CHARACTERIZATION AND GENETIC DIVERSITY OF SPONGE GOURD (*Luffa cylindrica* L.)

By

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CERTIFICATE

This is to certify that the thesis entitled, **"CHARACTERIZATION AND GENETIC DIVERGENCE OF SPONGE GOURD (*Luffa cylindrica* L.)"** submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE** in **GENETICS and PLANT BREEDING**, embodies the result of a piece of bona fide research work, carried out by **Md. Abdul Gaffar, Registration No.: 01062,** 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 sources of information, as has been availed of during the course of this investigation has duly been acknowledged.

Dated: June, 2008
Place: Dhaka, Bangladesh

(Prof. Dr. Md. Sarowar Hossain)
Supervisor


Dedicated to
My
Parents

LIST OF ABBREVIATIONS

Symbols	Acronyms
%	Percentage
°C	Degrees Celsius
ANOVA	Analysis of variance
BBS	Bangladesh Bureau of Statistics
cm	Centimeter
CV	Coefficient of variation
e.g.	Exempli gratia (by way of example)
et al.	et alu=other people
etc.	et cetera (means and the rest)
FAO	Food and Agriculture Organization
Fig.	Figure
g	Gram
gl^{-1}	Gram per litre
GDP	Gross Domestic Product
ha	Hectare
hrs.	Hours
i.e.	ed est (means That is)
IARI	Indian Agricultural Research Institute
ICRISAT	International Crop Research Institute for the Semi-arid Tropics
IRRI	International Rice Research Institute
j.	Journal
LB	Left border
mgl^{-1}	Milligram per litre
ml	Mili litre
Na_2-EDTA	Sodium salt of ferric ethylene diamine tetraacetate
No.	Number
NS	Non significant
pH	Negative logarithm of hydrogen ion concentration (-log $[H^+]$)

LIST OF ABBREVIATIONS

Symbols	Acronyms
req.	Required
Spp.	Species (plural)
t	Ton
T-DNA	Transfer DNA
TK	Taka
UK	United Kingdom
var.	Variety
via	By way of
viz.	Namely
DSG	Days to seed germination
INL	Inter node length
LL	Leaf length
LB	Leaf breadth
PTL	Petiole length
DFMF	Days to first male flower
DFFF	Days to first female flower
NFMF	Node no. of first female flower
SR	Sex ratio
FDM	Fruit diameter
PDL	Peduncle length
NFPP	No. of fruit per plant
AFW	Average fruit weight
YPP	Yield per plant
NSPP	No. of seed per fruit
SL	Seed length
SB	Seed breadth
ST	Seed thickness
HSW	Hundred seed weight
DF	Degrees of freedom

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Dated: June, 2008
Place: SAU, Dhaka.

The Author

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CHARACTERIZATION AND GENETIC DIVERSITY OF SPONGE GOURD (*Luffa cylindrica* L.)

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ABSTRACT

The morphological character, genetic diversity, genotypic and phenotypic variance, genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean were studied for 15 genotypes of sponge gourd were determined in a field experiment conducted at the farm of Sher-e-Bangla Agricultural University, Dhaka during April, 2007 to October, 2007. Significant genotypic differences were observed for all the characters studied. The phenotypic coefficient of variation was higher than genotypic coefficient of variation in all the characters. The phenotypic coefficient of variation (PCV) estimates were high for all the characters. Heritability estimates were high for days to seed germination, days to first male flower, days to first female flower, peduncle length, fruit length and no. of seed per plant. In spite of high heritability values for most traits, the expected genetic advance as percentage of mean ranged from 1.14 to 121.30. Multivariate analysis was performed through principal component analysis (PCA); principal coordinate analysis, cluster analysis and canonical variate analysis were used to classify 15 sponge gourd genotypes. As per as PCA, D^2 and cluster analysis, the genotypes were grouped into five different clusters. Cluster I and cluster IV had the maximum of four and minimum of one genotypes respectively. The highest inter-genotypic distance was found between G01 and G02 and the lowest distance between G02 and G07. The maximum inter-cluster distance was observed between the clusters IV and cluster V, whereas the lowest-inter cluster distance was found between the cluster I and cluster IV. The highest intra-cluster distance was identified in cluster III and the lowest intra cluster distance was found in cluster IV. Genotypes included in cluster I suitable for yield per plant, cluster III for having the highest mean value for inter node length, cluster V for leaf length, leaf breadth, petiole length, days to first male flower, days to first female flower, node no. of first male flower, node no. of first female flower and sex ratio. Considering diversity pattern and other agronomic performances the genotypic crosses between G01and G02; G01 and G07; G01 and G15; G01 and G04; G01 and G14; G01 and G10; G11 and G 07; G05 and G14; G02 and G03; G04 and G11, might be used for future hybridization programme

Chapter I

Introduction

CHAPTER I
INTRODUCTION

Sponge gourd (*Luffa cylindrica* L.) belongs to the family Cucurbitaceae having chromosome number, 2n = 26, under the order cucurbitales, subclass polypatae and class Dicotyledon (Hooker, 1979). It is an annually cultivated monoecious climbing type herbaceous vegetable crop. It is probably originated in the tropical Asia and Africa. Now it is extended to the Indian subcontinent, China, America and other countries.

Sponge gourd is named as smooth, loofash, vegetable sponge, disa-rug gourd etc. It is named in Bangladesh as Dhundal. It is mainly used in Bangladesh as vegetable. It is also used for different purposes in other countries. It's fruits contain a fibrous vascular system. The fibre network is used as a bathroom sponge. It is useful for the preparation of soup, filters, slipper soles, baskets etc.

In Bangladesh, vegetable production is not uniform round the year due to climatic and edaphic factors. Vegetables are produced on large scale during the winter. There is a scaricity of vegetables during summer or rainy season and only small number of vegetables are produced during the period from April to October. Among these vegetables, sponge gourd contributes a significant portion of vegetable production during lean period of vegetable supply in summer and rainy season of Bangladesh.

Morphological characterization is important to identify the species, to classify the species into different group and give an idea about the crop canopy. Variability is a desirable goal in germplasm collection since the material conserved in such collection represents the stock material for breeding programme. Knowledge of the interrelationship between yield and yield contributing characters is necessary. Thus, determination of correlation among the characters is a matter of considerable importance in selection of correlated response.

In crop improvement programme, genetic diversity has been considered as an important factor and an essential pre-requisite for hybridization programme. If the genotype are identified on the basis of diverse analysis, the resulting recombinants through hybridization would be more promising. Several methods of multivariate analysis such as D^2 cluster and factor analysis have been proved to be useful in selecting germplasm for hybridization. Mahalanobis (1936) D^2 analysis has been successfully used in measuring the diversity in several cucurbitaceous crops (Masud *et al.* 2001, Badade *et al.* 2001. Rashed *et al.* 2002).

A good number of landraces of sponge gourd are present in Bangladesh. But till now no recommended or released varieties are available. Systematic research was not made in the past to evaluate the potentialities of the available genotype. Considering the above facts, the present study was undertaken with the following objectives:

- To characterize the genotypes on the basis of different morphological and yield contributing characters,
- To study the genetic variability for different quantative characters involved among sponge gourd genotypes,
- To study the genetic diversity among the materials,
- To study the genetically diverged parents to involve them in the future hybridization programme.

Chapter II
Review of Literature

CHAPTER II
REVIEW OF LITERATURE

Though sponge gourd is an important vegetable cultivated in Bangladesh, there are few reports related to the present study in this country as well as other countries of the world. Therefore, the literature relevant to the present study on sponge gourd and some other related vegetables under the family Cucurbitaceae are reviewed in this chapter under the following headings.

2.1 Morphological characterization

Arora *et al.* (1983) reported in sponge gourd that days to first male and female flowering ranged from 56 to 118 days and 61 to 125 days, respectively.

Akand (1193) observed in ridge gourd that in five parental lines first male flower opened within 42 to 46 days, and the first female flower opened within 48 to 52 days, while for hybrids it ranged from 40 to 45 days and 43 to 51 days for male and female flower anthesis, respectively.

Latif (1993) noted in ridge gourd that the number of days to male flower opening of five parental lines and for their hybrids ranged from 46 to 49 and 46 to 51 days, and that for female flowers it ranged from 51 to 54 and 50 to 55 days, respectively. Female flowering was late as compared to male flowering in all genotypes and hybrids tested.

Sahni *et al.* (1987) found non-additive gene effects in first female flowering node as well as female flower number per stem in ridge gourd.

In a study Rahman *et al.* (1990) observed significant variation for days to first flowering among the genotypes of ridge gourd. They reported that days to male and female flowering ranged from 35 to 37 days and 37 to 43 days, respectively.

Rahman *et al.* (1990, 1991) also concluded that days to male flowering was earlier than days to female flowering in the genotypes of ridge gourd studied.

Krishna Prasad and Singh (1989) noted in ridge gourd that the number of node at which first male and female flowers opened was an average of 7 to 16.

Arora *et al.* (1983) observed in sponge gourd that the node number of first female flowers opened ranged from 8 to 20.

Rashid (1993) reported that the fruits of ridge gourd are tubular shaped or club shaped, deep green in colour and ten ridge are present on the surface of fruit.

Choudhury (1967) observed the fruits of hermaphrodite variety known as satputia are small and are born in clusters.

Rashid (1993) noted that the length of ridge gourd fruit varied from 15 to 401 cm.

Rahman *et al.* (1990, 1991) found significant variations in fruit length and breadth of ribbed gourd genotypes. They reported that fruit length varied from 11 to 16 cm and fruit breadth varied from 2.8 to 4.1 cm.

Sahni *et al.* (1987) studied the genotypic and phenotypic variability in ribbed gourd and found that fruit length and fruit breadth showed potentiality for improvement by heterosis breedin0g.

Sahni *et al.* (1987) studied genotypic and phenotypic variability in ribbed gourd and found that heritability was high for most of the characters studied. They also reported that fruit weight was controlled by additive genes.

Rahman *et al.* (1990, 1991) reported significant variations in fruit weight among a number of genotypes of ribbed gourd. They reported that the average weight per fruit varied from 50 g to 95 g. The genotypes with longest fruits did not have highest individual fruit weight, on the contry the genotypes with smallest fruits showed the highest fruit weight.

Akand (1993) studied mean performance of fruits per plant of 20 ridge gourd hybrids and their parents. He reported that the total number of fruits per plant ranged from 5.22 to 6.11.

Latif (1993) reported that the range of total number of fruits per plant of 5 ridge gourd inbred lines and their 10 F_1 hybrids were 17.43 to 25.35.

Krishna *et al.* (1989) observed that the range of total number of fruits per plant of 11 varieties of ridge gourd was 26 to 86.

In study Rahman *et al.* (1990) reported significant variation in biter gourd, ribbed gourd, sweet gourd genotypes for number of fruits per plant.

Rahman *et al.* (1990) reported in ridge gourd that the average yield per plant varied from 1.83 kg to 3.00 kg with no significant difference. They also mentioned that weight per fruit appeared to be unrelated with yield per plant.

Latif (1993) noted that the range of yield per plant of 5 ridge gourd inbred lines and their 10 F_1 hybrids was 1.01 kg to 2.14 kg. After evaluation of 20 hybrids of ridge gourd and their parents, Akand (1993) reported that the range of yield per plant was 215 to 385 g.

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 on 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.

Ninety eight hybrids of cucumber derived from crosses involving 14 male and 7 female parents were carried out by Singh *et at.* (2002) and found that fruit weight, fruit girth and fruit length had high correlations with fruit yield. Genotypic correlation co-efficients were higher than the phenotypic co-efficient which

indicated strong association among these traits. Path coefficient analysis also indicated that fruit weight had the highest direct effect on fruit yield.

Badade *et al.* (2001) carried out 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.

Miah *et al.* (2000) noted that fruit yield 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. 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.

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

Number of fruits per plant, average fruit weight, fruiting rate and leaf area of cucumber genotypes were positively correlated to yield. Days to flowering and vine length were negatively correlated. From path analysis, they also concluded that fruits per plant and average fruit weight affected the yield directly (Li *et al.*, 1997).

Paranjape and Rajpute (1995) stated that the genotypic correlation of 21 bitter gourd genotypes revealed, yield was mainly contributed by number of fruits/vine, average fruit weight and fruit length. The physiological attributes like vine length, primary branches and average leaf area were mutually associated and had effects on yield.

2.2 Genetic diversity

Guar *et al.* (1978) studied genetic diversity is one of the important tools to quantify genetic variability in both self and cross-pollinated crops Twenty six genotypes of snake gourd were tested using multivariate analysis and the genotypes were grouped into seven distinct clusters. No relationship was found between genetic divergence and geographic all distribution of genotypes. The highest inter genotypes distance was observed between the genotypes SG 026 and SG 0.10 (1.897).

Banik, (2003) found that the inter cluster distance was maximum between cluster II and IV (17.74). Main vine length, node number for first female flower, nodes on main vine, fruit length and number of seeds per fruit had the highest contribution towards the divergence

Raseed *et al.* (2002) studied the genetic divergence of 47 pumpkin genotypes collected from different parts of Bangladesh using Mahalanobis's D^2 and principal component analyses. The genotypes were grouped into seven clusters. Clusters III had the maximum (11) and cluster IV and VII had the minimum (4) number of genotypes. The characters like fruit weight, yield per plant contributed maximum towards total divergence.

Masud *et al.* (2001) studied genetic divergence in 19 genotypes of sponge gourd (*Luffa cylindrical*) collected from local and exotic sources. The genotypes were grouped into five clusters. The genetic divergence of the genotypes did not follow their geographical distribution and was fairly at random. There was no evidence of relationship between geographical distribution and genetic divergence as estimated by D2 statistics. Maximum intercluster distance (45.9) was observed between cluster II and V and minimum (10.3) between cluster II and IV. Fruit length and diameter were significant contributors to genetic divergence.

Cluster analysis was performed by Ram *et al.* (2001) in 167 Pointed gourd genotypes (*T. dioica*) collected from different ecogeographic region of India. On

the basis of different yield contributing agro morphological traits, the genotypes were grouped into eight cluster which were non-overlapping. Cluster IV comprising the most number of genotypes (37 accessions) and cluster VI comprising the lowest number of genotypes (6 accessions). Intra-cluster distance ranged from 1.258 in cluster I and 1.655 in cluster VII. Cluster VIII and V were the most diverse as indicated by maximum inter cluster distance between them (6.049). The results indicated the potential for wide scope of varietal improvement through hybridization and selection due to the wide genetic diversity present in the accession studied.

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, no. of branches, fruit/vine, length and diameter of fruit and yield per vine. Rashid (2000) found no relationship between geographic distribution and genetic diversity in pumpkin. The result suggested that geographic isolation in not the only factor causing genetic diversity and this point should be considered in selecting parents for hybridization.

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 grouped into seven cluster. No relationship was found between genetic divergence and geographic distribution of the genotypes. Maximkum inter cluster distance was observed between cluster II & VII and was minimum between V & VI. Number of fruits per plant and yield per plant showed maximum contributed to the total divergence. The results obtained by D^2 analysis were confirmed by principal component analysis.

Varalaksmi *et al.* (1994) conducted an experiment with 58 genotypes of ridge gourd collected from different regions of India to analyze genetic divergence. Nineteen (19) quantitative characters were selected to study genetic

divergence using Mahalanobi's D^2 statistics and Tocher method to form cluster. The 58 genotypes were grouped into five clusters but, in general, there was no association between geographical distance and genetic divergence. There was substantial variation in cluster means for whole plant sex ratio, fruit number per plant, fruit weight and yield per plant. The intercluster D^2 value indicated that cluster III was most divergent from the other clusters.

Chapter III

Materials and Methods

CHAPTER III
MATERIALS AND METHODS

3.1 Experimental Site

The experiment was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka-1207, during April, 2007 to October, 2007. The Location of the experimental site was situated at $23^0$41' N latitude and $90^0$22' E longitude with an elevation of 8.6 meter from the sea level. The physical and chemical characteristics of the soil have been presented in Appendix I.

3.2 Climate and Soil

The experimental site was situated in the subtropical zone. The soil of the experimental site lies in Agro ecological region of "Madhupur Tract" (AEZ No. 28) of Norda soil series. The soil is sandy loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH is 5.47 to 5.63 and organic carbon content is 0.82% (Appendix I). The mean temperature during the research period was 24.21^0C with average maximum and minimum being 29.4^0C and 19.03^0C respectively. The record of air temperature, humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka Appendix II).

3.3 Genotypes

A total number of 15 (Fifteen) genotypes were used in this experiment. The seeds of the fifteen genotypes were collected from several area and market of Bangladesh. Sources of genotypes is presented in Table 1.

3.4 Design and Layout

The experiment was laid out in Randomized complete Block Design (RCBD) with three replications. The total area of the experiment was 29.2m × 9.9 m,

and the distance between two units was 2 m. of fifteen genotypes with the spacing of 2 m × 1.25 m. The thirty four genotypes were distributed to each plot within each unit randomly.

Table 1. Sources of 15 sponge gourd genotypes

Sl. No.	Designation	Sources
01	G-01	Fujian (LTSC)
02	G-02	Rajshahi (L)
03	G-03	Shuvra (MSC)
04	G-04	Chuadanga (L)
05	G-05	Majnushah (MSC)
06	G-06	Lalonshah (MSC)
07	G-07	Tangail (L)
08	G-08	Shrabani (USC)
09	G-09	Mayabi (USC)
10	G-10	Dhaka (L)
11	G-11	Laksmi (IN)
12	G-12	Comilla (L)
13	G-13	Karnaphuli (T)
14	G-14	Munshigonj (L)
15	G-15	Jessore (L)

3.5 Raising of Seedling

Individual poly bag was prepared for different varieties following standard method of poly bag soil preparation. Seeds were sown in well prepared poly bag seed beds on 6th April 2007. The seeds were sown at about 1.25 cm depth and were covered uniformly with light soil for proper germination. Heptachlor was dusted over the seedbed to prevent the seedling mainly from ant attack. The seed bed was watered as and when necessary for proper germination as well for normal growth of the seedling. After germination shading was arranged to protect the young seedling from scorching sunshine and was kept exposed during night, morning and afternoon. Proper nursing was done for developing healthy seedlings. At the attainment of 30 days of age the seedlings were transplanted to the Experimental Plot.

3.6 Land Preparation

The experimental plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with power tiller and country plough to bring about good tilth. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly. The final land preparation was done on 06 April 2007.

3.7 Pit preparation

After final land preparation, pits of 50 × 50 × 30 cm were prepared in each plot with a spacing of 2 × 2.5 m. Pits were kept open in the sun for 7 days. To control field cricket, Furadan was also mixed with the soils of each pit before transplanting of seedling.

3.8 Application of manures and fertilizers

Manures and fertilizer was applicable by the rule of horticultural division of BARI which was shown Table 2.

3.9 Transplanting of Seedling

Thirty days old seedlings were transplanted in well prepared experimental plot on 6th May, 2007. Two plants were planted for each genotype in single pit in each replication maintaining plant spacing. Field view of the experiment was shown in Plate 1a. and Plate 1b.

3.10 Intercultural operations

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

3.10.2 Thinning Out and Gap filling

Keeping only one healthy seedlings between the two seedlings per pit, to avoid crowded situation. On the contrary, gap filling was done where needed.

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

Fertilizer	Total Amount	Basal dose /Decimal	Dose of fertilizer per Pit				
			7-10 DBT	10-15 DAT	30-35 DAT	50-55 DAT	70-75 DAT
Cow dung	80 Kg.	20 Kg.	10 Kg.	-	-	-	-
TSP	700 g.	350 g.	60 g.	-	-	-	-
Urea	700 g.		-	30 g.	30 g.	30 g.	30 g.
MOP	600 g.	200 g.	50 g.	25g.	-	-	-
Gypsum	400 g.	400 g.	-	-	-	-	-
Zn fertilizer	50 g.	50 g.	-	-	-	-	-
Borax	40 g.	4 g.	-	-	-	-	-
MgO	50 g.	-	8 g.	-	-	-	-

Plate 1a. Field view of the experimental site

Plate 1b. Field view of the experimental field

3.10.3 Weeding and Mulching

Weeding and mulching were necessary to keep the plots free from weeds at initial stage for ease of aeration and to conserve soil moisture. Seven weeding were done to keep the plot free from weeds. The soil was mulched after each irrigation to prevent crust formation and to facilitate good aeration

3.10.4 Irrigation

In the early stage of transplanting, watering was done twice daily by water cane. In mature stage, flood irrigation was done to the field when it was necessary for the crop.

3.11 Pendel preparation

Pendel was made with bamboo wire and net for proper growth and development of the sponge gourd plants.

3.12 Plant Protection Measures

At seedling stage, especially at cotyledonary leaves, the seedling were attacked by red pumpkin beetle. In primary stage of infestation, ash was used. Besides that Malathion was used in case of severe infestation. Fruit fly caused serious damage to the fruits. Preventive and curative measures were taken against the attack of fruit fly by using and poison bait.

3.13 Harvesting

Harvesting of fruits was started from the 9 June, 2007 and continued up to 25 October, 2007. Sponge gourd fruits were picked on the basis of horticultural maturity, Size, colour and age being determined for the purpose of consumption as the sponge gourd grew rapidly and soon get beyond the marketable stage. Picking at three days interval was done throughout the harvesting period. Fruits were picked with a sharp knife and care was taken to avoid injury of the vine.

3.14 Data Collection

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

3.14.1 Seed Germination

Days of seed germination for each genotype was recorded.

3.14.2 Length of leaf

The length of three matured leaves were measured by a measuring scale from leaf base to the tip and expressed in centimeter.

3.14.3 Breadth of leaf

The breadth of three leaves were measured at the broadest part of leaves by a measuring scale and expressed in centimeter.

3.14.4 Leaf blade lobbing

The data were recorded by observing leaf structure phenotypically as per as the following structure:

- Weak
- Intermediate
- Strong

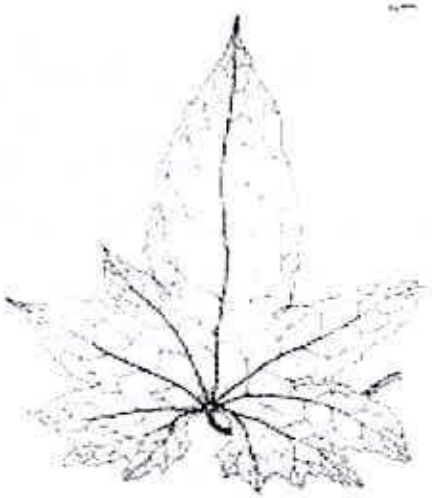
3.14.5 Leaf Shape

The data were recorded by observing leaf shape phenotypically as per as the following structure (Figure 1):

- Ovate
- Orbicular
- Reniform

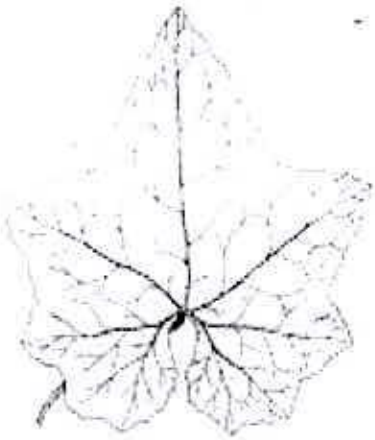
3.14.6 Length of petiole

The lengths of petiole of three mature leaves were measured in centimeter with the help of measuring scale.



Ovate

Orbicular



Reniform

Figure 1: Different shape of fruit

3.14.7 Days to first male flowering

Each germplasm was keenly observed for appearance of male flower and days to first male flower opening were recorded in each case.

3.14.8 Days to first female flowering

Each germplasm was keenly observed for appearance of female flower and days to first female follower opening were recorded in each case.

3.14.9 Nodal position of first male flower opening

The order of node at which male flower appeared was recorded by counting the number of nodes from ground level.

3.14.10 Nodal position of first female flower opening

The order of nodes at which first female flower appeared was recorded by counting the number of nodes in each replication.

3.14.11 Sex ratio of flower

Sex ratio (male flower: female flower) of flower was recorded in each germplasm.

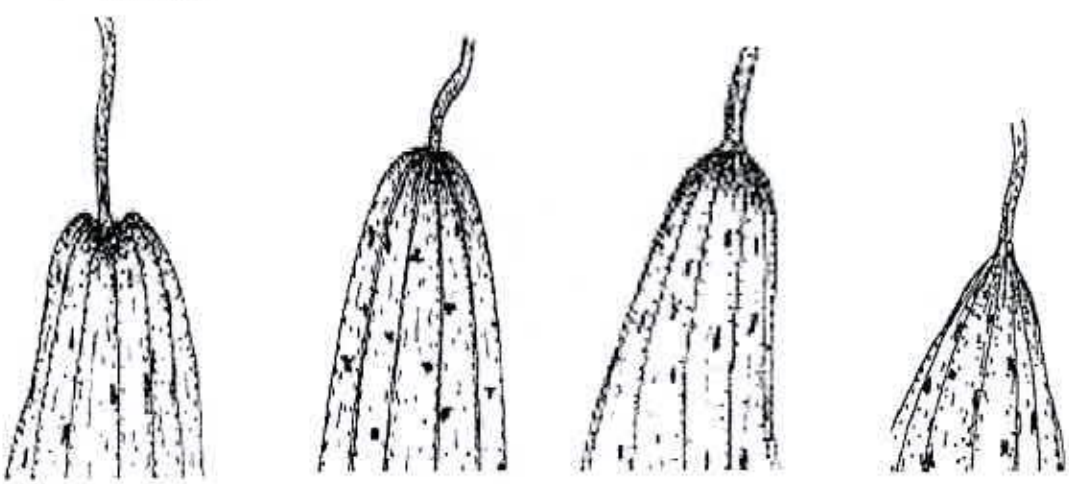
3.14.12 Time of anthesis

Anthesis time of the day in different sex types and their duration for full blooming were recorded.

3.14.13 Stem-end fruit shape

Stem-end fruit shape was recorded by watching under the following structure of the fruits.

- Depressed
- Flattened
- Rounded
- Pointed



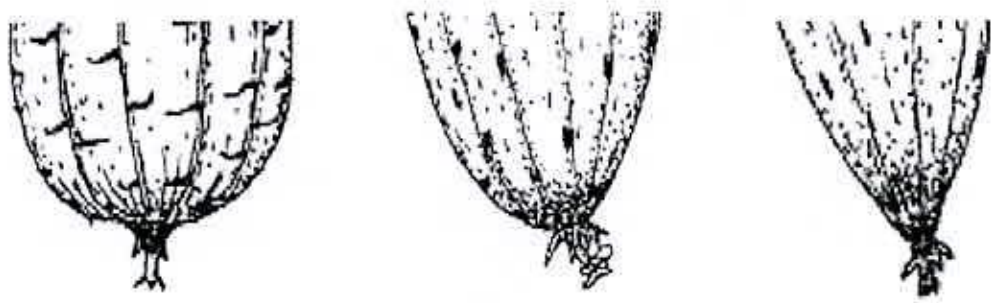
Depressed **Flattened** **Rounded** **Pointed**

Figure 2: Different shape of stem-end fruit

3.14.14 Blossom-end fruit shape

Blossom-end fruit shape was recorded by watching under the following structure of the fruits.

- Flattened
- Rounded
- Pointed



Flattened **Rounded** **Pointed**

Figure 3: Different shape of blossom-end fruit

3.14.15 Length of fruit

Three randomly selected fruits from selected plants of each germplasm were taken and mean length was measured at harvest.

3.14.16 Breadth of fruit

Diameter of three randomly selected green fruits from selected plants of each genotypes was measured with the help of slide calipers in centimeter.

3.14.17 Color of fruit

The fruit colour of 15 (fifteen) sponge gourd genotypes were recorded

3.14.18 Shape of fruit

The fruit of different genotypes showed differences in their shape. The fruit of every genotype was recorded as per as the following shapes:

- Elongate tapered
- Elliptical
- Oblong blocky
- Elongate slim
- Elongate elliptical

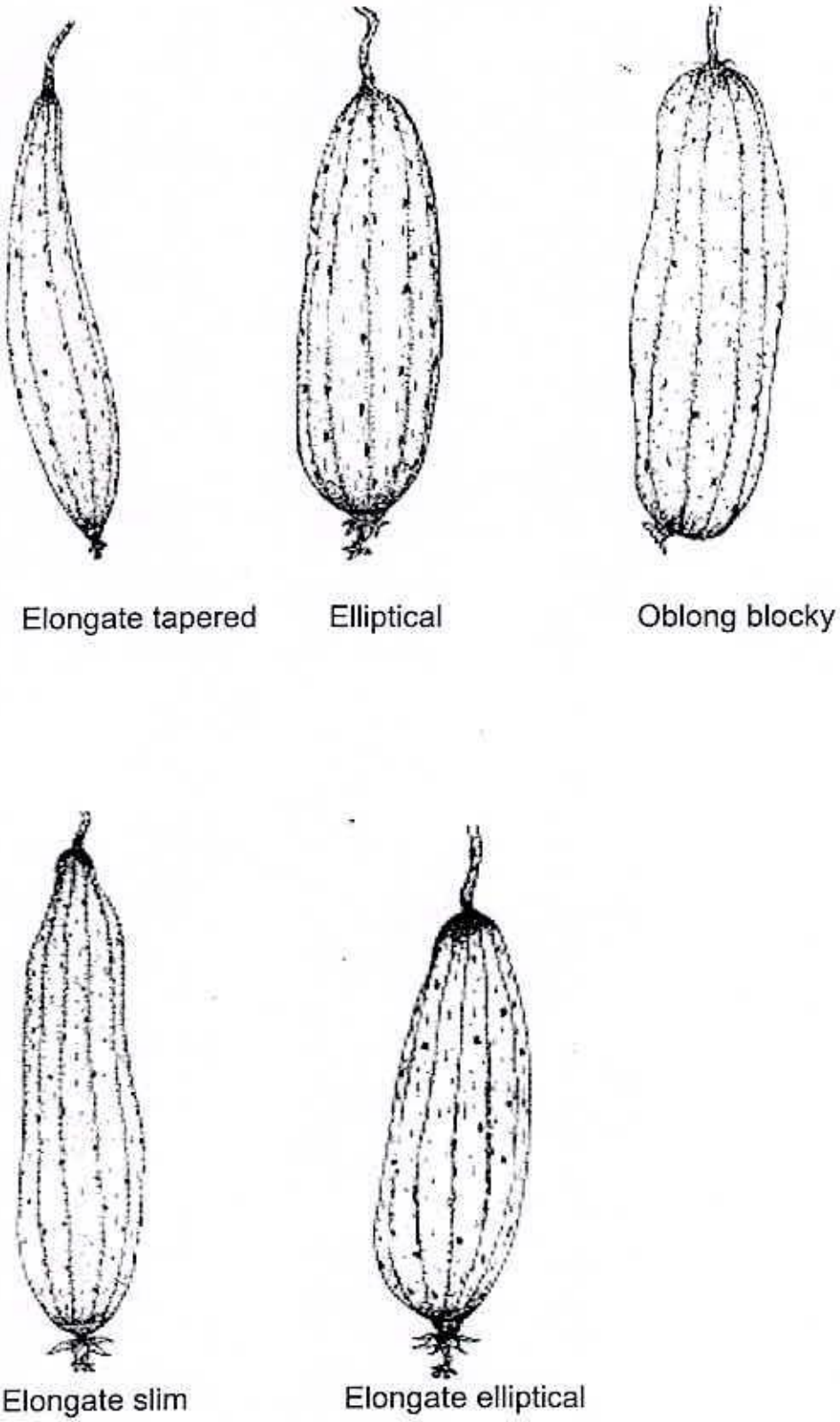


Figure 4: Different shape fruit

3.14.19 Peduncle length

Three randomly selected fruits were taken from selected plants of each germplasm and mean peduncle length was measured in centimeter.

Number of stripe per fruit: Three randomly selected fruits were taken from selected plants of each germplasm and mean number of stripe per fruit was recorded.

3.14.20 Number of fruits per plant

The total number of fruits of selected plants from each germplasm was recorded and mean was found out.

3.14.21 Average fruit weight

Weight of three randomly selected fruits at horticultural maturity stage from each germplasm was taken in gram and mean was calculated.

3.14.22 Yield per plant

Weight of fruits of selected plants from each germplasm was weighed in kilogram.

3.14.23 Inter node length of main stem

Average length of inter node from the 10^{th} node to the 15^{th} node was measured in cm.

3.14.24 Amount of seed in the fruit

Amount of seed was observing by cutting five fruits of every genotype. By observing amount of seed in the fruit the data were recorded.

3.14.25 Seed coat color

Different seed coat color was recorded.

3.14.26 Seed length

Average lengths of three mature seeds of each germplasm was measured by slide calipers in centimeter and mean was calculated.

3.14.27 Seed breadth

Average breadth of three mature seeds of each germplasm was measured by slide calipers in centimeter and mean was calculated.

3.14.28 Seed thickness

Three randomly selected seeds from selected plants of each germplasm was measured in centimeter by slide calipers and mean was calculated.

3.14.29 Hundred-seed weight

Hundred seeds were weighed by electric balance in gram.

3.15 Statistical analysis

Genetic divergence is one of the most important parameters evaluated by plant breeders in starting a breeding program. This is a necessary, but not sufficient, condition for the occurrence of heterosis and the generation of a population with broad genetic variability. Subsequently, heterosis is directly proportional to genetic divergence and to dominance squared (Falconer, 1981; Cruz, 1990; Ferreira, 1993) and is also associated with adaptation. A second approach is to use multivariate methods to estimate genetic divergence and then predict hybrid performance. In this case, it is not necessary to make crosses. Furthermore, a large number of materials may be successfully evaluated (Hallauer and Miranda Filho, 1981).

In the latter approach, a large number of traits must be measured. A canonical variate technique is often used to reduce the number of these traits, through a linear combination of them, without a significant loss of the total variation. Additionally, this technique takes into account the structure of residual covariances. Thus, it allows plant breeders to obtain information about traits that are important for genetic divergence among varieties.

The concept of D^2 statistics was originally developed by P. C. Mahalanobis in 1928. He used this technique in the study of Antropomatry and Psychometry. Rao (1952) suggested the application of this technique for the assessment of

genetic diversity in plant breeding. Now this technique is extensively used in plant breeding and genetics for the study of genetic divergence in the various breeding materials. This is one of the potent techniques of measuring genetic divergence. In plant breeding, Genetic diversity plays an important because hybrids between lines of diverse origin, generally, display a greater heterosis than those between closely related parents. This has been observed in fescue, maize, alfalfa, cotton and several other crops. Genetic diversity arises due to geographical separation or due to genetic barriers to crossability.

Statistical analysis such as Mahalanobis D^2 and Canonical Variate Analysis (CVA), which quantify the differences among several quantitative traits are efficient method of evaluating genetic diversity. Mean data of each quantitative character were subjected to both univariate and multivariate analysis. For univariate analysis of variance, analysis was done individually and least of significance was done by F- Test (Pense and Shukhatme, 1978). Mean, range, co-efficient of variation (CV) and correlation was estimated using MSTAT computer program. Multivariate analysis viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CLU) and Canonical Variate Analysis (CVA) were done by using GENSTAT program.

The hierarchical nature of the grouping into various number of classes could impose undue constrains and the statistical properties of the resulting groups were not at all clear Peyne *et al.* (1989). Therefore, they have suggested non-hierarchical classification, as an alternative approach to optimize some suitability choosing criteria directly from the data matrix. Peyne *et al.* (1989) also reported that the squared distance between means were Mahalanobis's D^2 statistics when all the dimensions were used, could be computed using principal coordinate analysis (PCO). They also commended the Canonical Variate Analysis (CVA) for discriminatory purpose.

3.15.1 Variability of Sponge Gourd Genotypes

3.15.1.1 Estimation of Phenotypic and Genotypic Variance

Genotypic and phenotypic variances were estimated by Johnson *et al.* (1955). Genotypic variance (6^2_g) was obtained by subtracting genotype mean sum of squire to error mean sum of squire and dividing by the number of replication as given below:

$$\textbf{Genotypic Variance } (\sigma^2_g) = \frac{\textbf{GMS-EMS}}{\textbf{Number of replication (r)}}$$

Where,

GMS = Genotypic mean sum of squire

EMS = Error mean sum of squire

The phenotypic variances (σ^2_p) were come from by adding genotypic variances (σ^2_g) with error variance (σ^2_e) as shown by the given formula:

$$\sigma^2_p = \sigma^2_g + \sigma^2_e$$

3.15.1.2 Estimation of Genotypic and Phenotypic Coefficient of Variation

According to the Johnson *et al.* (1955) genotypic and phenotypic coefficient of variation were estimated.

$$\textbf{Genotypic coefficient of Variation (GCV)} = \frac{\sigma_g}{\textbf{Grand Mean}}$$

Where,

σ_g = Genotypic standard deviations

$$\textbf{Phenotypic Coefficient of Variation (PCV)} = \frac{\sigma_p}{\textbf{Grand Mean}}$$

Where,

σ_p = Phenotypic standard deviations

3.15.1.3 Estimation of Heritability

Johnson et al. (1955) was suggesting a formula for estimating broad sense heritability.

$$\% h^2b = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where, h^2b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

3.15.1.4 Estimation of Genetic Advance

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

$$\text{Genetic Advance (GA)} = \frac{\sigma^2_g}{\sigma^2_p} \times K \times \sigma_p$$

Where,

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

σ_p = Phenotypic standard deviation

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

3.15.1.5 Estimation of Genetic Advance in Percentage of Mean

Genetic advance in percentage of mean was calculated from the formula given by Comstock and Robinson (1952).

$$\text{Genetic Advance in Percentage of Mean} = \frac{\text{Genetic Advance}}{\text{Grand Mean}} \times 100$$

3.15.2 Genetic Diversity Analysis

3.15.2.1 Principal Component Analysis (PCA)

It is a way of identifying patterns in data, and expressing the data in such a way as to highlight their similarities and differences. Since patterns in data can be hard to find in data of high dimension, where the luxury of graphical representation is not available, PCA is a powerful tool for analyzing data. The

purpose of principal component analysis it to derive a small number of linear combinations (principal components) of a set of variables that retain as much of the information in the original variables as possible.

Principal Component Analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters. It can be done from the sum of squares and products matrix for the characters. Principal components were computed from the correlation matrix and genotype scores obtained for the first components and succeeding components with latent roots greater than unity (Jeger *et al.* 1983). Contributions of different morphological characters towards divergence were 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 is used to calculate inter unit distances. Through the use of all dimensions 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 Clustering

The term *cluster analysis* (first used by Tryon, 1939) encompasses a number of different algorithms and methods for grouping objects of similar kind into respective categories.

In multivariate analysis, cluster analysis refers to methods used to divide up objects into similar groups, or, more precisely, groups whose members are all close to one another on various dimensions being measured. In cluster analysis, one does not start with any apriori notion of group characteristics. The definition of clusters emerges entirely from the cluster analysis-i.e. from the process of identifying "clumps" of objects.

Cluster analysis is an exploratory data analysis tool for solving classification problems. Its object is to sort cases (People, plant, things, events, etc) into groups, or clusters, so that the degree of association is strong between

members of the same cluster and weak between members of different clusters. Each cluster thus describes, in terms of the data collected, the class to which its members belong; and this description may be abstracted through use from the particular to the general class or type.

To divide the genotypes of a data set into some number of mutually exclusive groups clustering was done using non-hierarchical classification. In GENSTAT, algorithm was used to search for optimal values of chosen criteria which proceed as follows:

Starting from some initial classification of the genotypes in required number of group, 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 could be found to improve the criterion, he algorithm switched to a second stage, which examined the effect of swapping two genotypes of different classes and so on.

3.15.2.4 Canonical Variate Analysis (CVA)

Discriminant function or canonical variate analysis attempt to establish whether a set of variables can be used to distinguish between two or more groups.

Canonical variate analysis complementary to D^2 statistic is sort of multivariate analysis where canonical vectors and roots representing different axes of differentiation and the amount of variation accounted for by each of such axes respectively and derived. Canonical variate analysis computed linear combination of original variability that maximized the ratio between ground and within group variations, thereby giving functions of the original variables that could be used to discriminate between the groups. Thus in this analysis, a series of orthogonal transformation sequentially maximized the ratio of the groups to within group variations.Several techniques that seek to illuminate the ways in which sets of variables are related one another. The term refers to regression analysis, MANOVA, discriminant analysis, and, most often, to canonical correlation analysis.

3.15.2.5 Cluster Diagram

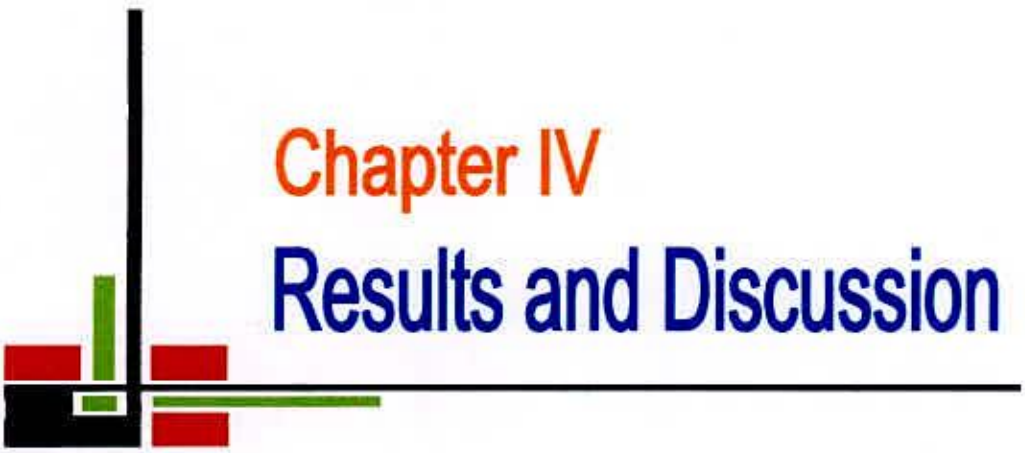
In D^2 analysis a line diagram is constructed with the help of D^2 values which is known as cluster diagram. The squires roots of average intra and inter cluster D^2 value are used in the construction of cluster diagram. This diagram provides information on the following aspects:

- The depicts the genetic diversity in an easily understandable manner.
- The number of cluster represents the number of groups in which a population can be classified on the basis of D^2 analysis.
- The distance between two clusters in the measure of the degree of diversification. The greater the distance between two cluster the greater the divergence and vice versa.
- The genotypes filling in the same cluster are more closely related then those belonging to another cluster. In other words, the genotypes grouped together in one cluster are less divergent than those which are placed in different cluster.
- It provides information about relationship between various clusters.

A cluster diagram was drawn using the values ($\sqrt{D^2}$) of intra and inter-cluster distance. The diagram represented the brief idea of the patter diversity among the genotypes and relationships between different genotypes included in the cluster.

3.15.2.6 Selection of Genotypes for Future Hybridization Programme

Genotypes were selected from the study for future hybridization programme considering genetic variability and other performances related to yield (kg), number of fruit per plant, color of fruit and presence and absence of prickle, number of primary branches, number of secondary branches, no. of flower per inflorescence, days to first flowering, weight per fruit (gm), percent insect infestation of fruits, percent insect infestation of plants, curvature of the fruit, fruit length (cm) and fruit circumference (cm).



Chapter IV

Results and Discussion

CHAPTER IV
RESULTS AND DISCUSSION

The knowledge of genotypic variation within genotypes in relation to morphology, phenology and yield would help to screen better genotypes. Therefore, to generate information in characterization and the degree of diversity of fifteen genotypes of sponge gourd (*Luffa cylindrica* L.) were raised in the kharif season of 2007 at the field of Sher-e-Bangla Agricultural University, Dhaka. The data were recorded, analyzed and presented in this chapter.

The availability of transgressive segregants in breeding program depends upon the divergence of the parents. So, the accurate information on the nature and degree of diversity of the parents is the pre-requisite of an effective breeding program. Performance of 15 genotypes of sponge gourd was investigated in summer season and the findings of present study have been discussed under different morphological characters. The result of the study showed marked variation in different characters and the variation of different characters are presented in the following Tables, Figures and Plates.

The data pertaining to several characters were computed and statistically analyzed and the results obtained are described below:

4.1 Characterization of sponge gourd

- 4.1.1 Morphological characterization based on grading
- 4.1.2 Characterization of sponge gourd on the basis of yield and yield contributing characters

4.2 Variability of sponge gourd on the basis of yield and yield contributing characters

4.3 Genetic diversity presents among the sponge gourd genotypes

4.1 Characterization of sponge gourd

4.1.1 Morphological characterization based on grading

4.1.1.1 Leaf blade lobbing

Leaf blade lobbing is an important traits to choice a sponge gourd genotypes for future breeding programme. Leaf blade lobbing can help to a breeder to know the information on photosynthesis rate. Strong leaves can help a grater opportunity to get maximum sunlight than the weaker leaves. Among the 15 genotypes, four genotypes (G1, G7, G10 and G11) were seen weaker leaf blade; six genotypes (G2, G3, G6, G8, G13 and G14) were strong leaf blade and rest of the genotypes were intermediate habit in their leaf blade lobbing (Table 3). The intermediate leaf blade lobbing genotypes were produced better yield than the strong and weaker leaves holder genotypes (Table 3). A comparative leaf blade lobbing morphology of 15 genotypes are presented in Plate 2.

4.1.1.2 Leaf shape

Leaf shape is an important trait in sponge gourd. Various types of sponge gourd were found according to their different shape. From the fifteen genotypes reniform, ovate and orbicular shaped sponge gourd were observed (Table 3). Among the fifteen genotypes G1, G14 and G15, produced reniform leaf, genotypes G2, G3, G6, G7, G8 and G13 produced ovate leaves and the rest of genotype produce orbicular leaves (Table 3). The reniform leaves holder genotypes were shown better yield than the ovate and orbicular leaf shaped genotypes (Table 3). A comparative leaf shape of 15 genotypes are also presented in Plate 2.

4.1.1.3 Fruits colour

Fruit color is one of the important traits for consumer preference in sponge gourd marketing. Generally light green, green, and dark green color fruits are commonly found in the market. In the present study, variations in fruit color were found in the present study and that could be classified in distinct groups: like light green, green, and dark green (Table 3). Among the fifteen genotypes, six (G1, G2, G8, G10, G11 and G15) produced light green fruit and another six genotypes (G3, G4, G5, G7, G12 and G14) produced green fruits and the rest of the genotypes were produced dark green. This variation offered a good scope for breeding of consumer preference attributes (Plate 3).

Table 3. Characterization of 15 Sponge gourd genotypes

No. of Genotype	Leaf Lobbing	Leaf Shape	Fruit Color	Blossom-end Fruit Shape	Stem-end Fruit Shape	Fruit Shape	Seed color
G1	Weak	Reniform	Light green	Rounded	Depreshed	Elongate tapered	Black
G2	Strong	Ovate	Light green	Rounded	Rounded	Elongate tapered	Black
G3	Strong	Ovate	Green	Pointed	Pointed	Elongate tapered	Black
G4	Intermediate	Reniform	Green	Rounded	Flattened	Elliptical	Black
G5	Intermediate	Reniform	Green	Rounded	Rounded	Elongate tapered	Brown
G6	Strong	Ovate	Dark green	Pointed	Flattened	Oblong blocky	White
G7	Weak	Ovate	Green	Pointed	Flattened	Elongate elliptical	Black
G8	Strong	Ovate	Light green	Flattened	Flattened	Elongate slim	Brown
G9	Intermediate	Orbicular	Dark green	Rounded	Flattened	Elongate slim	White
G10	Weak	Orbicular	Light green	Rounded	Pointed	Elliptical	Black
G11	Weak	Orbicular	Light green	Pointed	Pointed	Elongate elliptical	White
G12	Strong	Ovate	Green	Pointed	Rounded	Elongate tapered	Brown
G13	Strong	Reniform	Dark green	Pointed	Pointed	Elongate elliptical	Black
G14	Intermediate	Reniform	Green	Pointed	Pointed	Elongate tapered	Black
G15	Intermediate	Reniform	Light green	Rounded	Flattened	Elongate slim	Brown

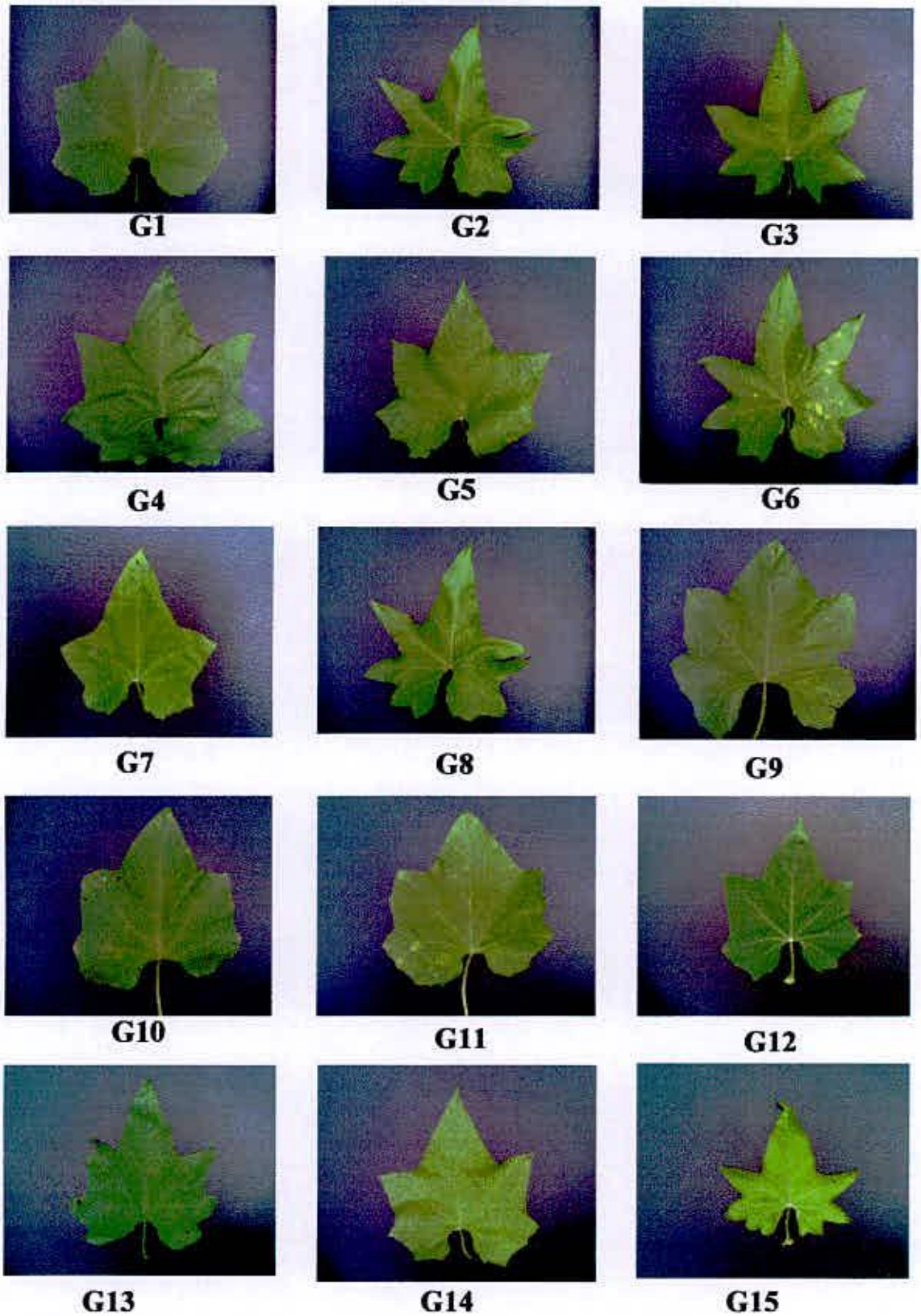


Plate 2: Different leaf morphology (leaf lobbing and leaf shape) of 15 genotypes sponge gourd

Plate 5: Different fruit morphology of 15 sponge gourd genotypes

4.1.1.4 Blossom-end Fruit Shape

Blossom-end shape is important character for sponge gourd, because it plays a critical impact on consumer preference. Blossom-end fruit shape was divided into three groups: rounded, pointed and flattened. Genotype G1, G2, G4, G9, G10 and G15 produced rounded blossom-end fruit shape, genotype G3, G5, G6, G7, G11, G12, G13 and G14 produced pointed blossom-end fruit shape while the rest of the genotypes produced flattened blossom-end shape fruits (Table 3). The round shaped genotypes were produced better yield than the pointed and flattened shaped genotypes (Table 3).

4.1.1.5 Stem-end Fruit Shape

Stem-end shape is another important character for sponge gourd, because it plays a critical impact on consumer preference. Stem-end fruit shape was divided into four groups: depressed, rounded, pointed and flattened. Genotype-1 produced depressed blossom-end fruit shape, genotype G2, G5 and G12 produced rounded blossom-end fruit shape, genotype G3, G10, G11, G13 and G14 produced pointed blossom-end fruit shape while the rest of the genotypes produced flattened blossom-end shape fruits (Table 3). The round shaped genotypes were produced better yield than the pointed and flattened shaped genotypes

4.1.1.6 Fruit shape

Fruit shape is an important consumer preference trait in sponge gourd marketing. Various types of sponge gourd were found according to their different shape. From the fifteen genotypes elongate tapered, elliptical, oblong blocky, elongate slim and elongate elliptical shaped sponge gourd were observed. The genotypes G1, G2, G3, G5, G12 and G14 produced elongate tapered, genotypes G4 and G10 produced elliptical fruits, genotypes G-6, produced oblong blocky fruits, genotype G7, G11 and G13 produced elongate elliptical fruits. The rest of the genotypes produced elongate slim fruits (Table 3). The elongate type fruit shape genotypes were produce better yield than other. (Table 3)

4.1.1.7 Seed colour

Seed color is one of the important traits in sponge gourd. Generally black, brown and white color seeds are common in the market. However, variations in seed color were found in the present study and that could be classified in distinct groups: black, brown and white (Table 3). The genotype G5, G8, G12, and G14 produced brown seed; white seeds were produced in G6, G9 and G11; the rest of the genotypes were produced black (Plate 4). The black colored genotypes were shown better yield than the brown and white colored seed genotypes (Table 3)

4.1.2 Characterization of sponge gourd on the basis of yield and yield contributing characters

4.1.2.1 Days to seed germination

The analysis of variance indicates that significant difference was present among the sponge gourd genotype for seed germination (Table 5). Minimum days (8.14) for seed germination was recorded in G5 and maximum days (15.35) to seed germination was recorded in genotype number G2 (Table 4). Rahman (2005) also found significant difference in seed germination of sponge gourd which varied from 2 to 3 weeks

4.1.2.2 Internodes length (cm) of main stem

Significant difference was observed in case of internodes length of sponge gourd (Table 5). The mean value of internodes length was 15.82 cm. The length varied from 13.14 to 18.96 cm (Table 4), the minimum length was found in G3 and the maximum length was found in G15. Rahman (2005) evaluated thirty nine genotypes of sponge gourd of diverse origin and reported that Internode length of main stem varied from 10.66 to 17.33 cm.

4.1.2.3 Leaf length

It was observed that leaf length varied significantly ranging from 16.45 to 32.08 cm with a mean value of 24.56 cm. The minimum leaf length was recorded in G1 and the maximum leaf length was recorded in G7, which differed

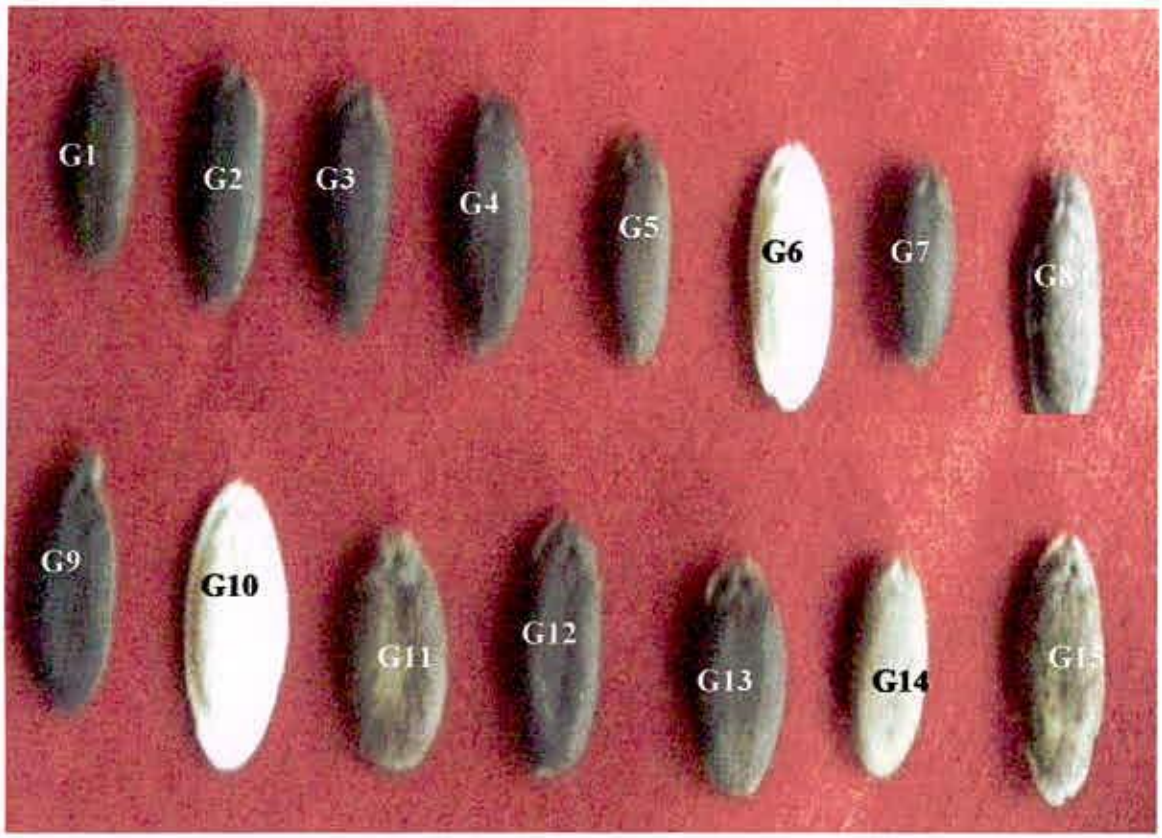


Plate 4. Variation in Seeds of 15 sponge gourd genotypes

Table 4: Mean performance of 15 sponge gourd genotypes

Genotype	DSG	INL	LL	LB	PTL	DFMF	DFFF	NFMF	NFFF	SR
G1	10.20	14.74	16.42	13.41	6.49	43.33	49.82	10.92	13.89	21.93
G2	15.35	17.29	31.94	27.23	15.45	85.06	92.46	22.00	26.04	31.61
G3	9.17	13.14	21.79	17.60	7.78	44.87	46.70	9.76	12.80	23.60
G4	12.31	17.45	28.15	21.86	12.39	82.54	85.96	24.08	27.47	31.84
G5	8.14	14.63	22.83	22.20	10.50	44.71	48.12	12.69	16.10	24.74
G6	10.21	13.97	22.11	19.14	8.53	44.48	48.47	10.89	13.31	25.28
G7	13.73	17.29	32.08	25.52	12.83	77.47	80.92	20.83	24.19	28.92
G8	10.27	13.87	22.05	18.92	9.54	50.72	52.41	13.63	18.70	26.26
G9	10.34	14.92	24.47	19.13	13.70	51.44	52.87	13.55	16.59	27.22
G10	13.32	17.66	31.29	26.93	13.61	73.46	76.88	19.12	22.95	30.67
G11	9.20	15.37	20.17	15.22	6.83	38.48	41.04	9.20	13.38	25.35
G12	11.34	16.23	20.87	15.20	11.73	63.69	72.22	14.90	18.73	28.92
G13	10.39	14.97	19.32	15.89	8.49	55.01	57.82	14.01	17.81	31.82
G14	14.33	16.76	29.55	23.99	12.46	87.96	91.78	23.14	29.10	31.57
G15	14.40	18.96	25.44	20.11	10.66	71.15	74.77	18.64	29.31	30.14
Range	8.14-15.35	13.14-18.96	16.45-32.08	13.41-27.23	6.49-15.45	38.48-87.96	41.04-92.46	9.20-24.08	12.80-29.31	21.93-31.84
Mean	11.51	15.817	24.564	20.157	10.733	80.957	84.816	15.823	20.025	27.990
STD	2.325	1.749	4.951	4.611	3.927	16.988	17.654	5.174	6.037	3.524
SE	0.347	0.261	0.738	0.687	0.585	2.532	2.632	0.771	0.900	0.525
%CV	2.68	3.930	4.860	10.230	32.430	3.370	2.470	11.090	7.660	3.300
lsd(0.05)	0.298	0.600	1.152	1.991	3.361	2.635	2.023	1.694	1.482	0.891
lsd(0.01)	0.401	0.809	1.554	2.686	4.534	3.555	2.729	2.285	1.999	1.202

DSG= Days to seed germination, INL=Inter node length, LL= Leaf length, LB=Leaf breadth, PTL= Petiole length, DFMF= Days to first male flower, DFFF= Days to first female flower, NFMF= Node no. of first male flower, NFFF= Node no. of first female flower, SR= Sex ratio

Table 4: (continued)

Genotype	FL	FDM	PDL	NFPP	AFW	YPP	NSPF	SL	SB	ST	HSW
G1	33.65	17.28	15.44	20.31	501.77	10.19	134.33	0.97	0.70	0.23	6.68
G2	38.00	14.96	9.37	9.27	164.62	1.54	343.16	1.10	0.80	0.33	6.57
G3	45.01	14.99	12.50	15.74	176.83	2.79	159.62	1.20	0.80	0.27	7.68
G4	32.74	15.96	8.52	12.50	196.04	2.46	334.73	0.90	0.70	0.23	6.38
G5	35.87	18.02	11.48	19.74	419.16	8.29	218.74	0.96	0.80	0.30	6.68
G6	20.28	16.91	10.48	20.42	241.96	4.94	156.91	1.20	0.70	0.27	7.16
G7	31.73	16.37	6.56	7.32	223.83	1.62	330.73	1.10	0.70	0.23	7.11
G8	49.92	17.96	14.58	16.43	319.02	5.26	208.82	1.10	0.80	0.23	6.46
G9	47.24	16.01	16.48	12.87	152.66	1.97	341.11	1.33	0.60	0.23	6.58
G10	20.15	16.00	6.69	7.43	425.39	3.15	182.05	1.00	0.90	0.27	6.40
G11	35.10	16.95	14.51	20.39	185.26	3.76	149.44	0.93	0.80	0.27	6.45
G12	36.24	16.99	11.59	11.10	215.44	2.40	188.55	1.30	0.90	0.30	6.47
G13	28.84	17.23	13.48	12.55	263.92	3.32	180.19	0.87	0.80	0.23	6.43
G14	36.20	14.30	7.65	8.40	408.69	3.44	205.34	1.03	0.90	0.23	6.50
G15	31.50	12.12	9.48	10.01	180.92	1.80	204.03	1.17	0.80	0.30	6.41
Range	28.84-49.92	12.12-18.02	6.56-16.48	7.32-20.42	152.66-501.77	1.54-10.19	134.33-343.16	0.80-1.33	0.70-0.90	0.23-0.33	6.38-7.68
Mean	280.59	16.136	11.25	34.83	13.63	3.79	222.51	1.07	0.72	0.26	6.66
STD	111.64	1.776	3.237	8.328	4.844	2.573	74.325	74.325	0.106	0.053	0.707
SE	16.643	0.265	0.482	1.242	0.722	0.384	11.08	0.024	0.016	0.008	0.105
%CV	9.270	6.118	1.760	3.870	7.800	26.94	5.1	6.31	7.24	19.28	8.78
lsd(0.05)	25.122	5.093	0.191	1.301	1.026	0.987	11.114	0.068	0.053	0.259	0.565
lsd(0.01)	33.893	6.871	0.257	1.755	1.384	1.331	14.994	0.092	0.071	0.349	0.763

FL= Fruit length, FDM= Fruit diameter, PDL= Peduncle length, NFPP= No. of fruit per plant, AFW= Average fruit weight, YPP= Yield per plant, NSPP= No. of seed per fruit, SL= seed length, SB= seed breadth, ST= seed thickness, HSW= Hundred seed weight.

significantly from the other genotype (Table 5). Rahman (2005) evaluated thirty nine genotypes of sponge gourd of diverse origin and reported that Leaf length varied from 18.41 to 33.00 cm.

4.1.2.4 Leaf breadth

It was observed that leaf breadth varied significantly among the genotype ranging from 13.41 to 27.23 cm (Table 4 and Table 5). The plants of G1 showed lowest value of leaf breadth and G2 showed highest value of leaf breadth. Rahman (2005) observed thirty nine genotypes of sponge gourd of diverse origin and reported that Leaf breadth varied from 17.21 to 26.43 cm.

4.1.2.5 Petiole length

Petiole length varied significantly among the genotype and ranged from 6.94 to 15.45 cm. (Table 4 and Table 5). The mean value for this character was 10.73. Haque (1971) found that petiole length for bottle gourd, sweet gourd and white gourd were 13.84 cm, 14.53 cm and 12.14 cm, respectively. The lowest value of petiole length was recorded for G1 and G2 showed highest value (Table 4).

4.1.2.6 Days to first male flowering

It is one of the most important plant characters. Among 15 genotypes G-11 showed, early flowering. It took the shortest time to flowering. The highest time for flowering (87.96 days) which was statistically similar to G2 and G4 (Table 4). Banik (2003) and Joseph (1978) found significant differences for days to 1st male flower opening in snake gourd.

4.1.2.7 Days to first female flowering

It is another important character that influences the yield. Analysis of variance indicated that there was wide range of variability among the 15 genotype of sponge gourd (Table 5). The range varied from 41.01 days to 92.46 days. G11 showed early female flowering and G2 showed late female flowering (92.46 days) (Table 4). Arora *et al.* (1983) reported in sponge gourd that days to first female flowering ranged from 61 to 125 days.

4.1.2.8 Node number for first male flower

Nodal position for first male flowering varied significantly among the genotype and ranged from 9.20 to 28.08 (Table 4 and Table 5). The mean value was 15.83. The minimum value was recorded for G3 and the maximum value was recorded for G14. Rahman (2005) found significant (Table 5) differences for node no. for 1st male flower opening in sponge gourd.

4.1.2.9 Node number for first female flower

Significant difference was found for this character (Table 5). The range varied from 12.80 to 29.31. The lowest value was found in G3 (12.80) while the highest value (29.31) was found in G15 (Table 4). Arora *et al.* (1983) observed in sponge gourd that the node number of first female flowers opened ranged from 8 to 20.

4.1.2.10 Sex ratio (male : female)

Significant difference was also observed in this trait (Table 5). It ranged from 21.93 to 31.84. The minimum value was found in G1 and the maximum value was found in G14 (Table 4). The mean value was 27.99. Rahman (2005) found significant differences for sex ratio of sponge gourd and its ranged from 15.09 to 26.88.

4.1.2.11 Length of fruit

Significant difference was observed in fruit length among 15 genotypes (Table 5). Among the genotype studied, longest fruit (49.92 cm) was observed in G8 while the shortest fruit length (20.15 cm) was recorded in G10 (Table 4). Significant variation for fruit length was noticed in sponge gourd (Arora *et al.*, 1983; Prosad and Singh, 1990), ribbed gourd and bottle gourd (Rahman *et al.*, 1991).

4.1.2.12 Fruit diameter

Diameter of edible fruit at middle position varied significantly among 15 sponge gourd genotypes and ranged from 12.12 to 18.02 cm. The mean value was 16.14 cm. The highest diameter recorded in G5 and the lowest diameter were observed in G15 (Table 4). Rahman (2005) also found significant differences for this character of sponge gourd.

Table 5: Mean sum square from the ANOVA of 15 sponge gourd genotypes in respect of 21 characters

Character	DF			Means Square		
	Replication	Treatment	Error	Replication	Treatment	Error
DSG	2	14	28	13.217	14.91**	0.095
INL	2	14	28	1.88	8.58**	0.39
LL	2	14	28	2.72	73.81**	1.42
LB	2	14	28	4.19	57.7**	4.25
PTL	2	14	28	13.74	22.25**	12.12
DFMF	2	14	28	9.11	890.79**	7.45
DFFF	2	14	28	35.29	965.71**	4.39
NFMF	2	14	28	10.76	76.44**	3.08
NFFF	2	14	28	18.03	107.27**	2.36
SR	2	14	28	31.17	32.87**	0.85
TPP	2	14	28	0.26	18.69**	1.05
PDL	2	14	28	14.09	30.83**	0.04
FL	2	14	28	15.23	212.18**	1.82
NFPP	2	14	28	0.84	71.37**	1.13
AFW	2	14	28	1757.72	37569**	677.11
FDM	2	14	28	4.91	7.22**	0.99
NSPP	2	14	28	95.32	17082.96**	132.53
SL	2	14	28	0.06	0.06**	0.06
SB	2	14	28	0.1	0.014**	0.003
ST	2	14	28	0.03	0.06^{ns}	0.03
HSW	2	14	28	3.32	0.416^{ns}	0.343

DSG= Days to seed germination, INL=Inter node length, LL= Leaf length, LB=Leaf breadth, PTL= Petiole length, DFMF= Days to first male flower, DFFF= Days to first female flower, NFMF= Node no. of first male flower, NFFF= Node no. of first female flower, SR= Sex ratio, FL= Fruit length, FDM= Fruit diameter, PDL= Peduncle length, NFPP= No. of fruit per plant, AFW= Average fruit weight, YPP= Yield per plant, NSPP= No. of seed per fruit, SL= seed length, SB= seed breadth, ST= seed thickness, HSW= Hundred seed weight, DF= Degrees of freedom, **= Significant at 5%, ns= Non significant.

4.1.2.13 Peduncle length

The peduncle length of fruits varied significantly among the genotype (Table 5). Among the genotype studied longest peduncle length (16.48 cm) was observed in G8 while the shortest peduncle length (6.56 cm) was recorded in G7 (Table 4). The mean peduncle length was 11.25 cm.). Rahman (2005) evaluated thirty nine genotypes of sponge gourd of diverse origin and reported that peduncle length varied from 7.23 to 17.06 cm.

4.1.2.14 Number of fruits per plant

It is one of the most important yield contributing characters. Analysis of variance revealed that significant variation existed among the genotype for number of fruits per plant (Table 5). The lowest number of fruits (7.32) per plant was recorded in G7 which was statistically similar to G6 (7.43) and the highest number of fruits (20.39) was recorded in G11 (Table 4). Rahman (2005) observed thirty nine genotypes of sponge gourd of diverse origin and reported that number of fruits per plant varied from 4.50 to 15.17.

4.1.2.15 Average fruit weight

In case of average fruit weight, significant difference was observed among the 15 genotype of sponge gourd ranging from 152.66 to 501.77 g. It is also an important yield contributing character. The highest value was obtained from G1 and the lowest value was obtained from G9 (Table 4). This findings are in agreement with Rahman (2005) in sponge gourd.

4.1.2.16 Yield per plant

Significant difference was found among the 15 sponge gourd genotype for the yield per plant (Table 5). The yield per plant ranged from 1.54 to 10.19 kg with the mean value of 3.79 kg per plant. The lowest yield was found in G2 while G1 was the highest yield per plant. (Table 4). This results support the findings of Abusaleha and Datta (1990) in cucumber.

4.1.2.17 Number of seeds per fruit

It is also an important yield contributing character. Significant difference was observed among the genotype in this trait (Table 5). Number of seeds per fruit

varied from 134.33 to 343.16 The mean value was observed as 222.51 seeds per fruit. The highest number of seeds per fruit was recorded in G2 and the lowest number was recorded in G1 (Table 4). Swamy *et al.* (1984) and Mannan (1992) also reported wide variability among genotypes of snake gourd, musk melon and bitter gourd. Rahman (2005) also found the similar result.

4.1.2.18 Seed length

Significant variation was observed in seed length among 15 genotypes of sponge gourd (Table 5). The seed length varied from 0.87 to 1.33 cm. The lowest seed length was recorded in G13 and the highest length was recorded in G9 (Table 4). The mean value was 1.07 cm. Rahman (2005) found significant differences for seed length of sponge gourd.

4.1.2.19 Seed breadth

Significant difference was found among 15 genotypes of sponge gourd in this character (Table 5). The highest seed breadth was found in G10, G12 and G14 (0.90 cm) and the lowest was found in G1, G4, G6, G7 (0.70 cm) which are shown in (Table 4). This findings support with the agreement of Rahman (2005) in sponge gourd.

4.1.2.20 Seed thickness

The seed thickness varyied from 0.23 to 0.33 cm. The highest thickness was recorded in genotype G2 and the lowest value from G4, G7, G8, G9, G13 and G14 (Table 4). Rahman (2005) also found non significant differences for sponge gourd.

4.1.2.21 Hundred seed weight

Hundred seed weight was found among 15 genotypes of sponge gourd in respect of 100 seed weight. It varied from 6.38 to 7.68 g. The highest weight of 100 seed weight was recorded in G3 and the lowest in G10 The highest weight of 100 seed weight was recorded in G3 and the lowest in G4 (Table 4). Rahman (2005) observed thirty nine genotypes of sponge gourd of diverse origin and reported that hundred seed weight varied from 8.06 to 9.46 gm.

4.2 Variability of sponge gourd on the basis of yield and yield contributing characters

4.2.1 Days to seed germination

The genotypic and phenotypic variance was 4.94 and 5.03. Genotypic co-efficient of variation (GCV) was lower than phenotypic coefficient of variation (19.30% and 19.49%) which indicated that little role of environment on the performance of particular character. Heritability in broad sense was calculated also was 99% with low genetic advance (4.53) and genetic advance in percent of mean (39.39) was considerable for this trait indicating apparent variation was due to genotypes. So selection based on this trait would be effective. This result also has the agreement with the findings of Saha *et al.* (1992).

4.2.2 Internodes length (cm) of main stem

The genotypic and phenotypic variances for inter node length were 2.73 and 3.12, respectively. The GCV and PCV were 10.45% and 11.16%, respectively (Table 6). Little role were observed between genotypic and phenotypic variance as well as genotypic and phenotypic co-efficient of variation indicating low environmental influence on this trait. The heritability in broad sense (h^2b) for inter node length was high (94%) with moderate genetic advance (3.19) and genetic advance in percent of mean (20.14) was considerable for this trait indicating apparent variation was due to genotypes. So selection based on this trait would be effective. This result also has the agreement with the findings of Singh *et al.* (2002).

4.2.3 Leaf length

The genotypic and phenotypic variances were 24.13 and 25.55, respectively. The GCV (20.00%) was slightly lower than PCV (20.58%), which indicated low environmental influence on the expression of this trait (Table 6). Heritability in broad sense for this character 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. So selection based on this trait would be effective. This result also has the agreement with the findings of Rahman (2005).

Table 6: Genetic parameters of different characters

Characters	$\sigma^2 g$	$\sigma^2 e$	$\sigma^2 p$	%GCV	%PCV	$h^2 b$	GA	GAPM
DSG	4.94	0.095	5.03	19.30	19.49	0.99	4.53	39.39
INL	2.73	0.386	3.12	10.45	11.16	0.94	3.19	20.14
LL	24.13	1.424	25.55	20.00	20.58	0.97	9.83	40.03
LB	17.82	4.253	22.07	20.94	23.31	0.90	7.81	38.76
PTL	3.38	12.118	15.50	17.12	36.68	0.47	1.77	16.47
DFMF	294.45	7.45	301.90	21.20	21.46	0.99	34.91	43.12
DFFF	320.44	4.39	324.83	21.11	21.25	0.99	36.63	43.18
NFMF	24.45	3.078	27.53	31.25	33.16	0.94	9.60	60.67
NFFF	34.97	2.355	37.33	29.53	30.51	0.97	11.79	58.88
SR	10.67	0.851	11.52	11.67	12.13	0.96	6.48	23.14
FL	70.12	1.816	71.94	24.04	24.35	0.99	17.03	48.90
FDM	24.41	27.829	52.24	30.62	44.79	0.68	6.96	43.12
PDL	10.26	0.039	10.30	28.47	28.52	1.00	6.59	58.53
NFPP	23.41	1.129	24.54	35.49	36.34	0.98	9.74	71.42
AFW	12297.30	677.111	12974.41	39.52	40.59	0.97	222.40	79.26
YPP	5.88	1.045	6.93	63.90	69.35	0.92	4.60	121.30
NSPP	5650.14	132.526	5782.67	33.78	34.17	0.99	153.06	68.79
SL	0.02	0.005	0.02	12.68	14.28	0.89	0.25	23.20
SB	0.00	0.003	0.01	8.41	11.34	0.74	0.09	12.85
ST	0.01	0.072	0.08	35.50	108.31	0.33	0.06	23.97
HSW	0.02	0.343	0.37	2.24	9.07	0.25	0.08	1.14

DSG= Days to seed germination, INL=Inter node length, LL= Leaf length, LB=Leaf breadth, PTL= Petiole length, DFMF= Days to first male flower, DFFF= Days to first female flower, NFMF= Node no. of first male flower, NFFF= Node no. of first female flower, SR= Sex ratio, FL= Fruit length, FDM= Fruit diameter, PDL= Peduncle length, NFPP= No. of fruit per plant, AFW= Average fruit weight, YPP= Yield per plant, NSPP= No. of seed per plant, SL= seed length, SB= seed breadth, ST= seed thickness, HSW= Hundred seed weight, $\sigma^2 g$= Genotypic variance, $\sigma^2 e$= Environmental variance, $\sigma^2 p$= Phenotypic variance, GCV= Genotypic co-efficient of variance, PCV= Phenotypic co-efficient of variance, $h^2 b$= Heritability in broad sense, GA= Genetic advance, GAPM= Genetic advance in percent of mean.

4.2.4 Leaf breadth

The heritability for this characters was 90%. GCV (20.94%) was slightly lower than the PCV (23.31%) indicating that there was low environmental influence on the expression of this traits (Table 6). The heritability in broad sense (h^2b) for leaf breadth was high (94%) with moderate genetic advance (7.81) and genetic advance in percent of mean (38.76) was considerable for this trait indicating apparent variation was due to genotypes. So selection based on this trait would be effective. This result is in agreement with the findings of Rahman (2005).

4.2.5 Petiole length

The GCV and PCV were 17.12% and 36.68%, respectively. The PCV was very high to GCV which indicated that there was highly environmental influence on the expression of this trait (Table 6). The heritability in broad sense (h^2b) for petiol length was high (47%) with low genetic advance (1.77) and genetic advance in percent of mean (16.47) was considerable for this trait indicating apparent variation was due to genotypes. So selection based on this trait would be effective.

4.2.6 Days to first male flowering

The genotypic (294.45) and phenotypic (301.90) variances were very high and the GCV (20.20%) and PCV (21.46%) were indicated high environmental effect upon the expression of this trait (Table 6). Heritability (h^2b) was high (99%). The genetic advance (34.91) and genetic advance in percent of mean (43.12) was considerable for this trait indicating apparent variation was due to genotypes. So selection based on this trait would be effective. This result also has the agreement with the findings of Rahman (2005).

4.2.7 Days to first female flowering

Phenotypic variance (324.84) was moderately higher than genotypic variance (320.44). Also narrow difference was observed between GCV (21.11%) and PCV (21.25%). Heritability was high 99% (Table 6). Therefore, the plant breeder should select this trait for breeding purposes. The small difference between GCV and PCV was observed in water melon by Rajendran (1985).

Sharma and Dhankhar (1990) also found almost similar result in bitter gourd. The genetic advance (36.63) and genetic advance in percent of mean (43.18) was considerable for this trait indicating apparent variation was due to genotypes. So selection based on this trait would be effective. This result also has the agreement with the findings of Rahman (2005).

4.2.8 Node number for first male flower

The genotypic variance and phenotypic variance were 24.45 and 27.53, respectively. The difference between GCV (31.25%) and PCV (3.16%) was moderate which indicate that this character was moderately influenced by environment on the expression of this character. The heritability (h^2b) was high 94% (Table 6). Saha *et al.* (1986) found significant difference in node number for first male flowering in pumpkin genotypes. The genetic advance (9.60) and genetic advance in percent of mean (60.67) was considerable for this trait indicating apparent variation was due to genotypes. So selection based on this trait would be effective.

4.2.9 Node number for first female flower

The mean for this trait was 20.03. The genotypic variance (34.97) was moderately high than phenotypic variance (37.33) as well as GCV (29.53%) was lower than PCV (30.51%) indicating environmental influence on the expression of this trait. The heritability (h^2b) for this character was high (97%) (Table 6). Masud (1995) reported that generally female flower of pumpkin borne in 17.67-30.00 nodes. The genetic advance (11.79) and genetic advance in percent of mean (58.88) was considerable for this trait indicating apparent variation was due to genotypes. So selection based on this trait would be effective. This result also has the agreement with the findings of Rahman (2005).

4.2.10 Sex ratio (male : female)

The genotypic variance (10.67) was lower than phenotypic variance (11.52) as well as the PCV (12.13%) was, slightly higher than GCV (11.67%). It indicated that there was less environmental influence on the expression of this character

(Table 6). The genetic advance (6.48) and genetic advance in percent of mean (23.14) was considerable for this trait indicating apparent variation was due to genotypes. So selection based on this trait would be effective. These results are in agreement with Bose and Som (1986), Sharma and Nath (1971) and Rahman (2005).

4.2.11 Length of fruit

The GCV (24.04%) and PCV (24.35%), It indicated that there was low environmental influence on the expression of this traits. Heritability (h^2b) was high (99%) (Table 6). Rahman *et al.* (1986) reported similar result in bottle gourd. The genetic advance (17.03) and genetic advance in percent of mean (48.90) was considerable for this trait indicating apparent variation was due to genotypes. So selection based on this trait would be effective. This result also has the agreement with the findings of Rahman (2005).

4.2.12 Fruit diameter

The difference between GCV (30.62%) and PCV (44.79%), indicated the influence of environment on expression of this trait. Heritability (h^2b) was 68% (Table 6). Rahman *et al.* (2005) reported almost similar result in sponge gourd. The genetic advance (6.96) and genetic advance in percent of mean (43.12) was considerable for this trait indicating apparent variation was due to genotypes. So selection based on this trait would be effective. This result also has the agreement with the findings of Rahman (2005).

4.2.13 Peduncle length

The genotypic variance was (10.26%) and phenotypic variance was (10.30%). The GCV and PCV were (28.47%) and (28.52%), respectively. It indicated that there was very low environmental influence on the expression of the traits. Heritability (h^2b) was high (1.00%) (Table 6). The genetic advance (6.59) and genetic advance in percent of mean (58.53) was considerable for this trait indicating apparent variation was due to genotypes. So selection based on this trait would be effective. This result also has the agreement with the findings of Rahman (2005).

4.2.14 Number of fruits per plant

The genotypic variance was (23.41) and phenotypic was (12974.41). The GCV (35.49%) and PCV (36.34%). This indicated very much influenced on the expression of this trait. The heritability (h^2b) was very high (98%) indicating the selectivity of the character for further breeding purpose (Table 6). Prasad and Singh (1990) observed significant variation among the genotypes of pointed gourd in respect of number of fruits per plant. The genetic advance (9.74) and genetic advance in percent of mean (71.42) was considerable for this trait indicating variation was due to genotypes. So selection based on this trait would be effective. This result also has the agreement with the findings of Rashid (1993) in ridge gourd.

4.2.15 Average fruit weight

The genotypic (12297.32) and phenotypic variances (12974) were very high. The GCV (39.52) and PCV (40.59%) (Table 6). It indicated very much environmental influences on the expression of this character. The heritability (h^2b) was very high (97%). The genetic advance (222.40) and genetic advance in percent of mean (79.26) was considerable for this trait. So selection based on this trait would be less effective.

4.2.16 Yield per plant

The genotypic variance (5.88) and phenotypic variance (6.93) were high. The GCV (63.90%) and PCV (69.35%) were also high. The difference between GCV and PCV indicated moderate influence of environment on the expression of this trait (Table 6). That is it is moderately controlled by genetic makeup. Rahman *et al.* (1991) observed similar result in bottle gourd. Heritability (h^2b) of yield per plant was very high (92%) indicating potentiality in selection of this character for further breeding program (Table 6). The genetic advance (4.60) and genetic advance in percent of mean (121.30) was considerable for this trait indicating apparent variation was due to genotypes. These findings support the findings of Abusaleha and Dutta (1990) in cucumber.

4.2.17 Number of seeds per fruit

The genotypic (5650.14) and phenotypic variances (5782.67) were very high. The GCV and PCV were found 33.78% and 34.17%, respectively i.e. GCV and PCV values were high. This indicated that this traits is lower genetically controlled. The heritability was also very high (99%) (Table 6) The genetic advance (153.06) and genetic advance in percent of mean (68.79) was considerable for this trait indicating apparent variation was due to genotypes. Swamy *et al.* (1984) and Mannan (1992) also reported wide variability among genotypes of snake gourd, musk melon and bitter gourd.

4.2.18 Seed length

The genotypic and phenotypic variance were very low (0.02 and 0.02) with heritability (0.89%). The GCV and PCV were low i.e. 12.68% and 14.28%, respectively (Table 6) indicating very low environmental influence on this trait. The genetic advance (0.25) and genetic advance in percent of mean (23.20) was considerable for this trait indicating apparent variation was due to genotypes.

4.2.19 Seed breadth

The genotypic variance (0.004) and phenotypic variance (0.01) were very low. The GCV (8.41%) and PCV (11.34%) were low indicating this character is controlled by genetic make up. The estimated heritability was moderate (74%) (Table 6). The genetic advance (0.09) and genetic advance in percent of mean (12.85) was considerable for this trait indicating apparent variation was due to genotypes. Rahman (2005) also reported wide variability among genotypes of sponge gourd.

4.2.20 Seed thickness

The genotypic and phenotypic variances were 0.01 and 0.08, respectively. The difference between GCV (35.50%) and PCV (108.31%) were very high indicating this trait is genetically controlled. Heritability (h^2b) of this parameter was high (33%) (Table 6). The genetic advance (0.06) and genetic advance in percent of mean (23.97) was considerable for this trait indicating apparent variation was due to genotypes. Swamy *et al.* (1984) and Mannan (1992) also reported wide variability among genotypes of snake gourd, musk melon and bitter gourd.

4.2.21 Hundred seed weight

The genotypic (0.02) and phenotypic (0.37) variances were low. The GCV and PCV was 2.24% and 9.07%. Heritability in broad sense (0.25) was low (Table 6). The differences between GCV and PCV indicated low environmental influence on the expression of this trait that is it was controlled genetically. Low 100 seed weight would be better for the purpose of selecting a genotype in better trait. Varghese (1991) reported similar result in snake gourd. The genetic advance (0.08) and genetic advance in percent of mean (1.14) was considerable for this trait indicating apparent variation was due to genotypes.

4.3 Diversity of the Sponge gourd Genotypes

Genetic divergence in Sponge gourd was analyzed by using GENSTAT software programme. Genetic diversity analysis involved several steps i.e., estimation of distance between the genotypes, clusters and analysis of inter-cluster distance. Therefore, more than one multivariate technique was required to represent the results more clearly and it was obvious from the results of many researchers (Bashar, 2002; Uddin, 2001; Juned *et al.*1988 and Ario, 1987). In the analysis of genetic diversity in sponge gourd multivariate techniques were used.

4.3.1 Construction of scatter diagram

In multivariate analysis, cluster analysis refers to methods used to divide up objects into similar groups, or more precisely, groups whose members are all close to one another on various dimensions being measured. Depending on the values of principal component scores 2 and 1 obtained from the principal component analysis, a two dimensional scatter diagram (Z_1 - Z_2) using component score 1 as X-axis and component score 2 as Y-axis was constructed, which has been presented in Figure 5. The position of the genotypes in the scatter diagram was apparently distributed into six groups, which indicated that there existed considerable diversity among the genotypes.

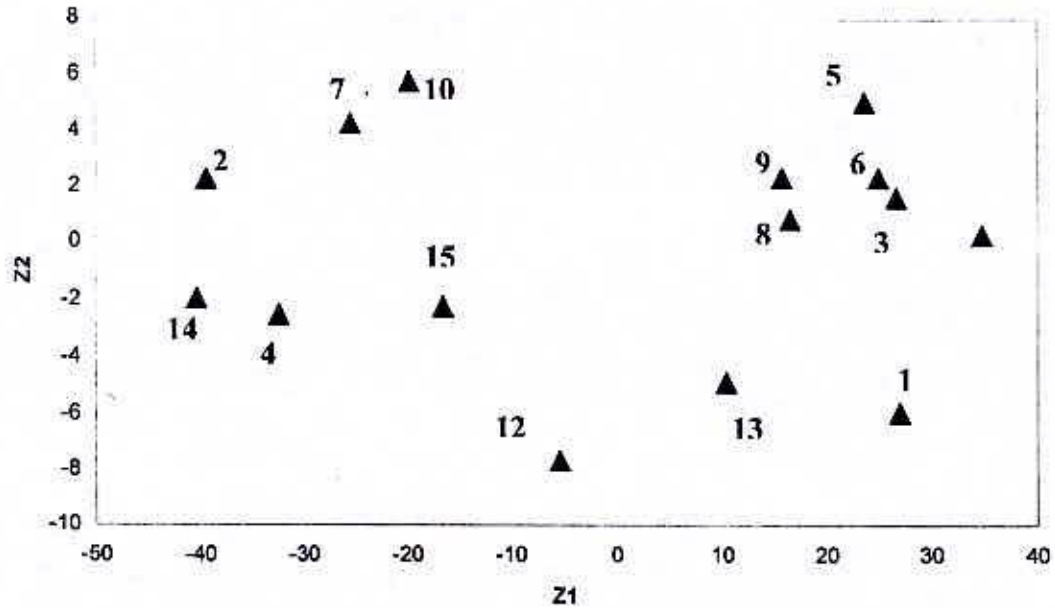


Figure 5. Scatter distribution of 15 sponge gourd genotypes based on their principle component scores

4.3.2 Principal component analysis

Principal components were computed from the correlation matrix from genotype scores obtained from first components and succeeding components with latent roots greater than the unity. Contributions of the different morphological characters towards divergence were discussed from the latent vectors of the first two principal components. The principal component analysis yielded eigen values of each principal component axes with the first axes totally accounting for the variation among the genotypes is 71.48, while two of these with eigen values above unity accounted for 91.99% (Table 7). The first three principal axes accounted for 96.57% of the total variation among the 10 characters describing 15 sponge gourd genotypes.

Based on principal component axes I and II, a two dimensional chart (Z_1 - Z_2) of the cultivars are presented in Figure 5. The scatter diagram revealed that apparently there were mainly five clusters. The genotypes were distantly located from each other.

Balasch *et al.* (1984) reported the use and the comparison of different multivariate techniques in classifying some important number of tomato varieties/lines. It was marked that three methods gave similar results. But factorial discriminate and Mahalanobis's D^2 distance methods required collecting data plant by plant, while the PCA method required taking data by plots.

Out of five cluster, cluster I was associated with four genotypes namely G01, G03, G25, G05 and G06 (Table 8). From the clustering mean values (Table 9), it was observed that cluster-I produced the highest mean for days to 1st female flowering (68.28) followed by days to 1st male flowering (64.35), and sex ratio similar findings were mentioned by Rahman (2005). The lowest mean value for cluster I (6.55) was the yield per plant.

Table 7. Eigen values and percentage of variation in respect of 10 characters in 15 genotypes

Principle Component Axis	Principal component characters	Eigen Value	% Total variation	Cumulative Parent
I	Internodes length	6.3269	71.48	71.48
II	Leaf length	1.8155	20.51	91.99
III	Leaf breadth	0.4055	4.58	96.57
IV	Petiole length	0.1473	1.66	98.23
V	Days to first male flower	0.0727	0.82	99.05
VI	Days to first female flower	0.0451	0.51	99.56
VII	Node no. of first male flower	0.024	0.28	99.84
VIII	Node no. of first female flower	0.0105	0.12	99.96
IX	Seed rate	0.0028	0.03	99.99
X	Yield per plant	0.0004	0	99.99

Table 8: Distribution of 15 sponge gourd genotypes in different clusters

Cluster	No. of genotypes Involved in cluster	Genotypes (Place of collection)
I	4 (G1, G 3, G 5, G 6)	G1=Fujian (Lalteer), G3=Shuvra (Mallik seed Co.), G5=Majnushah (Mallik seed Co.), G6=Lalonshah (Mallik seed Co.),
II	3 (G 8, G 9, G 13)	G8=Shrabony (United Seed Co.), G9=Mayaby (United Seed Co.), G13=Karnaphuli (Thailand)
III	3 (G 10, G 12, G 15)	G10=Dhaka Local, G12=Comilla Local, G15=Jessor local
IV	1 (G 11)	G11=Lakshmi (Local Market)
V	4 (G 2, G 4, G 7, G 14)	G2=Rajshahi Local, G4=Chuadanga Local, G7=Tangail Local, G14=Munshigong Local.

Table 9: Mean performance of five cluster of ten characters in 15 sponge gourd genotypes

SL N0.	Character	Cluster Mean				
		I	II	III	IV	V
01	Inter node length	14.12	14.59	17.62	15.37	17.20
02	Leaf length	20.79	21.95	25.87	20.17	30.43
03	Leaf breadth	18.09	17.98	20.75	15.22	24.65
04	Petiole length	8.32	8.49	13.25	6.83	13.28
05	Days to first male flower	64.35	72.37	89.43	58.50	103.28
06	Days to first female flower	68.28	74.37	94.63	61.00	107.80
07	Node number of first male flower	11.06	13.38	17.55	9.20	22.51
08	Node number of first male flower	14.03	17.70	23.66	13.38	26.70
09	Sex ratio	23.89	28.43	29.91	25.35	30.99
10	Yield per plant	6.55	3.52	2.45	2.09	2.29

Cluster II was associated with three genotypes namely G08, G09 and G13 (Table 8). These genotypes produced the highest mean for days to 1st female flowering (74.37) followed by days to 1st male flowering (72.37), and sex ratio. Similar findings were mentioned by Rahman (2005). The lowest mean value for cluster-II (3.52) was the yield per plant (Table 9)

Among the five clusters, cluster III composed of three genotypes. The genotypes were G10, G12 and G15 (Table 8). In cluster-III the highest mean for days to 1st female flowering (94.63) followed by days to 1st male flowering (89.43), and sex ratio. Similar findings were mentioned by Rahman (2005). The lowest mean value for cluster III (2.45) was the yield per plant (Table 9).

Cluster IV consists of one genotypes (G11) (Table 8). From the clustering mean values (Table 9), it was observed that cluster IV produced the highest mean values for days to 1st female flowering (61.00) and days to 1st male flowering (58.50). The lowest mean value for cluster IV (2.09) was the yield per plant.

Cluster V constituted with four genotypes. The genotypes were G02, G04, G07 and G14 (Table 8). In cluster-V the highest mean for days to 1st female flowering (107.80) followed by days to 1st male flowering (103.28). However, the lowest mean value for cluster V (2.29) was the yield per plant. (Table 9).

Joshi *et al.* (2003) assessed the nature and magnitude of genetic divergence using non hierarchical Euclidean cluster analysis in 73 tomato genotypes of diverse origin for different quantitative and qualitative traits. Maximum value of coefficient of variability (53.208) was recorded for shelf life of fruits while it was minimum of 69.208 for days to first picking. The grouping of the genotypes into 15 clusters indicated the presence of wide range of genetic diversity among the genotypes

Dharmatti *et al.* (2001) in a population of 402 tomato lines was observed 4 clusters based on the similarities of D^2 values. Considerable diversity within and between the clusters was noted, and it was observed that the characters

TLCV resistance, fruit yield per plant and number of whiteflies per plant contributed maximum to the divergence.

It was observed that all the cluster mean values for plant height, days to first flower, days to first harvest, fruit length, fruit circumference, number of fruits per plant, individual fruit weight were more or less similar. Information on genetic divergence of sweet potatoes was reported by Naskar *et al.* (1996). The genotypes were grouped into 7 different clusters.

Desai *et al.* (1997) evaluated thirty six genotypes of potato for genetic divergence by Mahalanobis's D^2 statistic. Nine clusters were identified; I being the largest, accommodating 7 genotypes. Cluster I, III, V, VI and VII showed larger genetic divergence.

4.3.3 Principal coordinate analysis

Inter-genotypic distances as obtained by Principal Coordinate analysis for selective combination showed that the highest distance (2.255) was observed between the G01 and G02, followed by G01 and G07 (2.078) and G01 and G15 (1.971) and the lowest distance was observed between G02 and G15 (0.493) followed by G07 and G10 (0.484), G07 and G15 (0.426) (Table 10).

By using these inter-genotypic distances intra-cluster genotypic distances were calculated (Table 11) as suggested by Singh *et al.* (1977). Cluster III which (0.999) composed of three genotypes showed the maximum intra cluster distances and cluster IV showed the lowest intra-cluster distance (0.000) which composed of one genotypes. The coordinates obtained from the Principal Component analysis (PCA) were used as input at Principal Coordinate Analysis (PCO) to calculate distances among the points reported by Digby *et al.* (1989). PCA was used for the graphical representation of the points while PCO was used to calculate the minimum distance straight line between each pair of points.

Table 10. Inter genotypic distances (D^2) of 10 higher and lower values of different clusters

Sl. No.	10 higher D^2 values of different clusters genotypes		Sl. No.	10 lower D^2 values of different clusters genotypes	
	Between Genotypes	Distance (D^2)		Between Genotypes	Distance (D^2)
01	G 01-G 02	2.26	01	G 02 - G 07	0.26
02	G 01-G 07	2.08	02	G 04 - G 14	0.29
03	G 01-G 15	1.97	03	G 10 - G 14	0.36
04	G 01-G 04	1.93	04	G 07 - G 15	0.39
05	G 01-G 14	1.86	05	G 07 - G 10	0.40
06	G 01-G 10	1.77	06	G 04 - G 07	0.41
07	G 11-G 07	1.58	07	G 06 - G 08	0.42
08	G 05-G 14	1.68	08	G 03 - G 11	0.43
09	G 02-G 03	1.59	09	G 04 - G 15	0.48
10	G 04-G 11	1.57	10	G 02 - G 15	0.49

Table 11: Intra and inter-cluster distances of 15 sponge gourd genotype

Cluster	I	II	III	IV	V
I	**0.805**	8.31	37.85	5.1	47.04
II		**0.603**	29.54	12.62	38.78
III			**0.999**	41.70	11.17
IV				**0.000**	51.31
V					**0.439**

4.3.4 Canonical variate analysis

To compute the inter-cluster Mahalanobis's D^2 values canonical variate analysis was used. The Table 10 indicates the intra and inter-cluster distance (D^2) values. The inter-cluster distances were higher than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups. Results indicated that the highest inter cluster distance was observed between cluster IV and Cluster V (7.163) followed by between cluster I to cluster V (6.859), Cluster III to Cluster IV (6.458), cluster II to Cluster V (6.227) and Cluster I to Cluster III (6.152) (Figure 6). The lowest inter-cluster distances was observed between the cluster I to Cluster IV (2.258), followed by cluster I to cluster II (2.883) and cluster II to cluster IV (3.552) (Figure 6). Inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups (Table 11 and Figure 6).

Islam *et al.* (1995) was carried out an experiment on groundnut (*Arachis Hypogaea* L.) and obtained larger inter-cluster distances than the intra-cluster distances in a multivariate analysis.

However the maximum inter-cluster distance was observed between cluster IV and Cluster V (7.163) maintaining more distances than other clusters, and the lowest inter-cluster distance found between cluster I to Cluster IV (2.258), maintaining less distance than other cluster. Genotypes from the cluster IV and Cluster V (7.163), if involved in hybridization might produce a wide spectrum of segregating population, as genetic variation was very distinct among these groups.

Results obtained from different multivariate techniques were superimposed in Figure 7 from which it might be concluded that all the techniques gave more or less similar results and one technique supplemented and confirmed the results of another one. The clustering revealed that varieties/genotype originating from the same places did not form a single cluster because of direct selection pressure. It has been observed that geographic diversity is not always related

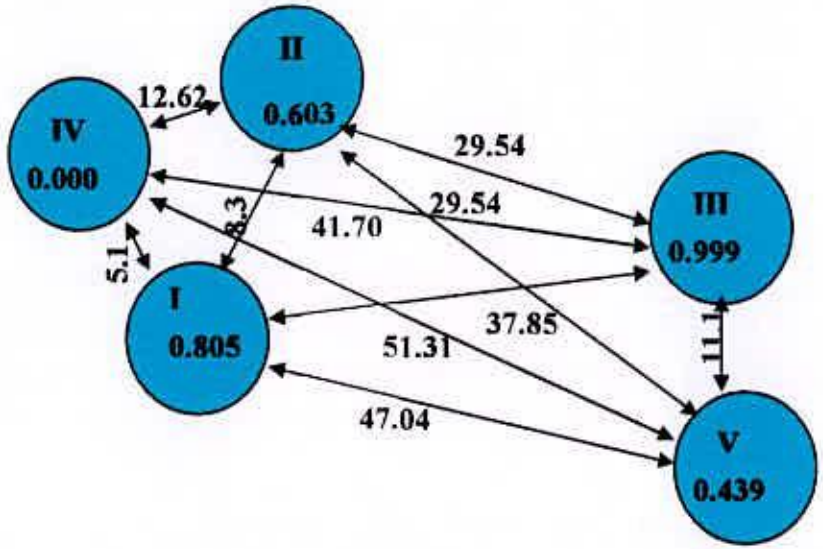


Figure 6: Cluster diagram showing intra (encircle value) and inter cluster distances ($D=\sqrt{D^2}$) of 15 sponge gourd genotypes

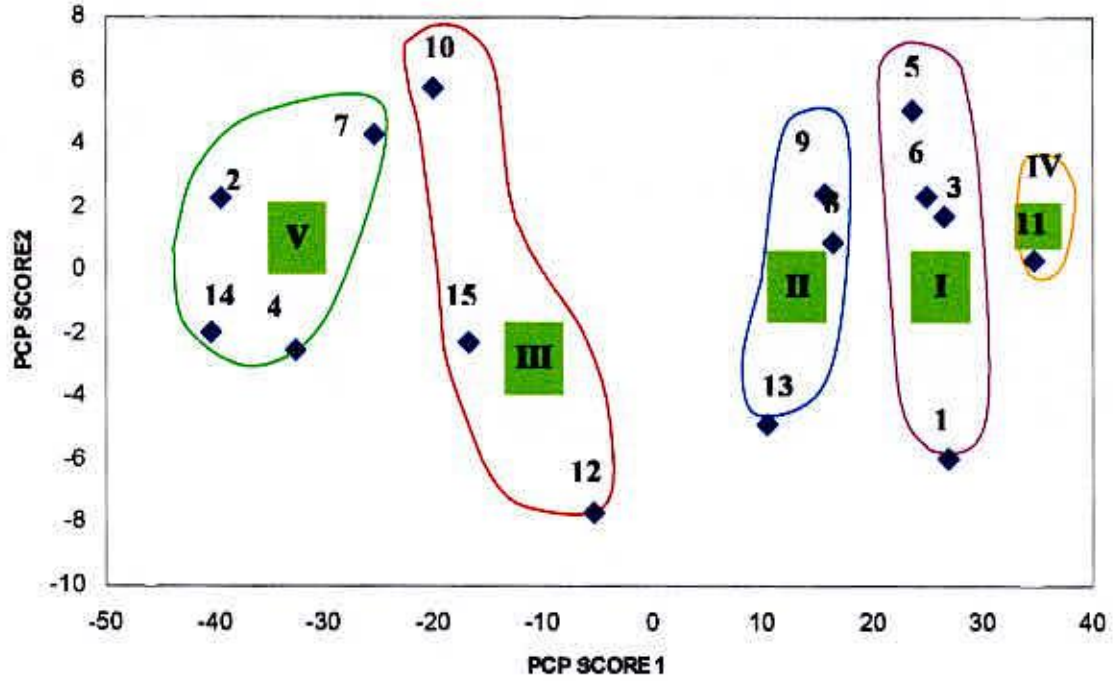


Figure 7: Cluster diagram showing five different clusters with principle component (PCP) scores

to genetic diversity and therefore, it is not adequate as an index of genetic diversity. Murty and Arunachalam (1966) studied that genetic drift and selection in different environment could cause greater diversity than geographic distance.

Furthermore, there is a free exchange of seed material among different region, as a consequence, the characters constellation that might be associated with particular region in nature loose their individuality under human interference and however, in some cases effect of geographic origin influenced clustering that is why geographic distribution was not the sole criterion of genetic diversity. The free cluster of the genotypes suggested dependence upon directional selection pressure applied for realizing maximum yield in different regions; the nicely evolved homeostatic devices would favor constance of the associated characters. This would suggest that it was not necessary to choose diverse parents for diverse geographic regions for hybridization.

4.3.5 Non-hierarchical Clustering

By using covariance matrix with the application of Non-hierarchical clustering, the 15 sponge gourd genotypes were grouped into 5 (five) clusters. These results confined the clustering pattern of the genotype according to the principle component analysis. Khan, (2006) reported five clustering Islam (2005) reported four clusters, and Kumar *et al.* (1998) reported six distinct clusters in different gourd. Compositions of different clusters with their corresponding genotypes in each cluster were presented in Table 8. These results confirmed the clustering pattern of the genotypes according to the principal component analysis. So, the results obtained through PCA were confirmed by non-hierarchical clustering.

Joshi *et al.* (2003) assessed the nature and magnitude of genetic divergence using non hierarchical Euclidean cluster analysis in 73 tomato (*Lycopersicon esculentum*) genotypes of diverse origin for different quantitative and qualitative traits. Maximum value of coefficient of variability (53.2008) was recorded for shelf life of fruits while it was minimum (69.208) for days to first picking. The grouping of the genotypes into 15 clusters indicted the presence of wide range

of genetic diversity among the genotypes. The clustering pattern of tomato genotypes indicated non-parallelism between geographic and genetic diversity.

4.3.5.1 Cluster I

Cluster I had four genotypes viz G01, G03, G05 and G06 (Table 8). From the clustering mean values (Table 9), it was observed that cluster I produced the highest number of mean values for the characters yield per plant (6.55). Cluster I also had the second lowest number of cluster mean values for leaf length (20.79), days to 1st male flower (64.35), days to 1st female flower (68.28), node no. of 1st male flower(11.06) and node no. of 1st female flower (14.03) (Table 9).

4.3.5.2 Cluster II

Cluster II was composed of three genotypes viz. G08, G09 and G13 (Table 8). These genotypes produced the 2nd highest mean values for yield per plant (3.52)

These group possessed genotypes with the second lowest cluster mean for inter node length (14.59) and leaf breadth (17.98) (Table 9).

4.3.5.3 Cluster III

From the clustering mean value it was observed that Cluster III was composed of 3 genotypes and consisted of genotypes (G10, G12 and G15) (Table 8). The genotypes of this cluster produced highest value for Inter node length (17.62) (Table 9).

The second lowest cluster mean for leaf length (25.87), leaf breadth (20.75), petiole length (13.25), days to 1st male flower (89.43), days to 1st female flower (94.63), node no. of 1st male flower(17.55), node no. of 1st female flower (23.66) and sex ratio (29.91) (Table 9).

4.3.5.3 Cluster IV

From the clustering mean value (Table 8) it was observed that Cluster IV was composed of 1 genotypes and consisted of genotypes G11 (Table 9). The genotypes of this cluster produced lowest value for leaf length (20.17), leaf breadth (15.22), petiole length (6.83) days to 1st male flower (58.55), days to 1st

female flower (61.00), node no. of 1st male flower (9.20), node no. of 1st female flower (13.38) and yield per plant (2.09) (Table 9).

4.3.5.2 Cluster V

Cluster V was composed of four genotypes viz. G02, G04, G07 and G14 (Table 8). These genotypes produced the highest mean values for leaf length (30.43), leaf breadth (24.65), petiole length (13.28) days to 1st male flower (103.28), days to 1st female flower (107.80), node no. of 1st male flower (22.51), node no. of 1st female flower (26.70) and sex ratio (30.99) (Table 9). These group possessed genotypes with the second highest cluster mean for inter node length (17.20) (Table 9).

4.4 Contribution of Characters towards Divergence of the Genotypes

Contribution of the characters towards divergence is presented in Table 10. The character contributing maximum to the divergence were given greater emphasis for deciding on the cluster for the purpose of future selection and choice of parents for hybridization (Jagadev *et al.* 1991). The vector-1 (Z_1) obtained from PCA, the important characters responsible for genetic divergence in the major axis of differentiation was yield per plant (0.203) (Table 12)

In vector II (Z_2) that was the second axis of differentiation for genetic divergence were inter node length (0.100) and seed rate (0.340) (Table 12).

4.5 Comparison of Different Multivariate Techniques

The cluster pattern of D^2 analysis though non-hierchical clustering has taken care of simultaneous variation in all the character under study. However, the distribution of genotypes in different cluster of the D^2 analysis has followed more or less similar trend of the Z_1 and Z_2 vector of the principal component analysis were found to be alternative methods in giving the information regarding the clustering pattern of genotypes. However the principal component analysis provides the information regarding the contribution of characters towards divergence of sponge gourd.

Table 12. Latent vectors for ten characters of 15 sponge gourd genotypes

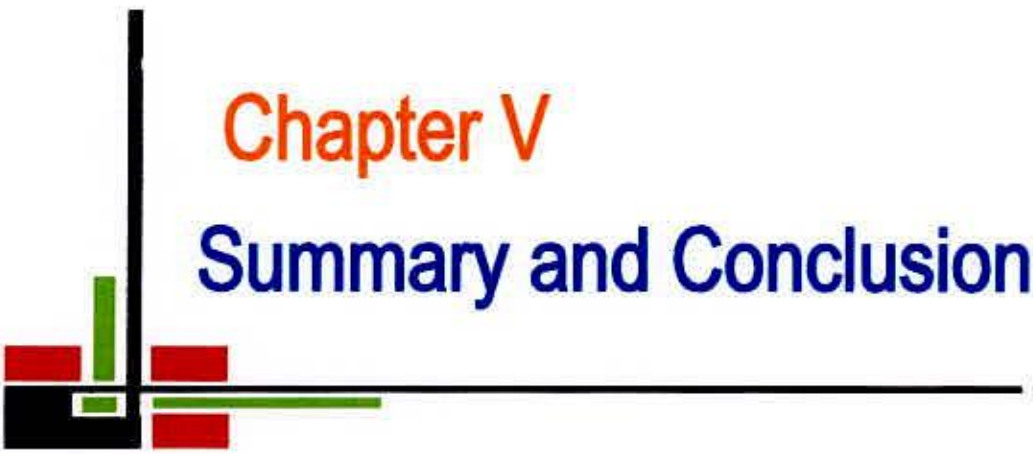
Sl. No.	Characters	Vector-I	Vector-II
01	Internodes length	-0.301	0.100
02	Leaf length	-0.321	-0.187
03	Leaf breadth	-0.286	-0.426
04	Petiole length	-0.330	-0.147
05	Days to first male flower	-0.349	-0.026
06	Days to first female flower	-0.344	-0.041
07	Node no. of first male flower	-0.345	-0.105
08	Node no. of first female flower	-0.338	-0.0211
09	Seed rate	-0.340	0.340
10	Yield per plant	0.203	-0.789

4.6 Selection of Genotypes for Further Hybridization Programme

selection of genetically divergent genotypes is an important step for hybridization programme. So, the genotypes were to be selected on the basis of specific objectives. A higher heterosis could be produced from the crosses between genetically distant parents (Falconer, 1960; Moll *et al.* 1962; Ramanujam *et al.* 1974; Ghaderi *et al* 1989; Main and Bhal, 1989).

Considering the magnitude of genetic distance and agronomic performance, the genotypes G01 and G05 from cluster I and G8 from cluster II would be suitable for highest yield per plant, maximum yield per plant.

Therefore, considering group distance and other agronomic performance, the inter genotypic crosses between G01 and G02; G01 and G07; G01 and G15; G01 and G04; G01 and G14; G01 and G10; G11 and G 07; G05 and G14; G02 and G03; G04 and G11, might be used for future hybridization programme.



Chapter V

Summary and Conclusion

CHAPTER V
SUMMARY AND CONCLUSION

In order to study the variability and genetic diversity, an experiment was conducted with 15 sponge gourd genotypes at the experimental farm of Sher-e-Bangla Agricultural University, during April, 2007 to October, 2007. Seeds of the different genotypes were sown in separate poly bag and thirty days old seedlings were transplanted in the main field in a RCBD with three replications. Data on different morphological and yield contributing characters like days to seed germination, inter node length, leaf length, leaf breath, petiole length, days to first male flowering, days to first female flowering, node number of first male flower, node number of first female flower, sex ratio, peduncle length, number of fruit per plant, average fruit weight, fruit length, fruit perimeter, yield per plant, number of seed per fruit, seed length, seed breath, seed thickness and hundred seed weight were recorded. Analysis of variance revealed significant differences among all the genotypes for all the characters under study.

The phenotypic variance was higher than the corresponding genotypic variance for all the characters indicating greater influence of environment for the expression of these characters. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters. The maximum differences between phenotypic and genotypic coefficient of variation were 108.31 and 35.50 respectively which indicated that the seed thickness was mostly depended on the environmental effect.

Amongst the characters the highest genotypic coefficient of variation was recorded for yield per plant (63.90) followed by top fruit perimeter (46.60) and average fruit weight (39.52 cm).

The highest estimated heritability amongst twenty three characters of sponge gourd was 100% for peduncle length, also 99% was found for days to seed germination, days to first male flower, days to first female flower, fruit length

and number of fruit per plant fruit weight. The lowest was 25% for hundred seed weight. The highest GA amongst all the characters was found in average fruit weight 222.40 gm the lowest genetic advance was carried out in seed thickness (0.06).

The maximum genetic advance in percent of mean was observed for top fruit perimeter (80.05) and average fruit weight (79.26), where as the lowest was for hundred seed weight (1.14). The low heritability (25%) with low genetic advance in percent of mean (1.14) indicated additive gene action for expression of the characters.

The significant variations among the genotypes for twenty three characters of sponge gourd were observed. Multivariate analysis was performed through principal component analysis, principal coordinate analysis, cluster analysis and canonical variate analysis using GENSTAT 513 software programme. The first three principal component characters with eigen values were greater than unity contributed a total of 96.57% variation towards divergence. As per as principal component analysis (PCA), D^2 and cluster analysis, the genotypes were grouped into five different cluster. These clusters were found from a scatter diagram formed by Z_1 and Z_2 values obtained from PCA. Cluster I, II, III, IV and V composed of four, three, three, one and four genotypes respectively. The maximum intra-cluster distance was observed between the clusters IV and V (7.163), followed by cluster II and cluster V (6.227). The lowest-inter cluster distance was found between the cluster I and cluster IV (2.258), followed by cluster I and cluster II (2.883).

The highest intra-cluster distance was identified in cluster III (0.999) and the lowest intra cluster distance was found in cluster IV (0.000). Genotypes included in cluster I were suitable for yield per plant (6.55), cluster III for having the highest mean value for inter node length (17.62), cluster V for leaf length (30.43), leaf breadth (24.65), petiole length (13.28), days to first male flower(103.28), days to first female flower (107.80), node no. of first male flower (22.51), node no. of first female flower (26.7) and sex ratio (30.99).

Findings of the present investigation indicated significant differences among the cultivars for all the characters studied. Generally, diversity was influenced by the morphological characters, but not by the distribution of genotypes, which indicated the importance of consumer preference and growers suitability. Considering diversity pattern and other agronomic performances, the genotypes G1, G3, G5 and G6 from cluster I and genotypes G12 from cluster III could be considered as suitable parents for efficient hybridization in future breeding programme. Inter-genotypic crosses between the diverse genotypes, *viz.* G12 and G3; G14 and G1; G9 and G5; G13 and G6; G12 and G13; G8 and G6, G15 and G11, might be able to produce desirable segregants.

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Appendices

Appendix I. Morphological, physical and chemical characteristics of initial soil (0 – 15 cm depth)

A. Physical Composition of the Soil

Sl. No.	Soil Separates	%	Methods Employed
01	Sand	36.90	Hydrometer Methods (Day, 1915)
02	Silt	26.40	Same
03	Clay	36.66	Same
04	Texture Class	Clay Loam	Same

B. Chemical Composition of the Soil

Sl. No.	Soil Characters	Analytical Data	Methods Employed
01	Organic Carbon (%)	0.82	Walkley And Black, 1947
02	Total Nitrogen (Kg/ha)	1790.00	Bremner and Mulvaney, 1965
03	Total S (ppm)	225.00	Bardsley and Lanester, 1965
04	Total Phosphorous	840.00	Olsen and Sommers, 1982
05	Available Nitrogen (Kg/ha)	54.00	Bremner, 1965
06	Available Phosphorous	69.00	Olsen and dean, 1965
07	Exchangeable K (Kg/ha)	89.50	Pratt, 1965
08	Available S (Kg/ha)	16.00	Hunter, 1984
09	pH (1:2.5 Soil to Water)	5055	Jackson, 1958
10	CEC	11.23	Chapman, 1965

Appendix II. Weather data of the experimental station, SAU during April, 2007 to October, 2007

Month	Air Temperature (^{0}C)			RH (%)	Total rainfall (mm)	Sunshine hour
	Max.	Min.	Mean			
Apr.	33.74	23.87	28.81	69.41	185	234.6
May	34.7	25.9	30.3	70	185	241.8
June	32.4	25.5	28.95	81	628	96.0
July	31.4	25.7	28.55	84	753	127.1
Aug.	32.4	26.4	29.4	80	505	108.5
Sep.	32.4	25.3	28.85	76	203	193.3
Oct.	32.3	24.7	28.50	72	88	303.25