another on various dimensions being measured. Depending on the values of principal component scores 2 and 1 obtained from the principal component analysis, a two-dimensional scatter diagram (Z1 - Z2) using component score 1 as X-axis and component score 2 as Y-axis was constructed, which has been presented in (Figure 1). The position of the genotypes in the scatter diagram was apparently distributed into five groups, which indicated that there existed considerable diversity among the genotypes.

#### 4.4.1 Principal Component Analysis (PCA)

Principal components were computed from the correlation matrix from genotype scores obtained from first components and succeeding components with latent roots greater than the unity. The principal component analysis yielded Eigen values of each principal component axes with the first axes totally accounting for the variation. Principal component analysis was carried out with 28 genotypes of sweet gourd. The computed eigen values for the 14 variables with 5 vectors 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 85%. In summary, the principal component analysis resulted in the reduction of the 14 original variables to five independent linear

combination, principal component of variables. The first principal component accounted for 22.506% of the total variation while principal components two, three, four, five accounted for 16.642%, 12.235%, 11.347%, 9.538 respectively (Table 6).

### 4.4.2 Non-Hierarchical Clustering

Twenty-eight sweet gourd 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. Husna, A. (2009) reported five clusters in sweet gourd. Gaffar (2008) reported similar number of clustering in fifteen sponge gourd genotypes. In this study cluster IV had the highest number of genotypes IX, cluster III and cluster V constitute five genotypes. Cluster II had six genotype and cluster I had 3 genotypes (Table 7).

### 4.4.3 Principal coordinate analysis (PCO)

By using these inter-genotypic distances intra-cluster genotypic distances were calculated (Table 7 & Figure 1) as suggested by Singh *et al.* (1977). Cluster-II which (1.547) composed of two genotypes cluster III showed the maximum intra distances (3.352) and cluster II showed the lowest intra-cluster distance (2.362) which composed of four genotypes. The coordinates obtained from the Principal Component analysis (PCA) were used as iCPut at Principal Coordinate Analysis (PCO) to calculate distances among the points reported. PCA was used for the graphical representation of the points while PCO was used to calculate the minimum distance straight line between each pair of points.

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

| Principal component axes | Eigen value | % Variance | Cumulative (%) total variance |
|---|---|---|---|
| I | 3.15 | 22.506 | 22.505 |
| II | 2.329 | 16.642 | 39.147 |
| III | 1.712 | 12.235 | 51.382 |
| IV | 1.588 | 11.347 | 62.729 |
| V | 1.335 | 9.538 | 72.268 |
| VI | 0.993 | 7.085 | 79.363 |
| VII | 0.899 | 6.428 | 85.791 |
| VIII | 0.528 | 3.774 | 89.565 |
| IX | 0.493 | 3.524 | 93.089 |
| X | 0.41 | 2.934 | 96.023 |
| XI | 0.276 | 1.973 | 97.997 |
| XII | 0.255 | 1.821 | 99.819 |
| XIII | 0.022 | 0.160 | 99.979 |
| XIV | .002 | 0.020 | 100 |

**Table 7. Distribution of genotypes in different clusters**

| Cluster number | Number of genotypes | Percent (%) | Name of genotypes |
|---|---|---|---|
| I | 3 | 10.714 | G12, G13, and G22 |
| II | 6 | 21.428 | G9, G10, G17, G20, G21, and G23 |
| III | 4 | 14.285 | G15, G24, G27, and G28 |
| IV | 9 | 32.142 | G7, G8, G11, G14, G16, G18, G19, G25and G26 |
| V | 6 | 21.428 | G1, G2, G3, G4, G5 and G6 |

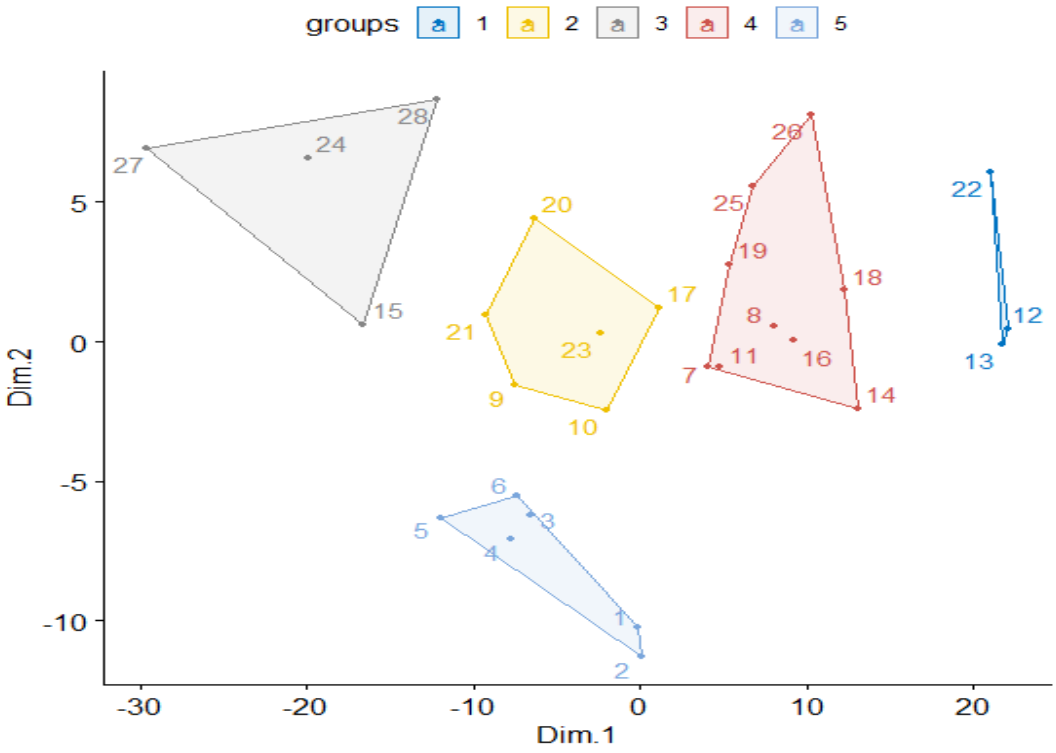


**Fig1.Scattereddiagram of twenty-eight sweet gourd genotype**

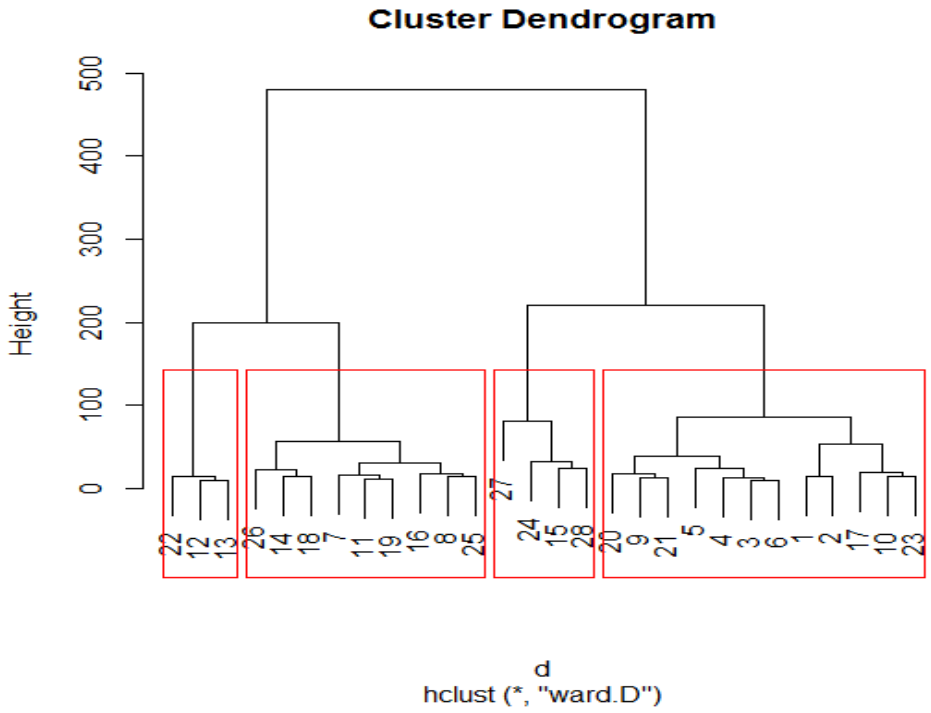


**Fig. 2. Dendrogram of twenty-eight sweet gourd genotypes**

### 4.4.4 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 8). 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 I and III (3.735), followed by between cluster I and IV (3.675), cluster III and IV (3.174), cluster II and IV (2.992), and between cluster III and V (2.751). The However, the maximum inter-cluster distance was observed between the Clusters I and III (3.735), 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 III (3.352), which contained of 4 genotypes, while the minimum distance was found in cluster IV (2.249) that comprises 9 genotypes. The different multivariate analysis was superimposed from which it could be concluded that different multivariate techniques supplemented and confirmed one another.

### 4.4.5 Contribution of characters towards divergence of the genotypes

#### 4.4.5.1. Cluster-I

Cluster-I had three genotypes $G_{12}$, $G_{13}$, $G_{22}$ (Table 7). From the clustering mean values (Table 9), it was observed that cluster-I produced the highest mean for number of male flower (0.176) followed by days to Chlorophyll percentage (0.093) and all other traits shows negative value, leaf length without petiole (-0.258), leaf breadth (-0.298), internode distance (-0.223), pedicel length of male flower (-0.084), pedicel length of female flower (-0.35), number of female flower per plant (-0.011), fruit length (-0.049), fruit Breadth (-0.291), Pericarp length (-0.252), Fruit per plant (-0.445), Fruit Yield per plant (-0.467) The lowest mean value for cluster-I (-0.222) was fruit weight (cm). (Table 8)

**Table 8. Intra (Bold) and inter cluster distances ($D^2$) for 28 genotypes**

| Cluster | I | II | III | IV | V |
|---|---|---|---|---|---|
| I | **3.136** | | | | |
| II | 2.425 | **2.362** | | | |
| III | 3.735 | 2.546 | **3.352** | | |
| IV | 2.294 | 2.992 | 3.174 | **2.675** | |
| V | 2.465 | 3.143 | 2.751 | 3.243 | **2.252** |

#### 4.4.5.2. Cluster-II

Cluster-II had six genotypes $G_9$, $G_{10}$, $G_{17}$, $G_{20}$, $G_{21}$, $G_{23}$ (Table 8). From the clustering mean values (Table 9), it was observed that cluster-II produced the highest mean for fruit weight (4.297) followed by Fruit Yield per plant (3.627), Internode distance (1.609), , Pedicel length of female flower (0.191), Chlorophyll percentage per plant (1.387), Fruit length (0.111), Leaf breadth (0.108), Fruit Breadth (0.122), Pericarp length (0.063), Fruit per plant (0.068), negative mean value also founded Number of male flower per plant (-1.703), Number of female flower per plant ( -1.381), Leaf length without petiole (-0.813), Pedicel length of male flower (-0.107), The lowest mean value for cluster-II (0.28) was the seed thickness (cm).

#### 4.4.5.3. Cluster-III

Cluster-III had four genotypes $G_{15}$, $G_{24}$, $G_{27}$, and $G_{28}$ namely (Table 10). From the clustering mean values (Table 9), it was observed that cluster-III produced the highest mean for Fruit per plant (1.049), followed by Pedicel length of female flower (0.807), Leaf length without petiole (0.714), Leaf breadth (0.694), Internode distance (0.328), Pedicel length of male flower (0.215), , Number of male flower per plant (0.633), Number of female flower per plant (0.198), Fruit length (0.103), Fruit Breadth (0.676), Pericarp length (0.591), Fruit Yield per plant (0.64) also showed negative mean value Chlorophyll percentage per plant (-0.396), Fruit weight (-0.009) is also lowest mean value for cluster-III .

**Table 9. Cluster mean for fourteen yield and yield characters of 28 sweet gourd genotypes**

| | I | II | III | IV | V |
|---|---|---|---|---|---|
| LLWP | -0.258 | -0.813 | 0.714 | 0.694 | 0.723 |
| LB | -0.298 | 0.108 | 0.694 | -0.582 | -0.491 |
| ID | -0.223 | 1.609 | 0.328 | 0.783 | 0.875 |
| PLMF | -0.084 | -0.107 | 0.215 | 0.342 | -0.436 |
| PLFF | -0.35 | 0.191 | 0.807 | 0.962 | 542 |
| CP | 0.093 | 1.387 | -0.396 | -0.247 | 0.763 |
| NMF | 0.176 | -1.703 | 0.633 | 0.742 | 0.754 |
| NFF | -0.011 | -1.381 | 0.198 | -0.874 | -0.641 |
| FL | -0.049 | 0.111 | 0.103 | 0.451 | 0.863 |
| FB | -0.291 | 0.122 | 0.676 | 0.759 | 0.245 |
| PL | -0.252 | 0.063 | 0.591 | 0.987 | 0.734 |
| FPP | -0.445 | 0.068 | 1.049 | 0.459 | 0.634 |
| FW | -0.222 | 4.297 | -0.009 | 0.776 | 0.852 |
| FYPP | -0.467 | 3.627 | 0.64 | 0.453 | 0.763 |

LLWP= Leaf length without petiole (cm), LB= Leaf breadth (cm), ID= Internode distance (cm), PLMF= Pedicel length of male flower (cm), PLFF= Pedicel length of female flower (cm), CP= Chlorophyll percentage per plant, NMF= Number of male flower per plant, NFF= Number of female flower per plant, FL= Fruit length (cm), FB= Fruit Breadth (cm), PL= Pericarp length (cm), FPP= Fruit per plant (kg), FW =Fruit weight (kg), FYPP= Fruit Yield per plant (kg)

#### 4.4.5.4. Cluster-IV

Cluster-IV had nine genotypes $G_7$, $G_8$, $G_{11}$, $G_{14}$, $G_{16}$, $G_{18}$, G19, $G_{25}$ and $G_{26}$ . From the clustering mean values (Table 9), it was observed that cluster IV produced the highest mean for Pericarp length (0.987), Pedicel length of female flower (0.961) followed by Leaf length without petiole (0.694), Internode distance (0.783), Fruit weight (0.776), Fruit Breadth (0.759), Number of male flower per plant (0.742), Fruit length (0.451), ,Fruit per plant (0.459), Fruit Yield per plant (0.453), Pedicel length of male flower (0.342) also showed highest negative value Number of female flower per plant (-0.874), Leaf breadth (-0.582), Chlorophyll percentage per plant (-0.247), The lowest mean positive value for cluster-IV Pedicel length of male flower (0.342)

#### 4.4.5.5. Cluster-V

Cluster-V had six genotypes $G_1$, $G_2$, $G_3$, $G_4$, $G_5$, and G6 (Table 6). From the clustering mean values (Table 8), it was observed that cluster-V produced the highest mean for Internode distance (0.875), Fruit length (0.863), Fruit weight (0.852), Fruit Yield per plant (0.763), Number of male flower per plant (0.754), Pericarp length (0.734), Chlorophyll percentage per plant (0.763), Leaf length without petiole (0.723), Pedicel length of female flower (0.542), Fruit per plant (0.634), also showed negative value Leaf breadth (-0.491), Pedicel length of male flower (-0.436), Number of female flower per plant(- 0.641) The lowest mean value for cluster-V was the Fruit Breadth (0.245).

### 4.6 Comparison of different multivariate techniques

the cluster pattern of $D^2$ analysis though non-hierarchical clustering has taken care of simultaneous variation in all the character under study. However, the distribution of genotypes in different cluster of the D2 analysis has followed more or less similar trend of principal component analysis were found to be alternative methods in giving the information regarding the clustering pattern of genotypes. However, the principal component analysis provides the information regarding the contribution of characters towards divergence of sweet gourd.

### 4.4.7 Selection of genotype as parents for future hybridization program

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 means and agronomic performance the genotype

G15 (BD 290) for the minimum female flowering from cluster III, G10 (BD 277) for the maximum number of fruit yield and for the maximum number of female flowerings from cluster V, G20 (BD 2153) for the maximum fruit breadth from cluster IV, G12 (279) for the maximum fruit weight from cluster II. Therefore, considering group distance and other agronomic performances the inter genotypic crosses between G15 (BD 246) and G10 (BD 309); G20 (9492) and G12 (BD 309); may be suggested for future hybridization program

**5. Qualitative analysis of 28 genotype of sweet gourd**

**LGYS**: Light Greenish Yellow Strip; **D.G.Y.S**: Deep Greenish Yellow Strip; **D.Y**: Deep Yellow,

**Among 28 Genotype**

**Deep Greenish Yellow Strip** (D.G.Y.S): $G_4$, $G_6$, $G_8$, $G_{10}$, $G_{12}$, $G_{13}$, $G_{14}$, $G_{16}$, $G_{18}$, $G_{19}$, $G_{20}$, $G_{23}$, $G_{26}$, $G_{27}$, $G_{28}$

**Light Greenish Yellow Strip** (L.G.Y.S) = $G_1$, $G_2$, $G_3$, and $G_5$

**Deep Yellow** (D.Y): $G_7$, $G_9$, $G_{15}$, $G_{17}$, $G_{21}$, $G_{22}$, $G_{24}$, $G_{25}$

**According to Shape**

**Round:** $G_1$, $G_3$, $G_7$, $G_9$, $G_{14}$, $G_{15}$, $G_{17}$, G20, $G_{23}$

**Round Strip:** $G_2$, $G_{10}$, $G_{11}$, $G_{16}$, $G_{18}$, $G_{19}$, $G_{21}$, $G_{22}$, $G_{24}$, $G_{25}$, $G_{26}$, $G_{27}$, $G_{28}$

**Oval:** $G_4$, $G_6$, $G_{12}$, $G_{13}$. (Those all character is represented on plate 6a and plate 6b)

**Table 10. Fruit shape variation of 28 genotype of sweet gourd**

| Sl. No. | Genotype | BARI ACC Number | Fruit Color | Fruit Shape |
|---|---|---|---|---|
| 1 | $G_1$ | BD- 232 | L.G.Y. S | Round |
| 2 | $G_2$ | BD-264 | L.G.Y. S | Round Strip |
| 3 | $G_3$ | BD- 265 | L.G.Y. S | Round |
| 4 | $G_4$ | BD- 266 | D.G | Oval |
| 5 | $G_5$ | BD- 268 | D.G.Y. S | Christy |
| 6 | $G_6$ | BD- 269 | D.G.Y. S | Oval |
| 7 | $G_7$ | BD- 273 | D.Y | Round |
| 8 | $G_8$ | BD- 274 | D.G.Y. S | Chirsty |
| 9 | $G_9$ | BD- 275 | D.Y | Round |
| 10 | $G_{10}$ | BD- 277 | D.G.Y. S | Round Strip |
| 11 | $G_{11}$ | BD- 278 | L.G.Y. S | Round Strip |
| 12 | $G_{12}$ | BD- 279 | D.G.Y. S | Oval |
| 13 | $G_{13}$ | BD- 282 | D.G.Y. S | Oval |
| 14 | $G_{14}$ | BD- 288 | D.G.Y. S | Round |
| 15 | $G_{15}$ | BD- 290 | D.Y | Round |
| 16 | $G_{16}$ | BD- 306 | D.G.Y. S | Round Strip |
| 17 | $G_{17}$ | BD- 309 | D.Y | Round |
| 18 | $G_{18}$ | BD- 2150 | D.G.Y. S | Round Strip |
| 19 | $G_{19}$ | BD- 2151 | D.G.Y. S | Round Strip |
| 20 | $G_{20}$ | BD- 2153 | D.G.Y. S | Round |
| 21 | $G_{21}$ | BD- 2157 | D.Y | Round Strip |
| 22 | $G_{22}$ | BD-2174 | D.Y | Round Strip |
| 23 | $G_{23}$ | BD-2177 | D.G.Y. S | Round |
| 24 | $G_{24}$ | BD-2196 | D.Y | Round Strip |
| 25 | $G_{25}$ | BD-2205 | D.Y | Round Strip |
| 26 | $G_{26}$ | BD-2212 | D.G.Y. S | Round Strip |
| 27 | $G_{27}$ | BARI-(v) 2 | D.G.Y. S | Round Strip |
| 28 | $G_{28}$ | BARI-(H) 1 | D.G.Y. S | Round Strip |

# CHAPTER V

## SUMMARY AND CONCLUSION

The present investigation entitled “genetic variation and inter relationship between yield and yield contributing characters of Sweet gourd (Cucurbita maxima L.)” was conducted during robi season (November to March) in 2020 at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh. The experiment was comprised of 28 genotypes of bottle gourd laid out in Randomized Complete Block Design (RCBD) with three replications to estimate the genetic variability, correlation coefficient and path analysis. It was observed that significant variation exists among all the genotypes used for most of the characters studied.

plants were considered for observations of different characters viz., (LLWP) leaf length without petiole (cm), (LB) leaf breadth (cm), (ID) internode distance (cm), (PLMF) pedicel length of male flower (cm), (PLFF) pedicel length of female flower (cm), (CP) Chlorophyll percentage per plant, (NMF) number of male flower per plant, (NFF) number of female flower per plant, (FL) fruit length (cm), (FB) fruit Breadth (cm), (PL) Pericarp length (cm), (FPP) fruit per plant (kg), (FW) fruit weight (kg), (FYPP) fruit Yield per plant (kg)

This analysis of variance revealed that mean sum of squares due to genotypes were highly significant for all characters. Significant mean sum of squares due to fruit yield and attributing characters revealed existence of considerable variability in material studied for improvement of various traits.

The maximum leaf length without petiole in G28 was 21.17 cm and in G1 the minimum was 12.50 cm and the mean value was 12.832.The maximum leaf breadth was found 21.14 cm in G24 (BD-2196) and the minimum was recorded 5.44 cm in G2 (BD-264) with mean value 13.280 (Appendix V) The maximum internodes distance was found 12.05 cm in G27 (BD 258) and the minimum was recorded 4.02 in G4 (BD 4587) with mean value 08.38 (Appendix IV).The maximum male flowers pedicel length was found 16.87 in G24 and the minimum was recorded 6.27 in G1 (BD 288) with mean value 11.593 (Appendix V). The maximum female flowers pedicel length was found 8.63 in BD-2214 and the minimum was recorded 2.07 in BARI mistikmmra-l with mean value 4.45 The highest Chlorophyll percentage was found 36.52 in G19 and the minimum was recorded 28.37 in G2 with mean value 33.326 .The maximum no. of male flower was found (70.25) in 1313-9491 and the

minimum was recorded (21.3) in BARI mistikumra-l & BARI mistikumra-Z with mean value 42.32 The maximum no. of female flower was found 17.12 in BB-266 and the minimum was recorded 6.55 in BARI mistikumra-l & BARI mistikumra-2 with mean value 12.302 . The maximum fruit length was found 10.47 cm in G28 and the minimum was recorded 4.56 cm in G6 with mean value 7.160. The maximum fruit breadth was found 10.47 cm in G28 and the minimum was recorded 4.56 cm in G23 with mean value 7.160. The maximum Pericarp length was found 9.92 cm in G27 and the minimum was recorded 0.80 cm in G1 with mean value 4.01. The maximum fruit per plant was found 5 in BD-2150 and the minimum was recorded 1.67 kg in BARI mistikumra-1 with mean value 3.33. The maximum weight per fruit was found 5.01 kg in G27 and the minimum was recorded 1.67 kg in G1 with mean value 3.33. The highest yield per plant was found 9.92 kg in G10 followed by BD-2151 (9.41kg), BD-266 (8.14) and BD-2150 (7.15) and the minimum was recorded 0.80 kg in G15 with mean value 4.01 kg (Appendix V)

The highest genotypic and phenotypic coefficient of variation was recorded, fruit yield per plant (31.40 % and 54.05%). The phenotypic coefficients of variation were higher than the genotypic coefficient of variation, indicating greater influence of environment on the expression of these characters. The highest heritability was recorded in yield contributing characters were number of pedicel length of male flower (0.98), internode distance (0.97), leaf breadth (0.96), pedicel length of female flower (0.94), fruit length without petiole (0.88), Pericarp length (0.79), fruit breadth (0.74) fruit length (0.73), number of female flower (0.63), Chlorophyll percentage (0.51), fruit per plant (0.43).Whereas, highest heritability coupled with highest genetic advance were observed for characters viz., fruit yield per plant (0.33), leaf breadth (0.96) number of male flower (0.36), pedicel length of male flower (o.98), number of female flower (0.63), Chlorophyll percentage (0.51).

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 was 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, corresponding phenotypic correlation co-efficient were higher than their 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.

Correlation analysis revealed that fruit yield per plant showed the high positive and significant correlation with Number of leaf breadth (g=0.730, p=0.698) fruit weight (g=0.721, p=0.807), pedicel length of male flower (g=0.651, p=0.621) Fruit per plant (g= 0.585, p=0.588) and Pericarp length (g=0.669, p=0.253) at both genotypic and phenotypic level.

Leaf length without petiole showed negatively direct effect (- 0.011) on yield , leaf breadth showed negatively direct effect (- 0.013) on yield Internode distance showed negatively direct effect (- 0.011)Pedicel length of male flower showed highest negatively direct effect (-5.907)Pedicel length of female flower showed negatively direct effect (- 0.012)Chlorophyll Percentage per plant showed negatively direct effect (-0.11) on yield number of male flower showed positively direct effect on yield (0.036). Number of female flower showed negatively direct effect on yield (-0.011), fruit length showed negatively direct effect on yield (- 0.025), fruit breadth showed positively direct effect on yield (0.027), Pericarp length showed highest positively direct effect on yield (9.671), fruit per plant showed positively direct effect on yield (0.565), Fruit Weight showed positively direct effect on yield (0.802)

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 I and III (3.735), followed by between cluster I and IV (3.675), cluster III and IV (3.174), cluster II and IV (2.992), and between cluster III and V (2.751). The However, the maximum inter-cluster distance was observed between the Clusters I and III (3.735), 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 III (3.352), which contained of 4 genotypes, while the minimum distance was found in cluster IV (2.249)

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

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

ii. The mean performance for yield of BD-2150, BD- 2175, BD-282 was superior among all the genotypes, which indicated that the genotype may be utilize as an elite genotype for future varietal development breeding program.

Recommendations

I. There is need of in-depth study on qualitative and processing parameters along with resistance to different biotic and abiotic stresses.

II. More number of genotypes may be collected from different sources of Bangladesh and included in further studies.

III. In order to improve the fruit yield per plant and other important attributes, the genotypes which in distant characters may be utilized in future breeding program.

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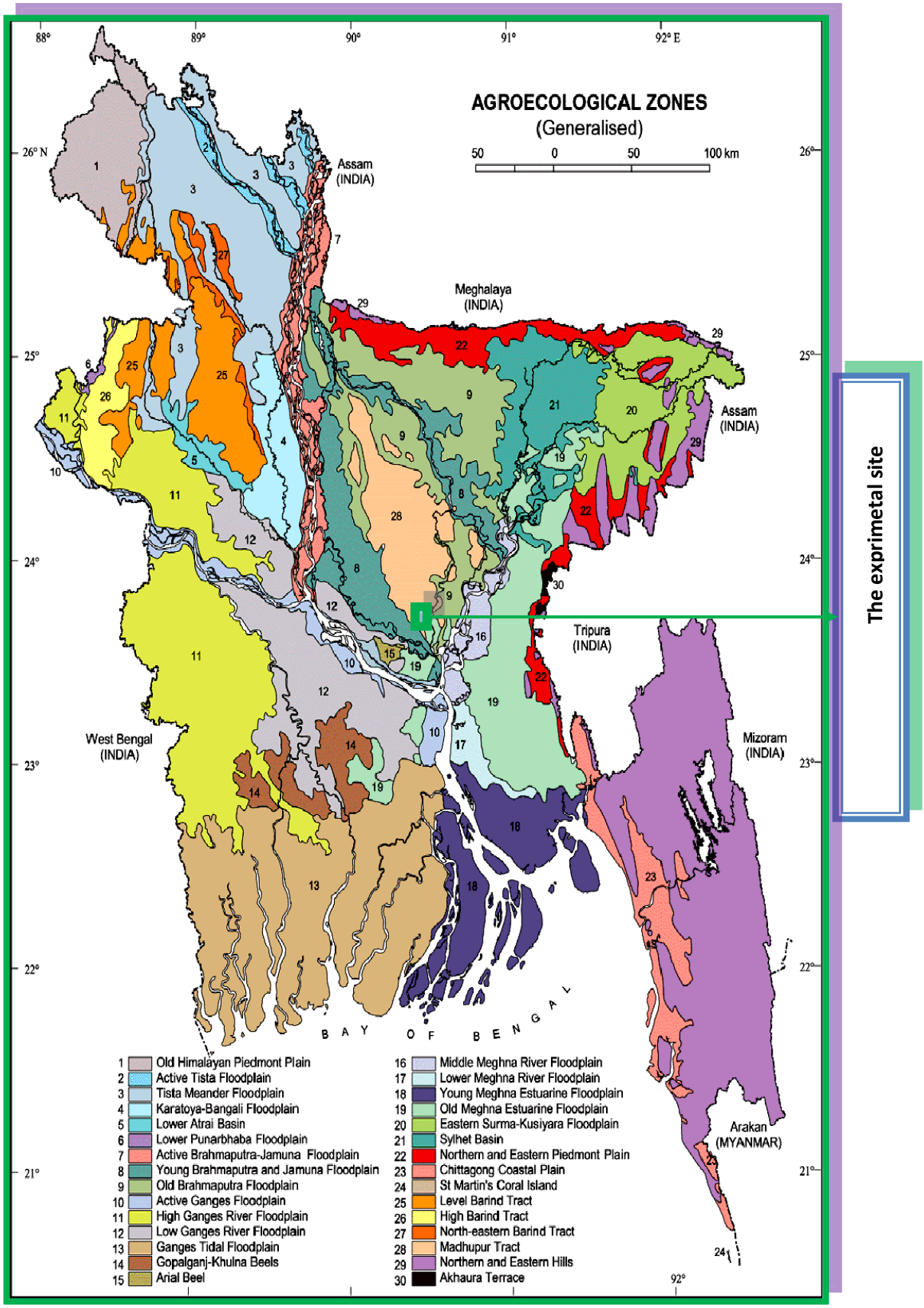
# APPENDICES

## Appendix I. Map showing the experimental site under the study.




The exprimetal site

**Appendix II.** Monthly records of air temperature, relative humidity, rainfall and sunshine hours during the period from November 2019 to March 2020

| Month | Year | Monthly average air temperature ($C^0$) | Average relative humidity (%) | Total rainfall (mm) | Sea Level Pressure | Total sunshine (hours) |
|---|---|---|---|---|---|---|
| **November** | **2019** | **27.6** | **78** | **188** | **1010.1** | **3.15** |
| **November** | **2019** | **24.9** | **74** | **37** | **1011.5** | **3.0** |
| **December** | **2019** | **19.3** | **74** | **5** | **1015.2** | **3.1** |
| **January** | **2020** | **18.5** | **76** | **21** | **1014.7** | **2.5** |
| **February** | **2020** | **21.6** | **59** | **1** | **1014.5** | **3.2** |
| **March** | **2020** | **26.4** | **57** | **30** | **1010.7** | **7.7** |

**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** | **20%** |
| **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 Chlorophyll | 0.072 soil |
| Phosphorus | 22.08 µg/g soil |
| Sulphur | 25.98 µg/g |
| Boron | 0.48 µg/g soil |
| Iron | 262.6 µg/g soil |
| Manganese | 164 µg/g soil |
| Zinc | 3.32 µg/g soil |
| Copper | 3.54 µg/g soil |

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

**Appendix IV. Analysis of variance for different yield contributing characters of 28 sweet gourd genotypes.**

| Characters | d.f | LLWP | LB | ID | PLMF | PLFF | CP | NMF | NFF | FL | FB | PL | FPP | FW | FYPP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Replication | 2 | 0.933 | 0.673 | 1.823 | 0.640 | 0.381 | 2.611 | 336.04 | 0.723 | 0.555 | 6.456 | 0.193 | 1.0833 | 0.123 | 6.151 |
| Genotypes | 27 | 6.805*** | 26.05**** | 7.881*** | 23.351*** | 5.840*** | 29.917*** | 986.74*** | 33.114*** | 5.800*** | 12.615*** | 0.485*** | 1.98*** | 1.124** | 21.61** |
| Error | 54 | 0.303 | 0.397 | 0.091 | 0.165 | 0.128 | 7.277 | 364.48 | 5.39 | 0.638 | 1.338 | 0.040 | 0.614 | 0.387 | 8.794 |
| P value | | <0 | <0 | <0 | <0 | <0 | <0 | <0 | <0 | <0 | <0 | <0 | <0 | <0.001 | <0.001 |

Acronyms indicate that

d.f = Degrees of freedom

LLWP =Leaf length without petiole (cm), (LB) Leaf breadth (cm), (ID) Internode distance (cm), (PLMF) Pedicel length of male flower (cm), (PLFF) Pedicel length of female flower (cm), (CP) Chlorophyll percentage per plant, (NMF) Number of male flower per plant, (NFF) Number of female flower per plant, (FL) Fruit length (cm), (FB) Fruit Breadth (cm), (PL) Pericarp length (cm), (FPP) Fruit per plant (kg), (FW) Fruit weight (kg), (FYPP) Fruit Yield per plant (kg)

## Appendix V: Mean comparison of different character of 28 genotype of sweet gourd

| Geno | LLWP | LB | ID | PLMF | PLFF | CP | NMF | NFF | FL | FB | PL | FPP | FW | FYPP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 8.07h | 10.0ef | 6.01e-g | 6.27i | 6.74 a-d | 34.06a-d | 43.56abc | 6.55d | 6.22b-h | 10.05bcd | 2.60h | 2.67efg | 1.77f | 3.76 a-h |
| 2 | 9.33gh | 5.44f | 4.69fg | 7.84hi | 6.26 a-h | 28.37d | 43.44abc | 8.11cd | 5.05gh | 10.30bcd | 2.74gh | 3.00def | 1.85ef | 5.381a |
| 3 | 11.40d-h | 10.61def | 6.85d-g | 8.11hi | 7.63efg | 31.99a-d | 49.33abc | 9.67bcd | 7.22b-h | 11.06b | 3.20e-h | 5.00ab | 2.48b-f | 8.26efg |
| 4 | 10.35fgh | 9.92ef | 4.02g | 10.59b-i | 7.66 b-f | 35.04abc | 50.55abc | 8.89cd | 8.28a-f | 10.22bcd | 3.04fgh | 2.67efg | 2.55b-f | 5.83 def |
| 5 | 12.37b-g | 12.92b-e | 4.80fg | 8.30f-i | 7.43abc | 34.41abc | 54.43abc | 10.11a-d | 5.72d-h | 9.86bcd | 3.00fgh | 2.33fg | 2.34c-f | 4.86 a-h |
| 6 | 11.77c-h | 11.83c-f | 6.84d-g | 9.55ef-i | 8.00 e-h | 30.71bcd | 49.99abc | 11.01a-d | 4.56h | 7.58de | 2.81gh | 3.00def | 2.27def | 5.45cde |
| 7 | 11.83c-g | 11.97c-e | 7.19b-g | 9.94ef-i | 7.60efg | 36.45ab | 38.87abc | 16.90ab | 5.78c-h | 7.06e | 3.14e-h | 2.33fg | 3.04a-f | 5.95 a-d |
| 8 | 11.73c-h | 11.92c-e | 7.88a-g | 10.99b-i | 7.96 a-d | 30.42cd | 34.76abc | 17.12a | 5.39fgh | 10.28bcd | 3.42e-h | 2.67efg | 2.62b-f | 4.83 c-g |
| 9 | 13.90a-f | 14.42b-e | 7.64a-g | 10.29c-i | 10.39efg | 32.28a-d | 49.64abc | 11.68ad | 5.84c-h | 9.84b-e | 3.83c-h | 4.00bcd | 2.92a-f | 6.16 b-f |
| 10 | 11.83c-g | 12.64b-e | 5.94e-g | 10.10d-i | 8.59 a-g | 34.18abc | 44.53abc | 12.23a-d | 6.89b-h | 11.56b | 4.01b-h | 5.67a | 3.28a-f | 10.86efg |
| 11 | 11.63c-h | 12.72b-e | 7.43a-g | 10.78b-i | 10.53efg | 35.26abc | 38.08abc | 13.13a-d | 6.90b-h | 9.84b-e | 3.68c-h | 3.67cde | 3.05a-f | 7.48abc |
| 12 | 11.60d-h | 12.87b-e | 9.58a-e | 11.01a-i | 7.53 c-g | 36.03abc | 21.30c | 8.68cd | 6.95b-h | 10.67b | 3.76c-h | 3.33c-f | 4.83ab | 16.31bc |
| 13 | 11.80c-g | 13.83b-e | 9.02a-f | 9.79e-i | 7.611a | 30.93a-d | 21.52c | 10.24a-d | 5.62e-h | 10.50bc | 3.50d-h | 3.33c-f | 2.97a-f | 5.281a |
| 14 | 11.05e-h | 13.44b-e | 7.03b-g | 8.16g-i | 6.11bc | 35.94abc | 30.07bc | 10.46a-d | 6.57b-h | 11.17b | 3.80c-h | 3.00def | 3.15a-f | 5.51bc |
| 15 | 13.38a-f | 13.39b-e | 8.04a-g | 16.44ab | 8.14 def | 31.58a-d | 58.29ab | 12.35a-d | 6.51b-h | 10.51bc | 3.32e-h | 1.67g | 2.86a-f | 3.16 e-h |
| 16 | 12.43b-g | 12.22b-e | 10.40a-e | 9.81e-i | 7.06 a-h | 35.84abc | 33.84bc | 11.58a-d | 7.12b-h | 11.62b | 3.83c-h | 3.33cdef | 3.14a-f | 5.06 a-d |
| 17 | 14.37a-e | 13.31b-e | 6.96c-g | 12.90a-h | 7.61 a-d | 31.12a-d | 41.06abc | 12.80a-d | 8.90a-d | 10.87b | 3.78ch | 2.67efg | 3.16a-f | 4.77 a-d |
| 18 | 12.73b-g | 11.47c-f | 8.08a-g | 14.27a-e | 7.28cde | 34.38abc | 30.61bc | 12.36a-d | 7.35a-h | 10.84b | 4.49a-g | 3.00def | 3.46a-f | 5.45 c-g |
| 19 | 13.57a-f | 14.11b-e | 8.43a-g | 14.03a-g | 7.94 c-g | 36.52a | 37.16abc | 12.25a-d | 7.13b-h | 11.17b | 4.23a-h | 3.33c-f | 3.47a-f | 5.81efg |
| 20 | 14.22a-e | 16.58a-d | 9.21a-f | 13.12a-h | 7.39 b-f | 34.11a-d | 48.05abc | 15.14abc | 7.40a-h | 12.56ab | 4.75a-f | 3.67cde | 3.88a-f | 5.91 def |
| 21 | 14.73a-e | 15.03a-e | 9.99a-e | 9.90e-i | 7.73bc | 34.03a-d | 51.27abc | 12.70a-d | 8.02a-g | 10.73b | 4.22a-h | 3.00def | 3.54a-f | 4.65 a-h |
| 22 | 14.90a-d | 13.14b-e | 10.81a-d | 14.08a-f | 7.801a | 34.06a-d | 21.82c | 13.59a-d | 8.13a-g | 10.98b | 4.85a-e | 3.33c-f | 3.84a-f | 5.19 a-g |
| 23 | 14.02a-f | 14.11b-e | 10.82a-d | 9.55ef-i | 6.5 def | 32.70a-d | 44.71abc | 11.81a-d | 9.07ab | 7.79cde | 4.47a-g | 2.67efg | 4.01a-f | 5.21efg |
| 24 | 14.33a-e | 21.14a | 11.04a-d | 16.87a | 10.29efg | 31.77a-d | 60.59ab | 12.04a-d | 8.79a-e | 11.23b | 4.68a-f | 3.00def | 4.20a-e | 6.45 b-f |
| 25 | 14.07a-f | 13.31b-e | 9.83a-e | 15.88a-d | 8.69 a-d | 31.21a-d | 35.48abc | 14.93abc | 8.30a-f | 10.40bc | 5.26a-d | 3.67cde | 4.29a-d | 7.94bc |
| 26 | 15.37a-c | 13.36b-e | 11.65a-c | 15.99a-c | 9.42abc | 32.98a-d | 32.03bc | 16.82ab | 7.35a-h | 11.34b | 5.37abc | 3.67cde | 4.67abc | 9.56 a-d |
| 27 | 15.75ab | 17.59a-c | 12.05a | 15.17a-e | 9.52bc | 34.60abc | 70.25a | 16.38ab | 8.96abc | 14.62a | 5.85a | 4.33bc | 5.01a | 10.25abc |
| 28 | 16.77a | 18.56ab | 11.78ab | 14.87a-e | 13.95 a-h | 32.15a-d | 53.13abc | 14.93abc | 10.47a | 14.57a | 5.62ab | 3.67cde | 4.72ab | 8.92 a-h |
| Maximum | 16.77 | 21.14 | 12.05 | 16.87 | 13.95 | 36.52 | 70.25 | 17.12 | 10.47 | 14.62 | 5.85 | 5.67 | 5.01 | 16.31 |
| Minimum | 8.07 | 5.44 | 4.02 | 6.27 | 6.11 | 28.37 | 21.3 | 6.55 | 4.56 | 7.06 | 2.6 | 1.67 | 1.77 | 3.16 |
| Mean | 12.83214 | 13.28036 | 8.3875 | 11.59286 | 8.1915 | 33.325 | 42.4414 | 12.30219 | 7.16035 | 10.68138 | 3.39732 | 3.973214 | 3.33465 | 3.327428 |
| %CV | 17.78 | 29.64 | 34.78 | 30.97 | 19.10 | 10.60 | 52.19 | 36.64 | 27.18 | 16.04 | 27.45 | 23.85 | 43.35 | 3.16 |
| LSD | 3.74 | 6.44 | 4.75 | 5.87 | 6.76 | 5.78 | 36.26 | 7.37 | 3.18 | 2.80 | 1.78 | 1.27 | 2.36 | 2.99 |

(LLWP) Leaf length without petiole (cm), (LB) Leaf breadth (cm), (ID) Internode distance (cm), (PLMF) Pedicel length of male flower (cm), (PLFF) Pedicel length of female flower (cm), (CP) Chlorophyll percentage per plant, (NMF) Number of male flower per plant, (NFF) Number of female flower per plant, (FL) Fruit length (cm), (FB) Fruit Breadth (cm), (PL) Pericarp length (cm), (FPP) Fruit per plant (kg), (FW) Fruit weight (kg), (FYPP) Fruit Yield per plant (kg)