GENETIC VARIABILITY STUDIES IN MUSKMELON (*Cucumis melo* L.)

AYEASA AKTER

DEPARTMENT OF GENETICS AND PLANT BREEDING

SHER-E-BANGLA AGRICULTURAL UNIVERSITY

DHAKA-1207

JUNE, 2022

GENETIC VARIABILITY STUDIES IN MUSKMELON (*Cucumis melo L.*)

By

AYEASA AKTER

REGISTRATION N0. 15-06826

A Thesis
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

SEMESTER: JANUARY-JUNE, 2022

Approved by:

Prof. Dr. Md. Abdur Rahim	**Prof. Dr. Naheed Zeba**
Supervisor	**Co-Supervisor**

Assoc. Prof. Dr. Shahanaz Parveen

Chairman

Examination Committee

DEPARTMENT OF GENETICS AND PLANT BREEDING

Sher-e-Bangla Agricultural University

Sher-e-Bangla Nagar

Dhaka-1207

CERTIFICATE

This is to certify that thesis entitled, "GENETIC VARIABILITY STUDIES IN MUSKMELON (*Cucumis melo* L.)" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE** in Genetics and Plant Breeding, embodies the result of a piece of bonafide research work carried out by Ayeasa Akter, Registration No. 15-06826 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: June, 2022
Place: Dhaka, Bangladesh

Prof. Dr. Md. Abdur Rahim
Supervisor

DEDICATED TO
MY
BELOVED PARENTS

ACKNOWLEDGEMENTS

All praises to the Almighty Allah, the great, the gracious, merciful and supreme ruler of the universe who enables the author to complete this present piece of work for the degree of Master of Science (MS) in the Department of Genetics and Plant Breeding.

The author would like to express her deepest sense of gratitude, respect to her research supervisor, Prof. Dr. Md. Abdur Rahim**,** Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, for his kind and scholastic guidance, untiring effort, valuable suggestions, inspiration, extending generous help and encouragement during the research work and guidance in preparation of manuscript of the thesis.

The author sincerely expresses her deepest respect and boundless gratitude to her co-supervisor Prof. Dr. Naheed Zeba, Department of Genetics and Plant Breeding, for her helpful suggestion and valuable advice during the preparation of this manuscript.

It is highly appreciating words for chairman Assoc. Prof Dr. Shahanaz Parveen, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, for the facilities provided, in carrying out this work.

The author also acknowledges with deep regards the help and cooperation received from her honourable teachers, Prof. Dr. Md. Shahidur Rashid Bhuiyan (Vice Chancellor), Prof. Dr. Md. Sarowar Hossain, Prof. Dr. Naheed Zeba, Prof. Dr. Firoz Mahmud, Prof. Dr. Jamilur Rahman, Prof. Dr. Mohammad Saiful Islam, Prof. Dr. Md. Ashaduzzaman Siddikee, Prof. Dr. Kazi Md. Kamrul Huda and and all other staffs of Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for their teaching, direct and indirect advice, encouragement and co-operation during the study period.

At last but not the least, the author feels indebtedness to her beloved parents and friends whose sacrifice, inspiration, encouragement and continuous blessing paved the way to her higher education and reach at this stage. May Allah bless us all.

The Author

GENETIC VARIABILITY STUDIES IN MUSKMELON (*Cucumis melo L.*)

By

AYEASA AKTER

ABSTRACT

An experiment was conducted at Sher-e-Bangla Agricultural University Dhaka, during *Kharif I*, 2020 using thirteen muskmelon (*Cucumis melo* L.) genotype to study the genetic variability among the genotype in a randomized complete block design with three replications. The analysis of variance revealed significant differences for various traits among genotypes. For all of the characters, phenotypic variance are greater than genotypic variance. The number of fruits per plant (47.73), single fruit weight (52.55), and yield plant per plant (90.40) all had high genotypic co-efficients of variation (GCV). High heritability with high genetic advance in percent of mean was observed in number of fruits per plant (86.05), single fruit weight (99.12), rind thickness (24.33) and yield plant per plant (93.47) 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 flowering (59.93) and days to first female flowering (60.15). The result revealed a highly significant positive correlation with plant height (rg= 0.615, rp= 0.541), number of branches per plant (rg= 0.698, rp= 0.530), number of fruits per plant (rg= 0.652, rp= 0.703), single fruit weight(rg= 0.854, rp= 0.778), rind thickness (rg= 0.579, rp= 0.517), and flash thickness (rg= 0.664, rp= 0.649) to yield per plant. Thirteen muskmelon genotypes were grouped into four cluster. Cluster III exhibited maximum 5 genotypes while cluster I had only 2 genotypes. Among four cluster, the highest inter-cluster distance (8.13) was observed between clusters II and IV, while the lowest (5.164) was observed between clusters I and III. Cluster IV had the highest intra cluster distance (3.144), while Cluster II had the lowest (0.874). Considering group distance and phenotypic performances, the inter genotypic crosses between G13 (BD-11268) and G11 (BD-11266); G13 and G12 (BD-11267); G13 and G2 (BD-11254); G12 and G11; G12 and G2; and G11 and G2 might be suggested for future hybridization program.

LIST OF CONTENTS

LIST OF CONTENTS (Cont'd)

LIST OF CONTENTS (Cont'd)

LIST OF CONTENTS (Cont'd)

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

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 Number	Sl. No.

CHAPTER I

INTRODUCTION

The muskmelon (*Cucumis melo* L., 2n=24) is one of the most nutritive and commercially important fruit crop of the cucurbitaceae in the world (Choudhary *et al*., 2019). Generally, it is considered as a crop of tropical and subtropical regions, and also extensively cultivated in different temperate regions. Desert and savannah regions of Africa, Arabia, southwestern Asia and Australia are the origin of wild populations of muskmelons (Molla *et al*., 2017). The USA is the world largest consumers of muskmelon. According to Behe (2020), Americans consume around 28 pound melon per year. Muskmelon is normally eaten as a fresh fruit, salad, or dessert with ice cream or custard. In Bangladesh, people consume both unripe and ripe fruits. Unripe fruits are used as salad and processed food as soup, stew, curry, stir-fry or pickle while mature ripe fruits are eaten fresh as a desert fruit and sometimes slightly processed as canned, syrup, jam or dehydrated slices (Malek *et al*., 2012). Moreover, it is a source of antioxidants, chemicals which can regulate the formation of nitric oxide, a vital chemical for prevention of heart attacks.

In Bangladesh, it is considered as a minor fruit crop and is cultivated all over the country. According to the latest statistics provided by BBS (2021), it was indicated that the area and production of muskmelon are 4053 ha and 49572 tons, respectively and contributes 1.45% to total fruit production in Bangladesh.

Despite the variation in habit, size, shape, colour, maturity time and yield observed in Bangladeshi muskmelon genotypes, very little work has been done on genetical improvement of this crop. Muskmelon being predominantly andromonoecious, is a cross pollinated crop and provide ample scope for utilization of the hybrid vigor. Assessment of genetic variability and selection of suitable genotypes is the foremost criterion for genetical improvement of crop species. Plant Genetic Resources Centre (PGRC) of Bangladesh Agricultural Research Institute (BARI) has conserved different types of muskmelon genotypes collected from different parts of Bangladesh. Islam *et al.* (2017) reported that a total of 131 genotypes in PGRC, BARI. Among these genotypes, diverse genotypes could be used as a source of genetic material for improving the yield, earliness,

uniformity, quality and resistance to biotic and abiotic stresses in muskmelon. In this crop, practically all plant characters of economic importance are quantitatively inherited and therefore, improvement in yield through yield contributing traits depends on the nature and magnitude of heritable variation. Information like genetic variability, heritability and genetic advance helps in planning an efficient breeding programme.

The information's on variability present in the material, extent of heritability and genetic gain for a particular trait and contributing effect of one character on the other are prerequisite for formulating a suitable breeding technique to bring out a high jump in yield of any crop. Since muskmelon is an under exploited cucurbitaceous vegetable, very little attempts have been made to gather genetic information in this crop (Choudhary and Pandey, 2016). Owing to the favorable environmental conditions, it is grown almost every districts of Bangladesh. Due to non-availability of improved lines, farmers are still growing existing land races, which give poor yield and are also low in quality. Seeing the importance of muskmelon in the culture of people, particularly of rural and urban areas of Bangladesh and the wide existing variability, the present investigation was envisaged to gather basic information on the genetic parameters needed for crop improvement in muskmelon.

Crop improvement depends largely on availability of genetic variability in genotypes, their effective evaluation and utilization. This genetic variability is responsible for the different traits in species and enables crop species to adapt to the variety of environments that exist in the world. It also provides the raw materials by which new species arise through evolution. Before aiming at an improvement in melon for yield, quality and disease resistance, it is necessary to have a thorough knowledge of genetic variability present in the crop. Adequate genetic variability ensures better chances of producing new forms (Begna, 2021). During the domestication process, although plants retained several horticultural important traits like big fruit, desirable flavor and high yield but they lost other undesirable traits which confer disease resistance and high secondary metabolites. Thus, plants lost some of the alleles related to horticulturally undesirable or non-selected traits and decreased the genetic base of following population (Salgotra and Stewart, 2020). However, today’s modern breeding methodologies produce high-yielding crops

which are important for the agriculturist and the genetic variation of crop plants becomes narrower because as varieties are developed from crosses between genetically related species (Qaim, 2020). Unfortunately, crop species have been driven into a genetic bottleneck. The allelic variation of genes in a population starts to decrease and it brings a dramatic loss of heterogeneity. The narrow genetic base of some plant species poses serious threat to these species. Crop species with narrow genetic variation are more susceptible to diseases, insect-pests and environmental changes (Skendzic *et al.*, 2021). Pests and diseases cause great losses to melon crops around the world. Their distribution and impact on melon plants varies around the world (Tahir, 2020). Melon and its related species and genera co-exist in Asia and have rich genetic resources, which are characterized by a considerable amount of variability for horticultural traits and insect-pests and disease resistance (Toyzhigitova *et al.*, 2019). Therefore, efforts should be made to collect, conserve and evaluate the genetic resources of melon in Bangladesh. To enhance the utilization of such genetic resources, systematic evaluation for different characters are prime important.

Correlations are helpful to ascertain the real components of a complex character like yield. Correlation coefficient indicates the degree of relationship between characters, but it alone does not give a clear picture of the association between yield and its components. Thus, interrelationship between various traits along with direct and indirect influence of component characters on yield is of prime importance to the plant breeder from practical stand point, since selection involves two or more characters. However, only correlation studies do not provide an exact magnitude of direct and indirect effects towards the yield. In this context, Wright (1921) proposed estimation of path coefficient analysis as an important tool in partitioning the correlation coefficient into direct and indirect effects found useful to breeder in identifying important biometrical characters to achieve desirable goals.

Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization. Conventionally, varietal identification and genetic diversity in plants is based on phenotypic evaluation of morphological characteristics that demands collection of extensive data at different

locations, however, many traits having polygenic control are influenced by environment. Also, the level of polymorphism for morphological characteristic in elite genotypes is sometimes too limited and inadequate to allow for varietal discrimination (Wang *et al.*, 2008). A method suggested by Mahalanobis (1936) known as 'Mahalanobis D^2-statistic' is a powerful tool for quantifying the divergence.

Inspite of the fact that muskmelon is grown extensively and have aesthetic value, not much work has been done on the improvement of complex quantitative characters. Therefore, the present investigation was conducted with the following objectives.

i. to determine the genetic variability among muskmelon 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

The main concern of the plant breeder is the improvement of both quantitative and qualitative plant characteristics. Adequate genetic knowledge of different characteristics is therefore very important in the vegetable breeding programme to achieve desired results in future generations. However, the success of plant breeding depends on the extent and the magnitude of variability existing in the genotypes. At the same time, improvement is possible on the basis of heritable variation. In the present investigation, an attempt has been made to study the genetic variability in muskmelon genotypes. The relevant literature available on various aspects included in the present study is reviewed under the following sub heads:

2.1 Genetic variability, heritability and genetic advance
2.2 Correlation coefficient
2.3 Path coefficient analysis
2.4 Genetic divergence

2.1 Genetic variability, heritability and genetic advance

The importance of plants and evolving new varieties depends upon the variability present in the base population. The variation among the individuals occurs due to differences in genetic composition and/or the environment in which they are raised. The phenotypic variation in a population arises due to genotypic and environmental effects. Genetic variance is divided it into three components, *viz*., additive, dominance and epistatic components of genetic variance. Out of these, additive genetic variance corresponds to the fixable component of heritable variation and can be exploited for genetic improvement through selection, while, the other two components possess the unfixable characteristics. Yield and its contributing traits usually show quantitative inheritance patterns and they are usually influenced by the environment. Since environmental effects are not heritable and cannot be passed on to the progeny. Therefore, the contribution of genotype to the phenotype should be estimate for the formulation of a breeding

programme in desirable direction. Estimates of genetic parameters for heritability and heritable components of variation such as genotypic and phenotypic coefficients of variation help in gaining the knowledge about the genetic nature of characters under study. These parameters provide information concerning the maximum effect of selection for complex characters such as yield and how closely this maximum can be approached. Brief reviews on the genetic variability, heritability and genetic advance present in muskmelon and other cucurbitaceous crops are described below.

Costa *et al.* (2019) evaluated forty-one treatments of melon genotypes of *Momordica* group, the significant positive GCA and SCA effects showed the importance of the additive and non-additive genes effects. The additive gene action contributes the larger role in the control of most characters like mean fruit mass, mean fruit length, mean fruit diameter, fruit length per diameter ratio, fruit internal cavity and mean pulp thickness.

Muthuselvi *et al*. (2019) performed variability in twenty-three snap melon (*Cucumis melo* var. *momordica*) genotypes. Analysis of variance revealed that there was a considerable variability exists among the genotypes for all the twenty-one characters. High phenotypic and genotypic coefficients of variation were recorded for number of primary branches (28.16 and 28.22), node at which first male flower appearance (34.19 and 34.26), length of the fruit (27.50 and 27.67), weight of the fruit (29.54 and 29.69), number of fruits per plant (29.79 and 29.92) and fruit yield per plant (34.54 and 34.63). High level of heritability with moderate genetic advance as percentage mean was recorded by days to first male flower appearance (89.53 and 14.09%) and days to first female flower appearance (90.11 and 18.94 percent).

Pasha *et al*. (2019) evaluated fifteen snap melon (*Cucumis melo* L. var. *momordica*) genotypes to assess genetic variability for yield and its component traits. Analysis of variance showed significance differences for days to male flowering, days to female flowering, number of fruits per plant, fruit length, fruit girth, flesh thickness, average fruit weight and fruit yield per plant indicating considerable amount of genetic variation. The low difference between GCV and PCV depicted that a little or no influence of environment on the expression of the various quantitative traits. High heritability coupled with high genetic advance was depicted by for average fruit weight and number of fruits

per plant indicated predominance of additive gene effects and the possibilities of effective selection based on these traits for snap melon improvement.

Torkadi *et al.* (2019) studied genetic variability among fifty-one genotypes of muskmelon for sixteen characters. High magnitude of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for average weight of fruit, number of fruits per plant, fruit weight and fruit yield/ plant, which indicated the presence of significant amount of variation for these characters. High estimate of heritability coupled with high genetic advance for average weight were recorded for fruit length, suggesting the presence of additive gene action and efficacy of direct selection for these traits.

Janghel *et al.* (2018) evaluated 18 varieties of muskmelon for genetic variability, heritability and genetic advance for 18 contributing characters and found the widest range of variation in fruit volume, days to first fruit harvest, days to fruit set, days to first female flower appearance and days to 50% flowering. Maximum GCV and PCV was observed for rind thickness followed by average fruit weight, fruit yield plot^{-1}, fruit volume, node number of first female flower, node number at first male flower appear, whereas, high magnitude of heritability (%) was observed for fruit volume (98.8) followed by yield plot^{-1} (94.6), average fruit weight (89.6), rind thickness (84.5) and fruit girth (82.3). The maximum genetic advance as per cent of mean was observed for fruit length (91.9), fruit girth (90.5) and rind thickness (86.8).

Kamagoud *et al.* (2018) studied genetic variability for yield and its attributing characters of forty oriental pickling melon. Analysis of variance revealed that highly significant (P = 0.01) difference among genotypes for all the twenty characters related to growth and yield traits except for number of primary branches. The estimate of PCV was higher than GCV in all the characters studied indicating the influence of environment towards expression of characters. Higher PCV and GCV were recorded for nodes at first female flower appears, number of male flowers, number of female flowers, average fruit weight, number of fruits per plant and fruit yield per plant indicating the higher variability present for these characters. High heritability coupled with high GAM recorded for 16 characters

indicating predominance of additive components and hence, these traits can be improved by following simple selection.

Mishra *et al.* (2017) evaluated forty genotypes of muskmelon (*Cucumis melo* L.) to study genetic variability among the traits to determine selection criteria for breeding programmes for fruit yield and related characters. The results reported that drought stress caused reduction in fruit yield and most of the characters studied. Significant variations for all the characters were found under different water regimes (non-stress, 50% and 25%). High genotypic (GCV) and phenotypic (PCV) coefficients of variations were observed for fruit yield per plant, fruit weightand fruit length 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 and fruit yield per plant in both the non-stress and stress conditions. This shows that these traits 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.

Saha *et al.* (2018) evaluated twenty-one F_1 hybrids of muskmelon (*Cucumis melo* L.) in a half-diallel set involving seven characters *viz*. day to first female flower opening, number of fruits per plant, average fruit weight, fruit length, flesh thickness and number of primary branches per plant. Result showed high narrow-sense heritability for node number of first female flower, average fruit weight and yield per plant which indicated that the non-additive type of gene action played an important role in the inheritance of this trait.

Bhimappa *et al*. (2017) performed genetic variability, heritability and genetic advance among sixty-seven diverse muskmelon (*Cucumis melo* L.) genotypes for yield and its contributing characters. Average fruit weight showed the highest phenotypic and genotypic coefficients of variation closely followed by fruit yield per plant. The lowest value was recorded for number of fruits per plant followed by number of primary branches per plant, days to female flowering. Traits like days to female flowering and fruit length showed nearly equal GCV and PCV values indicated the least influence of environment on their expression. The heritability estimates were generally high (above 80%) for fruit length, fruit girth, flesh thickness, TSS, number of primary branches and

days to female flowering. Genetic advance as percentage of mean was the highest for average fruit weight (kg) followed by fruit length (cm) and yield per plant (kg). High heritability coupled with high GAM was observed for fruit length indicated additive gene action and could be effectively improved through selection.

Venkatesan *et al.* (2016) evaluated the performance of fifty-one muskmelon genotypes (*Cucumis melo* L.) for different traits attributing for growth, yield and quality traits. Among the genotypes used for investigation, Dharwad Local recorded the highest number of fruits per plant followed by GWL-1. The genotype Dharwad Local recorded the highest yield followed by Mysore Local and Tindivanam Local. The maximum β carotene content was observed in the genotypes KashiMadhu followed by Yanakandla and Tindivanam Local. The genotype Yanakandla recorded the highest value of TSS (14.04° Brix) followed by KashiMadhu (11.60° Brix). Based on their performance Dharwad Local, KashiMadhu, Yanakandla and Tindivanam Local can be used for further breeding programme to produce promising hybrids that could be exploited for cultivation in muskmelon.

Mali *et al*. (2015) carried out genetic variability and interrelationship among different traits in seven F_3 muskmelon (*Cucumis melo* L.) progenies. Significant differences among progenies were observed for all the traits under study. The high value of genotypic and phenotypic coefficients of variability and heritability estimates were associated with greater value of genetic advance as percent of mean as observed for fruit length, number of primary branches per plant, fruit weight, flesh thickness, TSS, number of fruits per plant and fruit yield per plant.

Potekar *et al*. (2014) evaluated twenty-two genotypes of muskmelon to study genetic variability. A wide range of genetic variability was observed for all the characters. GCV and PCV werethe highest for fruit length, fruit weight, flesh thickness and fruit yield per plant. High estimate of heritability in broad sense were recorded for fruit length, fruit weight, flesh thickness, TSS and fruit yield per plant. The lowest value of heritability was recorded for days required for appearance of first female flower. High heritability values with high genetic advance were obtained for fruit length and fruit weight.

Devendra *et al.* (2013) carried out variability studies in ten snap melon (*Cucumis melo* var. *momordica*) genotypes. They select various parameters viz., length of fruits (cm), weight of fruits (kg) and total soluble solid (TSS). Genotype V_5 had the maximum fruit length (27 cm), whereas, V_6 had highest weight (3 kg) and TSS content (50 Brix). The minimum fruit length was recorded in genotypes V_7 (12cm). Whereas, the minimum fruit size was recorded in genotype V_9 (8cm). The minimum fruit weight was recorded in V_2 (0.90 kg),while, the lowest TSS was observed in V_5 (40 Brix). Snap melon V_1, V_2, V_6, V_8 and V_9 were found compact in nature whereas V_3 and V_{10} were found less compact. Melon V_1 and V_8 had banana like aroma rather than snap melon V_2 and V_5 had light banana like aroma.

Ibrahim and Ramadan (2013) evaluated thirteen Egyptian sweet melon (*Cucumis melo aegyptiacus* L.) genotypes for variability, heritability and genetic advance under irrigation as well as drought stress condition. Significant differences were observed among genotypes for all the studies traits under normal irrigation and water stress. The estimates of phenotypic coefficient of variation were higher than the estimates of genotypic coefficient of variation for all the characters which suggested that the apparent variation was not only due to the genotypes but also due to the influence of environment. High heritability coupled with high genetic advance was noted for fruit weight and yield per plant. Fruit length was very less affected by water stress, but yield per plant was very high affected by water stress.

Kumar *et al.* (2013) reported the highest GCV and PCV for total fruit yield per vine followed by average fruit weight and TSS while, the average fruit weight showed high heritability with high genetic advance.

Reddy and Shanthi (2013) reported wide variability for characters *viz.*,vine length (129.9 to 290.9 cm), fruit cavity size (5.40 to 11.15 cm) and TSS (3.56 to 12.80 °brix). Moderate GCV, PCV along with high heritibality and high genetic advance as per cent of mean was observed in vine length and fruit cavity size. Whereas, high GCV and PCV coupled with high heritability and GAM was recorded for TSS in 24 accessions of muskmelon.

Choudhary *et al.* (2011) performed genetic variability, heritability and genetic advance among seventy genotypes of muskmelon for fifteen yield contributing character. Yield per plant and average fruit weight exhibited higher values of genotypic and phenotypic coefficients of variation. High heritability and genetic advance observed for fruit yield per plant and average fruit weight indicated existence of considerable amount of genetic variability.

Fergany *et al.* (2011) analyzed variation among fifty melon (*Cucumis melo*) landraces from the humid tropics of southern India. They observed that the number of fruits per plant ranges from 2.5 to 9.0, fruit weight from 0.17 to 1.73kg, average fruit yield per plant varied between 0.87 and 5.33 kg. The three accessions with the highest fruit weight had yielded less number of fruits per plant. Variability in melon landraces was also observed for fruit length, fruit girth, primary branches per pant and flesh thickness.

Szamosi *et al.* (2010) studied morphological evaluation and comparison of fifty eight Hungarian and Turkish melon genotypes and reported wide range of diversity among melon genotypes belonging to these regions. Among Hungarian melon, the average fruit weight ranged from 734.0 to 1333.7 g, fruit diameter from 8.5 to 24.5 cm, fruit length from 7.9 to 29.8 cm, however, among Turkish melon the average fruit weight ranged from 653.50 to 1017.70 g, fruit girth from 4.2 to 16.7 cm, fruit length from 5.5 to 26.7 cm.

Lotti *et al.* (2008) assessed one hundred and fifty-three genotypes of muskmelon belonging to inodorus and cantalupensis. The result revealed wide range of variability among the accessions in fruit weight (0.6 to 4.1kg), fruit length (12.2 to 35.6cm) and fruit girth (10.7 to 20.2cm). High heritability in broad sense was recorded in characters like fruit length, fruit girth, fruit weight, node at which first female flower appear and total soluble solids content. The estimates of heritability in broad sense were found low for fruits per plant. The Node at which first female flower appear showed the highest expected genetic advance.

Tomar *et al.* (2008) evaluated fifty genotypes of muskmelon (*Cucumis melo* L.) to study the variability for yield and its contributing characters. The analysis of variance showed significant variation for all the characters indicated presence of sufficient variability in the material studied. The moderately high genotypic and phenotypic coefficients of variation were observed for fruit yield per plant, fruits per plant and total soluble sugar. Very high heritability observed for total soluble sugars, total soluble solids and fruit yield per plant. Traits like fruit yield per plant, total soluble sugars, number of fruits per plant, number of the node at which first female flower appeared and fruit weight (having very high to moderately high heritability) coupled with high to moderately high genetic advance (as per cent mean) suggested that these characters can be improved by effective selection of genotypes.

Dhillon *et al.* (2007) reported large variation in twenty-seven snap melon accessions collected from different regions of India. They found that the number of primary branches varied from 2.9 to 11.8, number of fruits per plant 1 to 3.5, average fruit weight from 0.24 to 1.4 kg within accessions. High heritability and medium genetic advance as per cent of mean exhibited by fruit yield per plant, number of fruits per plant and fruit weight indicated that hybridization followed by selection was effective for genetic improvement of these traits.

Samadia (2007) studied genetic variability, heritability and genetic advance in round melon using eighteen land races/genotypes under hot arid environment to identify desirable genotypes for crop improvement programme. On the basis of fruit quality characters along with a greater number of fruits and early yield per plant, the genotype AHRM-1 (1.91 kg), KPT-3, ArkaTinda and KCM/BKP 01 were observed to be the most potential. The estimates of GCV were high for fruit yield and number of fruits per plant and moderate for node to female flower appearance, fruit weightand number of primary branches per plants indicated better scope of improvement through selection. The genetic advance as percentage of mean ranged from 10.62 to 91.17. High estimates of heritability values accompanied with high genetic gain were observed for fruit yield per plant, number of fruits per plant and node to first female flower appearance.

Iathet and Piluek (2006) assessed two inbred lines (RM1 and LM2) of slicing melon (*Cucumis melo* L. var. *conomon markino*) and their related progenies were determined for their quantitative inheritance of fruit girth, fruit length, fruit weight, number of fruits per plant and fruit yield per plant. The results indicated that heritability based on fruit girth, fruit length and fruit weight were relatively high at 0.60, 0.68 and 0.71 respectively. The heritability as considered from number of fruits per plant and fruit yield per plant were also high at 0.60 and 0.61.

Rakhi and Rajamony (2006) evaluated forty-two landraces of culinary melons (*Cucumis melo* L.) and noted high heritability coupled with high genetic advance for fruit length and average fruit weight. The result indicated the scope for improvement of culinary melon through selection in these traits. The characters like number of primary branches per plant recorded low heritability. Although heritability was high for fruit length, fruit girth and fruit yield per plant, genetic advance was moderate to low, indicated the role of non-additive gene action, which may result in no scope of selection. Overall, selection for high yielding melon types should focus on average fruit weight, number of fruits per plant and keeping quality.

Fageria and Luthra (2005) carried out genetic variability among one hundred and twelve diverse genotypes of muskmelon (*Cucumis melo* L). They observed sufficient genetic variability for fruit shape, fruit colour, average fruit weight and TSS. The fruit weight varied from 200 to 700g. Total soluble solids ranged from 7 to 17º brix.

Prasad *et al.* (2004) carried out analysis of genetic variation in thirty-four muskmelon (*Cucumis melo* L.) genotype in which they found highly significant variation among 34 muskmelons inbred with regard to the characters like fruit weight, fruit length, primary branches per plant and TSS except node at which female flower appeared.

Ram *et al.* (2004) evaluated one hundred and sixty-nine muskmelon genotypes to study the variation among the genotypes. They found huge variation for fruit weight (100-2500 g), fruit length (4-25 cm), flesh thickness (2-4 cm), TSS (4-14 %), number of fruits per plant (2-12) and fruit yield per hectare (80-268 q per ha).

Singh and Ram (2003) conducted a study on variability of twenty-eight genotypes of muskmelon and reported variation for fruit shape and fruit colour. The fruit colour showed enough variability. Approximately half of the genotypes were sweet tasting with pleasant flavor and good flesh thickness. Fruit weight ranged from 350 to 1460 g. Flesh thickness varied from 1.3 to 3.0 cm.

Kadi and Sambhaj (2003) performed variability study among fifty-one genotypes of muskmelon. They found genotypic coefficient of variation were low as compared to correspondent phenotypic coefficient of variation. The highest genotypic as well as phenotypic coefficient of variation was observed for economically important characters such as average weight of fruit followed by fruit girth and number of fruits per plant. The characters *viz*., flesh thickness, length of fruit and weight of fruits per plant showed high heritability. While, the characters average weight of fruit, fruit girth and number of fruits per plant recorded high percentage of genetic advance along with higher estimates of heritability indicated additive gene effects in their inheritance and scope for selection. High heritability coupled with medium or low genetic advance as exhibited by length of fruit and pulp thickness were attributable to the non-additive gene effects. This indicates that hybridization followed by selection might be effective for genetic improvement.

2.2 Correlation coefficient

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.

Pasha *et al*. (2019) evaluated fifteen snap melon (*Cucumis melo* L. var. *momordica*) genotypes to assess correlation coefficient analysis. The result revealed that days to first

male flowering, days to first female flowering, number of fruits plant, fruit length, fruit girth, flesh thickness and average fruit weight had shown significant positive correlation with yield per plant at both phenotypic and genotypic levels representing that any improvement in these traits may increase the yield in snap melon.

Sunisa *et al.* (2018) reported a significant positive correlation among the fruit weight, fruit length, fruit width and fruit thickness traits of muskmelon.

Bhimappa and Choudhary (2017) performed correlation coefficient analysis among sixty seven diverse muskmelon (*Cucumis melo* L.) genotypes for yield and its contributing characters. The genotypic and phenotypic correlation coefficients among different quantitative traits along with fruit yield per plant exhibited highly significant and positive association with average fruit weight, fruit length, fruit girth and flesh thickness. The total soluble solid showed highly significant and positive association with days to male flowering, days to female flowering, fruit length and flesh thickness.

Shivaprasad *et al.* (2017) analyzed correlation of eight muskmelon hybrids with one commercial check for sixteen different growths, yield and quality attributing characters. Number of primary branches per plant had positive association with number of fruits per plant and total sugars. while, it was negatively associated with fruit length, number of primary branches per plant, fruit weight, flesh thickness and fruit yield per plant. Fruit weight and fruit yield per plant negatively correlated with days to first male flowering and days to first female flowering. Positive and highly significant correlation of total soluble sugar was observed with total soluble solids.

Mali *et al*. (2015) carried out correlation analysis among different traits in seven F_3 muskmelon (*Cucumis melo* L.) progenies which revealed that fruit yield per plant showed highly significant positive correlation with yield contributing character such as fruit length, number of primary branches per plant, average fruit weight, flesh thickness, number of fruits per plant and fruit girth. This suggested that characters *viz*., number of fruits per plant and average fruit weight should be given priority for selecting high yielding genotypes.

Potekar *et al*. (2014) evaluated twenty-two genotypes of muskmelon (*Cucumis melo* L.) to study correlation coefficient analysis. They reported that the yield per plant was closely associated with weight of fruit at both genotypic and phenotypic levels with significant and positive correlation. While, characters days for first female flowering, fruit length, number of fruits per plant, length of fruit, fruit girth, flesh thickness and TSS exhibited positive and non-significant correlation with fruit yield per plant. Node at which primary branches per plant showed negative and non-significant correlation with fruit yield per plant.

Malik and Vashisht (2012) studied Correlation among growth, yield and quality attributes in *Cucumis melo* L. among ninety-six variable lines representing different melon types. They reported that number of fruits per plant exhibits a significantly negative correlation with the fruit weight, fruit length and flesh thickness, while, fruit weight showed positive correlation with the fruit length. The negative correlation between number of fruits per plant and average fruit weight. This indicated that the development of genotypes may possibly having moderate number of fruits along with commercially acceptable fruit size.

Nasrabadi *et al*. (2012) examined the characteristics of eleven Iranian melon cultivars for quantitative traits and results showed greater diversity. Correlation analysis between the traits reported a significantly positive relation between length of fruit and total soluble sugar. Similarly, fruit weight was positively correlated with fruit girth, fruit length, flesh thickness and total soluble sugar content. Negative correlation was reported among fruit length, fruit girth and flesh thickness.

Reddy *et al.* (2012) evaluated a set of thirty-five germplasm lines of muskmelon (*Cucumis melo* L.) to study the correlation among 18 quantitative traits pertaining to growth, earliness, and yield characters and to help breeders to determine the selection criteria for breeding programmes for fruit yield improvement. They observed that the fruit yield per plant had a positive correlation with fruit length, number of primary branches per plant, fruit length, fruit girth, average fruit weight and number of fruits per plant, while, it had a negative correlation with the flesh thickness.

Cheema *et al.* (2011) carried out correlation analysis of forty-five muskmelon [(*Cucumis melo* L (Reticulatus group)] genotypes. Correlation indicated that fruit yield per plant was positively correlated with number of fruits per plants and fruit weight. Number of fruits per plants was positively correlated with total soluble solids (TSS) and fruit yield per plant and may be used as a morphological marker for selection of higher TSS and yield.

Mehta *et al*. (2009) evaluated forty-four muskmelon genotypes (*Cucumis melo* L.) to study the association between yield and contributing traits by correlation analysis. Fruit yield was positively and significantly correlated with fruits per plant, fruit weight, fruit girth and pulp thickness and at both genotypic and phenotypic levels. Fruit yield showed significant and negative correlation with total soluble solids at both genotypic and phenotypic levels. Therefore, fruit yield may be improved by selecting genotypes having higher fruit weight, fruit length, fruit girth, fruits per plant and pulp thickness with less total soluble solids.

Tomar *et al.* (2008) investigated fifty genotypes of muskmelon (*Cucumis melo* L.) to study genotypic and phenotypic correlations. They concluded that the genotypic correlations were higher than those of their respective phenotypic correlation coefficients in majority of the cases suggesting that genotypic correlations were stronger, reliable and free from the environment factors. Fruit yield per plant was positively correlated with fruit weight, fruit girth, flesh thickness and number of fruits per plant at both the genotypic and phenotypic levels, while, it had significant and positive correlation with fruit length at the genotypic level only. On the other hand, it showed significant and negative correlation with total soluble solids at both the phenotypic and genotypic levels.

Samadia (2007) conducted correlation coefficient analysis for round melon using eighteen land races/genotypes under hot arid environment to identify desirable genotypes for crop improvement programme. A very strong positive and significant correlation was recorded between fruit yield per plant with number of fruits per plant (0.921) and fruit length (0.808) indicating that effective improvement through these characters could be achieved in round melon. Negative and significant association of days to appearance of female flower with number of fruits per plant which indicated that early genotypes bear a greater number of fruits per plant.

Iathet and Piluek (2006) assessed two inbred lines (RM1 and LM2) of slicing melon (*Cucumis melo* L. var. *conomon markino*) and their related progenies were determined for their correlations among fruit girth, fruit length, fruit weight, number of fruits per plant and fruit yield per plant. The results indicated that the girth of marketable immature fruit showed negative correlation to fruit length and fruit shape. Fruit shape and size were not related to number of fruits per plant and fruit yield per plant, while, number of fruits per plant had highly positive correlation to fruit yield per plant.

Pandey *et al.* (2005) carried out correlation analysis of thirty-five accession of muskmelon (*Cucumis melo* L.). Positive and significant correlation were found between fruit weight, fruit girth, fruit length, rind thickness and flesh thickness at both phenotypic and genotypic levels. The fruit weight, fruit girth, fruit length and flesh thickness had positive correlation coefficient among themselves.

Rolania (2005) estimated correlation coefficient among one hundred and twelve genotypes of muskmelon. On the basis of overall performance, out of 112 genotypes, fourteen were categorized as most promising. These were GP-105, GP102, GP-39, GP-98, GP-116, GP-115, GP-151, GP-187, GP-194, GP-195, GP-204, GP-59, GP-36 and GP-140. The fruit yield per plant had positive and significant association with fruit weight and flesh thickness.

Choudhary *et al.* (2004) studied correlation analysis among eight genotypes of muskmelon (*Cucumis melo* L.) and found that fruit yield per plant had positive and significant correlation with fruit weight, fruits per plant, fruit length and flesh thickness at both phenotypic and genotypic levels.

Kadi and Sambhaj (2003) performed correlation analysis among fifty-one genotypes of muskmelon. The estimates of genotypic correlation were slightly higher than phenotypic correlation, indicated the minimum effect of environment on the expression of characters. The weight of fruits per vine depicted positive correlation with average weight of fruit and pulp thickness at genotypic level. Thus, these characters can be considered as yield contributing characters in muskmelon. Significant and negative correlation showed with

TSS at genotypic level. The number of fruits per vine showed significant and negative correlation with average weight of fruit, length of fruit and pulp thickness.

Singh and Ram (2003) examined correlation among twenty-eight genotypes of muskmelon (*Cucumis melo* L.) and observed positive correlation of fruit weight with flesh thickness. The total soluble solid contents were not significantly correlated with fruit yield per plant.

Taha *et al.* (2003) estimated correlation among growth, yield and quality attributes in *Cucumis melo* L. with thirteen variable lines representing different melon genotypes. Positive and significant association were found between the number of fruits per plant with the number of primary branches (+0.82); pulp thickness (+0.39); and total soluble solids (+0.67); fruit weight withfruit length (+0.59). Total soluble solids with number of primary branches manifested negative and significant association between them.

Yadav and Ram (2002) conducted correlation in fifty-six genotypes of melon (*Cucumis melo*) revealed that fruit weight had positive and significant correlation with fruit girth, fruit length and flesh thickness. The total soluble solids (TSS) content showed non-significant correlation with fruit girth, fruit length, flesh thickness and fruit weight. The large fruits tended to have less total soluble solids content. However, this could not be considered as a barrier in combining desirable fruit size and total soluble solids content in one genotype, since the negative correlation between total soluble solids and fruit size components was, low and non-significant.

2.3 Path coefficient analysis

The path coefficient analysis is simply a standardized partial regression analysis, which may be useful in choosing the characters that have direct and indirect effects on yield. Such a study found useful in effective selection for simultaneous improvement of component characters that really contribute towards yield. Path analysis was initially suggested by Wright (1921) but was applied for the first time in plant breeding by Dewey and Lu (1959). 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.

Silpa *et al*. (2020) carried out path analysis in fifty-three accession of oriental pickling melon (*Cucumis melo* L var. *conomon* Mak.). The result revealed that fruit yield per plant showed high positive direct effect to number of primary branches per plant (0.84), number of fruits per plant (0.81) and fruit length (0.57), while, fruit weight showed high positive direct effect to fruit length (1.06), fruit girth (0.85) and flesh thickness (0.99).

Pasha *et al*. (2019) evaluated fifteen snap melon (*Cucumis melo* L var. *momordica*.) genotypes to assess path analysis. The result revealed that the characters *viz*., days to female flowering, number of fruits per plant, fruit length, fruit girth, flesh thickness and average fruit weight showed positive direct effect on fruit yield per plant at the both phenotypic and genotypic levels indicating the effectiveness of direct selection, Therefore these traits may selected for crop improvement programme.

Kamagoud (2018) studied forty oriental pickling melon (*Cucumis melo* var. *conomon*) genotypes for the path analysis for yield and its contributing traits of different morphological characters. The result revealed that the traits like days to first male and female flowering, number of fruits per plant, average fruit weight, fruit length, flesh thickness and fruit girth had significant and positive correlation with fruit yield per plant with positive direct effect. Therefore, direct selection of these traits could effective for increasing the fruit yield per plant.

Kumari *et al.* (2018) found in path coefficient analysis that the traits like a number of fruits per plant and average fruit weight (g) have positive and direct genotypic and phenotypic effects towards the fruit yield.

Bhimappa *et al*. (2017) performed path analysis among sixty-seven diverse muskmelon (*Cucumis melo* L.) genotypes for yield and its contributing characters. Path coefficient analysis at genotypic level revealed that total soluble solids had a direct positive effect (0.003) and indirect effect via average fruit weight (0.143) and negative indirect effect via fruit length (-0.381) and days to first male flowering (-0.120).

Karadi *et al.* (2017) investigated twenty-four genotypes of wild melon (*Cucumis melo* sub sp. *agrestis*) for the path analysis of different quantitative and qualitative characters.

The result revealed that fruit yield per plant showed direct positive effect to number of fruits per plant, fruit length, fruit girth and flesh thickness. Total soluble solids had exhibited true association with direct positive effect on fruit yield per plant. The direct selection for these traits would be rewarding for improvement in the total yield per plant.

Potekar *et al*. (2014) evaluated twenty-two genotypes of muskmelon (*Cucumis melo* L.) to study path analysis. The result indicated the importance of yield contributing characters viz., fruit length, number of fruits per plant, fruit girth and weight of fruit which showed high positive direct effects as the major yield contributing traits, for enhancing the yield of muskmelon. Based on direct and indirect effects of different yield components on yield it appears that it would be rewarding to give stress on the number of fruits per plant, fruit girth and weight of fruit followed by days for first female flowering, length of fruit and flesh thickness, while formulating selection indices for improvement of yield in muskmelon.

Babu (2013) studied forty-six genotypes of oriental pickling melon (*Cucumis melo* L. var *conomon*) to determine path analysis between different traits. The result revealed that fruit weight, fruit length and number of fruits per plant exerted high positive direct effect on fruit yield per plant and these traits also recorded significant positive correlation with fruit yield per plant signifying the importance of these traits in selection programme for crop improvement.

Reddy *et al.* (2012) carried out path analysis in a set of thirty-five germplasm lines of muskmelon (*Cucumis melo* L.). They found that the number of primary branches per plant, fruit length and fruit weight exhibited positive correlation with fruit yield but, direct effects on fruit yield were negative or negligible. The traits *viz*., the days to first female flowering and number of fruits per plant had high positive direct effect on fruit yield.

Mehta *et al*. (2009) evaluated forty-four muskmelon (*Cucumis melo* L.) genotypes for path analysis. The result revealed that fruits per plant and fruit weight were the main yield attributing characters in fruit yield of muskmelon, because of their high positive

direct effect and positive correlation with fruit yield per plant. In addition to fruit weight and fruits per plant, total soluble solids also exhibited positive direct effect on fruit yield per plant.

Tomar *et al.* (2008) studied path analysis among fifty genotypes of muskmelon. The path analysis based on genotypic associations revealed that the fruits per plant was the main yield attributing character in fruit yield of muskmelon, because of its high positive direct effect and positive correlation with fruit yield per plant. In addition to fruits per plant; total soluble solids also exhibited positive direct effect on fruit yield per plant. Thus, it could be advocated that fruits per plant and total soluble solids should be given more weightage for an effective selection programme to improve the fruit yield in muskmelon.

Pandey *et al.* (2005) carried out path coefficient analysis of thirty-five accession of muskmelon (*Cucumis melo* L.). The result revealed that the highest and positive direct effect on yield was exerted by fruit girth followed by number of fruits per plant, fruit weight and flesh thickness. Direct selection based on fruit weight and fruit girth results in an appreciable improvement for total yield. Besides direct selection for fruit yield, indirect selection though the fruit length and number of fruits per plant should be considered for further improvement of yield.

Rolania (2005) examined one hundred and twelve genotypes of muskmelon to determine path analysis between different traits. The result revealed that flesh thickness, days to first male and female flowering, number of fruits per plant and fruit weight had positive direct effect on fruit yield per plant.

Choudhary *et al.* (2004) studied path coefficient analysis among eight genotypes of muskmelon and found positive direct effect of fruit weight, fruits per plant, flesh thickness and TSS on yield per plant. While, days to first female flower had negative direct effect.

Yadav and Ram (2002) studied path coefficient analysis of fifty-six genotypes of muskmelon (*Cucumis melo* L.) and found positive direct effect of fruit weight, fruit girth, flesh thickness, TSS and number of fruits per plant on fruit yield per plant, while, negative direct effect of primary branches per plant on fruit yield per plant.

2.4 Genetic divergence

Several methods have been developed for measuring divergence between population using multivariate analysis such as coefficient of racial likeness (Pearson, 1926), multiple regression (Hotelling, 1935), discriminate function (Fisher, 1936) and D^2 statistic (Mahalanobis, 1936). Out of these, D^2 statistic is a powerful tool in quantifying the degree of divergence among biological populations at genotypic level and to assess the relative contributions of different components to total divergence. The importance of genetic diversity has long been appreciated by breeders. Selection of parents based on individual attributes may not be as advantageous as that based on number of important components taken collectively, especially if the aim is to seek improvement in complex quantitative character such as yield.

Indraja *et al.* (2018) evaluated twenty-five genotypes of muskmelon (*Cucumis melo* L.) for assessment of genetic diversity based on 29 morphological traits. Cluster analysis revealed distinct clustering pattern and grouping of genotypes in to six clusters. Cluster II was the largest (7 genotypes) followed by cluster I and III (5 genotypes) followed by cluster IV (3 genotypes), while, cluster VI consisted of only one genotype. Intra cluster D^2 values ranged from 0.00 (cluster VI) to 1980.14 (cluster II), while, intercluster D^2 values ranged from 2286.05 (cluster I and II) to 17401 (cluster VI and V). Cluster V and VI were extremely diverse from the rest of the clusters. Hence, the genotypes falling in these clusters being genetically more divergent, can be used in hybridization programme.

Senthilvadivu *et al.* (2018) evaluated thirty-five muskmelon (*Cucumis melo* L.) genotypes to check its genetic diversity. Based on D^2 analysis these genotypes were grouped in to 11 clusters. Out of eleven clusters, cluster I was the largest, comprising of seven genotypes. Among 21 characters studied, fruit yield per plant (24.54%) contributed the maximum towards expression of genetic divergence followed by beta carotene (23.53%), total soluble sugars (6.72%) and number of fruits per plant (5.21%). The maximum intra cluster distance was found in the cluster VII followed by clusters XI, X and I. The genotypes in the most divergent clusters VI and VIII could be used for hybridization programme to develop hybrids.

Reddy *et al.* (2017) studied genetic diversity among thirty-five genotypes of muskmelon. Cluster analysis revealed distinct clustering pattern and grouping of genotypes into six distinct clusters. Cluster II was the largest (22 genotypes) followed by cluster I (8 genotypes) and cluster IV (2 genotypes), while, cluster III, V and VI were solitary consisting of single genotype. Intracluster D^2 values ranged from 0.00 (cluster III, V and VI) to 85.514 (cluster IV), while, the intercluster D2 values ranged from 94.56 (clusters I and II) to 753.29 (clusters I and VI).

Karadi *et al.* (2017) investigated twenty-four genotypes of wild melon to study the diversity for different quantitative and qualitative characters. The genotypes were grouped into eight clusters with irrespective of geographic divergence, indicating no parallelism between geographic and genetic diversity. The maximum number of genotypes (17) was found in cluster 1 with intra-cluster distance of (22.12). The maximum inter-cluster distance was observed between cluster III and cluster VIII (97.23). Hence, genotypes belonging to these clusters may be utilized for involving in hybridization program for crop improvement. Among 18 characters included for D^2 analysis, fruit length (71.01%) and fruit flesh thickness (20.65%)contributed more for genetic divergence.

Rahman *et al.* (2016) evaluated sixty-four genotypes of muskmelon (*Cucumis melo* L.) to assess genetic divergence using D^2 statistics. The genotypes were grouped into six clusters to indicate the existence of considerable among the genotypes. The highest number of genotypes possessed in Cluster I. The highest intra cluster distance was computed for cluster III (0.839) followed by cluster I (0.751). Cluster VI showed the least intra cluster distance which indicated that the genotypes in this cluster were more or less homogeneous. The inter cluster distances were larger than the intra cluster distances suggesting wider genetic diversity among the genotypes of different clusters. Similarly, the highest total fruit weight per plant was found in cluster IV (13.5 kg) which was also far different from other clusters. So, it revealed that genotypes of this cluster could be used for developing high yielding variety. Cluster VI showed the highest brix reading (5.6%).

Koli and Murthy (2013) assessed the phenotypic diversity among thirty-three landraces of C. melo and these were clustered into three clusters based on principle component analysis. Accessions in cluster I showed large variation in number of primary branches per plant on 60^{th} day (12 to 20), length of fruit (15 to 43 cm), width of fruit (7 to 12 cm) and these collections were basically from the group acidulous. Genotypes having large fruit length and high fruit weight and short growth duration (within 90 days) were grouped in the cluster II, comprised of group momordica. Cluster III having landraces which had almost similar characters were of group momordica. There existed single unclustered landrace CmKc-9 having higher heavy fruit weight and high fruit breadth and with the medium growth durations (less than 120 days), which belongs to acidulous group.

Manohar and Murthy (2012) studied phenotypic divergence with 44 melon accessions, from two important snapmelon varieties, *Cucumis melo* var. *momordica* and *Cucumis melo* var. *acidulus*. In scatter diagram, acidulus and momordica accessions grouped into different clusters. The maximum and the minimum vine length and the nodes per plant were same in both the genotypes; except in one accession, CMC 108 (momordica group) in which the highest vine length was 291.1 cm. Mean number of branches in group acidulus (6.63 ± 1.65) was higher as compared to momordica group (5.90 ± 2.15). Length of fruit varied widely, from 12.1- 40.7 cm and 12.1-6.1 cm in acidulus and momordica, respectively. The mean fruit weight (g) in acidulus group (1109.36 ± 362.72) was more as compared to momordica group (883.40 ± 5.08).

Reddy *et al.* (2012) studied genetic divergence among thirty-five genotypes of muskmelon (*Cucumis melo* L.). Cluster analysis revealed distinct clustering pattern and grouping of genotypes into six distinct clusters. Cluster II was the largest (22 genotypes) followed by cluster I (8 genotypes) and cluster IV (2 genotypes), while, cluster III, V and VI were solitary consisting of single genotypes. Intra cluster D^2 values ranged from 0.00 (cluster III, V and VI) to 85.514 (cluster IV), while, the inter cluster D^2 values ranged from 94.56 (clusters I and II) to 753.29 (clusters I and VI). The genotype of the most divergent clusters I and VI (753.29), clusters IV and VI (590.55) and clusters II and IV (529.79) could be used in hybridization programmes. Total soluble solids, fruit yield,

days to appearance of first staminate flower and average fruit weight contributed the maximum towards divergence.

Soltani *et al.* (2010) assessed diversity among Iranian melon land races of groups flexuosus and dudaim for morphological and physiological traits. They reported that thirty-one morphological and physiological traits had significant variation among accessions. Cluster analysis of morphological and physiological characters divided Iranian melon into seven groups. Dudaim (cluster VII) was clearly separated from flexuosus in which typical (cluster I) accessions and atypical accessions (clusters III-VI) were grouped separately.

Phan *et al.* (2010) studied genetic diversity among fifty-nine melon land races from Vietnam and reported that morphological characters of the melon land race fruits were highly diversified. Among the five types of cultivated melon, Dua le and Duavang were classified as conomon var. makuwa. Whereas, Dua gang as conomon var. conomon, and Duabo as momordica, however, Duathom could not be classified into a proper group or variety. A cluster analysis revealed that Duabo, Dua le, Duavang and Dua gang were grouped in cluster II. Clusters III and IV consisted mainly of conomon accessions from China and Japan. Duathom was classified into cluster V with landraces from Yunnan Province, China. The other four types were related closely with conomon and agrestis accessions from China, Korea, and Japan, indicating their involvement in the differentiation and establishment of the conomon group in East Asia.

Yi-San *et al.* (2009) studied genetic diversity in forty-one accessions of melon, of which thirty-six accessions were of small-seed type. The gene diversity was 0.239, higher than that for group conomon from East Asia and equivalent to Indian melon populations. Melon accessions were classified into six major clusters, however, the largest cluster IV mainly comprised group conomon which was closely related to cluster V consisting of mainly group agrestis. The accessions of group cantalupensis were grouped into clusters II or VII which were distantly related to groups conomon and agrestis.

Tomar *et al.* (2008) investigated fifty genotypes of muskmelon to study genetic divergence. Analysis of variance for yield attributing character showed significant

variation for all the traits, indicating presence of sufficient variability. D^2 values distributed all the genotypes in seven clusters. The maximum genetic distance was obtained between clusters II and V, while, clusters III and VII displayed the lowest degree of divergence. Total soluble sugars followed by total soluble solids and fruit yield per plant contributed the most towards divergence.

Tanaka *et al*. (2007) classified genetic diversity of sixty-nine accessions from India, Myanmar, Korea and Japan which were grouped into three major clusters and sub clusters. Cluster I and II comprised group conomon var. makuwa and var. conomon from East India, which indicated that genetic variation decreased from India towards East.

Gurjinder and Dhillon (2006) studied genetic diversity among thirty muskmelon genotypes for 14 characters. The varieties differed significantly for all the characters. The 30 strains were grouped in 11 clusters depending on similarities of their D^2 values. The clustering pattern of the genotypes did not follow the geographical distribution pattern. The intracluster distance was the maximum in cluster VIII and the minimum in clusters VIII, IX, X and XI. The maximum inter-cluster distance was calculated between X and VII clusters and the minimum between clusters V and III. This indicated that muskmelon crop improvement programme may be tried with the genotypes of divergent clusters X and VII for better heterotic effects.

Singh and Dhillon (2006) carried out genetic divergence among fourteen characters and grouped them into eleven clusters based on D^2 values. The clustering pattern of the genotypes did not follow the geographical distribution pattern. The intra cluster distance was the maximum in cluster VIII and the minimum in clusters VIII, IX, X and XI. The maximum inter cluster distance was calculated between X and VII clusters, whereas, the minimum between V and III.

McCreight *et al.* (2004) analyzed genetic divergence of three hundred and seventy-eight melons accessions collected from India and twenty-six accessions from China with nineteen isozyme loci. ‘Top Mark’ and ‘Green Flesh Honeydew’ which represented two distinct *Cucumis melo* ssp melo groups: cantalupensis and inodorus, respectively, were used as reference cultivars. They calculated genetic distance and initial cluster analysis

among accessions. Group 1 was unique and consisted of only two *Cucumis melo* ssp *agrestis* accessions. Two large branches were detected at cluster node 2. One branch comprised three groups of 3, 12 and 34 accessions, while, other branch contained seven groups of 2, 3, 14, 16 and 47 accessions and reference accessions. From the one hundred and forty-eight accessions, one hundred and thirty-two were distributed unequally across the 11 groups. The fourteen Chinese accessions originating from seven provinces were also dispersed unequally in the four major cluster groups. 'Top Mark' and 'Green Flesh Honeydew' were genetically distinct and uniquely clustered in the same group.

Staub *et al*. (2004) assessed genetic diversity among seventeen melon land races and inbred lines of group cantalupensis, inodorus and flexuosus in which average fruit weight ranged from 176 to 439 g, number of fruits per vine from 0.8 to 4.3. Fruits of group flexuosus were mostly elongated in shape, while mostly ovoid in groups inodorus and cantalupensis.

Singh and Lal (2003) performed multivariate analysis by using fifty-one accessions of muskmelon and grouped them into thirteen clusters. The maximum intercluster distance was between cluster VII and XII as well as the minimum between cluster I and II. The maximum divergence was depicted by node at which first female flower opens (11.0%) followed by fruit weight (10.1%) and TSS content (9.3%) emphasizing the importance of these characters in breeding programme.

More and Seshadri (2002) evaluated ninety-eight geographically diverse muskmelon genotypes. Based on their statistical significance, all ninety-eight genotypes were classified into twelve clusters. Consideration of the different classes of genotypes led to the inference that in this out breeding taxon, genetic variability and diversification occurred over wide geographical locations.

Rizzo and Braz (2002) studied the genetic divergence with five cultivars (JAB20, JAB-21, JAB-22, JAB-23 and Bonus no. 2) of muskmelon (*Cucumis melo* var. *reticulates*) and estimated the relative contribution of the sixteen characteristics to genetic divergence. Two similar groups were formed between the genitors based on the values of D^2, one of them constituted the genotypes JAB-20, JAB-21 and Bonus no. 2 and the other comprised of JAB-22 and JAB-23. The characters *viz*.,length of fruit, girth of fruit,

number of fruits per plant and total soluble solid percentage contributed more to the genetic divergence between the progenitors.

Sanjay and Tarsem (2000) tested the fifty-one genotypes of melon for various plant parameters to assess their genetic divergence using D^2 statistics. The genotypes were grouped into thirteen clusters. The intra-cluster distance was the greatest in cluster I and II. The maximum divergence was manifested by node at which first female flower opened. While, the minimum divergence was provided by total fruit yield per vine.

CHAPTER III

MATERIALS AND METHODS

The experiment was conducted at Sher-e-Bangla Agricultural University, Dhaka to study the genetic variability in muskmelon genotypes. 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 13 muskmelon (*Cucumis melo* L.) 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, thirteen genotypes of muskmelon were used as experimental materials. The purity and germination percentage were leveled as around 100 and 80, respectively. The seeds of the muskmelon genotypes were collected from the Plant Genetic Resources Center (PGRC) of the Bangladesh Agricultural Research Institute (BARI), Gazipur (Table 1).

3.4 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. Seedling of different muskmelon in polybag showed in plate 1.

Table 1. List of muskmelon genotypes with their accession and source

Sl. No.	Genotype No.	BARI ACC Number	Source
1	G1	BD-11252	PGRC, BARI
2	G2	BD-11254	PGRC, BARI
3	G3	BD-11255	PGRC, BARI
4	G4	BD-11257	PGRC, BARI
5	G5	BD-11258	PGRC, BARI
6	G6	BD-11259	PGRC, BARI
7	G7	BD-11260	PGRC, BARI
8	G8	BD-11262	PGRC, BARI
9	G9	BD-11264	PGRC, BARI
10	G10	BD-11265	PGRC, BARI
11	G11	BD-11266	PGRC, BARI
12	G12	BD-11267	PGRC, BARI
13	G13	BD-11268	PGRC, BARI

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

Plate 1. Seedling of different muskmelon in polybag

3.5 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 plot size was 4.0 × 5.0 m and block spacing was 2.0 × 1.0 m. The experimental plot was carefully cleared of weeds and other debris and leveled as needed.

3.6 Pit preparation

Pits measuring 55 cm × 55 cm × 50 cm with a spacing of 1 m × 1 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.

3.7 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.

3.8 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.

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

	Fertilizers/Manures	Dose
1	Cowdung	10 ton per ha
2	Urea	150 kg per ha
3	TSP	100 kg per ha
4	MOP	150 kg per ha
5	Gypsum	80 kg per ha
6	Zinc Oxide	10 kg per ha

3.9 Intercultural operations

3.9.1 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.

3.9.2 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.

3.9.3 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.

3.9.4 Pesticide application

Malathion 57EC (organophosphate insecticide) and Ripcord 10 EC (Cypermethrin) were applied in the field in response to the red 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 wereutilized as fruit fly defenses.

3.10 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.

3.11 Data recording

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

i. Plant height

The height of the selected plant was measured from the ground level to the tip of the plant at harvest. Mean plant height of soybean plant were calculated and expressed in cm.

ii. Primary branches per plant

Number of primary branches were counted and the mean value for each of the three random plants were computed for each replication.

iii. Days to 50% male flowering

The days to 50% male flowering were calculated on plot basis. The character was recorded by computing the days required for appearing male flower in 50% plants of the plot from the date of sowing.

iv. Days to 50 % female flowering

The days to 50% female flowering were calculated on plot basis. The character was recorded by computing the days required for appearing female flower in 50% plants of the plot from the date of sowing.

v. Number of fruits per plant

number of fruits per plant were recorded by counting all the marketable fruits harvested from all picking of plants from each replication.

vi. Fruit weight (g)

The same three marketable fruits selected for measuring fruit length and fruit girth were weighed individually. The observations were then averaged to compute fruit weight in grams per plant.

vii. Fruit yield per plant (g)

The total marketable fruits obtained from all plants during the individual picking were weighed and summed up. The observations were then averaged to compute yield in grams per plant.

viii. Flesh thickness (cm)

The same three marketable fruits selected for fruit length, fruit girth and fruit weight were taken from the plants from each replication and cut the fruits equatorially. The observations were then averaged to compute flesh thickness in cm using the ruler.

ix. Rind thickness (cm)

The same three marketable fruits selected for fruit length, fruit girth and fruit weight were taken from the plants from each replication and cut the fruits equatorially. The observations were then averaged to compute flesh thickness in cm using the Vernier caliper.

3.12 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).

3.12.1 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:

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

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

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

Where,

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

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

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

3.12.2 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)

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

B) Phenotypic Coefficient of Variation (PCV)

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

3.12.3 Heritability (in broad sense)

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

$$\text{Heritability (\%)} = \frac{Vg}{Vp} \times 100$$

Where,

Vg = Genotypic variance [Vg = (Mg - Me) / r]

Vp = Phenotypic variance [Vg + Ve]

3.12.4 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)

σp = Phenotypic standard deviation

H = Heritability in broad sense

3.12.5 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):

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

3.12.6 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:

3.12.7 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:

$$VeXY = MP_2$$

$$VgXY = (MP_1 - MP_2)/r$$

$$VpXY = VgXY + VeXY$$

Where, VeXY = Environmental covariance between X and Y

Vg = Genetic covariance between X and Y

XYVpXY = Phenotypic Covariance between X and Y

3.12.8 Coefficients of correlation

a. Genotypic correlation coefficient between X and Y

$$r_g = \frac{Vg\ XY}{\sqrt{(Vg\ X \times Vg\ Y)}}$$

Where,

Vg XY = Genotypic covariance between X and Y

Vg X = Genotypic variance of X

Vg Y = Genotypic variance of Y

b. Phenotypic correlation coefficient between X and Y

$$r_p = \frac{Vp\ XY}{\sqrt{(Vp\ X \times Vp\ Y)}}$$

Vp XY = Phenotypic covariance between X and Y

Vp X = Phenotypic variance of X

Vp Y = Phenotypic variance of Y

Genotypic variance (Vg) = (Mg-Me) / r

Phenotypic variance (Vp) = (Vg+Ve)

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.

3.12.9 Path coefficient analysis

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985) using simple correlation values. In path analysis, correlation co-efficient is partitioned into direct and indirect independent variables on the dependent variable. In order to estimate direct & indirect effect of the correlated characters, say x1, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

$r_{yx1} = P_{yx1} + P_{yx2}r_{x1x2} + P_{yx3}r_{x1x3}$

$r_{yx2} = P_{yx1}r_{x1x2} + P_{yx2} + P_{yx3}r_{x2x3}$

$r_{yx3} = P_{yx1}r_{x1x3} + P_{yx2}r_{x2x3} + P_{yx3}$

Where, r's denotes simple correlation co-efficient and P's denote path co-efficient (Unknown). P's in the above equations may be conveniently solved by arranging them in matrix from.

Total correlation, say between x1 and y is thus partitioned as follows:

P_{yx1} = The direct effect of x1 on y.

$P_{yx2}r_{x1x2}$ = The indirect effect of x1 via x2 on y.

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

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

$P^2RY = 1- \sum P_{iy} .Riy$

Where,

$P^2RY = (R^2)$; and hence residual effect, $R= (P^2RY)^{1/2}$

Piy = Direct effect of the character on yield

Riy = Correlation of the character with yield.

3.12.10 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:

3.12.11 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.

3.12.12 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.

3.12.13 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.

3.12.14 Calculation of D^2 values

According to Rao (1952) and Singh and Chaudhury (1985), the Mahalanobls 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.

$D^2 = \Sigma_1^x d_1^2 = \Sigma_1^x (Y_i^j - Y_j^k)^2 \quad (j \neq k)$

Where,

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

x = Number of characters.

3.12.15 Computation of average intra-cluster distances

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

$$\text{Average intra-cluster distance} = \frac{\Sigma Di^2}{n}$$

Where,

Di^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.

3.12.16 Computation of average inter-cluster distances

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

$$\text{Average inter-cluster distance} = \frac{\Sigma Di^2 j}{ni \times nj}$$

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

Ni= Number of populations in cluster i.

nj = Number of populations in cluster j.

3.12.17 Cluster diagram

The cluster diagram proposed by Singh and Chaudhury (1985) was drawn using the values of intra- and inter-cluster distances (D = Dz). 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 genetic variability in muskmelon genotypes. 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 muskmelon genotypes. Table 3 displayed the mean, 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 (m)

The plant height of 13 genotypes of muskmelon showed significant variation. Significant mean sum of squares for plant height (0.061) suggested that the genotypes under study showed a great deal of variation (Table 3). The genotype G13 (BD-11268) had the tallest plants (2.34 m), while G2 (BD-11254) had the shortest plants (1.92 m), with a mean height of 2.11 m (Appendix IV). The phenotypic variance (0.031) appeared to be slightly higher than the genotypic variance (0.030). The phenotypic co-efficient of variation (PCV) 8.34% and the genotypic co-efficient of variation expression (GCV) 8.21% were rather close to one another. Moderately high PCV and GCV estimates indicate that these traits are under genetic control and are less affected by environment. The plant height showed the highest heritability with (98.37) with moderate genetic advance in percent of mean (8.44%) indicated that this trait has additive genetic control. Thus the selection based on this character would be effective. Reddy and Shanthi (2013) found a wide range of variation in the vine length of muskmelon.

Plate 2. Pictures showing morphological variation in fruits among different muskmelon genotypes

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

Parameters	Range		MS	Mean	CV (%)	σ^2p	σ^2g	σ^2e	PCV	GCV	h^2b	GA (5%)	GA (%) mean
	Max	Min											
PH	2.34	1.92	0.061**	2.11	1.751	0.031	0.03	0.001	8.34	8.21	98.37	0.18	8.44
NBP	9.67	5.67	4.333**	7.67	9.341	2.423	1.91	0.513	20.29	18.02	88.78	1.42	18.54
DFMF	21.00	17.33	4.003**	19.34	4.812	2.945	1.058	1.887	8.87	5.32	59.93	1.06	5.47
DFFF	26.33	22.00	4.030*	24.46	5.618	2.96	1.071	1.889	7.03	4.23	60.15	1.06	4.35
DFH	91.00	81.00	29.692**	85.69	1.768	15.994	13.699	2.295	4.66	4.32	92.54	3.8	4.44
NFP	7.33	2.00	11.526**	4.64	28.242	6.622	4.904	1.718	55.45	47.73	86.05	2.28	49.11
SFW	1.70	0.49	0.338**	0.78	7.244	0.171	0.168	0.003	53.01	52.55	99.12	0.42	54.08
RT	0.50	0.25	0.018**	0.39	4.892	0.01	0.009	0.001	25.64	24.33	94.86	0.09	25.03
FT	3.90	2.10	0.508**	2.99	9.534	0.295	0.214	0.081	18.17	15.47	85.17	0.47	15.92
YPP	12.42	1.22	24.517**	3.74	34.391	13.085	11.432	1.653	96.72	90.4	93.47	3.57	95.45

PH = Plant height (m), NBP = Number of branches per plant, DFMF = Days to first male flowering, DFFF = Days to first female flowering, DFH = Days to first harvest, NFP = Number of fruits per plant, SFW = Single fruit weight (kg), FT – Flash thickness (cm), YPP = Yield per plant (kg), σ^2p = Phenotypic variance, σ^2g = Genotypic variance, σ^2e = 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.

4.1.2 Number of branches per plant

The mean sum of squares of the number of branches per plant of muskmelon was found to be significant (4.333) (Table 3). The mean number of branches per plant was 7.67, with G13 (BD-11268) having the highest number of branches per plant at 9.67 and G2 (BD-11254) having the lowest number of branches per plant at 5.67 . The phenotypic variance (2.423) appeared to be larger than the genotypic variance (1.910), indicating that the environment had less influence on the expression of this gene controlling the trait. The PCV (20.29%) was higher than GCV (18.02%). The higher heritability (88.78) with genetic advance in percent of mean (18.54) was found for this trait suggesting moderate additive gene effects. Thus the selection based on this character would be effective. The high value of genotypic and phenotypic coefficients of variability and heritability estimates were associated with greater value of genetic advance as percent of mean as observed for number of primary branches per plant (Mali *et al*., 2015)

4.1.3 Days to first male flowering

Days to first male flowering revealed highly significant variation among the muskmelon genotypes. G13 (BD-11268) required the longest duration (20.67) for the emergence of the first male flower, while G4 (BD-11257) required the shortest duration (17.33), with a mean value of 19.34. (Table 3). There was a considerable difference between the phenotypic variance (2.945) and genotypic variance (1.058), suggested less influence of environment on the expression of the genes controlling this character (Table 3). The difference between phenotypic coefficient of variation (8.87%) and genotypic coefficient of variation (5.32) was comparatively larger in terms of days to first male flower. This character showed a moderate heritability (59.93), genetic advance (1.06), and genetic advance in percent of mean (5.47). However Muthuselvi *et al*. (2019) reported that high level of heritability with moderate genetic advance as percentage mean was recorded by days to first male flower appearance (89.53 and 14.09 percent).

4.1.4 Days to first female flowering

The mean sum of squares of the days to first female flowering revealed highly significant muskmelon genotype variation (4.030). With a mean value of 24.46, G12 (BD-11267) required the longest time (26.33) and G2 (BD-11254) required the shortest time (22.00), respectively, for the emergence of the first female flower. (Table 3). The phenotypic variance (2.960) and genotypic variance (1.071) differed significantly, indicating that environmental factors may have influenced the traits expressed (Table 3). The phenotypic co-efficient of variation (7.03%), higher than the genotypic co-efficient of variation (4.23%) had significant effect due to phenotypic variation. Heritability was (60.15), genetic advance (1.06), and genetic advance in percent of mean (4.35), indicating that this character was influenced by additive gene effects. Similar result also observed by Kamagoud *et al.* (2018) reported that higher PCV and GCV were recorded for nodes at first female flower appears of forty oriental pickling melon, indicating the higher variability present for this character.

4.1.5 Days to first harvest

Days to first harvest of muskmelon genotypes mean square of sum was significant (29.692). Among different genotypes, G8 (BD-11262) required the longest duration (91.00) for first harvest of muskmelon, while G1 (BD-11252) required the shortest duration (81.00), with a mean value of 85.69 (Table3). The phenotypic variance (15.994) and genotypic variance (13.699) 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 (4.66%) was only marginally greater than the genotypic co-efficient of variation (4.32%). Heritability was high (92.54), genetic advance (3.8) and genetic advance in percent of mean (4.44) indicating successful selection based on this feature as the character was governed by additive genes. The result was similar with the findings of Janghel *et al.* (2018) who evaluated 18 varieties of muskmelon for genetic variability, heritability and genetic advance for 18 contributing characters and found the widest range of variation in days to first fruit harvest.

4.1.6 Number of fruits per plant

The mean sum of squares of fruit number per plant of muskmelon was found to be highly significant (11.526). With a mean value of 4.64, the highest fruit number per plant (7.33) was found in G13 (BD-11268) and G11 (BD-11266), while the lowest fruit number per plant (2) was found in G12 (BD-11267). The fact that the phenotypic variance (6.622) was greater than the genotypic variance (4.904). The genotypic and phenotypic co-efficients of variation were both 55.45% and 47.73% respectively. This character showed a high heritability (86.05) with high genetic advance in percent of mean (49.11) indicating that this trait was governed by additive genes. Therefore, selection based on this character would be rewarding. The result was similar with the findings of Kamagoud *et al.* (2018) who studied genetic variability for yield and its attributing characters of forty oriental pickling melon reported that higher PCV and GCV were observed for number of fruits per plant indicating the higher variability present for these characters. Dhillon *et al.* (2007) reported large variation in twenty-seven snap melon accessions collected from different regions of India. They found that the number of fruits per plant varied from 1 to 3.5 within accessions. High heritability and moderate genetic advance as per cent of mean exhibited by fruit yield per plant.

4.1.7 Single fruit weight (kg)

A significant mean sum of squares of single fruit weight was discovered (0.30). The mean single fruit weight was 0.338, with the maximum single fruit weight of 1.70 kg found in G13 (BD-11268) and the minimum single fruit weight of 0.49 kg found in G4 (BD-11257). The fact that the phenotypic variance (0.171) was slightly greater than the genotypic variance (0.168) suggested that the environment had less of an impact on the expression of the gene responsible for this feature (Table 3). The phenotypic and genotypic co-efficients of variation were 53.01% and 52.55%, respectively. Heritability was found to be high (99.12%), with a genetic advance (0.42) and highly genetic advance in percent of mean (54.08), indicating that the character was controlled by an additive gene, so selection based on this character would be effective. According to Pasha *et al*. (2019), analysis of variance revealed significant differences in average fruit weight

among fifteen snap melon (*Cucumis melo* L. var. *momordica*) genotypes. The low difference between GCV and PCV depicted that a little or no influence of environment on the expression of the various quantitative traits. High heritability coupled with high genetic advance was depicted by for average fruit weight indicated predominance of additive gene effects and the possibilities of effective selection.

4.1.8 Rind thickness (cm)

The mean sum of squares of rind thickness was discovered to be significant (0.018). The average rind thickness was 0.39 cm, with G13 (BD-11268) having the highest rind thickness of 0.50 cm and G4 having the lowest rind thickness of 0.25 cm. The fact that the phenotypic variance (0.01) was slightly higher than the genotypic variance (0.009) indicated that the environment had less of an effect on the expression of the gene responsible for this feature (Table 3). The phenotypic and genotypic co-efficients of variation were respectively 25.64% and 24.33%. Heritability was found to be high (94.86%), with a low genetic advance (0.09) and a high genetic advance in terms of percent of mean (25.03), indicating that the character was controlled by an additive gene, so selection based on this character would be effective. Janghel *et al.* (2018) reported similar result in muskmelon.

4.1.9 Flash thickness (cm)

It was discovered that the mean sum of squares of flash thickness of muskmelon genotypes was significant (0.508). The average flash thickness was 2.99 cm, with G13 (BD-11268) having the thickest flash at 3.90 cm and G4 having the thinnest at 2.10 cm. The phenotypic variance (0.295) was slightly higher than the genotypic variance (0.214), indicating that the environment had less of an effect on the expression of the gene responsible for this feature (Table 3). The phenotypic and genotypic coefficients of variation were respectively 18.17% and 15.47%. Heritability was found to be high (85.17%), with a low genetic advance (0.47) and a moderate genetic advance in terms of percent of mean (15.92), indicating that the character was controlled by an additive gene, so selection based on this character would be effective. Fergany *et al.* (2011) also found similar results in muskmelon.

4.1.10. Yield per plant

Significant mean sum of squares of yield per plant was found (24.517). The mean yield per plant was 3.74, with the maximum yield per plant of 12.42 kg discovered in G13 (BD-11268) and the minimum yield per plant of 1.22 kg discovered in G12 (BD-11268). The fact that the phenotypic variance (13.085) was larger than the genotypic variance (11.432) suggested that the environment had an impact on the expression of the gene responsible for this feature (Table 3). Both the genotypic and phenotypic co-efficients of variance were 96.72% and 90.4%, respectively. Heritability was found high (93.47%) with a low genetic advance (3.57) and a high genetic advance in percent of mean (95.45), revealed that the character was controlled by additive gene so the selection based on this character would be effective. Choudhary *et al.* (2011) reported that high heritability and genetic advance observed for fruit yield per plant and average fruit weight in muskmelon.

4.2. Correlation coefficient

4.2.1 Plant height (cm)

Plant height showed highly significant positive correlation with number of branches per plant(rg = 0.909, rp = 0.847), days to first female flowering(rg = 0.767, rp = 0.364), single fruit weight (rg = 0.550, rp = 0.532), rind thickness (rg = 0.387, rp = 0.367), flash thickness (rg = 0.556, rp = 0.449) and yield per plant (rg = 0.615, rp = 0.541) indicating that if plant height increase these parameters will also be increased (Table 4). Non-significant positive correlation was found in days to first male flowering(rg = 0.524, rp = 0.240), days to first harvest (rg = 0.017, rp = 0.049) and number of fruits per plant(rg = 0.394 , rp = 0.305). Plant height was an important component of plant ecological strategy. It is strongly related to life span, seed mass, and maturity time, and it is a major determinant of a species' ability to compete for light. Pandey *et al.* (2005) also found similar result which supported the present findings.

Table 4. Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters of muskmelon

Characters		NBP	DFMF	DFFF	DFH	NFP	SFW	RT	FT	YPP
PH	rg	0.909**	0.524	0.767**	0.017	0.394	0.550**	0.387*	0.556**	0.615**
	rp	0.847**	0.240	0.364*	0.049	0.305	0.532**	0.367*	0.449**	0.541**
NBP	rg		0.630**	0.988**	0.113	0.560**	0.563**	0.275	0.551**	0.698**
	rp		0.275**	0.445**	0.124	0.379*	0.470**	0.230	0.366*	0.530**
DFMF	rg			0.002**	-0.141	0.325	0.733**	0.922**	1.000**	0.716**
	rp			0.728**	-0.006	0.111	0.354*	0.466**	0.386*	0.291**
DFFF	rg				-0.200	0.193	0.230	-0.057	0.406**	0.287
	rp				-0.034	0.055	0.096	-0.030	0.099**	0.089
DFH	rg					-0.128	0.151	0.072	0.334	0.089
	rp					-0.171	0.134	0.051	0.197	0.028
NFP	rg						0.201**	0.087	0.017	0.652**
	rp						0.168**	0.084	0.155	0.703**
SFW	rg							0.767**	0.852**	0.854**
	rp							0.724**	0.680**	0.778**
RT	rg								0.908**	0.579**
	rp								0.698**	0.517**
FT	rg									0.664**
	rp									0.649**

PH = Plant height (m), NBP = Number of branches per plant, DFMF = Days to first male flowering, DFFF = Days to first female flowering, DFH = Days to first harvest, NFP = Number of fruits per plant, SFW = Single fruit weight (kg), RT – Rind thickness (cm), FT – Flash thickness (cm) and YPP = Yield per plant (kg).

4.2.2 Number of branches per plant

Number of branches per plant showed highly significant positive correlation with days to first male flowering(rg = 0.630, rp = 0.275), days to first female flowering(rg = 0.988, rp = 0.445), number of fruits per plant(rg = 0.560, rp = 0.379), single fruit weight (rg = 0.563, rp = 0.470), flash thickness(rg = 0.551, rp = 0.366) and yield per plant (rg = 0.698, rp = 0.530) 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 days to first harvest (rg = 0.113, rp = 0.124) and rind thickness (rg = 0.275, rp = 0.230). Shivaprasad *et al.* (2017) analyzed correlation in muskmelon and reported that the number of primary branches per plant had positive association with number of fruits per plant and total sugars while, it was negatively associated with fruit length, number of primary branches per plant, fruit weight, flesh thickness and fruit yield per plant. Mali *et al*. (2015) also reported highly significant positive correlation with yield contributing character such as number of primary branches per plant.

4.2.3 Days to first male flowering

Days to first male flower showed highly significant and positive correlation with days to first female flowering (rg = 0.002, rp = 0.728), single fruit weight (rg = 0.733, rp = 0.354), rind thickness(rg = 0.922, rp = 0.466), flash thickness (rg = 1.000, rp = 0.386) and yield per plant (rg = 0.716, rp = 0.291)at both genotypic and phenotypic level indicating that the traits were governed by same gene and in that case, phenotypic selection would be effective (Table 4). Non significant but positive correlation was observed with number of fruits per plant (rg = 0.325, rp = 0.111) while non significant and negative correlation was observed with days to first harvest (rg = -0.141, rp = -0.006). Pasha *et al*. (2019) showed that days to first male flowering had shown significant positive correlation with yield per plant at both phenotypic and genotypic levels.

4.2.4 Days to first female flowering

Days to first female flowering showed highly significant and positive correlation with flash thickness (rg = 0.406, rp = 0.099) at both genotypic and phenotypic level (Table 4) while non significant but positive correlation was observed with number of fruits per plant(rg = 0.193, rp = 0.055), single fruit weight (rg = 0.230, rp = 0.096) and yield per plant (rg = 0.287, rp = 0.089). However a non significant and negative correlation was observed with days to first harvest (rg = -0.200, rp = -0.034) and rind thickness (rg = -0.057, rp = -0.030). Similar result was reported by Potekar *et al*. (2014) in muskmelon.

4.2.5 Days to first harvest

Days to first harvest showed non significant but positive correlation with single fruit weight (rg = 0.151, rp = 0.134), rind thickness (rg = 0.072, rp = 0.051), flash thickness (rg = 0.334 , rp = 0.197) and yield per plant (rg = 0.089, rp = 0.028). While non significant and negative correlation was observed with number of fruits per plant (rg = -0.128, rp = -0.171) (Table 4). In muskmelon, *Janghel et al.* (2018) reported a similar result.

4.2.6 Number of fruits per plant

At both genotypic and phenotypic level, number of fruits per plant demonstrated a significant positive correlation with single fruit weight (rg = 0.201, rp = 0.168) and yield per plant (rg = 0.652, rp = 0.703) indicating that fruit weight and yield per plant increasing significantly if the number of fruits per plant increased (Table 4). While not statistically significant, there is a positive correlation between rind thickness (rg = 0.087, rp = 0.084) and flash thickness (rg = 0.017, rp = 0.155) at both the genotypic and phenotypic levels, and the association between these traits is heavily influenced by environmental factors. The result was similar with the findings of Cheema *et al.* (2011) who carried out analysis of muskmelon.

4.2.7 Single fruit weight

Single fruit weight showed highly significant and positive correlation with rind thickness (rg = 0.767, rp = 0.724), flash thickness (rg = 0.852, rp = 0.680) and yield per plant (rg = 0.854, rp = 0.778), at both genotypic and phenotypic level (Table 4). The result suggested that phenotypic selection would be effective. Sunisa *et al.* (2018) reported a significant positive correlation among the fruit weight traits of muskmelon.

4.2.8 Rind thickness

Rind thickness showed a highly significant and positive correlation with flash thickness (rg = 0.908, rp = 0.698) and yield per plant (rg = 0.579, rp = 0.517) at both the genotypic and phenotypic levels, indicating that if the rind thickness was increased the flash thickness and yield per plant was increasing significantly (Table 4). Pandey *et al*. (2005) reported a similar result in muskmelon.

4.2.9 Flash thickness

Flash thickness demonstrated a highly significant and positive correlation with yield per plant (rg = 0.664, rp = 0.649) at both genotypic and phenotypic level (Table 4). Bhimappa and Choudhary (2017) found that yield per plant exhibited highly significant and positive association with flesh thickness.

4.3 Path analysis

4.3.1 Plant height (cm)

Plant height had a negative direct impact on yield (-0.109) (Table 5). This character exhibite negative indirect effect on days to first female flowering (-0.678), days to first harvest (-0.002), number of fruits per plant (-0.157), rind thickness (-0.107) and flash thickness (-0.114). The character also showed positive indirect effect on number of branches per plant (0.233), days to first male flowering (0.367) and shelf life (0.761) which finally made significant positive correlation with yield (0.615). Pandey *et al.* (2005) reported that in addition to direct selection for fruit yield, indirect selection

through growth and yield contributing characteristics should be considered for further yield improvement.

4.3.2 Number of branches per plant

Number of branches per plant showed positive direct effect on yield (0.256) (Table5). This character produce negative indirect effect on plant height (-0.992), days to first female flowering (-0.895), days to first harvest (-0.014), number of fruits per plant (-0.224), rind thickness (-0.076) and flash thickness (-0.113). The character also showed positive indirect effect on days to first male flowering (0.441), single fruit weight (0.345) and shelf life (0.679) which finally made significant positive correlation with yield (0.698). The result was similar with Silpa *et al*. (2020) who carried out path analysis in melon.

4.3.3 Days to first male flowering

Days to first male flower showed positive direct effect (0.700) on yield (Table 5). This character showed positive indirect effect on number of branches per plant (0.161), days to first harvest (0.017), single fruit weight (0.449) and shelf life (0.115). This character also showed negative indirect effect on plant height (-0.572), days to first female flowering (-0.002), number of fruits per plant (-0.130), rind thickness (-0.254) and flash thickness (-0.225). The cumulative effect produced a positive and highly significant correlation with yield (0.716). Kamagoud (2018) revealed that the traits like days to first male and female flowering, number of fruits per plant, average fruit weight, fruit length, flesh thickness and fruit girth had significant and positive correlation with fruit yield per plant with positive direct effect. Therefore, direct selection of these traits could effective for increasing the fruit yield per plant.

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

Characters	Direct effect	PH	NBP	DFMF	DFFF	DFH	NFP	SFW	RT	FT	Genotypic correlation with yield
PH	-0.109		0.233	0.367	-0.678	-0.002	-0.157	0.337	-0.107	-0.114	0.615**
NBP	0.256	-0.992		0.441	-0.895	-0.014	-0.224	0.345	-0.076	-0.113	0.698**
DFMF	0.700	-0.572	0.161		-0.002	0.017	-0.130	0.449	-0.254	-0.225	0.716**
DFFF	-0.884	-0.837	0.259	0.002		0.024	-0.077	0.141	0.016	-0.832	0.287
DFH	-0.120	-0.019	0.290	-0.099	0.177		0.051	0.092	-0.020	-0.685	0.089
NFP	0.399	-0.430	0.144	0.228	-0.171	0.015		0.123	-0.024	-0.035	0.652**
SFW	0.613	-0.600	0.144	0.513	-0.203	-0.018	-0.080		-0.212	-0.175	0.854**
RT	-0.276	-0.423	0.704	0.645	0.051	-0.009	-0.035	0.470		-0.186	0.579**
FT	0.205	-0.607	0.141	0.768	-0.359	-0.040	-0.007	0.523	-0.250		0.664**

Residual effect (R) = 0.14

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

PH = Plant height (m), NBP = Number of branches per plant, DFMF = Days to first male flowering, DFFF = Days to first female flowering, DFH = Days to first harvest, NFP = Number of fruits per plant, SFW = Single fruit weight (kg), RT – Rind thickness (cm), FT – Flash thickness (cm) and YPP = Yield per plant (kg).

4.3.4 Days to first female flowering

Days to first female flower showed negative direct effect (-0.884) on yield (Table 5). This character produce negative indirect effect on plant height (-0.837), number of fruits per plant (-0.077) and flash thickness (-0.832). This character also produce positive indirect effect on number of branches per plant (0.259), days to first male flowering (0.002), days to first harvest (0.024), single fruit weight (0.141), rind thickness (0.016) and shelf life (0.143). The cumulative effect produced a positive but non-significant correlation with yield (0.287). The result was differ with the findings of Pasha *et al*. (2019) who evaluated snap melon genotypes and found that the characters *viz*., days to female flowering showed positive direct effect on fruit yield per plant.

4.3.5 Days to first harvest

Days to first harvest had a non favorable negative direct impact on yield (-0.120) (Table5). This character showed positive indirect effect on number of branches per plant (0.290), days to first female flowering (0.177), number of fruits per plant (0.051), single fruit weight (0.092) and shelf life (0.421). This character showed also showed negative indirect effect on plant height (-0.019), days to first male flowering (-0.099), rind thickness (-0.020) and flash thickness (-0.685). The cumulative effect showed a positive but non significant association with yield (0.089).

4.3.6 Number of fruits per plant

The character showed a positive direct effect (0.399) on yield (Table 5). This character showed positive indirect effect on number of branches per plant (0.144), days to first male flowering (0.228), days to first harvest (0.015) and single fruit weight (0.123). This character also showed negative indirect effect on plant height (-0.430), days to first female flowering (-0.171), rind thickness (-0.024), flash thickness (-0.035) and shelf life (-0.090). The cumulative effect showed a positive significant association with yield (0.652). Kumari *et al.* (2018) found number of fruits per plant and average fruit weight (g) have positive and direct genotypic and phenotypic effects towards the fruit yield.

4.3.7 Single fruit weight

Single fruit weight showed positive direct effect (0.613) on yield (Table 5). This character showed positive indirect effect on number of branches per plant (0.144), days to first male flowering (0.513) and shelf life (0.115). This character also showed negative indirect effect on plant height (-0.600), days to first female flowering (-0.203), days to first harvest (-0.018), number of fruits per plant (-0.080), rind thickness (-0.212) and flash thickness (-0.175). The cumulative effect resulted in a positive highly significant correlation on yield (0.854). Kumari *et al.* (2018) found in path coefficient analysis that the traits like a number of fruits per plant and average fruit weight (g) have positive and direct genotypic and phenotypic effects towards the fruit yield. Babu (2013) showed that fruit weight exerted high positive direct effect on fruit yield per plant.

4.3.8 Rind thickness

Rind thickness showed negative direct effect (-0.276) on yield (Table 5). This character showed positive indirect effect on number of branches per plant (0.704), days to first male flowering (0.645), days to first female flowering (0.051), single fruit weight (0.470) and shelf life (0.131). This character also showed negative indirect effect on plant height (-0.423), days to first harvest (-0.009), number of fruits per plant (-0.035) and flash thickness (-0.186). The cumulative effect resulted in a positive highly significant correlation on yield (0.579).

4.3.9 Flash thickness

Flash thickness showed positive direct effect (0.205) on yield (Table 5). This character showed positive indirect effect on number of branches per plant (0.141), days to first male flowering (0.768), single fruit weight (0.523) and shelf life (0.128). This character also showed negative indirect effect on plant height (-0.607), days to first female flowering (-0.359), days to first harvest (-0.040), number of fruits per plant (-0.007) and rind thickness (-0.250). The cumulative effect resulted in a positive highly significant correlation on yield (0.664). Karadi *et al.* (2017) reported that fruit yield per plant

showed direct positive effect to flesh thickness. The direct selection for this trait would be rewarding for improvement in the total yield per plant.

4.4 Genetic diversity analysis

Genetic diversity among the muskmelon genotypes are shown in Tables 6-10 and Figure 1.

4.4.1 Principal Component Analysis (PCA)

The muskmelon genotypes were subjected to principal component analysis (PCA) and the results are presented in Table 6. 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 PCA, the 11 initial variables were reduced to three principal components, which are independent linear combinations of variables. Principle components two and three each accounted for 17.80% and 10.90% of the total variation, whereas the first principal component contributed 50.30% to the overall variation.

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

Principal component axes	Eigen values	% of total variation accounted for	Cumulative percent
PH	5.538	50.30	50.30
NBP	1.961	17.80	68.20
DFMF	1.199	10.90	79.10
DFFF	1.078	9.80	88.90
DFH	0.591	5.40	94.20
NFP	0.317	2.90	97.10
SFW	0.151	1.40	98.50
RT	0.077	0.70	99.20
FT	0.056	0.50	99.70
YPP	0.003	0.00	100.00

Here, PH = Plant height (m), NBP = Number of branches per plant, DFMF = Days to first male flowering, DFFF = Days to first female flowering, DFH = Days to first harvest, NFP = Number of fruits per plant, SFW = Single fruit weight (kg), RT – Rind thickness (cm), FT – Flash thickness (cm), YPP = Yield per plant (kg).

4.4.2 Non-Hierarchical clustering

Muskmelon genotypes were grouped into four cluster (Table 7) through non-hierarchical clustering. Reddy *et al.* (2017) also cluster 35 muskmelon genotypes into six distinct clusters. Cluster III in this study had the most genotypes (5) while cluster II and cluster IV each had an equal number (3) genotypes and cluster I had (2) genotypes of muskmelon (Table 7). Cluster I had G2 (BD-11254) and G4 (BD-11257) genotypes. Cluster II had G6 (BD-11259), G8 (BD-11262) and G12 (BD-11267) genotypes. Cluster III accumulated G1 (BD-11252), G3 (BD-11255), G5 (BD-11258), G7 (BD-11260) and G10 (BD-11265) genotypes and Cluster IV accumulated G9 (BD-11264), G11 (BD-11266) and G13 (BD-11268) genotypes. Among the thirteen genotypes cluster IV estimated the maximum cluster mean value for plant height (2.23), number of branches per plant (9.00), days to first male flowering (20.22), days to first female flowering (24.89), number of fruits per plant (7.33), single fruit weight (1.00), rind thickness (0.43), flash thickness (3.37) and yield per plant (7.34). In cluster II, the highest mean value was observed in days to first harvest (89.67).

Table 7. Distribution of thirteen muskmelon genotypes in four different clusters

Cluster	Total no. of line	Genotype Number	Genotype Designation
I	2	2, 4	BD-11254, BD-11257
II	3	6, 8, 12	BD-11259, BD-11262, BD-11267
III	5	1, 3, 5, 7, 10	BD-11252, BD-11255, BD-11258, BD-11260, BD-11265
IV	3	9, 11, 13	BD-11264, BD-11266, BD-11268

Table 8. Cluster means for eleven characters of thirteen muskmelon genotypes

Characters	Cluster			
	I	II	III	IV
PH	1.97	2.07	2.12	2.23
NBP	6.33	7.33	7.60	9.00
DFMF	17.50	19.33	19.53	20.22
DFFF	22.50	24.67	24.87	24.89
DFH	86.00	89.67	82.40	87.00
NFP	4.50	2.44	4.40	7.33
SEW	0.52	0.71	0.79	1.00
RT	0.30	0.38	0.40	0.43
FT	2.50	3.07	2.91	3.37
YPP	2.24	1.75	3.37	7.34

Here, PH = Plant height (m), NBP = Number of branches per plant, DFMF = Days to first male flowering, DFFF = Days to first female flowering, DFH = Days to first harvest, NFP = Number of fruits per plant, SFW = Single fruit weight (kg), RT – Rind thickness (cm), FT – Flash thickness (cm) and YPP = Yield per plant (kg).

4.4.3 Canonical Variant Analysis (CVA)

After the canonical variant analysis was completed, the inter-cluster distances were calculated. The intra and inter-cluster distance (D^2) values were shown in Table 9. In this experiment, inter-cluster distances were greater than intra-cluster distances, indicating greater genetic variation between genotypes of different groups. Clusters II and IV had the greatest inter cluster distance (8.130), followed by clusters II and III (7.712), cluster I and cluster IV (7.654), cluster III and cluster IV (6.973), cluster I and cluster II (5.357), and cluster I and III (5.164) (Table 9). Clusters II and IV had the greatest inter cluster distance (8.130) 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 three genotypes had the highest intra-cluster distance (3.144), whereas cluster II, which had three genotypes, had the smallest distance (0.874). From the Fig. 1 it was noticed that all of the genotypes were reportedly grouped into four clusters according to the scatter plot. The genotype combinations from the most divergent clusters were predicted to result in the greatest number of heterosis manifestations. It is recommended that future plant breeders increase production levels in addition to heterosis levels. As a result, in addition to selecting genotypes from these clusters with high inter-cluster distance for hybridization, one can consider selecting parents based on the extent of genetic divergence in relation to a specific 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. Indraja *et al.* (2018) also reported similar result. Hence, the genotypes falling in these clusters being genetically more divergent, can be used in hybridization programme.

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

Cluster	I	II	III	IV
I	**1.952**	5.357	5.164	7.654
II		**0.874**	7.712	8.130
III			**2.063**	6.973
IV				**3.144**

*Bold figures denotes intra-cluster distance

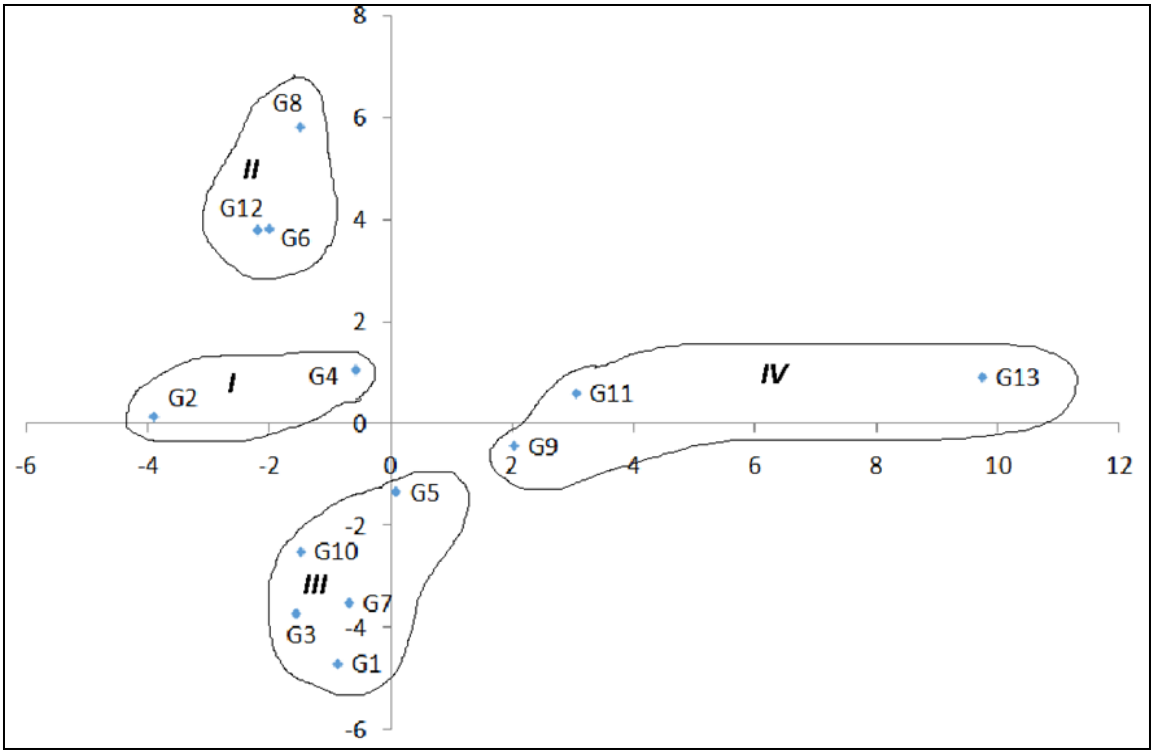


Figure 1. Scattered distribution of thirteen muskmelon genotypes on principal component score

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, days to first male flowering, days to first female flowering, days to first harvest, number of fruits per plant, single fruit weight, rind thickness flash thickness, shelf life and yield per plant. In vector-2 the important characters responsible for genetic divergence were days to first male flowering, days to first harvest, number of fruits per plant, single fruit weight, rind thickness flash thickness and yield per plant. In vector-2 negative value determined the lower contribution of genetic divergence.

4.4.5 Selection of parents for future hybridization

This genotype selection method is critical and difficult for the upcoming future breeding program. In the meantime, considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and phenotypic traits, the genotype G13 (BD-11268) for maximum plant height, number of branches per plant, number of fruits per plant, single fruit weight, rind thickness, flash thickness, shelf life, and yield plant per plant from cluster IV. G11 (BD-11268) and G12 for second highest number of branches per plant from cluster IV and II and G2 (BD-11254) for the minimum number of days needed to male and female flower appearance from cluster I should be considered. Therefore, for a future hybridization program, it may be proposed to make the inter genotypic crosses between G13 (BD-11268) and G11 (BD-11266); G13 and G12 (BD-11267); G13 and G2 (BD-11254); G12 and G11; G12 and G2; and G11 and G2 might be suggested for future hybridization program. Senthilvadivu *et al.* (2018) also reported similar result in muskmelon.

Table 10. Relative contribution of eleven characters towards divergence of the muskmelon genotypes

Character no.	Vector-1	Vector-2
PH	0.027	-0.003
NBP	0.254	-0.005
DFMF	0.171	0.053
DFFF	0.087	-0.059
DFH	0.167	0.969
NFP	0.418	0.201
SEW	0.075	0.006
RT	0.012	0.000
FT	0.078	0.026
YPP	0.814	0.092

Here, PH = Plant height (m), NBP = Number of branches per plant, DFMF = Days to first male flowering, DFFF = Days to first female flowering, DFH = Days to first harvest, NFP = Number of fruits per plant, SFW = Single fruit weight (kg), RT = Rind thickness (cm), FT = Flash thickness (cm) and YPP = Yield per plant (kg).

CHAPTER V

SUMMARY AND CONCLUSION

An experiment was conducted at Sher-e-Bangla Agricultural University Dhaka, during the period from *Kharif-I*, 2020 using 13 muskmelon (*Cucumis melo L*.) genotypes to study the genetic variability in muskmelon genotypes in a randomized complete block design with three replications.

The experimental results revealed significant differences for studied traits among genotypes. For all of the characters, phenotypic variance was greater than genotypic variance. The number of fruits per plant (47.73), single fruit weight (52.55), and yield plant per plant (90.40) all had high genotypic co-efficients of variation (GCV). High heritability with high genetic advance in percent of mean was observed in number of fruits per plant (86.05), single fruit weight (99.12) and yield plant per plant (93.47) 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 flowering (59.93) and days to first female flowering (60.15).

The result revealed a highly significant positive correlation with plant height (rg= 0.615, rp= 0.541), number of branches per plant (rg= 0.698, rp= 0.530), number of fruits per plant(rg= 0.652, rp= 0.703), single fruit weight(rg= 0.854, rp= 0.778), rind thickness (rg= 0.579, rp= 0.517), and flash thickness (rg= 0.664, rp= 0.649) to yield per plant.

The thirteen muskmelon genotypes were grouped into four cluster. Cluster III exhibited maximum 5 genotypes while cluster had only 2 genotypes. Among four cluster the highest inter-cluster distance (8.13) was observed in clusters II and IV, while the lowest (5.164) was observed in clusters I and III. Cluster IV had the highest intra cluster distance (3.144), while Cluster II had the lowest (0.874).

Considering the magnitude of genetic distance, cluster mean and phenotypic traits, the genotype G13 (BD-11268) for maximum plant height, number of branches per plant, number of fruits per plant, single fruit weight, rind thickness, flash thickness, shelf life, and yield plant per plant from cluster IV, G11 (BD-11268) and G12 for second highest

number of branches per plant from cluster IV and II and G2 (BD-11254) for the minimum number of days needed to male and female flower appearance from cluster I should be considered. Therefore, for a future hybridization program, it may be proposed to make the inter genotypic crosses between G13 (BD-11268) and G11 (BD-11266); G13 and G12 (BD-11267); G13 and G2 (BD-11254); G12 and G11; G12 and G2; and G11 and G2 might be suggested for future hybridization program.

REFERENCES

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.

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.

Babu, R.R. (2013). Genetic divergence studies in oriental pickling melon (*Cucumis melo* L. var. *conomon*) germplasm. Unpublished doctoral dissertation submitted to Dr. YSR horticultural university, Andhra Pradesh.

BBS. (2021). Yearly statistical bulletin of Bangladesh, Bangladesh Bureau of Statistics, Ministry of Planning, Government of the People's Republic of Bangladesh, Dhaka. pp. 8.

Begna, T. (2021). Role and economic importance of crop genetic diversity in food security. *J Agric. Sci. Food Technol*. **7**(1): 164-169.

Behe, B.K. (2020). Characterizing the U.S. melon market. *Hortscience* **55**(6): 795–803.

Bhimappa, B.B. and Choudhary, H. (2017). Genetic variability, heritability and genetic advance in muskmelon (*Cucumis melo* L.). *Veg. Sci.* **44**(1): 28- 34.

Bhimappa, B.B., Choudhary, H., Behera, T.K., and Sharma, V.K. (2017). Correlation and path analysis study for yield and its contributing traits in different horticultural groups of muskmelon (*Cucumis melo* L.). *Veg. Sci.* **44**(1): 54-59.

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.

Cheema, K.L., Iqbal, M., Niaz, S. and Shafique, M. (2011). Assessment of variability of muskmelon. *Int. J. Veg. Sci.* **17**(4): 322-332.

Choudhary, B. and Pandey, S. (2016). Muskmelon genetics, breeding, and cultural practices. In book: Handbook of cucurbits: growth, cultural practices, and physiology. pp. 213-236.

Choudhary, B.R., Fageria, M.S. and Dhaka, R.S. (2004). Correlation and path coefficient analysis in muskmelon (*Cucumis melo* L.). *Indian J. Hort.* **61**(2): 158-162.

Choudhary, B.R., Singh, D. and Saroj, P.L. (2019). Development and characterization of intraspecific hybrids derived from *Cucumis melo* L. *Bangladesh J. Bot.* **48**(2): 359-366.

Choudhary, H., Ram, H.H. and Singh, D.K. (2011). Genetic variability study in muskmelon. *Prog. Hort.* **43**: 231-233.

Comstock, R. and Robinson, H. (1954). An analysis of quantitative variability in Nicotiana tabacum. *Heredity.* **8**: 365-376.

Costa, I.J.N., de Normandes, V.R., Nóbrega, D.A., Mendes, A.Q., Silva, F.S. and Menezes, D. (2019). Heterosis and combining ability of melon genotypes of Momordica group. *J. Exp. Agric. Int.* **15**: 1-9.

Devendra, K., Ram, R.B., Sanjay, K., Sutanu, M. and Manoj, K. (2013). Variability and physico-chemical studies in snap melon (*Cucumis melo* var. *momordica*). *Asian J. Hort.* **8**(2): 751-753.

Dewey, D.R. and Lu, K.H. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *J. Agron.* **57**: 515-518.

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.

Dhillon, N.P.S., Ranjana, R., Singh, K., Eduardo, I., Monforte, A. J., Pitrat, M. and Singh, P.P. (2007). Diversity among landraces of Indian snapmelon (*Cucumismelo* var. *momordica*). *Genetic Res. Crop Evolution.* **54**(6): 1267-1283.

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.

Fageria, M.S. and Luthra, J.P. (2005). Genetic variability in muskmelon (*Cucumis melo*L.). In: National Seminar on Cucurbits, 22-23 Sept. (2005), GBPUAT, Pantnagar, pp. 142.

Fergany, M., Kaur, B., Monforte, A.J., Pitrat, M., Rys, C., Lecoq, H. and Dhaliwal, S.S. (2011). Variation in melon (*Cucumis melo*) landraces adapted to the humidtropics of southern India. *Genetic Res. Crop Evolution.* **58**(2): 225-243.

Fisher, R.A. (1936). The use of multiple measurement in taxonomic problems. *Ann. Eugenics. London.* **7**: 179.

Fisher, R.A. and Yates, F. (1963) Statistical Tables for Biological, Agricultural and Medical Research. 6th ed. Oliver and Boyd Ltd, London. pp. 146.

Gurjinder, S. and Dhillon, N.P.S. (2006). Genetic divergence in muskmelon germplasm. *Haryana J. Hort. Sci.* **35**(3/4): 340-341.

Hotelling, H. (1935). Relation between two sets of variables. *Biometrics*. 28: 321-377.

Iathet, C. and Piluek, K. (2006). Heritability, heterosis and correlations of fruit characters and yield in Thai slicing melon (*Cucumis melo* L.). *Agric. Nat. Res.* **40**(1): 20-25.

Ibrahim, E.A. and Ramadan, A.Y. (2013). Correlation and path coefficient analyses in sweet melon (*Cucumis melo* Var. *Aegyptiacus* L.) under irrigated and drought conditions. *Pakistan J. Biol. Sci.* **16**(13): 610-616.

Indraja, G., Sadarunnisa, S., Madhumathi, C., Tanuja, P.B. and Reddi, S.M. (2018). Genetic divergence analysis in muskmelon (*Cucumis melo* L.). *Int. J. Chem. Stud.* **6**(6): 2623-2626.

Islam, M.T., Malek, M.A.and Islam, M.N. (2017). Characterization of muskmelon germplasm (summer-2015-16). **In**: Islam, M.T. Afroz, R., Rahman, S. and Molla, M.R. (Eds). Annual research report on plant genetic resources conservation and management 2016-17. Plant Genetic Resources Centre, Bangladesh Agricultural Research Institute, Joydebpur, Gazipur-1701. pp. 104-111.

Janghel, A.K., Trivedi, J., Sharma, D., Lodhi, Y.K. and Kumar, L. (2018). Genetic variability in muskmelon (*Cucumis melo* L.). .). *Intl. J. Cur. Micro. App. Sci.* **6**: 211-217.

Janghel, A.K., Trivedi, J., Sharma, D., Lodhi, Y.K. and Kumar, L. (2018). Genetic variability in muskmelon (*Cucumis melo* L.) under protected condition. *Int. J. Cur. Micro. App. Sci.* **6**: 211-217.

Kadi, T. and Sambhaj, M.S. (2003). Genetic variability in muskmelon *(Cucumis melo* L.). Unpublished doctoral dissertation submitted to Mahatma Phule Krishi Vidyapeeth, Rahuri-413722, Dist. Ahmednagar, Maharashtra, India.

Kamagoud, S. (2018). Morphological and molecular characterization of oriental pickling melon (*Cucumis melo* var. *conomon*) genotypes for productivity traits. Unpublished doctoral dissertation submitted to College of Horticulture, Ph.D. thesis, UHS, Bagalkot, India.

Kamagoud, S., Shet, R.M., Nishani, S., Hongal, S., Hanchinmani, C.N. and Prashanta, A. (2018). Assessment of genetic variability among oriental pickling melon (*Cucumis melo* L.) genotypes. *Int. J. Chem. Stud.* **6**(4): 2630-2633.

Karadi, S.M., Ganiger, V.M., Bhuvaneshwari, G., Hadimani, H.P., Madalageri, M.B. and Pallavi, H.M. (2017). Path analysis and diversity studies for growth, earliness, yield and quality parameters in wild melon (*Cucumis melo* subsp. *agrestis*) genotypes. *Int. J. Cur. Micro. App. Sci.* **6**(12): 1612-1618.

Koli, S.P. and Murthy, H.N. (2013). Estimation of phenotypic divergence in a collectionof *Cucumis melo* from Kerala State, Southern India.

Kumar, R., Ameta, K.D., Dubey, R.B. and Pareek, S. (2013). Genetic variability, correlation and path analysis in sponge gourd (*Luffa cylindrical* Roem.). *African J. Biotech.* **12**(6): 539-543.

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.

Lotti, C., Marcotrigiano, A.R., De Giovanni, C., Resta, P., Ricciardi, A., Zonno, V. and Ricciardi, L. (2008). Univariate and multivariate analysis performed on bio-agronomical traits of *Cucumis melo* L. germplasm. *Genetic Res. Crop Evolution*. **55**(4): 511-522.

Mahalanobis, P.C. (1936). On the generalized distance in statistics. *Pro. Nat. Ins. Sci. India*. **2**: 49-55.

Malek, M.A., Islam, M.O., Haque, M.M. and Sultan, M.K. (2012). Screening of muskmelon (*Cucumis melo* L.) germplasm against salinity. *Bangladesh J. Agric. Res.* **37**(3):465-472.

Mali, M.D., Musmade, A.M. and Ranpise, S.A. (2015). Genetic variability and interrelationship among different traits in F3 Progenies of muskmelon (*Cucumis melo* L.). Bio. *Qua. J. Life Sci.* **12**(3b): 733-738.

Malik, A.A. and Vashisht, V.K. (2012). Correlation among growth, yield and quality attributes in the indigenous and exotic accessions of *Cucumis melo* L. *J. Agric. Tech.* **8**(7): 2273-2281.

Manohar, S.H. and Murthy, H.N. (2012). Estimation of phenotypic divergence in a collection of *Cucumis melo,* including shelf-life of fruit. *Sci. Hort.* **148**: 74-82.

McCreight, J.D., Staub, J.E., Lopez-Sese, A. and Chung, S. (2004). Isozyme variationin Indian and Chinese melon (*Cucumis melo* L.) germplasm collections. *J. American Soc. Hort. Sci.* **129**: 811-818.

Mehta, R., Singh, D. and Bhalala, M.K. (2009). Correlation and path analysis in muskmelon. *Indian J. Hort.* **66**(3): 396-399.

Mishra, S., Sharma, A.K. and Sharma, V. (2017). Genetic variability studies in responseto drought under different water regimes in muskmelon (*Cucumis melo* L.). *J. App. Nat. Sci.* **9**(3): 1744-1750.

Molla, M.R., Ahmed, I., Rahman, S., Hossain, M.A., Salam, M.A., Chowdhury, M.A.Z. and Rohman, M.M. (2017). Genetic diversity among muskmelon (*cucumis melo* L.) germplasm in Bangladesh as revealed by microsatellite markers. *African J. Agric. Res.* **12**(44): 3203-3213.

More, T.A. and Seshadri, V.S. (2002). Studies on genetic divergence in muskmelon (*Cucumis melo* L.). *J. Maharashtra Agric. Uni.* **27**(2): 127-131.

Muthuselvi, R., Praneetha, S. and Uma, Z.J.K.D. (2019). Assessment of variability in snap melon (*Cucumis melo* var. *Momordica*) genotypes. *J. Pharma. Phytochem.* **8**(4): 654-657.

Nasrabadi, H.N., Nemati, H., Sobhani, A., and Sharifi, M. (2012). Study on morphologic variation of different Iranian melon cultivars (*Cucumis melo* L.). *African J. Agric. Res.* **7**(18): 2764-2769.

Pandey. S., Mathura, R. and Singh, B. (2005). Genetic variability and character association in muskmelon (*Cucumis melo* L.). *Indian J. Plant Genetic Res.* **18**: 25.

Pasha, S.G., Marker, S. and Chandra, G.S. (2019). Genetic variability, correlation and path analysis study on snap melon (*Cucumis melo* L. var. *momordica*) farmer's varieties. *Int. J. Bio-res. Stress Manage.* **10**(6): 636-644.

Pearson, K. (1926). On the cofficient of racial likeness. *Biometrika.* **18**(1/2): 105-117.

Phan. T., Akashi. Y., Tran-Thi-Minh-Hang, Tanaka. K., Aierken. Y., Yamamoto. T., Nishida. H, Long, C., and Kato, K. (2010). Genetic diversity in Vietnamese melon landraces revealed by the analyses of morphological traits and nuclear and cytoplasmic molecular markers. *Breed. Sci.* **60** (3): 255-266.

Potekar, S.V., Nagre, P.K. and Sawant, S.N. (2014). Correlation coefficient and path analysis in muskmelon (*Cucumis melo* L.). *Int. J. Trop. Agric.* **32**(3/4): 335-340.

Prasad, V.S.R., Pitchaimuthu, M. and Dutta, O.P. (2004). Variation diversity pattern and choice of parental selection in musk melon (*Cucumis melo* L.). *J. Hort. Sci.* **61**: 319-322.

Qaim, M. (2020). Role of new plant breeding technologies for food security and Sustainable Agricultural Development. *App. Eco. Pers. Poli.* **42**(2): 129-150.

Rahman, S., Miah, M.A.K. and Rahman, H. (2016). Genetic diversity of muskmelon using multivariate technique. *Bangladesh J. Agric. Res.* **41**(2): 273-286.

Rakhi, R. and Rajamony, L. (2006). Variability, heritability and genetic advance in landraces of culinary melon (*Cucumis melo* L.). *J. Tropical Agric.* **43**: 79-82.

Ram, H.H., Singh, D.K., Dubey, R.K. Chaubey, A.K. and Jaiswal, H.R. (2004). Studies on genetic variability in muskmelon in Tarai region of Uttaranchal. In: International Seminar on Recent Trends in Hi-tech Horticulture and Post Harvest Technology, CSAUAT, Kanpur, February 4-6, 2004.

Rao, C.R. (1952). Advanced statistical method in biometrics research. john wiley and sons, New York. pp. 390.

Reddy, B.P.K., Begum, H., Sunil, N., Reddy, M.T., Babu, J.D., Reddy, R.S.K., and Reddy, B.P. (2017). Genetic divergence analysis in muskmelon (*Cucumis melo* L.). *Int. J. Cur. Micro. App. Sci.* **6**(6): 2251-2260.

Reddy, P.K., Begum, H., Sunil, N., Reddy, M.T., Babu, J.D., Reddy, S.K. and Reddy, B.P. (2012). Genetic divergence analysis in muskmelon (*Cucumis melo* L.). *Asian J. Sci. Tech.* **4**(12): 001-006.

Reddy, S.A.K. and Shanthi, A. (2013). Variability and genetic diversity studies of muskmelon accession in the coastal region of Karaikal. *Green Farm.* **4**(6): 764-766.

Rizzo, A.A.N. and Braz, L.T. (2002). Genetic divergence among five muskmelon cultivars. *Hort. Brasileria*. **20**(2): 171-173.

Rolania, S. (2005). Studies on genetic variability and development of hybrids in muskmelon (*Cucumis melo* L.). Unpublished doctoral dissertation submitted to SKN Agricultural University, SKNAU, Rajasthan.

Saha, K., Mishra, S., Choudhary, H. and Mahapatra, S. (2018). Estimates of genetic component of variation in muskmelon (*Cucumis melo* L.). *Int. J. Cur. Micro. App. Sci.* **7**(7): 1144-1151.

Salgotra, R.K. and Stewart, C.N.J. (2020). Functional markers for precision plant breeding. *Int. J. Mol. Sci*. **21**(13): 4792.

Samadia, D.K. (2007). Studies on genetic variability and scope of improvement in round melon under hot arid conditions. *J. Trop. Agric.* 32: 72-78.

Sanjay, S. and Tarsem, L. (2000). Assessment of genetic divergence in melon (*Cucumis melo* L.). *J. Res. Punjab Agric. Uni.* **37**(1/2): 36-41.

Senthilvadivu, G., Arumugam, T., Vethamoni, P.I. and Jeyaprakash, P. (2018). Genetic divergence studies in muskmelon (*Cucumis melo* L.). *Elec. J. Plant Breed.* **9**(3): 985-992.

Shivaprasad, M.K., Ganiger, V.M., 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.

Silpa, R., Anitha, P., Pradeepkumar, T. and John, C.L. (2020). Character associations and path analysis in oriental pickling melon (*Cucumis melo* var. *conomon* Mak.). *Veg. Sci.* **47**(1): 85-92.

Singh, D.K. and Ram, H.H. (2003). Correlations among fruit characters in theindigenous germplasm lines of muskmelon. *Progress Hort.* **35**(1): 69-72.

Singh, G. and Dhillon, N.P.S. (2006). Genetic divergence in muskmelon germplasm. *Harayana J. Hort. Sci.* **35**: 340-341.

Singh, H. and Lal, B.S. (2003). Genetic divergence in muskmelon germplasm. *Euphytica*. 119: 170-178.

Singh, R.K. and Chaudhury, B.D. (1985). Biometrical methods of quantitative genetic analysis. *Haryana J. Hort. Sci.* **12**(2): 151-156.

Skendzic, S., Zovko, M., Zivkovic, I.P., Lesic, V., Lemic, D. (2021). The impact of climate change on agricultural insect pests. *Insects.* **12**(5): 440

Soltani, F., Akashi, Y., Kashi, A., Zamani, Z., Mostofi, Y. and Kato, K. (2010). Characterization of Iranian melon landraces of *Cucumis melo* L. Groups Flexuosus and Dudaim by analysis of morphological characters and random amplified polymorphic DNA. *Breed. Sci*. **60**: 34-45.

Staub, J.E., Lopez-Sese. A.I. and Fanourakis, N. (2004). Diversity among melon landraces (*Cucumis melo*. L) from Greece and their genetic relationships withother melon germplasm of diverse origins. *Euphytica.* **136**: 151-166.

Sunisa, S., Sompong, C. and Jirawat, S. (2018). Genetics analysis and heritability of fruit characters in muskmelon (*Cucumis melo* L.) using extreme parental differences. *Agrivita J. Agric. Sci.* **40**(1): 1-7.

Szamosi, C., Solmaz, I., Sari, N. and Barsony, C. (2010). Morphological evaluation and comparison of Hungarian and Turkish melon (*Cucumis melo* L.) germplasm. *Sci. Hort.* **124**: 170-182.

Taha, M., Omaraz, K. and Jack, A.E. (2003). Correlation among growth, yield and quality characters in (*Cucumis melo* L.) muskmelon. *Genetics Coo. Rep.* **26**: 9-11.

Tahir, N., Hashim, N., Tahir, A. and Azmi, W. (2020). Pests and diseases incidence at different growth stages of melon manis terengganu (*Cucumis melo* var. Inodorus cv. Melon Manis Terengganu). *Serangga*. **25**: 1-14.

Tanaka, K., Nishitani, A., Akashi, Y., Sakata, Y., Nishida, H., Yoshino, H. and Kato, K. (2007). Molecular characterization of South and East Asian melon, *Cucumis melo* L. and the origin of the group conomon var. *makuwa* and var *conomon* revealed by RAPD analysis. *Euphytica.* **153**: 233-247.

Tomar, R.S., Kulkarni, G.U. and Kakade, D.K. (2008). Genetic analysis in (*Cucumis melo* L.). *J. Hort. Sci.* **3**(2): 112-118.

Torkadi, S.S., Musmade, A.M. and Mangave, K.K. (2019). Genetic variability studies in muskmelon (*Cucumis melo* L.). *J. Soil. Crop*. **17**(2): 308-311.

Toyzhigitova, B., Yskak, S., Lozowicka, B. (2019). Biological and chemical protection of melon crops against *Myiopardalis pardalina Bigot*. *J. Plant Dis. Prot*. **126**: 359-366.

Venkatesan, K., Reddy, B.M. and Senthil, N. (2016). Evaluation of Muskmelon (*Cucumis melo* L.) genotypes for growth, yield and quality traits. *Electronic J. Plant Breed.* **7**(2): 443-447.

Wang, J, Yao, J. and Li, W. (2008). Construction of a molecular map for melon (*Cucumis melo* L.) based on SRAP. *Front Agric. China.* **2**: 451-55.

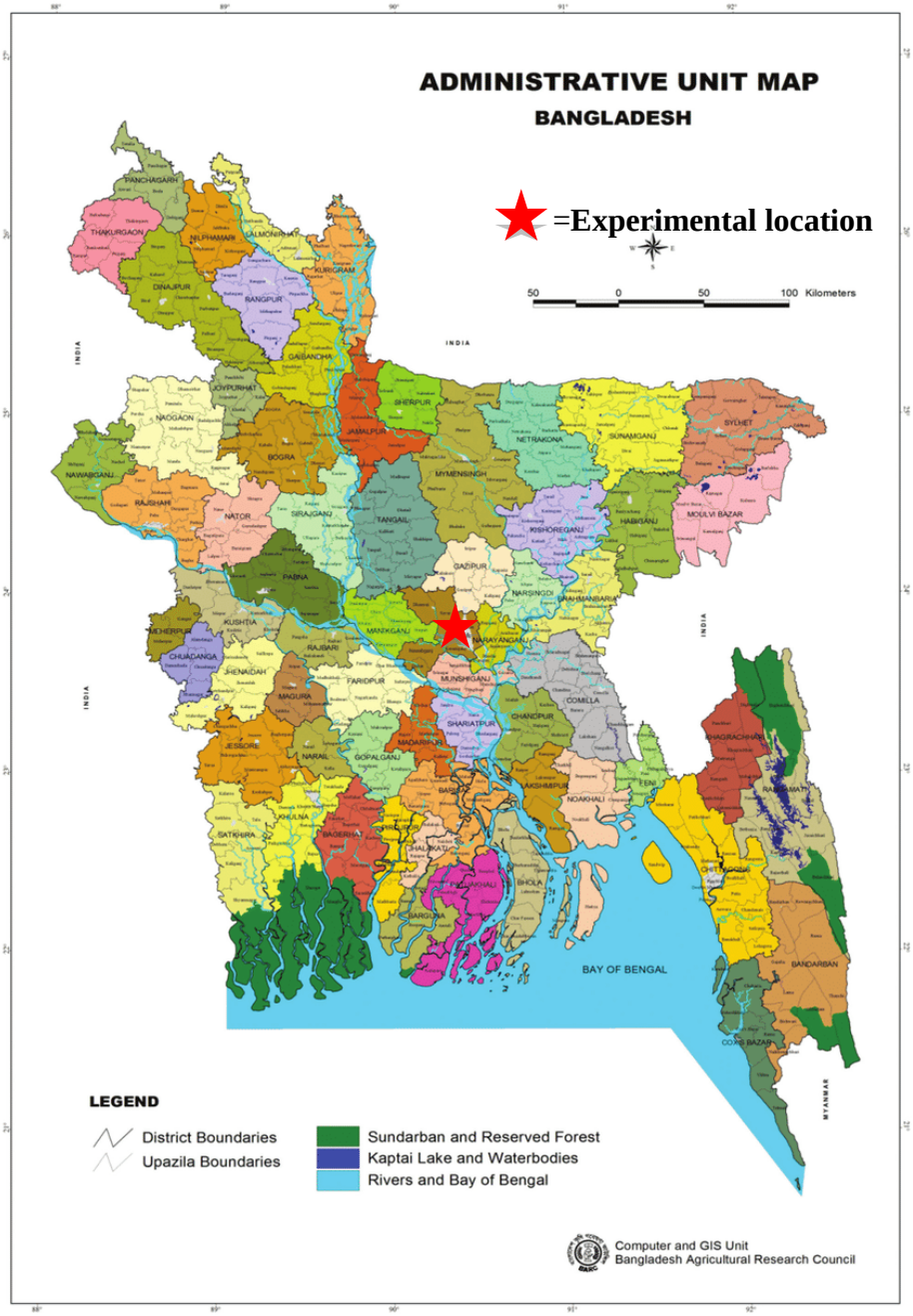
Wright, S. (1921). The methods of the path coefficients. *The Ann. Math. Stat.* **5**: 161-215.

Yadav, R.K. and Ram, H.H. (2002). Correlation and path coefficient analysis in muskmelon. *Harayana J. Hort. Sci.* **31**(1-2): 74-76.

Yi-San, A.Y., Tanaka, K., Cho, T., Khaing, M., Yoshino, H., Nishida,H., Yamamoto, T., Win, K. and Kato, K. (2009). Molecular analysis of genetic diversity in melon land races (*Cucumis melo* L.) from Myanmar and their relationship with melon germplasm from East and South Asia. *Genetic Res.* Crop *Evol.* **56**: 1149-1161.

APPENDICES

Appendix I. Map showing the experimental location under study



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

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

Appendix III. Monthly meteorological information during the period from Kharif, I, 2020.

Year	Month	Air temperature (^{0}C)		Relative humidity (%)	Average rainfall (mm)
		Maximum	Minimum		
2020	March	32.9	20.1	61	54
	April	34.1	23.6	67	138
	May	33.4	24.7	76	269
	June	34	27.3	76	134
	July	32.6	26.8	81	114
	August	32.6	25.5	80	106
	September	32.4	25.7	80	86

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

Appendix IV. Mean performance for 11 different characters in 13 muskmelon genotype

Genotype		PH	NBP	DFMF	DFFF	DFH	NFP	SFW	RT	FT	YPP
G1	BD-11252	1.97	6.33	21.00	24.00	81.00	5.00	0.72	0.45	2.95	3.64
G2	BD-11254	1.92	5.67	17.67	22.00	85.00	2.67	0.54	0.35	2.90	1.44
G3	BD-11255	2.14	7.67	17.67	25.33	82.00	5.33	0.52	0.30	2.50	2.80
G4	BD-11257	2.01	7.00	17.33	23.00	87.00	6.33	0.49	0.25	2.10	3.04
G5	BD-11258	2.19	8.33	19.67	24.33	84.00	3.33	1.26	0.48	3.10	4.25
G6	BD-11259	1.99	6.33	19.67	24.00	89.00	2.67	0.72	0.40	3.00	1.91
G7	BD-11260	2.31	8.67	19.67	25.33	82.00	4.33	0.74	0.40	3.00	3.22
G8	BD-11262	2.03	7.00	18.67	23.67	91.00	2.67	0.80	0.45	3.20	2.13
G9	BD-11264	2.04	8.67	20.00	25.33	86.00	7.33	0.59	0.35	2.90	4.34
G10	BD-11265	2.01	7.00	19.67	25.33	83.00	4.00	0.73	0.35	3.00	2.92
G11	BD-11266	2.30	8.67	20.00	24.33	87.00	7.33	0.72	0.45	3.30	5.26
G12	BD-11267	2.19	8.67	19.67	26.33	89.00	2.00	0.62	0.30	3.00	1.22
G13	BD-11268	2.34	9.67	20.67	25.00	88.00	7.33	1.70	0.50	3.90	12.42
CV(%)		1.751	9.341	4.812	5.618	1.768	28.242	7.244	4.892	9.534	34.391

PH = Plant height (m), NBP = Number of branches per plant, DFMF = Days to first male flowering, DFFF = Days to first female flowering, DFH = Days to first harvest, NFP = Number of fruits per plant, SFW = Single fruit weight (kg), RT – Rind thickness (cm), FT – Flash thickness (cm), YPP = Yield per plant (kg)