

GENETIC DIVERSITY STUDIES IN PUMPKIN

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CERTIFICATE

*This is to certify that thesis entitled, “**GENETIC DIVERSITY STUDIES IN PUMPKIN**” 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 **AFIA ANJUM**, **Registration No.19-10207** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

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**DEDICATED TO
MY
BELOVED PARENTS**

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The Author

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ABSTRACT

An experiment was conducted at Sher-e-Bangla Agricultural University Dhaka, during the period from March 2020 to September 2020 using eighteen pumpkin (*Cucurbita maxima* Duch.) genotypes to study the genetic variability and diversity of pumpkin in a randomized complete block design with three replications. Experimental results showed significant differences among the genotypes. For all the traits, phenotypic variance exceeded genotypic variance. High genotypic co-efficient of variation was found in number of fruits per plant, fruit length, fruit breadth, individual fruit weight, and yield per plant. Low GCV was observed for plant height, number of branches per plant, leaf length, days to first male flower, and days to first harvest. High heritability with high genetic advance in percent of mean was observed fruit length, fruit breadth, individual fruit weight, and yield per plant which indicated that these traits would be effective for genetic improvement. High heritability with low genetic advance in percent of mean was observed in days to first male flower, days to first female flower, days to first female flower anthesis, and days to first harvest. Correlation studies showed that positive and significant correlation of fruit yield per plant with plant height, days to first harvest, number of fruits per plant, fruit length, fruit breadth, individual fruit weight and fruit yield per plant. The highest intra cluster distance was found in cluster IV (4.244) and the lowest was found in cluster II (1.246). Among five clusters, the highest inter cluster distance was found in between cluster IV (47.008) and V (55.141) and the lowest between cluster II (26.200) and III (20.165). Considering group distance and phenotypic performances, the inter genotypic crosses between G4 "Hazari (Local)" and G13; G4 "Hazari (Local)" and G14 (BD-4371) and G13 (BD-4391) and G14 (BD-4371) might be suggested for future hybridization program.

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SOME COMMONLY USED ABBREVIATIONS

Full word	Abbreviations
Agriculture	Agr.
Agro-Ecological Zone	AEZ
Bangladesh Bureau of Statistics	BBS
Biology	Biol.
Biotechnology	Biotechnol.
Botany	Bot.
Cultivar	Cv.
Dry weight	DW
Editors	Eds.
Emulsifiable concentrate	EC
Entomology	Entomol.
Environments	Environ.
Food and Agriculture Organization	FAO
Fresh weight	FW
International	Intl.
Journal	J.
Least Significant Difference	LSD
Liter	L
Triple super phosphate	TSP
Science	Sci.
Soil Resource Development Institute	SRDI
Technology	Technol.
Serial	Sl.

CHAPTER I

INTRODUCTION

Pumpkin (*Cucurbita maxima* Duch.) is the most important seed propagated monoecious climbing vegetable crop that belongs to the family Cucurbitaceae, with the chromosome number $2n=40$ (Katyal and Chadha, 2000). It is one of the most common fruit vegetables in Bangladesh. It is locally known as Misti kumra or Misti lau or Misti kadu (Jahan *et al.*, 2012). It is grown round the year in the country and has the longest storability among the cucurbits. The well-matured fruits can be stored for 2 to 4 months. It has a great demand in Bangladesh due to its good storability, nutritive value, long period of availability, better transport potential and reasonable market price.

Pumpkin is grown in all over the country and in most areas, local land races are cultivated. The yield of this fruity vegetable is still very low. During 2018-2019, average yield was 7.89 t/ha (BBS, 2020) which is much lower than our neighboring country India. During 2018-2019, the average pumpkin production was 9.5 t/ha in India, 18.59 t/ha in China, 21.31 t/ha in Russia, 20.0 t/ha in Mexico, 29.89 t/ha in Italy and 24.63 t/ha in USA (FAO, 2020). The per capita consumption of vegetable in Bangladesh is about 50g/day, which is the lowest among the countries of South and South Asia. However, the daily per capita requirement is 220 g (AVRDC, 2011). There is a big gap between the demand and supply of vegetables in Bangladesh. Thus, improvement of crop yield and production of this vegetable is most desirable and important to mitigate the future demand.

Cultivated species that belong *Cucurbita* genus are *Cucurbita maxima*, *C. moschata*, *C. pepo*, *C. mixta* and *C. ficifolia* (Naik *et al.*, 2015). From archaeological remains, it has been possible to trace man's association with these plants backward in time, for a maximum of 10 thousand years (Seshadri and Parthasarthy, 2002). Cytogenetically, the species of *Cucurbita* show uniformity of chromosome number and they are considered as a secondary polyploids probably with a basic number of $x=10$ (Seshadri and Parthasarthy, 2002). Archaeological evidences show that *C. moschata* was distributed in both North and South America, Mexico and Peru being the primary centre of origin.

Though, there is a wide range of genetic variability available in Asia, not much attention has been given to the genetical improvement (Govindaraj *et al.*, 2015). The role of genetic variability in crops is of paramount importance in selecting the best genotypes for making rapid improvement in yield and related characters as well as to select the most potential parents for making the hybridization program successful (Islam *et al.*, 2015). With the limited variability, nothing can be achieved and the breeder will have to enrich the germplasm or he can resort to creation of greater variability by hybridization, mutation and polyploidy breeding.

The phenotypic expression of the plant character is mainly controlled by the genetic makeup of the plant and the environment, in which it is grown and the interaction between the genotype and environment (Pham and Mc Connaughay, 2014). Further, the genetic variance of any quantitative trait is composed of additive variance (heritable) and non-additive variance (non-heritable), which include dominance and epistasis (non-allelic interaction). Therefore, it becomes necessary to partition the observed phenotypic variability into its genotypic (partly heritable) and environmental (non-heritable) components with suitable parameters, such as phenotypic and genotypic coefficient of variation and heritability in broad sense. Further, genetic advance can be used to predict the efficiency of selection (Sztepanacz *et al.*, 2017).

Fruit yield is a complex character controlled by various yield contributing characters and their interactions. A study of correlation between different quantitative characters provides an idea of association that could be effectively exploited to formulate selection strategies for improving yield and quality of a crop (Li *et al.*, 2019). In order to have clearer picture of yield components for effective selection program, it would be desirable to consider the relative magnitude of association of various characters with yield. The path coefficient technique developed by Wright (1921) helps in estimating direct and indirect contribution of various components in building up the total correlation towards yield. On the basis of these studies, the quantum importance of individual character is marked to facilitate the selection program for better gains.

Generally diverse plants of compatible taxa are expected to give high hybrid vigor (Harrington, 1940) and hence, it necessitates study of genetic divergence among the

existing varieties and germplasm collection for identification of more heterotic parents for hybridization program. The information on genetic divergence of various traits particularly of those that contribute to yield and quality would be most useful in planning the breeding programs. The D^2 statistic developed by Mahalanobis (1936) provides a measure of magnitude of divergence between two groups under comparison. It considers the variation produced by any character and their consequent effect that it bears on other characters. This technique has been applied in several crops to select genotypes for further breeding programs. Grouping of genotypes based on D^2 analysis will be useful in choosing suitable parental lines for heterosis breeding. Such studies are also useful in selection of parents for hybridisation to recover superior transgressive segregants and it can further result into release of improved open-pollinated varieties for commercial cultivation (Thippeswamy *et al.*, 2016).

Pumpkin is considered as a major cucurbit crop after cucumber and watermelon (Naik *et al.*, 2015). Despite of so much variability and genetic diversity very little work has been done to estimate the amount of genetic divergence in pumpkin crop. Wide range of variability is reported but very limited attempt had been made for improvement of quantitative as well as qualitative characters (Ozturk *et al.*, 2022). Hence, in order to develop high yielding varieties with good quality and desirable yield contributing characters it would be worthy to identify parents with good quality traits, high yielding ability and the nature of gene action governing yield, quality and their component traits, which could be of great help in selecting parents for the hybridization program to get the maximum heterosis (Ganapati *et al.*, 2020). Keeping this in view, the present investigation carried out to identify the most suitable diverse genotypes with superior morphological characters and the investigation in pumpkin has been planned with following major objectives:

- i. To determine the genetic variability among pumpkin genotypes;
- ii. To know the interrelationship among various yield contributing traits; and
- iii. To identify potential genotype for further hybridization program.

CHAPTER II

REVIEW OF LITERATURE

Pumpkin (*Cucurbita maxima* Duch.), is considered as a nutritious crop due to its relatively elevated nutritional content. Among cucurbits, it is a very good source of β -carotene and ascorbic acid that have a major role in nutrition in the form of pro-vitamin A and vitamin C as antioxidants. Pumpkin is produced round the year and extensively grown during rainy and summer season in different parts of the country. Also it has long storage quality than other cucurbitaceous crops. Though pumpkin is considered to have its primary centre of origin in Central America, but a huge diversity can also be found in Asia. It is grown almost in all tropical and sub-tropical parts of the country. Diversity observed for fruit shape, fruit size, fruit colour, fruit pattern etc in various pumpkin genotypes. A wide variation of total carotenoid contents and yield contributing traits in the Indian germplasms of pumpkin has been reported (Pandey *et al.*, 2003). Variability in agronomic traits is the key component of breeding program for broadening the gene pool and requires reliable estimates of heritability to plan an efficient breeding program (Akinwale *et al.*, 2011). Therefore, before initiating the crop improvement program knowledge of variability among and between the genotypes is very important. Decision of method of breeding program for crop improvement is crucial. Before going for genetic improvement of any crop species, one should have a thorough knowledge of all the genetic parameters to estimate and a brief idea about the previous done research. Under this chapter an attempt has been made to review the available relevant literature on pertinent aspects of research under study “Genetic variability and diversity studies in pumpkin” and review are grouped here under the following headings.

2.1 Genetic variability analysis;

2.2 Correlation coefficient analysis;

2.3 Path coefficient analysis; and

2.4 Genetic divergence analysis.

2.1 Genetic variability analysis

Genetic variability is an amount of variation or differences seen within a particular population. It is a measure of the tendency of individual genotypes in a population to vary from one another. Variability is the pre-requisite for any plant breeding program. The knowledge of genetic variability for characters of economic importance, their heritability and genetic advance is very important for planning future breeding in any crop. In favor of that it was suggested that co-efficient of variability together with heritability estimate will give a good picture of amount of genetic advance to be expected from selection. Variability observed for any character is due to differences in the genetic constitution of the populations as well as variation arising due to environmental conditions. The coefficients of genotypic variation and phenotypic variation are used as an aid in the plant breeding work. Brief reviews on the genetic variability present in pumpkin and other cucurbitaceous crops are described below.

Tyagi *et al.* (2018) worked on bitter gourd at Faizabad (UP) and noted that estimates of phenotypic coefficient of variation were higher than corresponding genotypic coefficient of variation in thirty one genotypes of bitter gourd which indicated that variation is not only due to genotypes, but also due to the influence of environment. Characters showing high heritability in broad sense coupled with high genetic advance indicating such characters were controlled by additive gene action. Selection on the basis of these characters could be more effective for crop improvement.

Tamang *et al.* (2018) observed that ten genotypes of cucumber performed differently in biochemical parameters at Sikkim (India). High phenotypic coefficient of variability, genotypic coefficient of variability and heritability estimates coupled with high genetic gain was observed for the fruit weight, fruit length, fruit girth, and fruit yield per plant. Fruit weight and vine length are highly correlated with fruit yield per plant. It indicated the existence of a wide range of variation and offers wide scope for selection of the traits.

At Sirsi (Karnataka), Shet *et al.* (2018) evaluated thirty cucumber cultivars for growth and yield traits. Results revealed that significant genetic variability were present among genotypes for various traits, a high range of variation; high GCV and high

heritability coupled with high genetic advance was recorded for node at first female flower, number of male flower, number of female flower, fruit weight, flesh thickness, fruit length and fruit width. It reveals broad genetic base, less environmental influence and these traits are under control of additive genes.

Rana *et al.* (2018) carried out an investigation with eighteen genotypes of bottle gourd at Bharsar (Uttarakhand). The analysis of variance showed significant variation among different genotypes for all the traits under study. Genetic analysis indicated that phenotypic coefficient of variation was higher than genotypic coefficient of variation in all of the attributes studied. High heritability estimates coupled with high genetic advance as percentage of mean were observed for yield and other horticultural traits.

Doddamani *et al.* (2018) revealed significant differences among the twenty local collection of cucumber for all the traits studied indicating the presence of sufficient variability in genotypes. The phenotypic coefficient of variation was higher than genotypic coefficient of variation and the difference between PCV and GCV was narrow for most of the characters revealing little influence of the environment in the expression of these traits at Arabhavi, Karnataka conditions.

Deepa *et al.* (2018) assessed genetic variability, heritability and genetic gain for various yield and its constituent traits in thirty cucumber genotypes in Arabhavi, Karnataka. Estimates of phenotypic coefficient of variation were higher than the corresponding values of genotypic coefficient of variation, though difference was very less in majority of the cases, thus showing these traits were less influenced by environmental factors. High heritability coupled with high to moderate genetic advance were observed for all the characters except for days to first male and female flowering and fruit set percentage.

Tamilselvi and Jansirani (2017) started an experiment to find out suitable pumpkin genotype for earliness, high yield and quality in Tamil Nadu. About 15 pumpkin genotypes collected from various places were evaluated for different quantitative characters viz., vine length, days to first female flower appearance, node number for first female flower appearance, sex ratio, days to first harvest, fruit number per vine, fruit

weight, flesh thickness, fruit yield per vine and quality parameters viz., total carbohydrate content and total carotenoid content. Analysis of variance revealed that mean sum of squares due to genotypes was highly significant for all characters.

Shrikant *et al.* (2017) indicated that significant differences were observed among 60 F4 generation pumpkin genotypes used to study variability, heritability and genetic advance under Bagalkot, Karnataka conditions. High estimates of heritability coupled with high values of genetic advance over mean was observed for average fruit weight, β -carotene content of fruit, seed cavity length, sex ratio, number of seeds per fruit, fruit yield per vine, vine length at 45 and 75 DAS, number of primary branches per vine at 45 and 75 days after sowing, number of fruits per vine and fruit length. This indicates predominance of additive component for these traits and hence direct selection would be more effective in improving these traits.

Rambabu *et al.* (2017) revealed significant differences among twenty one genotypes of bottle gourd in West Bengal. In general PCV was marginally higher than the corresponding GCV indicated the less influence of environment in the expression of the characters under study. High heritability coupled with high genetic advance as percentage of mean was observed for few characters viz., vine length, number of primary branches, days to first male flower appearance, days to first female flower appearance, days to first harvest, number of fruits per vine, average fruit weight, fruit length, fruit width, fruit yield per plant, sex ratio, seed number per fruit, 100 seed weight, TSS of the pulp, total sugar content and ascorbic acid content of the pulp indicated that these characters were mainly controlled by additive gene effects and thus selection may be effective for improvement in these characters.

Rajawat and Collis (2017) conducted an experiment under Allahabad agro-climate condition to study genetic variability, heritability and genetic advance for some traits in twelve cucumber genotypes. The study indicated existence of considerable amount of genetic variability for all the traits in all the genotypes used in the experiment. High genetic advance over mean coupled with high heritability was observed in characters like number of male flowers per vine, vine length and fruit weight. Higher

heritability estimates were accompanied by lower genetic advance over the mean for vitamin C, TSS, fruit yield per vine and days to first fruit harvest.

Mohsin *et al.* (2017) recorded highest genotypic coefficient of variation for fruit length, fruit weight, TSS and yield per plant in twenty one diverse genotypes of pumpkin at Gazipur (Bangladesh) . Heritability estimates in broad sense were higher for almost all the characters. The characters namely, fruit length, single fruit weight, yield per plant and TSS had high genotypic coefficient of variation coupled with heritability gave high genetic advance expressed as percentage of mean ranged from 76.84 to 96.06 which indicated that these characters were less influenced by environment confirming additive gene action, and therefore, selection of these characters would be more effective for yield improvement of pumpkins.

Mishra *et al.* (2017) evaluated a set of forty genotypes of muskmelon to study genetic variability among the traits at New Delhi. The results reported high GCV and PCV for fruit yield per plant, fruit weight per plant, vine length and proline content in non-stress, 50% and 25% water stress conditions, respectively. High estimates of heritability along with high genetic advance as percentage of mean over the characters was recorded for fruit weight (128.79, 164.05 and 161.15), proline content (42.50, 72.86 and 69.26) and fruit yield per plant (149.61, 186.91 and 184.12) in both the non-stress and stress conditions .This shows that the setraits were under the control of additive genetic effects. Therefore, it was concluded that selection for these traits should lead rapid genetic improvement of the material.

Kandasamy (2017) evaluated twenty diverse genotypes of cucumber at Annamalai (Tamil Nadu) and found that maximum phenotypic and genotypic co-efficient of variation was for yield per plant followed by average fruit weight, fruit diameter and number of fruits per vine. High heritability was observed for all the characters except node number of first female flower. Genetic gain was reported to have maximum values for yield per plant followed by average fruit weight, fruit diameter, number of fruits per vine, number of secondary branches, fruit length, fruit girth and 1000 seed weight.

Hamdi *et al.* (2017) revealed a considerable genetic variability for most of the agromorphological parameters in fifteen local accessions of squash. Morphological variation was most apparent in fruit characteristics.

Oliveira *et al.* (2016) conducted an experiment to report the characterization and evaluation of fourteen pumpkin accessions at Rio de Janeiro. They revealed that there was a great variability among pumpkin landraces used during their experiment.

Nahar *et al.* (2016) reported that analysis of variance for different characters showed there was high degree of variation among those forty accessions of sweet gourd which were studied for evaluation of field performance and genetic variability. In all the traits genotypic coefficient of variation was smaller than phenotypic coefficient of variation. Results of their study revealed that wide variability exists among the sweet gourd accessions used in the experiment at Bangladesh.

In Nigeria, Fayeun *et al.* (2016) evaluated genetic variation among twenty one fluted pumpkin genotypes for seedling traits. High phenotypic coefficients of variation and genotypic coefficients of variation were observed for leaf area (75.44%) and dry shoot weight (55.85%) respectively, while heritability estimates above 50 percent was observed for leaf area (82.0%), dry weight (77.78%), emergence percent (70.84%) and seedling vigor index (51.98%).

Ene *et al.* (2016) observed that high coefficient of variation was recorded for most traits in both seasons and high variability was found among genotypes in sixteen cucumber genotypes in Nigerian situation. High heritability was associated with all the traits in both seasons, except for mean fruit weight in the early planting season and fruit girth, mean fruit weight, and total fruit yield in late planting season. Rani *et al.* (2015) observed that analysis of variance showed highly significant differences for all the characters studied in twenty eight F₁ which were evaluated to determine the various parameters of genetic variability and nature of inter relation among traits affecting yield in bitter gourd. High heritability in association with high genetic advance as percent mean was observed for yield per vine, number of fruits per vine, average fruit weight, fruit length and number of laterals per vine.

Khan *et al.* (2015) found that there was a great deal of significant variation for all the characters studied among seventeen genotypes of bitter gourd. Considering genetic parameters high GCV was observed for branches per vine, yield per plant and number of fruit per plant. However, low GCV was observed for days to first male and female flowering. In all the cases, it was found that PCV was greater than GCV. They concluded that highest genotypic and phenotypic co-efficient of variation was observed in branch per vine, fruit length, fruit weight and number of fruit per plant which indicated a wide variability among the genotypes and offered better scope of selection.

Pathak *et al.* (2014) analyzed variability among eight horticultural characters of twenty bitter gourd hybrids in Ludhiana (Punjab). They observed that for most of the parameters under study, PCV was found to be higher than GCV. High heritability with high genetic advance was observed for fruit weight, fruit length and fruits per vine which is an indicative of greater proportion of additive genetic variance and consequence a high genetic gain from selection. High heritability with low genetic advance was observed for days to first male and female flower anthesis and days to marketable maturity from anthesis, indicated that non-additive gene effects were involved for the expression of these characters.

Jat *et al.* (2014) evaluated genetic variability, heritability and genetic advance for some traits in sixteen genotypes of valankakri in Rajasthan. On the basis of this study they concluded that selection would be rewarding for acidity of fruit, total yield per vine, weight of fruit, number of fruits per vine, total soluble solids and diameter of fruit in bringing out the improvement in the valankakri because they appeared with high value of GCV, PCV, heritability and genetic gain.

Akter *et al.* (2013) reported that significant variations were found among thirty pumpkin genotypes for most of the characters studied under Bangladesh condition. High genotypic coefficient of variation and high heritability coupled with high genetic advance in percentage of mean were observed for beta-carotene followed by non-reducing sugar, number of seeds per fruit, yield per plant, dry weight, flesh thickness, number of male flowers per plant and number of female flowers per plant which indicated that these

characters were under additive gene control and selection for genetic improvement for these traits might be effective.

Yadav *et al.* (2012) revealed that the mean sum of square was highly significant for all traits, indicating the presence of wide variability in twenty genotypes of cucumber. In general, the phenotypic variance and phenotypic coefficients of variation were higher than the respective genotypic variance and genotypic coefficients of variation for all the traits indicating a considerable influence of environment on their expression. They found that genotypes were possessed a high to moderate phenotypic variation for various characters as revealed by PCV.

Sharma and Sengupta (2012) carried out a field trial with sixteen genotypes of bottle gourd for evaluating their performance for various horticultural characters. They showed that there was a great deal of significant variation for all the characters among the genotypes. High genotypic co-efficient of variation was observed for fruit weight (39.48%). In all cases, PCV were higher than the GCV. They found high heritability with high genetic advance as % of mean for all the characters and all characters were under additive gene control. Therefore, they suggested selection would be best for genetic improvement for these traits.

Gaikwad *et al.* (2011) noted that in eighteen genotypes of cucumber a high degree of variation was observed in respect of all the characters studied in Rahuri (Maharashtra). The estimates of genotypic coefficient of variation were slightly low as compared to estimates of phenotypic coefficient of variation indicating the substantial modifying effect of environment in the expression of the traits studied.

Balkaya *et al.* (2010) showed appreciable phenotypic variation in fruit shape, fruit color, fruit brightness, fruit dimension and fruit weight in winter squash in Turkey. Cluster analysis based on fourteen quantitative and seven qualitative variables identified ten different groups. They found first five principal component axes accounted for 65 percent of the total multivariate variation among the populations. The greater part of variance was accounted for fruit weight, fruit diameter, fruit length, length of seed cavity and flesh thickness.

Khan *et al.* (2009) worked with twenty four accessions of pointed gourd in Bangladesh. Evaluation of yield and yield components revealed high phenotypic and genotypic coefficients of variation and wide variations among the accessions in respect of plant, leaf, flower, fruit and seed characters were recorded. The accessions varied significantly for days required to first flowering, number of node at first harvest, inter node length at first harvest, vine length at first harvest, fruit length, breadth and weight, pulp weight per fruit, pulp seed ratio, number of fruits per vine, weight of fruits per vine, number of seeds per fruit, weight of seed per fruit and yield.

Islam *et al.* (2009) observed wide genetic variation among bitter gourd genotypes for branches per vine, yield per plant and number of fruits per plant under Bangladesh situation. Considering genetic parameters high GCV was observed for branches per vine, yield per plant and number of fruit per plant whereas, low GCV was observed for days to first male and female flowering. In all cases, phenotypic variances were higher than the genotypic variance.

Kanwar *et al.* (2003) found wide range of variation in twenty six indigenous and exotic cucumber genotypes in Nauni, Solan situation with respect to different traits, except for harvest duration. They observed high heritability estimates accompanied with high genetic gain for sex ratio, yield per plant and node of first female flower indicating additive gene control for inheritance of these traits.

In the northern region of Bangladesh during the kharif season, Ahamed *et al.* (2011) conducted an experiment to evaluate the morphological and yield characteristics of pumpkin (*Cucurbita moschata*). Different genotypes' leaf lengths, which varied from 30.6-47.2 cm, showed considerable diversity.

For this character in the bottle gourd, Husna (2009) discovered that GCV (22.87) was lower than PCV (23.04).

Gaffar (2008) noted that the GCV (20.94%) was marginally lower than the PCV (23.31 %). For this trait in sponge gourd, heritability in the broadest sense was high (94%) with a moderate genetic progress (7.81).

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

At the farm of the Olericulture Division, HRC and in various RARS, BAR] throughout the summer of 2005, Quamruzzaman *et al.* (2008) conducted an experiment to examine the genetic divergence among thirty genotypes of ridge gourd (*Luffa acutangula*). The genotypes RGNO3, RGN 12 had the lowest cluster mean values for days to the first female flower open (27.0 days) and single fruit weight (141.0 g), while RGNO5, RGNO6, RGNO7, RGNO8, RGN 13, RGN 17, RGN 18, RGN27, and RGN29 had the greatest values (85.0 g). The relevance of fruit width, single fruit weight, days to first male flower opening, days to first female flower opening, and fruit number in PCA in determining genetic divergence.

Significant genetic differences were discovered for all the features in snake gourd by Rajkumar and Karuppaiah (2007). With the exception of days to first female flower, all characters had high heritable estimates. According to Banik (2003) the parent P4 was the greatest general combiner for fruits per plant, first male and female flower.

Suresh babu(1989) study of 50 pumpkin genotypes, found significant variation in the times between the first male flower anthesis (41.0–73.0 days) and the first female flower opening (41.0-84.5 days). Prior to the first male flower anthesis, the lowest PCV was noted for days (13 .08).

At the Research Farm of the Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Salna, Gazipur, during the growing season 2011–12, Akter *et al.* (2013) conducted an experiment among thirty accessions of pumpkin genetic divergence. Beta-carotene, non-reducing sugar, the number of male flowers per plant, and the number of female flowers per plant all showed high genotypic coefficient of variation high heritability, and high genetic advance in percent of mean, indicating that these characters were under additive gene control and that selection for genetic improvement for these traits might be successful.

According to Husna (2009) research, the female bottle gourd flower pedicel length is 3.13–9 cm while the male flower pedicel length is 3.5-21 cm. Rashid (1993) reported that

the male flower pedicel length in bottle gourds is longer than the female flower pedicel length. According to Grubben (2004), female bottle gourd flowers have 2-10 cm long pedicels, but male flowers have 7-31 cm long pedicels.

Banik (2003) discovered that snake gourds have high heritability and high genetic progress for fruit length (GCV and PCV 29.92 and 30.04; h^2 99.19 percent).

According to Mathew and Khader (1999) the snake gourd had the highest GCV and PCV for fruit length.

High GCV and PCV were found by Saha *et al.* (1992) for fruit length (30.34 and 31.76), but low values were found for fruit diameter (8.87 and 10.23). Both the diameter (75.07) and the length (11.27%) were estimated to be high h^2 .

Rahman *et al.* (1986) reported high GCV and PCV for bottle gourd fruits that were 31.73 and 33.75 in length and 39.23 and 41.96 in diameter. Additionally, they noted the smallest difference between GCV and PCV. Characters with a high GCV have a greater chance of being selected successfully (Burton, 1952).

According to Mathew and Khader (1999) the maximum GCV and PCV were for mean fruit weight. In snake gourds, they found a strong heritability for the mean fruit weight.

According to Akter *et al.* (2013), there was a positive and very significant correlation between the yield per plant, the number of fruits per plant, and the weight of a single fruit. Path coefficient analysis showed that the number of fruits per plant provided the greatest direct contribution to yield, followed by the number of days until the first female flower and the weight of a single fruit, indicating that these characteristics should be regarded as the main contributors to yield.

Husna *et al.* (2012) investigated the variability, correlation, and path analysis among the 31 bottle gourd genotype's various features. Fruit weight and yield per plant showed high genotypic co-efficients of variation, whereas fruit breadth showed low genotypic co-efficients of variation. The quantity of fruits per plant, followed by fruit weight, had the greatest direct impact on production per plant, according to a path co-efficient analysis.

2.2 Correlation coefficient analysis

The statistic which measures the relation and its extent, between two or more variables is known as correlation coefficient. Interrelation among different characters is of great importance in plant breeding program. Correlation coefficient provides a measure of genotypic association between the characters and helps to decide the dependability of the characters with each other. If two traits are positively correlated, then one trait can be improved indirectly by improving the other trait. The knowledge about correlation to yield traits is necessary; we can do simultaneous selection of two or more characters. Brief reviews on the inter relationship between different yield and yield attributing characters among different cucurbitaceous crops are described below.

Maurya *et al.* (2019) evaluated the thirty genotypes of bitter gourd at Faizabad (Uttar Pradesh). In most cases the genotypic correlation coefficient was higher than the respective phenotypic correlation coefficients indicating the suppressive effect of environment modified phenotypic expression of these characters by reducing phenotypic correlation values. The phenotypic correlation coefficients between different characters were generally similar in magnitude and nature to the corresponding genotypic correlation coefficient. The significant and positive correlation with yield per plant was observed at phenotypic level with average fruit weight and number of fruits per vine.

Sultana *et al.* (2018) observed that yield were positively and significantly correlated with fruit weight, 100 seed weight, branes per plant and fruits per vine in thirty nine genotypes of bottle gourd at Gazipur (Uttar Pradesh). Negative associations of yield were noted with days to first male and female flower opening, days to harvest and length of fruit. Path analysis revealed that fruits per vine (0.93) and weight of fruit (0.467) had very high positive effect on fruit yield.

Sharma *et al.* (2018) conducted a study at Himachal Pradesh, to examine relationship between important traits of cucumber. Correlation studies revealed that yield per plot had positive and significant association with number of marketable fruits per vine, average fruit weight, harvest duration, seed germination and seed vigor index-I, while significant negative correlations were observed with node number bearing first female

flower, days to marketable maturity, anthracnose and angular leaf spot both at phenotypic and genotypic levels.

At Allahabad (U.P.) Ramesh *et al.* (2018) revealed that in fourteen genotypes of ridge gourd, fruit yield was positively and significantly correlated with fruit percent, number of fruits per vine, fruit length and average fruit weight, fruit diameter, vine length at 90 days, sex ratio and rind thickness while selecting a good hybrid for enhancing the yield of ridge gourd.

Panigrahi *et al.* (2018) noticed the fruit yield per vine and per hectare had positive and highly significant correlation with most of the characters viz., number of primary branches, vine length, number of fruits per vine and length of fruit in thirty seven genotypes of bottle gourd at Hisar (Haryana). Fruit yield per vine and yield per hectare were also positively correlated with each other at both genotypic and phenotypic level.

Kumari *et al.* (2018) showed that most of the traits have significant correlation among nineteen genotypes of cucumber at Varanasi. The fruit yield per plant had significant and positive correlations with both genotypic and phenotypic traits like average fruit weight, number of fruits per vine, number of pistillate flowers per plant, fruit width, vine length, and number of nodes per vine.

Kumar *et al.* (2018a) conducted an experiment to study correlation for yield and quality traits of twenty eight genotypes of pumpkin. The correlation coefficient analysis at genotypic level revealed that fruit yield per vine had positive and significant association with fruit number per vine (0.85), fruit weight (0.61), fruit equatorial diameter (0.53), ascorbic acid content (0.69) and crude fiber content (0.49).

Chetariya *et al.* (2018) observed that the values of genotypic correlation, in general, were higher as compared to the corresponding phenotypic correlation in fifty diverse genotypes of bottle gourd. This indicated that though there was high degree of association between two variables at genotypic level, its phenotypic expression was deflated by the influence of environment. The character fruit yield per vine was found to be significantly and positively correlated with fruit length, average fruit weight, vine length and fruit girth at both the genotypic and phenotypic levels.

Ahmed *et al.* (2018) evaluated nineteen pumpkin inbreds to measure the association among the characters and their contribution to yield. They found the positive and strong association of node number of first female flower, flesh thickness and fruit diameter with yield per plant. On the other hand, days to first male flower and days to first female flower correlated negatively and insignificantly with fruit yield per plant. Moreover, the results indicated that node number to first female flower, average fruit weight, flesh thickness, fruit length, fruit diameter and fruits per vine can be used as useful selection criteria to increase fruit yield per plant in pumpkin.

Saranyadevi *et al.* (2017) conducted the study at Tamil Nadu and found in correlation analysis of twenty genotypes of bitter gourd that fruit yield per vine was significant and positively correlated with vine length, nodes of female flower appearance, fruits per vine, fruit length, fruit girth, fruit weight, fruit thickness, seeds per fruit, momordicine content and protein content. However negative association was observed with days to first male flower appearance, days to first female flower appearance and nodes of first male flower appearance.

Shivprasad *et al.* (2017) estimated correlation among muskmelon hybrids at Bagalkot, Karnataka. They found that vine length, number of branches per plant and number of leaves per plant are having positive association with number of fruit per plant and total sugars. Vitamin C is negatively associated with vine length, number of branches per plant and number of leaves per plant, fruit weight flesh thickness and yield. Fruit weight and yield negatively correlated with node to first flowering, days to first female flower and sex ratio. Vitamin C is negatively associated with total sugars, whereas the total sugars highly positive significant with total soluble solids.

Thakur *et al.* (2017) revealed that fruits per vine and average fruit weight had highest significant positive association with yield at both phenotypic and genotypic levels and also had significant positive direct effect on fruit yield per hectare in seventy three bottle gourd genotypes at Raipur.

Yadagiri *et al.* (2017) carried out experiment at Gwalior (Madhya Pradesh) and observed that there was a great deal of significant correlation for all the characters among twenty genotypes of bitter gourd. Length of vine (0.640), number of branches per vine (0.577),

number of male flowers per vine (0.594), number of female flowers per vine (0.529), number of fruits per vine (0.649), fruit length (0.724), weight of fruit (0.961), number of seeds per fruit (0.360), seed weight per fruit (0.380) had significant positive correlation for yield.

Gautam *et al.* (2017) revealed in character association studies of forty two genotypes of ridge gourd that fruit yield had positive and significant correlation with average fruit weight (0.774), number of fruits per vine, vine length, number of primary branches, fruit length, seed length whereas, fruit yield had negative and significant correlation with number of node to first female/hermaphrodite flower, days to first female/hermaphrodite flower anthesis and days of first fruit harvesting.

Manikandan *et al.* (2017) studied correlation in six parents of ash gourd and their hybrids in Tamil Nadu climatic condition. Results indicated that yield per vine had highly significant and positive association with the individual fruit weight, number of fruits per vine, fruit length, fruit girth and flesh thickness.

Pal *et al.* (2017) carried out an trial on cucumber genotypes at Bangaluru, Karnataka and revealed that yield per plant had positive significant association with average fruit weight, fruit length and diameter, marketable fruits per vine, harvest duration, vine length, primary branches per plant, seed length, hundred seed weight, germination percentage, seed vigor index I and II, whereas, yield per plant had negative significant correlation with node number bearing first female flower, days to first harvest, total soluble solids and severity of four foliar diseases.

At Andhra Pradesh, Rani *et al.* (2017) observed in correlation analysis of bottle gourd that number of branches per vine, number of fruits per vine, fruit length, fruit girth, and number of seeds per fruit showed strong positive correlation with yield and among themselves. Therefore, these characters could be used as indices for selection of genotypes with high yielding potential.

Reddy *et al.* (2017) evaluated set of thirty five germplasm lines of muskmelon at Andhra Pradesh to study the relationship among eighteen quantitative traits pertaining to growth, earliness and yield characters. Their study showed that fruit yield had a positive

correlation with vine length, number of primary branches per vine, fruit length, fruit diameter, average fruit weight, number of fruits per vine, fruit cavity length, fruit cavity width, rind thickness and seed yield, while it had a negative correlation with the node numbers of the first pistillate flower, days to last fruit harvest and pulp thickness.

Ananthan and Krishnamoorthy (2017) found through genotypic and phenotypic correlation coefficients that yield per plant significantly contributed by fruit weight (0.722 and 0.681), fruit diameter (0.426 and 0.393), fruits per vine (0.504 and 0.477) and first female flower node (0.467 and 0.428) in correlation study of ridge gourd under Tamil Nadu location.

Deepthi *et al.* (2016) assessed the nature of association among yield and its contributing traits in twenty four bottle gourd genotypes including one check at Andhra Pradesh. Correlation studies showed that yield per vine had significant positive association with tendril length, number of nodes per vine, number of primary branches per vine, total vine length, inter nodal length, number of fruits per vine, fruit weight, fruit diameter, number of seeds per fruit and 100 seed weight both at phenotypic and genotypic levels indicating the importance of these traits in selection for yield and are identified as yield attributing characters. They concluded that simultaneous improvement can be made if selection is made for any one of the correlated traits.

Gupta *et al.* (2015) carried out an experiment with twenty six genotypes of bitter gourd including check Solan Hara at Palampur. They found that average fruit weight (0.726), marketable fruits per vine (0.547) and seeds per fruit (0.377) exhibited positive phenotypic association while marketable fruits per vine (0.684), seeds per fruit (0.625), average fruit weight (0.591) and node at which first female flower appears (0.338) showed genotypically positive association with total marketable fruit yield per hectare.

Iqbal (2015) revealed the positive and significant relationship between first male flower node position and pH value in correlation study of 12 genotypes of bitter gourd at Faisalabad, Pakistan. The study emphasized that first male node position is highly significant with first female node position. Increase in female node position will reduce the yield potential of plant. The above findings indicated that the lower the node at which first male or female flower appeared the higher and earlier would be the yield. Therefore,

they concluded that during the breeding of bitter gourd for higher yield, lines with lower position of first male and female flower node should be selected.

Janaranjani and Kanthaswamy (2015) studied correlation and direct and indirect effects of different characters on fruit yield of thirty six hybrids of bottle gourd at Puducherry (Tamil Nadu). The overall analysis revealed that fruit yield was positively and significantly correlated with fruit flesh thickness, number of fruits per vine and number of fruit pickings.

At Hyderabad, Rani *et al.* (2015) evaluated twenty eight F₁ of bitter gourd to determine the nature of inter relationships among traits affecting yield. They found that yield per vine expressed positive and significant genotypic association with number of fruits per vine, average fruit weight, vine length, number of laterals per vine and fruit length whereas, significant negative association with sex ratio, days to first female flower and node number at first female flower appeared.

Aliya *et al.* (2014) observed fruiting period and fruits per vine not only had positive significant correlation with fruit yield but also had positive high direct effect on it and are regarded as the main determinants of fruit yield in 50 genotypes of spine gourd. Days to first fruit harvest had positive moderate direct effect on fruit yield and its association was negatively significant, days to last fruit harvest had negative high direct effect on fruit yield and its association was significant positive.

Rashid *et al.* (2014) tested eight F₁ genotypes for correlation coefficient in snake gourd. They found that days to female male flowering, node number of first bearing of female and male flower, days to first harvest, number of fruits per vine, total number of fruits, total weight of fruit per plant and yield, individual fruit weight, fruit length and fruit diameter were major contributing factors towards yield and selection based on these characters can be effective for developing high yielding varieties.

Singh *et al.* (2014) found that the characters like fruits per vine and fruit length had significant and positive correlation with yield in bitter gourd. Fruits per vine and average fruit weight had the highest positive direct effect on fruit yield per plant.

Ullah *et al.* (2012) observed that fruit yield per plant showed high significant positive correlation with fruits per vine, fruit weight, flesh thickness, fruit diameter and leaves per plant in 12 genotypes of cucumber at Bangladesh. Partial correlation was significant for fruits per vine and indicated these traits contributed over 70 percent to total fruit yield. By variability, correlation and regression analysis it was concluded that more fruits per vine and more fruit weight are major yield contributing factors in selecting high yielding cucumber cultivars.

Kumar *et al.* (2013) noted that total yield per vine was found to be positively and significantly correlated with number of fruits per vine, average weight of fruit and number of seeds per fruit in twenty sponge gourd genotypes.

Reshmi and Sreelathakumary (2012) found that vine length had positive correlation with yield and was mainly due to their positive indirect effects through fruit length in twenty genotypes of ash gourd at Thiruvananthapuram condition. At the same time, sex ratio, fruit girth and seeds per fruit made high positive correlation with yield due to their positive indirect effects through average fruit weight. Direct effects of vine length, node to first female flower and sex ratio were negligible, but their indirect effect through fruit length and average fruit weight were consistently high.

Rabbani *et al.* (2012) indicated that in sixty genotypes of ridge gourd, yield per plant had highly significant positive relationship with the number of fruits per vine, average fruit weight, vine length at harvest and length of fruit. On the other hand, the sex ratio and circumference of fruit exhibited negative association with yield, when the experiment was conducted at Bangladesh.

Aruah *et al.* (2012) revealed that in ten pumpkin accessions, number of seeds per fruit had a significant positive correlation with the number of male flowers per plant and fruit diameter at Nigeria. A significant positive correlation was also obtained between the number of flowers and the fruits per vine that was an indication that both traits increased or decreased simultaneously. Therefore, they concluded that the days to flowering, fruit diameter and number of seeds per fruit can be used as selection criteria to increase fruit yield in pumpkin.

Kumar *et al.* (2011) conducted an experiment at Solan (Himachal Pradesh) and revealed that in cucumber genotypes yield had significant positive association with marketable fruits per vine, fruit length and breadth, average fruit weight, harvest duration, total soluble solids, seed germination, and seed vigour index-I and II, while significant negative correlations were observed with node number bearing first female flower, days to marketable maturity, severity of powdery mildew, anthracnose and angular leaf spot, both at phenotypic and genotypic levels.

Husna *et al.* (2011) observed highest significant association of yield per plant with reproductive characters number of fruit per plant followed by fruit weight at genotypic and phenotypic level in bottle gourd genotypes under correlation studies.

2.3 Path coefficient analysis

Path analysis provides knowledge of direct and indirect cause of association and partitions the correlation coefficient into the direct and indirect effect of a set of independent variables on dependent variables (Nagariya *et al.*, 2015). Brief reviews on the research related to inter relationship and direct and indirect effect on yield and yield attributing characters among different cucurbitaceous crops are described below.

Sharma *et al.* (2018) examined path coefficient analysis in 30 genotypes of cucumber at Solan, Himachal Pradesh and showed that severity of powdery mildew had maximum positive direct effect on yield per plot followed by TSS, fruit length, average fruit weight, days to marketable maturity, number of marketable fruits per vine, seed vigor index-I, severity of anthracnose, harvest duration, fruit breadth, severity of angular leaf spot and seed vigor index-II. While, negative direct effect of seed germination and node number bearing first female flower was observed on yield per plot. Hence they concluded that future breeding should focus on selecting the characters having direct effects to improve yield per plot.

Kumar *et al.* (2018a) conducted an experiment to study path analysis for yield and quality traits of twenty eight genotypes of pumpkin and noted that number of fruits per vine exerted the highest positive direct effect (3.64) on total yield per plant followed by sex ratio (2.29), fruit polar diameter (1.83), days to first harvest (1.57) and fruit equatorial diameter (0.92) at genotypic level. Besides this negative direct effect on yield

per plant was recorded by 100 seed weight (-2.06), ascorbic acid content (-1.12), fruit weight (1.03), β -carotene (-0.90) and days to first female flower appearance (-0.39).

Kumar *et al.* (2018b) assessed the nature and magnitude of association among yield and its contributing traits in thirty two genotypes of cucumber. The path coefficient analysis revealed that the number of fruits per vine, fruit weight, number of primary branches per plant, fruit length, 100 seed weight, number of seeds per fruit, days to last fruit harvest, fruit diameter and number of nodes per vine have direct positive phenotypic and genotypic effect on yield. Hence, direct selection for these traits can be done for improving fruit yield per plant.

Yadagiri *et al.* (2017) noted yield was found to be directly correlated with crop duration (0.004), length of vine (0.030), number of seeds per fruit (0.045) and length of fruit (0.094). Hence, they concluded that selection based on these characters would be more rewarding in bitter gourd.

Sampath and Krishnamoorthy (2017) evaluated thirty two pumpkin genotypes and path analysis study revealed that the characters like fruit weight (1.367) and flesh thickness (5.348) were the most important yield determinants, because of their high direct effects and high indirect effects via many other yield and quality improving characters. The indirect effect also showed that most of the characters influenced the yield through vine length (0.282), days to first female flower anthesis (0.414) and fruit length (0.524). Hence, they suggested that emphasis must be given to such traits while exercising selection to improve the yield in pumpkin.

Ahirwar *et al.* (2017) revealed that fruits per vine (0.860) showed positive significant correlation with yield, among forty four genotypes with two checks Pant Khira-1 and Pointsette of cucumber. Analysis was conducted under Pantnagar (Uttarakhand) climatic conditions. Values of direct and indirect contribution of different traits revealed the maximum direct effect of fruits per vine (0.837) and maximum positive indirect effect of fruits per vine (0.110) on yield per plant.

Jena *et al.* (2017) worked on path analysis study in twenty two genotypes of pointed gourd they revealed that fruits per vine and number of nodes per vine had the

greatest direct effect on yield both at phenotypic and genotypic level. Thus, selection for these characters will improve the yield. The results indicated that fruits per vine and number of nodes per vine can be considered during selection for improved yield in pointed gourd.

Manikandan *et al.* (2017) found in path analysis that the fruit characters such as flesh thickness, fruit length, fruit weight, fruit girth and number of fruits per vine are considered as important traits which directly and indirectly influences yield. This study confirm that individual fruit weight, number of fruit per plant, fruit length, fruit girth and flesh thickness were the important characters for varietal selection of ash gourd.

Pal *et al.* (2017) observed that path analysis provide a clear picture that, harvest duration had maximum positive direct effect, followed by marketable fruits per vine while, days to first harvest had maximum negative direct effect followed by severity of downy mildew on yield per plant in thirty cucumber genotypes. Further, harvest duration exerted maximum positive indirect effect via marketable fruits per vine whereas; severity of powdery mildew showed maximum negative indirect effect via harvest duration on yield per plant. Thus, while conducting selection for yield improvement in cucumber, a breeder will have to emphasize on these characters.

Singh *et al.* (2016) studied path coefficient analysis in determining the important yield attributing characters for the selection of high yielding types of pointed gourd. They found that the leaf width (4.733 cm), number of seeds per fruit (3.634), petiole length (0.812 cm), seed pulp ratio (2.284), fruit diameter (1.729 cm), length of vines (1.225 cm) and fruit length (0.671 cm) have got the maximum positive effect on the yield.

Kumar *et al.* (2013) observed that average diameter of fruit, number of primary branches, number of fruits per vine, average weight of fruit and total soluble solids showed positive direct effects on total yield per vine in sponge gourd. Hence, selection for these traits for improving yield per vine is suggested.

Kumar *et al.* (2011) revealed in path coefficient analysis of cucumber genotypes that average fruit weight had maximum positive direct effect on yield followed by harvest duration, seed vigor index-II, severity of angular leaf spot, anthracnose and powdery

mildew, marketable fruits per vine and total soluble solids whereas, negative direct effect of fruit length and breadth, seed vigor index-I, days to marketable maturity, seed germination, fruit length and node number bearing first female flower was observed on yield. Hence, direct selection for fruit weight, harvest duration and fruits per vine with minimum disease severity may be reliable for yield improvement in cucumber.

In path analysis of thirty one bottle gourd genotypes, Husna *et al.* (2011) observed that highest significant association of yield per plant with reproductive characters number of fruit per plant followed by fruit weight at genotypic and phenotypic level. Path co-efficient analysis revealed maximum direct contribution towards yield per plant with of number of fruit per plant followed by fruit weight.

Tomar *et al.* (2008) evaluated fifty genotypes of musk melon at Anand (Gujarat) and path analysis based on genotypic associations revealed that fruits per vine and moisture percentage were the main yield attributing characters in fruit yield of muskmelon, because of its high positive direct effect and positive correlation with fruit yield per plant. In addition to moisture percentage and fruits per vine, total soluble solids also exhibited positive direct effect on fruit yield per plant. Thus, it could be advocated that fruits per vine, moisture percentage and total soluble solids should be given more importance for an effective selection program to improve the fruit yield in muskmelon.

2.4 Genetic divergence analysis

Genetic diversity is the variation in the amount of genetic information within and among individuals of a population, a species, an assemblage, or a community (United Nations, 1992). Swingland (2001) defined genetic diversity as the variation of heritable characteristics present in a population of same species. The improvement of cultivated plants considerably depends on the extent of genetic variability available between the populations. Knowledge of genetic diversity among existing cultivars of any crop is essential for long term success in breeding program and to maximize the exploitation of the germplasm resources (Belaj *et al.*, 2002). It is also a pre-requisite for hybridization program to obtain high heterosis among hybrids. It provides opportunity to develop improved cultivars with desirable traits.

Genetic diversity facilitates breeders to develop varieties for specific traits like quality improvement and tolerance to biotic and abiotic stresses (Bhandari *et al.*, 2017). For planning and executing of genetic improvement program a clear understanding of the magnitudes of genetic diversities for yield and its component characteristics are important to plant breeders for both cross and self pollinated crops (Griffing and Lindstrom, 1954). Brief reviews on the genetic diversity present in pumpkin and other cucurbitaceous crops are described below.

Shah *et al.* (2018) revealed that there was a wide genetic diversity among the 13 cucumber genotypes studied for the nature and magnitude of genetic divergence in Srinagar (Uttarakhand). All genotypes were grouped into four clusters based on Mahalanobis D^2 statistics using Tocher's method. They concluded that diverse genotypes can be extensively used for further breeding program to generate new material.

Simmi *et al.* (2018) reported that characters like branches per plant, male and female flowers per plant, fruit length, fruit weight, fruits per vine, fruit yield per plant contributed the maximum variability towards divergence among thirty nine cucumber genotypes which were grouped into six clusters under Bangladesh conditions.

Sultana *et al.* (2018) observed genetic diversity for yield and its component traits on twenty one genotypes of pumpkin in Bangladesh. They found that high degree of variation exhibited within the collection, as reflected by mean diversity index value of 0.80. The genotypes were grouped into five different clusters. Based on inter cluster distance, inter genotypic distance and consideration of desirable characters for high yield potential, they declared some genotypes belonging to different clusters can be selected as better parents for future hybridization program.

Verma *et al.* (2017) estimated the genetic divergence for twelve characters on thirty five genotypes of pointed gourd under tarai conditions of Pantnagar. Cluster analysis and principal component analysis were used to identify the most discerning trait responsible for greater variability in the lines and on the basis of mean performance; genotypes were classified into seven clusters. The high diversity found in the genotypes showed its great potential for improving qualitative as well as quantitative traits in pointed gourd.

Gautamet *et al.*(2017)at Faizabad (Uttar Pradesh), for genetic divergence using principal component analysis (PCA) and non-hierarchical cluster analysis. The first ten principal component score grouped the genotypes into three cluster accommodating 5, 22 and 15 genotypes in cluster I, II, and III, respectively. The intra-cluster distances ranged from 2.724 (cluster I) to 3.550 (cluster II). The inter cluster distances were found maximum (5.984) between cluster I and II, and minimum (3.419) between cluster II and III suggesting scope for exploiting heterosis upon hybridization between genotypes of these groups of desired traits.

Kumar *et al.* (2017) conducted an investigation using thirty two germplasm of ridge gourd. Genetic divergence analysis following Mahalanobis D^2 statistics revealed wide range of genetic diversity among germplasm of ridge gourd for all the eleven characters which was pertaining to growth, yield and quality traits. Genetic variation within and between different clusters were observed.

Rani and Reddy (2017) noted that thirty five ridge gourd germplasm which were grouped into five clusters based on D^2 values, exhibited no association between geographical and genetic divergence. They concluded by results of the study that on the basis of mean performance of different clusters, genotypes having better performance could be utilized as donor parents for respective traits in hybridization program.

Debata *et al.* (2017) assessed genetic diversity among thirty six genotypes of pointed gourd under climatic condition of Pantnagar (Uttarakhand). All the thirty nine genotypes of pointed gourd were classified into seven non-overlapping clusters on the basis of D^2 analysis. Maximum inter cluster distance was found between cluster VII and IV (72.42). This indicates that inter genotypic crosses between the members of cluster VII and IV would exhibit high heterosis and is also likely to produce new recombinants with desired traits.

Chaudhari *et al.* (2017) studied the genetic divergence on forty diverse genotypes of pumpkin in Gujarat and grouped them into fourteen clusters. They found that total sugar content contributed maximum to total genetic divergence followed by fruit weight, fruit yield per plant, β -carotene, flesh thickness, first male flowering node, test weight of 100 seeds, equatorial circumferences of fruit and number of seeds per fruit among the

clusters. Their results indicated the potential for a wide scope of varietal improvement through hybridization and selection due to the wide genetic diversity present in the accessions studied.

Hasan *et al.* (2015) grouped seven cucumber genotypes into three different clusters in Bangladesh. The highest inter-cluster distance (4.078) was observed between cluster I and II whereas, lowest inter-cluster distances (1.011) was observed between the clusters I and III. Cluster II showed highest mean for length of main vine, nodes per plant, primary branches per plant, days to first male flowering, length of internodes per plant, fruits per vine and yield per plant whereas, cluster III produced highest mean for leaf length, leaf breadth, fruit length, fruit diameter and fruit weight. Cluster II and III contributed 53.8 and 38.4 percent, respectively towards divergence.

Similarly, Iqbal (2015) evaluated twelve entries of bitter melon and reported that wide genetic diversity occurred for all the traits under Pakistan condition. Differences between genotypic co-efficient of variation and phenotypic coefficient of variation indicated the majority of variation in traits was due to genetics. Node position of the first male flower, fruit length, pH, vitamin C content and yield were additive based upon high broad sense heritability coupled with high genetic advance over percentage of mean. These traits could be improved through direct selection.

Naik and Prasad (2015) tested twenty five cultivars of pumpkin in Allahabad. The results of their study indicated significant differences among all the genotypes for all the characters under study. The genotypes were grouped into five different clusters. Clustering pattern revealed that geographical diversity was not associated with genetic diversity. The wider genetic diversity was observed in cluster II, III and VI which indicate the potentiality of this diverse genotype collection for providing basic material for future breeding program.

Extreme genetic divergence have reported by Visen *et al.* (2015) among five major clusters of thirty one bottle gourd genotypes which were used to analyze genetic diversity for yield and its contributing traits. They found that characters such as fruit length, fruit girth and average fruit weight contributes maximum towards genetic divergence under climatic conditions of Raipur.

Ara *et al.* (2014) grouped twenty eight genotypes of bottle gourd into five different clusters on the basis of D^2 values and showed the existence of wide genetic diversity among them. They also suggested that the genotypes within a cluster might have some degree of ancestral relationship and geographic diversity may not necessarily be related with genetic diversity. Therefore, the selection of genotypes for hybridization should be based on genetic diversity rather than on geographic diversity.

Haque *et al.* (2014) evaluated performance of eight snake gourd genotypes in Bangladesh. Wide ranges of variability were found in the studied characters among the genotypes. Flowering period was significantly correlated with yield contributing characters. Number of fruits per vine, total number of fruits per plot and individual fruit weight was significantly and positively correlated with yield of snake gourd.

Singh *et al.* (2014) assessed thirty two bitter gourd genotypes including two checks, i.e. Pusa Do Mausami and Kalyanpur Sona, based on cluster and principal component for yield and its eleven contributing traits. The cluster analysis categorized all bitter gourd genotypes into 6 major clusters and they found extreme genetic divergence among clusters. Based on cluster and principal component analyses promising diverse parents identified and selected for future hybridization program in Bhagalpur (Bihar).

Abd El-Hamed *et al.* (2015) reported a wide range of variability among thirteen summer squash and one winter squash germplasm accessions in Egypt, for morphological and chemical characteristics. At a similarity level of 82 percent the genotypes were divided into two clusters. The first cluster consisted of eight genotypes (PI 506466, PI 292014, PI 518688, PI 615119, PI 136448, Butternut, Copi, and Eskandrani). The second cluster contained only two genotypes (Yellow Crookneck and Shamamy). Results of evaluation were proved with the help of RAPD markers which provides clear evidence that there is a considerable variation among summer squash genotypes. Therefore, their results were helpful in development of breeding programs in squash since high genetic variability in its accessions and landraces has been found.

Onyishi *et al.* (2013) determined the extent of variability in twelve accessions of tropical pumpkin at Nigeria. Results of the study showed that there exists a

sufficient genetic variability among the accessions that could be utilized as a germplasm pool for further improvement of the crop.

Kumar *et al.* (2013) revealed that selection of divergent parents should be based on the cluster distances to obtain favorable hybrids and transgressive segregants. They analyzed cucumber genotypes to know the nature and magnitude of variability and genetic divergence under Udaipur, Rajasthan condition. The genotypes were grouped into 4 clusters and the highest (6.168) inter cluster distance was recorded between cluster II and III. The diverse genotypes characterized by maximum inter cluster distance and were different in phenotypic performance.

Golabadi *et al.* (2012) noted that there was a high significant variation for all of the studied traits between twenty cucumber genotypes. Cluster analysis with Ward method divided the genotypes to four distinct groups. They concluded that, selection of superior genotypes in view point of desirable morphological traits, with high genetic distance could be selected for hybridization programs and recognition of best genotypes for different traits to produce new elite hybrids.

Kundu *et al.* (2012) assessed genetic diversity of thirty six genotypes of bitter gourd based on twenty two characters through principle component analysis. Their results showed that first three components accounted for 60.04 percent of the total variation. Days to first male flower opening, number of primary branches per vine, fruit yield per vine, days to green fruit maturity, seed weight per fruit, mature seed width had the highest contribution towards the divergence.

Bharthi and Vishalnath (2011) indicated that twenty two land races of pointed gourd, based on D^2 values the accessions were grouped into five clusters. The pattern of group constellations indicated that genetic diversity was not directly correlated to the geographic diversity.

Kabir *et al.* (2009) conducted an experiment to estimate the genetic diversity among twenty four genotypes of pointed gourd by using Mahalanobis D^2 statistics for nine characters. The genotypes were grouped into five clusters. The clustering pattern of the genotypes under this study revealed that the genotypes collected from the same location

were grouped into different clusters. The inter cluster distance were larger than the intra cluster distance suggesting wider genetic diversity among the genotypes of different groups under Bangladesh condition.

Khan *et al.* (2008) analyzed sixty four pointed gourd genotypes in Bangladesh condition through multivariate analysis. The genotypes were grouped into twelve clusters. The clustering pattern of the genotypes under this study revealed that the genotypes collected from the same location were grouped into different clusters. Fruit weight, seeds per fruit and fruit weight per plant contributed maximum to the total divergence.

Sharma and Sharma (2006) grouped the genotypes of cucumber into seven clusters through cluster analysis in Solan (Himachal Pradesh). From the information regarding cluster distance they concluded that parents selected from distantly related clusters may provide a broader genetic base for crop improvement program and may produce heterotic hybrids or transgressive segregants in later generations.

CHAPTER III

MATERIALS AND METHODS

The experiment was conducted at Sher-e-Bangla Agricultural University, Dhaka to study the evaluation of morphological traits and genetic diversity of pumpkin germplasm. Materials used and methodologies followed in the present investigation have been described in this chapter.

3.1 Experimental period

The experiment was conducted during the period from March to September 2020 using 18 pumpkin (*Cucurbita maxima* Duch.) genotypes.

3.2 Description of the experimental site

3.2.1 Geographical location

The experiment was conducted both in the field of Sher-e-Bangla Agricultural University (SAU). The experimental site was geographically situated at 23°77' N latitude and 90°33' E longitude at an altitude of 8.6 meter above sea level (Anonymous, 2004).

3.2.2 Agro-Ecological Zone

The experimental field belongs to the Agro-ecological zone (AEZ) of “The Madhupur Tract”, AEZ-28 (Anonymous, 1988 a). This was a region of complex relief and soils developed over the Modhupur clay, where floodplain sediments buried the dissected edges of the Modhupur Tract leaving small hillocks of red soils as ‘islands’ surrounded by floodplain (Anonymous, 1988 b). For better understanding about the experimental site has been shown in the Map of AEZ of Bangladesh in Appendix-I.

3.2.3 Soil

The soil texture was silty clay with pH 6.1. The morphological, physical and chemical characteristics of the experimental soil have been presented in Appendix- II.

3.2.4 Climate and weather

The climate of the experimental site was subtropical, characterized by the winter season from November to February and the pre-monsoon period or hot season from March to April and the monsoon period from May to October (Edris *et al.*, 1979). Meteorological data related to the temperature, relative humidity and rainfall during the experiment period of was collected from Bangladesh Meteorological Department (Climate division), Sher-e-Bangla Nagar, Dhaka and has been presented in Appendix-III.

3.3 Planting materials

For the purposes of the current research, eighteen genotypes of pumpkin were used as experimental materials. The purity and germination percentage were leveled as around 100 and 80, respectively. The seeds of the pumpkin genotypes were collected from the Plant Genetic Resources Center (PGRC) of the Bangladesh Agricultural Research Institute (BARI), Gazipur and local market (Table 1).

3.4 Design and layout of the experiment

The experiment was laid out using a randomized complete block design (RCBD) with three replications. The genotypes were distributed across the blocks of the planned experiment via randomization technique. Pits were kept 1 meter apart from one another.

Polybag preparation for different genotypes of pumpkin is presented in Plate 1 and germination stage of different genotype is presented in plate 2.

Table 1. List of eighteen pumpkin genotypes with their accession and source

Sl. No.	Genotype No.	BARI ACC Number	Source
1	G1	BD-4396	PGRC,BARI
2	G2	BD-4381	PGRC, BARI
3	G3	BD-4352	PGRC, BARI
4	G4	Hazari (Local)	Local market
5	G5	BD-4398	PGRC, BARI
6	G6	Gadikata (Local)	Local market
7	G7	BD-4389	PGRC, BARI
8	G8	BD-4361	PGRC, BARI
9	G9	BD-4380	PGRC, BARI
10	G10	BD-4368	PGRC, BARI
11	G11	BD-4357	PGRC, BARI
12	G12	BD-4356	PGRC, BARI
13	G13	BD-4391	PGRC, BARI
14	G14	BD-4371	PGRC, BARI
15	G15	BD-4382	PGRC, BARI
16	G16	Diamond(local)	Local market
17	G17	BD-4351	PGRC, BARI
18	G18	Black super (local)	Local market

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



Plate 1. Picture showing poly bag preparation for different genotype of pumpkin



Plate 2. Picture showing germination of different genotype of pumpkin

3.5 Poly bag preparation and raising seedling

To increase the germination rate and produce healthy seedlings, the seeds were dibbled into poly bags. The seedlings were moved into the pits at the main field when they were 12 days old. Before sowing, seeds were treated with Bavistin for 5 minutes.

3.6 Land preparation

The experiment plot was prepared by multiple ploughing and cross ploughing, followed by laddering and harrowing with a tractor and power tiller to create good tilth. The experimental plot was carefully cleared of weeds and other debris and leveled as needed.

3.7 Pit preparation

Pits measuring 55 cm × 55 cm × 50 cm with a spacing of 3 m × 3 m were constructed in each block after the final land preparation. To get rid of hazardous insects and bacteria, pits were left exposed to the sun for seven days. Furadan (5 mg) was also mixed with the soils of each pit before making it ready for dibbling.

3.8 Application of manure and fertilizers

During the last stage of land preparation, all cowdung, half of TSP, and one-third of MOP were applied on the field. One week before transplantation, remaining TSP, a third of MOP, complete gypsum, zinc oxide, and a third of urea were applied in the pit. At 20, 40, 60, and 75 days after transplanting, the remaining urea and MOP were applied in four installments as top dressing. Table 2 displays the manure dosages and fertilizers utilized in the study.

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

	Fertilizers/Manures	Dose
1	Cowdung	5 ton per ha
2	Urea	125kgperha
3	TSP	125 kgperha
4	MOP	150 kgperha
5	Gypsum	75 kgperha
6	Zinc Oxide	10 kgperha

3.9 Transplanting of seedlings

The seeds germinated in under ten days, and then seedlings from several accessions were placed in the pit. Two seedlings were placed in each pit, and the soil around each plant was thoroughly packed by hand. Mulching straw given to different genotypes is presented in plate 3.

3.10 Intercultural operations

3.10.1 Thinning and gap filling

For appropriate development and to avoid a crowded environment, only one healthy seedling was preserved per pit. When necessary, thinning and gap filling were carried out for this.

3.10.2 Weeding and mulching

Several weeding and mulching were done as per requirement. For better aeration and less competition for seedling growth, weeding was done at the very beginning. Mulch was used following watering to minimize crust formation and promote good aeration.

3.10.3 Irrigation and after-care

Early on, water cane was used for twice-daily for irrigation. Flood irrigation was used at the mature stage as needed.

3.10.4 Pesticide application

Malathion 57EC (organophosphate insecticide) and Ripcord 10 EC (Cypermethrin) were applied in the field in response to the red pumpkin beetle attacking sensitive leaves at the seedling stage. Cucurbit fruit flies inflicted serious damage on the fruit when it was mature. MSGT (Mashed Sweet Gourd Trap), pheromone bait, Ripcord, and Sevin powders were utilized as fruit fly defenses.

3.11 Harvesting

From setting to marketable stage, the fruit needs roughly 7 to 10 days. Fruits were selected frequently throughout the harvesting season based on horticultural maturity, size, color, and age being determined for eating purposes as the fruit developed quickly and soon got past the marketable stage. Sharp knives were used to carefully harvest the fruits while taking care to protect the plant.



Plate 3. Picture showing mulching straw given to different genotype of pumpkin

3.12 Data recording

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

3.12.1. Plant characteristics

i. Leaf length (cm)

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

ii. Leaf breadth (cm)

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

iii. Internode distance (cm)

Internode distance was measured in three to five internodes in each germplasm in cm and average data was recorded.

3.12.2 Flower characteristics

i. Days to first male flowering

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

ii. Days to first female flowering

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

iii. Pedicel length of male flower

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

iv. Pedicel length of female flower

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

3.12.3 Fruit characteristics

i. Fruit length

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

ii. Fruit breadth

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

iii. Fruit weight (Kg)

Weight of three to five fruits in each genotype during harvest for vegetable use was measured in kilogram (kg).

iv. Fruit yield per plant (Kg)

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

3.13 Statistical analysis

All characters under examination underwent a univariate analysis of the individual character using the mean values (Singh and Chaudhury, 1985), which was estimated using the MSTAT-C computer program. To examine the differences between the genotype means, Duncan's Multiple Range Test (DMRT) was run on each character. Using MSTAT-C, it was also possible to estimate the mean, range, and co-efficient of variation (CV percent). Multivariate analysis was performed on the character mean data. Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA), and Canonical Vector Analysis were the four V methods (Volume, Variety, Variation and Visibility) used in the multivariate analysis carried out by computer utilizing GENSTAT 5.13 and Microsoft Excel 2000 software (CVA).

3.13.1 Analysis of variance

Source of variation	Degree of freedom	Sum of squares	Mean sum of squares	Variance ratio (V.R.)
Replication (r)	r-1	SSr	SSr/(r-1) =MSSr	MSSr/MSSe
Genotypes (g)	g-1	SSg	SSg/(g-1) = MSSg	MSSg/MSSe
Error (e)	(r-1) (g-1)	SSe	SSe/(r-1) (g-1) =MSSe	

Where,

r = Number of replications

g = Number of genotypes

SSr = Sum of squares due to replications

SSg = Sum of squares due to genotypes

SSe = Sum of squares due to error

MSSr = Mean sum of squares due to replications

MSSg = Mean sum of squares due to genotypes

MSSe = Mean sum of squares due to error

The calculated F-value was compared with tabulated F-value. When F-test was found significant, critical difference was calculated to find out the superiority of one entry over the others.

The standard error and critical differences were calculated as follows:

$$SE(m)\pm = \sqrt{Me/r}$$

$$SE(d)\pm = \sqrt{2Me/r}$$

$$CD_{0.05} = S.E.(d) \times t_{(0.05)(r-1)(g-1)df}$$

$$SE(m)\pm = \text{Standard error of mean}$$

Where,

$$SE(d)\pm = \text{Standard error of difference}$$

$$CD_{0.05} = \text{Critical difference at 5\% level of significance}$$

3.13.2 Mean performance and genetic variability

The genotypic and phenotypic coefficients of variability were calculated as per formulae given by Burton and De Vane (1953).

A) Genotypic Coefficient of Variation (GCV)

$$GCV (\%) = \frac{\sqrt{\text{Genotypic variance (Vg)}}}{\text{General mean of population } (\bar{x})} \times 100$$

B) Phenotypic Coefficient of Variation (PCV)

$$\text{PCV (\%)} = \frac{\sqrt{\text{Phenotypic variance (Vp)}}}{\text{General mean of population } (\bar{x})} \times 100$$

3.13.3 Heritability (in broad sense)

Heritability in broad sense was calculated by the formula as suggested by Allard (1960).

$$\text{Heritability (\%)} = \frac{V_g}{V_p} \times 100$$

Where,

V_g = Genotypic variance [$V_g = (M_g - M_e) / r$]

V_p = Phenotypic variance [$V_g + V_e$]

3.13.4 Genetic advance (GA)

The expected genetic advance (GA) resulting from selection of 5% superior individuals was worked out as suggested by Allard (1960).

Genetic advance = $H \times \sigma_p \times K$

Where,

K = 2.06 (Selection differential at 5% selection index)

σ_p = Phenotypic standard deviation

H = Heritability in broad sense

3.13.5 Estimation of genetic advance percentage of mean

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

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

3.13.6 Correlations

The genotypic and phenotypic correlations were calculated as per Al-Jibouri *et al.* (1958) by using analysis of variance and covariance matrix in which total variability has splited

into replications, genotypes and errors. All the components of variance were estimated from the analysis of covariance as given below:

3.13.7 Analysis of variance and covariance

Source of variation	Degree of freedom	Mean sum of squares		Mean sum of products	Variance
		X	Y		
Replication (r)	r-1				
Genotypes (g)	g-1	Mg X	Mg Y	Mg XY= MP ₁	MP ₁ / MP ₂
Error (e)	(r-1) (g-1)	Me X	Me Y	Me XY= MP ₂	

Genotypic, phenotypic and environmental co-variances between X and Y characters were worked out as under:

$$V_{eXY} = MP_2$$

$$V_{gXY} = (MP_1 - MP_2)/r$$

$$V_{pXY} = V_{gXY} + V_{eXY}$$

Where, V_{eXY} = Environmental covariance between X and Y

V_g = Genetic covariance between X and Y

V_{pXY} = Phenotypic Covariance between X and Y

3.13.8 Coefficients of correlation

a. Genotypic correlation coefficient between X and Y

$$r_g = \frac{V_{gXY}}{\sqrt{V_{gX} \times V_{gY}}}$$

Where,

V_{gXY} = Genotypic covariance between X and Y

V_{gX} = Genotypic variance of X

$V_g Y =$ Genotypic variance of Y

b. Phenotypic correlation coefficient between X and Y

$$r_p = \frac{V_{pXY}}{\sqrt{V_{pX} \times V_{pY}}}$$

$V_{pXY} =$ Phenotypic covariance between X and Y

$V_{pX} =$ Phenotypic variance of X

$V_{pY} =$ Phenotypic variance of Y

Genotypic variance (V_g) = $(M_g - M_e) / r$

Phenotypic variance (V_p) = $(V_g + V_e)$

The calculated correlation coefficients (r) values were compared with ‘r’ tabulated values as given by Fisher and Yates (1963) at (n-2) degrees of freedom to test their significance, where ‘n’ denotes number of genotypes. If calculated ‘r’ value at 5% level of significance was greater than tabulated value of ‘r’, the correlation was said to be significant.

3.13.9 Path coefficient analysis

Using the phenotypic correlation coefficient value, path coefficient analysis was carried out in accordance with the method used by Dewey and Lu (1959), as quoted in Singh and Chaudhary (1985). In route analysis, the direct and indirect impacts of yield contributing characters on grain yield per hectare were divided by the correlation coefficients between yield and yield contributing characters. The correlated characters, 1, 2, 3..... and 13 have direct and indirect effects on yield y, and in order to assess these effects, a series of simultaneous. It is necessary to formulate equations (eight equations in this example), as illustrated below:

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

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

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

$$r_{4,y} = r_{1.4} P_{1,y} + r_{2.4} P_{2,y} + r_{3.4} P_{3,y} + P_{4,y} + r_{4.5} P_{5,y} + r_{4.6} P_{6,y} + r_{4.7} P_{7,y} + r_{4.8} P_{8,y} + r_{4.9} P_{9,y} + r_{4.10} P_{10,y} + r_{4.11} P_{11,y} + r_{4.12} P_{12,y}$$

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

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

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

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

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

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

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

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

Where,

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

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

1 = Days to first male flowering

2 = Days to first female flowering

3 = Leaf length (cm)

- 4 = Leaf breadth (cm)
- 5 = Internode distance (cm)
- 6 = Pedicel length of male flower (cm)
- 7 = Pedicel length of female flower (cm)
- 8 = Number of male flower per plant
- 9 = Number of female flower per plant
- 10 = Fruit weight (kg)
- 11 = Fruit length (cm)
- 12 = Fruit breadth (cm)

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

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

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

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

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

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

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

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

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

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

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

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

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

Where,

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

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

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

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

Where,

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

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

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

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

3.13.10 Multivariate analysis

Mahalanobis' (1936) general distance (D^2) statistic and its auxiliary analyses were used to evaluate the genetic diversity among the genotypes. Mahalanobis' D^2 statistic was used to pick the parents in hybridization programs, and it was considered to be a more reliable method because the required information on the parents' multitude of features was accessible before crossing. Rao (1952) proposed that the selection of genetically diverse parents for a hybridization program had been made practicable by the assessment of genetic diversity through biometrical processes. Multivariate analysis, such as Principal Component, Cluster, and Canonical Vector analysis (CVA), which quantifies the differences between a number of quantitative variables, is an effective way to assess genetic diversity. These are listed below:

3.13.11 Principal component analysis (PCA)

The sum of squares and products matrix for the characters can be used to do principal component analysis, one of the multivariate approaches, to evaluate the correlations between various characters. In order to display the majority of the original variability in fewer dimensions, PCA searches for linear combinations of a set variate that maximize the variation contained within them. The correlation matrix and genotype scores for the

first component, which has the feature of accounting for the largest variance, and subsequent components with latent roots greater than unity were used to compute the principal components. The latent vectors of the first two main components are used to discuss how the various morphological characteristics contributed to divergence.

3.13.12 Cluster analysis (CA)

The genotypes of a data set are divided by cluster analysis into a number of mutually exclusive groups. Non-hierarchical classification was used for clustering. The algorithm used by Genstat to look for the best values of a selected criterion works as follows. The algorithm repeatedly moved genotypes from one group to another as long as the transfer enhanced the criterion's value after initially classifying the genotypes into the necessary number of groups. The algorithm moves on to the second stage, where it looks at the impact of merging two genotypes of different classes, and so forth, if no additional transfer can be discovered to improve the criterion.

3.13.13 Canonical vector analysis (CVA)

By identifying linear combinations of the original variables that maximize the ratio of between-group to within-group variance, canonical vector analysis (CVA) produces functions of the original variables that can be used to distinguish between the groups. As a result, a number of orthogonal transformations were used in this analysis to maximize the ratio of variation between groups to variation within groups. The roots and vectors of WB , where W is the pooled within groups covariance matrix and B is the among groups covariance matrix, serve as the foundation for canonical vectors.

3.13.14 Calculation of D^2 values

According to Rao (1952) and Singh and Chaudhury (1985), the Mahalanobis distance (D^2) values were derived using converted uncorrelated means of characters. For all conceivable genotype combinations, the D^2 values were estimated. The formula defines D^2 statistic in a more straightforward manner.

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

Where,

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

x = Number of characters.

3.13.15 Computation of average intra-cluster distances

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

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

Where,

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

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

3.13.16 Computation of average inter-cluster distances

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

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

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

N_i = Number of populations in cluster i.

n_j = Number of populations in cluster j.

3.13.17 Cluster diagram

The cluster diagram proposed by Singh and Chaudhury (1985) was drawn using the values of intra- and inter-cluster distances ($D = D_z$). The pattern of variety among the genotypes included in a cluster is briefly described

CHAPTER IV

RESULTS AND DISCUSSION

Results obtained from the present study have been presented and discussed in this chapter with a view to study the evaluation of morphological traits and genetic diversity of pumpkin germplasm. The results have been discussed, and possible interpretations are given under the following headings.

4.1. Genetic variability

The results of the analysis of variance showed that there was significant genetic variation among the pumpkin genotypes. Table 3 displayed the mean, standard deviation, mean sum of squares, variance components, genotypic and phenotypic coefficients of variance, heritability, genetic advance, and genetic advance expressed as a percentage of the mean.

4.1.1. Plant height (cm)

The plant height of 18 genotypes of pumpkin showed significant variation. Significant mean sum of squares for plant height (322.29) suggested that the genotypes under study showed a great deal of variation (Table3).The genotype G8 (BD-4361) had the tallest plants (229.33 cm), while G13 (BD-4391) had the shortest plants (195.00 cm), with a mean height of 210.59 cm (Appendix IV). The phenotypic variance (127.32) seemed to be larger than the genotypic variance (97.49), which indicated that the phenotypic coefficient of variation (5.35%) and the environment's influence on expression (4.68%) were rather near to one another. High PCV and GCV estimates suggesting that these traits were under the influence of genetic control and less affected by environment. Highest heritability (76.57) and moderate genetic advance (17.79) and genetic advance in percent of mean (8.45 %) revealed that the character was controlled by additive genes. Thus the selection based on this character would be effective. Hence, these traits can be relied upon, and simple selection can be practiced for further improvement. Doddamani *et al.* (2018) revealed significant differences among the twenty local collection of cucumber for all the traits studied indicating the presence of sufficient variability in genotypes. The phenotypic coefficient of variation was higher than genotypic coefficient of variation and the difference between PCV and GCV was narrow for most of the

characters revealing little influence of the environment in the expression of these traits at Arabhavi, Karnataka conditions.

4.1.2 Number of branches per plant

Significant mean sum of squares of number of branches per plant was observed (1.65) (Table 3). The mean number of branches per plant was 9.00, with the maximum number of branches per plant being 11.00 in G4 (Hazari Local) and the lowest number of branches per plant (7.67) was found in G11 (BD-4357). The phenotypic variance (1.01) seemed to be slightly larger than the genotypic variance (0.32), suggests less influence of environment on the expression of this gene controlling the trait. The phenotypic coefficient of variation (11.17 %) and the environment's influence on expression (6.27 %) was large which indicated presence of environmental influence for the expression of the characters. Highest heritability (31.47) and moderate genetic advance (0.65) and genetic advance in percent of mean (7.24%) revealed that the character was controlled by additive genes. Thus the selection based on this character would be effective. Rambabu *et al.* (2017) found significant differences among twenty one genotypes of bottle gourd in West Bengal. In general PCV was marginally higher than the corresponding GCV indicated the less influence of environment in the expression of the characters under study. High heritability coupled with high genetic advance as percentage of mean was observed for few characters *viz.*: number of branches per plant and this characters was mainly controlled by additive gene effects and thus selection may be effective for improvement in these characters.

4.1.3 Leaf length (cm)

In case of leaf length, significant differences were found among 18 genotypes of pumpkin. Highly significant mean sum of square for leaf length (9.23) suggested that the genotypes under study showed a great deal of variation (Table 3). The mean leaf length was 24.43, with the maximum leaf length being 25.99 in G15 (BD-4382) and the smallest leaf length being 20.50 in G10 (BD-4368) in (Appendix IV). The phenotypic variance (4.08), which seemed to be slightly greater than the genotypic variance (2.58), suggested that the phenotypic co-efficient of variation (8.27%), which was close to the genotypic co-efficient of variation (6.57%), had little effect on phenotypic variation. This

characteristic demonstrated substantial genetic advance in percent of mean (10.76) and heritability (63.12%), indicating that the characteristic is governed by additive genes and selection based on this character would be effective. Ahamed *et al.* (2011) reported that in different genotypes' leaf lengths, which varied from 30.6-47.2cm, showed considerable diversity.

4.1.4 Leaf breadth (cm)

In case of leaf breadth, significant differences were found among eighteen genotypes of pumpkin. Significant mean sum of square for leaf breadth (2.46) suggested that the genotypes under study showed a great deal of variation (Table 3). The mean leaf breadth was 20.24, with the maximum leaf breadth being 20.85 in G16 (Diamond local) and the smallest leaf breadth being 17.78 in G17 (BD-4368) (Appendix IV). The phenotypic variance (1.05), which seemed to be slightly greater than the genotypic variance (0.71), suggested that the phenotypic co-efficient of variation (5.06%), which was close to the genotypic co-efficient of variation (4.16%), had little effect on phenotypic variation. This characteristic demonstrated substantial genetic advance in percent of mean (7.03) and heritability (67.37 %) indicating that the trait is governed by additive genes and selection based on this character would be effective.

4.1.5 Days to first male flower

Significant variation of genotype was found of days to first male flower variation as mean sum of square was significant (230.27). Among different genotype G12 (BD-4356) had the longest duration (66.67) require for first male flower blooming, while G1 (BD-4396) had the shortest duration (40.33) required for first male flower blooming, with a mean value of 49.24. (Table3).there was a significant difference between the phenotypic variance (86.67) and genotypic variance (71.80) (Table 3) and it is because of environmental influence. The phenotypic co-efficient of variation (18.90 %), which was close to the genotypic co-efficient of variation (17.21 %), and here is little effect on phenotypic variation. Selection based on this trait would be successful since heritability was high (82.84) and genetic advance in percent of mean (32.26) suggested that the character was governed by additive genes. Shet *et al.* (2018) observed, significant genetic variability among cucumber genotypes for various traits, a high range of

variation; high GCV and high heritability coupled with high genetic advance was recorded for node at first female flower, number of male flower, number of female flower, fruit weight, flesh thickness, fruit length and fruit width. It reveals broad genetic base, less environmental influence and these traits are under control of additive genes.

4.1.6 Days to first female flower

Days to first male flowering revealed highly significant pumpkin genotypes variation as mean sum of square was significant (190.51). Among different genotype, G12 (BD-4356) required the longest duration (68.67) for the emergence of the first female flower, while G13 (BD-4391) required the shortest duration (42.33), with a mean value of 52.11. (Table 3). There was a considerable difference between the phenotypic variance (75.22) and genotypic variance (57.64), suggesting that environmental factors may have affected the traits expressed (Table 3). The phenotypic co-efficient of variation (16.64%), slightly higher than the genotypic co-efficient of variation (14.57 %) had little effect due to phenotypic variation. Heritability was high (76.63) and genetic advance in percent of mean (26.27) indicating successful selection based on this feature as the character was governed by additive genes. Similar result also observed by Rambabu *et al.* (2017) who revealed significant differences among twenty one genotypes of bottle gourd in West Bengal. In general PCV was marginally higher than the corresponding GCV indicated the less influence of environment in the expression of the characters under study. High heritability coupled with high genetic advance as percentage of mean was observed for few characters viz., vine length, number of primary branches, days to first male flower appearance, days to first female flower appearance, days to first harvest, number of fruits per vine, average fruit weight, fruit length, fruit width, fruit yield per plant, sex ratio, seed number per fruit, 100 seed weight, TSS of the pulp, total sugar content and ascorbic acid content of the pulp indicated that these characters were mainly controlled by additive gene effects and thus selection may be effective for improvement in these characters.

4.1.7 Days to first female flower anthesis

Days to first male flowering anthesis revealed highly significant pumpkin genotypes variation as mean sum of square was significant (189.78). Among different genotype, G12 (BD-4356) required the longest duration (71.00) for the emergence of the first female flower anthesis, while G13 (BD-4391) required the shortest duration (45.00), with a mean value of 54.28. (Table3). The phenotypic variance (75.86) and genotypic variance (56.96) differed significantly, indicating that environmental influences may have had an impact on how the traits were manifested (Table 3). Phenotypic variation had little impact as the phenotypic co-efficient of variation (16.05%) was only marginally greater than the genotypic co-efficient of variation (13.91%). Heritability was high (75.09) and genetic advance in percent of mean (24.82) indicating successful selection based on this feature as the character was governed by additive genes. Pathak *et al.* (2014) reported that high heritability with low genetic advance was observed for days to first male and female flower anthesis and days to marketable maturity from anthesis, indicated that non-additive gene effects were involved for the expression of these characters.

4.1.8 Days to first harvest

Days to first harvest of pumpkin genotypes mean square of sum was significant (86.98). Among different genotype, G12 (BD-4356) required the longest duration (114.33) for first harvest of pumpkin, while G15 (BD-4382) required the shortest duration (97.33), with a mean value of 104.30 (Table3). The phenotypic variance (30.94) and genotypic variance (28.02) differed significantly, indicating that environmental influences may have had an impact on how the traits were manifested (Table 3). Phenotypic variation had little impact as the phenotypic co-efficient of variation (5.33%) was only marginally greater than the genotypic co-efficient of variation (5.07%). Heritability was high (90.56) and genetic advance in percent of mean (9.95) indicating successful selection based on this feature as the character was governed by additive genes. Tamilselvi and Jansirani (2017) also reported that the mean sum of squares due to genotypes was highly significant for days to first harvest of pumpkin.

4.1.9 Number of fruits per plant

Highly significant mean sum of square of fruit number per plant was found (1.81). The highest fruit number per plant found 4.33 in G18 (Black super) and G14 (BD-4371) while the lowest number per plant found 1.33 in G12 (BD-4356) with a mean value of 3.19. The fact that the phenotypic variance (0.94) was slightly larger than the genotypic variance (0.44) suggested that the environment had less of an impact on the expression of the gene responsible for this feature. Both the genotypic and phenotypic co-efficient of variations were 30.45% and 20.72%, respectively. Since the character was controlled by an additive gene and heritability was determined to be high (46.29) with a moderately high genetic advance in percent of mean (29.05), the selection based on this character would be successful. Rambabu *et al.* (2017) reported that in general PCV was marginally higher than the corresponding GCV indicated the less influence of environment in the expression of the characters under study. High heritability coupled with high genetic advance as percentage of mean was observed for few characters which indicated that those characters were mainly controlled by additive gene effect. In this case selection may be effective for improvement in these characters. Fruits of different pumpkin genotypes is presented in plate 4.



Plate4. Picture showing morphological variation in fruits among different pumpkin genotypes

4.1.10 Fruit length

Significant fruit length of mean sum square was found in pumpkin genotype (105.10). The mean fruit length was 19.41, with the maximum fruit length being 37.25 in G4 (Hazari) and the lowest fruit length being 12.53 in G12 (BD-4356). The fact that the genotypic variation (34.01) was slightly lower than the phenotypic variation (37.09) suggested that the environment had an impact on the expression of the gene responsible for this feature (Table 3). The genotypic and phenotypic co-efficient of variation were 30.04% and 31.37%, respectively. It was determined that heritability was high (91.69%) and that genetic advance in percent of mean (59.26) was strongly higher, indicating that the character is controlled by an additive gene and that character-based selection will be successful. Rani *et al.* (2015) reported that high heritability in association with high genetic advance as percent mean was observed for number of fruits per of bitter gourd.

4.1.11 Fruit breadth

Pumpkin genotype revealed significant mean sum of square of fruit breadth (572.42). The average fruit breadth was 26.83, with G4 (Hazari) having the highest fruit breadth of 57.57 and G12 (BD-4356) having the lowest fruit breadth of 12.11 (Table 3). The genotypic variation (185.17) was lower than the phenotypic variance (202.10), indicating that the environment may have affected how this trait was expressed by the gene responsible. The phenotypic and genotypic co-efficients of variation were 54.88% and 52.53% respectively. It was found that the character was controlled by an additive gene. So character-based selection will be effective since heritability (91.62) and genetic advance in percent of mean (96.53) was strongly high. Rahman *et al.* (1991) reported high GCV and PCV for bottle gourd fruits that were 31.73 and 33.75 in length and 39.23 and 41.96 in diameter. Additionally, they noted the smallest difference between GCV and PCV. Characters with a high GCV have a greater chance of being selected successfully (Burton, 1952).

4.1.12 Individual fruit weight

Significant mean sum of squares of individual fruit weight was found (0.30). The mean individual fruit weight was 0.76, with the maximum fruit weight of 1.57 kg was found in

G4 (Hazari) and the minimum fruit weight of 0.62 kg was found in G1 (BD-4396) and G13 (BD-4391). The fact that the phenotypic variance (0.11) was slightly larger than the genotypic variance (0.10) suggested that the environment had less of an impact on the expression of the gene responsible for this feature (Table 3). Both the genotypic and phenotypic co-efficients of variation were 40.95% and 43.22%, respectively. Heritability was found high (89.75%) with high genetic advance in percent of mean (79.92) revealed that the character was controlled by additive gene so the selection based on this character would be effective. According to Mathew and Khader (1999) the maximum GCV and PCV were for mean fruit weight. In snake gourds, they found a strong heritability for the mean fruit weight.

4.1.13 Yield per plant

Significant mean sum of squares of yield per plant was found (4.99). The mean yield per plant was 2.51, with the maximum yield per plant of 5.15 kg discovered in G14 (BD-4371) and the minimum yield per plant of 0.57 kg discovered in G12 (BD-4356). The fact that the phenotypic variance (1.86) was slightly larger than the genotypic variance (1.56) suggested that the environment had less of an impact on the expression of the gene responsible for this feature (Table 3). Both the genotypic and phenotypic co-efficients of variance were 49.88% and 54.36%, respectively. Heritability was found high (84.17 %) with high genetic advance in percent of mean (94.26) revealed that the character was controlled by additive gene so the selection based on this character would be effective. Husna *et al.* (2012) reported that in bottle gourd, fruit weight and yield per plant showed high genotypic co-efficients of variation (GCV), whereas fruit breadth showed low genotypic co-efficients of variation. The quantity of fruits per plant, followed by fruit weight, had direct impact on production per plant, according to a path co-efficient analysis. Kanwar *et al.* (2003) reported that in cucumber heritability estimates accompanied with high genetic gain for sex ratio, yield per plant and node of first female flower indicating additive gene control for inheritance of these traits.

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

Parameters	Range		MS	Mean	CV (%)	σ^2_p	σ^2_g	σ^2_e	PCV	GCV	h^2_b	GA (5%)	GA (%) mean
	Max	Min											
PH	229.33	195.00	322.29 **	210.59	6.29	127.32	97.49	29.83	5.35	4.68	76.57	17.79	8.45
NBP	11.00	7.67	1.65**	9.00	4.45	1.01	0.32	0.69	11.17	6.27	31.47	0.65	7.24
LLP	25.99	20.50	9.23**	24.43	8.07	4.08	2.58	1.51	8.27	6.57	63.12	2.63	10.76
LBP	20.85	17.78	2.46**	20.24	6.57	1.05	0.71	0.34	5.06	4.16	67.37	1.42	7.03
DFMF	66.67	40.33	230.27**	49.24	4.68	86.67	71.80	14.88	18.90	17.21	82.84	15.89	32.26
DFFF	68.67	42.33	190.51**	52.11	10.92	75.22	57.64	17.59	16.64	14.57	76.63	13.69	26.27
DFFFA	71.00	45.00	189.78**	54.28	3.82	75.86	56.96	18.89	16.05	13.91	75.09	13.47	24.82
DFH	114.33	97.33	86.98**	104.30	3.49	30.94	28.02	2.92	5.33	5.07	90.56	10.37	9.95
NFP	4.33	1.33	1.81**	3.19	5.26	0.94	0.44	0.51	30.45	20.72	46.29	0.93	29.05
FLP	37.25	12.53	105.10**	19.41	3.42	37.09	34.01	3.08	31.37	30.04	91.69	11.50	59.26
FBP	57.57	12.11	572.42**	26.83	5.46	202.10	185.17	16.93	54.88	52.53	91.62	25.90	96.53
IFW	1.57	0.42	0.30**	0.76	4.08	0.11	0.10	0.01	43.22	40.95	89.75	0.61	79.92
YPP	5.15	0.57	4.99**	2.51	11.84	1.86	1.56	0.29	54.36	49.88	84.17	2.36	94.26

Here, PH = Plant height (cm), NBP = Number of branches per plant, LLP = Leaf length(cm), LBP = Leaf breadth(cm), DFMF = Days to first male flower, DFFFA = Days to first female flower, DFFFA = Days to first female flower anthesis, DFH = Days to first harvest, NFP = Number of fruits per plant, FLP = Fruit length(cm), FBP = Fruit breadth(cm), IFW = Individual fruit weight (kg), YPP = Yield per plant (kg), Range, σ^2_p = Phenotypic variance, σ^2_g = Genotypic variance, σ^2_e = Environmental variance, PCV = Phenotypic Coefficient of Variation, GCV = Genotypic Coefficient of variation, h^2_b = Heritability, GA = Genetic advanced, GA(%) mean = Genetic advance in percent of mean, ** = significant at 1%, and * = significant at 5% level of probability, respectively.

4.2. Correlation coefficient

Yield is a complicated product that is influenced by a number of interconnected quantitative traits. As a result, yield selection may not be successful unless other yield components that directly or indirectly affect it are taken into account. A number of other correlated traits are impacted at the same time when selection pressure is applied to improve a feature that is strongly connected with yield. Therefore, knowledge of the relationship between character and yield as well as among themselves offers guidance to plant breeders for making improvements through selection and clarifies the role of genetic and non-genetic elements in generating the relationship. Thirteen yield-contributing characters of the pumpkin were calculated separately as vegetative character and reproductive character as a result of genotypic and phenotypic correlation coefficient study in Table 4 which discussed character wise below:

4.2.1 Plant height(cm)

Plant height showed highly significant positive correlation with number of branches (Table 4) per plant, days to first harvest, fruit length, fruit and individual fruit weight and yield per plant at both genotypic and phenotypic level, indicating that if plant height increase these parameters will also be increased. Non-significant positive correlation was found in leaf leanth, leaf breadth, days to first male flower, days to first female flower and days to first female flower anthesis. Non-significant and negative correlation was found in number of fruits per plant. Plant height was a central part of plant ecological strategy. It is strongly correlated with life span, seed mass and time to maturity, and is a major determinant of a species ability to compete for light. Plant height was also related to critical ecosystem variables such as animal diversity and carbon storage capacity.

4.2.2 Number of branches per plant

Number of branches per plant showed highly significant positive correlation with fruit length per plant, days to first harvest and individual fruit weight both at genotypic and phenotypic level indicating that if number of branches per plant increase, these parameters will also be increased (Table 4). Non-significant positive correlation was found in leaf length, leaf breadth, days to first male flower, days to first female flower, and days to first female flower anthesis, and yield per plant. Non-significant and negative

correlation was found in number of fruits per plant. Panigrahi *et al.* (2018) noticed that the fruit yield per vine and per hectare had positive and highly significant correlation with most of the characters viz., number of primary branches, vine length, number of fruits per vine and length of fruit in thirty seven genotypes of bottle gourd at Hisar (Haryana).

4.2.3 Leaf length (cm)

Leaf length was highly positive correlation with leaf breadth both in genotypic and phenotypic level indicating that association of this traits was largely influenced by environmental factor (Table 4). While Non-significant and positive correlation was found with days to first male flower, days to first female flower, days to first female flower anthesis, days to first harvest, fruit breadth individual fruit weight and yield per plant. Whereas non-significant and negative correlation was found in number of fruits per plant and fruit length at both phenotypic and genotypic level.

4.2.4 Leaf breadth (cm)

Leaf breadth showed non significant but positive correlation with days to first male flower, days to first harvest, fruit breadth, individual fruit weight and yield per plant (Table 4), where negative and non significant correlation found with days to first female flower, days to first female flower anthesis, and number of fruits per plant at phenotypic level.

4.2.5 Days to first male flower

Days to first male flower showed highly significant and positive correlation with days to first female flower and days to first female flower anthesis, at both genotypic and phenotypic level indicating that the traits were governed by same gene and in that case, simultaneous improvement would be effective (Table 4), while highly significant but negative correlation was observed with number of fruits per plant, fruit length, individual fruit weight and yield per plant at phenotypic level. Non significant but positive correlation was observed with days to first harvest. While non significant and negative correlation was observed with days to first harvest at both genotypic and phenotypic level. Yadagiri *et al.* (2017) observed that there was a great deal of significant correlation

for all the characters among twenty genotypes of bitter gourd. Length of vine (0.640), number of branches per vine (0.577), number of male flowers per vine (0.594), number of female flowers per vine (0.529), number of fruits per vine (0.649), fruit length (0.724), weight of fruit (0.961), number of seeds per fruit (0.360), seed weight per fruit (0.380) had significant positive correlation for yield at both genotypic and phenotypic level.

4.2.6 Days to first female flower anthesis

The character showed highly significant and positive correlation with days to first female flower anthesis at both genotypic and phenotypic level. Highly significant but negative correlation with number of fruits per plant, fruit length, individual fruit weight and yield per plant (Table 4). Non significant but positive correlation with days to first harvest while non significant but negative correlation with fruit breadth. Ahmed *et al.* (2018) found the positive and strong association of node number of first female flower, flesh thickness and fruit diameter with yield per plant.

4.2.7 Days to first female flower anthesis

Days to first female flower anthesis showed highly significant but negative correlation with number of fruits per plant, fruit length, individual fruit weight and yield per plant at phenotypic level and association among these traits was largely influenced by environmental (Table 4). These character was highly significant with days to first female flower anthesis, While non significant but positive correlation with days to first harvest and non significant and negative correlation with fruit breadth that both genotypic and phenotypic level. Kumari *et al.* (2018) showed that most of the traits have significant correlation among nineteen genotypes of cucumber at Varanasi. The fruit yield per plant had significant and positive correlations with both genotypic and phenotypic traits like average fruit weight, number of fruits per vine, number of pistillate flowers per plant, fruit width, vine length, and number of nodes per vine.

4.2.8 Days to first harvest

Days to first harvest showed highly significant and positive correlation with individual fruit weight and significant with yield per plant at both genotypic and phenotypic level indicated that if days to days to first harvest increased fruit yield would be highly increased (Table 4). Non significant but positive correlation with fruit length and fruit

breadth indicated the qualities were governed by same gene and improvement would be effective. Sharma *et al.* (2018) reported that in correlation studies yield per plot had positive and significant association with number of marketable fruits per vine, average fruit weight, harvest duration, seed germination and seed vigor index-I, while significant negative correlations were observed with node number bearing first female flower, days to marketable maturity, anthracnose and angular leaf spot both at phenotypic and genotypic levels.

4.2.9 Number of fruits per plant

At phenotypic level, this trait demonstrated a strong positive connection with individual fruit weight and yield per plant indicating that fruit weight and yield per plant increasing significantly if the number of fruits per plant increased (Table 4). While not significant but positive correlation with fruit length and fruit bread that both genotypic and phenotypic level and association among these traits is largely influenced by environmental. Janaranjani and Kanthaswamy (2015) reported that fruit yield was positively and significantly correlated with fruit flesh thickness, number of fruits per vine and number of fruit pickings.

4.2.10 Fruit length (cm)

At both the genotypic and phenotypic levels, this trait demonstrated a strong positive connection with fruit breadth, individual fruit weight and yield per plant indicating that fruit weight and yield per plant increasing significantly if the number of number of fruits per plant increase (Table 4). Singh *et al.* (2014) found that the characters like fruits per vine and fruit length had significant and positive correlation with yield in bitter gourd. Fruits per vine and average fruit weight had the highest positive direct effect on fruit yield per plant.

4.2.11 Fruit breadth (cm)

Fruit breadth showed highly significant and positive correlation with individual fruit weight, and yield per plant indicated that if days to days to first harvest increases fruit yield would be highly increased (Table 4). Ullah *et al.* (2012) observed that fruit yield per plant showed high significant positive correlation with fruits per vine, fruit weight,

flesh thickness, fruit diameter and leaves per plant in 12 genotypes of cucumber at Bangladesh.

4.2.12 Individual fruit weight (kg)

Individual fruit weight showed highly significant and positive correlation genotypic (0.957) and phenotypic (0.873) variation with yield per plant (Table 4). Maurya *et al.* (2019) reported that in bitter gourd the significant and positive correlation with yield per plant was observed at phenotypic level with average fruit weight and number of fruits per vine.

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

Characters		NBP	LLP	LBP	DFMF	DFFF	DFFFA	DFH	NFP	FLP	FBP	IFW	YPP
PH	G	0.756**	0.462	0.370	0.099	0.031	0.024	0.558**	-0.167	0.271	0.374*	0.511**	0.334*
	P	0.411**	0.258	0.211	0.101	0.074	0.083	0.512**	-0.071	0.207	0.335*	0.454**	0.308*
NBP	G		0.302	0.206	0.147	0.207	0.175	0.516*	-0.263	0.775**	0.639	0.586*	0.366
	P		0.198	0.131	0.080	0.078	0.050	0.343*	-0.181	0.424**	0.386**	0.336*	0.160
LLP	G			0.800**	0.308	0.286	0.279	0.334	-0.254	-0.066	0.107	0.124	0.006
	P			0.668**	0.147	0.037	0.034	0.231	-0.158	0.046	0.086	0.115	0.006
LBP	G				0.114	0.025	0.011	0.409	0.115	0.117	0.203	0.255	0.264
	P				0.038	-0.114	-0.137	0.251	-0.011	0.107	0.192	0.225	0.167
DFMF	G					0.982**	0.988	0.244	-0.601**	-0.516**	-0.194	-0.445**	-0.528**
	P					0.948**	0.934**	0.206	-0.400**	-0.444**	-0.217	-0.411**	-0.472**
DFFF	G						1.000**	0.179	-0.718**	-0.509**	-0.192	-0.533**	-0.640**
	P						0.991**	0.182	-0.407**	-0.454**	-0.206	-0.480**	-0.528**
DFFFA	G							0.156	-0.734**	-0.536**	-0.196	-0.551**	-0.662**
	P							0.169	-0.404**	-0.469**	-0.209	-0.497**	-0.541**
DFH	G								-0.311	0.234	0.035	0.432**	0.313*
	P								-0.218	0.209	0.041	0.405**	0.274*
NFP	G									0.424	0.277	0.538*	0.735*
	P									0.241	0.189	0.301*	0.701**
FLP	G										0.792	0.825**	0.757**
	P										0.742**	0.778**	0.669**
FBP	G											0.576**	0.477**
	P											0.573**	0.457**
IFW	G												0.957**
	P												0.873**

Here, PH = Plant height (cm), NBP = Number of branches per plant, LLP = Leaf length(cm), LBP = Leaf breadth(cm), DFMF = Days to first male flower, DFFFA = Days to first female flower, DFFFA = Days to first female flower anthesis, DFH = Days to first harvest, NFP = Number of fruits per plant, FLP = Fruit length(cm), FBP = Fruit breadth(cm), IFW = Individual fruit weight (kg), YPP = Yield per plant (kg), ** = significant at 1%, and * = significant at 5% level of probability, respectively

4.3 Path analysis

The correlation coefficient's determination of association of character may not accurately provide the exact picture of each yield component's direct and indirect influence. Using path analysis at the phenotypic level, which also quantified the relative significance of each component, direct and indirect impacts were worked out in order to obtain a clear picture of the interrelationship between yield per plant and other yield parameters. Path coefficient analysis estimation of the pumpkin's direct and indirect effects is provided in Table 5.

4.3.1 Plant height (cm)

Plant height had a favorable direct impact on yield (0.015) (Table5) .This character produce negative indirect on number of branches per plant (-0.0322), leaf breadth(-0.0186), days to first female male flower (-0.0171), number of fruits per plant (-0.0552), and fruit breadth (-0.0536). The character also showed positive indirect effect on leaf length (0.0272), days to first male flower (0.0529), days to first female flower anthesis (0.0005), days to first harvest (0.0507), fruit length (0.0791), and individual fruit weight (0.2856) which finally made significant positive correlation with yield (0.334). Deepthi *et al.* (2016) reported that in bottle gourd, correlation studies showed that yield per vine had significant positive association with tendril length, number of nodes per vine, number of primary branches per vine, total vine length, inter nodal length, number of fruits per vine, fruit weight, fruit diameter, number of seeds per fruit and 100 seed weight both at phenotypic and genotypic levels indicating the importance of these traits in selection for yield and are identified as yield attributing characters. They concluded that simultaneous improvement can be made if selection is made for any one of the correlated traits.

4.3.2 Number of branches per plant

Number of branches per plant showed negative effect on yield (-0.043). (Table5). This character produce negative indirect on leaf breadth (-0.0104), days to first female male flower (-0.1148), number of fruits per plant (-0.0868), and fruit breadth (0.0917). The character also showed positive indirect effect on plant height (0.0114), leaf length(0.0177), days to first male flower (0.0789), days to first female flower anthesis (0.0035), days to first harvest (0.0470), fruit length (0.2261) and individual fruit weight

(0.3275) which finally made highly significant positive correlation with yield (0.366). Reddy *et al.* (2017) showed that in muskmelon, fruit yield had a positive correlation with vine length, number of primary branches per vine, fruit length, fruit diameter, average fruit weight, number of fruits per vine, fruit cavity length, fruit cavity width, rind thickness and seed yield, while it had a negative correlation with the node numbers of the first pistillate flower, days to last fruit harvest and pulp thickness.

4.3.3 Leaf length (cm)

Fruit length had a favorable direct effect on yield (0.059). (Table5). This character showed positive indirect effect on plant height (0.0070), days to first male flower (0.1654), days to first female flower anthesis (0.0056), days to first harvest (0.0304) and individual fruit weight (0.0691). The character also showed negative indirect effect on number of branches per plant (0.0129), leaf breadth (-0.0403), days to first female flower (-0.1587), number of fruits per plant(-0.0836), fruit length(-0.0193), fruit breadth(-0.0154), which finally made non-significant but positive correlation with yield (0.006).

4.3.4 Leaf breadth (cm)

Fruit breadth had negative direct effect on yield (-0.050). (Table5). This character showed positive indirect effect on plant height (0.0056), leaf length (0.0470), days to first male flower (0.0611), days to first female flower anthesis (0.0002), days to first harvest (0.0372), number of fruits per plant (0.0381), fruit length(0.0341), and individual fruit weight (0.1428). The character also showed negative indirect effect on number of branches per plant (-0.0088), days to first female flower (-0.0140), fruit breadth(-0.0291), which finally made non-significant but positive correlation with yield (0.264).

4.3.5 Days to first male flower (cm)

Days to first male flower showed positive direct effect (0.537) on yield (Table 5). This character showed positive indirect effect on plant height (0.0015), leaf length (0.0168), days to first female flower anthesis (0.0202), days to first harvest (0.0163), and fruit breadth (0.0275). This character also showed negative indirect effect on number of branches per plant(-0.0063), leaf breadth (-0.0057), days to first female flower (-0.5453), number of fruits per plant (-0.1982), fruit length (-0.1504), and individual fruit weight (-0.2487). The cumulative effect produced a negative but highly significant correlation

with yield (-0.528). Aruah *et al.* (2012) revealed that in ten pumpkin accessions, number of seeds per fruit had a significant positive correlation with the number of male flowers per plant and fruit diameter at Nigeria.

4.3.6 Days to first female flower

Days to first female flower showed negative direct effect (-0.555) on yield (Table 5). This character showed positive indirect effect on plant height (0.0015), leaf length (0.0181), days to first female flower anthesis (0.0198), days to first harvest (0.0222) and fruit breadth (0.0278). plant height (0.0005), leaf length (0.0168), days to first male flower (0.5269), days to first female flower anthesis (0.0202), days to first harvest (0.0163), fruit breadth (0.0275). This character also showed negative indirect effect on number of branches per plant (-0.0088), leaf breadth (-0.0013), number of fruits per plant (-0.2365), fruit length (-0.1485) and individual fruit weight (-0.2982). The cumulative effect produced a negative but significant correlation with yield (-0.640). Kumar *et al.* (2011) revealed that in cucumber genotypes yield had significant positive association with marketable fruits per vine, fruit length and breadth, average fruit weight, harvest duration, total soluble solids, seed germination, and seed vigor index-I and II, while significant negative correlations were observed with node number bearing first female flower, days to marketable maturity, severity of powdery mildew, anthracnose and angular leaf spot, both at phenotypic and genotypic levels.

4.3.7 Days to first female flower anthesis

Days to first female flower anthesis had a favorable positive direct impact on yield (0.020) (Table5). This character showed positive indirect effect on plant height (0.0004), leaf length (0.0164), days to first male flower (0.5300), days to first harvest (0.0142), and fruit breadth (0.0282). This character also showed negative indirect effect on number of branches per plant(-0.0075), leaf breadth (-0.0006), days to first female flower (-0.5573), number of fruits per plant (-0.2420), fruit length per plant (-0.1562), and individual fruit weight (-0.3079). The cumulative effect showed a negative significant association with yield (-0.662). Future breeding should focus on selecting the characters having direct effects to improve yield per plot.

4.3.8 Days to first harvest

Days to first harvest had a favorable positive direct impact on yield (0.091). (Table5). This character showed highest indirect effect on plant height (0.0084), leaf length (0.0196), days to first male flower (0.1308), days to first female flower anthesis (0.0031), fruit length (0.0682), and individual fruit weight (0.2417). This character also showed negative indirect effect on number of branches per plant(-0.0220), leaf breadth (-0.0206), days to first female flower (-0.0994), number of fruits per plant (-0.1025) and fruit breadth (-0.0050). The cumulative effect showed a positive significant association with yield (0.313). Kumar *et al.* (2018b) assessed the nature and magnitude of association among yield and its contributing traits in thirty two genotypes of cucumber. The path coefficient analysis revealed that the number of fruits per vine, fruit weight, number of primary branches per plant, fruit length, 100 seed weight, number of seeds per fruit, days to fast fruit harvest, fruit diameter and number of nodes per vine have direct positive phenotypic and genotypic effect on yield.

4.3.9 Number of fruits per plant

The character showed a positive direct effect (0.33) on yield (Table 5). This character showed positive indirect effect on number of branches per plant(0.0112), days to first female flower (0.3985), fruit length (0.1237) and individual fruit weight (0.3006). This character also showed negative indirect effect on plant height (-0.0025), leaf length (-0.0149) leaf breadth (-0.0058), days to first male flower (-0.3227), days to first female flower anthesis(-0.0147), days to first harvest (-0.0283) and fruit breadth (-0.0347). The cumulative effect showed a positive significant association with yield (0.735). Kumar *et al.* (2018 a) noted that number of fruits per vine exerted the positive direct effect (3.64) on total yield per plant followed by sex ratio (2.29), fruit polar diameter (1.83), days to first harvest (1.57), and fruit equatorial diameter (0.92). Besides this negative direct effect on yield per plant was recorded by 100 seed weight (-2.06), ascorbic acid content (-1.12), fruit weight (1.03), β -carotene (-0.90) and days to first female flower appearance (-0.39). AHIRWAR *et al.* (2017)revealed that fruits per vine (0.860) showed positive significant correlation with yield, among forty four genotypes with two checks Pant Khira-1 and Pointsette of cucumber.

4.3.10 Fruit length (cm)

Fruit length showed positive direct effect (0.292) on yield (Table 5). This character showed positive indirect effect on plant height (0.0041), days to first female flower (0.2829), days to first harvest (0.0213), number of fruits per plant (0.1399) and individual fruit weight (0.4613). This character also showed negative indirect effect on number of branches per plant(-0.0331), leaf length (-0.0039), leaf breadth(0.0059), days to first male flower (-0.2767), days to first female flower anthesis (-0.0108) and fruit breadth (-0.1136) which finally resulted in a positive highly significant correlation on yield (0.757). Yadagiri *et al.* (2017) reported that in bitter gourd yield was found to be directly correlated with crop duration (0.004), length of vine (0.030), number of seeds per fruit (0.045) and length of fruit (0.094). Hence, they concluded that selection based on these characters would be more rewarding in bitter gourd.

4.3.11 Fruit breadth (cm)

Fruit breadth showed negative direct effect (-0.143) on yield (Table 5). This character showed highest positive indirect effect on plant height (0.0056), leaf length (0.0063), days to first female flower (0.1065), days to first harvest (0.0032), number of fruits per plant (0.0913), fruit length (0.2309), and individual fruit weight (0.3222). This character also showed negative indirect effect on number of branches per plant(-0.0273), leaf breadth (-0.0102), days to first male flower (-0.1041) and days to first female flower anthesis (-0.0039) which finally resulted in a positive highly significant correlation on yield (0.477). Kumar *et al.* (2018a) reported that in cucumber number of fruits per vine exerted the highest positive direct effect (3.64) on total yield per plant followed by sex ratio (2.29), fruit polar diameter (1.83), days to first harvest (1.57), and fruit equatorial diameter (0.92) at genotypic level.

4.3.12 Individual fruit weight (kg)

Individual fruit weight showed direct effect (0.559) on yield (Table 5). This character showed positive indirect effect on plant height (0.0077), leaf length (0.0073), days to first female flower (0.2962), days to first harvest (0.0393), number of fruits per plant (0.1772), and fruit length (0.2406). This character also showed negative indirect effect on number

of branches per plant(-0.0250), leaf breadth (-0.0129), days to first male flower (-0.2387), days to first female flower anthesis (-0.0111) and fruit breadth (-0.0827) which finally resulted in a positive highly significant association on yield (0.957). Sampath and Krishnamoorthy (2017) evaluated thirty two pumpkin genotypes and path analysis study revealed that the characters like fruit weight (1.367) and flesh thickness (5.348) were the most important yield determinants, because of their high direct effects and high indirect effects via many other yield and quality improving characters.

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

Characters	Direct effect	PH	NBP	LLP	LBP	DFMF	DFFF	DFFFA	DFH	NFP	FLP	FBP	IFW	Genotypic correlation with yield
PH	0.015	-	-0.0322	0.0272	-0.0186	0.0529	-0.0171	0.0005	0.0507	-0.0552	0.0791	-0.0536	0.2856	0.334*
NBP	-0.043	0.0114	-	0.0177	-0.0104	0.0789	-0.1148	0.0035	0.0470	-0.0868	0.2261	-0.0917	0.3275	0.366**
LLP	0.059	0.0070	-0.0129	-	-0.0403	0.1654	-0.1587	0.0056	0.0304	-0.0836	-0.0193	-0.0154	0.0691	0.006NS
LBP	-0.050	0.0056	-0.0088	0.0470	-	0.0611	-0.0140	0.0002	0.0372	0.0381	0.0341	-0.0291	0.1428	0.264NS
DFMF	0.537	0.0015	-0.0063	0.0181	-0.0057	-	-0.5453	0.0198	0.0222	-0.1982	-0.1504	0.0278	-0.2487	-0.528**
DFFF	-0.555	0.0005	-0.0088	0.0168	-0.0013	0.5269	-	0.0202	0.0163	-0.2365	-0.1485	0.0275	-0.2982	-0.640**
DFFFA	0.020	0.0004	-0.0075	0.0164	-0.0006	0.5300	-0.5573	-	0.0142	-0.2420	-0.1562	0.0282	-0.3079	-0.662**
DFH	0.091	0.0084	-0.0220	0.0196	-0.0206	0.1308	-0.0994	0.0031	-	-0.1025	0.0682	-0.0050	0.2417	0.313*
NFP	0.33	-0.0025	0.0112	-0.0149	-0.0058	-0.3227	0.3985	-0.0147	-0.0283	-	0.1237	-0.0397	0.3006	0.735**
FLP	0.292	0.0041	-0.0331	-0.0039	-0.0059	-0.2767	0.2829	-0.0108	0.0213	0.1399	-	-0.1136	0.4613	0.757**
FBP	-0.143	0.0056	-0.0273	0.0063	-0.0102	-0.1041	0.1065	-0.0039	0.0032	0.0913	0.2309	-	0.3222	0.477**
IFW	0.559	0.0077	-0.0250	0.0073	-0.0129	-0.2387	0.2962	-0.0111	0.0393	0.1772	0.2406	-0.0827	-	0.957**

Residual Effect (R) = 0.00681

Here, **, * Correlation is significant at the 0.01 and 0.05 level, respectively.

PH = Plant height (cm), NBP = Number of branches per plant, LLP = Leaf length(cm), LBP = Leaf breadth(cm), DFMF = Days to first male flower, DFFFA = Days to first female flower, DFFFA = Days to first female flower anthesis, DFH = Days to first harvest, NFP = Number of fruits per plant, FLP = Fruit length(cm), FBP = Fruit breadth(cm), IFW = Individual fruit weight (kg), YPP = Yield per plant (kg).

4.4 Genetic diversity analysis

Advanced pumpkin lines' genetic diversity was shown in Tables 6 to Tables 10 and in Figures 1 and 3.

4.4.1 Principal Component Analysis (PCA)

With 18 pumpkin genotypes, principal component analysis was performed. Table 6 showed the calculated Eigen values for the 13 variables that were subjected to principal component analysis along with the corresponding proportion and cumulative explained variance. Only one main component was kept after applying the proportion of variance criterion, and these are the principal components whose total explained variances were equal to or higher than 99%. As a consequence of the principal component analysis, the 13 initial variables were reduced to three principal components, which are independent linear combinations of variables. Principle components two and three each accounted for 25.90% and 11.20% of the total variation, whereas the first principal component contributed 39.80% to the variation overall (Table 6). Hamdi *et al.* (2017) revealed a considerable genetic variability for most of the agro-morphological parameters in fifteen local accessions of squash. Morphological variation was most apparent in fruit characteristics. PCA helped to produce a dendrogram which classifies these local varieties into three homogenous groups. Analysis of the biochemical constituents revealed a significant difference between these groups for all the traits.

Table 6. Eigen values and % of total variation and cumulative percent in respect of thirteen characters in eighteen pumpkin genotypes

Principal component axis	Eigen values	% of total variation accounted for	Cumulative percent
PH	5.18	39.80	39.80
NBP	3.37	25.90	65.80
LLP	1.45	11.20	77.00
LBP	0.95	7.30	84.20
DFMF	0.83	6.40	90.60
DFFF	0.51	3.90	94.50
DFFFA	0.32	2.50	97.00
DFH	0.23	1.80	98.70
NFP	0.11	0.90	99.60
FLP	0.03	0.20	99.80
FBP	0.02	0.10	100.00
IFW	0.00	0.00	100.00
YPP	0.00	0.00	100.00

Here, PH = Plant height (cm), NBP = Number of branches per plant, LLP = Leaf length(cm), LBP = Leaf breadth(cm), DFMF = Days to first male flower, DFFFA = Days to first female flower, DFFFA = Days to first female flower anthesis, DFH = Days to first harvest, NFP = Number of fruits per plant, FLP = Fruit length(cm), FBP = Fruit breadth(cm), IFW = Individual fruit weight (kg), YPP = Yield per plant (kg).

4.4.2 Non-Hierarchical Clustering

Five separate clusters were formed using non-hierarchical clustering from 18 pumpkin genotypes (Table 7). Non-hierarchical clustering was used to put the 18 pumpkin genotypes into five distinct clusters (Table 7). The genotype grouping pattern obtained through using principal component analysis. Sultana *et al.* (2018) observed genetic diversity for yield and its component traits on twenty one genotypes of pumpkin in Bangladesh. They found that high degree of variation exhibited within the collection, as reflected by mean diversity index value of 0.80. The genotypes were grouped into five different clusters. Balkaya *et al.* (2010) reported that in winter squash cluster analysis based on fourteen quantitative and seven qualitative variables identified ten different groups. They found first five principal component axes accounted for 65 percent of the total multivariate variation among the populations.

Cluster II in this study had the most genotypes six while Cluster IV and Cluster V each had an equal number of two genotypes. Number 3 and 5 genotypes were present in clusters I and III cluster (Table 7). Cluster I had G7 (BD-4389), G10 (BD-4368) and G16 (Diamond). Cluster II accumulated G1 (BD-4396), G2 (BD-4381), G3 (BD-4352), G5 (BD-4398), G9 (BD-4380) and G18 (Black super). Cluster III accumulated G11 (BD-4357), G13 (BD-4391), G14 (BD-4371), G15 (BD-4382), and G17 (BD-4351). Cluster IV consisted G4 (Hazari), and G8 (BD-4361), and Cluster V consisted G6 (Gadikata) and G12 (BD-4356). Among the thirteen genotypes cluster IV estimated the maximum cluster mean value for plant height (227.00), fruit length (30.06), fruit breadth (51.65), individual fruit weight (51.65) and yield per plant (4.43) (Table 8). In cluster V were highest mean value for leaf length (25.51), leaf breadth (20.54), days to first male flower (64.67), days to first female flower (66.84), days to first female flower anthesis (68.84), and days to first harvest (113.00). In cluster II highest mean value was observed in number of fruits per plant (3.55).

Table 7. Distribution of eighteen pumpkin genotypes in five different clusters

Cluster	Total no. of genotype	Genotype number	Genotype designation
I	3	7, 10, 16	BD-4389, BD-4368, Diamond (local)
II	6	1, 2, 3, 5, 9, 18	BD-4396, BD-4381, BD-4352, BD-4398, BD-4380, Black super (local)
III	5	11, 13, 14, 15, 17	BD-4357, BD-4391, BD-4371, BD-4382, BD-4351
IV	2	4, 8	Hazari (Local), BD-4361
V	2	6, 12	Gadikata (Local), BD-4356

Table 8. Cluster means for thirteen characters of eighteen pumpkin genotypes

Character	Cluster				
	I	II	III	IV	V
PH	202.67	214.72	203.34	227.00	217.17
NBP	8.89	9.06	8.57	10.00	9.50
LLP	24.06	24.44	23.99	25.18	25.51
LBP	19.98	20.40	20.05	20.46	20.54
DFMF	58.89	44.17	46.68	45.84	64.67
DFFF	60.67	48.22	49.46	47.84	66.84
DFFFA	62.67	50.45	51.68	50.00	68.84
DFH	100.78	103.06	102.22	109.50	113.00
NFP	3.44	3.55	3.33	3.17	1.50
FLP	17.27	20.56	17.98	30.06	13.04
FBP	27.94	29.77	19.11	51.65	12.24
IFW	0.60	0.77	0.70	51.65	0.43
YPP	2.08	2.74	2.45	4.43	0.64

Here, PH = Plant height (cm), NBP = Number of branches per plant, LLP = Leaf length(cm), LBP = Leaf breadth(cm), DFMF = Days to first male flower, DFFFA = Days to first female flower, DFFFA = Days to first female flower anthesis, DFH = Days to first harvest, NFP = Number of fruits per plant, FLP = Fruit length(cm), FBP = Fruit breadth(cm), IFW = Individual fruit weight (kg), YPP = Yield per plant (kg).

4.4.3 Canonical Variant Analysis (CVA)

The inter-cluster distances were calculated after the completion of the canonical variant analysis. Table 9 displayed the intra and inter-cluster distance (D^2) values. The inter-cluster distances in this experiment were greater than the intra-cluster distances, indicating greater genetic variation between the genotypes of various groups. Clusters IV and V had the greatest inter cluster distance (55.141), followed by clusters III and IV (47.008), cluster I and cluster IV (43.567), cluster III and cluster V (39.327), and cluster II and V (39.800). (Table9). Clusters IV and V had the greatest inter-cluster distance (55.141), indicating that genotypes from these two clusters could result in a variety of segregating populations if used in breeding programs. Alternatively, Cluster IV, which had two genotypes, had the highest intra-cluster distance (4.244), whereas cluster II, which had six genotypes, had the smallest distance (1.246). From the Fig. 1 it was noticed that all of the genotypes were reportedly grouped into five clusters according to the scatter plot. It was anticipated that the genotype combinations from the most divergent clusters will result in the maximum number of heterosis manifestations. Future plant breeders are advised to increase production levels in addition to heterosis levels. Hence, apart from selecting genotypes from these clusters which had high inter-cluster distance for hybridization, one can also think of selecting parents based on extent of genetic divergence in respect to a particular character of interest. This was to mean that, if breeder's intention is to improve fruit yield, they could be selected parents which were highly divergent with respect to these characters. Naik and Prasad (2015) tested twenty five cultivars of pumpkin in Allahabad and reported significant differences among all the genotypes for all the characters under study. The genotypes were grouped into five different clusters. Clustering pattern revealed that geographical diversity was not associated with genetic diversity. The wider genetic diversity was observed in cluster II, III and VI which indicate the potentiality of this diverse genotype collection for providing basic material for future breeding program.

Table 9. Average intra and inter-cluster distances (D^2) for eighteen pumpkin genotypes

Cluster	I	II	III	IV	V
I	2.035	26.200	26.630	43.567	27.245
II		1.246	20.165	27.728	39.800
III			2.643	47.008	39.327
IV				4.244	55.141
V					3.271

*Bold figures denotes intra-cluster distance

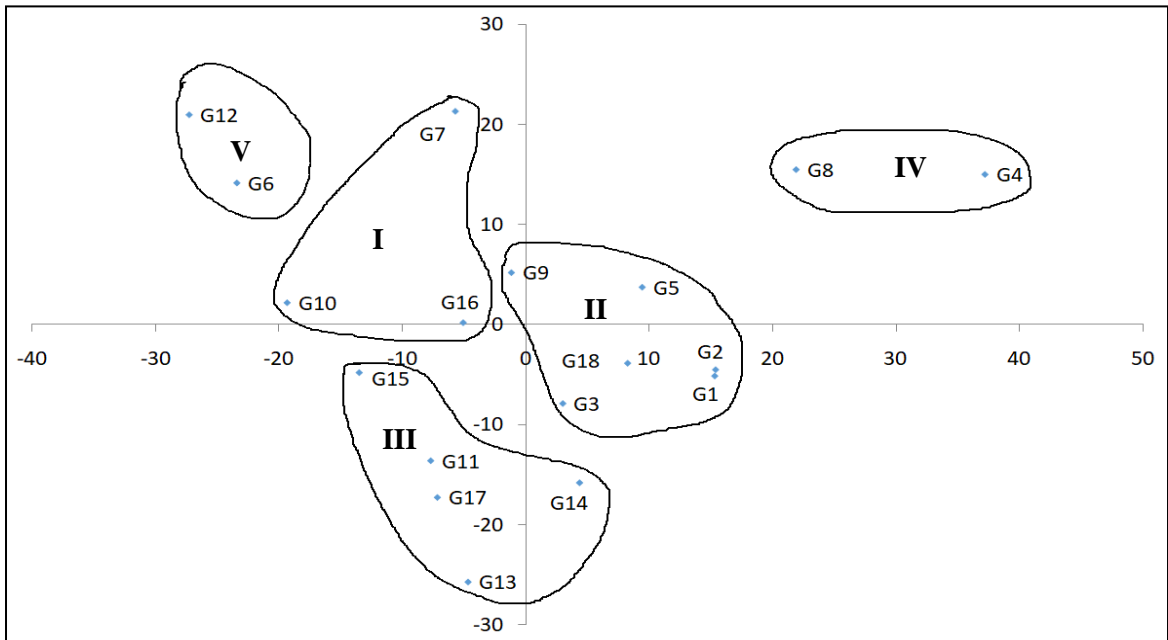


Figure 1. Scattered distribution of eighteen pumpkin genotypes on principal component score

Here, G1 = BD-4396, G2 = BD-4381, G3 = BD-4352, G4 = Hazari (Local), G5 = BD-4398, G6 = Gadikata (Local), G7 = BD-4389, G8 = BD-4361, G9 = BD-4380, G10 = BD-4368, G11= BD 4357, G12 = BD-4356, G13 = BD-4391, G14 = BD-4371, G15 = BD-4382, G16=Diamond (local) ,G17 = BD-4351, and G18 = Black super (local).

4.4.4 Contribution of phenotypic traits towards divergence of the genotypes

In Table 10 the values of Vector I and Vector II are presented. Character assembled in vector-1 that were major contribution to the genetic divergence like plant height, number of branches per plant, leaf length, leaf breadth, days to first harvest, number of fruits per plant, fruit length, fruit breadth, individual fruit weight and yield per plant. In vector-2 the important characters responsible for genetic divergence were plant height, number of branches per plant, leaf length, leaf breadth, days to first male flower, days to first female flower, days to first female flower anthesis, days to first harvest, fruit length, fruit breadth, and individual fruit weight. Both vectors negative value determined the lower contribution of genetic divergence. Rani and Reddy (2017) noted that thirty five ridge gourd germplasm which were grouped into five clusters based on D^2 values, exhibited no association between geographical and genetic divergence. They concluded by results of the study that on the basis of mean performance of different clusters, genotypes having better performance could be utilized as donor parents for respective traits in hybridization program.

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

Character no.	Vector-1	Vector-2
PH	0.225	0.467
NBP	0.018	0.030
LLP	0.001	0.047
LBP	0.010	0.016
DFMF	-0.354	0.462
DFFF	-0.326	0.413
DFFFA	-0.328	0.409
DFH	0.011	0.171
NFP	0.021	-0.022
FLP	0.314	0.035
FBP	0.712	0.442
IFW	0.015	0.002
YPP	0.056	-0.008

Here, PH = Plant height (cm), NBP = Number of branches per plant, LLP = Leaf length(cm),LBP = Leaf breadth(cm), DFMF = Days to first male flower, DFFFA = Days to first female flower, DFFFA = Days to first female flower anthesis, DFH = Days to first harvest, NFP = Number of fruits per plant, FLP = Fruit length(cm), FBP = Fruit breadth(cm), IFW = Individual fruit weight (kg), YPP = Yield per plant (kg).

4.4.5 Selection of parents for future hybridization

This method of genotype selection for upcoming future breeding programme is crucial and challenging. In the meantime, considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and phenotypic traits, the genotype G₄ (Hazari (Local)) for maximum fruit length, fruit breadth, and individual fruit weight from cluster IV, G₁₃ for the minimum number of days needed to reach first female flower anthesis from cluster III, and G₁₄ for fruit number per plant and yield per plant from cluster III should be considered. Therefore, for a future hybridization program, it may be proposed to make inter-genotypic crosses between G₄ "Hazari (Local)" and G₁₃; G₄ "Hazari (Local)" and G₁₄ (BD-4371); and G₁₃ (BD-4391) and G₁₄ (BD-4371). Ara *et al.* (2014) grouped twenty eight genotypes of bottle gourd into five different clusters on the basis of D² values and showed the existence of wide genetic diversity among them. They also suggested that the genotypes within a cluster might have some degree of ancestral relationship and geographic diversity may not necessarily be related with genetic diversity. Therefore, the selection of genotypes for hybridization should be based on genetic diversity rather than on geographic diversity.

CHAPTER V

SUMMARY AND CONCLUSION

An experiment was conducted at Sher-e-Bangla Agricultural University Dhaka, during the period from March 2020 to September 2020 using eighteen pumpkin (*Cucurbita maxima* Duch.) genotypes to study the genetic diversity of pumpkin in a randomized complete block design with three replications.

Experimental result showed significant differences among the genotypes. Phenotypic variance was higher than that of genotypic variance for all the characters. High genotypic co-efficient of variation was found in number of fruits per plant, fruit length, fruit breadth, individual fruit weight and yield per plant. Low GCV was observed for plant height, number of branches per plant, leaf length, days to first male flower, and days to first harvest.

High heritability with high genetic advance in percent of mean was observed fruit length, fruit breadth, individual fruit weight and yield per plant which indicated that these traits would be effective for genetic improvement. High heritability with low genetic advance in percent of mean was observed in days to first male flower, days to first female flower, days to first female flower anthesis, and days to first harvest.

Correlation studies showed that highly positive and significant correlation of fruit yield per plant with plant height, days to first harvest, number of fruits per plant, fruit length, fruit breadth, individual fruit weight, and yield per plant. The highest intra cluster distance was found in cluster IV and the lowest was found in cluster III. Among five clusters the highest inter cluster distance was found in between cluster IV and V and the lowest between cluster II and III.

Considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and phenotypic traits, the genotype G4 (Hazari (Local) for maximum fruit length, fruit breadth, and individual fruit weight from cluster IV, G13 for the minimum number of days needed to reach first female flower anthesis from cluster III, and G14 for fruit number per plant and yield per plant from cluster III should be considered. Therefore, for a future hybridization program, it may be proposed to make inter-genotypic crosses between G4 "Hazari (Local)" and G13, G4 "Hazari

(Local)", and G14 (BD-4371), and G13 (BD-4391) and G14 (BD-4371) for betting's better heterotic hybrid.

REFERENCES

- Abd el-hamed, K.E., Elwan, M.W.M. and Mohamed, F.H. (2015). Genetic diversity and relationship in squash using morphological, chemical and molecular analyses. *Int. J. Hort.* **5**(12): 1-10.
- Ahamed, K.U., Akhter, B., Islam M.R., Ara N. and Humauan, M.R. (2011). An assessment of morphology and yield characteristics of pumpkin (*Cucurbita moschata*) genotypes in northern Bangladesh. *Tropic. Agril. Res. ext.* **14**(1): 1-10.
- Ahirwar, C.S., Singh, D.K. and Kushwaha, M.L. (2017). Assessment of genetic variation in cucumber (*Cucumis sativus* L.) germplasm on correlation, path analysis and cluster analysis. *Chem. Sci. Rev. Letter.* **6**(23): 1886-1893.
- Ahmed, B., Masud, M.A.T., Zakaria, M., Hossain, M.M. and Mian, M.A.K. (2018). Variability, correlations and path co-efficient analysis in pumpkin (*Cucurbita moschata* Duch. ex Poir). *J. App. Life Sci. Int.* **16**(1): 1-8.
- Akinwale, M., Gregorio, G., Nwilene, F., Akinyele, B., Ogunbayo, S.A. and Odiyi, A.C. (2011). Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.). *African J. Plant Sci.* **5**: 207-212.
- Akter, S., Rasul, M.G., Aminul, A.K.M. and Hossain, M.M. (2013). Genetic variability, correlation and path coefficient analysis of yield and quality traits in pumpkin (*Cucurbita moschata* Duch ex poir.). *Bangladesh J. Plant Breed. Gen.* **26**(1): 25-33.
- Aliya, F., Begum, H., Reddy, M.T., Sivaraj, N., Pandravada, S.R. and Narshimulu, G. (2014). Correlation and path coefficient analysis of quantitative characters in spine gourd (*Momordica dioica* Roxb.). *Pakistan J. Bio. Sci.* **17**: 659-666.
- Al-Jibouri, H.W., Miller, P.A. and Robinson, H.F. (1958) Genotypic and environmental variances and co-variances in an upland cotton cross of interspecific origin. *Agron. J.* **50**: 633-636.

- Allard, R.W. (1960). Principles of Plant Breeding. John Wiley & Sons, Inc., New York, USA. pp. 485.
- Ananthan, M. and Krishnamoorthy, V. (2017). Genetic variability, correlation and path analysis in ridge gourd (*Luffa acutangula* (Roxb) L.). *Int. J. Cur. Micro. App. Sci.* **6**(9): 3022-3026.
- Anonymous. (1988 a). The Year Book of Production. FAO, Rome, Italy.
- Anonymous. (1988 b). Land resources appraisal of Bangladesh for agricultural development. Report No.2. Agro-ecological regions of Bangladesh, UNDP and FAO. pp. 472–496.
- Anonymous. (2004). Effect of seedling throwing on the grain yield of wart landrice compared to other planting methods. Crop Soil Water Management Program Agronomy Division, BRRI, Gazipur-1710.
- Ara, Z.G., Zakaria, M., Uddin, M.Z., Rahman, M.M., Rasu, M.G. and Kabir, A.F.M.R. (2014). Genetic divergence in bottle gourd. *Int. J. Nat. Soc. Sci.* **1**: 20-25.
- Aruah, B.C., Uguru, M.I. and Oyiga, B.C. (2012). Genetic variability and inter-relationship among some Nigerian pumpkin accessions (*Cucurbita* spp.). *Int. J. Plant Breed.* **6**(1): 34-41.
- AVRDC. (2011). Inception workshop on improving incomes, nutrition and health in Bangladesh through potato, sweet potato and vegetables, 17-18 January. pp. 1
- Balkaya, A., Ozbakir, M. and Kurtar, E.S. (2010). The phenotypic diversity and fruit characterization of winter squash (*Cucurbita maxima*) populations from the Black Sea Region of Turkey. *African J. Biotech.* **9**(2): 152-162.
- Banik, B. R.(2003). Variability, gene action and heterosis in snake gourd (*Trichosanthes anguina* L.). Ph.D. Thesis, BSMRAU, Gazipur. pp. 18-29.

- BBS. (Bangladesh Bureau of Statistics). (2020). Statistical Year Book of Bangladesh 2018-2019. Bangladesh Bureau of Statistics Division, Ministry of Planning, Govt. of the People's Republic of Bangladesh, Dhaka.
- Belaj, A., Satovic, Z., Rallo, L. and Trujillo, I. (2002). Genetic diversity and relationship in olive (*Olea europea* L.) germplasm collection as determined by RAPD. *Theoro. App. Gen.* **105**(4): 638-644.
- Bhandari, H.R., Bhanu, A.N., Srivastava, K. and Singh, M.N. (2017). Assessment of genetic diversity in crop plants-an overview. *Adv. Pl. Agric. Res.* **7**(3): 200-255.
- Bharathi, L.K. and Vishalnath. (2011). Phenotypic diversity analysis in pointed gourd (*Trichosanthes dioica* Roxb.). *Cucurbit Gen. Coop. Rep.* **34**: 62-64.
- Burton, G. W. (1952). Quantitative inheritance in Grasses. *Int. Grassland Cong.* **1**: 277-283.
- Burton, G.W. and De Vane, D.H. (1953) Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clover materials. *Agron. J.* **45**: 478-481.
- Chaudhari, D.J., Acharya, R.R., Patel, J.N., Gohil, S.B. and Bhalala, K.C. (2017). Variability, correlation and path analysis in pumpkin (*Cucurbita moschata* Duch. ex. Poir.). *J. Pharma. Phytochem.* **6**(6): 142-145.
- Chetariya, C.P., Jalu, R.K., Vaddoria, M.A. and Madariya, R.B. (2018). Character association and path analysis in bottle gourd [*Ligenaria siceraria* (Mol.) Standl.]. *The Pharma Inn. J.* **7**(7): 579-583.
- Comstock, R and Robinson, H. (1954). An analysis of quantitative variability in *Nicotiana tabacum*. *Heredity.* **8**: 365–376.
- Debata, J., Maurya, S.K., Yadav, H. and Bhatt, L. (2017). Study on genetic diversity of pointed gourd using morphological traits. *Int. J. Cur. Microb. App. Sci.* **6**(12): 1511-1519.

- Deepa, S.K., Hadimani, H.P., Hanchinamani, C.P., Shet, R., Koulgi, S. and Ashok. (2018). Estimation of genetic variability in cucumber (*Cucumis sativus* L.). *Int. J. Chem. Stud.* **6**(6): 115-118.
- Deepthi, B., Reddy, P.S.S., Kumar, A.S. and Reddy, A.R. (2016). Character association and path coefficient analysis in bottle gourd (*Lagenaria Siceraria* Mol.) genotypes. *Plant Arc.* **16**(2): 531-536.
- Dewey, D.R. and Lu, K.H. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.* **51**: 515-518.
- Doddamani, S.M., Satish, D., Nishani, S., Masuthi, D.A., Seetaramu, G.K. and Tatagar, M.H. (2018). Assessment of genetic variability in local collections of cucumber (*Cucumis sativus* L.) genotypes for productivity traits. *Int. J. Gen.* **8**(1): 01-05.
- Edris, K.M., Islam, A.M.T., Chowdhury, M.S. and Haque, A.K.M.M. (1979). Detailed Soil Survey of Bangladesh, Dept. Soil Survey, BAU and Govt. Peoples Republic of Bangladesh. pp. 118.
- Ene, C.O., Ogbonna, P.E., Agbo, C.U. and Chukwudi, U.P. (2016). Studies of phenotypic and genotypic variation in sixteen cucumber genotypes. *Chilean J. Agric. Res.* **76**(1): 307-312.
- FAO. (2020). Vegetable Statistics. Food and Agriculture Organization of the United Nations, Rome, Italy. <http://www.faostat.fao.org>.
- Fayeun, L.S., Hammed, L.A., Oduwaye, O.A., Madike, J.U. and Ushie, E.U. (2016). Estimates of genetic variability for seedling traits in fluted pumpkin (*Telfairia occidentalis* Hook. F). *Plant Breed. Biotech.* **4**(2): 262-270.
- Fisher, R.A. and Yates, F. (1963) Statistical Tables for Biological, Agricultural and Medical Research. 6th ed. Oliver and Boyd Ltd, London. pp. 146.
- Gaffar, A. (2008). Characterization and genetic diversity of sponge gourd (*Luffa cylindrica* L.). MS Thesis, SAU, Dhaka-1207. Gaur, P., Gupta, C. and Kishore, H. (1978). Studies on genetic divergence in potato. *Euphytica.* **27**: 361-368.

- Gaikwad, A.G., Musmade, A.M., Dhumal, S.S. and Sonawane, H.G. (2011). Variability studies in cucumber (*Cucumis sativus* L.). *Eco. Environ. Conser.* **17**(4): 799-802.
- Ganapati, R.K., Rasul, M.G. and Sarker, U. (2020). Gene action of yield and yield contributing traits of submergence tolerant rice (*Oryza sativa* L.) in Bangladesh. *Bull. Natl. Res. Cent.* **44**: 8.
- Gautam, D.K., Yadav, G.C., Kumar, P., Kumar, V. and Singh, M. (2017). Estimation of heterosis for growth, yield and quality traits in bottle gourd [*Lagenaria siceraria* (Mol.) Standl.]. *Int. J. Cur. Micro. App. Sci.* **6**(8): 789-802.
- Gautam, D.K., Yadav, G.C., Kumar, P., Kumar, V. and Singh, M. (2017). Estimation of heterosis for growth, yield and quality traits in bottle gourd [*Lagenaria siceraria* (Mol.) Standl.]. *Int. J. Cur. Microb. App. Sci.* **6**(8): 789-802.
- Golabadi, M., Golkar, P. and Eghtedary, A.R. (2012). Assessment of genetic variation in cucumber (*Cucumis sativus* L.) genotypes. *European J. Exp. Bio.* **2**(5): 1382-1388.
- Govindaraj, M., Vetriventhan, M. and Srinivasan, M. (2015). Importance of genetic diversity assessment in crop plants and its recent advances: An overview of its analytical perspectives. *Gen. Res. Int.* **1**: 1-14.
- Griffing, B. and Lindstorm, E.W. (1954). A study of combining abilities of com inbreeds having varying proportions of com belt and non com belt germplasm. *Agronomy J.* **46**: 545-552.
- Grubben, G.J.H. (2004). *Vegetables*, backhuys publishers, Leiden. pp. 354-357.
- Gupta, N., Bhardwaj, M.L., Singh, S.P. and Sood, S. (2015). Correlation study among morpho-physiological attributes in bitter gourd (*Momordica charantia* L.). *J. Agric. Res.* **53**(3): 345-349.

- Hamdi, K., Be Amor, J., Mokrani, K., Mezghanni, N. and Tarchoun, N. (2017). Assessment of the genetic diversity of some local squash (*Cucurbita maxima* Duchesne) populations revealed by agromorphological and chemical traits. *J. New Sci. Agric. Biotech.* **42**(5): 2306-2317.
- Haque, M.M., Uddin, M.S., Mehraj, H. and Jamal Uddin, A.F.M. (2014). Evaluation of snake gourd (*Trichosanthes anguina* L.) test hybrids comparing with four popular checks. *Int. J. App. Sci. Biotech.* **2**(4): 525-528.
- Harrington, J.B. (1940). Yielding capacity of wheat crosses as indicated by bulk hybrid tests. *Canadian J. Res.* **18**: 578-584.
- Hasan, R., Hossain, M.K., Alam, N., Bashar, A., Islam, S. and Tarafder, M.J.A. (2015). Genetic divergenc in commercial cucumber (*Cucumis sativus* L.) genotypes. *Bangladesh J. Bot.* **44**(2): 201-207.
- Husna, A. (2009). Genetic diversity, correlation and path co-efficient analysis in bottle gourd (*Lagenaria siceraria* L.). MS Thesis. SAU, Dhaka-1207. pp. 12-19.
- Husna, A. Mahmud, F., Islam, M. R., Mahmud. M. A. A. and Ratna, M. M. (2012). Genetic Variability, correlation and path co-efficient analysis in bottle gourd (*Lagenaria siceraria* L.). *Adv. Biol. Res.* **5**(6): 323-327.
- Husna, A., Mahmud, F., Islam, M.R., Mahmud, M.A.A. and Ratna, M. (2011). Genetic variabilty, correlation and path co-efficient analysis in bottle gourd (*Lagenaria siceraria* L.). *Adv. Bio. Res.* **5**(6): 323-327.
- Iqbal, M. (2015). Study of correlation among morpho-physiological attributes in bitter gourd (*Momordica charantia* L.). *J. Agric. Res.* **53**(3): 345-349.
- Iqbal, M.S. (2015). Correlation and path analysis of yield and yield components in some genetic stocks of bitter gourd (*Momordica charantia* L.). *J. Breed. Gen.* **47**(4): 475-481.

- Islam, M., Raffi, S., Hossain, M. and Hasan, A. (2015). Analysis of genetic variability, heritability and genetic advance for yield and yield associated traits in some promising advanced lines of rice. *Prog. Agric.* **26**(1): 26-31.
- Islam, M.S. Mia, M.A.B., Das, M.R., Hossain, T., Ahmed, J.U. and Hossain, M.M. (2009). Sex phenology of bitter melon (*Momordica charantia* L.) landraces and its relation to yield potential and fruit quality. *Pak. J. Agri. Sci.* **51**(3): 651-658.
- Jahan, T.A., Islam, A.K.M.A., Rasul, M.G., Mian, M.A.K. and Haque, M.M. (2012). Heterosis of qualitative and quantitative characters in sweet melon (*Cucurbita moschata* Duch.ex Poir). *AJFAND* online. Published by ASSCAT, Nairobi, Kenya. **12**(3): 6186 - 6199.
- Janaranjani, K.G. and Kanthaswamy, V.J. (2015). Correlation studies and path analysis in bottle melon. *Hort.* **2**: 1.
- Jat, R.K., Ameta, K.D. and Choudhary, R.C. (2014). Genetic variability, heritability and genetic advance for yield and yield attributing traits in valan kakri (*Cucumis sativus* var. *utilimus* L.). *The bioscan: An Int. Quart. J. Environ. Sci.* **1**: 317-322.
- Jena, T., Suseela, T.S., Kiran Patro, K.K. and Sujatha, R.V. (2017). Correlation and path analysis for yield and yield components in pointed melon (*Trichosanthes dioica* Roxb.). *Int. J. Cur. Micro. App. Sci.* **8**: 1864-1869.
- Kabir, M.Y., Khan, A.S.M.M.R. and Hassain, M.S. (2009). Genetic divergence in pointed melon. *J. Agric. Rural Develop.* **7**(1-2): 87-89.
- Kandasamy, R. (2017). Variability studies in cucumber (*Cucumis sativus* L.). *Asian J. Hort.* **12** (1): 84-87.
- Kanwar, M.S., Korla, B.N. and Kumar, S. (2003). Evaluation of cucumber genotypes for yield and qualitative traits. *Himachal J. Agric. Res.* **29**(1-2): 43-47.
- Kanwar, M.S., Korla, B.N. and Kumar, S. (2003). Evaluation of cucumber genotypes for yield and qualitative traits. *Himachal J. Agric. Res.* **29**(1&2): 43-7.

- Katyal, S.L. and Chadha, M.L. (2000). Vegetables growing in India. Oxford and IBH Publishing Co. New Delhi, India. pp.92-93.
- Khan, A.S.M.M.R., Kabir, M.Y. and Alam, M.M. (2009). Variability, correlation path analysis of yield and yield components of pointed gourd. *J. Agric. Rural Develop.* **1**: 93-98.
- Khan, A.S.M.R., Rabbani, M.G., Siddique, M.A. and Hossain, M.I. (2008). Study on genetic diversity of pointed gourd using morphological characters. *Bangladesh J. Agric. Res.* **33**(3): 607-616.
- Khan, M.H., Bhuiyan, S.R., Saha, K.C., Bhuyin, M.R. and Ali, A.S.M.Y. (2015). Variability, correlation and path co-efficient analysis of bitter gourd (*Momordica charantia* L.). *Bangladesh J. Agric. Res.* **40**(4): 607-618.
- Kumar, D., Kumar, R., Kumar, S., Bhardwaj, M.L., Thakur, M.C., Kumar, R. (2013). Genetic variability, correlation and path coefficient analysis in tomato. *Int. J. Vegetable Sci.* **19**:313-323.
- Kumar, J. Phani., Syed, S., Reddy, S.S., Lakshmi, M.L. and Reddy, S. (2018 b). Studies on correlation and path-coefficient analysis for yield and its contributing characters in cucumber (*Cucumis sativus* L.). *Int. J. Chem. Stud.* **6**(6): 1649-1653.
- Kumar, P., Singh, V.B., Ram, C.N. and Gautam, D.K. (2017). Genetic divergence study in ridge gourd [*Luffa acutangula* L. (Roxb.)] germplasm. *Res. Environ. Life Sci.* **10**(3): 232-234.
- Kumar, R., Ameta, K.D., Dubey, R.B. and Pareek, S. (2013). Genetic variability, correlation and path analysis in sponge gourd (*Luffa cylindrica* Roem.). *African J. Biotechn.* **12**(6): 539-543.
- Kumar, R., Rajasree, V., Praneetha, S., Rajeswari, S. and Tripura, U. (2018 a). Correlation and path coefficient analysis studies in pumpkin (*Cucurbita moschata* Duch. Ex poir) for yield and quality traits. *Int. J. Cur. Micro. App. Sci.* **7**(5): 3067-3075.

- Kumar, S., Kumar, R., Gupta, R.K. and Sephia, R. (2011). Studies on correlation and path-coefficient analysis for yield and its contributing traits in cucumber. *Crop Improv.* **38**(1): 18-23.
- Kumari, A., Singh, A.K., Moharana, D.P., Kumar, A. and Kumar, N. (2018). Character relationship and path coefficient analysis for yield and yield components in diverse genotypes of cucumber (*Cucumis sativus* L.). *The Pharma Inn. J.* **7**(5): 33-38.
- Kundu, B.C., Hossain, M.M.M., Khaleque, M.A. and Mian, I.H. (2012). Genetic divergence in bitter gourd (*Momordica charntia* L.). *J. Asiatic Soc. Bangladesh.* **38**(2): 125-134.
- Li, R., Li, M., Ashraf, U., Liu, S. and Zhang, J. (2019). Exploring the relationships between yield and yield-related traits for rice varieties released in China from 1978 to 2017. *Front. Plant Sci.* **10**: 543.
- Mahalanobis, P.C. (1936). On the generalized distance in statistics. *Proc. Nat. Inst. Sci., India.* **2**: 49-55.
- Mahalanobis, P.C. (1936). Proceedings of the national academy of sciences on the generalized distance in statistics. *Stat.* **19**: 201-208.
- Manikandan, M., Yassin, G.M., Kanthaswamy, V. and Kamaladevi, S. (2017). Correlation and path coefficient analysis in ash gourd (*Benincasa hispida* (Thunb) cogn.) for yield and yield attributing traits. *Chemical Sci. Rev. Let.* **6**(23): 1399-1403.
- Manikandan, M., Yassin, G.M., Kanthaswamy, V. and Kamaladevi, S. (2017). Correlation and path coefficient analysis in ash gourd [*Benincasa hispida* (Thunb) Cogn.] for yield and yield attributing traits. *Chemical Sci. Rev. Letter.* **6**(23): 1399-1403.
- Mathew, S.S. and Khader, K.M.A. (1999). Genetic studies in snake gourd (*Trichosanthes anguina* L.). *J. Trop. Agril.* **37**(1-2): 71-72.

- Mathew, S.S. and Khader, K.M.A. (1999). Genetic studies in snake gourd (*Trichosanthes anguina* L.). *J. Trop. Agril.* **37**(1-2): 71-72.
- Maurya, D., Singh, V.B., Yadav, G.C., Kumar, G.C., Dubey, S. and Pandey, A.K. (2019). Study the correlation coefficient and path coefficient for the yield and yield component of bitter gourd (*Momordica charantia* L.). *Int. J. Cur. Micro. App. Sci.* **8**(2): 952-960.
- Mishra, S., Sharma, A.K. and Sharma, V. (2017). Genetic variability studies in response to drought under different water regimes in muskmelon (*Cucumis melo* L.). *J. App. Nat. Sci.* **9** (3): 1744 -1750.
- Mohsin, G.M., Islam, M.S., Rahman, M.S., Ali, L. and Hasanuzzaman, M. (2017). Genetic variability, correlation and path coefficients of yield and its components analysis in pumpkin (*Cucurbita moschata* Duch Ex Poir). *Int. J. Agric. Res. Inn. Tech.* **7**(1): 8-13.
- Nagariya, N.K., Bhardwaj, R., Sharma, N., Mukherjee, S. and Umesh. (2015). Correlation and path analysis in tomato (*Solanum lycopersicon* L.). *Int. J. Farm Sci.* **5**(4): 111-117.
- Nahar, B.A.U., Rabbani, M.G. and Karim, M.R. (2016). Genetic variability and field performance of some sweet gourd (*Cucurbita moschata* Duch) accessions. *J. Sci. Tech. Environ. Inf.* **04**(2): 301-312.
- Naik, M.L. and Prasad, V.M. (2015). Studies on genetic divergence in studies on genetic divergence in pumpkin. The Bioscan: *Int. Quaternly J. Life Sci.* **10**(4): 2085-2088.
- Naik, M.L., Prasad, V.M. and L.P. Rajya. (2015). A study on character association and path analysis in pumpkin (*Cucurbita moschata* Duch. ex Poir.). *Int. J. Adv. Res.* **3**: 1030-1034.

- Oliveira, R.L.D., Gonçalves, L.S.A., Rodrigues, R., Baba, V.Y., Sudre, C.P., Santos, M.H.D. and Aranha, F.A. (2016). Genetic divergence among pumpkin landraces. *Semina: Ciências Agrárias. Londrina*. **37**(2): 547-556.
- Onyishi, G.C., Ngwuta, A.A., Onwuteaka, C. and Okporie, E.O. (2013). Assessment of genetic variation in twelve accessions of tropical pumpkin (*Cucurbita maxima*) of S.E. Nigeria. *World App. Sci. J.* **24**(2): 252-255.
- Ozturk, H., Donderalp, V., Bulut, H. and Korkut, R. (2022). Morphological and molecular characterization of some pumpkin (*Cucurbita pepo* L.) genotypes collected from Erzincan province of Turkey. *Sci. Rep.* **12**(1): 1-7.
- Pal, S., Sharma, H.R., Das, A. and Pandav, A.K. (2017). Character association and path analysis for fruit yield and its contributing traits in cucumber (*Cucumis sativus* L.). *Int. J. Agric. Environ. Biotech.* **10**(2): 163-170.
- Pandey, S., Singh, J., Updhaya, A.K., Ram, D. and Rai, M. (2003). Ascorbate and carotenoid content in Indian collection of pumpkin (*Cucurbita moschata* Duch. ex Poir.). *Cucurbit Gen. Coop. Rep.* **26**: 51-53.
- Panigrahi, I., Duhan, D.S., Panghal, V.P.S., Tehlan, S.K. and Yadav, S.K. (2018). Correlation coefficient analysis between yield defining traits of cultivated genotypes of bottle gourd (*Lagenaria siceraria* (Mol.) Stdl.). *J. Pharma. Phytochem.* **7**(2): 1378-1380.
- Pathak, M., Manpreet and Pahwa, K. (2014). Genetic variability, correlation and path coefficient analysis in bittergourd (*Momordica charantia* L.). *Int. J. Adv. Res.* **2**(8): 179-184.
- Pham, B. and McConnaughay, K. (2014). Plant phenotypic expression in variable environments. *ecology and the environment*. pp.119-141.
- Quamruzzaman, A.K.M., Rashid, M.A, Ali, M.M, Alam, A.K.M.M. and Mashiur, R.M. (2008). Genetic diversity in bitter gourd (*Momordica charantia* L.). *Bangladesh J. Agril. Res.* **33**(1): 129-134.

- Quamruzzaman, A.K.M., Rashid, M.A., Masud. M.A.T. and Uddin, M.N. (2009). Heterosis in bottle gourd. *Bangladesh J. Agril. Res.* **34**(3): 465-472.
- Rabbani, M.G., Naher, M.J. and Hoque, S. (2012). Variability, character association and diversity analysis of ridge gourd (*Luffa acutangula* Roxb.) genotypes of Bangladesh. *SAARC J. Agric.* **10**(2): 01-10.
- Rahman, A.K.M.M., Das, M.K. and Haque, M.M. (1986). Variability, correlation and path co-efficient analysis in bottle gourd (*Lagenaria vulgaris* L.). *Bangladesh J. Agric.* **11**(3): 13-19.
- Rahman, M.M., Dey, S.K. and Wazuddin, S. (1991). Study of yield, yield components and vine characters of some cucurbit genotypes. *BAU Res Pro.* **5**: 75-85.
- Rajawat, K.S. and Collis. (2017). Genetic variability, heritability and genetic advances analysis for quantitative and qualitative traits in cucumber (*Cucumis sativus* L.). *J. Pharm. Phyto.* **6**(4): 882-885.
- Rajkumar, M., and Karuppaiah, P. (2007). Variability studies in snake gourd (*Trichosanthes anguina* L.). *Plant Archives.* **7**(2): 699-701.
- Rambabu, E., Mandal, A.R., Hazra, P., Senapati, B.K. and Thapa, U. (2017). Morphological characterization and genetic variability studies in bottle gourd (*Lagenaria siceraria* (Mol.) Standley.). *Int. J. Cur. Micro. App. Sci.* **6**(9): 3585-3592.
- Ramesh, N.D., Choyal, P., Dewangan, R., Gudadinni, P.S., Ligade, P.P. and Seervi, K.S. (2018). Correlation and path analysis study in studied in ridge gourd (*Luffa acutangula* (L.) Roxb.). *Int. J. Cur. Micro. App. Sci.* **7**(8): 1511-1519.
- Rana, H ., Pant, S.C., Paliwal, A., Bahuguna, P. and Veena, A.M. (2018). Studies on Genetic Variability among various horticultural traits of bottle gourd. *Int. J. Pure App. Biosci.* **6**(6): 1-7.

- Rani, E.A., Jansirani, P. and Kannan Bapu, J.R. (2017). Assessment of breeding potential of ridge gourd [*Luffa acutangula* (roxb.) L.] germplasm for growth, yield and quality using diversity (D2) analysis. *Int. J. Cur. Micro. App. Sci.* **6**(3): 128-133.
- Rani, K. Radha, Raju, C.S. and Reddy, K.R. (2015). Variability, correlation and path analysis studies in bitter gourd (*Momordica charantia* L.). *Agric. Sci. Dig.* **35**(2): 106-110.
- Rani, K., Radha, R.C.S. and Reddy, K.R. (2015). Variability, correlation and path analysis studies in bitter gourd (*Momordica charantia* L.). *Agric. Sci. Dig.* **35**(2): 106-110.
- Rani, K.U. and Reddy, E.N. (2017). Variability and correlation studies in bottlegourd. *Int. J. Pure App. Biosci.* **5**(2): 723-731.
- Rao, C.R. (1952). Advanced statistical method in biometrics research. John Wiley and sons, New York. p. 390.
- Rao, M.N., Roy, P.V., and Reddy, B.M.M. (2000). Correlation and path analysis in segregating population of ridge gourd. *Crop Res. Hisar.* **20**(2): 338-342.
- Rashid, M.M. (1993). Vegetable Science (in Bangla). 1st ed., Bangla Academy. Dhaka. Bangladesh. pp. 265-336.
- Rashid, M.M., Haque, M.M., Moniruzzaman, M. and Jamal, M.A.H.M. (2014). Characterizations and correlation coefficient analysis of snake gourd (*Trichosanthes anguina* L.). *J. Res. Agric. Ani. Sci.* **2**(9): 01-06.
- Reddy, B.P.K., Begum, B., Sunil, N. and Reddy, M.T. (2017). Correlation and path coefficient analysis in muskmelon (*Cucumis melo* L.). *Int. J. Cur. Micro. App. Sci.* **6**(6): 2261-2276.
- Reshmi, J. and Sreelathakumary, I. (2012). Character association and path coefficient studies in (*Benincasa hispida*). *Agric. Sci. Dig.* **32**(3): 251-255.

- Saha, R.R., Mitra, B.N., Hossain, A.E., Jamaluddin, M. and Hoque, A.M.M.M. (1992). Genetic variability, character association and path coefficient analysis in pumpkin (*Cucurbita moschata* L). *Bangladesh Hort. J.* **20**(1): 59-62.
- Sampath, S. and Krishnamoorthy, V. (2017). Genetic variability, correlation and path analysis in pumpkin (*Cucurbita moschata* Duch. ex. Poir). *Int. J. Cur. Micro. App. Sci.* **6**(6): 3027-3035.
- Saranyadevi, G., Lakshmanan and Rohini, N. (2017). Performance evaluation and correlation analysis in mithipagal genotypes (*Momordica charantia* var. muricata). *Elect. J. Plant Breeding.* **8**(2): 652-659.
- Seshadri, V.S. and Parthasarthy, V.A. (2002). Cucurbits, vegetable crops. Vol I. Third revised edition. Ed. Bose, T.K., Kabir, J., Maity, T.K., Parthasarathy, V.A. and Som, M.G. Naya Prakash Publication, Calcutta. pp. 502-503.
- Shah, K.N., Rana, D.K. and Singh, V. (2018). Studies on genetic divergence in cucumber (*Cucumis sativus* L.) under subtropical conditions of Garhwal Himalaya. *Int. J. Adv. Sci. Res. Manage.* **1**: 39-42.
- Sharma, A. and Sengupta, S.K. (2012). Genetic diversity, heritability and morphological characterization in bottle gourd (*Lagenaria siceraria*). The Bioscan: *Int. Qua. J. Life Sci.* **8**(4): 1461-1465.
- Sharma, H.R. and Sharma, D. (2006). Genetic divergence for yield and yield-contributing traits in cucumber (*Cucumis sativus* L.). *J. Hort. Sci.* **1**(2): 141-143.
- Sharma, S., Kumar, R., Chatterjee, S. and Sharma, H.R. (2018). Correlation and path analysis studies for yield and its attributes in cucumber (*Cucumis sativus* L.). *Int. J. Che. Stud.* **6**(2): 2045-2048.
- Shet, R.M., Ashok, S.T. and Gurumurthy, S.B. (2018). Genetic variability and correlation studies for productivity traits in cucumber (*Cucumis sativus* L.). *Int. J. Chem. Stud.* **6**(5): 236-238.

- Shivaprasad, M.K., Vasant, M., Ganiger, Halesh, G.K., Buvaneshwari, G. and Vinay, G.M. (2017). Correlation studies in muskmelon for growth yield and quality attributes. *Int. J. Pure App. Bio.* **5**(4): 1913-1916.
- Shrikant, M.M., Mulge, R., Gasti, V.D., Mastiholi A.B., Koulagi, S. and Nagesh, G.C. (2017) Genetic Variability Studies in F4 Generation of Pumpkins (*Cucurbita* spp.). *Int. J. Agric. Sci.* **9**(1): 3603-3605.
- Shrikant, M.M., Ravindra, M., Gasti, V.D., Mastiholi, A.B., Sumangala, K. and Nagesh, G.C. (2017). Genetic variability studies in F4 generation of pumpkins (*Cucurbita* Spp.). *Int. J. Agric. Sci.* **9**(1): 3603-3605.
- Simi, F., Dr. Akter, Nasrin, I., Saif, H.B. and Mohammad, A. (2018). Parental diversity study in cucumber submitted to agricultural studies. *Agric. Sci.* **2**: 31-43.
- Simmi, F., Ivy, N.A., Saif, H.B., Akter, S. and Anik, M.F.A. (2018). Heterosis in cucumber (*Cucumis sativus* L.). *Bangladesh J. Agril. Res.* **42**(4): 731-747.
- Singh, H.K., Singh, V.B., Kumar, R., Baranwal, D.K. and Ray, P.K. (2014). Assessment of genetic diversity based on cluster and principal component analyses for yield and its contributing characters in bitter gourd. *India national J. Hort.* **71**(1): 55-60.
- Singh, P., Moharana, D.P., Kurrey, V., Bara, S., Minz, R. and Anand, P.K. (2016). Path coefficient analysis among quantitative and qualitative traits in pointed gourd (*Trichosanthes dioica* Roxb.) in chhattisgarh region. *Prog. Res. Int. J.* **11**: 2146-2148.
- Singh, R.K. and Chaudhury, B.D. (1985). Biometrical methods of quantitative genetic analysis. *Haryana J. Hort. Sci.* **12**(2): 151-156.
- Sultana, S., Kawochar, M.A., Naznin, S., Raihan, H. and Mahmud, F. (2018). Genetic divergence in pumpkin (*Cucurbita moschata* L.) genotypes. *Bangladesh J. Agric. Res.* **40**(4): 683-692.

- Sureshababu, V. (1989). Divergence studies in pumpkin. M. Sc. Thesis, Kerala Agril. University, Thrissare, Kerala. pp. 35.
- Swingland, I.R. (2001). Biodiversity. Definition of Encyclopedia of Biodiversity. **1**: 377–390.
- Sztepanacz, J., McGuigan, K. and Blows, M. (2017). Heritable micro-environmental variance covaries with fitness in an outbred population of *Drosophila serrata*. *Genetics*. **206**(4): 2185-2198.
- Tamang, B., Bhutia, K.D., Kumar, R., Sharma, L. and Bamaniya, B.S. (2018). Genetic variation and character association study in local cucumber (*Cucumis sativus* L.) genotypes of Sikkim. *Cur. J. App. Sci. Tech.* **31**(1): 1-9.
- Tamilselvi, N.A. and Jansirani, P. (2017). Evaluation of pumpkin (*Cucurbita moschata* L.) genotypes for earliness, yield and quality. *Int. J. Cur. Micro. App. Sci.* **6**(3): 1554-1559.
- Thakur, P., Singh, J., Nair, S.K. and Das, S.P. (2017). Correlation and path analysis in bottle gourd [*Lagenaria siceraria* (Mol.) Standl.]. *Int. J. Cur. Micro. App. Sci.* **6**(12): 1478-1485.
- Thippeswamy, S., Chandramohan, Y., Srinivas, B. and Padmaja, D. (2016). Selection of diverse parental lines for heterotic hybrid development in rice (*Oryza sativa* L.). *SABRAO J. Breed. Gen.* **48**(3): 285-294.
- Tomar, R.S., Kulkarni, G.U., Kakade, D.K., Patel, A.D. and Acharya, R.R. (2008). Genetic variability, correlation and path analysis in muskmelon (*Cucumis melo* L.). *The Asian J. Hort.* **3**(1): 158-161.
- Tyagi, N., Singh, V.B. and Maurya, P.K. (2018). Studies on genetic variability, heritability and genetic advance in bitter melon (*Momordica charantia* L.) for yield and yield contributing traits. *Int. J. Cur. Microb. App. Sci.* **7**(3): 1788-1794.

- Ullah, M.Z., Hasan, M.J., Chowdhury, A.Z.M.K.A., Saki, A.I. and Rahman, A.H.M.A. (2012). Genetic variability and correlation in exotic cucumber (*Cucumis sativus* L.) varieties. *Bangladesh J. Plant Breed. Gen.* **25**(1): 17-23.
- United Nation. (1992). Environment and development (Terminology bulletin: 344). United Nations, New York, USA.
- Verma, P., Maurya, S.K., Yadav, H. and Panchbhaiya, A. (2017). Determination of genetic divergence in pointed gourd by principal component and non-hierarchical euclidean cluster analysis. *J. App. Nat. Sci.* **9**(4): 2421-2426.
- Visen, V.K., Thakur, P., Sharma, D. and Nair, S.K. (2015). Genetic divergence studies in bottle gourd [*Lagenaria siceraria* (Mol.) Stand L.]. *Plant Arch.* **15**(2): 1175-1178.
- Wright, S. (1921). Correlation and causation. *J. Agric. Res.* **20**: 557-587.
- Yadagiri, J., Gupta, NK., Deeksha, T. and Sheela, V. (2017). Genetic variability, correlation studies and path coefficient analysis in bitter gourd (*Momordica charantia* L.). *J. Pharma. Phyto.* **6**(2): 63-66.
- Yadav, Y.C., Kumar, S. and Singh, R. (2012). Studies on genetic variability, heritability and genetic advance in cucumber (*Cucumis sativus* L.). *Hort. Flora Res. Spec.* **1**(1): 34-37.

Appendix II. Soil characteristics of the experimental field

A. Morphological features of the experimental field

Morphological features	Characteristics
AEZ	AEZ-28, Modhupur Tract
General Soil Type	Shallow Red Brown Terrace Soil
Land type	High land
Location	Sher-e-Bangla Agricultural University Agronomy research field, Dhaka
Soil series	Tejgaon
Topography	Fairly leveled

B. The initial physical and chemical characteristics of soil of the experimental site (0- 15 cm depth)

Physical characteristics	
Constituents	Percent
Clay	29 %
Sand	26 %
Silt	45 %
Textural class	Silty clay

Chemical characteristics	
Soil characteristics	Value
Available P (ppm)	20.54
Exchangeable K (mg/100 g soil)	0.10
Organic carbon (%)	0.45
Organic matter (%)	0.78
pH	5.6
Total nitrogen (%)	0.03

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

Appendix III. Monthly meteorological information during the period from March to September, 2020

Year	Month	Air temperature (°C)		Relative humidity (%)	Average rainfall (mm)
		Maximum	Minimum		
2020	March	32.9°C	20.1°C	61%	54 mm
	April	34.1°C	23.6°C	67%	138 mm
	May	33.4°C	24.7°C	76%	269 mm
	June	34°C	27.3°C	76%	134 mm
	July	32.6°C	26.8°C	81%	114 mm
	August	32.6°C	25.5°C	80%	106 mm
	September	32.4°C	25.7°C	80%	86 mm

Source: Metrological Centre, Agargaon, Dhaka (Climate Division)

Appendix IV. Mean performance for thirteen different characters in eighteen genotypes of pumpkin (*Cucurbita moschata*)

Genotype		PH	NBP	LLP	LBP	DFMF	DFFF	DFFFA	DFH	NFP	FLP	FBP	IFW	YPP
G1	BD-4396	200.33	9.33	23.23	19.06	40.33	49.67	51.67	99.33	3.33	27.09	40.64	0.62	2.10
G2	BD-4381	210.33	8.67	21.76	20.79	41.67	45.67	48.00	99.00	3.33	19.47	38.10	0.56	1.91
G3	BD-4352	218.00	9.33	25.47	20.55	40.67	47.00	49.00	104.67	3.33	19.47	18.63	1.02	3.30
G4	Hazari (Local)	224.67	11.00	25.26	20.83	45.00	46.00	47.67	109.67	3.00	37.25	57.57	1.57	4.70
G5	BD-4398	219.00	9.00	25.01	20.45	47.00	49.00	51.33	107.33	3.00	20.32	32.17	0.82	2.43
G6	Gadikata (Local)	215.67	10.00	25.59	20.70	62.67	65.00	66.67	111.67	1.67	13.55	12.36	0.44	0.71
G7	BD-4389	203.00	9.00	25.82	20.80	64.67	66.00	68.33	98.67	3.33	16.26	42.33	0.55	1.83
G8	BD-4361	229.33	9.00	25.10	20.08	46.67	49.67	52.33	109.33	3.33	22.86	45.72	1.27	4.16
G9	BD-4380	218.67	8.67	25.56	20.81	52.00	53.00	55.67	103.33	4.00	18.37	24.55	0.77	3.09
G10	BD-4368	205.33	8.67	20.50	18.29	59.00	60.00	62.00	99.67	3.67	15.24	14.39	0.65	2.37
G11	BD-4357	199.67	7.67	23.84	20.39	47.00	48.67	51.00	105.33	3.67	17.36	15.24	0.72	2.69
G12	BD-4356	218.67	9.00	25.42	20.37	66.67	68.67	71.00	114.33	1.33	12.53	12.11	0.42	0.57
G13	BD-4391	195.00	7.67	25.53	20.64	40.67	42.33	45.00	98.67	3.00	14.99	13.38	0.62	1.87
G14	BD-4371	201.67	9.00	22.88	20.63	41.67	44.00	45.33	111.67	4.33	25.23	20.32	1.20	5.15
G15	BD-4382	209.67	9.00	25.99	20.53	52.00	54.00	56.00	97.33	2.67	14.39	12.70	0.52	1.40
G16	Diamond (local)	199.67	9.00	25.86	20.85	53.00	56.00	57.67	104.00	3.33	20.32	27.09	0.61	2.04
G17	BD-4351	200.00	8.67	21.21	17.78	42.33	48.33	51.33	98.67	2.67	16.09	14.39	0.45	1.21
G18	Black super (local)	222.00	9.33	25.60	20.73	43.33	45.00	47.00	104.67	4.33	18.63	24.55	0.83	3.60
SE(±)		4.459	0.68	1.002	0.478	3.149	3.423	3.550	1.395	0.580	1.433	3.360	0.086	0.443
CV(%)		6.291	4.456	8.072	6.574	4.685	10.92	3.824	3.492	5.267	3.424	5.468	4.086	11.848

Here, PH = Plant height (cm), NBP = Number of branches per plant, LLP = Leaf length(cm),LBP = Leaf breadth(cm), DFMF = Days to first male flower, DFFFA = Days to first female flower, DFFFA = Days to first female flower anthesis, DFH = Days to first harvest, NFP = Number of fruits per plant, FLP = Fruit length(cm), FBP = Fruit breadth(cm), IFW = Individual fruit weight (kg), YPP = Yield per plant (kg).

Appendix V. Analysis of variance of 13 yield and yield contributing characters of pumpkin

Source	Sum of square of various traits of pumpkin													
	DF	PH	NBP	LLP	LBP	DFMF	DFFF	DFFFA	DFH	NFP	FLP	FBP	IFW	YPP
Replication	2	28.822	28.914	46.593	48.223	13.488	26.711	4.976	8.367	27.036	23.603	26.317	20.538	73.849
Genotype	17	195,196.376 **	142,032.820**	239,159.861**	131,211.668**	144,574.584**	240,680.769**	131,398.825**	218,774.581**	124,130.023**	132,000.265**	207,279.506**	121,353.713**	146,054.924**
Error	34	314.307	131.181	535.689	308.836	132.750	1,000.210	111.389	80.777	156.957	64.526	199.348	121.649	538.166
Total	53	195,539.506	142,192.915	239,742.143	131,568.727	144,720.823	241,707.690	131,515.189	218,863.724	124,314.016	132,088.393	207,505.170	121,495.901	146,666.939

Here, PH = Plant height (cm), NBP = Number of branches per plant, LLP = Leaf length (cm), LBP = Leaf breadth (cm), DFMF = Days to first male flower, DFFFA = Days to first female flower, DFFFA = Days to first female flower anthesis, DFH = Days to first harvest, NFP = Number of fruits per plant, FLP = Fruit length (cm), FBP = Fruit breadth (cm), IFW = Individual fruit weight (kg), YPP = Yield per plant (kg), **, * significant at the 1% and 5% level, respectively.