GENETIC DIVERSITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS IN WAX GOURD

(*Benincasa hispida Thunb.*)

BY

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This to certify that thesis entitled, ***"GENETIC DIVERSITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS IN WAX GOURD (Benincasa hispida Thunb.)"*** *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* ***Fatema Tuj Zohra,*** *Registration No.**05-1568** 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, has been availed of during the course of this investigation has duly been acknowledged.

Dated: June, 2011
Place: Dhaka, Bangladesh

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Dedicated to
My
Beloved Family

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ABSTRACT

Twenty seven genotypes of wax gourd (*Benincasa hispida Thunb.*) were studied in a field experiment at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, during March 2010 to August 2010. The objectives of the study were to measure the variability among the genotypes for yield and yield contributing characters, estimate genetic parameters, association among the characters and their contribution to yield. There was a great deal of significant variation for all the characters among the genotypes. High genotypic co-efficient of variation (GCV) was observed for fruit yield per plant, number of male flower, number of female flower. Low genotypic co-efficient of variation (GCV) was observed for leaf length, leaf breadth, internodes distance, fruit length. In all cases phenotypic variances were higher than the genotypic variances. High heritability with low genetic advance in percent of mean was observed in leaf length and leaf breadth which indicated that non-additive gene effects were involved for the expression of these characters and selection for such trait might not be rewarding. High heritability with high genetic advance in percent of mean was observed in number of male flower, number of female flower, fruit breadth, and yield per plant indicated that this trait was under additive gene control and selection for genetic improvement for this trait would be effective. Correlation studies revealed that highest significant association of yield per plant with the characters fruit weight followed by fruit breadth, pedicel length of female flower, internodes distance at genotypic level. Path co-efficient analysis revealed that maximum direct contribution towards yield per plant with traits of fruit weight followed by fruit breadth, pedicel length of female flower and number male flower. Highest intra-cluster distance was found in cluster V, low in III and no distance was found in cluster I. Among six clusters the highest inter cluster distance was observed between cluster I and cluster IV and lowest between cluster III and cluster VI. Considering all the characters the G_{20} (BD-364), G_{17} (BD-354), G_1 (BD 319) and G_{16} (BD-349) were selected for future breeding programme .

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LIST OF ABBREVIATED TERMS

ABBREVIATION	FULL WORD
AEZ	Agro-Ecological Zone
et al.	And others
ACC	Accessions
BARI	Bangladesh Agricultural Research Institute
BBS	Bangladesh Bureau of Statistics
Cm	Centimeter
CV	Co-efficient of Variation
Etc	Etcetera
Fig	Figure
G	Genotype
GA	Genetic Advance
GCV	Genotypic Co-efficient of Variation
g	Gram
h^2b	Heritability in broad sense
j.	Journal
Kg	Kilogram
m	Meter
MSS	Mean Sum of Square
mm	Millimeter
MP	Muriate of Potash
No.	Number
%	Percent
PCV	Phenotypic Co-efficient of Variation
RCBD	Randomized Complete Block Design
R	Replication
Res.	Research
SAU	Sher-e-Bangla Agricultural University
SE	Standard Error
m^2	Square meter
TSP	Triple Super Phosphate

Chapter 1

Introduction

Chapter I

INTRODUCTION

Indian subcontinent has rich diversity of cucurbits and is believed to be the primary and secondary centers of origin of several gourds and melons (Choudhary 1996). Wax gourd (*Benincasa hispida* Thunb.) is a cucurbitaceous vegetable grown widely in summer season in Bangladesh. It is an important vegetable mainly valued for its long storage life and having a good scope for value addition. The fruits are consumed as baked, fried, boiled, pickled or candied/preserved (Robinson and Decker-Walters 1999). *Benincasa* is a monotypic genus belonging to the family Cucurbitaceae with a single species, *B. hispida* (Thunb.) Cogn. which has chromosome number 2n= 24. *Benincasa hispida* is the only cultivated species commonly known as wax gourd, winter melon, white gourd, ash gourd, white pumpkin, ash pumpkin, Chinese preserving melon, hairy melon (when immature) and "chaal kumra" in Bengali. Many of these names symbolize the powdery white flakes of wax that coat the fruit surface of some cultivars.

Wax gourd is one of the most common summer vegetables grown in almost every district of Bangladesh. Among the non-traditional crops, Bangladesh has been earning a handsome amount of foreign currency by exporting ash gourd to the UK, Pakistan and Middle East (Alamgir, 1981). It becomes available even in the lean period when other vegetables are scarce. Among the cucurbitaceous vegetables and other creepers, ash gourd has shown higher profitability for marginal farmers (Chowdhury, 1993). Green immature fruits and young twigs of wax gourd are used as vegetables and mature fruits are used for preparing candy, sweets, and sun dried delicacy called "kumra bori" and also for cooking as a vegetable.

There are two ecotypes of ash gourd, one is orange shaped generally called "gimi or chuna kumra" which is grown in winter and the other is oblong shaped "chaal kumra" which is grown in summer season. Winter types are of short vine and produce comparatively smaller fruits than summer types and do not require trellis. It becomes available even in the rainy season when other vegetables are scarce in Bangladesh. (BARI, 2006).

The total production of vegetables can support only about 34.73% that is about one third of the total need per capita per day in Bangladesh. The total production of most of the vegetable crops is much less than the total needs . In Bangladesh, vegetable consumption rate is 104 g per day per adult, against the optimum amount of about 300g per day per adult. The total area under cultivation of wax gourd was 10000 acres with a total annual production of 28000 metric ton in 2004 (BBS, 2005). The average yield of wax gourd is 5.97 t/ha, which is very low. The productivity of local genotypes ranged from 6.93 t/ha to 19.07 t/ha (Hamid *et al.*, 1989)

Wax gourd is best suited for moderately dry areas in the tropics. It is relatively drought tolerant. It grows well at temperatures above 25°C, the optimum temperature for growth ranging from 23–28°C (24 h average). It is suited to tropical lowland conditions and elevations up to 1000 m altitude. It prefers a well-drained light soil with pH 6.0–7.0.

The yield of wax gourd is a complex component character. In a breeding program for increasing yield, quality, resistance to disease and pests in the exploration of genetic variability in presence of available germplasms is pre-requisite. Therefore, evaluation of germplasm under local conditions is very important. Improvement of yield depends on the nature and extent of genetic variability and genetic advance in the base population from which selection is made.

The knowledge of the interrelationships between yield and yield components is necessary; determination of correlation among plant characteristics is a matter of considerable importance in selection of correlated response.

Correlation studies between yield and other traits of the crop is of interest to breeders in planning the hybridization program and evaluating the individual plants in segregating populations, but it does not give an exact position of the relative importance of direct and indirect effects of various traits on yield or any other attributes. Following correlation analysis, 'the path coefficient analysis' would provide a true picture of genetic association among different traits (Bhatt, 1970). Path coefficient analysis is useful for evaluating the relative contribution of each component traits both direct and indirect to the yield. Path co-efficient analysis helps specifying the cause and effect and measuring their relative significance. So, correlations in combination with the path co-efficient analysis quantify the direct and indirect contributions of one characteristic upon another (Dewey and Lu, 1959).

A good knowledge of genetic diversity helps to select the genetically divergent parents to obtain the desirable recombinant in the segregating generation upon crossing. It is the function of heterosis. It also helps in identifying the desirable cultivars for commercial cultivation. The availability of transgressive segregants in any breeding programme depends upon the divergence of involving parents. Precise information on the nature and degree of genetic divergence of the parents is the prerequisite of an effective breeding program among the cultivated land races; a wide range of genetic variability exists in this crop that can be exploited for its improvement. Successful attempts to improve the crop characteristics for the increased production of fruit yield of wax gourd per plant or per unit area will be beneficial for the farmers of Bangladesh. It is the touchstone to a breeder to develop high yielding varieties through selection, either from the existing genotypes or from the segregates of a cross. Hence, information on variability in respect of yield and its contributing characters required to be properly assessed for its improvement.

Considering the above facts, the present study has been under taken to fulfill the following objectives:

Objectives:

i. To assess the genetic diversity among the genotypes.

ii. To know the yield potentiality of genotypes

iii. To know the association of traits with yield and its contributing traits.

iv. To screen out the suitable parental groups which are likely to provide superior segregates on hybridization.

Chapter 2

Review of literature

CHAPTER II

REVIEW OF LITERATURE

Wax gourd (*Benincasa hispida* Thunb.) is a member of the family Cucurbitaceae. Among cucurbits and other vine vegetables, wax gourd production is profitable for small scale producers (Chowdhury, 1993). In Bangladesh, the production of vegetables is higher during winter (60 to 70%) and most districts produce marketable surplus during that season. Wax gourd can be good addition in the summer when production of other vegetables is low. It is an annual monoecious climbing type herbaceous crop. In spite of its economic importance very little attempt has so far been made for its improvement in Bangladesh and other countries in the world. However, research efforts on the genetic resources, diversity on genetic and molecular level, correlation, path co-efficient analysis, heritabilily and genetic advance seem to be meager. However, information available in these aspects of wax gourd and some other cucurbit crops have been reviewed and presented in this section.

2.1 Variability, Heritability and Genetic Advance:

Gangopadhyay *et al.* (2008) conducted a field experiment to study the genetic diversity, clustering pattern and ordination (principal components) analyses which were undertaken in 26 wax gourd accessions. The accessions showed significant inter-population differences and wide variation for quantitative and qualitative morphological descriptors observed. Low level of difference between the magnitude of PCV and GCV indicated that the descriptors were least influenced by environment and are genetically controlled. High heritability coupled with high genetic advance was observed for descriptors such as primary branches, fruits/plant and fruit weight/plant. These accessions were grouped into four major clusters. The clusters were homogenous within themselves and heterogeneous among each other. Cluster IV was the most distinct with more primary branches, higher individual fruit weight, more fruits/plant and highest fruit weight/plant. The PCA in general confirmed the groupings obtained through cluster analysis. PCA revealed four informative components accounting for 67.71% variance. PC1 was related with petiole length, node number at which first female flower appears and yield contributing descriptors like primary branches, fruit length, fruit width and fruit weight.

Sanwal *et al.* (2011) conducted a field experiment to study the optimum multivariate profile of a wax gourd genotype which include a pool of 56 genotypes, of which 10 are released cultivars and 46 indigenous lines collected from different parts of India, was studied in a two-year experiment. Various traits are important when breeding new cultivars, so an optimum multivariate performance is studied in this germplasm, with a special focus on traits of the greatest importance, namely fruit yield per plant, flesh thickness, vine length, and number of days to female and male flowering. Such performance is studied for the best-yielding genotypes, and promising genotypes in terms of multivariate performance are selected.

Pandey *et al.* (2008) made an attempt to assess the genetic diversity among 34 accessions (9 cultivars and 25 germplasm) of *Benincasa hispida* using quantitative traits and RAPD data. Variability was observed for characters like days to first female flower, fruit weight, equatorial and polar diameter. Cluster analysis based on quantitative traits revealed a high degree of diversity among the accessions. RAPD-based dendrogram showed dissimilarity values 0.64–0.943 suggesting that the accessions represent a genetically diverse population. A non-significant correlation was observed between the clustering based on quantitative traits and RAPD markers. But the accessions like IVAG-107 and IVAG-81 clearly separated from rest of the accessions based on the quantitative traits and as well as RAPD primers. Both the dendrogram revealed that the accessions from northeastern region of India are diverse from the accessions of other parts of India, as they cluster together in both the dendrogram. On the basis of clustering, it was indicated that cultivars had a narrower genetic diversity among themselves as compare to germplasm collected from different agro-ecological region. The information generated could be utilized in developing cultivars/hybrids for specific traits.

Dasen *et al.* (2005) showed the inherited tendency of heterosis of main agronomic characters in wax gourd and the correlation of characters between F_1 and parents were analysed. The results indicated that fruit weight, fruit width and flesh density expressed positive heterobeltiosis, negative transgressive inheritance and negative incomplete dominance respectively, that the fruit length, fruit shape index and viruses resistance were significantly positive correlation between F_1 and male parent, and expressed incomplete dominant inheritance ,and that the content of solids and the flesh thickness expressed positive transgressive inheritance ,and the former correlation coefficient between F_1 and male parent and the latter correlation coefficient between F_1 and parents all attained significance levels.

Dasen *et al.* (2005) showed eleven yield relative characters of thirty-three wax gourd self-cross lines from different regions were analyzed by grey relation degree analysis, the results revealed that the key traits which affected the yield were fruit weight, index of fruit shape, fruit length and thickness of fruit flesh, while thickness of fruit flesh, fruit length, fruit width and index of virus disease were the main traits which affected the fruit weight, the disease resistance had the greatest influence on the compactness of fruit flesh. Among 33 wax gourd cultivars, No.32 had the greatest yield potential, No.19 and No.13 followed next.

Verma *et al.* (2007) conducted an experiment on Heterosis studies in wax gourd for yield and related traits. Ten elite inbred lines of ash gourd (*Benincasa hispida*) were selected based on their performance and were crossed in a diallel mating system (without reciprocal crosses) to generate 45 F1 hybrids. These hybrids along with the parents were grown to study heterosis in 10 yield related characters. The mid and better parent heterosis was observed to be as high as ~165% for yield per vine in DAG-6 × DAG-11. The maximum negative heterosis over the best parent for days to fruit maturity was noticed in cross DAG-2 × DAG-9 (~ –10%) indicating that it can be successfully utilized in breeding for earliness in ash gourd. Two hybrids namely, DAG-1 × DAG-5 (34.33 kg) and DAG-4 × DAG-11 (31.67 kg) recording positive heterosis over the best parent to the extent of 23.5% and 14.0% respectively for yield per vine can be utilized for commercial cultivation.

Banik *et al.* (2010) conducted a field experiment to study the nature and extent of combining ability of parents and crosses and the mode of gene action in controlling the individual characters in 6x6 diallel including reciprocals in snake gourd. The significant mean sum of squares due to general and specific combining ability (GCA and SCA) for these characters indicated both additive and as well as non-additive type of gene actions were involved for the expression of these characters. The parent P4 was the best general combiner for fruits per plant, first male and female flower, node number. Higher significant SCA effects were found in the cross combinations P2 x P3 for early fruit maturity, P1 x P5 for early first male and female flower with longest vine, P1 x P2 for fruit weight per plant; P1 x P5 for average fruit weight. Significant reciprocal effects were observed for first male and female flower appearance node number, fruits per plant, flower opening days, fruit yield per plant, average weight of fruits per plant and seeds per fruit. Reciprocal cross P5 x P3 was found best for early flowering, P4 x P2 for yield per plant. The best heterotic crosses for earliness and fruit yield per plant were P6 x P2, P5 x P1 and P1 x P2, respectively. Such crosses could be used for exploitation of heterosis in desirable direction. The experiment was conducted at the experimental farm of Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Salna, Gazipur, Bangladesh during May 2001 to September 2002.

Rajkumar (2007) *et al.* conducted a field experiment in Tamil Nadu, India, from 2003 to 2005, to determine the genetic variation including the mean, genotypic (GCV) and phenotypic coefficients of variation (PCV), heritability and genetic advance with 30 genotypes of snake gourd (*Trichosanthes cucumerina*). Significant differences among genotype for all the characters were noted. All the characters exhibited less difference between GCV and PCV values. The characters flesh thickness, fruits per plant, days to fruit maturity and 100-seed weight showed equal GCV and PCV values indicating less influence of environment in their expression. The heritable estimate was high for all the characters except days to first female flower. The maximum heritability was observed for ascorbic acid content of the fruit, followed by the crude fiber content and nodes for first female flower. The genetic advance as a percentage of mean was high for fruits per plant and fruit length. High heritability coupled with high genetic advance was observed for fruits per plant and fruit length. They are governed by additive genes and could be effectively improved through selection.

Narayanankutty *et al.* (2006) estimates genetical parameters of 36 snake gourd (*Trichosanthes cucumerina*) genotypes indicated a good amount of genetic variation in the germplasm collections. Characters such as fruit yield, fruit weight and seeds per fruit exhibited high values of heritability and genetic gain indicating additive gene effects are important in determining these characters. The character association analysis revealed that yield was strongly correlated with fruit weight, fruits per plant, fruit girth, fruit length, days to first harvest, flesh thickness and days to first female flower opening. Fruit weight and fruits per plant have the maximum positive direct effects on yield and the indirect contribution of other characters was mainly through days to first harvest, seeds per fruit and 100-seed weight.

Banik (2003) conducted an experiment on variability and genetic advance of 26 genotypes of snake gourd with respect of 15 quantitative yield contributing characters and found significant difference among the characters like vine length at harvest (2.197 to 3.87 m), number of primary branches (5.23 to 11.88), days to first male flowering (41.67 to 68.67 days), days to first female flowering (48.67 to 71.33 days), node number of first male flower (6.33 to 17.67 days), fruit length (20.67 to 71.17 cm), seeds per fruit (39.03 to 69.50). Banik also found that significant differences in first female flower, node number (mean value 19.28) and fruits per plant. The highest phenotypic co-efficient of variation was observed for fruiting node on main vine, fruit yield per plant, fruit length and first male flower node. The PCV was lowest for days to maturity, 100 seed weight and days to first male flower opening. The GCV along with heritability was high for the above characters. High heritability coupled with high genetic advance was noticed for fruit yield per plant (GCV and PCV 30.75 and 30.96; h^2b 98.64%), fruit length (GCV and PCV 29.92, and 30.04; h^2b 99.19%) and first female flower node number (GCV and PCV 25.87 and 26.59; h^2b 94.63%) and number of fruits per plant (GCV and PCV 19.82 and 20.59; h^2b 92.67%).

Dora *et al.* (2003) eleven pointed gourd (T. dioica) selections were assessed to estimate genetic variability and correlation for yield and its attributes. High genetic coefficient of variation (GCV) estimate was observed for the characters such as node at which first female flower appears, length of vine, number of nodes per plant, and number of fruits per plant. The heritability estimate was high for all the characters. The characters having high GCV also exhibited high genetic advance. Yield per plant had a significant positive correlation with number of fruits per plant, fruit set and fruit retention.

Chowdhury and Sharma (2002) studied genetic variation, heritability, genetic advance, and correlation for yield and yield components (vine length, number of nodes, node on which the first flower appeared, number of fruits per plant, fruit length, fruit girth, and fruit weight) were studied in 12 *Luffa acutangula* cultivars

(AAUJ-1, AAUJ-2, AAUJ-3, Mangaldoi, Tezpeu, Tihu, Mirza Short, Rangamati Long, Borpeta Long, Tiniali Long, Pusa Nazder, and HRS C-2) grown in Gwuahati, Assam, India. The genetic coefficient of variation (GCV) was higher than the phenotypic coefficient of variation (PCV) for all characters. High values of heritability, PCV, GCV, and genetic advance were recorded for vine length, yield per hectare, and fruit weight, indicating that these traits were characterized by additive gene effects. The correlation coefficients revealed that yield per hectare can be improved through selection for greater fruit number per plant, fruit length and girth, and individual fruit weight.

Quamruzzaman *et al.* (2009) studied heterosis in bottle gourd in a set of 13 F, with 26 parents. Results indicated highly significant differences for all the character among the materials studied. Heterosis was higher for yield per plant, number of fruits per plant and individual fruit weight, medium in fruit length and fruit diameter, and lower in days to 1st harvest. Hybrids (F1) 10 x 17 and 19 x 26 manifested highest heterosis over mid parent (73.1%) and better parent (61.8%), respectively, for yield per plant.

Narayan *et al.* (1996) studied genetic variability, heritability in broad sense, genetic advance in 25 diverse populations of bottle gourd. Wide range of variation was observed in most of the characters. The high value of GCV and heritability estimates associated with greater genetic advance was observed for number of primary branches per plant and yield per plant indicated that these two characters had additive gene effect and, therefore, they are more reliable for effective selection.

Bharathi *et al.* assessed (2006) genetic variability for 10 characters (days to flowering, vine length, number of nodes on which first flower appears, internode length, fruit length, girth, weight and volume, number of fruits, and yield per plant) in 32 genotypes of spine gourd (*Momordica dioica*) during 2003/04, in

Bhubaneswar, Orissa, India. Analysis of variance revealed significant differences among the genotypes studied. Phenotypic coefficient of variation (PCV) ranged from 15.26% for fruit girth to 34.28% for fruit weight, while genotypic coefficient of variation (GCV) ranged from 14.38% for fruit girth to 33.52% for fruit weight. High heritability coupled with high genetic advance were recorded for fruit weight, fruit volume and number of fruits per plant, indicating the preponderance of additive gene effects for these characters and their potential use in selection programmes to improve spine gourd productivity.

Masud *et al.* (2006) conducted a field experiment with seven inbred lines and their twenty-one hybrids of bottle gourd. Result showed significant variation in seven characters of the twenty eight populations. Variabilities were high in all seven characters indicating the possibilities of improvement through selection. Specific combining ability variance were significant for all characters while general combining estimates were significant for days to anthesis, fruit length, fruit diameter and yield per plant which indicated the presence of dominance for all the characters but additivity is for only few characters. Parent-two showed good GCA for earliness and fruit length, Parent-five showed good GCA for fruit length only and parent-seven showed good GCA for fruit diameter and fruit yield per plant. The cross involving parent-three and parent-five, which is the best for earliness, fruit length (53.5%) and; fruit yield per plant (106.8%).

Rahman *et al.* (1991) reported that male flower were earlier than female flower in several genotypes of bottle gourd, ribbed gourd and sweet gourd. They reported significant variations for that character among the genotypes of bitter gourd, sweet gourd, ribbed gourd and bottle gourd. Significant variation for fruit length and diameter were also observed. They also reported that bitter gourd, sweet gourd, ribbed gourd and bottle gourd genotypes differed significantly for fruit breadth and weight per fruit.

Abusaleha and Dutta (1990) carried out a study with 65 genetic stocks to assess the genetic variation and heritability in ridge gourd. Significant variability was observed for all the characters at phenotypic as well as genotypic level with a very wide range of values.

Miah *et al.* (2000) studied 30 genotypes of bitter gourd and observed the highest genotypic as well as phenotypic co-efficient of variation were found for fruit length followed by days to female flowering, fruit yield per plant, fruit weight and nodes per vine.

Sharma *et al.* (2000) evaluated ten cucumber lines and testers under different environmental conditions and reported that day to first female flower, nodal position of fruits per plant, marketable yield per plant, fruit length and fruit diameter had wide range of variation.

2.1.1 Leaf Length (cm)

Husna (2009) conducted an experiment with thirty one genotypes of bottle gourd in Sher-e Bangla Agricultural University. She found that the genotypic variance (14.18) was appeared to be higher than the genotypic variance (14.14). The GCV (22.63) and PCV (22.67) were close to each other. Heritability (99.69%) estimates for this trait was very high, genetic advance (9.91) and genetic advance in percent of mean (59.65) were found moderately high indicating this trait was governed by the additive gene.

Gaffar (2008) conducted an experiment with fifteen genotypes of sponge gourd in Sher-e Bangla Agricultural University. He found that the genotypic and phenotypic variances of leaf length were 24.13 and 25.55, respectively. The GCV (20%) was slightly lower than PCV (20.58%). Heritability for this trait was 97% with moderate genetic advance (9.83) and genetic advance in percent of mean (40.03) was considerable for this trait indicating apparent variation was due to genotypes.

2.1.2 Leaf breadth

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

Gaffar (2008) observed GCV (20.94%) was slightly lower than the PCV (23.31%) heritability in broad sense was high (94%) with moderate genetic advance (7.81) for this character in sponge gourd.

2.1.3 Days to first flowering

Rajkumar (2007) *et al.* found significant differences among genotype for all the characters in snake gourd. The heritable estimate was high for all the characters except days to first female flower. Banik et al. (2010) found in his experiment the parent P4 was the best general combiner for fruits per plant, first male and female flower.

Rahman *et al.* (1991) reported that male flower were earlier than female flower in several genotypes of bottle gourd. In Bitter gourd, Mannan (1992) recorded considerable variability among eight lines for days to first male flower (66.70-81.60 days) and female flower (72.80-85.67 days) opening.

2.1. 4 Pedicel length of flower (cm)

Husna (2009) found that in bottle gourd male flower pedicel length is 3.5-21 cm and in female flower pedicel length is 3.13-9 cm.

Rashid (1993) reported that in bottle gourd, male flower pedicel length is longer than female flower pedicel length.

Grubben (2004) stated that male flowers have 7-31 cm long pedicel and female flowers have 2-10 cm long pedicel in bottle gourd.

2.1. 5 Internodes distance (cm)

Gaffar (2008) reported almost similar estimates of GCV and PCV (10.45% and 11.16%) and heritability in broad sense was high (94%) with moderate genetic advance (3.19) for internodes length in sponge gourd. Similar result was found by Singh *et al*. (2002)

2.1.6 Fruit length and breadth (cm)

Banik (2003) found high heritability coupled with high genetic advance for fruit length (GCV and PCV 29'.92, and 30.04; h^2b 99.19%) in snake gourd.

Husna (2009) found GCV (16.49) and PCV (17.50) in male flower and GCV (15.84) and PCV (17.39) in female flower of bottle gourd plant.

2.1.7 Fruit weight (Kg)

Mathew and Khader (1999) recorded the highest GCV and PCV were for mean fruit weight. They observed high heritability for mean fruit weight in snake gourd.

High GCV and PCV were reported (39.55 and 41.00) by Saha *et al.* (1992); (30.2 and 36.4) by Doijode and Sulladmath (1986) for fruit weight in pumpkin. Mannan (1992) reported narrow difference between GCV and PCV for this trait in bitter gourd indicating less environmental influence on this character. High h^2 coupled with genetic advance for average fruit weight was noticed in pumpkin (82.9% and 49.6) by Doijode and Sulladmath (1986); (93.03% and 78.58) by Saha *et al.* (1992).

2.1.8 Yield per plant (kg)

Singh *et al.* (2000) found high heritability along with high genetic advance for fruit yield per plant while number of fruits per plant and fruit weight showed only high genetic advance in wax gourd. Genotypic correlations were found higher than the phenotypic correlations. Fruit weight and number of fruits per plant exhibited maximum direct effect on fruit yield.

Banik (2003) also found that significant differences in fruits per plant. The highest phenotypic co-efficient of variation was observed for fruiting node on main vine, fruit yield per plant, fruit length and first male flower node.

High heritability coupled with high genetic advance was noticed for fruit yield per plant (GCV and PCV 30.75 and 30.96; h^2b 98.64%).

The variation for yield per plant was recorded in bottle gourd (Rahman *et al.*, 1991), water melon (chezhiyan, 1984), musk melon (Swamy *et al.*, 1984) and pumpkin (Rana *et al.*, 1986; Shaha *et al.*, 1992). Mangal *et al.* (1981) found high value (47759.63 and 55149.80) in bitter gourd while, low GCV and PCV were recorded for this character in water melon (0.44 and 1.15) and musk melon (0.04 and 0.07) by Vashistha *et al.* (1983) and Vijay (1987).

2.2 Correlation Co-efficient:

Singh *et al.* (2000) showed genotypic correlations were found higher than the phenotypic correlations. Fruit weight and number of fruits per plant exhibited maximum direct effect on fruit yield.

Dasen *et al.* (2005) 56 melon varieties of 13 traits, the genetic correlation and path analysis, results showed that the melon long, dense flesh, diameter, fruit weight and total output is closely related to, flesh dense constitute the melon fruit weight and total output of the trait, melons, long contribution to the production. Melon long, flesh dense with fruit weight was highly significant positive correlation in the cavity and fruit weight was highly significant negative correlation. The correlation and path analysis of 13 characters of wax gourd were carried out. The results showed that the length of fruit, compactness, width and average weight of fruit existed evident relativity to yield. Compactness was the most important component factor to the fruit weight and total yield. Fruit length contributed the most to the yield. Significant positive correlation was observed between fruit weight, fruit length and compactness.

Kumaresan *et al.* (2006) conducted field experiments in Madurai, Tamil Nadu, India, during the 2000 rabi season, to determine correlations among different economic parameters and their direct and indirect effects on fruit yield in 6 snake gourd (*Trichosanthes cucumerina*) cultivars and their 30 hybrids. Yield per vine in snake gourd was positively associated with main vine length, number of fruits per vine, fruit weight, and number of seeds per fruit, seed weight per fruit and ascorbic acid content of the fruits. However, negative association was observed with days to first female flower opening, days to first male flower opening, fruit length, fruit girth and acid content of the fruit. This indicates that the selection for the characters will simultaneously result in improving the yield per vine.

Kumar *et al.* (2007) conducted an experiment to study the correlation coefficient of 20 bottle gourd *(Lagenaria vulgaris)* genotypes. Fruit yield per vine in bottle gourd is the result of interaction of number of inter-related characters. Therefore, selection should be based on these components character after assessing their correlation with fruit yield per vine. The fruit yield per vine showed positive and significant correlation with number of branches per vine, vine length, nodes number of first male flower, nodes number of first female flower, length of edible fruits, and number of fruits per vine, number of seeds per fruits and 100-seed weight at genotypic and phenotypic levels. This indicated that fruit yield can be improved by making selection on the basis of no. of branches per vive, vine length, nodes no. of first female flower, length of edible fruit and no. of fruit per vine.

Hazra *et al.* (2003) studied sixty-eight diverse female clones of T. dioica. These were grown at the Horticultural Research Station, Mondouri, West Bengal, India to evaluate growth, morphological, yield and quality characters and their relationship through correlation and path analysis. The magnitude of genotypic correlation coefficients was higher than phenotypic correlation coefficients for all the pairs of characters, and in most cases, a wide gap was recorded between the two estimates of correlation coefficients, indicating the influence of environment on the correlated response of the pair of characters. Most of the character pairs showed negligible or insignificant correlation that might have resulted due to simultaneous vegetative and reproductive growth in the plant. Only fruit number per plant had significant positive correlation with yield, whereas fruit weight showed highest positive direct effect on yield. However, from the overall study, most of the fruit characters, viz. fruit weight, pulp content of fruit, fruit number per plant and fruit volume, and growth traits, such as leaves per plant and leaf length, were identified as important yield contributors.

Prasana *et al.* (2002) studied the correlation between the yield and yield components of ridge gourd (*Luffa acutangula*) in Bangalore, Karnataka, India, during the rabi of 1999. Fruit yield per hectare was positively associated with vine length at 90 days after sowing (DAS), number of leaves at 90 DAS, number of female flowers, total dry weight of plant, number of fruits, and fruit girth and weight.

Badade *et al. (2001)* conducted an experiment to study the correlation of *20* bottle gourd *(Lagenaria vulgaris)* genotypes. Yield was found significantly and positively correlated with number of branch per vine, number of fruits per vine and significantly and negatively correlated with days to first male and female flower appearance and weight of deformed fruits per vine at both phenotypic and genotypic levels. Fruit length showed positive but non-significant correlation with fruit yield.

Narayan *et al.* (1996) studied correlation analysis in 25 diverse populations of bottle gourd. Correlation coefficient revealed that fruit yield per plant can be successfully improved by making selection or greater fruit number, higher fruit weight, greater number of primary branches and genotypes with lesser number of days to anthesis of first male flower.

Singh and Ram (2003) conducted an experiment on 28 musk melon genotypes to determine the correlation among fruit characters. The simple correlation among fruit traits showed that polar diameter, latitudinal diameter, flesh thickness and seed cavity size were positively correlated with fruit weight.

Shah and Kale (2002) conducted an experiment on correlation co-efficient analysis of yield components of 55 genotypes of ridge gourd. The fruit weight per vine was positively and significantly correlated with number of fruits per vine, average fruit weight, number of female flower per vine and vine length, indicating the close association and dependency of yield these characters. The fruit length was negatively correlated with fruit diameter and fruit number per vine, while it was positively correlated with average fruit weight.

Singh *et al.* (2002) carried out 98 hybrids of cucumber derived from crosses involving fourteen male and seven female parents and found that fruit weight, fruit girth and fruit length had high correlations with fruit yield. Genotypic correlation coefficient were higher than phenotypic co-efficient which indicated strong association among these traits.

Miah *et al.* (2000) noted that fruit yield in bitter gourd showed significant positive association with average fruit weight, fruit breadth and number of nodes per vine in genotypic and phenotypic correlation with days to male flowering.

Kumaran *et al.* (1998) carried out an experiment on correlation and path analysis studies in pumpkin. They found that positive and significant correlation of vine length, mean fruit weight, number of fruit per plant and number of seeds per fruit with fruit yield per plant.

Abusaleha and Dutta (1989) found that the yield of cucumber is positively correlated with vine length ($r = 0.35$), branches per vine ($r = 0.29$), fruits per vine ($r = 0.48$), fruit length ($r = 0.60$) and fruit girth ($r = 0.43$). Days to first male and female flowering, nodal position female flower, percentage of misshapen fruits and non-marketable yield were negatively correlated with yield.

2.3 Path Co-efficient:

Singh *et al.* (2000) conducted a field experiment to study the significant variances for all the eight characters studied under wax gourd genotypes.

Path coefficient analysis revealed that fruit weight and number of fruits per plant exhibited maximum direct effect on fruit yield.

Kumaresan *et al.* (2006) conducted field experiments in Madurai, Tamil Nadu, India, during the 2000 rabi season, to determine correlations among different economic parameters and their direct and indirect effects on fruit yield in 6 snake gourd (Trichosanthes cucumerina) cultivars and their 30 hybrids. Path coefficient analysis revealed that it would be highly rewarding to lay emphasis on the number of fruits per vine and fruit weight to increase the yield per vine directly.

Kumar *et al.* (2007) conducted an experiment to Study the path coefficient of 20 bottle gourd *(Lagenaria vulgaris)* genotypes. Path analysis revealed that number of branches per vine, vine length, nodes number of first female flower and number of fruit per vine had positive direct effect on fruit yield per vine. Narayan *et al.* (1996) studied path-coefficient analysis in 25 diverse populations of bottle gourd. Path coefficient analysis revealed that maximum weight age should be given primarily to days to first harvest followed by average weight of edible fruit, number of fruits per plant and days to anthesis of first female flower while formulating selection indices for improvement of yield in bottle gourd.

Singh *et al.* (2002) were carried out 98 hybrids of cucumber derived from crosses involving fourteen male and seven female parents. Path coefficient analysis indicated that fruit weight had the highest direct effect on fruit yield.

Rao *et al.* (2000) conducted an experiment on the segregating population of ridge gourd for correlation and path coefficient analysis. Path analysis revealed that yield improvement could be achieved by direct selection for days to 50% flowering, girth of fruit, fruits per plant or vine, fruit per branch and length of the vine of ridge gourd.

Miah *et al.* (2000) conducted an experiment on bitter gourd for correlation and path coefficient analysis. Path analysis revealed that average fruit weight, number of fruits per plant, days to male flowering and fruit length had positive direct effect on fruit yield.

Sarker *et al.* (1999) studied path co-efficient of 16 divergence types of pointed gourd. The path analysis revealed that fruit volume followed by fruit weight and fruit diameter had maximum positive direct effects on yield.

Kumaran *et al.* (1998) carried out an experiment on correlation and path analysis studies in pumpkin. They found that number of fruit per plant exhibited the highest direct effect on yield. High positive indirect effects were exerted by number of fruit per plant and mean fruit weight.

Li *et al.* (1997) conducted an experiment on cucumber genotypes. From path analysis, they concluded that fruits per plant and average fruit weight affected the yield directly.

Abusaleha and Dutta (1989) carried out an experiment on correlation and path analysis studies in cucumber. Path coefficient analysis revealed that fruits per vine and fruit length had the greatest direct effects on yield.

Parhi *et al.* (1995) studied correlation and path co-efficient of thirteen genotypes of bitter gourd. Path analysis revealed that fruit breadth, days to opening of first male and female flower, vine length and number of seeds per fruit had the maximum positive direct effect on yield in bitter gourd. The characters like fruit weight and fruit length though have significant positive correlation with yield, exhibited low direct effect. Besides direct selection for yield, indirect selection through number of seeds per fruit and fruit weight would prove worth for further improvement in yield of bitter gourd.

Prasanna *et al.* (2002) studied the correlation between the yield and yield components of ridge gourd *[Luffa acutangula]* in Bangalore, Karnataka, India, during the rabi of 1999. Fruit yield per hectare was positively associated with vine length at 90 days after sowing (DAS), number of leaves at 90 DAS, number of female flowers, total dry weight of plant, number of fruits, and fruit girth and weight. Path coefficient analysis showed that vine length at 90 DAS, number of female flowers per vine, number of branches per vine, number of fruits per vine, fruit girth, and fruit weight had direct positive effects on fruit yield, whereas the number of leaves at 90 DAS, total dry weight of the plant, and fruit length had negative direct effects on fruit yield. The fruit yield of ridge gourd can be enhanced through the improvement of vine length at 90 DAS, number of female flowers, number of branches, number of fruits per vine, fruit girth, and fruit weight.

Umamaheswarappa *et al.* (2004) conducted an experiment on the effect of various rates of nitrogen (0, 60 and 120 kg/ha), phosphorus (0, 50 and 100 kg/ha) and potassium (0, 30 and 60 kg/ha) on bottle gourd (*Lagenaria siceraria*), conducted in Bangalore, Karnataka, India, in 1999 showed that fruit yield/ha had strong positive association with vine length, number of leaves per vine, number of female flowers per vine, number of branches per vine, vine girth, total chlorophyll content in leaf, total dry weight of plant, number of fruits per vine, fruit weight, fruit length and fruit girth. Path coefficient analysis revealed that number of fruits per vine had maximum direct effect on fruit yield followed by fruit weight.

2.4 Genetic Divergence:

Genetic diversity is one of the important tools to quantify variability in both self and cross-pollinated crops (Griffing and Lindstone, 1954; Murty and Arunachalam, 1966: Guar *et al.* 1978).

The quantification of genetic diversity through biometrical procedure made it possible to choose genetically diverse plants for a successful hybridization programme. D^2 analysis (originally outlined by Mahalanobis, 1936) is one of potential methods of estimating the degree of genetic diversity. The wide diversity of genotypes can be shown by cluster˙ analysis from the same geographical regions. To understand the usable variability, grouping or classification of genotypes based on suitable scale. Multivariate analysis formulated by Mahalanobis (1936) is a powerful tool in quantifying the degree of divergence among biological population based on multiple characters. Studies on genetic diversity in bottle gourd carried out so far are presented as follows:

Afroze *et al.* (2007) studied the genetic divergence among 46 ash gourd genotypes from different origins was investigated to select the parents for hybridization using Mahalanobis D^2 statistics. Though the genotypes grouped into seven clusters, the pattern of distribution of the genotypes into different clusters were random indicating that the geographical isolation was not always related to genetic diversity. Characters like fruit weight, fruits per plant, days to first male flower and nodes for first male flower contributed considerably to the total divergence. Maximum inter-cluster distance between cluster III and IV indicating wide genetic divergence between the genotypes of these two clusters (cluster III and IV followed by cluster IV and VII). However, the intra-cluster distances were smaller than inter-cluster distances. Thus, crossing between the genotypes of these two groups (cluster III and IV) would produce high heterotic progeny and may produce new recombinants with desired traits. The experiment was conducted at the experimental farm of Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Salna, Gazipur, Bangladesh during the period from March 2005 to August 2005.

Verma *et al.* (2007) studied the genetic diversity of wax gourd inbred lines based on RAPD and ISSR markers and their hybrid performance where ten inbred lines of wax gourd were crossed to produce 45 F_1 hybrids (without reciprocal) which were evaluated along with the parents for 20 growth- and yield-related traits, in a replicated field trial. High level of heterosis was observed among the hybrids for most of the traits examined, including yield. These inbred lines were analysed by using 42 RAPD primers those produced 282 DNA marker bands. A total of 130 RAPD markers were obtained with a mean of 3.1 per primer, which in combination discriminated all the inbreds from each other. Pair-wise genetic distance measurements ranged from 0.07 to 0.31, suggesting a wide genetic diversity for these inbreds. These inberds were also analysed with five ISSR primers of which four were informative. Twenty-six ISSR marker bands were generated of which 11 were polymorphic with an average of 2.80 per primers. The percentage of polymorphic bands produced were higher in ISSR markers (>80%) than generated through RAPD markers (46%). Although the results indicated significant positive correlations of genetic distance with hybrid performance and heterosis, the RAPD based genetic distance measures and use of limited ISSR markers in this present study could not effectively predict hybrid performance in this crop. The genetic variation among ash gourd inbred lines examined, herein, defined a marker array (combined ISSR and RAPD) for the development of a standard reference for further genetic analyses, and the selection of potential parents for predicting hybrid performance and heterosis.

Khatun *et al.* (2010) conducted at the field and laboratory of the Department of Horticulture, Bangladesh Agricultural University, Mymensingh during the period from April 2004 to September 2004 to study the nature and magnitude of genetic diversity of 38 snake gourd genotypes collected from different regions of the country. Based on D2 analysis, the genotypes were grouped into four different clusters, where the cluster I possessed maximum number (21) of genotypes followed by the cluster 11(8), III (7), and IV (2). Clustering pattern revealed that geographical diversity was not associated with genetic diversity i.e., genotypes collected from same location were grouped into different clusters. The maximum inter-cluster distance was observed between the clusters III and IV and that of minimum in between the clusters I and II. In case of intra-cluster distance, the maximum distance was observed in the cluster IV and that of minimum was observed in the cluster III. Considering cluster mean, the genotypes of cluster IV could be selected for yield per plant and other yield contributing characters.

Banik (2003) studied 26 genotypes of snake gourd were tested using multivariate analysis and the genotypes were grouped into seven distinct cluster. No relationship was found between genetic divergence and geographical distribution of genotypes. The highest inter genotypes distance was observed between genotypes SG 026 and SG 010 (1.897). The inter cluster distance was maximum between cluster II and IV (17.74). Main vine length, first female flower node number, nodes on main vine, fruit length and number of seeds per fruit had the highest contribution towards the divergence.

BARI annual report 2008-09 revealed that Genetic divergence among 30 snake gourd genotypes was estimated using Mahalanobis's D^2 staistic. Cluster V contained the highest number of genotypes (13) and cluster III &IV contained the lowest (3). The highest intra-cluster distance was observed in cluster III (1.665) and the lowest in cluster V (0.430). The highest inter- cluster distance was observed between cluster I and III (26.954) and the lowest in cluster II and IV (5.693).

Islam *et al.* (2010) studied genetic divergence of twenty bitter gourd genotypes through Moahalanobis's D2 and principal component analysis in Pakistan. The genotypes under study fall into four clusters. The cluster I contained the highest number of genotypes and it was 10. Cluster IV contained the lowest number of genotypes. Cluster II produced the highest mean value for weight per fruit. The inter cluster distances were much higher than the intra cluster distances. Cluster I exhibit the highest intra cluster distance while the lowest distance was observed in cluster III. The highest inter cluster distance was observed between I and II while the lowest distance was observed between the cluster II and IV. The highest intra cluster means for weight per fruit and five important yield contributing characters were obtained from cluster II. Therefore, more emphasis should be given on the cluster for selecting genotypes as parents for crossing with the genotypes of cluster II which may produce new recombination with desired traits. Considering all the characters the G1 (Shaparan), G5, (Rampali gaj), G9 (Nabil), G12 (Nandita) G14 (Eureca), G16 (Tia) and G19 (Maharaj) were selected for future breeding programme.

Preeti *et al.* (2010) observed wide range of genetic diversity among twenty three germplasm lines of ash gourd collected from different parts of U.P. and Uttarakhand. Genotypes PAG-50, Pant Petha-1, PAG-64, PAG-12, PAG-14 and PAG-09 were high yielding lines while considering both the seasons summer and kharif 2006. Based on Mahalanobis D2 analysis all germplasm lines were grouped into 5 clusters. The clustering pattern indicated that geographical distribution need not necessarily be related to the genetic diversity. Cluster I was very large containing 14 genotypes (summer) and 10 genotypes (kharif) season. The commercially released cultivar Pant Petha-1 was grouped in cluster II along with other genotypes in both the seasons. The inter-cluster distance was found maximum between cluster III and cluster IV (summer) and cluster II and cluster V in (kharif) seasons. The genotypes in these clusters may possibly be utilized in hybrid breeding programme for successful exploitation of hybrid vigour in ash gourd.

Gaffar (2008) conducted an experiment with 15 sponge gourd genotypes at the experimental farm of Sher-e-Bangla Agricultural University, during April 2007 to October 2007. The genotypes were grouped into five clusters. The highest intra cluster distance was noticed for the cluster IIi (0.999) and the lowest for the cluster IV (0.439). The highest inter-cluster distance was observed between cluster IV and V (7.163) whereas the lowest was observed between cluster I and IV (2.258).

Khan *et al.* (2008) assessed the genetic diversity among 64 pointed gourd genotypes through multivariate analysis from an experiment conducted in Regional Agricultural Research Station, Ishurdi, Pabna during the growing season 2002-2003. The genotypes were grouped into twelve clusters. The cluster V consisted of highest number of genotypes and it was nine, the cluster VI and cluster VIII contained the lowest number of genotypes and it was two in each. The clustering pattern of the genotypes under this study revealed that the genotypes collected from the same location were grouped into different clusters. The genotypes of Jessore were distributed in different clusters. The highest inter genotype distance as 366.3 observed between the genotypes P0022 and P0007 and the lowest 2.6 as observed between the genotypes P0043 and P0044. Cluster V had the highest cluster mean value for internodes length, fruit weight per plant and yield the highest inter-cluster distance was noticed between cluster III and 11 (45.71) and the lowest between cluster VII acid Y VI (3.33). The highest intra cluster distance was computed for cluster III and that was lowest for the cluster II. The first five axes accounted for 77.65% of the total variation among the 13 characters describing 64 pointed gourd genotypes. Fruit weight, seeds per fruit and fruit weight per plant contributed maximum to the total divergence.

Kabir (2007) reported that genetic divergence studied 24 accessions of pointed gourd. The accessions were grouped into five clusters. The cluster I and III had the highest number of accessions (6) followed by cluster V (5), cluster 11 (4) & Cluster IV (3).The highest intra cluster distance was computed for cluster IV (35.80) followed by cluster I (28.12) and Cluster V (26.63). The minimum intra cluster distance was found in III (18.87).

Bharathi *et al.* (2005) studied genetic divergence among 32 genotypes of spine gourd (*Momordica dioica*) for 12 traits (vine length, number of days to flowering, node on which the first flower appeared, internode length, mature leaf size, pedicel length, petiole length, fruit weight, fruit length, fruit girth, number of fruits per plant, and yield per plant) was evaluated in Orissa, India. The analysis of variance revealed significant variation among the genotypes for all traits. The genotypes were grouped into 7 clusters based on D2 values. Cluster III had the highest number of genotypes (11), followed by clusters IV (9) and VI (4). The intracluster distance ranged from 30.34 (cluster I) to 371.56 (cluster III). The intercluster distance was greatest between clusters VI and VII (864.75). Genotypes included in cluster II were characterized by early flowering, and presence of the longest vines and internodes. Cluster VI recorded the greatest number of fruits, pedicel length and yield. Cluster VII was superior with regard to the node on which the first flower appeared. Cluster III had the greatest fruit weight, fruit length and fruit girth. Yield per plant, number of fruits, fruit weight, internode length, fruit length and pedicel length accounted for 93.55% of the diversity. Thus, selection for divergent parents based on these traits is recommended.

Genetic divergence using Mahalanobis D^2 statistics was studied for seven quantitative characters including yield per vine in a collection of twenty diverse cultivars of bottle gourd by Badade *et al.* (2001). The cultivars differed significantly for almost all of the characters and were grouped into 10 clusters based on the similarities of D^2 value. Considerable diversity within and between clusters was noted and it was observed for the characters viz. vine -length, number of branches, fruit per vine, length and diameter of fruit and yield per vine.

Karuppaiah *et al.* (2005) evaluated genetic divergence in 12 genotypes of bitter gourd *(Momordica charantia)* grown in Annamalai, Tamil Nadu, India, during JuneJuly 2001. Using Mahalanobis D^2 technique, the genotypes were grouped into clusters I (4 genotypes), II (one genotype), III (3 genotypes) and IV (four genotypes). Among the four clusters, cluster IV (LA-7, LA-9, LA-10 and LA-12) registered the highest mean values for vine length (6.2 m), number of male flowers per plant (79.3), number of female flowers per plant (23.2), yield per plant (5.2 kg), single fruit weight (242.2 g), fruit length (29.4 cm), number of fruits per plant (24.1), number of seeds per fruit (52.3), fruit size index (173.2). and 100-seed weight (18.6 g). Hence, it is desirable to involve LA-7, LA-9, La-10 and LA- 12 of cluster IV in breeding programmes.

Harshawardhan and Ram (2003) conducted an experiment on severity germplasms of musk melon lines to elucidate genetic divergence using a non-hierarchical Euciden cluster analysis for yield and its components. The genotypes were grouped into 11 clusters irrespective of geographic and genetic diversity. Group VIII contained the largest number of 11 genotypes. The maximum genetic distance occurred between cluster II and X.

Islam (2004) estimated genetic divergence among 42 bottle gourd (L. siceraria) accessions from Bangladesh was estimated in Japan during 2000 using D2 and canonical analysis. The accessions were grouped into five clusters. No clear relationship was observed between geographic origin and genetic diversity. The maximum intercluster distance was between cluster I and cluster II, and the minimum was between cluster III and cluster IV. Primary branches per plant, fruit length and weight, number of fruits and yield per plant contributed the most to the total genetic divergence. The results obtained by D2 analysis were also confirmed by canonical analysis. The accessions included in the most divergent clusters I and II, are promising parents for a hybridization programme for obtaining high heterosis and, thus, better segregants in bottle gourd.

Dora (2001) studied eleven genotypes of *Trihosanthes dioica* and the genotypes were grouped into four clusters based on Mahalanobis's D^2 statistics and found that intercluster distances were greater than intra cluster distances, indicating considerable genetic diversity among genotypes. The highest D^2 value (984.3) was recorded between cluster II and IV.

Masud *et al.* (1995) carried out an experiment to study the genetic divergence among 27 genotypes of pumpkin *(Cucurbita moschata)* collected from eight districts of Bangladesh was group into seven cluster. No relationship was found between genetic divergence and geographic distribution of the genotypes. Maximum inter cluster distance was observed between cluster II and VII and was minimum between V and VI. Number of fruits per plant and yield per plant showed maximum contribution to the total divergence. The results obtained by D^2 analysis were confirmed by principal component analysis.

Chapter 3

Materials and methods

CHAPTER III

MATERIALS AND METHODS

The investigation was carried out at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh during the period from March 2010 to August 2010 to study on the genetic diversity, correlation and path analysis in wax gourd. A brief description about the locations of the experimental site, characteristics of soil, climate, materials, layout and design of the experiment, land preparation, manuring and fertilizing, transplanting of seedlings, intercultural operations, harvesting, data recording procedure, economic and statistical analysis etc., which are presented as follows:

3.1. Experimental site

The research work was conducted at the Sher-e-Bangla Agricultural University Farm, Dhaka-1207 during March 2010 to August 2010.

3.2 Geographical Location

The experimental area was situated at 23°77'N latitude and 90°33'E longitude at an altitude of 8.6 meter above the sea level (Anon., 2004). The experimental field belongs to the Agro-ecological zone of "The Modhupur Tract, AEZ-28 (Anon., 1988). This was a region of complex relief and soils developed over the Modhupur clay, where floodplain sediments buried the dissected edges of the Modhupur Tract leaving small hillocks of red soils as `islands' surrounded by floodplain. The experimental site was shown in the map of AEZ of Bangladesh in (Appendix I).

3.3 Climate

Area has subtropical climate, characterized by high temperature, high relative humidity and heavy rainfall in Kharif season (March-August) and scanty rainfall associated with moderately low temperature during the Kharif season

(March-August). Meteorological information regarding temperature, relative humidity, rainfall and sunshine hours prevailed at the experimental site during the study period was presented in Appendix II.

3.4 Characteristics of soil

Soil of the experimental site belongs to the general soil type, Shallow Red Brown Terrace Soils under Tejgaon Series. Top soils were clay loam in texture, olive-gray with common fine to medium distinct dark yellowish brown mottles. Soil pH ranged from 6.0- 6.6 and had organic matter 0.84%. Experimental area was flat having available irrigation and drainage system and above flood level. Soil samples from 0-15 cm depths were collected from experimental field. The analyses were done by Soil Resource and Development Institute (SRDI), Dhaka. Physicochemical properties of the soil are presented in (Appendix III).

3.5 Planting materials

Twenty seven genotypes of wax gourd were used for the present research work. The purity and germination percentage were leveled as around 100 and 80, respectively. The genetically pure and physically healthy seeds of these genotypes were collected from Plant Genetic Resources Centre (PGRC) of Bangladesh Agricultural Research Institute (BARI) Gazipur. The name and origin of these genotypes are presented in (Table 1).

3.6 Design and layout of the experiment

The experiment was laid out Randomized Complete Block Design (RCBD) with three replications. The genotypes were distributed into the pit of each block of the prepared layout of the experiment. The twenty seven genotypes of the experiment were assigned at random into pits of each replication. The distance maintained spacing pit to pit 3 m. The distance maintained between two blocks was 1 m.

Table 1. Name and origin of Twenty seven Wax gourd genotypes used in the present study

SL No.	Genotype No.	BARI ACC Number	Origin
1	G_1	BD-319	PGRC,BARI
2	G_2	BD-320	PGRC, BARI
3	G_3	BD-321	PGRC, BARI
4	G_4	BD-322	PGRC, BARI
5	G_5	BD-323	PGRC, BARI
6	G_6	BD-324	PGRC, BARI
7	G_7	BD-325	PGRC, BARI
8	G_8	BD-328	PGRC, BARI
9	G_9	BD-329	PGRC, BARI
10	G_{10}	BD-333	PGRC, BARI
11	G_{11}	BD-337	PGRC, BARI
12	G_{12}	BD-338	PGRC, BARI
13	G_{13}	BD-340	PGRC, BARI
14	G_{14}	BD-342	PGRC, BARI
15	G_{15}	BD-348	PGRC, BARI
16	G_{16}	BD-349	PGRC, BARI
17	G_{17}	BD-354	PGRC, BARI
18	G_{18}	BD-358	PGRC, BARI
19	G_{19}	BD-361	PGRC, BARI
20	G_{20}	BD-364	PGRC, BARI
21	G_{21}	BD-368	PGRC, BARI
22	G_{22}	BD-370	PGRC, BARI
23	G_{23}	BD-374	PGRC, BARI
24	G_{24}	BD-2406	PGRC, BARI
25	G_{25}	BD-2412	PGRC, BARI
26	G_{26}	BARI chalkumra-1	PGRC, BARI
27	G_{27}	Local	PGRC, BARI

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

3.7 Poly bag preparation and raising seedling

Due to uncertain rainfall during the period of the study, the seeds were dibbled in Poly bag for higher germination percentage and to get healthy seedlings and when the seedlings become 20 days old; those were transplanted in the main field in the pit. Seeds were sown 10 March, 2010 before sowing seeds were treated with Bavistin for 5 minutes.

3.8 Land preparation

The experiment plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about good tilth in the first week of March, 2010. Weeds and other stables were removed carefully from the experimental plot and leveled properly.

3.9 Pit preparation

After final land preparation, pits of 55 cm x 55 cm x 45 cm were prepared in each block with spacing of 3 m x 1 m. Pits were kept open in the sun for 7 days to kill harmful insect and microorganisms. To control field cricket 5 mg Furadan was also mixed with the soils of each pit before making it ready for dibbling.

3.10 Manure and fertilizers application

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

3.11 Transplanting of seedlings

Within 12 days germination of seeds was completed and the seedlings of different accessions were planted in the pit on 4 April, 2010. In each pit two seedlings were planted and the soil around the plant was firmly pressed by hand.

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

SL No.	Fertilizer/Manure	Dose
1.	Cowdung	10 ton/ha
2.	Urea	125 kg/ha
3.	TSP	125 kg/ha
4.	MOP	150 kg/ha
5.	Gypsum	75 kg/ha
6.	Zinc Oxide	10 kg/ha

3.12 Intercultural operations

The following intercultural operations were done from time to time throughout the cropping season for proper growth and development of the plants.

3.12.1 Thinning and gap filling

Only one healthy seedling was kept per pit for the proper development and avoid crowd environment. For this whatever its need thinning and gap filling was done.

3.12.2 Weeding and mulching

Several weeding and mulching were done as per requirement. At the very first stage, weeding was done for ease of aeration and less competition seedling growth and mulch was provided after an irrigation to prevent crust formation and facilitate good aeration.

3.12.3 Irrigation and after-care

In the early stage irrigation was done twice daily by water cane. In mature stage flood irrigation was done whenever it is necessary.

3.12.4 Pesticide application

At the seedling stage red pumpkin beetle attacked tender leaves for this Malathion and Ripcord was sprayed in the field. In mature stage cucurbit fruit fly caused severe damage to the fruit. For a protection from fruit fly, MSGT, (Mashed Sweet Gourd Trap) and Pheromone bait was used along with ripcord, sevin powders.

3.13 Harvesting

The fruit takes about 7-10 days from setting to reach marketable stage. Fruits were picked on the basis of horticultural maturity, size, color and age being determined for the purpose of consumption as the fruit grew rapidly and soon get beyond the marketable stage, frequent picking was done throughout the harvesting period. Fruits were picked with sharp knife and care was taken to avoid injury of the vine.

3.14 Data recording

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

3.14.1 Plant characteristics

3.14.1.1 Leaf length (cm)

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

3.14.1.2 Leaf Breadth (cm)

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

3.14.1.3 Internode distance (cm)

Internode distance was measured in each germplasm in cm and average data was recorded.

3.14.2 Inflorescences characteristics

3.14.2.1 Days to first male flowering

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

3.14.2.2 Days to first female flowering

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

3.14.2.3 Pedicel length of Male flower (cm)

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

3.14.2.4 Pedicel length of Female flower (cm)

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

3.14.2.5 Number of male flower

The number of male flower per plant was counted and average data was recorded.

3.14.2.6 Number of female flower

The number of female flower per plant was counted and average data was recorded.

3.14.3 Fruit characteristics

3.14.3.1 Fruit length (cm)

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

3.14.3.2 Fruit breadth (cm)

Fruit diameter was measured in each germplasm in cm during fruit harvest for vegetable use.

3.14.3.3 Fruit weight (kg)

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

3.14.3.4 Fruit yield per plant (Kg)

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

3.15.1 Statistical analysis

Mean data of the characters were subjected to multivariate analysis. Univariate analysis of the individual character was done for all characters under study using the mean values (Singh and Chaudhury, 1985) and was estimated using MSTAT-C computer programme. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV %) were also estimated using MSTAT-C. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2000 software through four techniques viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA).

3.15.1.1 Estimation of genotypic and phenotypic variances

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

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

Where,

GMS = Genotypic mean sum of squares

EMS = Error mean sum of square

r = number of replications

Phenotypic variance (σ^2 ph) = σ^2_g + EMS

Where,

σ^2_g = Genotypic variance

EMS = Error mean sum of square

3.15.1.2 Estimation of genotypic and phenotypic correlation co-efficient

For calculating the genotypic and phenotypic correlation co-efficient for all possible combinations the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956) were adopted. The genotypic co-variance component between two traits and have the phenotypic covariance component were derived in the same way as for the corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows:

Genotypic correlation (r_{gxy}) = $\dfrac{\sigma_{gxy}}{\sqrt{\sigma^2_{gx}\ \sigma^2_{gy}}}$

Where,

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

σ^2_{gx} =Genotypic variance of the trait x

σ^2_{gy} =Genotypic variance of the trait y

Phenotypic correlation (r_{pxy}) = $\dfrac{\sigma_{pxy}}{\sqrt{\sigma^2_{px}\ \sigma^2_{py}}}$

Where,

σ_{pxy} =Phenotypic covariance between the traits x and y

σ^2_{px} =Phenotypic variance of the trait x

σ^2_{py} =Phenotypic variance of the trait y

3.15.1.3 Estimation of genotypic and phenotypic co-efficient of variation

Genotypic and phenotypic co-efficient of variation were calculated by the formula suggested by Burton (1952)

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

Where,

σ^2_g = Genotypic variance

x = Population mean similarly,

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

Phenotypic co-efficient variation (PCV) = $\sqrt{\dfrac{\sigma^2_{ph}}{\bar{x}}} \times 100$

Where,

σ^2_{ph} = Phenotypic variance

$\overline{x}$ = Population mean

3.15.1.4 Estimation of heritability

Broad sense heritability was estimated (Lush, 1943) by the following formula, suggested by Johnson *et al.* (1955):

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

Where,

$h^2 b$ = Heritability in broad sense

$\sigma^2{}_g$ = Genotypic variance

$\sigma^2{}_{ph}$ =Phenotypic variance

3.15.1.5 Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1943) and Johnson *et al.* (1955).

Genetic advance (GA) = K. h^2 b. σ_{ph}

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

Where,

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

σ_{ph} = Phenotypic standard deviation

$h^2 b$ = Heritability in broad sense

$\sigma^2{}_g$ = Genotypic variance

$\sigma^2{}_{ph}$ = Phenotypic variance

3.15.1.6 Estimation of genetic advance mean's percentage

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

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

3.14.1.7 Estimation of path co-efficient

Path coefficient analysis was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985), using phenotypic correlation coefficient valuers. In path analysis, correlation coefficients between yield and yield contributing characters were partitioned into direct and indirect effects of yield contributing characters on grain yield per hectare. In order to estimate direct and indirect effects of the correlated characters, i. e. 1, 2, 3……………….and 13 on yield y, a set of simultaneous equations (eight equations in this example) is required to be formulated as shown below:

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

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

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

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

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

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

$$r_{7.y} = r_{1.7}\,P1.y + r_{2.7}\,P_{2.y} + r_{3.7}\,P_{3.y} + r_{4.7}\,P_{4.y} + r_{5.7}\,P_{5.y} + r_{6.7}\,P_{6.y} + P_{7.y} + r_{7.8}\,P_{8.y} + r_{7.9}\,P_{9.y} + r_{7.10}\,P_{10.y} + r_{7.11}\,P_{11.y} + r_{7.12}\,P_{12.y}$$

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

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

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

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

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

Where,

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

P_{iy} = Path coefficient due to i th character (i= 1, 2, 3,……….,13)

1 = Days to first male flowering

2 = Days to first female flowering

3 = Leaf length (cm)

4 = Leaf breadth (cm)

5 = Internode distance (cm)

6 = Pedicel length of male flower (cm)

7 = Pedicel length of female flower (cm)

8 = Number of male flower per plant

9 = Number of female flower per plant

10 = Fruit weight (kg)

11 = Fruit length (cm)

12 = Fruit breadth (cm)

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

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

$r_{1.2} P_{2.y}$ = indirect effect of 1 via 2 on y

$r_{1.3} P_{3.y}$ = indirect effect of 1 via 3 on y

$r_{1.4} P_{4.y}$ = indirect effect of 1 via 4 on y

$r_{1.5} P_{5.y}$ = indirect effect of 1 via 5 on y

$r_{1.6} P_{6.y}$ = indirect effect of 1 via 6 on y

$r_{1.7} P_{7.y}$ = indirect effect of 1 via 7 on y

$r_{1.8} P_{8.y}$ = indirect effect of 1 via 8 on y

$r_{1.9} P_{9.y}$ = indirect effect of 1 via 9 on y

$r_{1.10} P_{10.y}$ = indirect effect of 1 via 10 on y

$r_{1.11} P_{11.y}$ = indirect effect of 1 via 11 on y

$r_{1.12} P_{12.y}$ = indirect effect of 1 via 12 on y

Where,

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

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

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

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

Where,

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

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

$P_{1.y}$ = Direct effect of the i th character on yield y.

$r_{1.y}$ = Correlation of the i th character with yield y.

3.15.2 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance (D^2) statistic and its auxiliary analyses. The parents selection in hybridization programme based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) suggested that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a hybridization programme. Multivariate analysis viz. Principal Component analysis, Principal Coordinate analysis, Cluster analysis and Canonical Vector analysis (CVA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

3.15.2.1 Principal Component analysis (PCA)

Principal Component analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, Principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity. Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.15.2.2 Principal Coordinate analysis (PCO)

Principal Coordinate analysis is equivalent to PCA but it is used to calculate inter unit distances. Through the use of all dimension of p it gives the minimum distance between each pair of the n points using similarity matrix (Digby *et al.*, 1989).

3.15.2.3 Cluster analysis (CA)

Cluster analysis divides the genotypes of a data set into some number of mutually exclusive groups. Clustering was done using non-hierarchical classification. In Genstat, the algorithm is used to search for optimal values of chosen criterion proceeds as follows. Starting from some initial classification of the genotypes into required number of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

3.15.2.4 Canonical Vector analysis (CVA)

Canonical vector analysis (CVA) finds linear combination of original variabilities that maximize the ratio of between group to within group variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing of the ratio of among groups to the within group variations. The canonical vector are based upon the roots and vectors of WB, where W is the pooled within groups covariance matrix and B is the among groups covariance matrix.

3.15.2.5 Calculation of D^2 values

The Mahalanobis's distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952), and Singh and Chaudhury (1985). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statistic is defined by the formula

$$D^2 = \sum_{i}^{x} d_i^2 = \sum_{i}^{x} (Y_i^j - Y_j^k)^2 \qquad (j \neq k)$$

Where,

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

x = Number of characters.

3.15.2.6 Computation of average intra-cluster distances

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

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

Where,

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

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

3.15.2.7 Computation of average inter-cluster distances

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

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

Where,

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

n_i= Number of populations in cluster i.

n_j = Number of populations in cluster j.

3.15.2.8 Cluster diagram

Using the values of intra and inter-cluster distances $(D = \sqrt{D^2})$, a cluster diagram was drawn as suggested by Singh and Chuadhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

3.15.2.9 Selection of varieties for future hybridization programme

Divergence analysis is usually performed to identify the diverse genotypes for hybridization purposes. The genotypes grouped together are less divergent among themselves than those, which fall into different clusters. Clusters separated by largest statistical distance (D^2) express the maximum divergence among the genotypes included into these different clusters. Variety (s) or line(s) were selected for efficient hybridization programme according to Singh and Chuadhury (1985). According to them the following points should be considered while selecting genotypes for hybridization programme:

i. Choice of cluster from which genotypes are selected for use as parent(s)
ii. Selection of particular genotype(s) from the selected cluster(s)
iii. Relative contribution of the characters to the total divergence
iv. Other important characters of the genotypes performance

Chapter 4

Results and Discussion

CHAPTER IV

RESULTS AND DISCUSSION

The results obtained from the study are presented and discussed in this chapter. The data pertaining to wax gourd genotypes as well as yield and its contributing characters were computed and statistically analyzed and the results thus obtained are discussed below under the following heads:

1. Genetic parameters
2. Correlation co efficient
3. Path co-efficient analysis
4. Multivariate analysis

4.1 GENETIC PARAMETERS

The analysis of variances indicated that the existence of highly significant variation among the genotypes studied. The mean sum of square, mean, range, variance components, genotypic and phenotypic coefficients of variations, heritability; genetic advance and genetic advance in percent of mean (GAPM) are presented in (Table 3).

The results are discussed character wise as follows:

4.1.1 Days to first male flowering

Significant variations were observed among all genotypes (221.94) studied for this character (Table 3). The mean performance of days to first male flowering indicated that the maximum duration (59.00days) to first flowering was produced by BD-340 and that of minimum (33.33days) by BD-364 with mean value 45.89days (Appendix IV). Highest genotypic and phenotypic variance was observed 72.41 and 77.12 respectively for days to first male flowering with large environmental influence and different between the genotypic co-efficient of variation (18.54) and phenotypic co-efficient of variation (19.14) indicating existence of less variation among the genotypes. Heritability for this trait was estimated very high (93.90%) and genetic advance (16.99) and genetic advance in percent of mean (37.02) were found high, indicated that the additive gene effect.

Table 3 Estimation of genetic parameters in thirteen characters of 27 genotypes in wax gourds

Parameters	Range	Mean	MSG	σ^2 p	σ^2g	σ^2 e
Days to first male flowering	33.33-59.00	45.89	221.94**	77.12	72.41	4.71
Days to first female flowering	53.67-79.67	66.41	169.80**	60.61	54.60	6.01
Leaf length (cm)	9.07-14.65	12.98	4.70*	3.17	0.77	2.40
Leaf breadth (cm)	12.92-19.98	16.96	8.31*	5.58	1.37	4.22
Internode distance (cm)	8.27-12.53	10.35	3.63**	1.51	1.06	0.44
Pedicel length of female flower (cm)	6.00-14.27	9.47	16.71**	5.67	5.53	0.14
Pedicel length of female flower (cm)	3.67-9.33	5.56	7.11**	2.41	2.35	0.06
Number of male flower per plant	11.00-48.33	24.56	324.50**	164.29	80.11	84.19
Number of female flower per plant	2.40-8.86	5.17	10.65**	4.84	2.91	1.93
Fruit weight (kg)	0.50-1.63	0.98	0.22**	0.10	0.06	0.04
Fruit length (cm)	19.55-32.53	23.76	18.71**	8.42	5.14	3.28
Fruit breadth (cm)	24.53-38.24	31.53	37.10**	15.93	10.59	5.35
Fruit yield per plant (kg)	0.50-3.18	1.75	1.72**	0.70	0.51	0.19

*** Signaficant at the 0.05 level** *** * Signaficant at the 0.01 level**

MS = mean sum of square, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance and σ^2 e = Environmental variance.

Table 3 Continued.

Parameters	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)	CV (%)	SE
Days to first male flowering	19.14	18.54	4.73	93.90	16.99	37.02	4.73	0.97
Days to first female flowering	11.72	11.13	3.69	90.09	14.45	21.76	3.69	0.85
Leaf length (cm)	13.71	6.76	11.93	24.31	0.89	6.87	11.93	0.26
Leaf breadth (cm)	13.93	6.89	12.11	24.47	1.19	7.02	12.11	0.34
Internode distance (cm)	11.87	9.97	6.44	70.56	1.79	17.25	6.44	0.13
Pedicel length of male flower (cm)	25.15	24.84	3.94	97.55	4.78	50.51	3.94	0.26
Pedicel length of female flower(cm)	27.92	27.56	4.45	97.46	3.12	56.08	4.45	0.17
Number of male flower per plant	52.19	36.44	37.36	48.76	12.87	52.42	37.36	1.70
Number of female flower per plant	42.56	32.97	26.91	60.03	2.72	52.62	26.91	0.30
Fruit weight (g)	31.95	25.33	19.47	62.87	0.41	41.57	19.47	0.03
Fruit length (cm)	12.21	9.55	7.62	61.09	3.65	15.37	7.62	0.34
Fruit breadth (cm)	12.66	10.32	7.33	66.45	5.46	17.33	7.33	0.49
Fruit yield per plant (kg)	47.70	40.81	24.70	73.19	1.26	72.10	24.70	0.18

PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation, CV% = Coefficient of variation and SE = standard error.

Mathew and Khader (1999) also observed high heritability for this trait in snake gourd. Singh *et al.* (2002) also found phenotypic co-efficient of variation higher than genotypic co-efficient of variation in respect to days to first male flower opening in cucumber. Husna (2009) estimated heritability for this trait was very high (90.20%) and genetic advance (15.70) and genetic advance in percent of mean (80.46) were found high revealed that the character is governed by additive gene.

4.1.2 Days to first female flowering

Days to first female flowering showed significant variation among genotype mean square (169.80). The maximum duration (79.67days) to first flowering was produced by BD-340 and that of minimum (53.67days) by BD-358 with mean value 66.41days (Appendix IV). The genotypic variance and phenotypic variance for this trait were 54.60 and 60.61 respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation (11.13) and phenotypic co-efficient of variation (11.72) were respectively (Table 3). Heritability for this trait was estimated very high (90.09%) and genetic advance (14.45) was high and genetic advance in percent of mean (21.76) was high, revealed that the character is governed by additive gene. Miah *et al.* (2000) and Yadav *et al.* (2009) estimated high GCV and PCV for days to first female flowering.

4.1.3 Leaf length (cm)

Mean sum of square for leaf length was 4.70 which was highly significant due to genotypes in wax gourd (Table 3) indicating existence of considerable difference for this trait. The maximum leaf length was found 14.65cm in BD-319 and the minimum was recorded 9.07cm in BD-2406 with mean value 12.98cm (Appendix IV). The phenotypic variance (3.17) appeared to be higher than the genotypic variance (0.77) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation (6.76) and phenotypic co-efficient of variation (13.71) were close to each other. Heritability (24.31) estimates for this trait was high, genotypic advance (0.89) and genotypic advance in percent of mean (6.87) were found low indicating this trait was governed by the non-additive gene. Husna (2009) found that the genotypic variance (14.18) was appeared to be higher than the genotypic variance (14.14) in bottle gourd. The GCV (22.63) and PCV (22.67) were close to each other. Heritability (99.69%) estimates for this trait was very high, genetic advance (9.91) and genetic advance in percent of mean (59.65) were found moderately high indicating this trait was governed by the additive gene. Gaffar (2008) found high heritability and moderate genetic advance for this trait in sponge gourd. Photograph showing variation of leaf length among different genotypes of wax gourd in Plate 1a and 1b.

4.1.4 Leaf breadth (cm)

Significant mean sum of square for leaf breadth (8.31) indicated considerable variation among the genotype studied (Table 3). The maximum leaf breadth was found 19.98cm in BD-354 and the minimum was recorded 12.92cm in BD-2406 with mean value 16.96cm (Appendix IV). The genotypic variance and phenotypic variance were 1.37 and 5.48 respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this character. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 6.89 and 13.93 respectively. Heritability (24.47%) estimates for this trait was moderately high, genotypic advance (1.19) was low and genotypic advance in percent of mean (7.02) was found low, indicated that this character was governed by non-additive gene. Husna (2009) found GCV (22.87) was lower than PCV (23.04) for this character in bottle gourd. Gaffar (2008) observed heritability in broad sense was high (94%) with moderate genetic advance (7.81) for this character in sponge gourd and also found the similar GCV (20.95%) and PCV (23.31%) in sponge gourd. Photograph showing variation of leaf breadth among different genotypes of wax gourd in Plate 1a and 1 b.

4.1.5 Internodes distance (cm)

Mean sum of square for internodes distance was significant (3.63) due to genotypes in wax gourd (Table 3) indicating existence of considerable differences for this trait. The maximum internodes distance was found 12.53cm in BD-329 and the minimum was recorded 8.27cm in BD-324 with mean value 10.35cm (Appendix IV). The differences in magnitudes in between genotypic (1.06) and phenotypic (1.51) variances was relatively

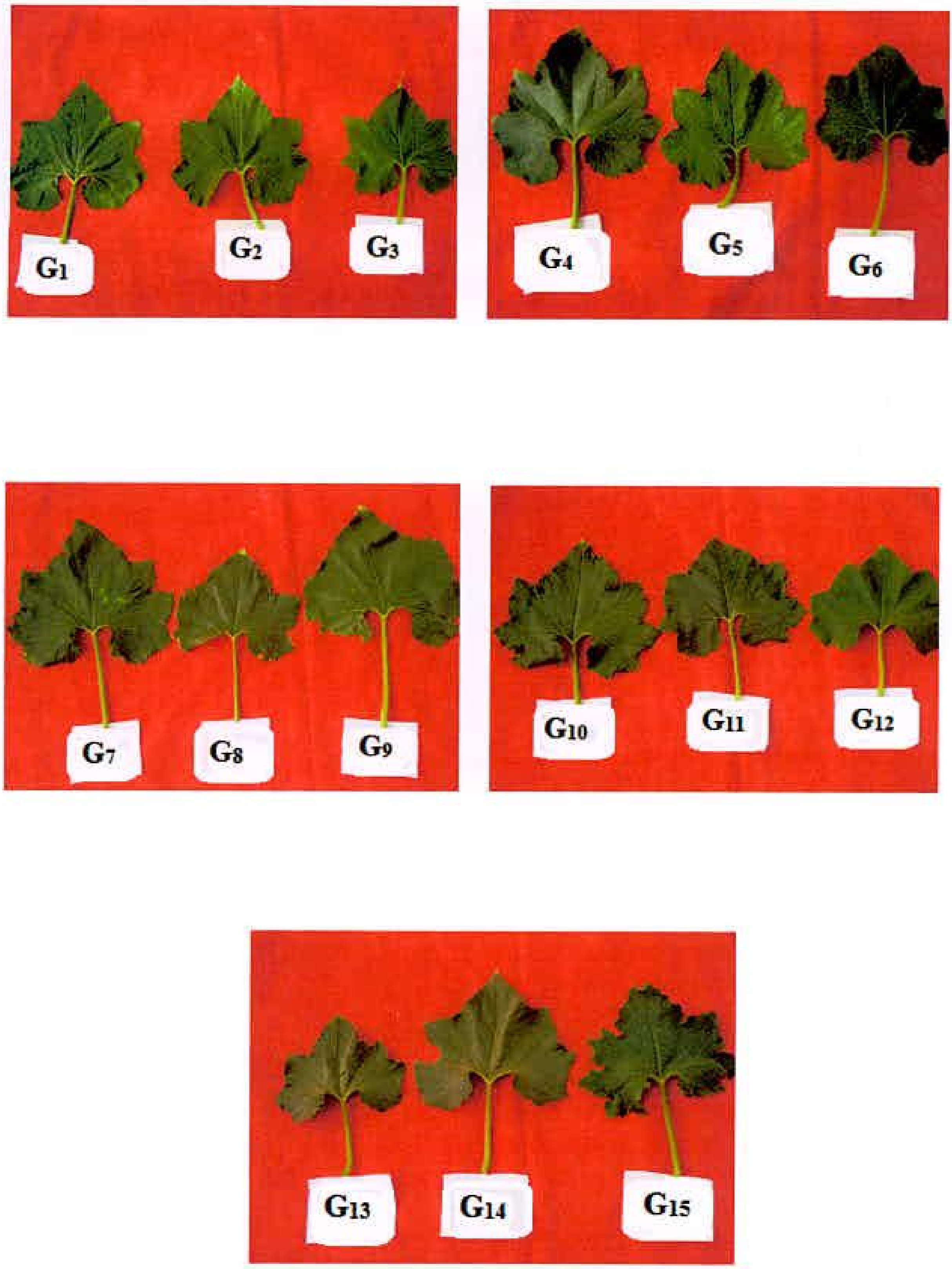

Plate 1a. Showing variation in leaf among different wax gourd genotypes (G_1-G_{15})

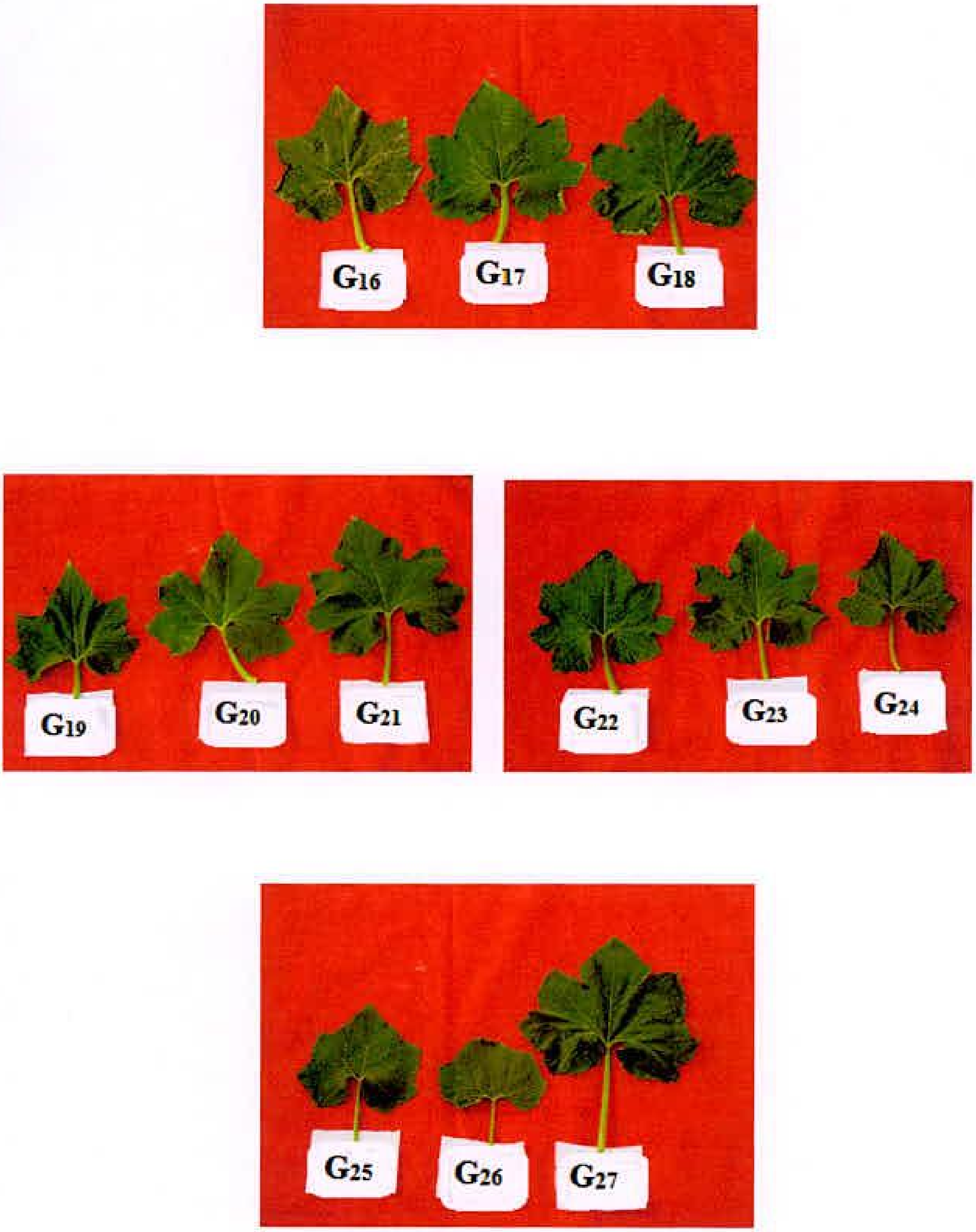

Plate 1b. Showing variation in leaf among different wax gourd genotypes (G_{16}- G_{27})

low for the internodes distance indicating less environmental influence on these characters. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 9.97 and 11.87 respectively. Heritability (70.56%) estimates for this trait was high, genotypic advance (1.79) and genotypic advance in percent of mean (17.25) were found moderately low, revealed that character was controlled by non-additive gene. Gaffar (2008) found high heritability (94%) and genetic advance for this trait in sponge gourd. Photograph showing variation of twig among different genotypes of wax gourd in Plate 1c.

4.1.6 Male flower pedicel length (cm)

Mean sum of square for male flower pedicel length was significant due to genotypes in wax gourd (Table 3) indicating existence of considerable difference for this trait. The maximum male flowers pedicel length was found 14.27cm in BD-364 and the minimum was recorded 6.00cm in BD-374 with mean value 9.47cm (Appendix IV). The genotypic variance was 5.53 and phenotypic variance was 5.67. The difference between genotypic co-efficient of variation (24.84) and phenotypic co-efficient of variation (25.15) was minimum. Heritability (97.55%) estimates for this trait was very high, genotypic advance (4.78) was low and genotypic advance in percent of mean (50.51) was found high. Indicating, this character was governed by additive gene effects. Husna (2009) found high heritability (99.55%) and genetic advance for this trait in bottle gourd . Photograph showing variation of male and female flower among some genotypes of wax gourd in Plate 2a and 2b.

4.1.7 Female flower pedicel length (cm)

Mean sum of square for female flower pedicel length was significant (7.11) due to genotypes in wax gourd (Table 3) indicating the existence of considerable variation for this trait. The maximum female flowers pedicel length was found 9.33cm in BD-354 and the minimum was recorded 3.67cm in BD-368 with mean value 5.56cm (Appendix IV). The genotypic variance and phenotypic variance for this trait were 2.35 and 2.41 respectively with minimum differences between

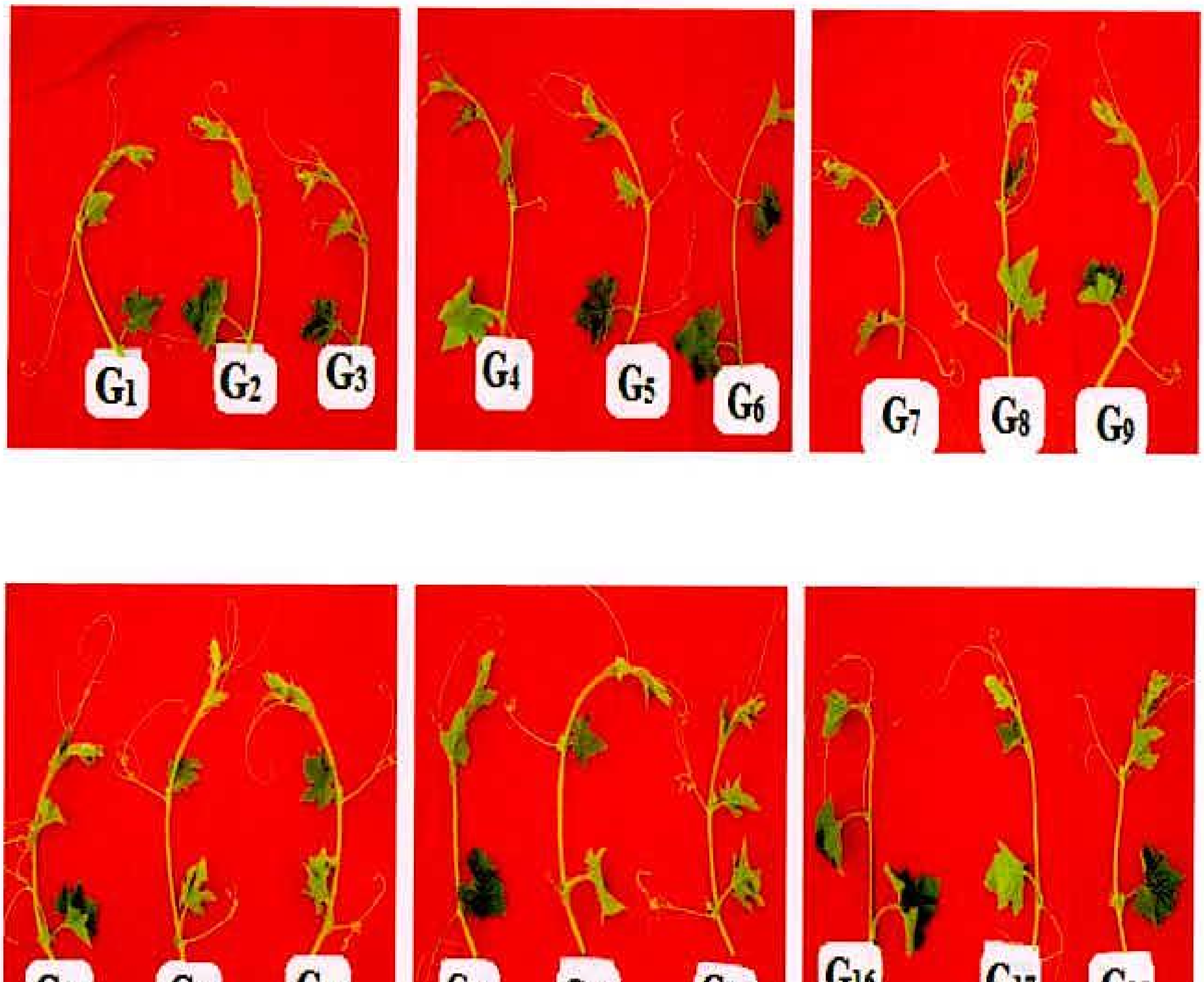

Plate 1c. Showing variation in twig among different Wax gourd genotypes

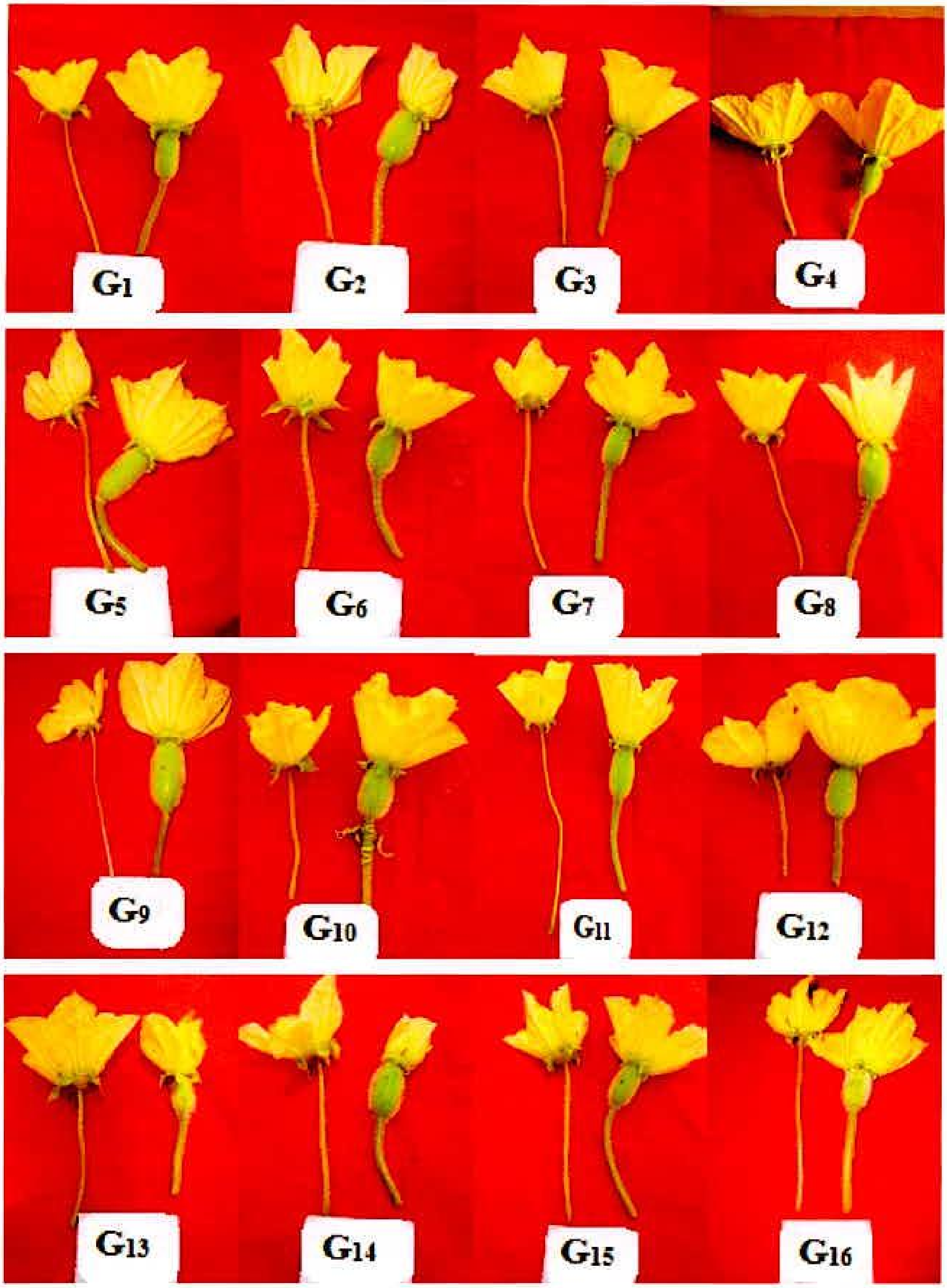

Plate 2a. Showing phenotypic variation in male and female flower among different genotypes of Wax gourd (G_1- G_{16})

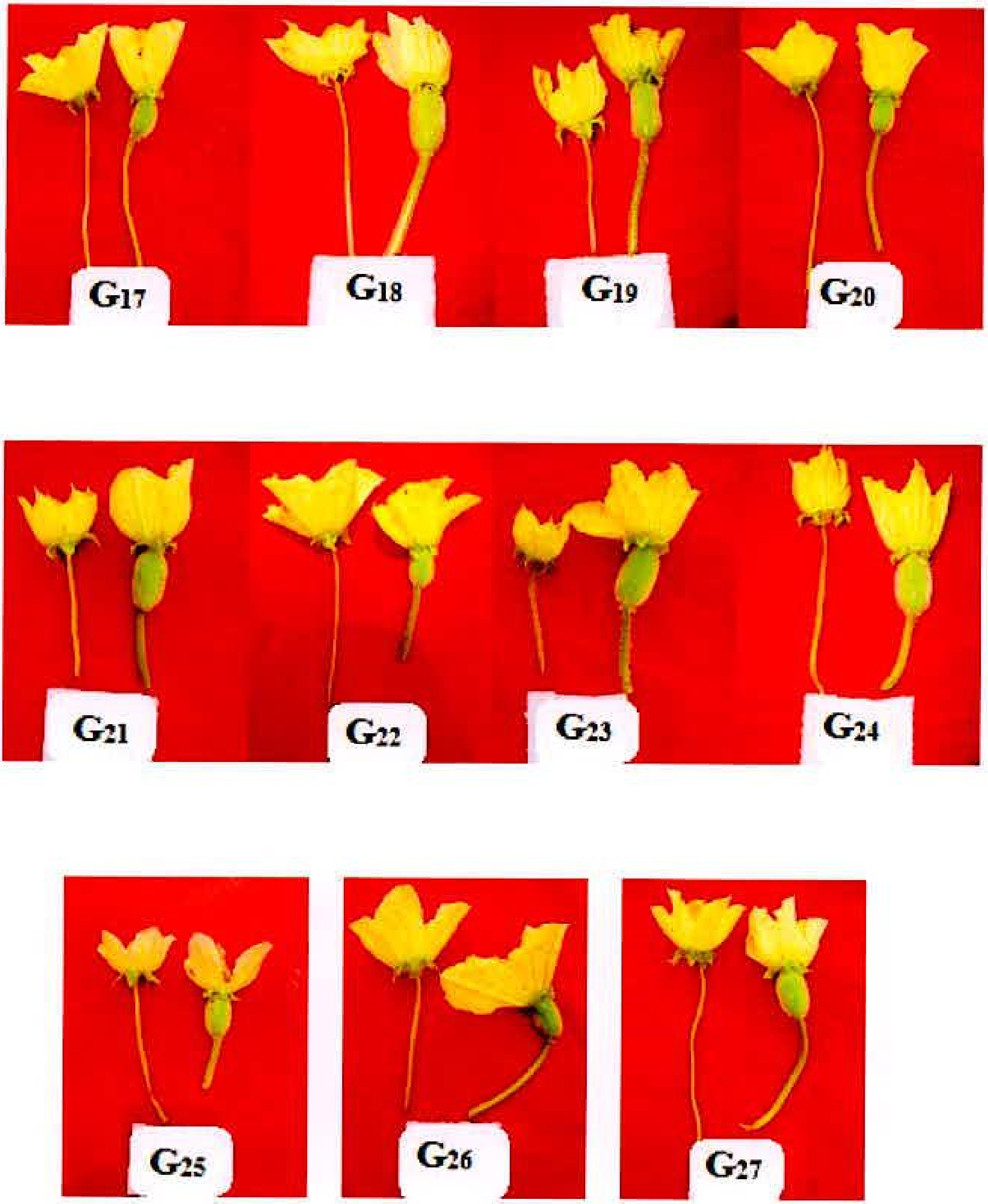

Plate 2b. Showing phenotypic variation in male and female flower among different genotypes of Wax gourd (G_{17}- G_{27})

them. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this character. The difference between phenotypic co-efficient of variation (27.92) and genotypic co-efficient of variation (27.56) was minimum in case of female flowers pedicel length. Heritability (97.46%) estimates for this trait was high, genotypic advance (3.12) was low and genotypic advance in percent of mean (56.08) was found moderately high, indicated that this character was controlled by additive gene effects. Husna (2009) found that in female flower pedicel length.

4.1.8 Number of male flower

Significant mean sum of square (324.50) for number of male flower indicated considerable variation among the genotypes studied (Table 3). The maximum number of male flower was found (48.33) in BD-325 and the minimum was recorded (11.00) in BD-323 with mean value 24.56 (Appendix IV). The phenotypic variance (164.29) appeared to be higher than the genotypic variance (80.11) suggested considerable influence of environment on the expression of the genes controlling this character. The genotypic co-efficient of variation was 36.44 and phenotypic co-efficient of variation was 52.19. Heritability (48.76%) estimates for this trait was high, genotypic advance (12.87) was moderately high and genotypic advance in percent of mean (52.42) was found high, indicated that the trait was governed by additive gene. Singh *et al.* (2002) also estimated high GCV and PCV for male flowers per plant in ridge gourd. Husna (2009) found genotypic co-efficient of variation was 31.86 and phenotypic co-efficient of variation was 31.95. Heritability (99.40%) estimates for this trait was very high, genotypic advance (4.47) was moderately high and genotypic advance in percent of mean (83.86) was found high in bottle gourd.

4.1.9 Number of female flower

Mean sum of square for number of female flower was significant (10.65) due to genotypes in wax gourd (Table 3) indicating existence of considerable difference for this trait. The maximum number of female flower was found 8.86 in BD-321 and the minimum was recorded 2.40 in BARI Chalkumra-1 with mean value 5.17 (Appendix IV). The differences in magnitudes in between genotypic (2.91) and phenotypic (4.84) variances was relatively high for this trait indicating large environmental influence on these characters. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 32.97 and 42.56 respectively. Heritability (60.03%) estimates for this trait was high, genotypic advance (2.72) was low and genotypic advance in percent of mean (52.62) was found high, revealed that the trait was controlled by additive gene. Husna (2009) also found the differences in magnitudes in between genotypic (13.41) and phenotypic (15.74) variances was relatively high for this trait in bottle gourd and the GCV and PCV were 35.14 and 38.08 respectively. She also found heritability (85.15%) high, genotypic advance (8.92) was moderately high and genotypic advance in percent of mean (85.60) was found high and also additive gene effect in bottle gourd.

4.1.10 Fruit weight (kg)

Mean sum of square for fruit weight was significant (0.22) in wax gourd (Table 3) indicating existence of considerable difference for this trait. The maximum weight per fruit was found 1.63 kg in BD-319 and the minimum was recorded 0.5 kg in BD-337 with mean value 0.98 (Appendix IV). The differences in magnitudes in between genotypic (0.06) and phenotypic (0.10) variances was relatively high for this trait indicating large environmental influence on these characters. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 25.33 and 31.95 respectively for fruit weight which indicating that significant variation exists among different genotypes. Heritability (62.87%) estimates for this trait was high together with considerable low genetic advance (0.41) and genetic advance in percent of mean (41.57) revealed that the trait was controlled by additive gene and selection for this character would be effective. Saha *et al.* (1992) found similar GCV (39.55) and PCV (41.00) for the fruit weight in pumpkin. This result is in consonance with the findings of Chowdhury and Sharma (2002) in ridge gourd and Rumaran *et al.* (1997) pumpkin. Rahman *et al.* (1986) also found the similar result in bottle gourd.

4.1.11 Fruit length (cm)

Significant mean sum of square for fruit length (18.71) indicated considerable difference among the genotypes studied (Table 3). The maximum fruit length was found 32.53cm in BD-321 and the minimum was recorded 19.55cm in BD-374 with mean value 23.76cm (Appendix IV). The genotypic variance and phenotypic variance were 5.14 and 8.42 respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this character. The genotypic co-efficient of variation (9.55) and phenotypic co-efficient of variation (12.21) were close to each other. Heritability (61.09%) estimates for this trait high, genotypic advance (3.65) and genotypic advance in percent of mean (15.37) were found moderately high, indicated that the trait was governed by additive gene and selection for this character would be effective. Banik (2003) found the highest phenotypic co-efficient of variation was for fruit length. Mathew and Khader (1999) also reported high heritability for fruit length in snake gourd. Rahman *et al.* (1986) indicated minimum differences between GCV and PCV in bottle gourd for fruit length. Photograph showing variation of fruit length among some genotypes of wax gourd in Plate 3a, 3b and 3c.

4.1.12 Fruit breadth (cm)

Mean sum of square fruit breadth was significant (37.10) due to genotypes in wax gourd (Table 3) indicating existence of considerable variation for this trait. The maximum fruit breadth was found 38.24cm in BD-349 and the minimum was recorded 24.53cm in BD-364 with mean value 31.53cm (Appendix IV). The genotypic variance and phenotypic variance were 10.59 and 15.93 respectively. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 10.32 and 12.66 respectively. Heritability (66.45%) estimates for this trait was high along with moderately high genetic advance (5.46) and genetic advance in percent of mean (17.33) indicated that this character was controlled by additive gene effects. Husna (2009) reported the GCV and PCV were 15.84 and 17.39 respectively in bottle gourd and heritability (82.93%) estimates for this trait was high along with moderately high genetic advance (8.76) and genetic advance in percent of mean (38.08) indicated that this character was controlled by additive gene effects.

4.1.13 Yield per plant (kg)

Significant mean sum of square for yield per plant (1.72) indicated considerable difference among the genotypes studied (Table 3). The maximum yield per plant was

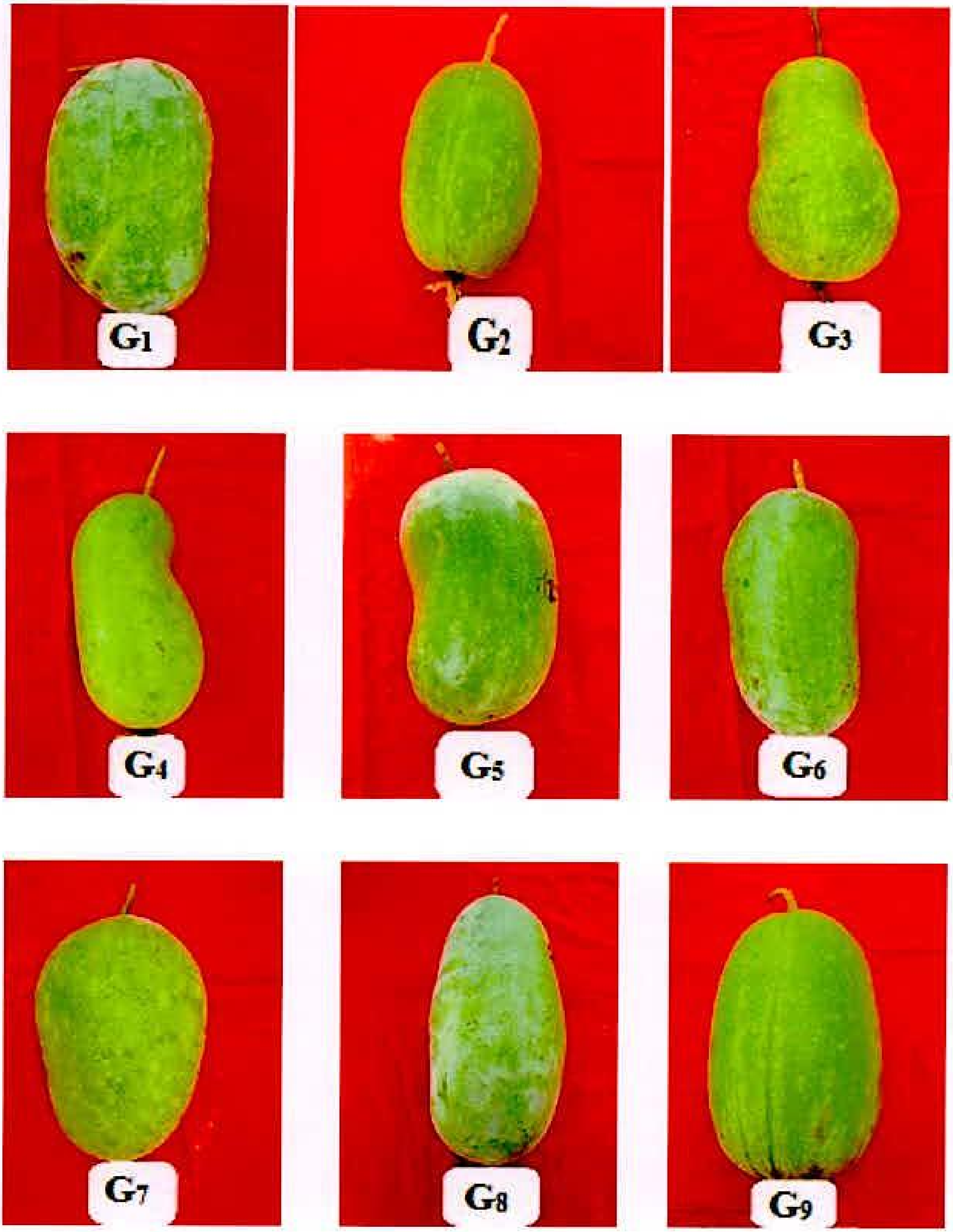

Plate 3a. Showing phenotypic variation in fruits among different genotypes of wax gourd (G_1-G_9)

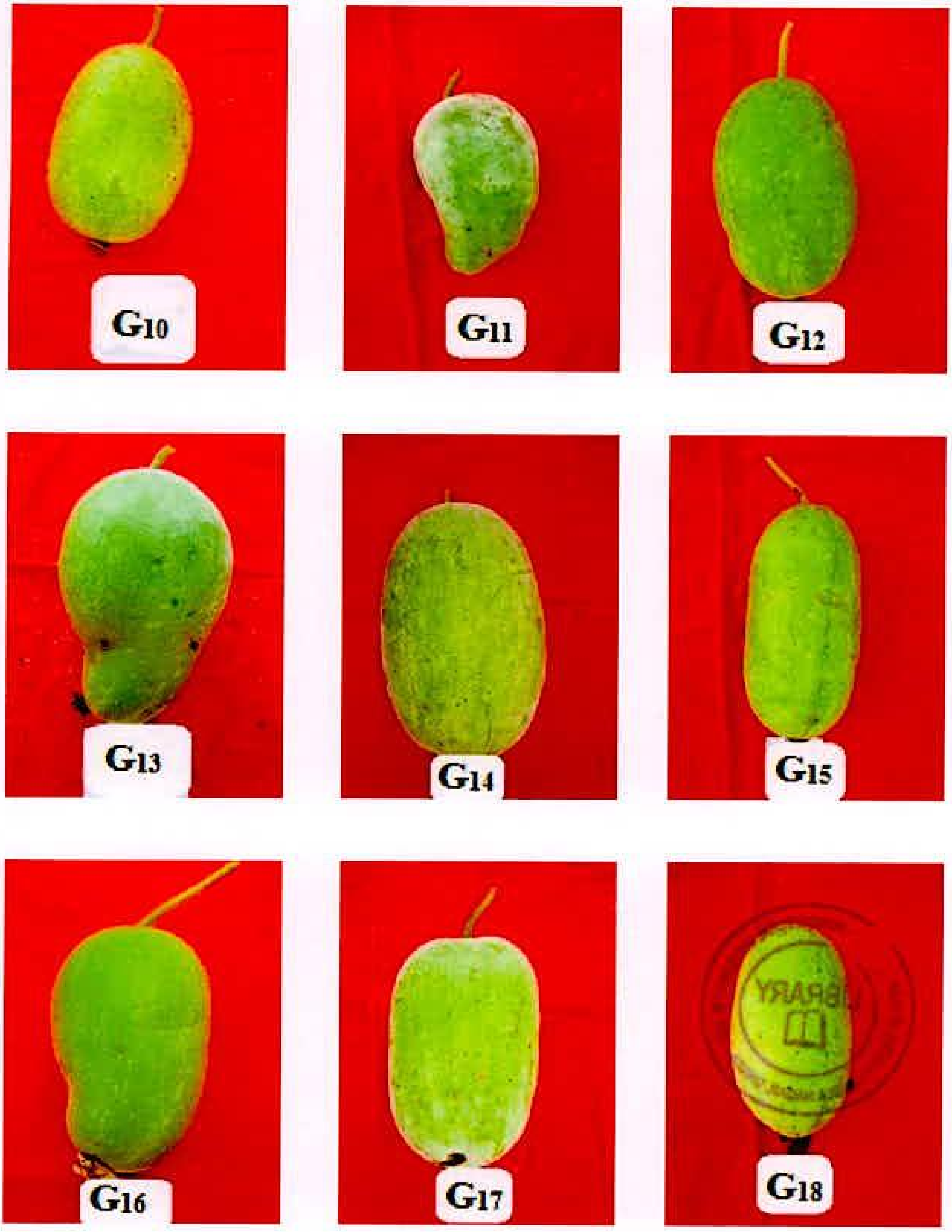

Plate 3b. Showing phenotypic variation in fruits among different genotypes of wax gourd (G_{10}-G_{18})

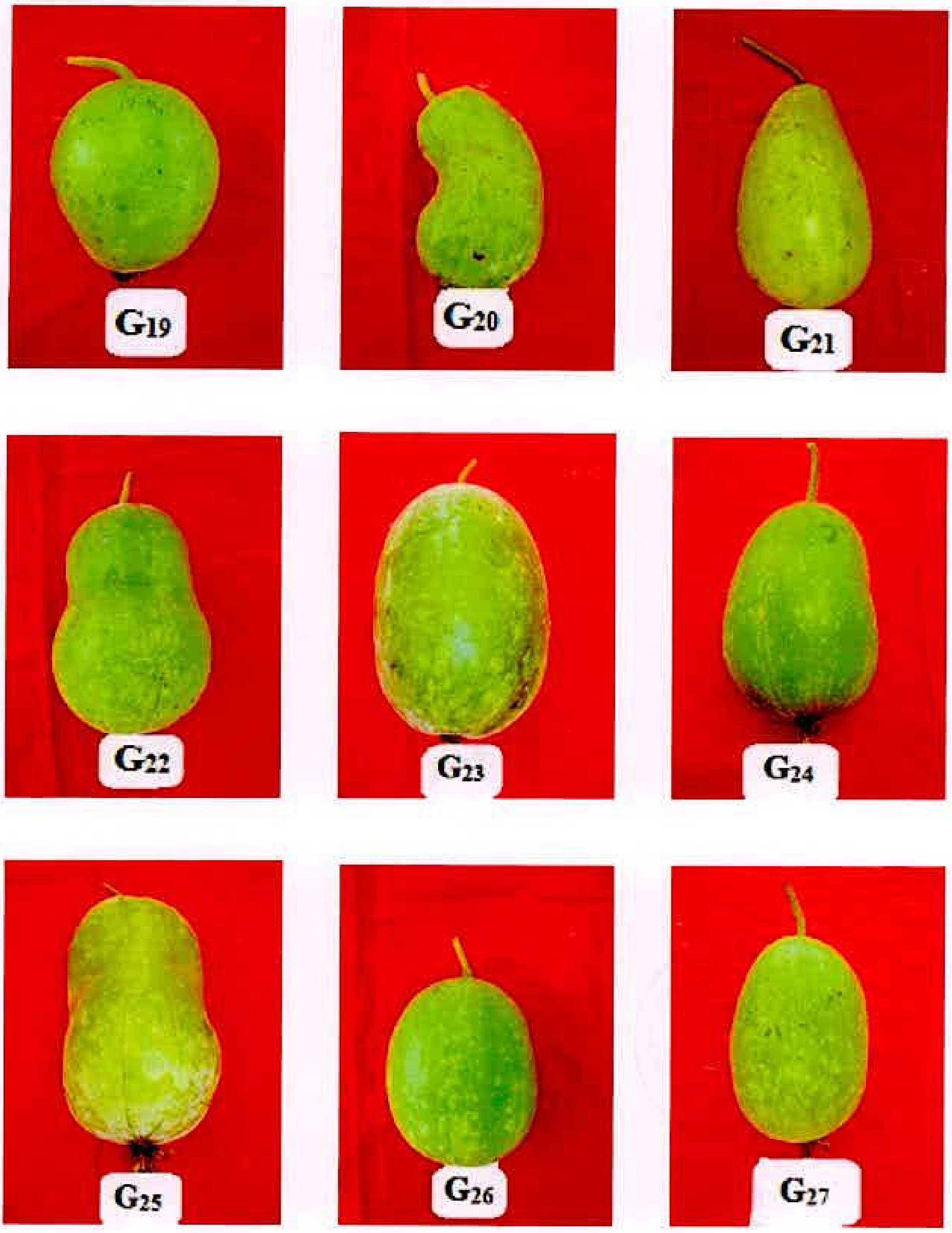

Plate 3c. Showing phenotypic variation in fruits among different genotypes of wax gourd (G_{19}-G_{27})

found 6.25 kg in BD-354 and the minimum was recorded 0.50 kg in BD-337 with mean value 1.75kg (Appendix IV) The differences in magnitudes in between genotypic (0.51) and phenotypic (0.70) variances for this trait indicating environmental influence on these characters. The genotypic coefficient of variation and phenotypic co-efficient of variation were 40.81 and 47.79 respectively for yield per plant which indicating that significant variation exists among different genotypes. The heritability value (73.19%) as well as genetic advance (1.26) and genetic advance in percent of mean (72.10) were observed very high. The very high heritability with moderate genetic advance provided opportunity for selecting high valued genotypes for breeding programme. This finding also supported Abusaleha and Dutta (1990) findings in cucumber. Narayanankutty *et al.* (2006) fruit yield exhibited high values of heritability and genetic gain indicating additive gene effects are important in determining the character. Mathew and Khader (1999) reported that highest GCV and PCV were recorded for fruit yield per plant in snake gourd.

4.2 CORRELATION CO-EFFICIENT

Yield is a complex product being influenced by several interdependent quantitative characters. Selection for yield may not be effective unless the directly or indirectly influences of other yield components are taken into consideration. When selection pressure is exercised for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated traits. Hence knowledge regarding association of character with yield and among themselves provides guideline to the plant breeder for making improvement through selection provide a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factors. Higher genotypic correlations than phenotypic one might be due to modifying or masking effect of environment in the expression of the character under study (Nandpuri *et al.* 1973). Results of genotypic and phenotypic correlation co-efficient of thirteen yield and its contributing traits of wax gourd 27 were estimated with yield and shown in Table 4 which discussed character wise as bellows:

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

Characters		DFFF	LLWP	LB	ID	PLMF	PLFF	NMF	NFF	FW	FL	FB	FYP
DFMF	**G**	0.936**	-0.043	-0.334**	-0.709**	-0.134	-0.183	-0.548**	-0.287*	-0.043	0.204	0.170	-0.210
	P	0.868**	-0.058	-0.209	-0.556**	-0.006	-0.166	-0.345**	-0.234*	-0.027	0.193	0.122	-0.175
DFFF	**G**		-0.039	-0.315**	-0.616**	-0.187	-0.155	-0.427**	-0.345**	-0.202	0.163	0.052	-0.325**
	P		-0.053	-0.151	-0.493**	-0.169	-0.140	-0.343**	-0.969**	-0.135	0.099	0.044	-0.256*
LLWP	**G**			0.787**	-0.155	0.387**	0.657**	0.228*	0.507**	0.288*	0.410**	0.474**	0.523**
	P			0.575**	0.052	0.202	0.312**	0.154	0.220*	0.167	0.181	0.180	0.088
LB	**G**				0.007	0.491**	0.773**	0.090	0.225*	0.092	-0.004	0.388**	0.441**
	P				0.013	0.229*	0.402**	0.107	0.066	0.078	-0.005	0.131	0.130
ID	**G**					-0.244*	-0.050	0.677**	0.322**	-0.069	-0.329**	-0.130	0.229*
	P					-0.192	-0.037	0.386**	0.205	-0.029	-0.224*	-0.104	0.113
PLMF	**G**						0.658**	0.191	0.241*	0.126	0.237*	0.074	0.091
	P						0.642**	0.123	0.189	0.092	0.178	0.055	0.073
PLFF	**G**							0.312**	0.261*	0.038	-0.004	0.115	0.370**
	P							0.202	0.178	0.017	-0.008	0.096	0.309**
NMF	**G**								0.695**	-0.198	0.017	-0.105	0.055
	P								0.543**	-0.037	0.105	0.017	0.088
NFF	**G**									-0.050	0.357**	-0.119	0.133
	P									-0.031	0.292*	-0.026	0.128
FW	**G**										0.382**	0.895**	0.535**
	P										0.414**	0.789**	0.520**
FL	**G**											0.370**	-0.194
	P											0.291*	-0.011
FB	**G**												0.460**
	P												0.412**

** Correlation is significant at the 0.01 level. * Correlation is significant at the 0.05 level.

DFMF= Days to first male flowering, DFFF=Days to first female flowering, LL=Leaf length (cm), LB=Leaf breadth (cm), ID= Internode distance (cm), PLMF=Pedicel length of male flower (cm), PLFF=Pedicel length of female flower (cm), NMF=Number of male flower per plant, NFF= Number of female flower per plant, FW= Fruit weight (kg), FL=Fruit length (cm), FB=Fruit breadth (cm) and FYP=Fruit yield per plant (kg)

4.2.1 Days to first male flowering

Significant positive relationships were found in both male and female flower for days to first flowering at both genotypic and phenotypic levels (Table 4). Highly significant positive association between days to first male and female flowering indicates that the traits are governed by same gene and simultaneous improvement would be effective. But this character showed significant but negative correlation at genotypic level and non- significant negative correlation at phenotypic level between this trait and leaf breadth. But this character showed significant and negative correlation at both genotypic and phenotypic level of internode distance, number of male flower, number of female flower. This character produced insignificant and negative correlation with leaf length, pedicel length of male flower, pedicel length of female flower, fruit weight and fruit yield per plant but insignificant and positive relation between fruit length and fruit breadth. Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Husna (2009) also reported same correlation of Days to first male flowering with yield in bottle gourd. Kumaresan *et al.* (2006) found negative association of yield per vine with days to first male flower opening; Badade *et al.* (2001) reported yield is significantly and negatively correlated with days to first male appearance.

4.2.2 Days to first female flowering

Days to first female flowering showed highly significant and negative correlation at both genotypic and phenotypic level between other traits like internode distance, no. of male flower, no. of female flower and fruit yield per plant. This indicated that if day to first female flowering is increased, then internode distance, no. of male flower, no. of female flower and fruit yield per plant decreased. This character showed insignificant and negative correlation at both genotypic and phenotypic level between leaf length, pedicel length of male flower, pedicel length of female flower and fruit weight but insignificant and positive relation with fruit length and fruit breadth. This trait also showed significant and negative relation at genotypic level and insignificant and negative relation with leaf breadth. Narayanankutty *et al.* (2006) reported that yield was strongly correlated days to first female flower opening in snake gourd. But

Kumaresan *et al.* (2006) found negative association with days to first female flower opening in snake gourd. Badade *et al. (2001)* found in bottle gourd this trait was significantly and negatively correlated with days to first male and female flower.

4.2.3 Leaf length (cm)

Leaf length showed highly significant and positive correlation with leaf breadth, pedicel length of female flower and no. of female flower at both genotypic and phenotypic levels (Table 4) revealed that if the leaf length is increased, then leaf breadth, pedicel length of female flower and no. of female flower also increased. This character also produced significant positive association at genotypic but insignificant positive association at phenotypic level with pedicel length of male flower, number of male flower per plant, fruit length, fruit breadth, fruit weight and fruit yield per plant. Husna (2009) also reported leaf length is significantly and positively correlated with leaf breadth at both genotypic and phenotypic levels.

4.2.4 Leaf breadth (cm)

Leaf breadth showed highly significant and positive correlation with pedicel length of male flower and pedicel length of female flower at both genotypic and phenotypic level (Table 4) indicated that if the leaf breadth is increased, then pedicel length of male flower and pedicel length of female flower also increased. On the other hand this character produced significant and positive correlation with number of female flower, fruit breadth and fruit yield per plant at genotypic level and insignificant and positive correlation at phenotypic level. This character also showed insignificant but positive relation with internodes distance, no. of male flower and fruit weight.

4.2.5 Internode distances (cm)

The character showed highly significant and positive relationship with no. of male flowers at both genotypic and phenotypic levels (Table 4) indicated that if internodes distance is increased, then no. of male flowers also increased. Positive and significant correlation between yield and internodes distance showed that selection of genotypes with higher internodes distance are expected to yield better. The character showed insignificant and negative relationship with pedicel length of female flower, fruit weight, fruit breadth at both genotypic and phenotypic level. On the other hand this character possessed significant but negative correlation with male flower pedicel length at genotypic and insignificant at phenotypic level. This character showed significant and positive at genotypic level but insignificant and positive with no. of female flower and fruit yield per plant. This character also showed significant but negative relation with fruit length.

4.2.6 Male flower pedicel length (cm)

Male flower pedicel length showed significant and positive correlation with only female flower pedicel length at both genotypic and phenotypic levels (Table 4). This character produced insignificant but positive correlation at both genotypic and phenotypic level with no. of male flower, fruit weight, fruit breadth and fruit yield per plant. This character also showed significant and positive at genotypic level but insignificant and positive relation at phenotypic level with no. of female flower and fruit length. Husna (2009) found same relation with female flower pedicel length with this trait in bottle gourd.

4.2.7 Female flower pedicel length (cm)

Female flower pedicel length showed significant and positive correlation with number of male flower and number of female flower at genotypic level and insignificant and positive at phenotypic level (Table 4). This character shows highly significant and positive correlation with fruit yield per plant indicated that if female flower pedicel length is increased, then yield is also increased. Insignificant positive association of female flower pedicel length was found with fruit weight and fruit breadth. But this character produced insignificant and negative correlation with fruit length at both genotypic and phenotypic level.

4.2.8 Number of male flower

The character number of male flower showed highly significant and positive correlation with number of female flower at both genotypic and phenotypic level (Table 4) which revealed that if number of male flower is increased then no. of female flower is also increased. But this character produced insignificant and negative correlation with fruit weight at both genotypic and phenotypic levels (Table 4) which indicated that if the number of male flower is increased then fruit is decreased. Insignificant but positive correlation was observed with fruit length and fruit yield per plant. This finding also supported Chadhury and Mandal (1987) findings in cucumber and Husna (2009) in bottle gourd.

4.2.9 Number of female flowers

Number of female flowers showed highly significant and positive correlation with fruit length at both genotypic and phenotypic level (Table 4). But insignificant and negative correlation of this character with fruit breadth, fruit weight both genotypic and phenotypic level indicated that the association among these traits largely influenced by environmental factors. This character showed insignificant but positive correlation with fruit yield per plant. Prasana *et al.* (2002) found that fruit yield per hectare was positively associated with number of female flowers in ridge gourd (*Luffa acutangula*).

4.2.10 Fruit weight (kg)

The trait fruit weight showed highly significant and positive correlation with fruit length, fruit breadth and yield per plant at both genotypic and phenotypic levels (Table 4) indicated that if the fruit weight is increased the fruit length, fruit breadth and yield per plant is also increased. Husna (2009) found same results with this trait in bottle gourd. Chowdhury and Sarma (2002) studied *Luffa acutangula* cultivars and observed that yield per hectare can be improved through selection individual fruit weight. Kumaresan *et al.* (2006) Yield per vine in snake gourd was positively associated with fruit weight. Prasana *et al.* (2002) found in ridge gourd (*Luffa acutangula*) fruit yield per hectare was positively associated with fruit weight.

4.2.11 Fruit length (cm)

Fruit length showed highly significant and positive correlation with fruit breadth. But it showed insignificant and negative relation with fruit yield per plant. Kumaresan *et al.* (2006) found fruit length showed negative association with fruit yield in snake gourd. Husna (2009) showed positive association of fruit length with fruit yield per plant.

4.2.12 Fruit breadth (cm)

Positive and highly significant correlation of fruit breadth was found with fruit yield per plant at both genotypic and phenotypic level (Table 4) revealed that any increased in this trait should bring about an enhancement in the yield. Narayanankutty *et al.* (2006) reported that yield is strongly correlated with fruit length in snake gourd. Prasana *et al.* (2002) studied the correlation between the yield and yield components of ridge gourd (*Luffa acutangula*). Fruit yield per hectare was positively associated with fruit girth and weight. Husna (2009) found similar result in bottle gourd and Miah *et al.* (2000) also found similar result for this trait in bitter gourd.

4.3 PATH CO-EFFICIENT ANALYSIS

Partitioning of genotypic correlation of different genotypes, yield and its contributing traits in wax gourd are shown in Table 5 and discussed character wise as follows:

4.3.1 Days to first male flowering

Days to first male flowering showed the positive direct effect (0.178) on yield (Table 5). The character also showed the maximum positive indirect effect through internode distance (0.068) followed by leaf breadth (0.019), number of female flower (0.014), pedicel length of male flower (0.011) and fruit breadth (0.003). The negative indirect effect of this character on yield via days to first female flowering (-0.119) was the highest followed by pedicel length of female flower (-0.057), fruit length (-0.021), number of male flower (-0.018), fruit weight (-0.011) and leaf length (-0.010) which finally made insignificant negative correlation between days to first male flowering and yield per plant (-0.044). Husna (2009) found similar result with fruit yield per plant regarding this character in bottle gourd. Miah *et al.* (2000) also found similar result for this trait in bitter gourd.

4.3.2 Days to first female flowering

Days to first female flowering showed a positive direct effect (0.137) on yield (Table 5) This character, also showed the highest positive indirect effect through days to first male flowering (0.068) followed by internodes distance (0.061), no. of female flower (0.017), pedicel length of male flower (0.015), leaf breadth (0.010) and fruit breadth (0.001) on yield. The character also produced negative indirect effect on yield via

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

Characters	Direct effect	Indirect effects												Pearson correlation with yield
		DFMF	DFFF	LLWP	LB	ID	PLMF	PLFF	NMF	NFF	FW	FL	FB	
DFMF	0.178	-	-0.119	-0.010	0.019	0.068	0.011	-0.057	-0.018	0.014	-0.011	-0.021	0.003	-0.044
DFFF	0.137	0.068	-	-0.009	0.010	0.061	0.015	-0.049	-0.019	0.017	-0.048	-0.011	0.001	-0.101
LLWP	0.074	-0.010	0.016	-	-0.185	-0.025	-0.012	0.082	0.004	-0.011	0.051	-0.006	0.004	-0.019
LB	-0.258	-0.006	0.005	0.053	-	-0.004	-0.019	0.098	0.003	-0.005	0.028	-0.008	0.002	-0.111
ID	-0.129	-0.041	0.065	0.014	-0.008	-	0.016	-0.010	0.016	-0.010	0.001	0.017	-0.002	-0.071
PLMF	-0.092	-0.009	0.022	0.010	-0.052	0.023	-	0.231	0.009	-0.008	0.012	-0.015	0.002	0.132
PLFF	0.46	-0.012	0.018	0.017	-0.070	0.004	-0.059	-	0.013	-0.007	0.006	0.001	0.004	0.274
NMF	0.261	-0.023	0.043	0.004	-0.014	-0.033	-0.014	0.074	-	-0.034	-0.011	-0.006	0.001	0.049
NFF	-0.065	-0.017	0.036	0.013	-0.020	-0.019	-0.011	0.036	0.031	-	-0.022	-0.012	0.001	-0.048
FW	0.84	-0.002	0.015	0.009	-0.016	0.000	-0.002	0.005	-0.001	0.003	-	-0.048	0.021	0.422**
FL	-0.097	0.017	-0.016	0.005	-0.021	0.022	-0.014	-0.002	0.004	-0.008	0.217	-	0.007	0.113
FB	0.628	0.007	-0.006	0.011	-0.017	0.011	-0.006	0.046	0.003	-0.002	0.330	-0.025	-	0.381**

Residual effect: 0.478, ** Correlation is significant at the 0.01 level. * Correlation is significant at the 0.05 level.

DFMF= Days to first male flowering, DFFF=Days to first female flowering, LL=Leaf length (cm), LB=Leaf breadth (cm), ID= Internode distance (cm), PLMF=Pedicel length of male flower (cm), PLFF=Pedicel length of female flower (cm), NMF=Number of male flower per plant, NFF= Number of female flower per plant, FW= Fruit weight (kg), FL=Fruit length (cm), FB=Fruit breadth (cm) and FYP=Fruit yield per plant (kg) pedicel length of female flower (-0.049), fruit weight (-0.048), number of male flower (-0.019), fruit length (-0.006) and leaf length (-0.009). The cumulative effects produced a negative genotypic correlation on yield (-0.101). The finding also supported Miah *et al.* (2000) also found similar result for this trait in bitter gourd.

4.3.3 Leaf length (cm)

Leaf length showed positively direct effect (0.074) on yield (Table 5). This character, however, showed positive indirect effect through pedicel length of female flower (0.082), fruit weight (0.051), days to first female flowering (0.016), number of male flower (0.004) and fruit breadth (0.004). The negative indirect effect via leaf breadth (-0.185) followed by internode distance (-0.025), pedicel length of male flower (-0.012), number of female flower (-0.011), days to first male flowering (-0.010) and fruit length (-0.006) and which were contributed to result insignificant negative genotypic correlation with yield per plant (-0.019). Husna (2009) showed insignificant and positive correlation with fruit yield per plant regarding this character in bottle gourd.

4.3.4 Leaf breadth (cm)

Leaf breadth showed a negative direct effect (-0.258) on yield (Table 5). This character, however, showed also positive indirect effect through pedicel length of female flower (0.098), leaf length (0.053), fruit weight (0.028), days to first female flowering (0.005), number of male flower (0.003) and fruit breadth (0.002). The negative indirect effects were also observed via pedicel length of male flower (-0.019) followed by fruit length (-0.008), days to first male flowering (-0.006), number of female flower (-0.005) and internodes distance which were contributed to result insignificant negative genotypic correlation with yield per plant (-0.111). Asmaul Husna (2009) found insignificant and positive correlation with fruit yield per plant regarding this character in bottle gourd.

4.3.5 Internodes distance (cm)

It was found that internodes distance showed the negative direct effect (-0.129) on yield (Table 5). This character also showed the highest positive indirect effect through length of male flower (0.016), number of male flower (0.016), leaf length (0.014) and fruit weight (0.001). The negative indirect effects of this character on yield were also observed via days to first male flowering (-0.041), pedicel length of female flower (-0.010), number of female flower (-0.010), leaf breadth (-0.008) and fruit breadth (-0.002) which finally made insignificant negative correlation between internodes distance and yield per plant (-0.071).

4.3.6 Pedicel length of male flower (cm)

Male flower pedicel length showed a negative direct effect (-0.092) on yield (Table 5). This character also showed the highest positive indirect effect through pedicel length of female flower (0.231) followed by internodes distance (0.023), days to first female flowering (0.022), fruit weight (0.012), leaf length (0.010), number of male flower (0.009), fruit breadth (0.002). The character also produced the negative indirect effect on yield via leaf breadth (-0.052), fruit length (-0.015), days to first male flowering (-0.009) and number of female flower (-0.008). The cumulative effects of these characters produced a positive genotypic correlation on yield (0.132). Figure 1 showing Path diagram of yield and its contributing traits in twenty seven genotypes of wax gourd.

4.3.7 Pedicel length of female flower (cm)

Female flower pedicel length showed a positive direct effect (0.46) on yield (Table 5). This character also showed the highest positive indirect effect through days to first female flowering (0.018) followed by leaf length (0.017), number of male flower (0.013), fruit weight (0.006), fruit breadth (0.004), internodes distance and fruit length (0.001). The character also produced the negative indirect effect on yield via leaf breadth (-0.070), pedicel length of male flower

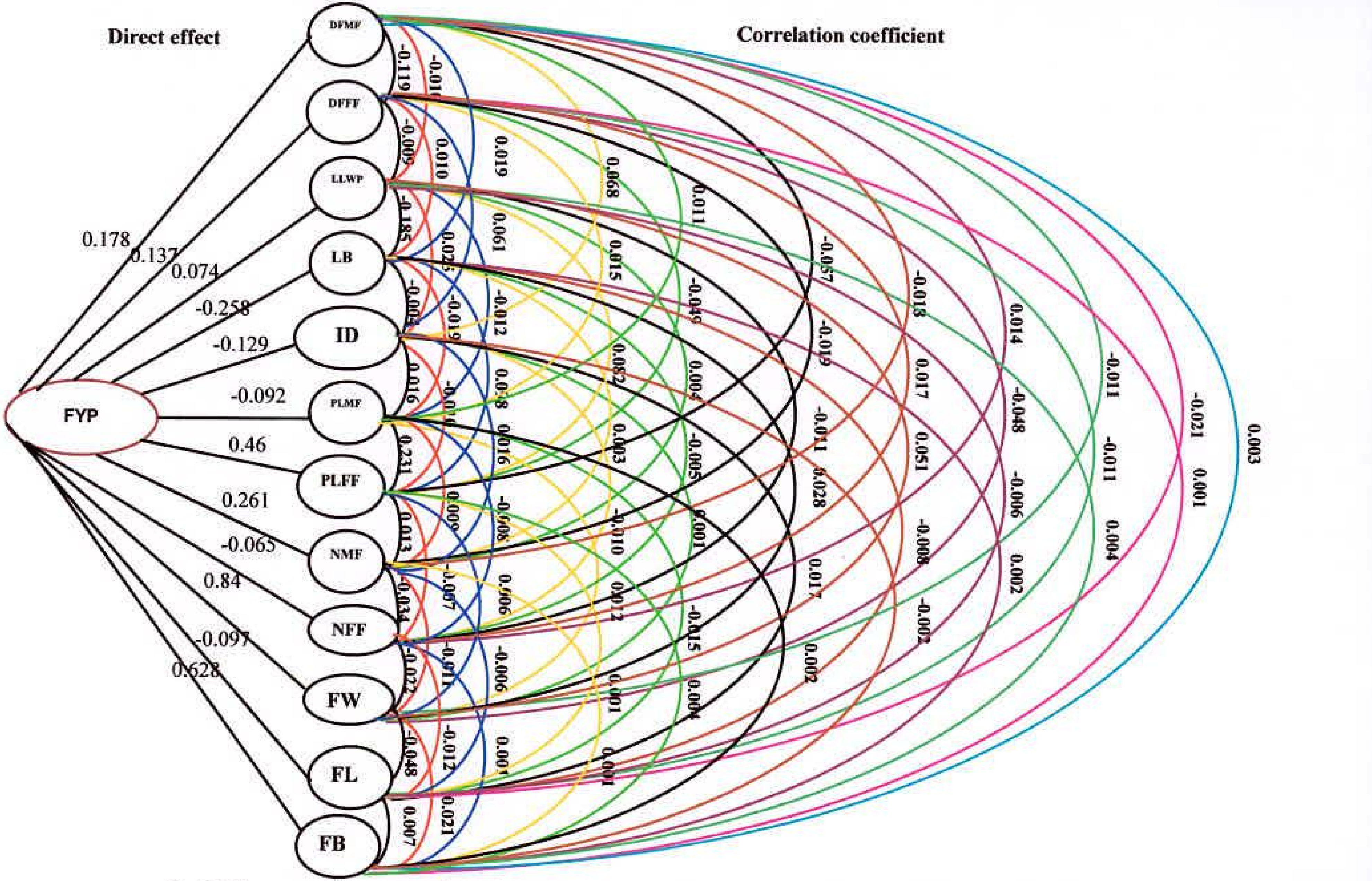

Fig.1: Diagrammatic representation of direct effects and correlation coefficients of variables on dependent variable in wax gourd genotypes

(-0.059), days to first male flowering (-0.012) and number of female flower (-0.007). The cumulative effects of these characters produced a positive genotypic correlation on yield (0.274). Husna (2009) found negative correlation with fruit yield per plant regarding this character in bottle gourd.

4.3.8 Number of male flower

Number of male flower showed a positive direct effect (0.261) on yield (Table 5). This character also showed the highest positive indirect effect through pedicel length of female flower (0.074), days to first female flowering (0.043), leaf length (0.004) and fruit breadth (0.001). This character, however, showed negative indirect effect through number of female flower (-0.034), internodes distance (-0.033), days to first male flowering (-0.023), leaf breadth (-0.014) pedicel length of male flower (-0.014) fruit weight (-0.011) and fruit length (-0.006) which were contributed to result in significant positive genotypic correlation with yield per plant (0.049). These findings also supported Chadhury and Mandal (1987) in cucumber.

4.3.9 Number of female flower

Number of female flower produced a negative direct effect (-0.065) on yield (Table 5). The character, however, showed also some positive indirect effect through days to first female flowering (0.036), pedicel length of female flower (0.036), number of male flower (0.031), leaf length (0.013) and fruit breadth (0.001). The negative indirect effects were also observed via fruit weight (-0.022) followed by leaf breadth (-0.020), internodes distance (-0.019), days to first male flowering (-0.017), fruit length (-0.012) and pedicel length of male flower (-0.011) which were contributed to result in significant negative genotypic correlation with yield per plant (-0.048). Figure 1 showing Path diagram of yield and its contributing traits in twenty seven genotypes of wax gourd.

4.3.10 Fruit weight (kg)

Weight per fruit had the positive direct effect (0.84) on yield (Table 5). This character also showed positive indirect effect through fruit breadth (0.021), days to first female flowering (0.015), leaf length (0.009), pedicel length of female flower (0.005) and number of female flower (0.003).But negative indirect effect through fruit length (-0.048) leaf breadth (-0.016), days to first male flowering (-0.002), pedicel length of male flower (-0.002) and. number of male flower (-0.001). However, all these effects contributed to result significant positive genotypic correlation with fruit yield per plant (0.422). Significant genotypic correlation between fruit weight and yield further strengthened their reliability in the process of selection for higher yield. Kumaresan *et al.* (2006) conducted an experiment in snake gourd and Path coefficient analysis revealed that it would be highly rewarding to lay emphasis on the number of fruits per vine and fruit weight to increase the yield per vine directly. The result is in consonance with the finding of Husna (2009) in bottle gourd, Kumarara *et al.* (1998) in pumpkim for this trait.

4.3.11 Fruit length (cm)

Fruit length showed negatively direct effect (-0.097) on yield (Table 5). This character, however, showed positive indirect effect through fruit weight (0.217) followed by internodes distance (0.022), days to first male flowering (0.017), fruit breadth (0.007), leaf length (0.005) and number of male flower (0.004). The negative indirect effects were also observed via leaf breadth (-0.021), days to first female flowering (-0.016), pedicel length of male flower (-0.014), number of female flower (-0.008) and pedicel length of female flower (-0.002) which were together contributed to result insignificant positive genotypic correlation with yield per plant (0.113). Husna (2009) in bottle gourd and Miah *et al.* (2000) also found similar result in bitter gourd.

4.3.12 Fruit breadth (cm)

Fruit breadth showed positively direct effect (0.628) on yield (Table 5). This character, however, showed positive indirect effect through fruit weight (0.330), pedicel length of female flower (0.046), leaf length (0.011), internodes distance (0.011), days to first male flowering (0.007) and number of male flower (0.003). The negative indirect effects were also found fruit length (-0.025), leaf breadth (-0.017), days to first female flowering (-0.006), pedicel length of male flower (-0.006) and number of female flower (-0.002) which were contributed to result significant positive genotypic correlation with yield per plant (0.381). The result is in also agreement with those of Asmaul Husna (2009) in bottle gourd, Rahman *et al.* (1986) in bottle gourd and Parhi *et al.* (1995) in bitter gourd. Chadhury and Mandal (1987) and Mondal *et al.* (1989) also found similar result for fruit breadth in cucumber and water melon respectively.

4.4 MULTI VARIATE ANALYSIS

4.4.1 Principal component analysis (PCA)

Principal component analysis was carried out with twenty seven genotypes of wax gourd. First three Eigen values for three principal coordination axes of genotypes accounted for 63.46% variation (Table 6). A two dimensional scattered diagram (Fig. 2) was developed on the basis of the principal component score; Z_1 and Z_2 score (Appendices V).

4.4.2 Principal coordinates analysis (PCO)

The results obtained from principal coordinate analysis showed that the highest inter genotypic distance was observed between genotypes G_7 and G_{22} (46.326) followed by G_7 and G_{13} (46.081) and the lowest distance was observed (0.381) between genotypes G_6 and G_{14} followed by the distance (1.923) between genotypes G_{19} and G_{25} (Table 7). The difference between the highest and the lowest inter genotypic distance indicated the moderate variability among the 27 genotypes of wax gourd. The highest intra-cluster distance was recorded in cluster V (0.358) having four genotypes viz. BD-338, BD-358, BD-364, BD-374containing. The lowest intra-cluster distance was observed in cluster I (0.000) which is BD-323. It favored to decide that intra-group diversity was the highest in cluster V and the lowest in cluster I. Cluster II having four genotypes BD-325, BD-328, BD-329, BD-354 and had the intra cluster distance 0.235. Cluster IV consisted ten genotypes BD-319, BD-321, BD-324, BD-340, BD-342, BD-368, BD-370, BD-2406, BARI chalkumra 1, Local and had an intra-cluster distance 0.038. The cluster VI consists six genotypes viz. BD-320, BD-322, BD-348, BD-349, BD-361, BD-2412 and had the intra cluster distance 0.117. Cluster III having two genotypes BD-333 and BD-337 (Table 8 and 10).

Table 6. Eigen values and yield percent contribution of 13 characters of twenty seven germplasm of wax gourd.

Characters	Eigen values	Percent variation	Cumulative variation
Days to first male flowering	3.597	27.67	27.67
Days to first female flowering	2.798	21.52	49.19
Leaf length without petiole (cm)	1.855	14.27	63.46
Leaf breadth (cm)	1.456	11.20	74.66
Internode distance (cm)	0.955	7.35	82.01
Pedicel length of male flower (cm)	0.766	5.89	87.9
Pedicel length of female flower (cm)	0.523	4.02	91.92
Number of male flower per plant	0.287	2.21	94.13
Number of female flower per plant	0.258	1.99	96.12
Fruit weight (kg)	0.219	1.69	97.81
Fruit length (cm)	0.170	1.31	99.12
Fruit breadth (cm)	0.062	0.48	99.60
Fruit yield per plant (kg)	0.052	0.40	100.00

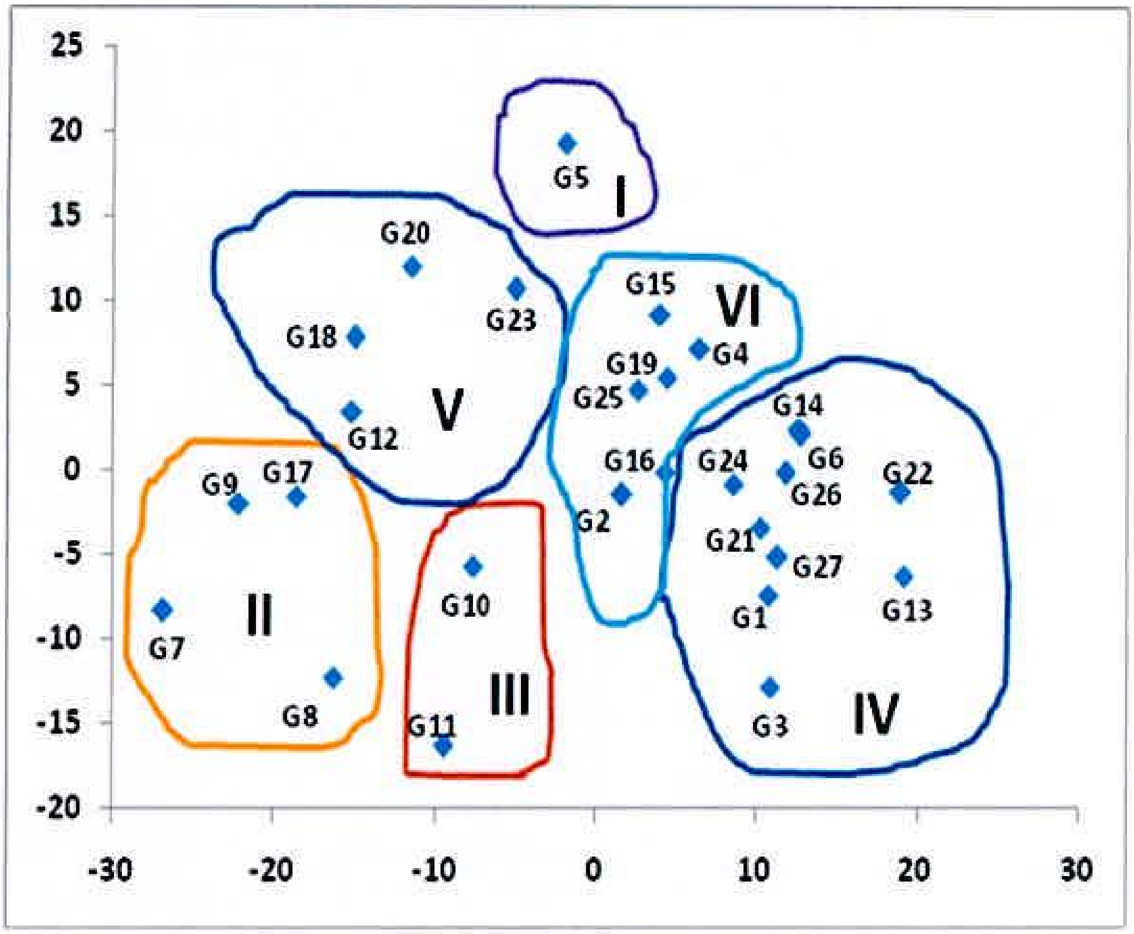

Figure 2: Scattered diagram of twenty seven wax gourd genotypes Superimpose cluster

Table 7. Ten highest and ten lowest inter genotypic distance among the 27 wax gourd genotypes

Highest distance				Lowest distance			
Sl No.	**Genotype**		**Distance**	**Sl No.**	**Genotype**		**Distance**
01	G_7	G_{22}	46.326	01	G_6	G_{14}	0.381
02	G_7	G_{13}	46.081	02	G_{19}	G_{25}	1.923
03	G_9	G_{13}	41.581	03	G_{21}	G_{27}	2.074
04	G_9	G_{22}	41.133	04	G_1	G_{27}	2.270
05	G_6	G_7	40.952	05	G_6	G_{26}	2.491
06	G_7	G_{14}	40.901	06	G_4	G_{19}	2.671
07	G_7	G_{26}	39.444	07	G_{14}	G_{26}	2.767
08	G_7	G_{27}	38.311	08	G_2	G_{16}	2.978
09	G_{13}	G_{17}	38.105	09	G_{21}	G_{24}	3.133
10	G_3	G_7	38.011	10	G_4	G_{15}	3.192

Table 8. Distribution of genotypes in different clusters

Cluster no.	No. of Genotypes	No. of population	varieties
I	G5	1	BD-323
II	G7, G8, G9, G17	4	BD-325, BD-328, BD-329, BD-354
III	G10, G11	2	BD-333, BD-337
IV	G1, G3, G6, G13, G14, G21, G22, G24, G26, G27	10	BD-319, BD-321, BD-324, BD-340, BD-342, BD-368, BD-370, BD-2406, BARI chalkumra 1, Local
V	G12, G18, G20, G23	4	BD-338, BD-358, BD-364, BD-374
VI	G2, G4, G15, G16, G19, G25	6	BD-320, BD-322, BD-348, BD-349, BD-361, BD-2412

4.4.3 Non-hierarchical clustering

The computations from covariance matrix gave non-hierarchical clustering among twenty seven genotypes of wax gourd and grouped them into six clusters. Khatun *et al.* (2010) conducted an experiment in 38 snake gourd genotypes and the genotypes were grouped into four different clusters. Husna (2009) reported five clusters in bottle gourd. Gaffar (2008) reported similar number of clustering in 15 sponge gourd genotypes. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. So the results obtained through PCA were confirmed by non-hierarchical clustering. Table 8 represents the clusters occupied by 27 genotypes of wax gourd. It explains that cluster IV contained the highest number of genotypes ten, cluster VI constitute by six genotypes, cluster II and cluster V constitute by four genotypes each and cluster III constitute by two genotypes and cluster I having only one genotypes. Cluster IV having ten genotypes BD-319, BD-321, BD-324, BD-340, BD-342, BD-368, BD-370, BD-2406, BARI chalkumra 1 and Local variety. The cluster IV genotypes are collected from Plant Genetic Resource Centre, BARI, Gazipur. Cluster mean for 13 traits are presented in (Table 9). From the Table 9, it was observed that the mean value of cluster IV ranked first for days to first male flowering (55.43) and days to first female flowering (73.30). Cluster VI was formed by six genotypes viz. BD-320, BD-322, BD-348, BD-349, BD-361, BD-2412. They were collected from Plant Genetic Resource Centre, BARI, Gazipur. These clusters were unable to lead in respect of the highest cluster mean value for maximum characters. Among 13 characters cluster II produced the maximum cluster mean for the seven characters viz, leaf length (13.40), internode distance (11.71), pedicel length of male flower (10.62), pedicel length of female flower (6.64), No. of male flowers (42.58), No. of female flowers (7.71) and fruit yield per plant (2.57). Similarly cluster I ranked first for fruit weight (1.53), fruit length (26.47) and fruit breadth (36.00) and had only one genotype BD 323.

Table 9. Cluster mean values of 13 different characters of 27 genotypes

Characters	I	II	III	IV	V	VI
Days to first male flowering	35.33	37.33	44.33	55.43	34.67	45.44
Days to first female flowering	56.33	57.92	69.33	73.30	57.67	67.11
Leaf length without petiole (cm)	11.27	13.40	12.72	12.82	13.39	13.07
Leaf breadth (cm)	15.68	17.91	15.72	16.53	17.94	17.00
Internode distance (cm)	9.64	11.71	10.30	9.51	11.09	10.48
Pedicel length of male flower (cm)	9.47	10.62	10.60	9.39	9.06	8.72
Pedicel length of female flower (cm)	4.50	6.64	6.32	5.25	5.35	5.43
Number of male flower per plant	11.00	42.58	38.33	18.84	25.76	18.94
Number of female flower per plant	5.29	7.71	5.89	4.76	5.33	3.79
Fruit weight (g)	1.53	1.11	0.60	0.98	0.84	1.04
Fruit length (cm)	26.47	23.97	23.53	24.01	21.87	24.10
Fruit breadth (cm)	36.00	33.69	27.28	31.94	28.10	32.35
Fruit yield per plant (kg)	1.53	2.57	0.69	1.60	1.58	1.98

Cluster V had four genotypes named BD-338, BD-358, BD-364, BD-374 were collected from Plant Genetic Resource Centre, BARI, Gazipur. The highest cluster mean value was achieved for leaf breadth (17.94). Cluster III and cluster VI are not high for any character.

4.4.4 Canonical variate analysis

The highest inter-cluster distance was observed (Table 10) between cluster I and cluster VI (16.607) followed by between clusters I and cluster III (14.677) and between cluster I and cluster II (14.175). Similarly, the lowest inter-cluster distance was observed between the clusters III and cluster VI (6.072). Moderate or intermediate distance was found between cluster I and cluster VI (11.708). On the other, the highest intra-cluster distance was found in cluster V (0.358) followed by cluster II (0.235). The lowest intra-cluster distance was observed between in cluster IV (0.038). The inter cluster distances were found much higher than the intra cluster distances suggesting wider genetic diversity existed among the genotype of different groups. Result of different multivariate analysis were superimposed in figure 2 from which it may be concluded from the above results that different multivariate techniques supplemented and confirmed one another.

Table 10. Intra (Bold) and inter cluster distances (D^2) for 27 genotypes of wax gourd

Cluster	I	II	III	IV	V	VI
I	**0.00**	14.175	14.677	16.607	10.500	11.708
II		**0.235**	7.393	13.230	6.553	8.962
III			**0.01**	8.510	7.487	6.072
IV				**0.038**	12.976	6.659
V					**0.358**	7.215
VI						**0.117**

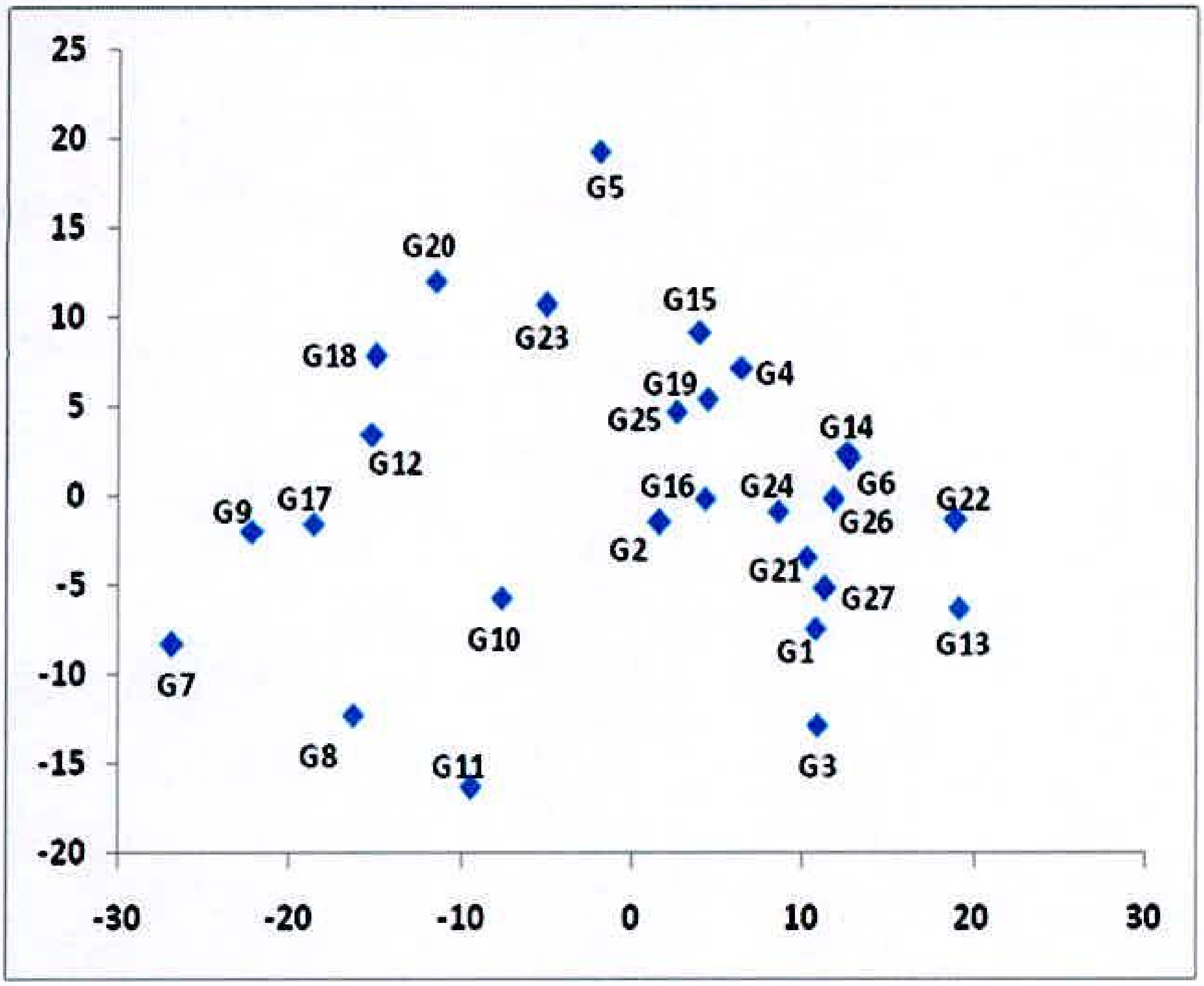

Fig 3. Scattered diagram of twenty seven wax gourd genotypes

As per scatter diagram the genotypes were apparently distributed into six clusters. It was also revealed that the genotype of cluster I was more diverse from the genotypes of cluster IV. Islam *et al.* (2004) also observed the similar result. It is assumed that maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. However, for a practical plant breeding the objective is not only high heterosis but also to achieved high-level production. In the present study the maximum distance existence between cluster I and cluster IV. But considering the yield and duration crosses involving cluster I and IV may be exhibit high heterosis for yield. Main and Bahl (1989) reported that the parents separated by D^2 values of moderate magnitude generally showed higher heterosis.

4.4.5 Contribution of characters towards divergence of the genotypes

The values of Vector I and Vector II are presented in Table 11. Vector I obtained from PCA expressed that days to first male flowering (0.6655), internodes distance (0.2649), pedicel length of male flower (0.2299), pedicel length of female flower (0.0452) and fruit weight (1.7582) were major characters that contribute to the genetic divergence. It was the reflection of first axis of differentiation. In vector II days to first female flowering (0.1025), pedicel length of female flower (0.2771), number of female flower (0.2677), fruit weight (1.5747), fruit length (0.1372) and fruit breadth (0. 1791) showed their important role toward genetic divergence. Negative values in both vectors for Leaf length, leaf breadth, number of male flower and fruit yield per plant had lower contribution towards the divergence.

Table 11. Relative contributions of the thirteen characters of 27 genotypes to the total divergence

Characters	Vector-1	Vector-2
Days to first male flowering	0.6655	-0.3640
Days to first female flowering	-0.0352	0.1025
Leaf length without petiole (cm)	-0.0325	-0.1051
Leaf breadth (cm)	-0.0509	-0.3680
Internode distance (cm)	0.2649	-0.6997
Pedicel length of male flower (cm)	0.2299	-0.3408
Pedicel length of female flower (cm)	0.0452	0.2771
Number of male flower per plant	-0.0358	-0.2856
Number of female flower per plant	-0.2924	0.2677
Fruit weight (g)	1.7582	1.5747
Fruit length (cm)	-0.0726	0.1372
Fruit breadth (cm)	-0.2167	0.1791
Fruit yield per plant (kg)	-0.0314	-1.1922

4.4.6 Selection of genotypes as parent for future hybridization programme

Selection of genetically diverse parents is an important step for hybridization program. So the genotypes were to be selected on the basis of specific objectives. A high heterosis could be produced from the crosses between genetically distant parents.

Considering the magnitude of cluster mean and agronomic performance the genotype G_{20} (BD-364) for minimum days of first male flower and maximum pedicel length of male flower from cluster V, G_{17} (BD-354) for maximum leaf breadth, maximum pedicel length of female flower and fruit yield per plant from cluster II; G_1 (BD 319) for maximum leaf length and maximum fruit weight from cluster IV and G_{16} (BD-349) for maximum fruit breadth from cluster VI were found promising. Therefore considering group distance and other agronomic performance the inter genotypic crosses between G_{20} (BD-364) and G_{17} (BD-354); G_1 (BD 319) and G_{16} (BD-349) may be suggested for future hybridization program.

Chapter 5

Summary and Conclusion

CHAPTER V
SUMMARY AND CONCLUSION

The present experiment was carried out in the Farm of Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka-1207, Bangladesh to evaluate the field performance, variability, character association, genetic divergence and characterization of twenty seven wax gourd genotypes using morphological characters.

The field experiment was laid out in Randomized Complete Block Design (RCBD) with three (3) replications. Data on different characters were recorded and analyzed statistically. The analysis of variance of all the traits was computed and significant differences were found among the accessions in respect of different characters studied. The maximum value in respect of days to first male flowering (59.00 days) was observed in G_{13} BD-340 and minimum days (33.33 days) to first male bud were recorded in G_{20} (BD-364). Genotype number G_{13} BD-340 recorded the maximum value (79.67 days) days to first female flowering and lowest days to first female flowering (53.67 days) was recorded in G_{18} (BD-358 days). In respect of leaf length, Genotype no.G_1 (BD-319) is the highest leaf length (14.65 cm) and genotype no. G_{24} (BD-2406) is the lowest leaf length (9.07 cm) was counted. In case of leaf breadth, the highest value (19.98 cm) was recorded in G_{17} (BD-354) and the lowest value was (12.92 cm) recorded in G_{24} (BD-2406). The maximum internodes distance was recorded in G_9 (BD-329) as 12.53 cm and minimum recorded in G_6 (BD-324) as 8.27 cm. In respect of male flowers pedicel length maximum value was found in G_{20} (BD-364) as 14.27 cm and the minimum was recorded in G_{23} (BD-374) as 6.00 cm. Genotype no G_{17} (BD-354) was the highest female flower pedicel length (9.33cm) and genotype no. G_{21} (BD-368) was the lowest female flower pedicel length (3.67 cm). In case of no. of male flower, the highest value (48.33) was observed in G_7 BD-325 and the lowest value (11.00) was recorded in G_5 (BD-323). In case of no. of female flower, the highest value (8.86) was observed in G_3 (BD-321) and the lowest value (2.40) was observed in G_{26} (BARI Chalkumra 1).). In case of average weight per fruit, the highest value (1.63 kg) was observed in G_1 (BD-319) and the lowest value (0.50 kg) was observed in G_{11} (BD-337). In respect of fruit length, longest fruit (32.53 cm) was observed in G_3 (BD-321) and the genotype no. G_{23} (BD-374) had the smallest length of (19.55cm). In case of fruit breadth, the highest value (38.24 cm) was observed in G_{16} (BD-349) and the lowest value (24.53 cm) was observed in G_{20} (BD-364). The highest average yield per plant (3.18 kg) was in G_{17} (BD-354) and the lowest yield per plant (0.50kg) was recorded in G_{11} (BD-337).

The phenotypic variance was higher than the corresponding genotypic variance in all the characters, indicating greater influence of environment on the expression of these characters. The maximum differences between phenotypic and genotypic coefficient of variation were 52.19% and 36.44%, respectively which indicated that the no. of male flower mostly depended on environmental effect. The highest estimated heritability among thirteen yield contributing characters 97.55%, 97.46%, 93.90%, 90.09% and 73.19% was in pedicel length of male flower, pedicel length of female flower, days to first male flower, days to first female flower and yield per plant. The lowest heritability was 24.31% in leaf length.

The maximum genetic advance was observed in respect of days to first male flower (16.99) and followed by maximum value was 14.45 in advance for days to first female flower among thirteen characters of wax gourd genotypes. The maximum genetic advance in percent of mean (GAMP) was obtained for yield per plant (72.10%) and the lowest was for leaf length (6.87%).

Multivariate analysis carried out through principal component analysis (PCA), principal coordinate analysis (PCO), cluster analysis, and canonical vector analysis (CVA) using Genstat 5.13 software programme. The first three principal characters with Eigen values were contributed 63.46% variation toward divergence. As per as PCA, D^2 and cluster analysis using the genotypes were grouped into six different clusters. Cluster I, II, III, IV, V and VI comprised one, four, two, ten, four and six genotypes, respectively.

The highest inter-cluster distance was observed between cluster I and cluster IV (16.607) followed by the distance between cluster I and cluster III (14.677), between cluster I and cluster II (14.175). Similarly, the lowest inter-cluster distance was observed between the cluster VI and cluster III (6.072) followed by IV and VI (6.659).

The highest intra-cluster distance was found in cluster V (0.358) followed by cluster II (0.235). The lowest intra-cluster distance was observed in cluster IV (0.038).

The highest intra-cluster distance was observed between genotypes G_7 and G_{22} (46.326) followed by G_7 and G_{13} (46.081) and the lowest distance was observed (0.381) between genotypes G_6 and G_{14} followed by the distance (1.923) between genotypes G_{19} and G_{25}. Cluster I ranked first for fruit weight (1.53kg), fruit length (26.47cm) and fruit breadth (36.00cm). leaf breadth (26.75), cluster II ranked first for leaf length (13.40cm), internodes distance (11.71cm), pedicel length of male flower (10.62cm), pedicel length of female flower (6.64cm), number of male flower (42.58), number of female flower (7.71) and fruit yield per plant (1.53kg) and cluster IV ranked first for days to first male flower (55.43) and days to first female flowering (73.30).

Findings of the present study indicated significant variation among the genotypes for all the characters studied. Considering diversity pattern and other field performances, the genotypes G_{20} (BD-364) from cluster V, G_{17} (BD-354) from cluster II; G_1 (BD 319) from cluster IV and G_{16} (BD-349) from cluster VI could be best choice as suitable parents for efficient hybridization program. Therefore considering group distance and other agronomic performance the inter genotypic crosses between G_{20} (BD-364) and G_{17} (BD-354); G_1 (BD 319) and G_{16} (BD-349), G_{20} (BD-364) and G_1 (BD 319), G_{20} (BD-364) and G_{16} (BD-349)), G_{17} (BD-354)and G_1 (BD 319), G_{17} (BD-354) and G_{16} (BD-349) may be suggested for future hybridization programme.

The result of present study revealed that a wide variability exists among the collected wax gourd genotypes. In addition, there was also genotypic variability of different yield contributing characters with yield of wax gourd. From the findings of the present study, the following conclusions could be drawn:

i. Wide range of genetic diversity existed among the wax gourd genotypes. That variability could be used for future breeding programme of wax gourd in Bangladesh.

ii. Selection procedure would be applied for desired characters such as leaf breadth, fruit breadth, fruit weight and fruit length and days to first male flower, days to first female flowering, pedicel length of male flower, female flower pedicel length to develop high yielding varieties.

iii. Further collection of wax gourd germplasm would be continued for getting more variability and desired traits in wax gourd.

iv. Highly significant positive association of yield per plant were observed with pedicel length of female flower, fruit breadth & fruit weight.

v. Path analysis showed that, yield per plant had the high direct effect on pedicel length of female flower, fruit breadth & fruit weight.

vi. **BD-364** from cluster **V; BD-354** from cluster **II; BD-319** from cluster **IV** and **BD-349** from cluster **VI** might be selected as suitable parents in future hybridization program.

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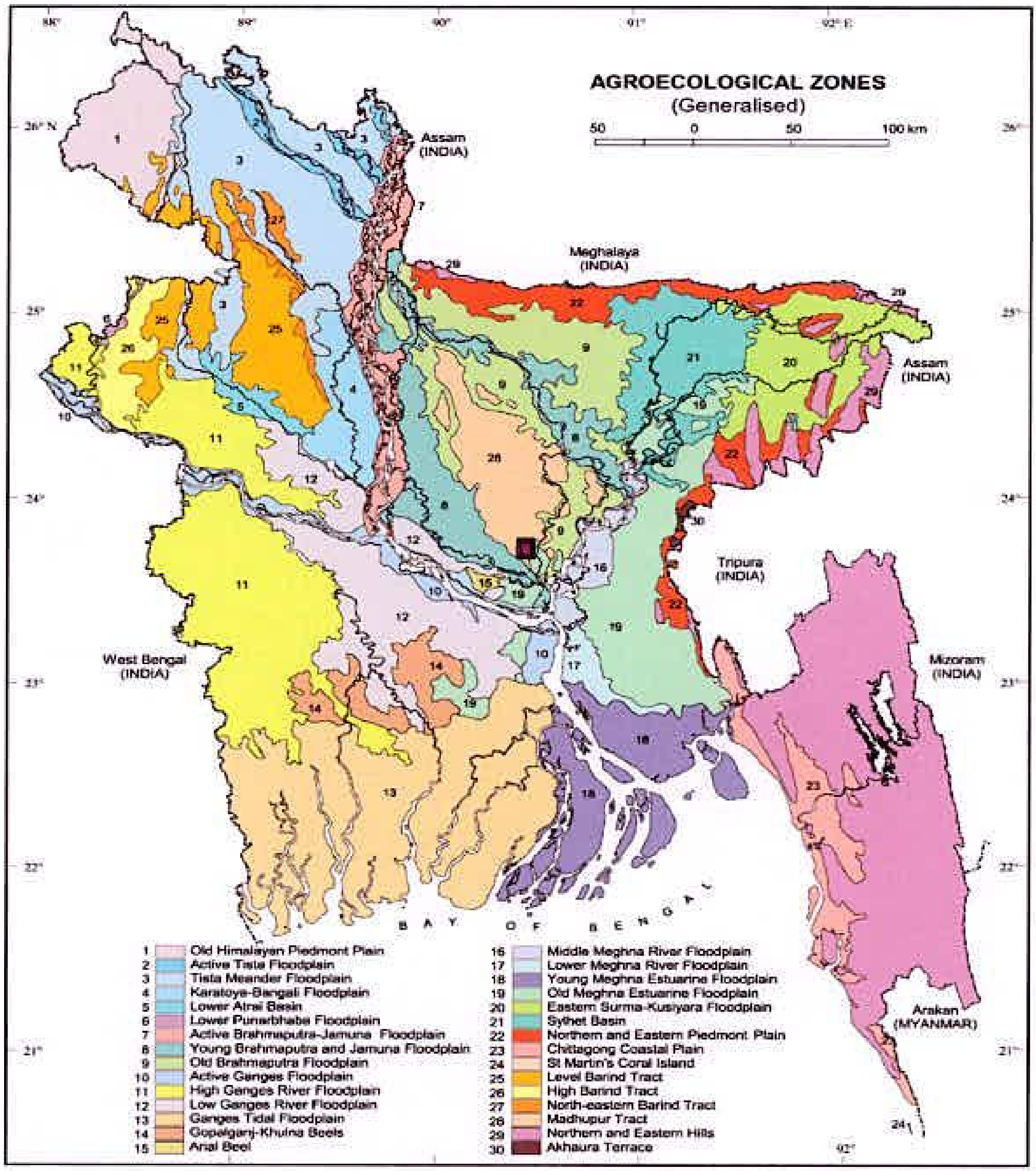
Appendices

APPENDICES

Appendix I . Map showing the experimental site under study



■ **The experimental site under study**

Appendix II. Monthly average Temperature, Relative Humidity and Total Rainfall of the experimental site during the period from March 2010 to August 2010

Month	Air temperature (°c) Maximum	Minimum	Relative Humidity (%) (total)	Rainfall (mm)	Sunshine (hr)
March, 2010	34.6	16.5	67	45	7.3
April, 2010	35.8	20.3	65	88	8.3
May, 2010	36.7	20.3	70	205	7.7
June, 2010	35.4	22.5	80	577	4.2
July, 2010	34	24.6	83	563	3.1
August, 2010	36	23.6	81	319	4.0

Source: Bangladesh Metrological Department (Climate and Weather division), Agargaon, Dhaka- 1212.

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

A. Physical composition of the soil

Soil separates	%	Methods employed
Sand	36.90	Hydrometer method (Day, 1915)
Silt	26.40	Do
Clay	36.66	Do
Texture class	Clay loam	Do

B. Chemical composition of the soil

Sl. No.	Soil characteristics	Analytical data	Methods employed
1	Organic carbon (%)	0.82	Walkley and Black, 1947
2	Total N (kg/ha)	1790.00	Bremner and Mulvaney, 1965
3	Total S (ppm)	225.00	Bardsley and Lanester, 1965
4	Total P (ppm)	840.00	Olsen and Sommers, 1982
5	Available N (kg/ha)	54.00	Bremner, 1965
6	Available P (kg/ha)	69.00	Olsen and Dean, 1965
7	Exchangeable K (kg/ha)	89.50	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	pH (1 : 2.5 soil to water)	5.55	Jackson, 1958
10	CEC	11.23	Chapman, 1965

Source: Soil Resource and Development Institute (SRDI), Dhaka

Appendix IV. Mean performance of different parameter of 27 genotypes of wax gourd

Genotype	DFMF	DFFF	LLWP	LB	ID	PLMF	PLFF	NMF	NFF	FW	FL	FB	FYP
BD-319	57.33	72.33	14.65	16.75	9.80	10.37	5.50	23.05	5.00	1.63	27.71	37.07	2.06
BD-320	45.67	69.67	13.08	17.08	10.58	6.93	4.87	24.67	4.00	0.92	24.60	33.48	2.24
BD-321	58.00	77.00	13.92	14.84	9.17	9.93	4.80	26.42	8.86	0.88	32.53	29.30	0.88
BD-322	45.67	67.00	13.08	16.90	10.77	6.67	3.70	14.78	6.51	0.90	23.92	28.64	2.08
BD-323	35.33	56.33	11.27	15.68	9.64	9.47	4.50	11.00	5.29	1.53	26.47	36.00	1.53
BD-324	54.33	69.33	13.17	17.75	8.27	7.97	4.37	15.00	3.67	1.01	24.53	30.13	2.06
BD-325	35.67	55.33	12.73	16.30	11.00	11.30	6.43	48.33	7.41	1.14	23.27	33.27	2.53
BD-328	42.33	63.67	13.58	17.87	12.17	6.83	6.13	44.33	8.30	1.04	23.33	34.83	2.39
BD-329	34.67	55.67	13.07	17.50	12.53	11.70	4.67	40.33	7.14	1.06	24.32	32.36	2.19
BD-333	43.00	66.67	14.03	15.26	10.10	12.73	6.37	33.67	5.96	0.70	22.73	28.28	0.89
BD-337	45.67	72.00	11.41	16.18	10.50	8.47	6.27	43.00	5.82	0.50	24.33	26.28	0.50
BD-338	34.67	58.67	13.87	17.83	11.93	6.13	3.80	32.00	5.71	0.75	20.46	27.57	1.54
BD-340	59.00	79.67	13.75	17.67	9.03	7.87	4.50	17.00	3.47	0.70	22.43	32.40	0.70
BD-342	56.67	66.33	12.89	15.88	9.67	9.50	5.33	14.67	6.36	1.03	22.15	33.21	2.81
BD-348	43.00	65.33	13.47	18.45	10.60	11.57	8.33	15.00	2.69	1.06	23.52	31.59	2.75
BD-349	47.00	69.67	14.56	18.66	9.67	12.10	6.37	21.75	3.03	1.40	25.71	38.24	2.18
BD-354	36.67	57.00	14.23	19.98	11.13	12.63	9.33	37.33	8.00	1.20	24.97	34.29	3.18
BD-358	35.00	53.67	13.92	19.28	10.07	9.83	5.73	28.33	6.00	1.00	24.85	32.24	1.00
BD-361	46.00	66.00	13.00	16.41	11.20	6.10	5.63	17.75	4.07	0.75	22.59	29.27	1.03
BD-364	33.33	56.33	13.64	19.50	11.03	14.27	7.40	22.67	5.86	0.61	22.62	24.53	0.96
BD-368	52.67	73.67	11.83	15.49	11.83	6.53	3.67	20.71	4.07	1.18	22.63	34.38	1.20
BD-370	56.33	77.67	11.65	18.53	8.87	10.43	4.67	13.34	3.51	0.84	23.30	32.33	1.12
BD-374	35.67	62.00	12.11	15.17	11.33	6.00	4.47	20.05	3.74	0.99	19.55	28.06	2.80
BD-2406	53.00	69.33	9.07	12.92	10.27	9.50	4.17	20.18	3.33	0.58	20.98	25.13	0.91
BD-2412	45.33	65.00	11.23	14.53	10.07	8.93	3.67	19.68	2.42	1.22	24.25	32.88	1.58
BARI Chalkumra-1	53.00	72.00	13.33	17.51	9.53	9.33	7.30	17.33	2.40	1.03	22.27	34.47	1.99
Local	54.00	75.67	13.90	18.00	8.63	12.47	8.23	20.75	6.94	0.93	21.53	30.97	2.27
Mean	45.89	66.41	12.98	16.96	10.35	9.47	5.56	24.56	5.17	0.98	23.76	31.53	1.75
Minimum.	**33.33**	**53.67**	**9.07**	**12.92**	**8.27**	**6.00**	**3.67**	**11.00**	**2.40**	**0.50**	**19.55**	**24.53**	**0.50**
Maximum.	**59.00**	**79.67**	**14.65**	**19.98**	**12.53**	**14.27**	**9.33**	**48.33**	**8.86**	**1.63**	**32.53**	**38.24**	**3.18**

LLWP = Leaf length (cm), LB = Leaf breadth, DFMF = Days to first male flowering, DFFF = Days to first female flowering, PLMF = Pedicel length of female flower (cm), PLFF = Pedicel length of female flower (cm), NMF = Number of male flower per plant, NFF = Number of female flower per plant , FL = Fruit length (cm), FB = Fruit breadth (cm), FW = Fruit weight (g), NFP = Number of fruits per plant and FYP = Fruit yield per plant (kg).

Appendix V. Principal Component score of 27 genotypes of wax gourd

Genotype	Z1	Z2
G_1	10.70	-7.33
G_2	1.62	-1.45
G_3	10.89	-12.80
G_4	6.41	7.20
G_5	-1.97	19.34
G_6	12.75	2.10
G_7	-26.86	-8.31
G_8	-16.36	-12.24
G_9	-22.19	-1.97
G_{10}	-7.67	-5.65
G_{11}	-9.44	-16.25
G_{12}	-15.22	3.50
G_{13}	19.18	-6.19
G_{14}	12.60	2.46
G_{15}	3.92	9.19
G_{16}	4.26	-0.08
G_{17}	-18.64	-1.49
G_{18}	-15.01	7.85
G_{19}	4.35	5.50
G_{20}	-11.55	12.00
G_{21}	10.21	-3.40
G_{22}	18.94	-1.32
G_{23}	-5.08	10.69
G_{24}	8.50	-0.77
G_{25}	2.58	4.74
G_{26}	11.74	-0.17
G_{27}	11.33	-5.15