# GENETIC VARIABILITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS OF SOME YIELD AND YIELD CONTRIBUTING CHARACTERS IN SWEETGOURD (*Cucurbita maxima* L.)

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JUNE, 2022

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By

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#### **REG. NO.: 20-11130**

A Thesis submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka in partial fulfilment of the requirements for the degree of

# MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING SEMESTER: JANUARY-JUNE, 2022

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### CERTIFICATE

This is to certify that the thesis entitled "GENETIC VARIABILITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS OF SOME YIELD AND YIELD CONTRIBUTING CHARACTERS IN SWEETGOURD (*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 bona fide research work carried out by Abu Hanjala, Registration number: 20-11130 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: June, 2022 Dhaka, Bangladesh

Prof. Dr. Md. Sarowar Hossain Supervisor

# **DEDICATED**

# ТО

# MY BELOVED PARENTS

#### ACKNOWLEDGEMENTS

All the praises are for the omniscient, omnipresent, and omnipotent Allah who has the Supreme Ruler of the universe, the merciful, the most benevolent whose blessings enabled the researcher to complete this experimental work successfully.

The author would like to exhibit his sincere appreciation and the profound sense of gratitude, and respect to his respectable research supervisor **Prof. Md. Sarowar Hossain**, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for his scholastic supervision, commentary help and unvarying inspiration throughout the entire session of the research work and the preparation of the thesis manuscript.

The author would also like to reveal his cordiality to respected Co-Supervisor, **Professor Dr. Firoz Mahmud** Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for his continuous support, constant inspiration, constructive criticism, advices, and suggestions throughout the research work and preparing this thesis paper.

The author would like to affirm his profound respect and gratitude to the Chairman, Associate Professor Dr. Shahanaz Parveen, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, and all of the department's respectable course instructors for their collegial guidance, constant encouragement, valuable suggestions, and kind cooperation throughout the entire experimental work period. The author wishes to extend his gratitude to the academic officers and staff of the Department of Genetics and Plant Breeding for their sincerity during this thesis preparation. The author desires to thank to the farmers and farm-staffs for cooperation during the field work and data collection.

The author would also like to show his respect and gratitude to **Professor Dr. Alok Kumar Paul**, Post Graduate Dean and **Professor Dr. Md. Shahidur Rashid Bhuiyan**, Vice-Chancellor, Sher-e-Bangla Agricultural University, Dhaka, for providing me all possible help to fulfill the research work successfully.

The author has received cordial cooperation from his seniors and juniors friends, during the research period and would like to thank them.

Finally, the author is highly indebted to his beloved parent for their blessings, endless encouragement and affection in all stages of his life.

June, 2022 SAV, Dhaka The Author

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Full word	Abbreviation
Agro Ecological Zone	AEZ
Analysis of variance	ANOVA
And others	et al.
At the rate	a
Bangladesh Agricultural Research Institute	BARI
Bangladesh Agricultural University	BAU
Bangladesh Institute of Nuclear Agriculture	BINA
Centimeter	Cm
Co-efficient of variation	$\mathrm{CV}$
Days after sowing	DAS
Degrees of Freedom	Df
Degree	$^{0}\mathrm{C}$
Environmental variance	$\sigma_e^2$
Et cetera	etc.
Food and Agricultural Organization	FAO
Genetic Advance	GA
Genotypic correlation	r <sub>g</sub>
Genotypic variance	$\sigma_{ m g}^2$
Genotypic Coefficient of variation	GCV
Gram	G
Heritability in broad sense	h <sup>2</sup> b
Kilogram	Kg
Meter	M
Milliliter	mL
Metric ton	MT
Muriate of Potash	MOP
Mean sum of square	MS
Number	No.
Percent	(%)
Percentage of Coefficient of Variation	CV%
Phenotypic variances	$\sigma_{\rm p}^2$
Phenotypic Coefficient of variation	PCV
Phenotypic correlation	r <sub>p</sub>
Randomized Complete Block Design	RCBD
Sher-e-Bangla Agricultural University	SAU
Species	sp.
Square meter	m <sup>2</sup>
Standard error	SE
Triple Super Phosphate	TSP

# SOME COMMONLY USED ABBREVIATIONS

# GENETIC VARIABILITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS OF SOME YIELD AND YIELD CONTRIBUTING CHARACTERS IN SWEETGOURD (Cucurbita maxima L.)

#### ABSTRACT

#### By

#### Abu Hanjala

The present study was laid on randomized complete block design on the experimental plot of Sher-e-Bangla Agricultural University, Dhaka- 1207 with three replications. Ten sweet gourd genotypes were used to estimate the genetic variability, correlation and path coefficient analysis of yield and yield contributing character in sweet gourd. Analysis of variance expressed that genotypic mean sum of square was found highly significant for all the studied characters. PCV for all the observed characters were found greater than the GCV. The highest value of PCV and GCV were 44.25% and 34.07%, respectively for yield per plant. High heritability along with high genetic advance were found for days to first male flowering, days to first female flowering, pedicle length of male flower, pedicle length of female flower, number of male flowers, and individual fruit weight. Through the correlation coefficient analysis, it was observed that, fruit yield per plant had positive and significant correlation with days to first male flowering, days to first female flowering, number of male flowers, number of female flowers, fruit length, number of fruits per plant and individual fruit weight. Path analysis exhibited that, positive and direct effect on yield per plant was recorded for days to first male flowering, number of male flowers, number of female flowers, leaf length, fruit length, number of fruits per plant, and individual fruit weight. From this observation, it was found that genotype G8 and genotype G4 were early in nature and genotype G6 was found to give best performance in number of male flowers, number of female flowers, number of fruits per plant, individual fruit weight, fruit yield per plant. So, that, these genotypes of sweet gourd could be used for future breeding programs.

#### CHAPTER I

#### **INTRODUCTION**

Sweet gourd (*Cucurbita maxima* L.) is commonly known as or 'Misti lau' or 'Misti kumra' or 'Misti kadu' or 'pumpkin'. It is also known as hubbard squash' or 'buttercup squash' in North America and 'Kabocha' in Japan. It is an annual plant and belonging to the Cucurbitaceae family and Cucurbita genus. The sweet gourd is one of the most common and highly consumed vegetables in the world. It ranked as the 10<sup>th</sup> most valuable crop worldwide in terms of production quality. In 2019, the global production of sweet gourd was estimated 33.5 million metric tons on 1.3 million hectares and China was the largest producer, accounting for almost 63% of total production, and it also had the largest area under sweet gourd cultivation, according to 70% of the global total. Other major producers of sweet gourd include Russia, India, Iran and Ukraine, (FAO, 2021). In Bangladesh sweet gourd is also a very popular and commonly grown vegetable. During 2017-2018, in Bangladesh, the total production of sweet gourd was 9.96 million metric tons and the area under production was 4,21,290 hectares (BBS, 2018).

The sweet gourd is an important crop in Bangladesh. It is providing food, income, traditional medicines, and significance to cultural. It plays a vital role in the economy and daily life of Bangladeshis. It provides nutrient value to the people. It generates the income of many farmers of Bangladesh. This crop can easy cultivated and requires minimum inputs, making it mor profitable to the small-scale farmers or entrepreneurs. Moreover, in the festival seasons or religious ceremonies, the sweet gourd become more precious to the local people and turns into a cash crop to the farmers.

It is unknown where sweet gourd actually originated, but it is believed that it was found in South America, especially in Peru and Ecuador, dating back to at least 4,000 years ago. It is one of the three main domesticated species of the Cucurbita genus, along with *C. moschata* and *C. pepo* (Decker-Walters, 2002). Then it is

distributed to Europe, Asia, and Africa. The sweet gourd is cultivated in tropical and temperate regions and nowadays it is commercially cultivated all over the world.

The sweet gourd is a very nutritious vegetable. It is rich in calories. It has Calories 137g of, protein 3gm, fat 7 gm, vitamin A 209% of the daily value, vitamin K 37% of the daily value, vitamin E 22% of the daily value, Iron 18% of the daily value, Magnesium 13% of the daily value, vitamin B 10% of the daily value, vitamin C 10% of the daily value, and Potassium 10% of the daily value in one cup (245 g) of the sweet gourd. Seeds of sweet gourd is also very nutritious. It is rich in protein and in one ounce of sweet gourd seed, 4 gm of protein is available (Tinsley, 2021).

The sweet gourd has many health-beneficial factors. Its extracts reduced inflammation by inhibiting the production of inflammatory cytokines. It has antidiabetic effects, anti-cancer effects, anti-microbial effects (Kim, *et al.*, 2014, Chen, *et al*, 2014, kim, *et al*, 2013, and Rios *et al*, 1988). Shoots, leaves, and flowers of the sweet gourd are also used as delicious vegetables. The fleshy large fruits can be consumed at immature and mature stages. People enjoy to have sweet gourd in many different ways and they also use them to make many traditional dishes, viz., 'pitha' a type of sweet cake, 'morobba' etc.

Various qualitative and quantitative parameters contribute to the yield of crops. These contributing characters are inter-related to each other and they exhibited different estimates because of their complex inter-relationship. The expression of the parameters is also highly affected by environmental conditions (Prasad *et al.*, 2001). The existence of genetic variability in a population is a valuable pre-requisite of a breeding program. To make the breeding program more efficient and productive, knowledge of genotypic and phenotypic co-efficient of the variation and the heritability with genetic advance among the genotypes for the desirable character is essential (Mishra *et al.*, 1988). Evaluation of the heritability is crucial for selection-based improvement, as it suggests the

transmissibility of a trait into future generations (Sabesan *et al.*, 2009). High that the heritability in a relationship with high genetic advance as a percent of the mean is very effective in predicting the suitable trait for the selection (Thomas and Lal, 2012). Estimated data from the analysis of correlation reveals that, the contribution of the parameters toward the final production (Panse, 1992). Evaluation of the path represents the direct and indirect effects of the traits. Thus, all these measurements help to identify the best characters for selection criteria for the better improvement of yield (Mustafa and Elsheikh, 2007; Akinwale *et al.*, 2011). This experiment were undertaking the following objectives-

- 1. To assess the genetic variability among the ten genotypes of sweet gourd,
- 2. To estimate the contribution of the yield-related traits on the yield of the ten genotypes of sweet gourd, and
- 3. To evaluate the direct and indirect effects of the qualitative characters on the yield of ten genotypes of the sweet gourd.

#### CHAPTER II

#### **REVIEW OF LITERATURE**

#### 2.1 Variability, heritability and genetic advance

Khatoon *et al.* (2022) carried out an experiment to monitor the growth and ion accumulation of fourteen sweet gourd inbred lines to identify superior genotypes. Electrical conductivity (EC) based salt was applied at 4, 8, 12 and 16 dS/m NaCl salinity levels for all the inbreeds. Treatments were imposed at the four to five-leaf stage. Salt stress resulted in significantly decreased growth and essential ion in sweet gourd inbred. Vine length (164.9 to149.5cm, control to 16 dS/m), internode length (9.67 to 9.83cm, control to 16 dS/m), the number of leaves (31 to 24.33, control to 16 dS/m), stem girth (16.38 to 15.87mm, control to 16 dS/m), and K+ ion accumulations were decreased (2.09 to 1.44, control to 16 dS/m) compared to the control. But the Na+ ion was increased (0.17 to 1.25, control to 16 dS/m) in all inbreeds under the salt conditions. Sweet gourd inbreeds were found as promising as salt-tolerant in respect of growth and the ion accumulation. These selected promising salt-tolerant sweet gourd genotypes can be used for breeding programs.

Venkatraman *et al.* (2021) conducted an experiment to analyze genetic variability for yield and its contributing characters in the thirty-five bottle gourd genotypes to assess the nature and magnitude of association among the yield and its contributing parameters in bottle gourd. Results indicated that, the PCV and the GCV were high (more than 20%), sex ratio for the PCV was 34.19 % and GCV registered as 24.79 per cent, respectively. Moderate PCV (14.28,16.10) and GCV (13.78,13.43) were recorded for vine length and primary branches, respectively. The high genetic advance (% mean) along with the high heritability was found for vine length (0.93%), fruit length (0.87%), fruit width (0.76%), fruits per vine (0.59 %), primary branches (0.69%), fruit yield (0.44%), sex ratio (0.52%), days to first female flower anthesis (0.42%), days to first harvest

(0.40%), the node at first female flower appears (0.41%), fruit thickness (0.37%), fruit weight, days to first male flower anthesis (0.37%), (0.35%) and node at first male flower appears (0.20%).

Sandilya et al. (2020) carried out a study on 31 genotypes of spine gourd to estimate genetic variability, correlation, and path coefficient analysis. They found, the high estimates of PCV for number of stems per plant and moderate GCV and PCV were observed for most of the studied parameters, which indicated that, the presence of adequate genetic variations among the genotypes. High heritability estimates combined with high genetic advance for the number of fruits per plant and fruit yield, which confirmed that these traits are under the control of additive gene action. Fruit yield exhibited significant positive associations with the days to first flowering, number of stems plant<sup>-1</sup>, fruit weight (gm) and number of fruits plant<sup>-1</sup>. The higher association of number of fruits plant<sup>-1</sup>, number of stem plant<sup>-1</sup>, fruit weight, days to first flowering, fruit diameter (cm) and ovary diameter (cm) may be attributed to their direct effect on fruit yield. The study showed that, the selection of characters with the high positive significant association and the high positive direct effect on the fruit yield can help in improving the yield of spine gourd. The coefficient is ranged from 0.33 to 0.94. In the pair-wise comparison, the maximum similarity was found between genotype with index of 0.32 to 0.50, whereas genotype exhibited the least similarity with other genotypes.

Srikanth *et al.* (2017) carried a study to assess genetic variability, heritability and genetic advance among the twenty-three pumpkin genotypes. Analysis of variance exhibited that, there was a highly significant variation for all of the examined traits between the genotypes. They also found the PCV was higher than the GCV for all the examined characters indicating the substantial modifying effect of environment in the reflection of all traits studied. The highest GCV, as well as PCV, was observed for vine length (cm) at 90 DAS, fruit cavity, rind thickness, number of seeds per fruit, and number of fruits per vine. The highest estimates of heritability (in a broad sense) were observed for fruit

cavities, followed by inter-nodal length and fruit yield per ha. The highest genetic advance (as a percent of the mean) was noted for the fruit cavity. Therefore, the selection of the superior genotypes from the viewpoint of desirable morphologic traits, with high genetic distance could be selected for the hybridization program and recognition of the best genotypes for different traits to produce new elite hybrids in pumpkins.

Singh *et al.* (2017) conducted research work in 2014 during the summer season to evaluate twenty strains. The main outcome of this field trial was to estimate the component of variance, phenotypic and genotypic coefficient, heritability, and genetic advance over mean for the different growth, yield, and quality parameters. The maximum difference between the PCV and GCV was found for fruit yield per vine, while the other parameters showed moderate to low PCV and GVC. This indicated the effect of environmental factors on these parameters is very negligible. The high to moderate heritability coupled with high to moderate genetic advance was recorded for all characters except total soluble solids. This indicated these traits are suitable for direct selection and improvement for future.

Rambabu *et al.* (2017) carried out an investigation during spring summer seasons of 2015, 2016 and 2017. The morphological characterization was done as per minimal descriptors. The results revealed that, the greatest diversity was observed in fruit characters, especially fruit shape and fruit color among the strains for various characters studied. Analysis of variance revealed significant differences among genotypes for all the characters. In general, the PCV was marginally higher than the corresponding GCV indicating less influence of the environment in the expression. High heritability coupled with the high genetic advance as a percentage of mean was observed for vine length, days to first male flower appearance, number of primary branches, days to first female flower appearance, number of primary branches, days to first female flower appearance, number of fruits per plant, days to first harvest, average fruit weight, fruit length, fruit yield per plant, fruit width, sex ratio, seed number per fruit, 100 seed weight (g), TSS of the pulp, total sugar content and ascorbic acid content of

the pulp indicated that these characters were controlled by additive gene effects and thus selection may be productive.

Nahar *et al.* (2016) conducted a study at the field and laboratory to collection, evaluation, conserve and the utilization of landraces and the wild relatives of some important vegetables and fruits in Bangladesh. Studies on the field the performance and the genetic variability of the sweet gourd accessions were carried out by using morphological traits. Analysis of variance for different parameters expressed a high degree of variation among the forty-three accessions. The accession CM152 was found to give the best performance in respect of the yield per plant (57.8 kg). The highest fruit weight (10.43 kg) was recorded in the CM154 accession. For the number of fruits per plant, CM145 gave a maximum number of fruits per plant (10.0). For all the parameters, the genotypic coefficient of variations was smaller than the phenotypic coefficient of variations. High heritability was observed for the vine length at final harvest time, number of male flowers per plant, average fruit weight, node for first male flowers, fruit cavity length and breadth, dry weight of 100 g flesh, and the number of seeds per fruit suggesting additive gene effects of these traits.

Mahbubur *et al.* (2016) estimated genetic variability, heritability and path coefficient analysis in 21 genotypes of the snake gourd. They observed, the phenotypic coefficient of variations was slightly higher than the genotypic coefficient of the variations for all studied characters; indicating that, the variation is not only genetic but also influenced by the growing environment in expression of the traits. The genotypic coefficient of variation was found high for the fruit yield (kg), length of fruit (cm), number of fruits per vine, and single fruit weight (gm). High heritability associated with high-to-moderate genetic advance was calculated for all characters studied. Correlation studies revealed that, the fruit yield (kg) had a significant and positive correlation with the number of fruits per vine, length of fruit (cm) and single fruit weight (gm). Importantly, more than 90% of genotypic total variation was contributed by the characters included in path analysis. The highest, direct and positive effect was recorded

for the number of fruits per vine. The divergence values for cluster analysis indicated that the genotypes from clusters II and III had the highest inter-cluster distances and were expected to provide high heterosis in hybridization program and to show wide variability in genetic architecture. The selection of the high yielding genotypes should give emphasis to the number of fruits per vine, length of fruit (cm) and single fruit weight (gm).

Aruah *et al.* (2012) used ten Nigerian pumpkin genotypes were evaluated to estimate the magnitude of genetic variability and the character association among some yield-contributing characters for two years. The results revealed that, wide genetic variability among the accessions. The genotypic variance and heritability estimates were high in the days to 50% emergence, fruit diameter, days to 50% flowering, and amount of seeds/fruit in both planting seasons. However, heritability estimates were low in the number of male and female flowers during both planting seasons. At both plantings, the number of seeds/fruit had a significant and positive correlation with the number of male flowers/plant and fruit diameter.

Rahman *et al.* (2011) evaluated eleven genotypes for 14 quantitative and two qualitative components for two years. The genotype × environment interactions were non-significant for all the studied characters, hence, the data were pooled over the years and discussed on the basis of the mean of the two years. Analysis of variance suggested significant differences for all the investigated characters. High GCV and PCV values were found for characters like primary branches per vine followed by total fruit yield per vine, fruit weight (gm), and protein content. The high heritability coupled with low genetic advance was observed for almost all quantitative and qualitative characters. High heritability coupled with exceptionally high genetic advance was found for total fruit yield per vine.

Mandal *et al.* (2015) conducted an investigation at Horticulture Farm of Institute of Agriculture, Sriniketan to assess the twenty-seven genotypes of bottle gourd. The analysis of variance exhibited highly significant differences for all the characters studied, indicating considerable variability among all genotypes. The highest GCV and PCV were found for the sex ratio. The differences between the GCV and PCV were high for fruit number/plant which indicates environmental influences. The high heritability associated with the high estimates of genetic advance in percent of mean were noted for node number of the first female flower, fruit length, sex ratio, fruit girth, number of fruits per plant, and fruit yield per plant. It indicated that the presence of additive gene action and selection for these traits would be productive.

#### 2.2 Correlation co-efficient

Reddy *et al.* (2022) carried out an experiment Rabi season of 2017-18. Twentyseven bitter gourd genotypes were evaluated for correlation and path co-efficient analysis of fruit yield and Yield attributes in bitter gourd. The fruit yield per vine expressed high positive and significant correlation with the vine length, fruit length, average fruit weight, number of fruits per vine, fruit diameter, fruit weight, and number of seeds per fruit. It was observed that with the increase in vine length, there is a corresponding increase in average fruit weight (g), number of fruits per vine, fruit length, fruit diameter, and the number of seeds per fruit.

Srikanth *et al.* (2021) investigated 57 genotypes of ridge gourd with 14 different traits to study the correlation of different parameters on fruit yield. The experiment was laid on randomized block design with two replications. The analysis reveals that, fruit yield per plant was positively and significant correlated with the days to first fruit harvest, fruit diameter, number of fruits per vine, fruit length, fruit flesh thickness, and average fruit weight (g) while selecting a good hybrid for enhancing the yield of the ridge gourd.

Kumari *et al.* (2021) conducted an experiment with bottle gourd genotypes. The correlation studied revealed that, the number of fruits/vine was found highly significant and positively correlated with the number of primary branches/vine, whereas negatively correlated with the days to 1<sup>st</sup> harvest was also recorded. The highest direct positive effect was expressed by the number of fruits/vine followed

by average fruit weight and fruit length while the negligible positive direct effect was shown by vine length, the total number of nodes/vine and the number of primary branches/vine.

Vijayakumar *et al.* (2020) evaluated F6 generation of ridge gourd to assess genetic variability, correlation and path analysis for yield and quality. The aim of this study was to develop high-yielding, medium size fruits and good-quality fruits of ridge gourd. The results revealed that, the moderate GCV, PCV, and high heritability along with the high genetic advance as a percentage of mean recorded for fruit length. Whereas, low GCV, PCV, and low heritability along with low genetic advance was recorded for the characters node to the first female flowering and rind thickness. Regarding correlation studies, the fruit yield was significantly and positively correlated with fruit weight and sex ratio.

Pradhan *et al.* (2020) conducted a study to evaluate the associations between the yield and the yield-contributing traits of ash gourd. Correlation of coefficients indicated that, the yield per vine had a significant and positive association with the number of branches per vine (0.318,0.137), sex ratio (0.579, 0.322), number of female flowers per vine (0.078, 0.565), fruit length (0.604, 0.463), average fruit weight (0.830, 0.758), fruit diameter (0.743, 0.565), number of seeds per fruit (0.387,0.286), weight of seeds per fruit (0.635, 0.478), and vine length (0.395, 0.340). They also found negative associations with the node to 1st female flower (-0.279, -0.280) and the days to 1st fruit setting (-0.465, -0.189). The number of fruits per vine (0.108) was positively combined with the yield per vine at the phenotypic level only.

Rashid *et al.* (2020) carried out an investigation with thirty bottle gourd genotypes. Observations of correlation revealed that, the fruit yield/ plant was positively associated with the parameters like node number at which the first male flower appeared, number of days to anthesis of first female flower, fruit diameter, node number at which first female flower appeared, dry matter content and total sugars. Moreover, the traits like days to last fruit harvested and number

of fruits/plant exhibited a significant positive genotypic correlation with the fruit yield/ plant, indicating that, the direct selection of these traits will be productive.

Som, *et al.* (2020) examined 15 genotypes of the sponge gourd to assess the parameters of variability, correlation, and path analysis for the fruit yield per plot and its attributing traits. Significant variations were recorded for all the characters in all the genotypes used in the study. The highest genotypic and phenotypic variation were noted for fruit yield (q/ha); followed by, fruit length, vine length, fruit yield per plot, number of fruits per plant, and average fruit weight. The fruit yield (q/ha); followed by, the fruit yield per plot, average fruit weight, number of fruits per plant, days to 1st fruit harvest, fruit girth, and fruit length expressed high heritability associated with high genetic advance. Correlation examination revealed that, the fruit yield per plot was noted to have positively and significantly correlated with the number of fruits per plant, fruit length, fruit plant, fru

Adarsh *et al.* (2019) used twenty-one bitter gourd strains to evaluate the morphological characters, fruit yield, and biochemical traits. The pistillate flowers were produced earlier than the staminate flowers in the proximal node in some bitter gourd genotypes. The results revealed that the small-fruited genotype had a larger number of fruits whereas larger-size fruits had the highest average weight. All the genotypes exhibited a wide range of scales for morphological and biochemical traits based on the Duncan multiple range test. The biochemical traits showed a considerable variation among the genotype. The phenotypic correlation matrix was higher than the genotypic correlation matrix for all the parameters. The variations in morphological, quantitative, and biochemical trait attributes lead to the development of high-yielding variety for qualitative and quantitative traits.

Vamsi *et al.* (2019) examined the genetic variability, heritability and correlation in 20 genotypes of bitter gourd. Genotype Co-1 and Susi Long exhibited high fruit yield per plant (kg). On the basis of the Analysis of variance a significant difference was noted for all the quantitative and qualitative parameters; indicating presence of a large amount of variability in the strains. The genotypic and phenotypic coefficient variation for fruit length (cm) indicating presence of a high amount of variation and the role of environment on the expression. The highest heritability estimate was found for characters viz., high for, fruit length (cm), fruit yield/ha (quintal), fruit yield/plant (kg), fruit width (cm), number of fruits/plant, seed germination (%), node number to which the first female flower had appeared, and fruit specific gravity (cc). Genotypic correlation analysis revealed that, the fruit yield per plant (kg) exhibited positive and highly significant association with fruit yield/ ha (0.999), fruit yield/ plant had positive and non-significant association co-efficient analysis revealed that, the fruit yield a positive and highly significant association with fruit specific gravity (0.241) and TSS (0.087). The phenotypic correlation co-efficient analysis revealed that, the fruit yield/ ha (1.000), Fruit yield/plant had a positive and non-significant association with fruit yield/ and non-significant association with fruit yield.

Panigrahi *et al.* (2018) conducted a study to assess the relationship between the different morphological parameters of 37 bottle gourd strains. The genotypes were laid on randomized block design with the three replications. Considerable amount of variability was noted for the 16 quantitative parameters. The per vine and fruit yield per hectare had highly significant positive correlation with the most of the characters viz., vine length, number of primary branches, number of fruits per vine, and length of fruit. The fruit yield per vine and fruit yield per hectare between the fruit yield per vine and phenotypic levels.

Mandal *et al.* (2015) conducted research to assess the twenty-seven genotypes of bottle gourd. Correlation analysis, Fruit yield/plant was found positively and significantly correlated at both genotypic and phenotypic levels with fruit length and fruit number/plant. Negative associations of fruit yield/plant were also observed with the node number of the first female flower, sex ratio, and days to

first harvest. Path analysis revealed that, days to first harvest and fruit girth had very high positive direct effects on fruit yield/plant.

Aruah *et al.* (2012) used ten Nigerian pumpkin strains to estimate the magnitude of genetic variability and the character association among some yieldcontributing characters. A significant positive correlation was also obtained between the number of female flowers and the amount of fruits/plant in the both planting seasons, suggesting that, both traits increased or decreased simultaneously. Thus, increasing the number of female flowers would favor fruiting in pumpkin.

Rahman *et al.* (2011) carried out an experiment with eleven genotypes to evaluated 14 quantitative and two qualitative components for two years. Correlation studies revealed that total fruit yield per vine was positively and significantly correlated to fruit weight (gm), fruit length (cm), fruit diameter (cm), fruit girth (cm), and protein content. Days to first female flower initiation which reflects the earliness to fruiting was positive with significantly associated with days to first male flower appearance and pedicel length (cm). Among the biochemical traits, protein content showed a significant and positive correlation with fruit weight, fruit girth, fruit length, fruit diameter, and total fruit yield/vine. Path analysis at the phenotypic level revealed that total fruit yield/vine was positively dependent on characteristics like the number of fruits/vine and fruit weight.

#### 2.3 Path co-efficient

Reddy *et al.* (2022) experimented twenty-seven bitter gourd genotypes in Rabi season of 2017-18. Path coefficient analysis of the different yield and yield contributing parameters on fruit yield per plant revealed that, the number of primary branches per vine, days to first male and female flower appearance, days to first and last fruit harvest, nodes at which first male and female flower appearance, fruit fly infestation percent, average fruit weight, and 100 seed weight expressed the positive and direct effects on fruit yield these characters

play a major role in recombination of breeding and suggested that the direct selection based on these traits will be effective.

Vijayakumar *et al.* (2020) investigated F6 generation to assess genetic variability, correlation and path analysis for yield and quality of ridge gourd. Path coefficient analysis showed that positive and direct effect on vine length, days to first harvest, fruit length, fruit weight, rind thickness, and number of fruits per plant. Of these traits, fruit weight exhibited the maximum positive direct effect on yield.

Pradhan *et al.* (2020) conducted a study to identify the direct and indirect effects of component characters on the fruit yield of ash gourd to enable the selection of promising lines. Path coefficient analysis revealed that, the number of female flowers per vine (6.221), fruit diameter (5.201), vine length (5.727), fruit length (0.647), number of branches per vine (1.300), days to 1st fruit setting (3.455), and weight of seeds per fruit (0.892) were directly related to the yield of ash gourd.

Rashid *et al.* (2020) conducted an experiment with thirty bottle gourd genotypes. Path analysis revealed that, the appreciable amount of direct positive effects of component traits like the number of nodes at which the first male flower has appeared, days to last fruit harvested, days to anthesis of the first female flower, number of fruits/ plant and total sugars on fruit/ yield plant.

Som, *et al.* (2020) investigated 15 genotypes of sponge gourd to evaluate the parameters of variability, correlation, and path analysis for the fruit yield and its attributing traits. Path coefficient analysis revealed that number of fruits per plant, fruit girth, days to female flower, duration of crop, number of branches per plant, 50% flowering, node number in male and female flower showed positive direct effects on fruit yield per plot. Hence, selection for these traits for improving fruit yield per plot in sponge gourd is suggested.

Harshitha *et al.* (2019) investigated twenty-five genotypes of the ridge gourd to know the effects of the independent variables on the yield (dependent variable). Character association and path analysis studies expressed that, the genotypic correlation and the path co-efficient were higher than the phenotypic correlations of path co-efficient for all the characters, indicating small influence of environmental components on genotypes. The result revealed that the number of fruits/ plant and the average fruit weight were the important contributing traits influencing yield through the direct effect coupled with the high positive correlation and selection based on these characteristics can be productive for developing high-yielding varieties.

Aruah *et al.* (2012) used ten Nigerian pumpkin genotypes to evaluated the magnitude of genetic variability and the character association among some yield-contributing characters for two years. Path analysis revealed that the days to 50% flowering had the highest positive direct effect on fruit weight and also, had a high direct contribution to the fruit yield. The significant positive correlation between fruit diameter and the weight of harvested fruits 1<sup>st</sup> season was due to the combination of the direct and indirect effects of fruit diameter on fruit yield. In 2008 planting, the number of female flowers recorded high positive direct effects on the weight of fruits/plants but its influence was nullified by high negative indirect effects of a number of fruits/plants. The results indicated that days to flowering, fruit diameter and the number of seeds/fruit can be used as selection criteria to increase fruit yield in Nigerian pumpkins.

Kumar *et al.* (2007) revealed in their path coefficient study of the 20 bottles of gourds that, all factors must be taken into the consideration are the number of branches per twig, length of twig, and the number of the nodes at which the first female flower blooms. And the fruits per twig was directly and positively in terms of fruits yield per twig. In the 25 various sweet gourd populations, examined path coefficient analysis. The analysis of the path coefficient exhibited this maximum The weight age must primarily be evaluated on the number of the days before the first harvest; followed by the average fruits weight per plant.

#### **CHAPTER III**

#### **MATERIALS AND METHODS**

The experimental work entitled "genetic variability, correlation and path coefficient analysis of some yield and yield contributing characters of sweet gourd" was executed in the research field of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh during the period November 2021 to March 2022. A detailed description of the test location, soil nature, climatic characteristics, materials, and experimental design is given in this section.

#### **3.1. Experimental site and soil**

The research plot of Sher-e-Bangla Agricultural University, Dhaka- 1207, Bangladesh was used for executing the research work. This place was located Zone of under the Agro-ecological Madhupur Tract (AEZ-28) (www.banglapedia.com) (Appendix I). This was a location of complex relief and soils build over the Modhupur clay, where the floodplain sediments buried the dissected the edges of the Modhupur Tract, leaving small hillocks of red soils as the 'islands' surrounded by floodplain (Anon., 1988) (Appendix III). It was at the 90° 22" E longitude and 23° 42" N latitude at an altitude of 8.6 meters from the level of sea (www.distancesfrom.com).

#### 3.2 Climate

The area had a subtropical climate, characterized by the high temperature, high relative humidity, and heavy rainfall in the Kharif season (March-August) and insufficient rainfall associated with moderate to low temperatures during that period (March-August). Meteorological information about the temperature, rainfall, relative humidity, and sunshine hours that prevailed at the experimental plot during the research period was presented in Appendix II.

Genotypes	Name of the Genotypes	Sources of Genotypes
G1	Cma-0001	GEPB, SAU
G2	Cma-0002	GEPB, SAU
G3	Cma-0003	GEPB, SAU
G4	Cma-0004	GEPB, SAU
G5	Cma-0005	GEPB, SAU
G6	Cma-0006	GEPB, SAU
G7	Cma-0007	GEPB, SAU
G8	Cma-0008	GEPB, SAU
G9	Baromashi	Local Market
G10	Baromashi	Local Market

Table 1. List of the sweet gourd genotypes and their sources of collection

Note:

GEPB= Genetics and Plant Breeding

SAU= Sher-e-Bangla Agricultural University

#### **3.3 Planting materials**

Ten genotypes of sweet gourd were used in this experiment and those samples were collected from Genetics and Plant Breeding (GEPB) of Sher-e-Bangla Agricultural University (SAU), Dhaka and Local Market. The name and source of collection of these genotypes are presented in (Table 1).

#### 3.4 Experimental design and layout

The experiment was executed by following Randomized Complete Block Design (RCBD) with three replications. The studied genotypes were distributed properly into the pit of each block of the built layout. The ten genotypes of the sweet gourd were assigned into pits of each replication randomly. The distance spacing was maintained as pit to pit 3 m and block to block 3m.

#### 3.5 Raising seeding into polybags

Small polybags are filled with soils and quality seeds had been dispersed into polybags for a higher germination rate. Seed were sown on 15 November, 2021. Proper irrigation was given and seedlings were raised carefully. After 3 weeks, healthy seedlings were transplanted in the pit of the main field. Plate 1 showing the polybags preparation. Seed showing and germination of seeds.

#### 3.6 Preparation of the main Land

Multiple snuffing, ploughing, and cross-ploughing were provided to prepare the area for the experiment, followed by the harrowing by a tractor and laddering. Weeds and other stubbles of the plots were carefully removed (Plate 2).

#### 3.7 Preparation of pits

After the final land preparation, pits of 55 cm x 55 cm x 50 cm were made in each block with a spacing of 3 x 3 m. Pits were kept in the open sun for a week to kill harmful insects, diseases, germs, and microorganisms. To control the



Plate 1. Growing the seedling in polybags (A) Prepared polybags, (B) Sowing the seeds into the polybags, & (C) Grown seedlings).



Plate 2. Preparation of main land



Plate 3. A. Preparation of pits B. Manure and fertilizer application

insect "field cricket" 5 mg Furadan was also mixed with the soils before making them ready for dibbling (Plate 3).

#### 3.8 Application of manure and fertilizers

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

SL No.	Fertilizers or Manures	Dose
1	Cow dung	10 ton/ha
2	Urea	125 kg/ha
3	МОР	150 kg/ha
4	Gypsum	75 kg/ha
5	TSP	125 kg/ha
6	Zinc Oxide	10 kg/ha

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

#### **3.9 Transplanting of seedlings**

Healthy and mature seedlings were transplanted into the pit of the main field on 6 December 2021. Two seedlings were planted in each pit and the soil was firmly pressed by hand around the plant (Plate 4).



Plate 4. A. Seedling transplantation and B. Field after seedling transplantation

#### **3.10 Intercultural Operation**

Following intercultural activities were conducted during the experimental work-

#### • Gap filling and thinning

The field was checked thoroughly and gap pits were filled with healthy seedlings. Only one healthy and perfect plant was maintained per pit, that's why extra plants were removed. So that, the plant can take sufficient amount of nutrient from the soil.

#### • Weeding and mulching

Weeding was carried out when that was necessary to keep the field clean, pest-insect free, and allow the availability of nutrients to the plant. Mulching was done several times to keep the soil moisture.

#### • Irrigation and drainage

Irrigation was conducted two times every week. It was done more if needed. Drainage was carried out if the water stands on the field.

#### • Application of pesticides

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

#### 3.11 Harvesting

The fruit took about 8-12 days from the setting stage to the marketable stage. The mature and ripped fruit had been harvested for consumption based on size, color, and age as the fruit grows quickly and was soon outdated in the marketable terms. A sharp knife was used to cut the fruit's twig from the plant and care was taken to avoid any twig injuries.

#### 3.12 Data recording

Data were recorded on the following parameters for the present experiment. The details of the data recording are given below on an individual plant basis.

#### • Days to first male flowering

The first day of male flower initiation was counted from the seed sowing day to determine the days to the first male flowering. Flowers were observed properly to identify the male flower.

#### • Days to first female flowering

The first day of female flower initiation was counted from the seed sowing day to determine the days to the first female flowering. Flowers were observed properly to identify the female flower.

#### • Pedicle length of male flower (cm)

Pedicle length was determined with the help of a scale. It was taken in centimeters.

#### • Pedicle length of female flower (cm)

Pedicle length was determined with the help of a scale. It was taken in centimeters.

#### • Number of Male Flowers

All the male flower of a plant is counted properly and carefully to identify the number of male flowers. Plate 5 showing data collection in the field.

#### • Number of female flowers

All the female flower of a plant is counted properly and carefully to identify the number of male flowers.

#### • Leaf length (cm)

For measuring Leaf length, three to five leaves in each germplasm were measured in centimeters with a scale and average data was recorded.

#### • Leaf breath (cm)

For counting Leaf breadth, three to five leaves from a single germplasm in centimeters with a scale and average data was recorded.

#### • Fruit length (cm)

The fruit length was measured in the three to five fruits in every genotype separately in centimeters and average data was recorded.



Plate 5. Data collection and field visit with supervisor.

#### • Fruit breath (cm)

The breath of three to five fruits of each genotype was measured in centimeters and average data was noted.

#### • Number of fruits per plant

Fruits from three different plants of each genotype were counted and average data was taken.

#### • Individual Fruit weight (kg)

Three to five fruits of each genotype were weighted properly and the average was taken.

#### • Fruits yield per plant(kg)

The weight of edible or marketable fruits of the selected plants from each germplasm was weighed in kilograms.

#### **3.13 Statistical analysis**

Data that were collected for different parameters for all the studied strains were statistically analyzed to find out the variances, phenotypic and genotypic coefficient of variations, heritability, genetic advance, correlation, and path analysis. The significance of the difference among the germplasms was computed with the help of statistix 10 (a software program). Analysis of variance was discovered by the F value test. The significant differences among the sweet gourd strains were achieved at 5% level of significance by the least significant of difference (LSD) test (Gomez and Gomez, 1984). The genotypic variances and phenotypic variances were found by the formula of Johnson et al. (1955). According to Burton's (1952) the PCV and the GCV were calculated. The broad sense of heritability was computed by using the formula given by Singh and Chaudhary (1985). In 1960, Allard gave a formula that was used for computing the genetic advance, whereas the genetic advance (% mean) was computed by the procedure provided by Comstock and Robinson (1952). The correlation coefficient analysis was computed by the formula given by Al-Jibouri et al. (1958). The path analysis was obtained by following the procedure of Dewey and Lu (1959).

#### • Analysis of variances:

For fourteen different studied parameters of all sweet gourd genotypes, an analysis of variances was carried out. The significant level was tested by using F test at 1% and %5. According to Cochran and Cox (1957), the sample of model ANOVA was -

Sources of	Degrees of	Mean sum of	Expected MS		
variation	freedom (D.F.)	squares (MS)			
Replications	(r-1)	Mr	$p \sigma_r^2 + \sigma_e^2$		
Genotypes	(g-1)	Mg	$r \sigma_p^2 + \sigma_e^2$		
Error	(p-1) (r-1)	Me	$\sigma_e^2$		
Total	(rp-1)				

Here,

g = number of genotypes;

r = number of replications;

 $\sigma_r^2$  = variance due to replications;

 $\sigma_g^2$  = variance due to genotypes; and

 $\sigma_e^2$  = variances due to error.

To test the significance of the differences between any two-adjusted genotypic means, the standard error of the mean was computed by using the formula:

S. E = 
$$\sqrt{\frac{2Me}{r}} (1 + \frac{rqu}{q+1})$$

Here,

S. E = Standard error of the mean;

r = No. of replications;

q = No. of populations in each sub-block;

u = Weightage factor computed; and

Me = Mean sum of the square for error (Intra block);

#### • Genotypic and phenotypic variance

The genotypic and phenotypic variances were estimated by the formula provide by Johnson et al. (1955).

a. Genotypic variances,  $\sigma_g^2 = \frac{\text{MSG-MSE}}{\text{r}}$ 

Here,

MSG = Mean sum of the square for genotypes;

MSE = Mean sum of the square for error; and

r = Number of the replications.

**b.** Phenotypic variances,  $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$ 

Here,

 $\sigma_p^2$  = Phenotypic variances;

 $\sigma_q^2$  = Genotypic variances; and

 $\sigma_e^2$  = Environmental variances = Mean square of error (MSE).

#### Phenotypic and genotypic co-efficient of variations

By using the provided method that given by Burton (1952), phenotypic coefficient of variations (GCV) and genotypic co-efficient of variations (PCV) for all the parameters of sweet gourd genotypes were estimated -

$$PCV = \frac{\sigma_p \times 100}{\bar{x}}$$
$$GCV = \frac{\sigma_g \times 100}{\bar{x}}$$

 $\sigma_g$ = Genotypic standard deviation;

 $\sigma_p$ = Phenotypic standard deviation; and

 $\bar{x}$  = Population means.

According to Sivasubramanian and Madhavamenon (1973), the PCV and GCV were categorized as -

#### • Broad sense heritability

Following method was used for computing the heritability in broad sense for all the traits. The formula was discoverd by Singh and Chaudhary in 1985.

$$h_b^2(\%) = \frac{\delta_g^2}{\delta_p^2} \times 100$$

Here,

h<sub>b</sub><sup>2</sup>=Heritability in the broad sense;

 $\sigma_g^2$ = Genotypic variances;

 $\sigma_p^2$  = Phenotypic variances.

Following listing was suggested by Robinson *et al.* in 1966 for estimating the heritability.

Low = 0-30% Moderate = 30-60% High = >60%

#### • Genetic Advance

Genetic advance was computed by the following process, which was presented by Allard in 1960.

$$GA=\,\frac{\sigma_g^2}{\sigma_p^2}\,.\,K\,.\,\sigma_p$$

Here,

GA = Genetic advance;

K= Standard selection differential, which is 2.06 at 5% selection intensity;

 $\sigma_g^2$  = Genotypic variance;

 $\sigma_p^2 =$  Phenotypic variance; and

 $\sigma_p$  = Phenotypic standard deviation.

Categories for genetic advance:

$$Low = (<10\%);$$

Moderate = (10-20%);

High = 
$$(>20\%)$$
.

#### Genetic advance in percent of mean

Comstock and Robinson (1952) gave the following equation for calculating the genetic advance in percent of mean –

GA in percent of mean = 
$$\frac{GA}{Grand mean} \times 100$$

Johnson et al. (1955) grouped the genetic advance in percent of mean as following -

Less than 10% = Low;

10-20% = Moderate;

More than 20% = High.

#### • Correlation coefficient analysis

Al-Jibouri *et al.* (1958) provided the following method for computing the relationship of yield contributing traits with the yield and among the yield attributing parameters.

$$r_{gxy} = \frac{Cov_{gxy}}{\sqrt{\sigma_{gx}^2} \sqrt{\sigma_{gy}^2}}$$
$$r_{pxy} = \frac{Cov_{pxy}}{\sqrt{\sigma_{px}^2} \sqrt{\sigma_{py}^2}}$$

Here,

 $r_g(xy)$  = the genotypic correlation coefficients of x and y;

 $r_p(xy)$  = the phenotypic correlation coefficients of x and y;

 $\sigma_{gx}^2$  = Genotypic variance of the trait x;

 $\sigma_{gy}^2$  = Genotypic variance of the trait y;

 $Cov_{gxy}$  = the genotypic covariance of x and y;

 $Cov_{pxy}$  = the phenotypic covariance of x and y;

 $\sigma_{px}^2$  = Phenotypic variance of the trait x; and

 $\sigma_{py}^2$  = Phenotypic variance of the trait y.

The estimated value of 'r' was compared with table 'r' value with n-2 degrees of the freedom at 5% and 1% level of significances,

here, n was referring to the number of pairs of the observation. Thus, the data obtained from various studied objectives were subjected to the pertinent statistical analysis to draw meaningful inference towards the genetic divergences of mustard populations.

#### Path analysis

According to the method given by Dewey and Lu (1959) also found in Singh and Chaudhary (1985). The path co-efficient analysis was done utilizing the simple correlation values. In the path analysis, the correlation co-efficient is divided into the direct and indirect independent variables on the dependent variable.

$$\mathbf{r}_{yx1} = \mathbf{P}_{yx1} + \mathbf{P}_{yx2}\mathbf{r}_{x1x2} + \mathbf{P}_{yx3}\mathbf{r}_{x1x3} + \dots + \mathbf{P}_{yx11}\mathbf{r}_{x1x11}$$

$$\mathbf{r}_{yx2} = \mathbf{P}_{yx1}\mathbf{r}_{x1x2} + \mathbf{P}_{yx2} + \mathbf{P}_{yx3}\mathbf{r}_{x2x3} + \dots + \mathbf{P}_{yx11}\mathbf{r}_{x2x11}$$

$$\mathbf{r}_{yx3} = \mathbf{P}_{yx1}\mathbf{r}_{x1x3} + \mathbf{P}_{yx2}\mathbf{r}_{x2x3} + \mathbf{P}_{yx3} + \dots + \mathbf{P}_{yx11}\mathbf{r}_{x3x11}$$

To calculate the direct and indirect effect of the correlated traits, say x1, x2 and x3 on yield y, a set of simultaneous equations (three equations in this example) is needed to be formulated as shown in below:

Where r's denoted as the simple correlation coefficient and P's indicates path coefficient (unknown).

P's in the above equations may be solved by arranging them in matrix form. Total correlation, say between x1 and y is thus partitioned as follows:  $P_{yx1}$  = The direct effect of x1 on y;

$$P_{yx2}r_{x1x2}$$
 = Indirect effect of x1 via x2 on y; and

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

After computing the direct and indirect effects of the traits, the residual effect (R) was found by using the following method given by Singh and Chaudhary in 1985.

$$P_{\rm RY}^2 = 1 - \sum P_{\rm iy} \, . \, r_{\rm iy}$$

Here,

$$P_{RY}^2 = (R^2);$$

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

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

 $r_{iy}$ =Correlation of the character with yield.

Categories:

#### **CHAPTER IV**

#### **RESULTS AND DISCUSSION**

The research activities were carried out in the experimental plot of Sher-e-Bangla Agricultural University, Dhaka during the Rabi season from November, 2021 to March, 2022 to investigate genetic variability, correlation among the parameters and direct and indirect effects of yield contributing characters on the yield of the sweet gourd. Genetic variation is fundamentally the most vital information to know, for introducing new cultivars through breeding programs. Thus, authentic information from the parents on the nature and degree of the diversity is the prerequisite for a productive breeding program.

The knowledge of genotypic variations within the strains in relation to morphology, and yield would help to find out better genotypes for hybridization or further breeding purposes. The accessibility of the transgressive segregants in the breeding techniques counts upon the dissimilarities of the parents. So, the appropriate data on the degree of diversity of the parents is crucial for a successful breeding program. The results on different traits have been interpreted, discussed, and presented in the following sub-headings:

# 4.1 Estimation of genetic variability, heritability, and genetic advance4.1.1 Days to first male flowering

Analysis of variance exhibited in Table 3 that, there were highly significant differences (239.70\*\*) among the genotypes for days to first male flowering. Maximum days to first male flowering was noticed in G1 (60.67), followed by G10 (58.00), G2 (57.67), and G7 (57.67), while minimum days were observed in G8 (31.33), followed by G5 (41.67), and G3 (48.00). The recorded value of mean was 50.17 days (Table 4). The genotypic and phenotypic variances for days to first male flowering was 74.10 and 91.51, respectively. The phenotypic variances were moderately higher than the genotypic variances, indicating moderate influence of environment on the genes expression for expressing this

trait. For days to first male flowering, The PCV and the GCV were noticed 18.76% and 16.88%, respectively. It was found that PCV is slightly greater than GCV, suggesting that, variations present among the genotypes (Table 5). High heritability (80.97%) coupled with high genetic advance % in mean (31.29%) was noticed for days to first male flowering, suggesting additive gene action. Therefore simple selection for this parameter would be productive. In sweet gourd, Rambabu *et al.* (2017) noticed similar result.

#### 4.1.2 Days to first female flowering

From the ANOVA Table 3, it was observed that, there was a highly significant differences (273.13\*\*) for to first female flower among the genotypes. Minimum days was recorded for first female flowering in G5 (34.33 days), followed by G8 (38.00 days) and G3 (48.00 days); whereas the maximum days to first female flowering in G6 (62.00 days), followed by G1 (60.67 days) and G7 (59.33 days). The estimated mean value was 51.75 days (Table 4). The days to first female flowering showed in Table 5, genotypic variances (87.00), phenotypic variances (99.13), PCV (18.98) and GCV (17.78). The PCV was little bit greater than the GCV, indicating effect of environment for exhibiting the trait. Days to first female flowering exhibited high genetic advance in percent of mean (87.77%) associated with high heritability (34.31%), that means there was presence of additive gene action. So, selection based on this character would be effective (Table 5). In sweet gourd, Rambabu *et al.* (2017) noticed similar result.

#### 4.1.3 Pedicle length of male flower (cm)

Pedicle length of male flower showed highly significant differences (76.92\*\*) among the genotypes in Table 3.

In Table 4, longest pedicle of male flower was noticed in G6 (28.05 cm), followed by G9 (24.02 cm) and G7 (22.60 cm); while smallest pedicle of male

Source of variance	DF	DFMF	DFFF	PLMF	PLFF	NMF	NFF	LL	LB
Replication	2	19.60	2.53	0.44	1.04	70.63	8.13	0.19	1.16
Genotype	9	239.70**	273.13**	76.92**	9.02**	239.34**	10.97**	7.37*	5.99**
Error	18	17.42	12.13	5.42	0.48	12.56	3.02	2.13	0.92
CV (%)		8.18	6.64	12.60	9.79	4.84	18.83	6.11	4.34

Table 3. Analysis of variance for different morphological plant characters of 10 sweet gourd

\* Indicates significant at 0.05 probability level & \*\* indicates significant at 0.01 probability level.

Table 3. Analysis of variance for different morphological plant characters of 10 sweet	gourd (Contd.)
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Source of variance	DF	LPL	ID	FL	FB	NFP	IFW	FYP
Replication	2	1.46	1.39	15.50	59.24	1.90	0.93	1.87
Genotype	9	20.09**	2.86**	12.02*	223.79**	1.86**	1.22**	28.38**
Error	18	4.37	0.97	4.10	33.95	0.46	0.21	5.29
CV (%)		10.53	5.41	6.72	8.73	23.27	15.44	28.24

\* Indicates significant at 0.05 probability level & \*\* indicates significant at 0.01 probability level.

DFMF=Days to first male flowering, DFFF=Days to first female flowering, PLMF=Pedicle length of male flower (cm), PLFF=Pedicle length of female flower (cm), NMF=Number of Male Flowers, NFF=Number of female flowers, LL=Leaf length (cm), LB=Leaf breath (cm), LPL=Leaf petiole length (cm), ID=Internode distance (cm), FL=Fruit length (cm), FB=Fruit breath (cm), NFP=Number of fruits per plant, IFW=Individual Fruit weight (kg), FYP=Fruits yield per plant(kg)

Genotypes	DFMF	DFFF	PLMF	PLFF	NMF	NFF	LL
G1	60.67a	60.67ab	14.97e	9.20ab	70.00de	7.33d	24.95ab
G2	57.67ab	56.00bcd	14.40e	6.79c	74.67cd	8.00cd	26.27a
G3	48.00cd	48.00e	14.20e	9.59a	64.33ef	7.00d	23.11bcd
G4	51.67bc	53.00de	12.61e	8.27b	81.00b	11.00ab	25.42ab
G5	41.67d	34.33f	18.10cd	8.63ab	69.33de	9.33bcd	24.00abc
G6	50.33c	62.00a	28.05a	6.14cde	89.33a	13.33a	22.15cd
G7	57.67ab	59.33abc	22.60bc	5.35ef	78.00bc	10.33bc	25.30ab
G8	31.33e	38.00f	15.54de	5.49def	61.00f	9.33bcd	23.42bcd
G9	53.00bc	58.67abcd	24.02b	4.69f	80.00bc	8.33bcd	23.01bcd
G10	58.00ab	54.67cd	19.40cd	6.56cd	64.67ef	8.33bcd	21.37d
Min	31.33	34.33	12.61	4.69	61.00	7.00	21.37
Max	60.67	62.00	28.05	9.59	89.33	13.33	26.27
Mean	50.17	51.75	18.79	7.08	73.56	9.39	23.89
SE	3.41	2.84	1.90	0.57	2.89	1.42	1.19
LSD (0.05)	7.16	5.97	3.99	1.19	6.08	2.98	2.51

Table 4. Mean performance of 10 sweet gourd genotypes based on different morphological traits related to yield

DFMF=Days to first male flowering, DFFF=Days to first female flowering, PLMF=Pedicle length of male flower (cm), PLFF=Pedicle length of female flower (cm), NMF=Number of Male Flowers, NFF=Number of female flowers, LL=Leaf length (cm)

Genotypes	LB	LPL	ID	FL	FB	NFP	IFW	FYP
G1	22.83abc	23.29a	18.94ab	30.69abcd	62.78b	3.33abc	2.59cd	9.01bc
G2	22.52bcd	17.59cd	18.18bc	28.14cd	68.36ab	2.67bcd	2.13d	5.73cd
G3	21.12def	15.46d	18.95ab	32.39ab	69.13ab	1.67d	2.94bc	4.84d
G4	22.72abcd	19.36bc	20.27a	31.31abc	74.95a	3.67ab	3.60ab	12.84ab
G5	22.17cde	18.12bcd	17.67bc	29.62bcd	72.11ab	2.33cd	3.57ab	8.26cd
<b>G6</b>	20.07f	20.62abc	17.16c	33.83a	73.26a	4.33a	3.90a	13.05a
<b>G7</b>	23.83ab	20.27abc	17.63bc	30.07bcd	44.63c	3.33abc	2.50cd	9.27abc
G8	24.21a	23.80a	18.69abc	29.39bcd	66.217ab	2.33cd	2.98bc	4.93d
G9	20.86ef	21.54ab	17.15c	28.33cd	65.31ab	2.33cd	2.07d	5.02d
G10	20.41f	18.58bcd	17.79bc	27.39d	70.92ab	3.00bc	3.38ab	8.48cd
Min	20.07	15.46	17.15	27.39	44.63	1.67	2.07	4.84
Max	24.21	23.80	20.27	33.83	74.95	4.33	3.89	13.05
Mean	22.08	19.82	18.32	30.20	65.60	2.92	2.97	8.28
SE	0.78	1.71	0.81	1.65	4.76	0.55	0.37	1.88
LSD (0.05)	1.64	3.59	1.69	3.47	10.00	1.16	0.78	3.94

Table 4. Mean performance of 10 sweet gourd genotypes based on different morphological traits related to yield (Contd.)

LB=Leaf breath (cm), LPL=Leaf petiole length (cm), ID=Internode distance (cm), FL=Fruit length (cm), FB=Fruit breath (cm), NFP=Number of fruits per plant, IFW=Individual Fruit weight (kg), and FYP=Fruits yield per plant (kg)

Characters	Phenotypic variance	Genotypic variance	PCV (%)	GCV (%)	Heritability (%)	GA	GA (%)
DFMF	91.51	74.10	18.76	16.88	80.97	15.96	31.29
DFFF	99.13	87.00	18.98	17.78	87.77	18.00	34.31
PLMF	29.26	23.83	29.27	26.42	81.47	9.08	49.12
PLFF	3.32	2.85	25.79	23.86	85.60	3.22	45.47
NMF	88.15	75.59	12.82	11.87	85.75	16.59	22.65
NFF	5.67	2.65	25.79	17.62	46.70	2.29	24.81
LL	3.88	1.75	8.24	5.53	44.98	1.83	7.64
LB	2.61	1.69	7.32	5.89	64.81	2.16	9.77
LPL	9.61	5.24	15.61	11.52	54.50	3.48	17.52
ID	1.60	0.63	6.94	4.34	39.18	1.02	5.60
FL	6.74	2.64	8.62	5.40	39.19	2.10	6.96
FB	97.23	63.28	14.77	11.91	65.08	13.22	19.80
NFP	0.92	0.47	33.11	23.56	50.60	1.00	34.52
IFW	0.55	0.34	24.93	19.57	61.65	0.94	31.66
FYP	12.98	7.70	44.25	34.07	59.29	4.40	54.04

Table 5. Estimation of genetic parameters for morphological characters related to yield

DFMF=Days to first male flowering, DFFF=Days to first female flowering, PLMF=Pedicle length of male flower (cm), PLFF=Pedicle length of female flower (cm), NMF=Number of Male Flowers, NFF=Number of female flowers, LL=Leaf length (cm), LB=Leaf breath (cm), LPL=Leaf petiole length (cm), ID=Internode distance (cm), FL=Fruit length (cm), FB=Fruit breath (cm), NFP=Number of fruits per plant, IFW=Individual Fruit weight (kg), and FYP=Fruits yield per plant(kg).

flower was noted in G4 (12.61 cm), followed by G3 (14.20 cm) and G2 (14.40 cm). the value of mean was 18.79. Phenotypic variance (29.26) was observed higher for pedicle length of male flower than the genotypic variance (23.83). Moreover, GCV (26.42) was noted a bit less than the PCV (29.27). That, indicating the presence of environmental factors for effecting this character. Apart from this, high heritability (81.47%) was observed to combine with high genetic advance in % of mean (49.12%), indicating additive action of gene. For that reason, simple selection on the basis of this character could be effective (Table 5).

#### 4.1.4 Pedicle length of female flower (cm)

Highly significant differences (9.02\*\*) among the genotypes was notice in table 3 for pedicle length of female flower. In table 4, largest pedicle length of female flower was noticed in G3 (9.59 cm), followed by G1 (9.20 cm) and G5 (8.63 cm); while shortest pedicle length of female flower was noted in G9 (4.69 cm), followed by G7 (5.35 cm) and G8 (5.49 cm). the calculated mean value was found 7.08. Phenotypic variance (3.32) was noticed greater for pedicle length of female flower than the genotypic variance (2.85). Additionally, GCV (23.86) was found a tiny bit smaller than the PCV (25.79). That, indicating the existence of environmental effects for releasing this parameter. Apart from this, high heritability (85.60%) was observed to couple with high genetic advance in % of mean (45.47%), indicating additive action of gene. For that reason, simple selection could be effective on the basis of this character (Table 5). Sandilya *et al.* (2020) noticed similar result in spine gourd. Morphological variation in male flowers among different genotypes is presented in Plate 6.

#### 4.1.5 Number of Male Flowers

In Table 3, highly significant differences  $(239.34^{**})$  were observed among the genotypes for number of male flowers. In Table 4, G6 (89.33) showed the maximum number of male flowers, followed by G4 (81.00) and G9 (80.00). On the other hand, G8 (61.00) was found to produce minimum number of male flowers, followed by G3 (64.33) and G10 (64.67). the estimated mean value was

73.56. Genotypic variance was (75.59) found smaller than the phenotypic variance (88.15). Besides, GCV was (11.87) noticed bit smaller than the PCV (12.82), indicating the existence of environmental effects for executing this trait. High heritability (85.75%) and high genetic advance in percent of mean (22.65%) was recorded, suggesting that, there was presence of additive gene activities. So that, on the basis of this parameter simple selection will be possible. In sweet gourd, Singh *et al.* (2017) found the similar result.

#### 4.1.6 Number of female flowers

In table 3, highly significant differences (10.97\*\*) among the genotypes were observed for the number of female flowers. In table 4, G6 (13.33) showed the highest number of female flowers, followed by G4 (11.00) and G7 (10.33). On the other hand, G3 (7.00) was noticed to produce lowest number of female flowers, followed by G1 (7.33) and G2 (8.00). The mean value was 9.39. Genotypic variance of number of female flowers was (2.65) recorded shorter than the phenotypic variance (5.67). Besides, GCV was (17.62) noted bit shorter than the PCV (25.79), indicating the presence of environmental effects for the execution of this trait. Moderate heritability (46.70%) associated with high genetic advance in percent of mean (24.81%) was found. Narayankutty et al. (2006) noticed similar result in snake gourd. Morphological variation in female flowers among different genotypes is presented in Plate 7.

#### 4.1.7 Leaf length (cm)

Leaf length in Table 3 showed highly significant differences (7.37\*) among the genotypes. In Table 4, largest length for leaf was noticed in G2 (26.27 cm), followed by G4 (25.42 cm) and G7 (25.30 cm); whereas, smallest length of leaf was recorded in G10 (21.37 cm), followed by G6 (22.15 cm) and G9 (23.01 cm). The mean value was 23.89. Phenotypic and genotypic variances were observed 3.88 and 1.75, respectively. GCV (5.53) was found smaller than the PCV (8.24), suggesting the effect of environment on this trait. Moderate heritability (44.98%) associated with low genetic advance in percent of mean (7.64%) was notice,



Plate 6. Showing morphological variations in male flowers among ten sweet Gourd genotypes.

indicating the non-additive gene action and suggesting selection based on this trait would not be productive (Table 5).

#### 4.1.8 Leaf breath (cm)

Highly significant differences  $(5.99^{**})$  in Table 3 was noticed for leaf breath among the genotypes. Longest leaf breath was found in G8 (24.21 cm), followed by G7 (23.83) and G1 (22.83 cm). On the other hand, smallest breath of leaf was noted in G6 (20.07 cm), followed by G10 (20.41 cm) and G9 (20.86 cm). The mean value was 22.08 (Table 4). Genotypic and phenotypic variance was found 1.69 and 2.61. PCV (7.32) was observed little bit higher than the GCV (5.89), indicating the existence of the environment factors for releasing this trait. High heritability (64.81%) coupled with low percent of mean genetic advance (9.77%), suggestion non-additive gene activities. So that, simple selection for this trait would not be possible (Table 5). Similar result was found by Sandilya *et al.* (2020) in spine gourd.

#### 4.1.9 Leaf petiole length (cm)

In Table 3, leaf petiole exhibited very highly significant of variances  $(20.09^{**})$  among the genotypes. Smallest length of petiole was found in G3 (15.46 cm), followed by G2 (17.59 cm) and G5 (18.12 cm). On the other hand, largest leaf petiole length was observed in G8 (23.80 cm), followed by G1 (23.29 cm) and G9 (21.54 cm). The mean value was19.82 (Table 4). Phenotypic variance (9.61) was little bit higher than the genotypic variance (5.24). PCV (15.61) was also found greater than the GCV (11.52). That means, environment have effect on this trait expression. Moderate genetic advance in percent of mean (17.52%) combined with moderate heritability (54.50%) was found for leaf petiole length,

#### 4.1.10 Internode distance (cm)

Internode distance exhibited in table 3 highly significant differences (2.86\*\*) among all the genotypes of sweet gourd.

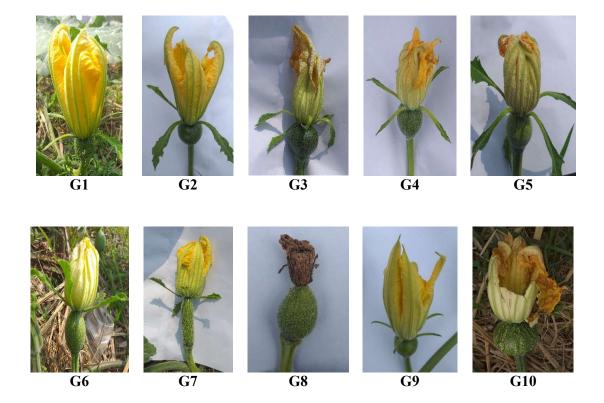


Plate 7. Showing morphological variations in female flowers among ten sweet Gourd genotypes.

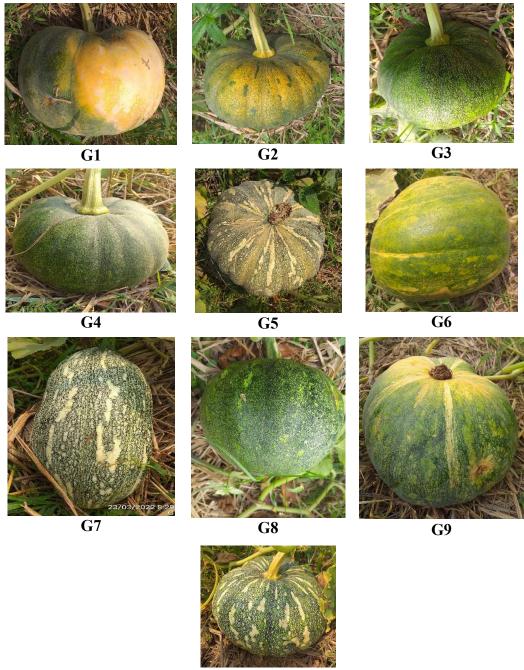
In table 4, the maximum distance for internode was noticed for G4 (20.27 cm), followed by G3 (18.95 cm) and G1 (18.94 cm). On the contrary, shortest internode distance was found in G9 (17.15 cm), followed by G6 (17.16 cm) and G7 (17.63 cm). The value of mean was 18.32. The phenotypic variance, genotypic variance, PCV, and GCV were observed 1.60, 0.63, 6.94, and 4.34, respectively. PCV was greater than the GCV, ensuring the environmental effect for expressing this parameter. Moderate heritability (39.18%) associated with low genetic advance in percent mean (5.60%) and low genetic advance (1.02), indicating non additive gene action. Fo that simple selection based on this trait will not be possible. Sandilya *et al.* (2020) noticed similar result in spine gourd.

#### 4.1.11 Fruit length (cm)

Fruit length showed highly significant of differences (12.02\*) among the genotypes of sweet gourd in table 3. In Table 4, largest fruit length was noticed in G6 (33.83 cm), followed by G3 (32.39 cm) and G4 (31.31 cm), while the G10 (27.39 cm) showed the lowest length for fruit, followed by G2 (28.14 cm) and G9 (28.33 cm). The value of mean was 30.20 cm. Genotypic variance and phenotypic variance were 2.64 and 6.74. PCV (8.62) was a bit greater than the GCV (5.40), expressing the presence of environmental effect. Moderate heritability (39.19%) along with low genetic advance in percent of mean (6.96%) was found for fruit length. High heritability associated with high genetic advance (%mean) was noticed by Venkatraman et al. (2021) in bottle gourd. Morphological variation in fruit among different genotypes is presented in Plate 8.

#### 4.1.12 Fruit breath (cm)

Fruit breath exhibited very highly significant of differences  $(223.79^{**})$  among the genotypes of sweet gourd in table 3. In table 4, largest breath of fruit was observed in G4 (74.95 cm), followed by G6 (73.26 cm) and G5 (72.11 cm), while the G7 (44.63 cm) expressed the smallest length for fruit, followed by G1 (62.78 cm) and G9 (65.31 cm). The value of mean was 65.60 cm.



G10

Plate 8. Showing morphological variations in fruits among ten sweet Gourd genotypes

Genotypic variance and phenotypic variance were 63.28 and 97.23, respectively. The PCV (14.77) was a bit larger than the GCV (11.91), expressing the existence of environmental effect. High heritability (65.08%) along with moderate genetic advance in percent of mean (19.80%) was found for fruit breath (Table 5). Similar result was recorded by Nahar *et al.* (2016).

#### 4.1.13 Number of fruits per plant

In Table 3, Highly significant differences (1.86\*\*) was observed for number of sweet gourd fruit per plant among the genotypes. Maximum number of fruits per plant were recorded in G6 (4.33 cm), followed by G4 (3.67 cm), G1(3.33 cm) and G7 (3.33 cm). On the other hand, Lowest number of fruits per plant were noticed in G3 (1.67 cm). The mean value was 2.92 (Table 4). The phenotypic variance (0.92) was a bit greater than the genotypic variance (0.47). Additionally, the PCV (33.11) was larger than the GCV (23.56), indicating that, there were environmental factors for expressing this character. Moderate heritability (50.60%) coupled with high genetic advance in percent of mean (34.52%) and genetic advance (1.00) was observed in table 5. Mahbubur *et al.* (2016) noted similar result in snake gourd.

#### 4.1.14 Individual Fruit weight (kg)

Individual fruit weight showed significant differences (1.22\*\*) in Table 3 among the sweet gourd genotypes. In Table 4, minimum weight for a fruit was recorded in G6 (3.90 kg), followed by G4 (3.60 kg) and G5 (3.57 kg). Whereas, highest weighted single fruit was noted in G9 (2.07 kg), followed by G2 (2.13 kg) and G7 (2.50 kg). The estimated mean was found 2.97 kg. Genotypic variance was (0.34) observed smaller than the phenotypic variance (0.55). PCV (24.93) was noticed a bit higher than the GCV (19.57). This indicating the environmental impact on this trait. It was also recorded high genetic advance in percent of mean (31.66%) associated with high heritability (61.65%), suggesting the additive gene action for exhibiting this parameter. So, selection on this trait basis would be productive in future. In sweet gourd, Rambabu *et al.* (2017) noticed similar result. Nahar *et al.* (2016) also found similar result in sweet gourd.

#### 4.1.15 Fruits yield per plant(kg)

Highly significant differences (28.38\*\*) were observed in Table 3 of the fruit yield per plant among the genotypes of sweet gourd. In Table 4, highest yield per plant was notices in G6 (13.05 kg), followed by G4 (12.84 kg) and G7 (9.27 kg). On the other hand, lowest yield per plant was noted in G3 (4.84 kg), followed by G8 (4.93 kg) and G9 (5.02 kg). The calculated mean value was 8.28 kg. The genotypic variance (7.70) was slightly lower than the phenotypic variance (12.98). The PCV (44.25) was slightly higher than the GCV (34.07). That suggesting the effect of environment on the expression of this trait. Moderate heritability (59.29%) along with high genetic advance in percent of mean (54.04%) and genetic advance (4.40) was observed in table 5. In bottle gourd Venkatraman *et al.* (2021) noticed high genetic advance in percent mean coupled with high genetic advance.

#### 4.2 Analysis of Correlation Coefficient

Yield of sweet gourd depends on the different yield attributing parameters. Calculation of co-efficient of correlation informs how several inter-dependable quantitative traits impacting the yield. For improving a particular qualitative character in the breeding program, it is important to compute the association of different yield contributing parameters with the yield and among themselves. It gives a good guideline to make development and improvement through selection to a plant breeder. The effect of every qualitative trait on the yield could be well-known through the analysis of correlation with a view to see the extent of relationships among yield and yield attributing traits. So, the genotypic and phenotypic correlation coefficient values for ten characters of sweet gourd genotypes are given in (Table 6).

#### 4.2.1 Days to first male flowering

**Days to first male flowering exhibited highly significant and positive correlation with** days to first female flowering (g=0.878, p=0.751), number of male flowers (g=0.400), number of fruits per plant (g=0.557) and fruits yield per plant (g=0.398). Moreover, it was negative and significantly correlated with individual fruit weight (g=-0.411). Besides, it was positively correlated with number of male flowers (p=0.304), leaf length (g=0.311, p=0.138), number of fruits per plant (p=0.186), and fruits yield per plant (p=0.10), while it was expressed negative and non-significant correlation with number of female flowers (g=-0.162, p=-0.168), leaf breath (g=-0.306, p=-0.210), fruit length (g=-0.123, p=-0.131) fruit breath (g=-0.316, p=-0.228), and individual fruit weight (p=-0.236). Mandal *et al.* (2015) noted similar results for bottle gourd.

#### 4.2.2 Days to first female flowering

It was recorded that, days to first female flowering had highly significant and positive correlation with number of male flowers (g=0.671, p=0.546), number of fruits per plant (g=0.718, p=0.454) and fruits yield per plant(kg) (g=0.454), while it exhibited significant and negative relation with leaf breath (g=-0.374). On the other hand, days to first female flowering showed positive relation with number of female flowers (g=0.226, p=0.087), leaf length (g=0.046, p=0.084), fruit length (g=0.231, p=0.062), and fruits yield per plant (p=0.238), whereas it showed negative relation with leaf breath (p=-0.231), fruit breath (cm) (g=-0.336, p=-0.213) and individual fruit weight (g=-0.328, p=-0.234). Similar result was observed by Aruah *et al.* (2012) in sweet gourd.

#### 4.2.3 Number of male flowers

Positive and highly significant correlation was shown by number of male flowers with number of female flowers with (g=0.905, p=0.483), fruit length (g= 0.492), number of fruits per plant (g=0.866, p=0.515), and fruits yield per plant (g=0.734, p=0.517); whereas positive correlation was observed with leaf length (g=0.215, p=0.066), fruit length (p=0.335), fruit breath (g=0.021), and individual fruit weight (g=0.146, p=0.060). Additionally, it expressed negative correlation with leaf breath (g=-0.304, p=-0.261) and fruit breath (p=-0.041). Husna *et al.* (2014) found similar result for bottle gourd.

#### 4.2.4 Number of female flowers

number of female flowers exhibited positive and highly significant relationship with fruit length (cm) (g=0.737), number of fruits per plant (g=0.933, p=0.585), individual fruit weight (g=0.842, p=0.366), and fruits yield per plant (kg) (g=0.921, p=0.607). On the other hand, positive relation was found with fruit length (cm) (p=0.314) fruit breath (cm) (g=0.058, p=0.151); whereas it showed negative correlation with leaf length (cm) (g=-0.202, p=-0.032) and leaf breath (cm) (g=-0.105, p=-0.073).

#### 4.2.5 Leaf length (cm)

leaf length exhibited highly significant and positive correlation with leaf breath (g=0.851, p=0.527); whereas highly significant but negative correlation with fruit breath (g=-0.482) and individual fruit weight (g=-0.609). On the other hand positive and non-significant correlation with number of fruits per plant (p=0.131) and fruits yield per plant (g=0.063, p=0.002); while negative relation was observed with fruit length (g=-0.080, p=-0.052), fruit breath (p=-0.174), number of fruits per plant (g=-0.023), and individual fruit weight (p=-0.244).

#### 4.2.6 Leaf breath (cm)

Negative and non-significant correlation was noticed for leaf breath with fruit length (g=-0.256, p=-0.079), fruit breath (p=-0.294), number of fruits per plant (g=-0.129, p=-0.057), individual fruit weight (g=-0.316, p=-0.271), and fruits yield per plant (g=-0.166, p=-0.121). It showed highly significant but negative relation with only fruit breath (p=-0.691).

#### 4.2.7 Fruit length (cm)

Highly significant and positive correlation was noticed for fruit length with number of fruits per plant (g=0.550), individual fruit weight (g=0.657), and fruits yield per plant(kg) (g=0.573, p=0.463); while it expressed positive correlation with fruit breath (g=0.230, p=0.078), number of fruits per plant (g=, p=0.255),

Characters		DFMF	DFFF	NMF	NFF	LL	LB	FL	FB	NFP	IFW
DFFF	rg	0.878**									
	rp	0.751**									
NMF	rg	0.400*	0.671**								
	rp	0.304	0.546**								
NFF	rg	-0.162	0.226	0.905**							
	rp	-0.168	0.087	0.483**							
LL	rg	0.311	0.046	0.215	-0.202						
	rp	0.138	0.084	0.066	-0.032						
LB	rg	-0.306	-0.374*	-0.304	-0.105	0.851**					
	rp	-0.210	-0.231	-0.261	-0.073	0.527**					
FL	rg	-0.123	0.231	0.492**	0.737**	-0.080	-0.256				
	rp	-0.131	0.062	0.335	0.314	-0.052	-0.079				
FB	rg	-0.316	-0.336	0.021	0.058	-0.482**	-0.691**	0.230			
	rp	-0.228	-0.213	-0.041	0.151	-0.174	-0.294	0.078			
NFP	rg	0.557**	0.718**	0.866**	0.933**	-0.023	-0.129	0.550**	-0.088		
	rp	0.186	0.454*	0.515**	0.585**	0.131	-0.057	0.255	0.083		
IFW	rg	-0.411*	-0.328	0.146	0.842**	-0.609**	-0.316	0.657**	0.693**	0.537**	
	rp	-0.236	-0.234	0.060	0.366*	-0.244	-0.271	0.355	0.396*	0.279	
FYP	rg	0.398*	0.454*	0.734**	0.921**	0.063	-0.166	0.573**	0.159	0.973**	0.779**
	rp	0.103NS	0.238	0.517**	0.607**	0.002	-0.121	0.463**	0.166	0.832**	0.527**

Table 6. Coefficients of phenotypic and genotypic correlation among different yield components

Here, \* Indicates significant at 0.05 probability level & \*\* indicates significant at 0.01 probability level.

DFMF=Days to first male flowering, DFFF=Days to first female flowering, PLMF=Pedicle length of male flower (cm), PLFF=Pedicle length of female flower (cm), NMF=Number of Male Flowers, NFF=Number of female flowers, LL=Leaf length (cm), LB=Leaf breath (cm), LPL=Leaf petiole length (cm), ID=Internode distance (cm), FL=Fruit length (cm), FB=Fruit breath (cm), NFP=Number of fruits per plant, IFW=Individual Fruit weight (kg), and FYP=Fruits yield per plant(kg).

and individual fruit weight (p=0.355). Similar results were observed by Srikanth *et al.* (2021) in ridge gourd.

#### 4.2.8 Fruit breath (cm)

Fruit breath exhibited significant and positive correlation with individual fruit weight (g=0.693, p=0.396). Moreover, it presented positive correlation with number of fruits per plant (p=0.083) and fruits yield per plant (g=0.159, p=0.166), whereas it showed negative correlation with number of fruits per plant (g=-0.088). Adarsh *et al.* (2019) noted similar result in bitter gourd. Husna *et al.* (2014) found similar result for bottle gourd.

#### 4.2.9 Number of fruits per plant

Highly significant and positive relationship was observed for number of fruits per plant with individual fruit weight (kg) (g=0.537) and fruits yield per plant(kg) (g=0.973, p=0.832), while positive correlation was noted with individual fruit weight (kg) (p=0.279). Reddy *et al.* (2022) noted the similar results for bitter gourd.

#### 4.2.10 Individual fruit weight (kg)

Positive and highly significant correlation was noticed for individual fruit weight with fruits yield per plant (g=0.779, p=0.527). Srikanth *et al.* (2021) noticed similar results in ridge gourd. Kumari *et al.* (2021) found similar kinds of results for bottle gourd.

#### 4.3 Analysis of path coefficient

By the help of path analysis, the direct and indirect effects of the qualitative traits on yield per plant and among traits can be understood. This technique of this analysis was discovered by Wright (1921) and clearly demonstrated by Deway and Lu (1959). It estimates the direct effect of one variable upon the another. Such kinds of data would be an important value in enabling the breeders to identify the necessary traits specifically of yield and utilize the genetic resources for the improvement. Estimation of direct and indirect influence of path coefficient analysis of sweet gourd is presented in Table 7.

#### 4.3.1 Days to first male flowering

Days to first male flowering exhibited positive and direct impact (1.305) on fruit yield per plant. Moreover, it expressed positive and indirect effect days to first female flowering (1.146), number of male flowers (0.522), leaf length (0.405), and number of fruits per plant (0.726); whereas the negative indirect effects were noticed in number of female flowers (-0.212), leaf breath (-0.400), fruit length (-0.161), fruit breath (-0.412), and individual fruit weight (-0.537). Kumar *et al.* (2007) noticed similar results.

#### 4.3.2 Days to first female flowering

It was found that, on fruit yield per plant, days to first female flowering had negative and direct effect (-1.757). It also showed indirect positive effects on leaf breath (0.657), fruit breath (0.590), and individual fruit weight (0.576). on the other hand, It was found to give negative indirect effects on days to first male flowering (-1.543), number of male flowers (-1.178), number of female flowers (-0.397), leaf length (-0.082), fruit length (-0.406), number of fruits per plant (-1.261). Som *et al.* (2020) noticed similar results in sponge gourd. Reddy (2022) found similar estimation in bitter gourd.

#### 4.3.3 Number of Male Flowers

Number of male flowers exhibited direct and positive effect on fruit yield per plant (0.338). Additionally, I gave indirect but positive impacts on days to first male flowering (0.136), days to first female flowering (0.227), number of female flowers (0.306), leaf length (0.073), fruit length (0.166), fruit breath (0.007), number of fruits per plant (0.293), and individual fruit weight (0.049); whereas to leaf breath (-0.103), it showed negative and indirect effect. Vamsi et al (2019) found similar results in bitter gourd.

#### 4.3.4 Number of female flowers

Number of female flowers was noticed to show positive and direct effect (0.206) on fruit yield per plant. Besides, it exhibited indirect but positive effects on days to first female flowering (0.047), number of male flowers (0.186), fruit length (0.152), fruit breath (0.012), number of fruits per plant (0.192), and individual fruit weight (0.173); whereas it produced indirect negative effects on days to first male flowering (-0.033), leaf length (-0.042), and leaf breath (-0.022). Pradhan *et al.* (2020) found similar result for female flower number in ash gourd.

#### 4.3.5 Leaf length (cm)

Leaf length was found to give direct and positive impact (0.084) on fruit yield per plant. Moreover, it showed indirect but positive effects on days to first male flowering (0.026), days to first female flowering (0.004), number of male flowers (0.018), and leaf breath (0.072); while negative indirect effects were observed on number of female flowers (-0.017), fruit length (-0.007), fruit breath (-0.041), number of fruits per plant (-0.002), and individual fruit weight (-0.051).

#### 4.3.6 Leaf breath (cm)

On the fruits yield per plant, leaf breath was found to produce negative direct effect (-0.523). Additionally, it was observed to gave indirect positive effects on days to first male flowering (0.160), days to first female flowering (0.195), number of male flowers (0.159), number of female flowers (0.055), fruit length (0.134), fruit breath (0.361), number of fruits per plant (0.067), and individual fruit weight (0.165); whereas, it had negative indirect effects on only leaf length (-0.445).

#### 4.3.7 Fruit length (cm)

Fruit length was found to give positive direct effect (0.328) on fruits yield per plant. It was also observed to give negative indirect effects on days to first male flowering (-0.040), leaf length (-0.026), and leaf breath (-0.084); while, it had positive and indirect effects on days to first female flowering (0.076), number of

Traits	DFMF	DFFF	NMF	NFF	LL	LB	FL	FB	NFP	IFW	Genotypic correlation with FYP
DFMF	1.305	-1.543	0.136	-0.033	0.026	0.160	-0.040	0.182	0.321	-0.115	0.398*
DFFF	1.146	-1.757	0.227	0.047	0.004	0.195	0.076	0.194	0.413	-0.091	0.454*
NMF	0.522	-1.178	0.338	0.186	0.018	0.159	0.161	-0.012	0.499	0.041	0.734**
NFF	-0.212	-0.397	0.306	0.206	-0.017	0.055	0.242	-0.033	0.537	0.235	0.921**
LL	0.405	-0.082	0.073	-0.042	0.084	-0.445	-0.026	0.278	-0.013	-0.170	0.063
LB	-0.400	0.657	-0.103	-0.022	0.072	-0.523	-0.084	0.399	-0.074	-0.088	-0.166
FL	-0.161	-0.406	0.166	0.152	-0.007	0.134	0.328	-0.133	0.317	0.183	0.573**
FB	-0.412	0.590	0.007	0.012	-0.041	0.361	0.075	-0.577	-0.050	0.193	0.159
NFP	0.726	-1.261	0.293	0.192	-0.002	0.067	0.180	0.050	0.576	0.150	0.973**
IFW	-0.537	0.576	0.049	0.173	-0.051	0.165	0.215	-0.400	0.309	0.279	0.779**
Residual e	ffect 0.12										

Table 7. Partitioning of genotypic into direct and indirect effects of morphological characters of 10 sweet gourd genotypes bypath coefficient analysis

\* Indicates significant at 0.05 probability level.

\*\* indicates significant at 0.01 probability level.

DFMF=Days to first male flowering, DFFF=Days to first female flowering, PLMF=Pedicle length of male flower (cm), PLFF=Pedicle length of female flower (cm), NMF=Number of Male Flowers, NFF=Number of female flowers, LL=Leaf length (cm), LB=Leaf breath (cm), LPL=Leaf petiole length (cm), ID=Internode distance (cm), FL=Fruit length (cm), FB=Fruit breath (cm), NFP=Number of fruits per plant, IFW=Individual Fruit weight (kg), and FYP=Fruits yield per plant(kg).

male flowers (0.161), number of female flowers (0.242), fruit breath (0.075), number of fruits per plant (0.180), and individual fruit weight (0.215). Pradhan *et al.* (2020) found similar result for fruit length on yield per plant in ash gourd.

#### 4.3.8 Fruit breath (cm)

Fruit breath was found to had negative but direct effect (-0.577) on fruits yield per plant of sweet gourd. Moreover, it had positive indirect impact on days to first male flowering (0.182), days to first female flowering (0.194), leaf length (0.278), leaf breath (0.399), and number of fruits per plant (0.050); on the other hand, it had negative indirect effects on number of male flowers (-0.012), number of female flowers (-0.033), fruit length (-0.133), and individual fruit weight (-0.400). In 2020, Som *et al.* noticed similar results in sponge gourd.

#### 4.3.9 Number of fruits per plant

Positive and direct effect (0.576) of number of fruits per plant were recorded on fruits yield per plant. Additionally, it had positive but indirect effects on days to first male flowering (0.321), days to first female flowering (0.413), number of male flowers (0.499), number of female flowers (0.537), fruit length (0.317), and individual fruit weight (0.309); while' it showed negative indirect impacts on leaf length (-0.013), leaf breath (-0.074), and fruit breath (-0.050). Vijayakumar et al. (2020) recorded the similar positive and direct effect of number of fruits per plant on yield per plant of ridge gourd. Rashid *et al.* (2020) found similar result for bottle gourd.

#### 4.3.10 Individual Fruit weight (kg)

Individual fruit weight exhibited positive and direct effect (0.279) on the fruits yield per plant of sweet gourd. Moreover, positive and indirect effects were observed on number of male flowers (0.041), number of female flowers (0.235), fruit length (0.183), fruit breath (0.193), and number of fruits per plant (0.150); while. It had indirect negative effects on days to first male flowering (-0.115), days to first female flowering (-0.091), leaf length (-0.170), and leaf breath (-0.088). Reddy *et al.* (2022) also found similar results for bitter gourd.

#### **CHAPTER V**

#### SUMMARY AND CONCLUSION

The present experiment was entitled "genetic variation and inter relationship between yield and yield contributing characters of Sweet gourd (*Cucurbita maxima* L.)" was conducted during the Robi season (November, 2021 to March, 2022) at the experimental area of Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh. The experiment was comprised of ten sweet gourd genotypes laid out in Randomized Complete Block Design with three replications. to evaluated the genetic variability, correlation coefficient and path analysis. It was noticed that, significant variation exists among all the sweet gourd genotypes for all studied characters.

This analysis of variance expressed that genotypic means sum of square were found highly significant for all the studied characters. Minimum days for first male flowering was noted in G8 (31.33), while the maximum was observed in G1 (60.67). Days to first female flowering exhibited minimum in G5 (34.33), while maximum days was found in G6 (62.00). Longest length of pedicle of male flower was noted in G6 (28.05), whereas smallest length was in G4 (12.61). Largest pedicle length of female flower was recorded in G3 (9.59), while shortest one was found in G9 (4.69). Highest number of male flowers was noticed in G6 (89.33); on the other hand minimum number was noted in G8 (61.00). G6 (13.33) gave the maximum number of female flowers, while minimum number of female flowers was found in G3 (7.00). Longest length of leaf was recorded in G2 (26.27), while shortest length was in G10 (21.37). Breath of leaf was found longer in G8 (24.21), while smallest breath of leaf was found in G6 (20.07). Minimum length of petiole was observed in G3 (15.46), whereas minimum was found in G8 (23.80). Highest internodal distance was recorded in G4 (20.27), while G9 (17.15) gave the shortest one. G6 (33.83) gave maximum lengthen fruit, while minimum lengthen fruit was in G10 (27.39). Maximum breath of fruit was observed in G4 (74.95), whereas minimum breath of fruit was given by

G7 (44.63). Highest number of fruits per plant was recorded in G6 (4.33), on the other hand gave minimum number of fruits per plant. G3 (1.67). G6 (3.90) gave maximum individual fruit weight, while minimum was found in G9 (2.07). Highest yield per plant was noted in G6 (13.05), whereas lowest yield per plant was found in G3 (4.84).

Phenotypic variances were recorded slightly higher than the genotypic variances for all the observed trait. The highest phenotypic and genotypic value was noted 99.13 and 87.00 respectively for days to first female flowering. PCV for all the observed characters were found greater than the GCV. The highest value of PCV and GCV were 44.25% and 34.07% respectively for yield per plant. High heritability along with high genetic advance were found for days to first male flowering, days to first female flowering, pedicle length of male flower, pedicle length of female flower, number of male flowers, and individual fruit weight. Highest heritability was 87.77% for days to female flowering.

Through the correlation coefficient analysis, it was observed that, fruit yield per plant had positive and significant correlation with days to first male flowering (g=0.398), days to first female flowering (g=0.454), number of male flowers (g=0.734, p=0.517), number of female flowers (g=0.921, p=0.607), fruit length (g=0.573, p=0.463), number of fruit per plant (g=0.973, p=0.832), and individual fruit weight (g=0.779,p=0.527).

Path analysis exhibited that, positive and direct effect on yield per plant was recorded for days to first male flowering (1.305), number of male flowers (0.338), number of female flowers (0.206), leaf length (0.084), fruit length (0.328), number of fruits per plant (0.576), and individual fruit weight (0.279)

From this observation, it was found that G8, G4 were early in nature and G6 was found to give best performance in number of male flowers, number of female flowers, number of fruits per plant, individual fruit weight, fruit yield per plant. Therefore, these genotypes of sweet gourd could be used for future breeding programs.

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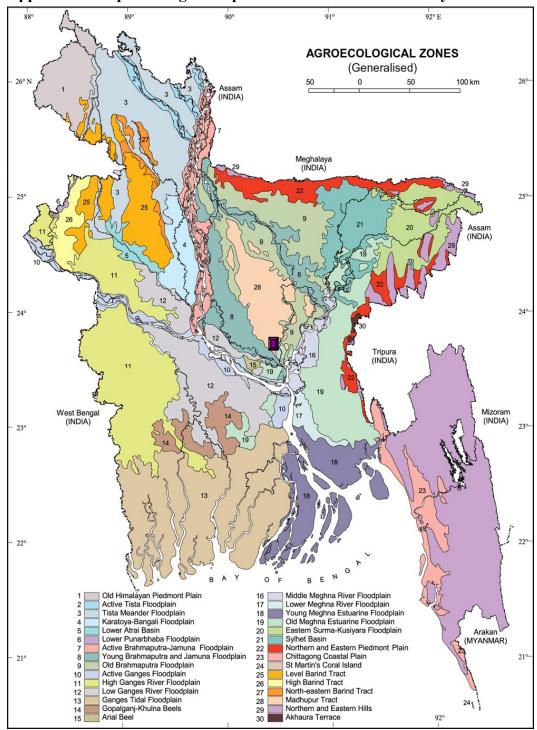
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#### **APPENDICES**



Appendix I. Map showing the experimental site under the study

The experimental site under study

Appendix II. Monthly average temperature, relative humidity and total
rainfall of the experimental site during the period from November, 2021 to
March, 2022

Month	Avg. Temperature (°C)	Relative Humidity (%)	Total Rainfall (mm)
November, 2021	24.5	6 7	34
December, 2021	21.3	6 4	7
January, 2022	20.5	6 8	18
February, 2022	23.6	5 8	1
March, 2022	26.5	5 6	28

**Source:** Bangladesh Meteorological Department (Climate Division, Dhaka Station), Agargaon, Dhaka – 1207

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

Soil separates	0/0
Sand	36.90
Silt	26.40
Clay	36.66
Texture class	Clay loam

## A. Physical composition of the soil

### B. Chemical composition of the soil

SI. No.	Soil characteristics	Analytical data	
1	Organic carbon (%)	0.81	
2	Total N (kg/ha)	1792.00	
3	Available N (kg/ha)	54.00	
4	Available P (kg/ha)	68.00	
5	Exchangeable K (kg/ha)	89.50	
6	Total S (ppm)	226.00	
7	Available S (ppm)	16.00	
8	Total P (ppm)	840.00	
9	pH (1:2.5 soil to water)	5.57	
10	CEC	11.23	

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