STUDY ON GENETIC DIVERSITY OF RIDGE GOURD (*Luffa acutangula* Roxb.)

BY

MD. EMADUDDIN

REGISTRATION NO. 00835

A Thesis

Submitted to the Faculty of Agriculture
Sher-e-Bangla Agricultural University, Dhaka,
In partial fulfillment of the requirements
for the degree of

MASTER OF SCIENCE
IN
GENETICS AND PLANT BREEDING

SEMESTER: JULY – DECEMBER, 2008

Approved by:

(Dr. Md. Sarowar Hossain)
Professor
Supervisor

(Dr. Md. Shahidur Rashid Bhuiyan)
Professor
Co-supervisor

(Dr. Firoz Mahmud)
Chairman
Examination Committee

Dr. Md. Sarowar Hossain
Professor
Department of Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Sher-e-Bangla Nagar, Dhaka-1207
Bangladesh
Mobile: 01552499169
E-mail: sarowar2001@rediffmail.com

Ref: ------------ Date: ____________

CERTIFICATE

This is to certify that thesis entitled, "STUDY ON GENETIC DIVERSITY OF RIDGE GOURD (Luffa acutangula Roxb.)" 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. EMADUDDIN****, Registration No.00835 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

Hossain

Dated: December, 2008
Place: Dhaka, Bangladesh

(Dr. Md. Sarowar Hossain)
Professor
Supervisor

DEDICATED
TO
MY BELOVED PARENTS
&
SIBLING

ACKNOWLEDGEMENTS

At first the author gratefully expresses his sincere gratitude Almighty Allah, who has kindly enabled the author to complete this research work and preparation of this thesis successfully.

The author like to express his heartfelt respect and deepest sense of gratitude to his honorable Supervisor, Professor Dr. Md. Sarowar Hossain, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for his dynamic guidance, constant encouragement, constructing criticism, valuable suggestions and kind advice during the research work and preparation of the thesis.

The author feels proud to express his sincere appreciation and profound respect to his research Co-supervisor, Professor Dr. Md. Shahidur Rashid Bhuiyan, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for his valuable guidance and helpful suggestions during the research work and in preparation of the thesis.

The author likes to his sincere thanks and deep sense of gratitude to Dr. Firoz Mahmud, Chairman, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, for his valuable and helpful suggestions during the research work and co-operation in preparing the thesis.

The author likes to record special word of gratefulness to professor Abu Akbar Mia, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, for his enormous help guidance and suggestions during the research period and thesis paper preparation.

The author also thankful to Professor Dr. Shah-E-Alam, Honorable Vice Chancellor, Sher-e-Bangla Agricultural University for providing necessary facilities and conductive atmosphere accomplish his research work

The author takes an opportunity to express his cordial thanks and sincere gratitude to all the respectable teachers and staff of the Department of Genetics and Plant Breeding for their valuable and helpful suggestions during the research work and co-operation in preparing the thesis of Sher-e-Bangla Agricultural University, Dhaka.

The author also expresses his cordial thanks and gratefulness to Co-ordinator of Advance Studies and Research (CASR), Professor Mohammad Hossain Bhuiyan, and library authorities of SAU, BARC, WB and BAU for providing necessary facilities and conductive atmosphere accomplish his research work.

The author thankfully remembers the students of the Genetic and Plant Breeding department for their cooperation in the entire period of study. He also feels please to all stuffs and workers of agriculture farm, Sher-e-Bangla Agricultural University, Dhaka for their sincere help in carrying out the research work.

The author would likes to express a heartfelt thank to A.K.M. Quamruzzaman, senior scientific officer, Olericulture division , BARI, Joydebpur, Gazipur for his sincere and enormous help in data analysis.

Finally, the author is ever grateful and expresses his deepest appreciation indebt ness to his beloved parents whose sacrifice, inspiration, encouragement and continuous blessing in carry out the study. He also grateful to his brothers, sisters, friends and relative, especially Dr. A.K.M. Tajuddin Bhuiyan, Nasrin Akter, Reza, Rowshan Ali, Parvez, Rafiq who continuously prayed for his success and without whose love, affection, inspiration and great sacrifice this would not have been completed.

Dated: December, 2008

Place:SAU, Dhaka The Author

ABBREVIATIONS & ACRONYMS

ABBREVIATION		FULL MEANING
Abst.	=	Abstract
Aca.	=	Academy
AEZ	=	Agro – Ecological Zone
AFW	=	Average fruit weight
Agric.	=	Agriculture
Agril.	=	Agricultural
Agron.	=	Agronomy
Appl.	=	Applied
BARI	=	Bangladesh Agricultural Research Institute
BARC	=	Bangladesh Agriculture Research Council
BAU	=	Bangladesh Agriculture University
BBS	=	Bangladesh Bureau of Statistics
Biol.	=	Biology
Breed.	=	Breeding
^{0}C	=	Degree Celsius
CA	=	Cluster Analysis
cm	=	Centimeter
Cong.	=	Congress
Cont'd	=	Continued
% CV	=	Co-efficient of variation
CVA	=	Canonical vector analysis
Dept.	=	Department
DFFF	=	Days to first female flower bud open
DFMF	=	Days to male flower bud open
DFVH	=	Days to first vegetable harvest
ECV	=	Environmental co-efficient of variation
e.g.	=	*exempli gratia* (For example)
EMS	=	Error mean sum of square
et al.	=	*et* alia (and others)
etc	=	*et cetera* (and the others and so forth)
FAO	=	Food and Agricultural Organization
FC	=	Fruit circumference
FL	=	Fruit length
g	=	gram (s)
G	=	Genotype
GA	=	Genetic Advance
GAMP	=	Genetic advance in mean percentage
Genet.	=	Genetics
GCV	=	Genotypic co- efficient of variation
GMS	=	Genotypic mean sum of squares
ha	=	Hectare
h^{2}b	=	Heritability in broad sense
Hort.	=	Horticulture

ABBREVIATIONS & ACRONYMS (Cont'd)

ABBREVIATION		FULL MEANING
HRC	=	Horticulture Research Center
HSW	=	Hundred seed weight
i.e.	=	*id est* (That is)
Inst.	=	Institute
IPSA	=	Institute of Post Graduate Studies
j.	=	Journal
kg	=	Kilogram (s)
kg/ha	=	kilogram/ hectare
mm	=	Millimeter
MOP	=	Murate of Potash
MSGT	=	Mashed Sweet Gourd Trap
Nat.	=	National
NFPP	=	Number of fruits per plant
No.	=	Number
NPB	=	Number of primary branches at harvest
NSPF	=	Number of seeds per fruit
PCA	=	Principal Component Analysis
PCO	=	Principal Coordinate Analysis
PCV	=	Phenotypic co-efficient of variation
PGRC	=	Plant Genetic Resources Center
Proc.	=	Proceeding
Prog.	=	Progress
q	=	Quintal
Res.	=	Research
Roxb.	=	William Roxburgh
SAU	=	Sher-e-Bangla Agricultural University
SB	=	Seed Breadth
Sci.	=	Science
SL	=	Seed Length
Tech.	=	Technology
TSP	=	Triple Super Phosphate
t/ha	=	ton/ hectare
UK.	=	United Kingdom
Univ.	=	University
USA	=	United States of America
viz.	=	*videlicet* (Namely)
Veg.	=	Vegetables
YPP	=	Yield per plant
WB	=	World Bank
%	=	Percent
σ^2_g	=	Genotypic variance
σ^2_{ph}	=	Phenotypic variance

TABLE OF CONTENTS

TABLE OF CONTENTS (Cont'd)

TABLE OF CONTENTS (Cont'd)

TABLE OF CONTENTS (Cont'd)

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

STUDY ON GENETIC DIVERSITY OF RIDGE GOURD (*Luffa acutangula* Roxb.)

By

MD. EMADUDDIN

ABSTRACT

An experiment was conducted to study the genetic diversity in ridge gourd at the experimental field of Genetics and Plant Breeding, Sher-e-Bangla Agriculture farm. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The study on genetic diversity of 25 ridge gourd genotypes were carried out using morphological traits and field performance during February, 2008 to August, 2008. The results of the experiment revealed that the characters under study varied significantly among the genotypes. Among the 25 genotypes G1 was the best in respect of number of fruits per plant (32.33) and average yield per plant (5.43 kg). The phenotypic variance was higher than the corresponding genotypic variance in all the characters, indicating greater influence of environment on the expression of these characters. Based on D^2 statistics and principal component analysis, the genotypes under study were grouped into five different clusters. Cluster I contained only G18 genotype and cluster V contained maximum number of genotypes (8) followed by cluster III (7), cluster IV (5) and cluster II (4). Clustering pattern revealed that the maximum inter-cluster distance was observed between cluster I and III (35.77) followed by the distance between clusters I and II (27.27), I and IV (22.34), III and V (21.05). The lowest inter-cluster distance was observed between cluster II and IV (6.92) followed by IV and V (8.00), II and III (9.25). The highest intra-cluster distance was identified in cluster II (0.915) and the lowest intra-cluster distance was observed in cluster I (0.00). Considering cluster mean, cluster IV could be selected for yield per plant, number of fruits per plant, average fruit weight and fruit length. The contribution of both fruit circumference and hundred seed weight were most responsible to the total divergence in ridge gourd genotypes. Vector I obtained from PCA expressed that first female flower bud, fruit circumference and hundred seed weight were major characters that contribute to genetic divergence, which was the reflection of first axis differentiation. In vector 2, fruit circumference, fruit weight, hundred seed weight and number of fruits per plant played major role on genetic divergence. Other characters have minor contribution in determining genetic divergence. Considering group distance and the agronomic performance, the inter genotypic crosses between G1 & G25, followed by G1 & G8; G1 & G9; G1 & G16; G9 & G25; G8 & G25; G1 & G10; G1 & G17; G17 & G25; G1 & G5 and G11 & G18 might be suitable choice for future hybridization programme.

Chapter 1

Introduction

CHAPTER 1
INTRODUCTION

Ridge gourd (*Luffa acutangula* Roxb.) is an annual monoecious (Bhandari, 1979) climbing type herbaceous vegetable crop belongs to the family Cucurbitaceae (consists of about 118 genera and 825 species) having the chromosome number 2n = 26 (Yawalker, 1985). The name "Luffa" or "Loofah" is of Arabic origin and refers to the spongy characteristics of the mature fruit. It is also known as ribbed gourd. Its origin is not definitely known, although wild forms of this crop are found in India, the Sunda Island and Java (Yawalkar, 1985). Now it is cultivated in Bangladesh, China and many regions of India such as Assam, West Bengal, Uttar Pradesh etc. (Bose and Som, 1986).

There is tremendous genetic diversity within the family, and the range of adaptation for *Luffa* species includes tropical and subtropical regions, arid deserts, and temperate regions. There are eight species originated in Indian Sub-continent of which only two *Luffa acutangula* and *Luffa cylindrica* (Sponge gourd) are important vegetable crops while others are wild type. It is one of the important summer vegetable crops in Bangladesh and available in the market from April to October when vegetables are scanty in the market. Less production and unequal supply of vegetable in market during various parts of the year resulted in the lowest per capita vegetable consumption (25 g/head/day) in Bangladesh (Hossain *et al.*, 1990). Now it is grown throughout the year except extreme winter season.

Ridge gourd is a popular vegetable with moderately high nutrition value. The fruits contain a reasonable amount of vitamin A, C and iron and other different nutrients (Appendix II). Its use is recommended for those who suffer from malaria and other seasonal fever for its easy digestibility and very appetizing quality (Yawalkar, 1985). The total production of ridge gourd in Bangladesh was about 41, 000 metric tons in 22,000 acres of land with an average yield of 1.83 metric tons per acres in the year 2007-2008 (BBS Monthly Bulletin August, 2008).

This figure indicates the low yield potentiality of cultivars. Several factors are responsible for such a low yield of ridge gourd. Among many reasons, the lack of high yielding variety is one of the important reasons for low yield of this crop in Bangladesh. For most of the improved cultivars, variety uniformity is one of the main requirements. On the other hand, variability is a desirable goal in germplasm collection, since the material observed in such collection can be used for breeding new varieties in near future. In crop improvement programme, genetic diversity is one of the important tools to quantify genetic variability in both cross and self pollinated crops (Gaur *et al.*, 1978).

The knowledge of genetic diversity is necessary to identify the diverse genotypes for breeding purpose. Characterization like disease resistance, earliness, quality or even performance of a particular character should also be considered in case of genetic divergence (Chowdhury *et al.*, 1975 and Belaj *et al.*, 2002). Because genetic diversity provides information about the relationship among elite breeding population and helps in selecting desirable parents for establishing new breeding population. But this genetic diversity within a population depends on the number and frequency of all loci and the genetic constitution of the population (Crossa *et al.*, 1993). Now the quantification of genetic diversity through biometrical procedure made it possible to choose genetically diverse parents (Jain *et al.*, 1975).

The genetic diversity is a must for a sound base selection. It is also essential to meet the diverse goals of plant breeding such as producing cultivars with increased yield and wider adaptation, desirable quality, pest and diseases resistance (Joshi and Dhawan, 1966).

Yield is complex character and various morphological and physiological characters contribute to yield. It is essential to have knowledge on variability of different characters for the yield improvement. The available variability in a population can be partitioned into heritable and non heritable parts with the aid of genetic parameters such as genetic coefficient of variation, heritability and genetic advance (Miller *et al.*, 1958). The variability of a biological population is an outcome of genetic constitution of individuals making up that population in relation to prevailing environment. It arises either due to geographical separation or due to genetic barriers to cross ability. A survey of genetic variability with the help of suitable parameters such as genotypic co-efficient of variation, heritability and genetic advance are absolutely necessary to start an efficient breeding programme (Mishra *et al.* 1988).

Multivariate analysis is a useful technique in quantifying the degree of divergence between biological populations at genotypic level and assessing the relative contribution of different components to the total divergence both at intra and inter-cluster levels (Murty and Arunachalam, 1966). The D^2 statistic is one of the frequently used models of multivariate analysis.

The varietals improvement of a crop population depends on the magnitude of the genetic diversities for yield and yield components. Although a good number of landraces of ridge gourd is present in our country, but not much systematic research was made in the past to evaluate the potentialities of the available population Thus, this information may promote to design efficient breeding programme for the development of new varieties of ridge gourd in Bangladesh. Under such circumstances, the present study was conducted with the following objectives:

1. To assess the field performance of the twenty-five collected ridge gourd genotypes.
2. To assess the variability and heritability for yield and yield contributing characters and their interrelationship in ridge gourd.
3. To study genetic diversity among the genotypes in respect of different morphological characters.
4. To sort out the suitable genotypes for future breeding programme.

Chapter 2

Review of Literature

CHAPTER 2
REVIEW OF LITERATURE

Ridge gourd is an important vegetable cultivated in Bangladesh, but there are few reports on it related to the present study in our country. For this, the literature relevant to the present study on ridge gourd and some other related vegetables under the family Cucurbitaceae are reviewed in this chapter the following headings:

2.1 Genotypic, phenotypic variability and field performances

Quamruzzaman *et al.* (2008) were conducted experiment the genetic divergence among thirty genotypes of ridge gourd (Luffa acutangula) at the farm of Olericulture Division, HRC and in different RARS, BARI during the summer season of 2005. The genotype RGN05, RGN06, RGN07, RGN08, RGN13, RGN17, RGN18, RGN27, RGN29 recorded highest cluster mean values for days to 1st male flower open (56.0 days) and single fruit weight (141.0 g) and RGN03, RGN12 l lowest mean values for days to 1st female flower open (27.0 days) and single fruit weight (85.0 g). The highest fruit length (23 cm), fruit number/plant (26) and yield/plant (9.7 kg) obtained from RGN16 and RGN20. The role of days to 1st male flower open, days to 1st female flower open, fruit diameter, single fruit weight and fruit number in PCA indicates their importance in genetic divergence.

Guffar (2008) was conducted an experiment with 15 sponge gourd genotypes at the experimental farm of Sher-e-Bangla Agricultural University, during April 2007 to October 2007. Among the characters the highest GCV recorded for yield per plant (63.90) followed by top fruit perimeter (46.60) and average fruit weight (39.52). 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) and other characters.

Ram *et al.* (2006) were evaluated twenty-four accessions of Luffa hermaphrodita in randomized complete block design for 12 economic characters to study genetic variability of traits and contribution towards yield and its association with each other. The analysis of variance revealed considerable genetic diversity among the accessions for aggregate effect of all the characters. Of the 24 genotypes, SP-59 recorded highest edible fruit yield/hectare (107.9 q) while DR/Y-1 expressed earliness with respect to days to first hermaphrodite flower anthesis (40.6) and maximum mean value for number of fruits per plant (185.3). High heritability for number of seeds per fruit, seed weight and edible fruit yield per hectare suggests that characters phenotypic value could provide fair and reliable measure of good genotype. High heritability and high genetic advance for number of seeds per fruit and edible fruit yield per hectare indicated the presence of high amount of fixable variation among genotypes for these traits, which provides ample scope for varietal improvement through hybridization and selection in Luffa hermaphrodita.

Zaman *et al.* (2004) reported the performance of three sponge gourd lines at the farm of Olericulture Division, HRC and in different RARS, BARI during the summer season of 2004. The line Sg 6-3-2-2-10-10 and Sg 6-3-1-2-1-6 produced the highest number of fruits per plant (34) and lower was recorded in Local (26). Maximum individual fruit weight was obtained form Local (189 g). The line Sg 6-3-2-2-10-10 gave the highest yield (20.0 t/ha) closely followed by Sg 6-3-1-2-1-6 (19.4 t/ha).

Shinde *et al.* (2003) evaluated that the fruit characteristics of 18 strains and 2 cultivars of *Luffa acutangula* during summer in India. The lowest number of days to fruit set was recorded in DPL-RG-12 (36.99), DPL-RG-4 (40.33) Punjab Sadabahar (40.66) and DPL-RG-2 (41.00). The average fruit number per vine (15.55) was recorded in DPL-RG-12, whereas Punjab Sadabahar recorded the highest average fruit length (28.73 cm) and fruit weight (115.33 g). The superior lines in terms of fruit yield and quality were DPl-RG-12, DPL-RG-2 and Punjab Sadabahar.

Singh *et al.* (2002) conducted an experiment on 80 ridge gourd genotypes to determine variability and heritability of nineteen yield contributing characters. High PCV and GCV were observed for node number for appearance of 1st male flower, male flowers per plant, sex ratio main axis and branches, fruit per plant, fruit weight, seeds per fruit, and yield per plant. The GCV and PCV values were almost equal for most of the characters studied. The broad sense heritability estimates were high for all the characters.

Hossain (1996) was conducted an experiment on floral biology of ridge gourd at the experimental farm of IPSA (Institute of Post Graduate Studies). Male, female and hermaphrodite flower buds appeared 29-38 days after seeding. The male flower buds developed earlier and in lower nodes than the female and hermaphrodite ones. The first male, female/hermaphrodite flowers were produced an average in the 10th to 21st node.

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

Abusaleha and Dutta (1990) carried out a study with 65 genetic stocks to assess the genetic variation and heritability in ridge gourd. Significant variability was observed for all the characters at phenotypic as well as genotypic level with a very wide range of values. Swamy *et al.* (1984) also conducted an experiment on muskmelon and reported a wide range of variability among the genotypes for number of seeds per fruit.

Rahman *et al.* (1990) in a study observed significant variation for days to first flowering among the genotypes of ribbed gourd, bitter gourd and sweet gourd. Rahman *et al.* (1990, 1991) also concluded that days to male flowering was earlier than days to female flowering in several genotypes of ribbed gourd, bitter gourd, bottle gourd and sweet gourd. They also reported that bitter gourd, sweet gourd, ribbed gourd and bottle gourd genotypes differed significantly for fruit breadth and weight per fruit.

Thirty *Luffa acutangula* varieties collected in Maharastra were scored for 14 quantitative traits. Most characters showed significant variation between entries. Yield was highest (1.77 kg/vine) in RGIII. High heritability and genetic advance estimates were obtained by Kadam and Kale (1987) for days to flowering, nodal position of female flower, fruit volume and powdery mildew intensity in ridge gourd.

Shani *et al.* (1987) reported that performances of 21 *Luffa acutangula* genotypes for yield and 8 related characters and on genetic parameters (Variance, coefficient of variation, heritability and expected genetic advance) for the characters. Heritability was high for most characters. Fruit weight was controlled by additive gene effects and fruit number per stem, female flower number per stem, first female flowering node and branch number per stem by non-additive effects. Fruit diameter and fruit length showed potential for improvement by heterosis breeding.

Chowdhury and Sharma (2002) were studied genetic variation, heritability, genetic advance and correlation for yield and yield components (vine length, number of nodes, node on which the first flower appeared, number of fruits per plant, fruit length, fruit girth and fruit weight) in 12 *Luffa acutangula* cultivars. The genetic coefficient of variation (GCV) was higher than the phenotypic coefficient variation (PCV) for all the characters. High values of variability, PCV, GCV and genetic advance have recorded for vine length, yield per hectare and fruit weight indicating that these characters were controlled by additive gene effects. The correlation coefficient revealed that yield per hectare could be improved through selection for higher fruit number per plant, fruit length and girth and individual fruit weight.

Banik (2003) conducted an experiment on variability and genetic advance of 26 genotypes of snake gourd with respect of 15 quantitative yield contributing characters and found significant difference among the characters like vine length at harvest (2.197 to 3.87 m), number of primary branches (5.23 to 11.88), days to 1st male flowering (41.67 to 68.67 days), days to 1st female flowering (48.67 to 71.33 days), node number of 1st male flower (6.33 to 17.67 days), fruit length (20.67 to 71.17 cm), seeds per fruit (39.03 to 69.50). Banik also found that significant differences in 1st female flower, node number (mean value 19.28) and fruits per plant. The highest phenotypic coefficient of variation was observed for fruiting node on main vine, fruit yield per plant, fruit length and first male flower node. The PCV was lowest for days to maturity, 100 seed weight and days to first male flower opening. The GCV along with heritability was high for the above characters. High heritability coupled with high genetic advance was noticed for fruit yield per plant (GCV and PCV 30.75 and 30.96; h^2b 98.64%), fruit length (GCV and PCV 29.92 and 30.04; h^2b 99.19%) and first female flower node number (GCV and PCV 25.87 and 26.59; h^2b 94.63%) and number of fruits per plant (GCV and PCV 19.82 and 20.59; h^2b 92.67%).

Kabir (2007) conducted an experiment on variability and estimation of genetic parameter, correlation, path analysis and genetic diversity of 24 accessions of pointed gourd with respect of different parameter such as days to flower, fruit length, fruit breadth, single fruit weight, pulp seed ratio, number of fruits per plant, weight of fruit per plant and yield of fruit. The accession PG020 showed the highest performance in weight of fruits per plant, single fruit weight and yield. The highest genotypic and phenotypic coefficients were recorded in the parameter number of fruits per plant (5415.55% and 5623.67%) and second highest was recorded from yield of fruits ton per hectare (410.30% and 410.98%). However, days require to first flowering (49.86% and 52.41%), fruit length (7.4% and 7.42%), fruit breadth (23.56% and 26.79%), single fruit weight (172.27% and 173.28%), and weight of fruit per plant (161.87% and 162.85%) recorded moderate GCV and PCV. Correlation coefficient indicated that fruit yield per plant was highly significant and there was a positive association with weight of fruit per plant, number of fruits per plant and single fruit weight. Path analysis indicates fruit breadth, number of fruits per plant and weight of fruits per plant directly contributed to the yield of pointed gourd accessions.

Seshadri *et al.* (2002) stated that *Cucumis melo* encompassed a wide variability of dessert melons and non-dessert forms and landraces found in India. There was a large array of varieties and types in these landraces.

Chen *et al.* (2002) evaluated two cultivars of cucumber for preliminary characterization of new species. From preliminary evaluation, they found that wild cultivars (*Cucumis hystrix* Chandr) were disease resistant and fruit morphology of the F_1 plants differed during the growing season.

Ashok and Rajan (2002) conducted an experiment with 25 accessions of snake gourd and the accessions were grouped into different clusters based on seed, growth and yield characters using principal component analysis and found that maximum seed index for TA 108 (178.63 mm^2); the maximum growth index value for TA 118 (91.533) and the maximum yield index value for TA 117 (2181.566) were revealed from the principal component analysis. Based upon the seed characters (seed size, seed coat colour and 100 seed weight); growth, leaf lobes, leaf pubescence and tendril length and fruit character (fruit skin colour, fruit girth, fruit length and fruit weight) keys were developed for varietal identification.

Sharma *et al.* (2000) evaluated 10 cucumber lines and testers under different environmental conditions and reported that day to first female flower, nodal position of fruits per plant, marketable yield per plant, fruit length and fruit diameter had wide range of variation.

Mathew and Khader (1999) conducted an experiment on genetic studies in snake gourd (*Trichosanthen anguina*) and observed the genetic variability and heritability of 12 traits in 34 *Trichosanthen anguina* in Kerela, India and reported that the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were almost equal for all characters. The highest GCV and PCV were recorded for mean fruit weight, seed per fruit,

fruit yield per plant and fruit length. High heritability was observed for mean fruit weight, seeds per fruit, fruit length, days to first male flower and fruit yield per plant.

Rumaran *et al.* (1997) was conducted 30 pumpkin genotypes in a field trial and reported that genotypic coefficient of variation was smaller than phenotypic coefficient of variation for most of the traits studied. However, GCV was high for mean fruit weight, number of fruits per plant, number of seeds per fruit, yield per plant and fruit, total soluble solids content. High heritability coupled with high genetic advance were observed for vine length, mean fruit weight, number of fruits per plant, number of seeds per fruit, fruit yield per plant and total soluble solids content of fruits. Islam (1993) reported that male flowering was earlier than female flowering in several genotypes of bottle gourd.

Varghese (1991) reported an experiment on the variability among 48 snake gourd genotypes in respect of different yield contributing characters and found significant differences among the characters. Main vine length varied from 3.035 to 7.85 m with high heritability (97.0%). In case of number of branches per vine, heritability was 91.0%. Moderate GCV and PCV in fruit length and breadth (32.15 and 32.51; 20.26 and 21.23) was also observed in snake gourd germplasms. Narrow differences between GCV and PCV in fruit weight with high heritability (h^2b) were also observed. GCV and PCV for yield per plant were 30.0 and 31.33 respectively. 100 seed weight varied from 20.0 to 41.0 g with high heritability 97.8% in snake gourd.

Mondal *et al.* (1989) studied the genetic variability of 31 watermelon genotypes and observed a wide range of variability for days to first fruit harvest, fruit length, fruit diameter, number of fruits per plant and fruit yield per plant.

2.2 Correlation, coefficient and path analysis

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

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

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

Singh *et al.* (2002) were carried out 98 hybrids of cucumber derived from crosses involving 14 male and 7 female parents and found that fruit weight, fruit girth and fruit length had high correlations with fruit yield. Genotypic correlation coefficient were higher than phenotypic co-efficient which indicated strong association among these traits. Path coefficient analysis also indicated that fruit weight had the highest direct effect on fruit yield.

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

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

Miah *et al.* (2000) noted that fruit yield in bitter gourd showed significant positive association with average fruit weight, fruit breadth and number of nodes per vine in genotypic and phenotypic correlation with days to male flowering. Path analysis revealed that average fruit weight, number of fruits per plant, days to male flowering and fruit length had positive direct effect on fruit yield.

Sarker *et al.* (1999) studied correlation and path coefficient of 16 divergence types of pointed gourd indicated that fruit weight, fruit diameter and number of primary branches per plant were positively and significantly correlated with yield per plant at genotypic and phenotypic levels. The path analysis revealed that fruit volume followed by fruit weight and fruit diameter had maximum positive direct effects on yield.

Li *et al.* (1997) noted that number of fruits per plant, average fruit 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.

Ananthan and Pappoah (1997) reported that fruit number per vine and seed number per fruit were positively correlated with total yield while days to first female flowering, days to first male flowering, sex ratio, fruit girth, pulp thickness and total soluble solids content were negatively correlated with total yield in cucmber.

Rajput *et al.* (1991) also found significant positive correlation between number of fruit and yield and number of branches with yield. Harvest period also influenced the yield and its degree of association with increasing vine length. The variability, heritability and scope of improvement were studied by Abusaleha and Dutta (1990) in cucumber. They found positive and significant correlation between yield and nodal position of first female flower ($r = 0.225$) in cucumber.

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

Sych (1990) conducted path coefficient analysis in 150 genotypes of watermelon and found that fruit weight and number of fruits per plant had considerable direct effects on yield.

Rastogi *et al.* (1990) conducted an experiment with 25 diverse cucumber cultivars and found that general genotypic correlation coefficient were higher than those related to phenotypic or environmental; factors. However, both genotypic and phenotypic coefficient for fruits per plant gave positive and significant association with number of primary branches, number of female flower, fruit weight and number of fruits per plant. Female flower per plant showed highly significant positive correlations with number of primary branches, fruit yield and fruit per plant. Longer vine length increased the number of male flowers and produced heavier fruits.

Mondal *et al.* (1989) studied path coefficient in 31 genotypes of watermelon and observed that the number of fruits per plant and fruit diameter affected fruit yield directly. Path coefficient analysis revealed that for increasing fruit yield selection should be based on plant having more number of fruits with larger diameter.

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

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

Prasad *et al.* (1988) in a study found that phenotypic and genotypic coefficient of variation of water melon were high for fruit per plant, average fruit weight, seed per fruit, 100 seed weight and fruit yield per plant. They also reported that fruit yield was correlated with vine length (r = 0.47), branches per plant (r = 0.75), fruit weight (r = 0.88), length (r = 0.63) and girth (r = 0.61).

Vijay (1987) worked with nine agronomic characters of 95 diverse musk melon stocks and found that fruits per vine, flesh thickness and yield per vine showed the greatest genotypic coefficient of variation. Heritability and genetic advance were high for fruit per vine, total soluble solids content, flesh thickness and yield per vine. Fruits per vine and fruit weight were positively correlated with yield.

Chadhury and Mandal (1987) conducted a study on 30 diverse cucumber genotypes and found high positive correlations at the genotypic and phenotypic levels between yield per plant with number of fruits and female flowers per plant, fruit length and weight. Path coefficient analysis revealed that the above characters and fruit diameter were the most important characters determining yield.

According to Singh *et al.* (1986) fruits per plant, fruit length and yield showed high heritability and genetic advance in pointed gourd. According them, yield was positively and significantly correlated with fruits per plant ($r = 0.60$) and days to flowering, days to fruit set and days to ripeness were negatively correlated with all the other characters with the exception of a positive correlation between days to flowering and fruit weight.

Reddy and Rao (1984) observed negative and non-significant correlation between these traits ($r = 0\ 0.222$) in ribbed gourd. Patil (1988) reported that main vine length had positive and significant correlation with yield in cucumber.

2.3 Genetic diversity

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

The quantification of genetic diversity through biometrical procedure made it possible to choose genetically diverse plants for a successful hybridization programme (Rao, 1952). D^2 analysis (originally outlined by Mahalanobis, 1936 and extended by Rao, 1952) is one of potential methods of estimating the degree of genetic diversity.

The wide diversity of genotypes can be shown by cluster analysis from the same geographical regions. To understand the usable variability, grouping or classification of genotypes based on suitable scale. Multivariate analysis formulated by Mahalanobis (1963) is a powerful tool in quantifying the degree of divergence among biological population based on multiple characters. Studies on genetic diversity in ridge gourd carried out so far are presented as follows:

Quamruzzaman *et al.* (2008) were studied the genetic divergence among thirty genotypes of ridge gourd (*Luffa acutangula*) using D^2 and principal component analysis. The genotypes were grouped into six clusters. The highest intra cluster distance was noticed for the cluster II (0.882) and the lowest for the cluster III (0.220). The highest inter-cluster distance was observed between cluster I and II (15.045) where as the lowest was observed between cluster IV and V (3.402).

Karuppaiah *et al.* (2005) were evaluated genetic divergence in 12 genotypes of ridge gourd (L. acutangula) grown in Annamalai, Tamil Nadu, India, during June-July 2001. Using Mahalanobis D2 technique, the genotypes were grouped into clusters I (4 genotypes), II (one genotype), III (3 genotypes) and IV (4 genotypes). Among the 4 clusters, cluster IV (LA-7, LA-9, LA-10 and LA-12) registered the highest mean values for vine length (6.2 m), number of male flowers per plant (79.3), number of female flowers per plant (23.2), yield per plant (5.2 kg), single fruit weight (242.2 g), fruit length (29.4 cm), number of fruits per plant (24.1), number of seeds per fruit (52.3), fruit size index (173.2), and 100-seed weight (18.6 g). Hence, it is desirable to involve LA-7, LA-9, La-10 and LA-12 of cluster IV in breeding programmes.

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

Sanwal *et al.* (2008) were evaluated thirty eight indigenous collections of chow-chow for eight quantitative and quality traits. High values of genotypic coefficient of variance along with high heritability and genetic advance were recorded for number of fruits/plant, fruit yield/plant, TSS, acidity and ascorbic acid. Number of fruits/plant and average fruit weight showed positive and significant correlation with fruit yield/plant. The number of fruit/plant and average fruit weight had high direct effect towards the fruit yield/plant. Hence, these characters should be given more emphasis while making selection for high yielding genotypes. On the basis of genetic divergence, relative magnitude of D^2 values thirty-eight genotypes were grouped into seven clusters. The maximum genetic divergence was observed between cluster III and VII followed by cluster II and VI. The cluster V and VI displayed lowest degree of divergence. The minimum intra-cluster distance was exhibited for cluster VI followed by cluster V. However, it was highest for cluster III. The mean values were higher in cluster I and IV for two characters i.e. fruit length and average fruit weight, while cluster II had high mean values for number of fruits/plant.

Masud *et al.* (2001) studied genetic divergence in 19 genotypes of sponge gourd (*Luffa cylindrica*) collected from local and exotic resources. 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 close relationship between geographical distribution and genetic divergence as estimated by D^2 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.

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

Hazra *et al.* (2003) reported that genetic divergence studied on 167 accessions of pointed gourd and grouped in eight non-overlapping clusters, with cluster IV comprising of the highest number of accessions (37 accessions) and cluster VI comprising of the lowest number of genotypes (6 accessions). Intercluster distance ranged from 1.25 in cluster I to 1.65 in cluster VII. Cluster VIII and V were the most diverse as indicated by the maximum intercluster distance between them (6.04).

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

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

Dora *et al.* (2003) conducted an experiment on eleven genotypes of pointed gourd to find out genetic divergence following Mahalanobis's D^2 statistics. The eleven genotypes were grouped into four clusters. Cluster I and II comprised of four genotypes each, cluster III comprised of two genotypes and cluster IV comprised of only single genotype. Genetic draft and natural selection in different environment can cause high diversity among genotypes that is geographical isolation (Updhaya and Mutry, 1970).

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. Cluster III had the maximum (11) and cluster IV and VII had the minimum number (4) of genotypes. The characters like fruit weight yield per plant contributed maximum towards total divergence.

More and Seshadri (2002) studied the genetic divergence in muskmelon. After evaluation, based on statistical analysis they classified 98 genotypes into 12 clusters. The crosses involving parent belonging to medium divergent cluster may also exhibit significant and positive heterosis (Miah and Bhal, 1989).

Rahman *et al.* (2000) conducted a study involving 22 diverse genotypes of chilli revealed a high diversity. Depending on the genetic divergence the 22 genotypes were grouped into 5 clusters. Maximum distance at inter cluster level was 19.989 followed by 16.176. They also reported that the genotype usually did not cluster according to the geographical distance.

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

Ram *et al.* (2001) performed cluster analysis in 167 pointed gourd genotypes (*Trihosanthes dioica*) collected from different ecogeographic region of India. On the basis of different yield contributing agro morphological traits, the genotypes were grouped into eight clusters 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.

Principal component and grouping analyze of data on 31 plant morphological traits were used to estimate genetic divergence in 15 accessions of *Cucurbita* by Choer *et al.* (2000). It was observed that the accessions dispersed in a bidirectional space way, forming three groups, each on having two subgroups. Grouping analysis by the Ward method showed similar results to those obtained from principal component analysis. The traits that mostly contributed to genetic divergence were presence of thorns on the petiole internode number of the main vine up to the first female flower, fruit shape, fruit diameter, skin texture, predominant skin colour and number of days to the first male flower on the main vine.

Ramos *et al.* (2000) were evaluated the genetic diversity of 40 squash accessions collected from distinct areas of the Northeast region of Brazil. The data were analyzed using canonic variable and Tocher cluster analysis adopting Mahalanobis D^2 general distance. It was observed that 65% of the accessions were clustered in a group. The disperse results based on the first four canonic variables (71% of total variability) did not permit a correlation between genetic diversity and eco-geographical origin.

Rashid (2000) found that no relationship between geographic distribution and genetic diversity in pumpkin. The result suggested that geographic isolation is not the only factor causing genetic diversity and this point should be considered in selecting parents for hybridization.

Varalaksmi *et al.* (1994) conducted an experiment with 48 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 Mahalanobis 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 inter cluster D^2 value indicated that cluster III was most divergent from the other clusters.

Prasad *et al.* (1993) were evaluated 32 genotypes landraces of cucumber for 14 characters. Mahalanobis's D^2 analysis indicated considerable diversity among the genotypes that were grouped into 8 clusters independently of their geographical distribution.

Mathew *et al.* (1986) studied genetic distance among five botanical varieties of *Cucumis melo*. The genetic distance was calculated for nodes to first female flower, fruit weight, seeds per fruit and fruits per plant. Total D^2 was estimated according to Mahalanobis (1936). The magnitude of D^2 indicated closeness among the varieties. The character fruits per plant contributed maximum to total divergence (80%). Seeds per fruit did not contribute to the total divergence and concluded that selection of botanical varieties based on fruits per plant would be a logical step in the selection of divergence parents in crop improvement programme.

Sidhu and Gautam (1985) obtained higher inter cluster distance than cluster distance in watermelon and reported the low intra cluster and high inter cluster distance indicated that the population grouped were homozygous within and heterozygous between clusters.

Digby *et al.* (1989) reported that the coordinates obtained from the Principal Component Analysis (PCA) to calculate distances among the points. PCA is used for the graphical representation of the points while PCO is used to calculate the minimum distance straight line between each pair of points.

Pyene *et al.* (1989) worked on the hierarchical nature of the grouping into various numbers of classes could impose undue constrains and the statistical properties of the resulting groups were not clear. Therefore, they have suggested non-hierarchical classification, as an alternative approach to optimize some suitability choosing criteria directly from the data matrix. They 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 vector analysis (CVA) for discriminatory purpose.

Chapter 3

Materials and Methods

CHAPTER 3
MATERIALS AND METHODS

The investigation was carried out at the experimental field of Genetics and Plant Breeding Field Laboratory of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh during the period from March 2008 to August 2008 to study on the morphological characterization and genetic diversity in Ridge gourd. A brief description about the experimental site, characteristics of soil, climatic condition of the experimental site, materials, design of the experiment and method of cultivation, data collection and statistical analysis employed have been presented below:

3.1 Experimental site

The experiment was conducted at the experimental field of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University (SAU), Sher-e-Bangla Nagar, Dhaka-1206. The location of the experimental site was at 23^0 74' N latitude and $90^0$35'E longitude with an elevation of 8.2 meter from the mean sea level.

3.2 Characteristics of soil

The soil of the experimental field was belonging to Madhupur Tract in Agro Ecological Zone (AEZ) 28. The soil of the experimental field was clay-loam in texture having a pH of around 6.2.

3.3 Climatic condition of the experimental site

The experimental site is under the sub-tropical climatic zone. Details of the metrological data including maximum and minimum mean monthly temperature (^{O}C), relative humidity and sunshine (hour/day) for growing season was collected from the Weather Station of Bangladesh, Sher-e-Bangla Nagar, Dhaka-1207, presented in Appendix I.

3.4 Planting materials

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

Table 1: Name and origin of twenty-five ridge gourd genotypes used in the present study

Sl. No.	Genotypes No.	BARI ACC Number	Origin
1	G_1	BD 2972	PGRC, BARI
2	G_2	BD 2973	PGRC, BARI
3	G_3	BD 2974	PGRC, BARI
4	G_4	BD 2975	PGRC, BARI
5	G_5	BD 2977	PGRC, BARI
6	G_6	BD 2978	PGRC, BARI
7	G_7	BD 2979	PGRC, BARI
8	G_8	BD 2980	PGRC, BARI
9	G_9	BD 2982	PGRC, BARI
10	G_{10}	BD 2983	PGRC, BARI
11	G_{11}	BD 2984	PGRC, BARI
12	G_{12}	BD 2985	PGRC, BARI
13	G_{13}	BD 2986	PGRC, BARI
14	G_{14}	BD 2990	PGRC, BARI
15	G_{15}	BD 2992	PGRC, BARI
16	G_{16}	BD 2993	PGRC, BARI
17	G_{17}	BD 2994	PGRC, BARI
18	G_{18}	BD 2997	PGRC, BARI
19	G_{19}	BD 2999	PGRC, BARI
20	G_{20}	BD 3000	PGRC, BARI
21	G_{21}	BD 3002	PGRC, BARI
22	G_{22}	BD 3007	PGRC, BARI
23	G_{23}	BD 3009	PGRC, BARI
24	G_{24}	BD 3010	PGRC, BARI
25	G_{25}	BD 3011	PGRC, BARI

3.5 Design and layout of the experiment

The experiment was laid out Randomized Complete Block Design (RCBD) with three replications. The genotypes were distributed into the every plot of each block of the prepared layout of the experiment. The individual plot was 4 m × 1 m in size. The twenty-five genotypes of the experiment were assigned at random into plots of each replication. The distance maintained 50 cm × 3 m spacing row to row and plant to plant respectively. The distance maintained between two blocks was 1 m

3.6 Polybag preparation and raising seedling

Due to uncertain rainfall during the period of the study, the seeds were dibbled in Polybag for higher germination percentage and to get healthy seedlings and when the seedlings the seedlings become 25 days old; those were transplanted in the main field in the pit. Seeds were 8 March, 2008, before sowing, seeds were soaked in water for 24 hours and seeds were treated with Bavistin for 5 minutes.

3.7 Land preparation

The experiment plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about good tilth in the first week of February 2008. Weeds and other stables were removed carefully from the experimental plot and leveled properly.

3.8 Pit preparation

After final land preparation, pits of 50 cm × 50 cm × 45 cm were prepared in each plot with a spacing of a spacing of 3 m × 1.25 m. Pits were kept open in the sun for 7 days to kill harmful insect and microorganisms. To control field cricket 5 mg Furadan was also mixed with the soils of each pit before making it ready for dibbling.

3.9 Manure and fertilizers application

The following doses of manure and fertilizers were applied to the plots for ridge gourd cultivation (Anonymous, 1991 & Rashid, M. 1999)

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

Sl. No.	Fertilizer/Manure	Dose
1.	Cowdung	10 ton/ha
2.	Urea	150 kg/ha
3.	TSP	100 kg/ha
4.	MOP	150 kg/ha
5.	Gypsum	80 kg/ha
6.	Zinc Oxide	8 kg/ha

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

3.10 Transplanting of seedlings

Germination of seeds was completed within 12 days and the seedlings of different accessions were planted in the pit on 3rd April, 2008. In each pit two seedlings were planted and the soil around the plant was firmly pressed by hand. The field view of the experiment shown in Plate 1a and Plate 1b.

Plate 1a: Field view of the experiment

Plate 1b: Field view of the experiment

3.11 Intercultural operations

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

3.11.1 Thinning and gap filling

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

3.11.2 Weeding and mulching

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

3.11.3 Irrigation and after-care

In the early stage irrigation was done twice daily by water cane. In mature stage flood irrigation was done when ever it's necessary.

3.11.4 Pesticide application

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

3.12 Harvesting

Fruits were picked on the basis of horticultural maturity, size, colour and age being determined for the purpose of consumption as the fruit grew rapidly and soon get beyond the marketable stage, frequent picking was done throughout the harvesting period. Fruits were picked with sharp knife and care was taken to avoid injury of the vine.

3.13 Data recording

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

3.13.1 Plant characteristics

i. Cotyledon colour:

Cotyledon colour was observed in 3-5 plants at the first time leaf expanding stage.

ii. Number of primary branches:

At the time of final harvest, number of primary branches of selected plants from each accession was counted.

iii. Leaf shape:

Leaf shape of the 6th – 10th leaf was observed at the time of 20th leaf expanding from 3-4 plants.

3.13.2 Inflorescences characteristics

i. Days to first male flowering:

The number of days required for first male flower flowering was counted.

ii. Days to first female flowering:

The number of days required for first female flower flowering was recorded.

iii. Male female flower ratio:

Male and female flower ratio was observed in 3-5 plants.

3.13.3 Fruit characteristics

i. Peduncle separation from fruit:

After fruit harvest for vegetable use, the break strength and peduncle with fruit was evaluated

ii. Blossom-end fruit shape:

Blossom-end fruit shape was observed at the peak harvest season for vegetable use in 3-5 fruits in different plants.

iii. Stem-end fruit shape:

Stem-end fruit shape was observed at the peak harvest season for vegetable use in 3-5 fruits in different plants.

iv. Fruit shape:

Fruit shape was observed at the peak harvest season for vegetable use in 3-5 fruits in different plants.

v. Fruit ribs:

Intensity of rib was observed at harvest time for vegetable use in 3-5 fruits per plants.

vi. Fruit colour:

Fruit colour was observed at the peak harvest season for vegetable use in 3-5 fruits in different plants.

vii. Fruit skin texture:

Fruit skin texture was observed in 3-5 fruits of different plants at vegetable purpose harvest time. Hand feeling (sensory taste) with skin of fruit is the way of describing genotypes.

viii. Flesh moisture:

Fruit flesh moisture was observed in 3-5 fruits ready to harvest for vegetable use.

ix. Skin hardness:

Skin hardness was test by sensory taste in 3-5 fruits ready to harvest for vegetable use. Feel when it is cut.

xi. Days to first harvest for vegetable use:

For this descriptor, date of seeding and date of first harvest for kitchen purpose was recorded.

xii. Fruit length:

Fruit length was measured in 3-5 fruits of different plants in cm. It is length between blossom and stem end during fruit harvest for vegetable use.

xiii. Fruit Circumference:

Diameter in central part of fruit at harvest time for vegetable use was measured in 3-5 fruits of different plants in cm.

xiv. Fruit weight:

Weight of 3-5 fruits of different plants during harvest for vegetable use was measured in gram (g).

xv. Fruit per plant:

The number of fruit suitable for vegetable use during crop season was counted in 3-5 plants.

xvi. Fruit yield per plant:

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

xvii. Seed per fruit:

The total number of matured functional seeds in 3-5 fruits of different plants was recorded

3.13.4 Seed characteristics

i. Seed surface:

Seed surface was observed in 3-5 matured seeds.

ii. Seed length:

Seed length measured in mm in 3-5 matured functional and dry seeds collected randomly from different fruits.

iii. Seed breadth:

Seed breadth measured in 3-5 matured functional and dry seeds collected randomly from different fruits. Seed breadth was measured in the middle part of seed in mm.

iv. Hundred seed weight:

Weight of 100 mature functional and dry seeds collected randomly from 3-5 fruits of different plants.

3.14 Statistical analysis

Mean data of the characters were subjected to both univariate and multivariate analysis. Univariate analysis of the individual character (Analysis of variance) was done for all characters under study using the mean values (Singh and Chaudhury, 1985) and was estimated using MSTAT-C computer programme. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV %) were also estimated using MSTAT-C. The significance of the difference between treatments was evaluated by least significant difference (LSD) test for the interpretation of the results (Gomez and Gomez, 1984). Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2000 software through four techniques viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA).

3.14.1 Univariate analysis

All recorded data obtained for each character were subjected to the analysis of variance following the RCBD design. Means ($\bar{x}$), ranges and standard deviations (O_x) of characters studied in this experiment also were estimated.

3.14.1.1 Estimation of genotypic, phenotypic and error variances

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

Genotypic variance (σ^2_g) $= \frac{\text{GMS} - \text{EMS}}{\text{r}}$

Where,
GMS = Genotypic mean sum of squares
EMS = Error mean sum of square
r = number of replications

Phenotypic variance (σ^2_{ph}) $= \sigma^2_g + \text{EMS}$

Where,

σ^2_g = Genotypic variance

EMS = Error mean sum of square

σ^2_e = error variance

3.14.1.2 Estimation of genotypic and phenotypic co-efficient of variation

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

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

Where,

σ^2_g = Genotypic variance

σ_g = Genotypic standard deviation

$\bar{x}$ = Population mean

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

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

Where,

σ^2_{ph} = Phenotypic variance

σ_{ph} = Phenotypic standard deviation

$\bar{x}$ = Population mean

3.14.1.3 Estimation of heritability

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

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

Where,

$h^2{}_b$ = Heritability in broad sense

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

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

3.14.1.4 Estimation of genetic advance

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

Genetic advance (GA) = $K.\ h^2.\ \sigma_{ph}$

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

Where,

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

σ_{ph} =Phenotypic standard deviation

$h^2{}_b$ = Heritability in broad sense

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

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

3.14.1.5 Estimation of genetic advance mean's percentage

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

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

3.14.2 Multivariate analysis

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

3.14.2.1 Principal Component analysis (PCA)

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

3.14.2.2 Principal Coordinate analysis (PCO)

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

3.14.2.3 Cluster analysis (CA)

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

3.14.2.4 Canonical Vector analysis (CVA)

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

3.14.2.5 Calculation of D^2 values

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

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

Where,

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

x = Number of characters.

Superscript j and k to Y = A pair of any two genotypes.

3.14.2.6 Computation of average intra-cluster distances

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

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

Where,

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

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

3.14.2.7 Computation of average inter-cluster distances

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

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

Where,

$\sum D_{ij}^2$ = The sum of distances between all possible

ombinations of the populations in cluster i and j.

n_i = Number of populations in cluster i.

n_j = Number of populations in cluster j.

3.14.2.8 Cluster diagram

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

3.14.2.9 Selection of varieties for future hybridization programme

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

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

Chapter 4

Results and Discussion

CHAPTER 4
RESULTS AND DISCUSSIONS

The present experiment was carried out with a view to determine the field performance, variability, the breeding values relating to mean performance and genotypic effects of the twenty five different genotypes of ridge gourd through morphological traits. Firstly, the availability of transgressive segregants in breeding programme. For this, the mean performance of 25 ridge gourd in respect of different quantitative characters such as days to first male flowering, days to first female flowering, days to vegetable harvest (edible maturity), number of primary branches per plant, fruit length, fruit circumference, fruit weight, number of seed per fruit, length of seed, breadth of seed, hundred seed weight, number fruits per plant and yield per plant were analyzed by Duncan's Multiple Range Test (DMRT). Variability is the prerequisite for an effective breeding programme. The data pertaining to 13 characters were computed and statistically analyzed. The results related to various genetic parameters of the genotypes have been presented and interpreted under the following headings –

4.1 Characterization of ridge gourd
    4.1.1 Morphological characterization based on grading
    4.1.2 Characterization of ridge gourd on the basis of mean performance of yield and yield contributing characters
4.2 Variability, heritability and character association
4.3 Genetic diversity
4.4 Comparison of results based on different multivariate technique
4.5 Selection of the genotypes for future hybridization programme

4.1 Characterization of ridge gourd

4.1.1 Morphological characterization based on grading

4.1.1.1 Cotyledon colour

Cotyledon colour is an important traits for choose in a future breeding programme. As cotyledon the first and base for the development of a plant from seed. Three different color cotyledons were found in the accessions. Among the 25 genotypes, five genotypes (G1, G9, G14, G19 and G24) were observed intermediate cotyledon colour; ten genotypes were (G4, G6-G8, G11, G12, G17, G20, G21 and G25) light green and rest of the ten genotypes was dark green cotyledon colour. Cotyledon colour variations are presented in Table 3.

Karuppaiah *et al.* (2005) also reported findings related to cotyledon colour in ridge gourd.

4.1.1.2 Leaf shape

Leaf shape is one of the important traits for ridge gourd. Various types of leaves were found in ridge gourd genotypes. Among the genotypes, G13, G16 and G18 produced ovate leaves and rest of the twenty five genotype produced orbicular leaves (Table 3).

Guffar (2008) findings in sponge gourd were also similar to these findings.

4.1.1.3 Male female ratio

Male and female ratio is another important trait in ridge gourd, because male female ratio effect on yield plant. High female and male ratio impact on high yield as G1, G4, G5, G7, G10, G11, G16, G20, G21, G23 and G24 genotypes produced high male female flower ratio. Only G13 produced low ratio and the rest of the genotype were produced medium ratio male female flower (Table 3).

Table 3: Morphological characterization of 25 genotypes of ridge gourd genotypes

Genotype	Cotyledon Color	Leaf Shape	Male Female Ratio	Blossom-end Fruit Shape	Stem-end Fruit Shape	Fruit Shape
G1	Intermediate	Orbicular	High	Pointed	Pointed	Elongate Elliptical
G2	Dark Green	Orbicular	Medium	Round	Round	Elongate Elliptical
G3	Dark Green	Orbicular	Medium	Round	Round	Elongate Elliptical
G4	Light Green	Orbicular	High	Round	Round	Elongate Elliptical
G5	Dark Green	Orbicular	High	Round	Round	Elliptical
G6	Light Green	Orbicular	Medium	Pointed	Round	Elongate Tapered
G7	Light Green	Orbicular	High	Round	Flattened	Pyriform
G8	Light Green	Orbicular	Medium	Round	Round	Elongate Tapered
G9	Intermediate	Orbicular	Medium	Round	Round	Elliptical
G10	Dark Green	Orbicular	High	Round	Round	Elliptical
G11	Light Green	Orbicular	High	Round	Round	Elliptical
G12	Light Green	Orbicular	Medium	Round	Round	Elliptical
G13	Dark Green	Ovate	Low	Round	Round	Elongate
G14	Intermediate	Orbicular	Medium	Round	Round	Elliptical
G15	Dark Green	Orbicular	Medium	Round	Round	Elliptical
G16	Dark Green	Ovate	High	Round	Flattened	Pyriform
G17	Light Green	Orbicular	Medium	Round	Round	Elliptical
G18	Dark Green	Ovate	Medium	Pointed	Pointed	Elliptical
G19	Intermediate	Orbicular	Medium	Round	Round	Elliptical
G20	Light Green	Orbicular	High	Round	Round	Elliptical
G21	Light Green	Orbicular	High	Round	Round	Elliptical
G22	Dark Green	Orbicular	Medium	Pointed	Round	Elliptical
G23	Dark Green	Orbicular	High	Round	Round	Elliptical
G24	Intermediate	Orbicular	High	Round	Round	Elliptical
G25	Light Green	Orbicular	Medium	Round	Round	Elongate Elliptical

Table 3: (Cont'd)

Genotype	Fruit ribs	Fruit Colour	Fruit Skin Texture	Flesh Moisture	Fruit Skin Hardness	Seed Surface
G1	Deep	Green	Smooth	Intermediate	Soft	Smooth
G2	Deep	Light Green	Grainy	High	Intermediate	Smooth
G3	Deep	Light Green	Smooth	Intermediate	Intermediate	Shallow Pitted
G4	Deep	Dark Green	Smooth	Intermediate	Soft	Shallow Pitted
G5	Deep	Light Green	Grainy	Intermediate	Soft	Shallow Pitted
G6	Deep	Light Green	Smooth	High	Soft	Smooth
G7	Superficial	Light Green	Smooth	Intermediate	Soft	Shallow Pitted
G8	Deep	Light Green	Smooth	Intermediate	Soft	Shallow Pitted
G9	Deep	Light Green	Smooth	High	Soft	Shallow Pitted
G10	Deep	Light Green	Smooth	High	Soft	Shallow Pitted
G11	Deep	Dark Green	Smooth	High	Soft	Smooth
G12	Deep	Dark Green	Smooth	High	Soft	Smooth
G13	Deep	Green	Smooth	Intermediate	Soft	Shallow Pitted
G14	Deep	Green	Smooth	High	Soft	Shallow Pitted
G15	Deep	Light Green	Smooth	High	Soft	Shallow Pitted
G16	Deep	Green	Smooth	High	Soft	Smooth
G17	Deep	Dark Green	Smooth	Intermediate	Soft	Smooth
G18	Superficial	Dark Green	Smooth	High	Soft	Smooth
G19	Deep	Green	Smooth	Intermediate	Soft	Smooth
G20	Deep	Green	Smooth	Intermediate	Intermediate	Smooth
G21	Deep	Green	Smooth	Intermediate	Soft	Smooth
G22	Deep	Light Green	Smooth	High	Soft	Shallow Pitted
G23	Deep	Light Green	Smooth	High	Soft	Shallow Pitted
G24	Deep	Dark Green	Smooth	Intermediate	Soft	Shallow Pitted
G25	Deep	Green	Smooth	Intermediate	Soft	Shallow Pitted

This finding were also similar to Karuppaiah *et al.* (2005) findings in ridge gourd, where highest number of male flower was 79.3 and number of female flower was 23.2. Singh *et al.* (2002) reported high sex ratio in ridge gourd.

4.1.1.4 Blossom-end fruit shape

Blossom-end fruit shape is important character for ridge gourd, because it plays a critical impact on consumer preference. Genotype G1, G6, G18 and G22 produced pointed blossom-end fruit shape and the rest of the genotypes produced rounded blossom-end shape fruits (Table 3).

Guffar (2008) findings in sponge gourd were support this findings.

4.1.1.5 Stem-end fruit shape

Stem-end fruit shape is another important trait for ridge gourd, because it also plays a critical impact on consumer preference. Genotypes G1 and G18 produced pointed stem-end shape fruits and G7 and G16 produced flattened stem-end shape fruits and the rest of the genotypes produced rounded blossom-end shape fruits (Table 3).

This result was reported to Guffar (2008) findings in sponge gourd.

4.1.1.6 Fruit shape

Fruit shape is an important consumer preference trait in ridge gourd market. Different types of ridge gourd were found according to their shape. Genotypes G1-G4 and G25 produced elongate elliptical shape fruits and genotypes G6 and G8 produced elongate tapered, genotypes G7 and G16 produced pyriform shape fruits and the rest of the genotypes produced elliptical shape fruits (Table 3).

Chen *et al.* (2002) and Sharma *et al.* (2000), Guffar (2008) reported wide range of variation in respect to fruit shape in cucumber and sponge gourd, respectively.

4.1.1.7 Fruit ribs

Fruit rib is another trait for consumer preference in ridge gourd. Superficial type fruit ribs was observed in genotypes G7 and G18, the rest genotypes showed deep type fruit ribs (Table 3). Singh *et al.* (2002) also found significant variation in ridge gourd 80 genotypes.

4.1.1.8 Fruit colour

Fruit colour generally light green, green and dark colour found in the market effect on consumer preference. Among 25 genotypes, genotypes G4, G11, G12, G17, G18 and G24 were produced dark green fruits and genotypes G1, G13, G14, G19-21 and G25 were produced green fruits and rest genotypes were produced light green fruits. These variations offer a better scope for breeding of consumer preference (Table 3).

Singh *et al.* (2002), Chen *et al.* (2002) and Guffar (2008) also found significant variation in respect to fruit colour in ridge gourd, cucumber and sponge gourd genotypes.

4.1.1.9 Fruit skin texture

Fruit skin texture also plays an important role for future ridge gourd breeding. The genotype G2 and G5 were produced grainy skin fruits and rests of the genotypes were produced smooth skin fruits (Table 3). Choer *et al.* (2000) also found significant variation in respect to fruit skin texture in *cucurbita*.

4.1.1.10 Flesh moisture

Flesh moisture also an important trait for consumer liking. Genotypes G2, G6, G9, G10, G11, G12, G14, G15, G16, G18, G22 and G23 contain high flesh moisture when fruits were edible and other genotypes contains intermediate flesh moisture (Table 3).

Chen *et al.* (2002) in cucumber, Singh and Ram (2003) in muskmelon also found variation in respect to this character.

4.1.1.11 Fruit skin hardness

Fruit skin hardness is another important trait for consumer liking to ridge gourd in market. Because consumer prefer soft skin fruits to other types fruits. Among the genotypes, G2, G3 and G3 had intermediate type fruit skin hardness and other genotypes were soft feelings (Table 3). This trait might be an option for breeder for the developing new combination.

Ashok and Rajan (2002) findings in snake gourd was also related to fruit skin hardness.

4.1.1.12 Seed surface

Seed surface variation in ridge gourd is another trait. The genotypes G1, G2, G6, G11, G12, G16, G17, G18, G19, G20 and G21 had smooth seed surface and the rest of genotypes were shallow pitted (Table 3). Seed appearance of different ridge gourd accessions were shown in Plate 2.

Ashok and Rajan (2002) in snake gourd, Chen *et al.* (2002) in cucumber reported related observations.

Plate 2: Seed appearance of different ridge gourd accessions

4.1.2 Characterization of ridge gourd on the basis of mean performance of yield and yield contributing characters

4.1.2.1 Days to first male flowering

It was observed that days to first male flower buds appear varied significantly among the genotypes (Table 4) and ranged from 27.67 days to 35.33 days (Table 5). The maximum days (35.33 days) for first male flower bud appearance was observed in G23 and minimum days (27.67 days) to first male bud appearance was recorded in G10. Hossain (1996) also found significant difference in male, female and hermaphrodite flower buds appeared 29-38 days after seeding. Joseph (1978) also found significant difference in respect to days to first male flower opening in snake gourd.

4.1.2.2 Days to first female flowering

Similarly it was observed that days to first female flower buds appear varied significantly among the genotypes (Table 4) and ranged from 33.67 days to 45.00 days (Table 5). The minimum days (33.67 days) for first female flower bud appearance was observed in G2 and a maximum days (45.00 days) to first female bud appearance was recorded in G16. A minimum day to female flowering is desirable for vegetable producer.

Islam (1993) in bottle gourd, Rahman *et al.* (1990, 1991) also found significant variation for days to first flowering.

4.1.2.3 Days to vegetable harvest (Edible maturity)

Analysis of variance for days to vegetable harvest (Edible maturity) showed highly significant variation among the genotypes for the trait (Table 4). The mean value for this trait was 68.25 days and ranged from 56.00 days (G2) to 76.00 days (G23) (Table 5).

Mondal *et al.* (1989) and Rajput *et al.* (1991) were reported in related to edible fruit harvest in watermelon and in cucumber respectively.

Table 4: Analysis of variances for yield and yield related thirteen characters of twenty-five ridge gourd genotypes

Source of variation (Characters)	Degrees of freedom (df)			Mean sum of squares		
	Replication	Genotypes	Error	Replication	Genotypes	Error
Days to first male flower bud	2	24	48	23.373	16.147**	12.790
Days to first female flower bud	2	24	48	6.493	32.820**	13.493
Days to first vegetable Harvest	2	24	48	17.373	65.036**	25.137
Primary branch (PB)	2	24	48	0.013	0.998	0.166
Fruit length	2	24	48	101.004	33.853**	54.343
Fruit circumference	2	24	48	28.715	1.625	10.194
Fruit weight	2	24	48	1598.294	887.586**	5379.96
Number of seed per fruit	2	24	48	349.720	4982.570**	1529.88
Hundred Seed weight	2	24	48	0.093	5.250**	0.260
Seed length	2	24	48	0.760	0.526	0.399
Seed breadth (SB)	2	24	48	1.213	0.694	0.283
Number of fruit per plant	2	24	48	116.320	63.389**	16.834
Yield per plant	2	24	48	2.453	2.473**	0.366

**** Significant at 1% level of probability**

Table 5. Mean performance of twenty-five different ridge gourd genotypes in respect to thirteen quantitative characters

Genotype	DFMF (days)	DFFF (days)	DFVH (days)	NPB	FL (cm)	FC (cm)	AFW (g)
G1	30.33	36.33	65.67	2.33	32.87	12.56	167.8
G2	28.00	33.67	56.00	2.00	21.30	12.29	108.3
G3	29.33	36.00	60.00	3.33	26.51	11.99	124.9
G4	30.33	37.33	70.33	2.33	26.53	12.48	143.3
G5	30.00	39.33	71.00	3.00	30.36	11.40	116.0
G6	28.33	34.33	63.33	2.33	19.75	13.45	108.8
G7	28.00	44.00	69.33	2.33	23.00	13.17	133.9
G8	30.00	39.00	66.00	2.00	26.83	11.02	104.6
G9	30.67	40.00	70.33	2.00	22.67	14.20	103.9
G10	27.67	41.67	69.00	3.33	22.30	13.64	127.3
G11	28.33	40.33	66.33	3.00	25.85	12.62	144.7
G12	30.33	39.67	76.00	2.33	24.24	12.34	140.6
G13	29.33	43.67	68.67	2.00	25.85	11.91	122.9
G14	35.00	45.00	69.00	3.67	27.58	12.35	141.9
G15	30.00	36.00	70.67	4.00	26.84	11.54	132.0
G16	35.00	45.00	64.00	3.00	19.40	12.43	92.34
G17	31.00	36.33	71.33	3.00	26.13	13.40	122.4
G18	31.33	39.33	66.00	3.00	28.80	12.09	133.4
G19	29.33	44.67	71.00	3.00	21.67	11.80	119.1
G20	30.67	38.67	70.67	2.33	28.73	12.05	141.2
G21	28.00	38.00	71.00	2.00	22.45	12.35	120.4
G22	31.00	28.00	66.00	3.33	23.65	13.00	132.2
G23	35.33	37.00	76.00	3.00	24.25	12.07	123.8
G24	30.00	36.00	64.00	2.33	21.82	13.04	132.1
G25	35.00	36.67	74.67	2.33	28.37	12.34	157.0
Range	27.67-35.33	33.67-45.00	56.00-76.00	2.00-4.00	19.40-32.87	11.02-14.20	92.34-167.8
Mean	30.41	39.09	68.25	2.69	25.11	12.46	127.79
STD	3.76	4.42	6.15	0.65	6.99	2.81	61.81
SE	0.43	0.51	0.71	0.07	0.80	0.32	7.13
%CV	11.76	9.4	7.35	15.13	29.36	25.62	57.40
Lsd (0.05)	6.189	6.013	8.231	0.669	12.10	5.242	120.40

DFMF = Days to male flower bud open, DFFF = Days to first female flower bud open, DFVH = Days to first vegetable harvest, NPB = Number of primary branches at harvest, FL = Fruit length, FC= Fruit circumference, AFW = Average fruit weight.

Table 5. (Cont'd)

Genotype	NSPF	HSW (g)	SL (mm)	SB (mm)	NFPP	YPP (kg)
G1	122.0	10.33	11.00	6.00	32.33	5.428
G2	75.00	12.00	11.00	7.00	20.00	2.167
G3	110.0	12.00	11.33	7.00	19.33	2.415
G4	160.0	12.33	11.67	7.00	20.00	2.865
G5	165.0	10.00	12.00	7.67	15.67	1.816
G6	80.0	12.00	12.00	7.67	21.00	2.284
G7	165.0	14.00	11.00	7.33	18.00	2.411
G8	136.0	12.00	11.00	6.33	12.67	1.325
G9	110.0	12.00	11.33	6.00	13.33	1.385
G10	134.0	10.00	11.67	7.00	14.33	1.823
G11	70.00	14.00	11.00	7.00	23.67	3.425
G12	75.00	10.00	11.33	7.33	16.00	2.292
G13	80.33	12.00	11.67	7.33	17.00	2.090
G14	158.0	12.00	10.67	7.00	18.33	2.602
G15	136.0	12.33	11.00	8.00	24.67	3.256
G16	120.0	10.33	11.00	7.33	17.67	1.631
G17	80.33	12.00	10.67	7.00	15.33	1.877
G18	224.0	12.33	11.00	7.00	17.67	2.356
G19	142.0	10.33	11.67	7.00	22.67	2.699
G20	132.3	10.00	11.33	7.00	20.00	2.824
G21	164.0	14.00	11.67	7.33	24.00	2.891
G22	172.0	10.33	12.00	7.67	20.33	2.688
G23	80.0	12.00	11.67	7.33	18.33	2.269
G24	170.0	10.00	11.33	7.33	18.67	2.416
G25	170.0	10.00	12.00	7.67	29.00	4.554
Range	70.00-224.0	10.00-14.00	10.67-12.00	6.00-8.00	12.67-32.33	1.325-5.428
Mean	129.24	11.53	11.36	7.13	19.60	2.55
STD	51.16	1.36	0.67	0.66	5.88	1.05
SE	5.90	0.15	0.07	0.07	0.67	0.12
%CV	30.26	4.42	5.56	7.45	20.93	23.72
Lsd (0.05)	64.21	0.837	1.037	0.8733	6.736	0.9932

NSPF = Number of seeds per fruit, HSW = Hundred seed weight, SL = Seed Length, SB = Seed Breadth, NFPP = Number of fruits per plant, YPP= Yield per plant

4.1.2.4 Number of primary branches

Number of primary branches per plant showed a significant mean sum of squares due to genotypes, which indicated considerable range of variation among the genotypes for this character (Table 5). The mean value of primary branches number was 2.69 that ranged from 2.00 to 4.00 (Table 4).

Banik (2003) also found significant difference in number of primary branches (5.23-11.88) in 26 genotypes of snake gourd.

4.1.2.5 Fruit length (cm)

In respect of fruit length significant difference was observed among 25 accession of the ridge gourd (Table 4). Among the accessions studied, longest fruit (32.87 cm) was observed in G1 which was followed by G5 (30.36 cm), G18 (28.80 cm), while the shortest fruit length was recorded in G16 (19.40 cm) in average (Table 5). Fruit appearance of different ridge gourd accessions were shown in Plate 3. The mean fruit length was 25.11 cm. Shinde *et al.* (2003) reported wide range of fruit length variation in ridge gourd. Significant variation for the fruit length was noticed in ribbed gourd and bottle gourd (Rahman *et al.*, 1991).

4.1.2.6 Fruit circumference (cm)

Circumference of edible fruit varied significantly among 25 ridge gourd accessions (Table 4) and range observed from 11.02 cm to 14.20 cm. The mean value was 12.46 cm. The highest value (14.20 cm) was observed in G9 and the lowest value (11.02 cm) was observed in G8 (Table 5). Varghese (1991), Guffar (2008) in snake gourd, Mondal *et al.* (1989) in watermelon, Rahman *et al.* (1991) in bottle gourd and Quamruzzaman *et al.* (2008) in ridge gourd reported almost similar results to the above findings.

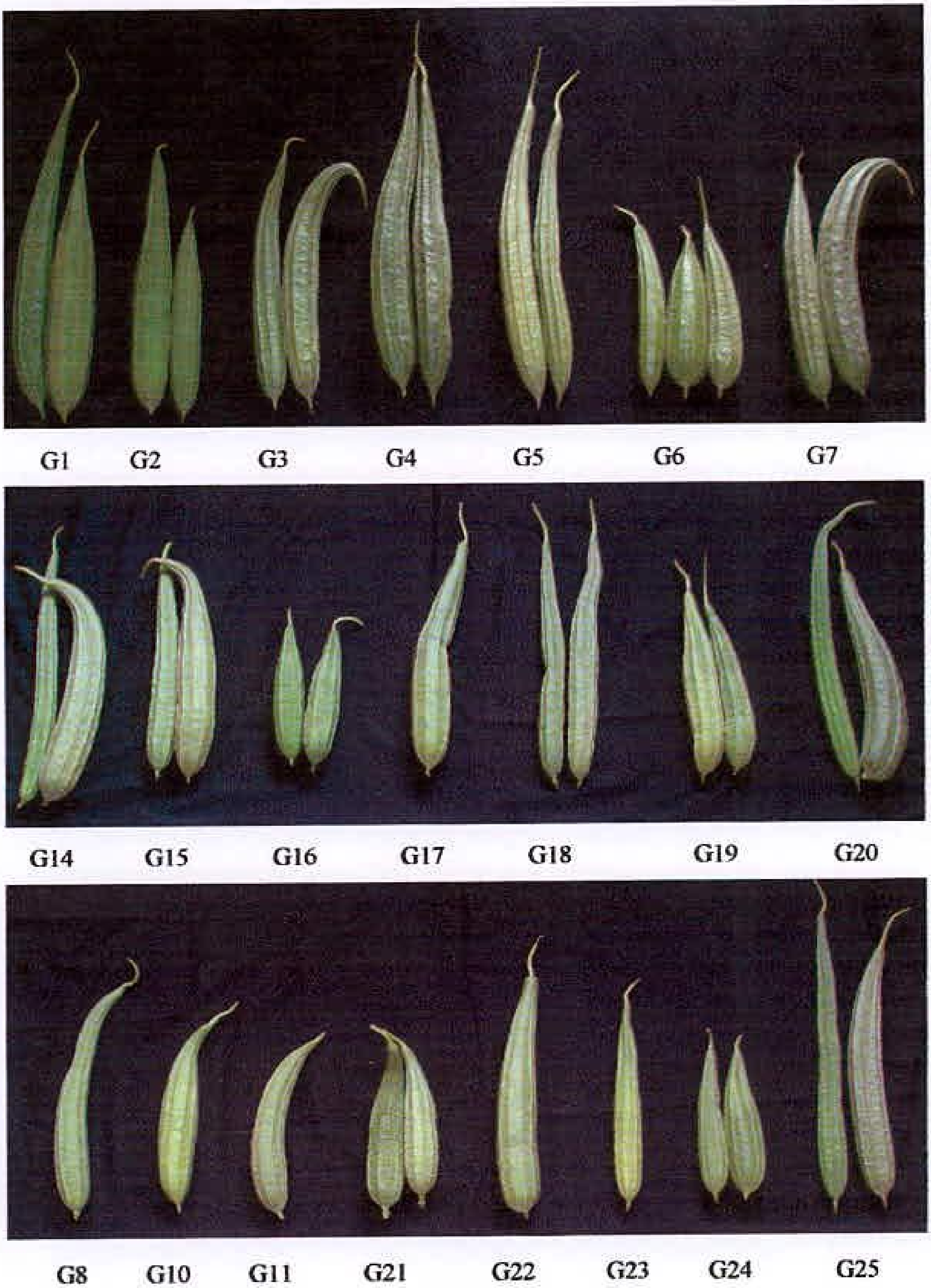

Plate 3: Fruit appearance of different ridge gourd genotypes

4.1.2.7 Average fruit weight (g)

In respect of average fruit weight, significant difference was observed among 25 ridge gourd accessions (Table 4) and ranged from 92.34 g to 167.8 g. The mean value was 127.8 g. The highest value was observed in G1 and the lowest value was observed in G16 (Table 5). These findings are in agreement with Quamruzzaman *et al.* (2008) in ridge gourd, Zaman *et al.* (2004) in snake gourd and Mannan (1992) and Varghese (1991) also reported similar results in bitter gourd and snake gourd, respectively.

4.1.2.8 Number of seeds per fruit

Significant difference was observed among the accessions in this yield contributing traits (Table 5). Number of seeds per fruit varied from 70.00 to 224.00. The mean value was observed as 129.24 seeds per fruit. The highest number of seeds per fruit was recorded in G18 and the lowest number was recorded in G11 (Table 4). In separate studies, Guffar (2008) and Banik (2003), Swamy *et al.* (1984) and Mannan (1992), Abusaleha and Dutta (1990) also reported wide variability in case of snake gourd, musk melon, bitter gourd and cucumber, respectively.

4.1.2.9 Hundred Seed weight (g)

Significant differences were found in respect of hundred (100) seed weight among the 25 ridge gourd accessions (Table 5). Hundred seed weight varied from 10.00 g to 14.00 g. The highest value was observed from G7, G11 and G21 and the lowest value was obtained from G25 similarly many other genotypes (Table 4). Khan *et al.* (2008) reported almost similar result in 64 genotypes of pointed gourd.

4.1.2.10 Seed Length (mm)

Significant difference was observed among the accessions of 25 ridge gourd genotypes in seed length traits (Table 5). The length varied from 10.67 mm to 12.00 mm. The highest seed length was recorded in G25 followed by G5, G6 and the lowest seed length obtained in G17 followed by G14 (Table 4). The mean value for seed length trait among the accession was 11.36 mm. Guffar (2008) were found significant differences in seed length of snake gourd.

4.1.2.11 Seed breadth (mm)

Significant difference was observed among the accessions in this trait (Table 5). The highest seed breadth was obtained in G15 (8.00 mm) and G1, followed by G9 (6.00 mm) showed lowest seed breadth among the accession (Table 4). Guffar (2008) were found significant differences in seed length of snake gourd.

4.1.2.12 Number of fruits per plant

Significant difference was existed among the accessions in the number of fruits per plant trait (Table 5). The highest number of fruits was recorded in G1 (32.33) and the lowest number of fruits per plant was observed in G8 (12.67) (Table 4). The value in respect of the traits was ranged from 12.67 to 32.33. Khan *et al.* (2008), Zaman *et al.* (2004) were found significant differences in number of fruits per plant of pointed gourd and snake gourd respectively.

4.1.2.13 Yield per plant (kg)

Significant difference was obtained among the accessions in the yield per plant trait (Table 5). The highest yield per plant was found in G1 (5.43 kg), similarly in G25 (4.55 kg) and the lowest yield per was observed in G8 (1.32 kg), followed by G9 (1.38 kg) (Table 4). The value in respect of the traits was ranged from 1.325 kg to 5.430 kg. The mean value of 25 ridge gourd genotypes in respect of this trait was 2.552 kg. Quamruzzaman *et al.* (2008), Guffar (2008) and Khan *et al.* (2008) were found significant differences in number of fruits per plant of ridge gourd and pointed gourd respectively.

4.2 Variability, heritability and character association of ridge gourd

4.2.1 Variability, heritability and genetic advance

The 25 genotypes variation significantly measured for all the characters (Table 6). Estimate of mean, range, genotypic variance (σ^2g), phenotypic variance (σ^2p) and environmental variance (σ^2e), genotypic coefficient of variation (GCV), phenotypic coefficients of variation (PCV), heritability (h^2b), genetic advance (GA) and Genetic advance in percentage of mean are presented in Table 6. Variability of twenty-five ridge gourd accessions are described below for each character.

4.2.2 Variability of ridge gourd on the basis of yield and yield contributing characters

4. 2.2.1 Days to first male flowering

The genotypic variance (1.12) was much fold lower than phenotypic variance (13.91) as well as GCV (19.19%) was much lower than PCV (67.62%) indicated much high environmental influence on the expression of this trait (Table 6). Heritability (8.05%), genetic advance (0.92), and genetic advance in percent of mean (2.03%) were considerable for this trait indicating apparent variation due to genotypes.

Singh *et al.* (2002) also found PCV higher than GCV in respect to days to first male flower opening.

Table 6: Genetic component of variation for thirteen yield and yield contributing characters of twenty-five ridge gourd genotypes

Characters	σ^2_g	σ^2_e	σ^2_p	GCV (%)	PCV (%)	h^2b (%)	GA	GAMP (%)
DFMF	1.12	12.79	13.91	19.19	67.62	8.05	0.62	2.03
DFFF	6.44	13.49	19.935	40.58	71.40	32.30	2.97	7.60
DVH	13.30	25.14	38.44	44.14	75.05	34.60	4.41	6.46
PB	0.277	0.166	0.443	32.07	40.55	62.52	0.89	33.05
FL	6.83	54.34	61.17	52.15	156.08	61.17	9.86	39.26
FC	2.86	10.19	13.05	47.90	104.72	21.91	1.62	13.00
FW	1497.46	5379.96	6877.42	342.31	733.59	21.77	37.19	29.10
SNPF	1150.90	1529.88	2680.78	298.41	455.44	42.93	45.79	35.43
HSW	1.66	0.26	1.92	37.94	40.80	86.46	2.47	21.42
SL	0.042	0.399	0.44	6.08	19.68	9.54	1.30	11.44
SW	0.137	0.283	0.42	13.86	24.27	57.11	0.76	10.66
FNPP	15.52	16.83	32.35	88.98	128.47	32.62	3.82	19.48
YPP	0.702	0.366	1.07	52.44	64.75	65.51	1.39	54.46

4.2.2.2 Days to first female flowering

The values of genotypic coefficient of variation (40.58%) and phenotypic coefficient of variation (71.40%) were moderate. Heritability was moderately low (32.30%) with 2.97 genetic advance and genetic advance in percent mean (7.60%) indicating moderate variation was due to accessions. So selection based on the trait would be effective. The results agree with the findings of Guffar (2008).

4.2.2.3 Days to vegetable harvest (Edible maturity)

The phenotypic and genotypic variances for this trait were 13.30 and 38.44, respectively (Table 6). The value of environmental variance suggested slight influence of environment on the expression of this trait. The phenotypic coefficient of variation and genotypic coefficient of variation was observed 75.05% and 44.14%, respectively. Heritability estimates for this trait was moderately low (34.60%) with genetic advance (4.41) indicated effective selection would be based on this trait.

Mondal *et al.* (1989) and Rajput *et al.* (1991) were reported in related to edible fruit harvest in watermelon and in cucumber respectively.

4.2.2.4 Number of primary branches

The phenotypic variance (0.443) was a little bit higher than genotypic variance (0.277). Such result indicated moderately influence of environment on the expression of the trait and genetic factor had significant role in controlling this trait. The phenotypic coefficient of variation (40.55%) and genotypic coefficient of variation (32.07%) indicated moderate influence of environment. Estimation of heritability (62.52%) for this trait was moderately high. However, the genetic advance was low (0.89). So selection based on this character would be effective. Banik (2003) also found significant difference in snake gourd.

4.2.2.5 Fruit length (cm)

The genotypic variance (6.83) and phenotypic variance (61.17) and the GCV (52.15%) and PCV (156.08%) difference were high. It indicated that there was high environmental influence on the expression of this trait (Table 6). Heritability (h^2b) was 9.86%. It indicated that this character might be used in future hybridization programme. Miah *et al.* (2000) reported the highest genotypic as well as phenotypic coefficient of variations for fruit length in bitter gourd.

4.2.2.6 Fruit circumference (cm)

The difference between GCV (47.90%) and PCV (104.72%) in circumference of edible fruit indicated great influence of environment on expression this trait (Table 6). Heritability (h^2b) was recorded low (21.91%). Quamruzzaman *et al.* (2008) in ridge gourd reported in respect to the above findings.

4.2.2.7 Average fruit weight (g)

Genotypic (342.31%) and phenotypic co-efficient of variation (733.59%) were very high for average edible fruit weight. There was a high difference between phenotypic variance (6877.42) and genotypic variance (1497.46) and co-efficient of variation indicated high environmental effects on the expression of this character (Table 6). The genetic advance (37.19%) and GAMP (29.10%) was considerable for this character. This indicated high potentiality for effective selection of this trait. Varghese (1991) also reported similar result in snake gourd. Chowdhury and Sharma (2002), Rumaran *et al.* (1997) also reported in respect to average fruit weight in ridge gourd and pumpkin respectively.

4.2.2.8 Number of seeds per fruit

The genotypic variance (1150.90) and phenotypic variance (2680.78) were very high. The GCV and PCV were found also high 298.41% and 455.44%, respectively (Table 6). The genetic advance (45.79%) and GAMP (35.43%) indicated that this trait controlled more by environment than additive gene. Selection would be based on this trait. Mannan (1992) reported related to this trait in bitter gourd. Mathew and Khader (1999) reported high heritability (98.24%) for number of seeds per fruit in snake gourd.

4.2.2.9 Hundred seed weight (g)

Significant difference were observed in case of genotypic (1.66) and phenotypic (1.92) variances in respect of 25 ridge gourd accessions. The GCV (37.94%) and PCV (40.80%) were moderate there were moderate environmental influence on this trait (Table 6). Heritability in broad sense (86.46%) was high indicating selectivity for future breeding programme. Varghese (1991) also reported similar results in snake gourd.

4.2.2.10 Seed length (mm)

The genotypic variance and phenotypic variance were very low (0.042 and 0.44) respectively with low heritability 9.54%. The GCV and PCV were very low i.e. 6.08% and 19.68%, respectively (Table 6) indicated low environmental influence on this character. The genetic advance (1.30) and GAMP (11.44%) in respect of seed length trait indicated considerable apparent variation was due to accessions of ridge gourd. Guffar (2008) also reported similar report in snake gourd genotypes.

4.2.2.11 Seed breadth (mm)

The genotypic variance (0.137) and phenotypic variance (0.42) were very low with 57.11% heritability. The GCV and PCV were very low 13.86% and 24.27%, respectively (Table 6) indicated low environmental influence on this character i.e this trait controlled genetically. The genetic advance (0.76) and GAMP (10.66%) in respect of seed breadth trait indicates considerable apparent variation was due to accessions of ridge gourd. Guffar (2008) also reported in respect to seed breadth in snake gourd genotypes.

4.2.2.12 Number of fruits per plant

Moderate range of genotypic (15.52) and phenotypic (32.35) variance was observed which also supported differences in GCV (88.98%) and PCV (128.47%). This indicated moderate environmental influence on the expression of the character. The heritability (h^2b) was 32.62% indicating selectivity of the character for further breeding programme (Table 6). High GCV and PCV indicate high potentiality for effective selection of this character for future breeding programme.

Sanwal *et al.*(2008), Prasad *et al.*(1988) also reported in related to number of fruits per plant in chow-chow and water melon respectively.

4.2.2.13 Yield per plant

The difference between genotypic variance (0.702) and phenotypic variance (1.07) were almost similar indicated this character very much controlled by genetically. But the difference between GCV (52.44%) and PCV (64.75%) was moderate. The difference between GCV and PCV was moderate indicating moderate influence of environment on the expression of this trait (Table 6). This observation was almost similar to Guffar (2008) in ridge gourd.

Heritability (h^2b) for yield per plant was 65.51% indicated potentiality in selection of this character for further breeding programme (Table 6). This finding also supported Abusaleha and Dutta (1990) findings in cucumber.

4.2.3 Character association

Yield is complex products being influenced by several inter dependable quantitative characters. Thus selection for yield may not be effective unless the other yield components influence it directly or indirectly are taken into consideration. When selection pressure is exercised for improvement of any character associated with yield. It simultaneously affects a number of other correlated characters. Hence, knowledge regarding association of characters with yield among themselves provides guideline to the breeder for making improvement through selection *viz.* provide a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factor.

4.3 Genetic diversity of twenty-five ridge gourd accessions

The results of the genetic diversity of among the ridge gourd accessions are represented in Table 4, 6 to Table 12 and Figure 1 to 3.

4.3.1 Principal component analysis

The principal component analysis produced thirteen eigen values of each principal component axes of coordination of genotypes in which the first axes accounted 41.15% of the total variation among the genotypes. The first two principal axes accounted for 71.10 % of the total variation among the 13 characters describing 25 genotypes (Table 7). Based on principal component scores I and II in Table 8, a two dimensional diagram ($Z_1 - Z_2$) of the genotypes are presented in Figure 1. The scattered diagram revealed that apparently there were mainly five clusters. Distantly located genotypes of different clusters were the genotype number 1, 8, 9, 16, 18, 25 etc.

Table 7: Eigen values and percentage of variation for corresponding 13 component characters in twenty five (25) ridge gourd genotypes

Principal component character	Eigen values	Percentage of total variation account for	Cumulative percentage
Days to first male flower bud (DFMF)	3.0808	41.15	41.15
Days to first female flower bud (DFFF)	2.2424	29.95	71.10
Days to first vegetable Harvest (DFVH)	0.7682	10.26	81.36
Primary branch (PB)	0.4922	6.58	87.94
Fruit length (FL)	0.2942	3.93	91.87
Fruit circumference (FC)	0.190	2.54	94.41
Fruit weight (FW)	0.1330	1.78	96.19
Seed number per fruit (SNPF)	0.1120	1.50	97.69
100 Seed weight (HSW)	0.0724	0.97	98.66
Seed length (SL)	0.0516	0.69	99.35
Seed breadth (SW)	0.0288	0.38	99.73
Fruit number per plant (FNPP)	0.0193	0.26	99.99
Yield per plant (YPP)	0.0009	0.01	100

Table 8. Principal component scores (PCS) for 25 genotypes of ridge gourd

Genotypes	Score 1 (Z_1)	Score 2 (Z_2)
G1	2.14	42.44
G2	56.15	-14.01
G3	19.33	-1.24
G4	-32.54	11.73
G5	-34.51	-15.54
G6	51.06	-13.45
G7	-31.42	1.57
G8	-4.23	-24.52
G9	21.71	-22.26
G10	-4.78	-2.47
G11	56.67	23.59
G12	51.86	21.07
G13	49.17	0.37
G14	-30.54	10.17
G15	-7.52	4.54
G16	13.03	-34.90
G17	49.34	0.06
G18	-94.99	-5.78
G19	-11.99	-9.88
G20	-4.61	13.27
G21	-33.90	-10.58
G22	-43.14	-1.06
G23	49.06	2.17
G24	-41.01	-1.57
G25	-44.33	26.25

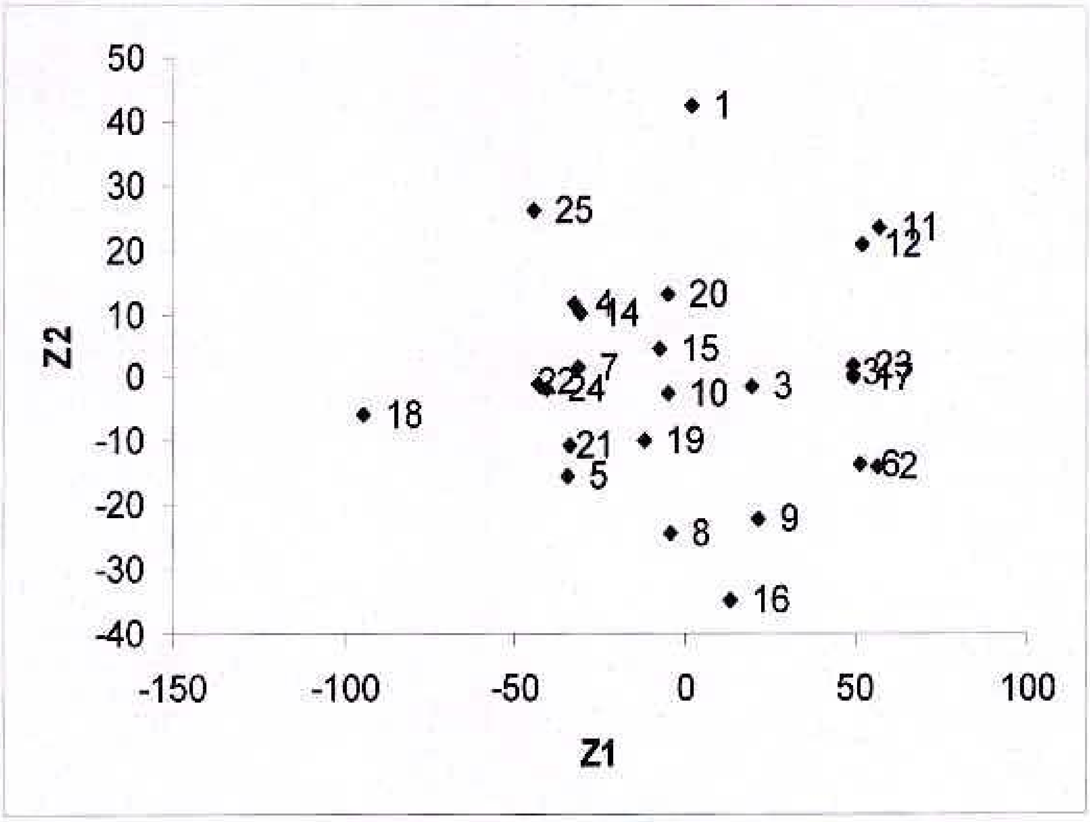

Figure 1. Scattered distribution of twenty-five ridge gourd genotypes based on their principal component scores (PCS)

4.3.2 Construction of a scatter diagram

Based 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. the position of the genotypes in the scatter diagram was apparently distributed into five groups, which indicated that considerable for the 25 ridge gourd genotypes of different clusters revealed that the genotype number 1, 8, 9, 16, 18, 25 were distantly located which suggesting more diverse from rest of the genotypes (Figure 1).

4.3.3 Principal Coordinate analysis (PCO)

The inter-genotypic distances are obtained by principal coordinate analysis. The results showed that the highest distance was observed between the genotype number G1 and G8 (1.464) followed by those of between G1 & G9 (1.4533), G1 and G16 (1.400), G9 and G25 (1.3439) and the lowest distance was observed between G2 and G6 (0.239) followed by G4 and G20 (0.2863), G12 and G13 (0.3023), G17 and G23 (0.3053) (Table 9).

By using (Table 9) these inter-genotypic distance intra-cluster distance were computed by the values of inter-genotypic distance matrix of PCO according to Singh and Chaudhury (1985). Cluster II showed highest intra cluster distance (0.91515) which composed of 4 genotypes and lowest distance in cluster 1 (0.00) composed of 1 genotypes (G18) that indicated within group diversity of the genotypes was maximum in cluster II and minimum in cluster in I (Table 10).

Table 9: Ten of each lower and higher inter-genotypic distances between pairs of genotypes

Ten higher D^2 Values	Genotype Combination	Ten lower D^2 Values	Genotype Combination
1.464	G1 & G8	0.239	G2 & G6
1.4533	G1 & G9	0.2863	G4 & G20
1.4001	G1 & G16	0.3023	G12 & G13
1.3439	G9 & G25	0.3053	G17 & G23
1.3184	G8 & G25	0.3297	G4 & G24
1.2839	G1 & G10	0.3346	G4 & G7
1.2702	G1 & G17	0.3351	G4 & G21
1.2611	G17 & G25	0.3355	G19 & G22
1.2496	G1 & G5	0.3536	G22 & G24
1.2381	G11 & G18	0.364	G7 & G8

Table 10: Average intra (Diagonal) and inter cluster distance (D^2) of five clusters formed by Tocher's method

Cluster	I	II	III	IV	V
I	0.00 (0.00)	27.27 (5.222)	35.77 (5.98)	22.34 (4.276)	14.87 (3.844)
II		0.91515 (0.956)	9.25 (3.041)	6.92 (2.630)	12.98 (3.602)
III			0.4957 (0.704)	14.13 (3.758)	21.05 (4.588)
IV				0.7341 (0.856)	8.00 (2.828)
V					0.5668 (0.752)

4.3.4 Canonical Vector Analysis

Canonical vector analysis was performed to obtain the inter-cluster distances .The intra and inter-cluster distance (D^2) is presented in Table 10. Statistical distances present the index of genetic diversity among the clusters. The inter-cluster distances were bigger than the intra cluster distances suggesting wider genetic diversity among the genotypes of different groups. Quamruzzaman *et al.* (2008) obtained larger inter-cluster distances than the intra-cluster distances in a multivariate analysis in ridge gourd. Results indicated that the highest inter cluster distance was observed between cluster I and III (35.77) followed by the distance between cluster I and II (27.27), I and IV (22.34), III and V (21.05). The higher inter-cluster distances between these clusters indicated to obtain wide spectrum of segregating population if parents chosen from these distant clusters are used in hybridization program. However, the highest inter-cluster distance was observed between clusters I and III indicated the genotypes in these clusters were far diverged than those of other clusters. The lowest inter-cluster distance was observed between cluster II and IV (6.92) followed by IV and V (8.00), II and III (9.25) suggesting a close relationship among these three clusters (Figure 2). The minimum values of inter-cluster distance indicated that the genotypes belonging to cluster II were closely related to the cluster IV, cluster IV to cluster V and cluster II to cluster III. These relationships were also reflected in the scattered diagram (fig.1). Similar reports were also made by Quamruzzaman *et al.* (2008), Guffar (2008) in ridge gourd and snake gourd genotypes respectively. The genotypes belonging to the cluster I and III having greater cluster distance recommended for inclusion in hybridization programme as they are expected to produce good segregants. Thus it could be suggested that crosses should be made between genotypes belonging to the distant clusters for higher heterotic response. Quamruzzaman *et al.* (2008) reported similar results in 30 genotypes, reported that selection of parents from distantly placed clusters exhibited

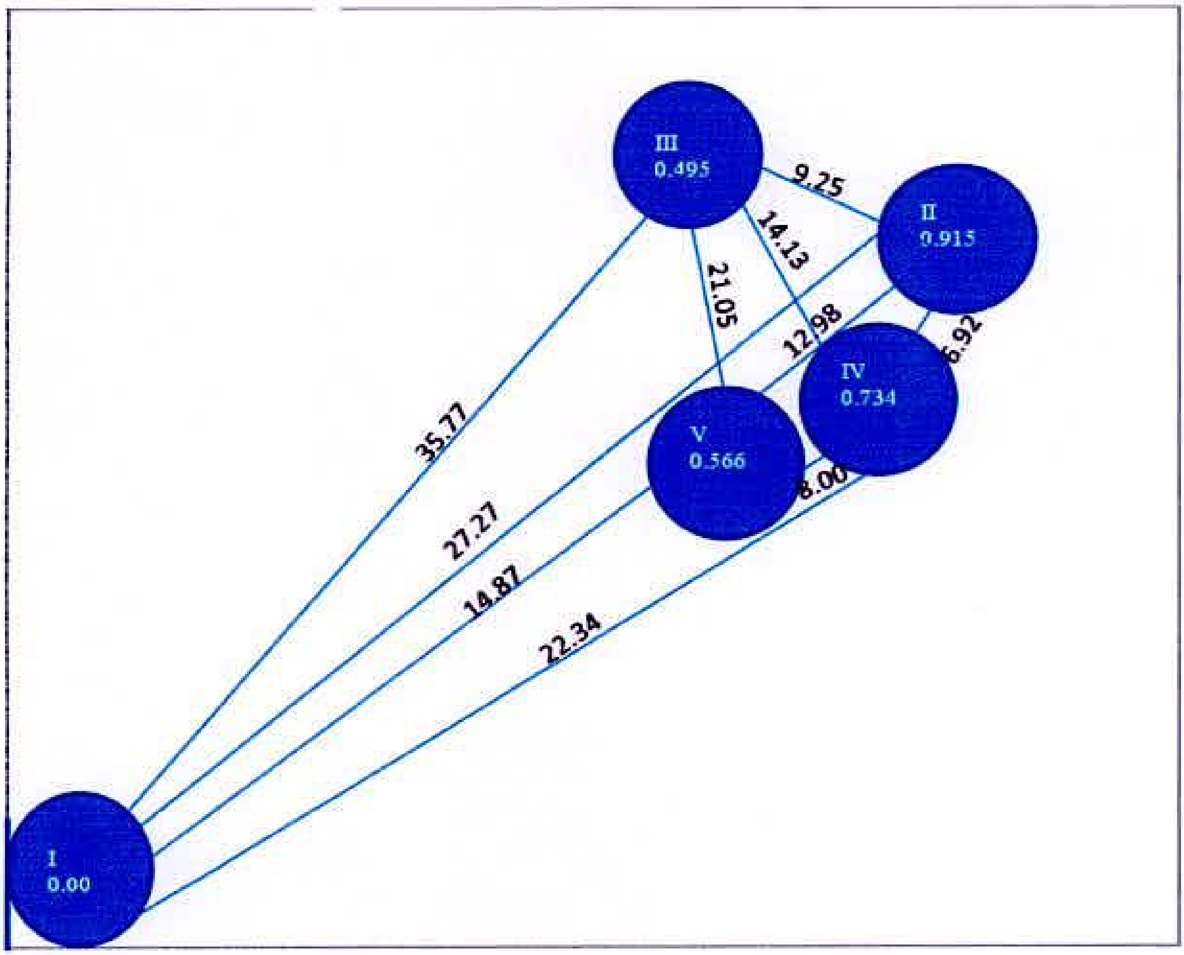

Figure 2: Diagram showing intra and inter-cluster distance of twenty-five ridge gourd genotypes

significant high heterosis in ridge gourd. Moderate type of inter-cluster distance has been existed between the cluster III and IV and also in I and V. The promising genotypes grouped in cluster III and IV (Table 11) could also be utilized in hybridization program considering genetic distances of the genotypes of different clusters. So the genotypes from these four clusters I, III, IV and V if involved in hybridization might be produce a wide range of segregating population, as genetic variation is very distinct among the group. The genotypes belonging to the distant clusters could be used in hybridization program for obtaining a wide range of variation among the segregants. Similar reports were also made by Quamruzzaman *et al.* (2008).

4.3.5 Non – hierarchical clustering

By application of non-hierarchical clustering using covariance matrix, the twenty-five (25) genotypes of ridge gourd were grouped into five different clusters. These results confirmed the clustering pattern of the genotype according to the principal component of analysis Quamruzzaman *et al.* (2008) reported that principal component analysis and cluster analysis in 30 genotypes and divided 30 varieties into 6 clusters. Guffar (2008) also carried out principal component analysis of 15 diverse snake gourd genotypes using multivariate D^2 analysis, which grouped into 5 clusters. These results confirmed the clustering pattern of the genotypes according to the principal component analysis.

Composition of different clusters with their corresponding genotypes and origin included in each cluster are presented in Table11. Cluster V had maximum eight (8) genotypes followed by cluster III and cluster IV, and cluster II which had 7, 5 and 4 genotypes respectively. Cluster I had minimum genotype namely G18. Eight genotypes number included in cluster V which are G4, G5, G7, G14, G21, G22, G24, G25 and cluster III

Table 11: Distribution of 25 ridge gourd genotypes in five clusters

Cluster	Total no. of genotypes (entry no.)	Name of the genotypes with local accession number
I	1 (G18)	G18 (BD 2997)
II	4 (G3, G8, G9, G16)	G3 (BD 2974), G8 (BD 2980), G9 (BD 2982), G16 (BD 2993)
III	7 (G2, G6, G11, G12, G13, G17, G23)	G2 (BD 2973), G6 (BD 2978), G11 (BD 2984), G12 (BD 2985), G13 (BD 2986), G17 (BD 2994), G23 (BD 3009)
IV	5 (G1, G10, G15, G19, G20)	G1 (BD 2972), G10 (BD 2983), G15 (BD 2992), G19 (BD 2999), G20 (BD 3000)
V	8 (G4, G5, G7, G14, G21, G22, G24, G25)	G4 (BD 2975), G5 (BD 2977), G7 (BD 2979), G14 (BD 2990), G21 (BD 3002), G22 (BD 3007), G24 (BD 3010), G25 (BD 3011)

constituted seven genotypes namely G2, G6, G11, G12, G13, G17, G23. Cluster IV and II was constituted of five and four accessions namely G1, G10, G15, G19, G20 and G3, G8, G9, G16 respectively.

4.3.6 Cluster mean value

Mean performance of different cluster for thirteen characters are shown in the Table 12. The data revealed that different clusters exhibited different mean values for almost all the characters.

The only genotype (G18) included in this cluster I produced the highest mean for the number of primary branches (3.00), fruit length (28.80 cm), number of seed per fruit (224.00) and highest mean for days to first male flower bud (31.00) and hundred seed weight (12.00 g) both in cluster I & II and I & III. The lowest mean value for fruit circumference (12.09 cm) was observed in the cluster I and lowest mean cluster value for seed length also observed both in I and II.

From mean values the cluster II the highest mean was obtained for days to first female blower bud (40.00 days) and the lowest means was found in respect of days to vegetable (edible maturity) harvest (65.00 days) which is desirable for producer and consumer. But other characters lowest mean for fruit length (23.85 cm), fruit weight (106.44 g), seed breadth (6.75 mm), number of fruit per plant (15.75) effect on low yield (1.69 kg) per plant in this cluster.

The genotypes (G2, G6, G11, G12, G13, G17, G23) of cluster III group produced the highest mean for fruit circumference (12.58 cm) and lowest means for number of seeds per

Table 12: Cluster mean of 5 clusters for 13 characters in 25 ridge gourd genotypes

Characters	Cluster mean				
	I	II	III	IV	V
Days to first male flower bud (DFMF)	31.00	31.00	29.86	29.60	30.75
Days to first female flower bud (DFFF)	39.00	40.00	37.86	39.60	39.50
Days to first vegetable Harvest (DFVH)	66.00	65.00	68.29	69.60	69.50
Primary branch (PB)	3.00	2.50	2.43	2.80	2.50
Fruit length (FL)	28.80	23.85	23.91	26.48	25.47
Fruit circumference (FC)	12.09	12.41	12.58	12.32	12.52
Average fruit weight (AFW)	133.40	106.44	124.88	137.47	134.60
Number of seed per fruit (NSPF)	224.00	119.00	77.14	133.20	164.87
100 Seed weight (HSW)	12.00	11.50	12.00	10.40	11.50
Seed length (SL)	11.00	11.00	11.43	11.40	11.63
Seed breadth (SW)	7.00	6.75	7.14	7.00	7.37
Number of fruit per plant (NFPP)	17.67	15.75	18.76	22.80	20.50
Yield per plant (YPP)	2.36	1.69	2.34	3.21	2.78

fruit (77.14) and second lower mean value for days to first male flower bud appears (29.86 days) might be desire for future breeding programme.

Accessions belongs to cluster IV namely G1, G10, G15, G19 and G20 produced the highest mean for fruit weight (137.47 g), number of fruits per plant (22.80), second highest fruit length (26.48 cm). Though highest mean value for days to vegetable harvest (69.60 dars) was observed, lowest days to first male flower bud appears (29.60 days) along with days to first female flower bud appears (39.60 days) impact on better yield per plant (3.21 kg).

Cluster V constituted highest number of genotypes namely G4, G5, G7, G14, G21, G22, G24 and G25. The genotype of these cluster produced highest value for seed length (11.63 mm), seed breadth (7.37 mm) and second highest value for fruit circumference (12.52 cm), fruit weight (134.60 g), number of seed per fruit (164.87), number of fruit per plant (20.50) and ultimate second highest value for yield (2.78 kg) tempted to choice in future hybridization programme.

The intra-cluster distance was computed by the values of inter-genotypic distance matrix of PCO according to Singh and Chaudhry (1985). There were not marked variations in intra-cluster distances, which ranged from 0.00 to 0.915 (Table 10). The highest intra-cluster distance was computed for cluster II (0.915) indicating genotypes in this cluster is highly heterogeneous. The lowest intra-cluster distance was computed for cluster I (0.00) composed of genotype G18 indicating genotypes in this cluster is highly homogeneous. In 25 accessions of ridge gourd the highest inter-cluster distance was observed (Table 10) between cluster I and III (35.77) followed by cluster I and II (27.27), I and IV (22.34) and the lowest inter-cluster distance was found between cluster II and IV (6.92) followed by cluster IV and V (8.00). The highest inter-cluster distance between clusters indicated that the genotypes belonging to each pair of clusters were genetically diverted. Similarly the lowest inter-cluster distance between clusters indicated that the genotypes belonging to each pair of clusters were genetically less diverged.

The clustering pattern of the genotypes revealed that varieties originating from country were grouped into different clusters (Table 11). This showed that geographic diversity is not always related to genetic diversity and therefore a single cluster, it is not adequate as an index of genetic diversity. Different response of the genotypes to the environments has altered the clustering pattern between environments. Furthermore, there is a free exchange of seed material among the different region, as a consequence, the characters constellation that might be loose their individuality under human interferences associate with particular region in nature.

4.3.7 Contribution of characters towards diversity

The PCA revealed contribution of characters towards divergence (Table 13). The PCA revealed that in vector 1 (Z_1) the important characters responsible for the genetic divergence in the major axis of differentiation were days to first female flower bud, fruit circumference and hundred seed weight having positive vector values. While in vector 2 (Z_2) which was the second axis of differentiation fruit circumference, fruit weight, hundred seed weight and number of fruits per plant having positive vector values. On the other hand days to first male flower bud, days to first vegetable harvest, number of primary branches, fruit length, fruit weight, number of seeds per fruit, seed length, seed breadth, number of fruits per plant and yield per plant in first axis differentiation had a minor role in the

Table 13: Latent vector values for 13 characters of 25 ridge gourd genotypes

Sl no.	Characters	Vector 1	Vector 2
1	Days to first male flower bud (DFMF)	-0.1666	-0.4302
2	Days to first female flower bud (DFFF)	0.1150	-0.3662
3	Days to first vegetable Harvest (DFVH)	-0.1957	-0.3036
4	Primary branch (PB)	-0.0369	-0.3747
5	Fruit length (FL)	-0.4008	-0.0178
6	Fruit circumference (FC)	0.1649	0.2021
7	Fruit weight (FW)	-0.4759	0.1301
8	Number of seed per fruit (NSPF)	-0.1831	-0.2370
9	100 Seed weight (HSW)	0.1375	0.2730
10	Seed length (SL)	-0.0546	-0.2355
11	Seed breadth (SW)	-0.0597	-0.3588
12	Number of fruit per plant (NFPP)	-0.4395	0.1892
13	Yield per plant (YPP)	-0.5029	0.1974

genetic divergence because of holding a negative signs. In second axis of differentiation, days to first male flower bud, first female flower bud, days to first vegetable harvest, number of primary branches, fruit length, number of seeds per fruit, seed length and seed breadth had a minor role in the genetic divergence because of holding a negative signs. The values of vector 1 and vector 2 revealed that both the vectors had positive value only for the two characters viz., fruit circumference and hundred seed weight among the thirteen characters studied in this experiment. These results indicated that these two characters had the highest contribution towards the divergence among the 25 accessions of ridge gourd. Quamruzzaman *et al* (2008) in ridge gourd reported days to first male flower open, days to first female flower open, fruit diameter, single fruit weight, fruit number/plant, in both the vectors indicated their importance in genetic divergence. Moreover Habib *et al.* (2007) in rice reported same result for grain/panicle, grain length and harvest index.

4.4 Comparison of results based on different multivariate (D^2) technique and principal component analysis

The cluster pattern of D^2 analysis through non-hierrachical clustering has taken care of simultaneous variation in all characters under study. Results combined from different multivariate techniques were superimposed in Figure 3. It could be concluded from this figure that all techniques gave more or less similar results and one technique supplemented and confirmed the results of the other. The cluster pattern of D^2 analysis through non-hierarchical clustering has been taken care of simultaneous variation in all the traits under study. However, the distribution of genotypes in different clusters based on D^2 analysis has followed more or less similar trend of the component score 1 (Z_1) and component score 2 (Z_2) of the Principal Component analysis. The D^2 and PCA were found to be alternative

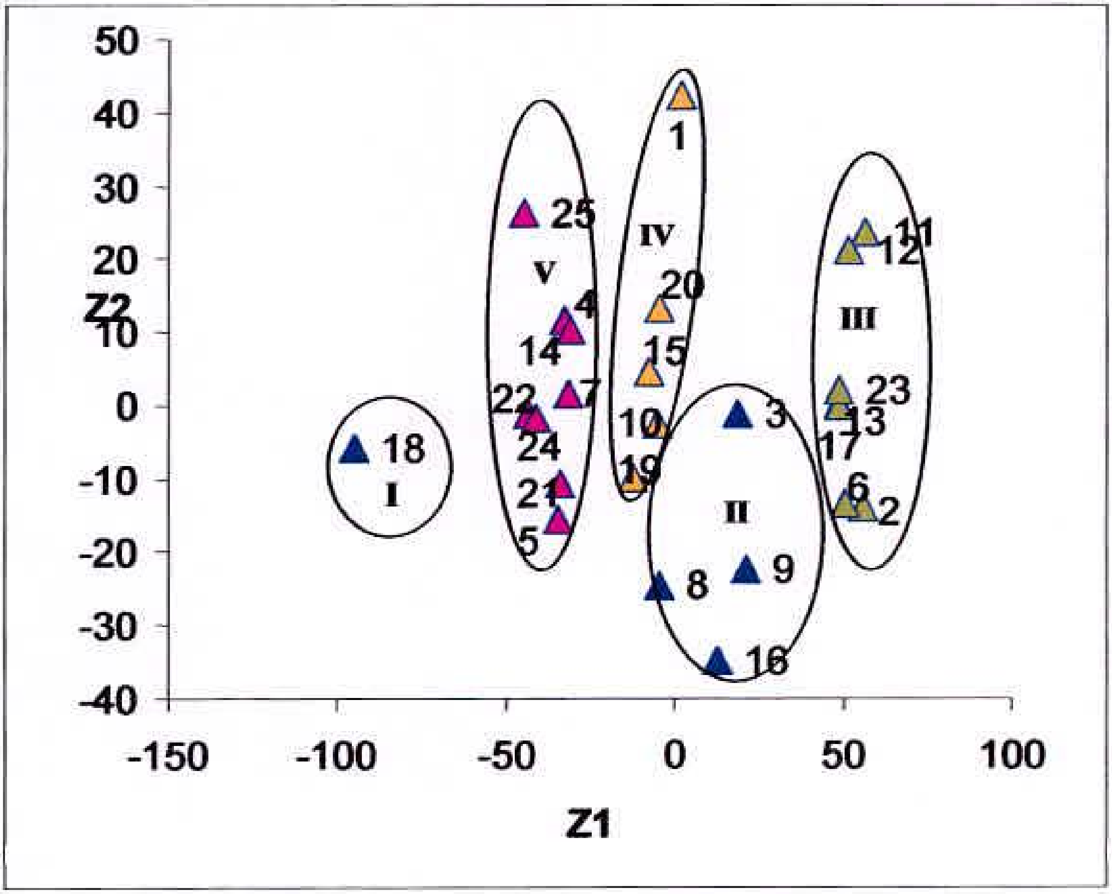

Figure 3. Scattered distribution of twenty-five ridge gourd genotypes based on their principal component scores (PCS) super imposed with clustering

methods in giving the information regarding the clustering pattern of genotypes. Nevertheless, the Canonical Vector Analysis (CVA) provides the information regarding the contribution of characters towards divergence of 25 ridge gourd accessions. So group constellation based on Tocher's method was fairly in good agreement with the scattered points of the Z_1-Z_2 graph as well as the clustering pattern obtained through dendograms.

4.5 Selection of the genotypes for future hybridization programme

Genetically distant parents are usually able to produce higher heterosis. Considering magnitude of genetic distance, contribution of different characters towards the total divergence, magnitude of cluster means for different characters and field performance the genotypes G1 from cluster IV and G25 from cluster V would be suitable for highest yield per plant for future hybridization programme.

It assumed that highest heterosis would be manifest in cross combination involving the genotypes belonging to divergent clusters. However for a practical plant breeder, the objective was not only high heterosis but also to achieve high level of production. Therefore, considering group distance and the agronomic performance, the inter genotypic crosses between G1 & G8; G1 & G9; G1 & G16; G9 & G25; G8 & G25; G1 & G10; G1 & G17; G17 & G25; G1 & G5 and G11 & G18 might be suitable choice for future hybridization programme.

Chapter 5

Summary and Conclusion

CHAPTER 5
SUMMARY AND CONCLUSION

The present experiment was conducted at the field, Department of Genetics & Plant Breeding, Sher-e-Bangla Agricultural University to evaluate the field performance, variability, character association, genetic divergence and characterization of 25 ridge gourd genotypes using morphological characters.

The field experiment was laid out in Randomized Complete Block Design (RCBD) with three (3) replications. Data on different characters were recorded and analyzed statistically.

The analysis of variance of all the traits was computed and significant differences were found among the genotypes in respect of different characters studied. The maximum value in respect of days to first male flower bud days (35.33 days) was observed in G23 and minimum days (27.67 days) to first male bud was recorded in G10. The genotype G16 recorded the maximum value 45 days to first female bud appearance and lowest days to first female bud appearance (33.64 days) was recorded in G2.

In respect of days to first vegetable harvest or edible maturity, genotype G23 recorded the highest value (76.00 days) and genotype G2 counted the lowest value (56.00 days). The genotype G13 exhibited the highest number of primary branches at harvest and the genotype G15 had the lowest number of primary branches.

In respect of fruit length, longest fruit (32.87 cm) was observed in G1 and the genotype G16 had the smallest length of 19.40 cm. In case of fruit circumference, the highest value 14.20 cm was recorded in G9 and the lowest value was 11.02 cm recorded in G8.

In case of average fruit weight, the highest value (167.8 g) was observed in G1 and the lowest value (92.34 g) was observed in G16.

In case of hundred seed weight, the highest value (14.00 g) was observed similarly in genotype G7, G11 and G21.

The highest number of seeds per fruit (224.00) was recorded in G18 and the lowest number of seeds per fruit (70.00) was recorded in G11. On the other hand, the highest number of fruits per plant (32.33) was recorded in G1 and the lowest number of fruits per plant (12.67) was observed in G8.

The highest seed length (12.00 mm) was recorded in G25 followed by G5, G6 and the lowest seed length (10.67 mm) was counted in G17 followed by in G14. In respect of seed breadth, highest seed breadth (8.00 mm) was obtained in G15 and the lowest value (6.00 mm) was counted in G1, followed by in G9.

The highest average yield per plant (5.430 kg) was in G1 and the lowest yield per plant (1.325 kg) was recorded in G8.

The phenotypic variance was higher than the corresponding genotypic variance in all the characters, indicating greater influence of environment on the expression of these characters. The maximum differences between phenotypic and genotypic coefficient of variation were 733.59% and 342.31% respectively which indicated that the average fruit weight mostly depended on environmental effect.

The highest estimated heritability among thirteen yield contributing characters 86.46%, 65.51%, 62.52% and 61.17% was in hundred seed weight, yield per plant, number of primary branches at harvest and fruit length respectively. The lowest heritability was 8.05% in days to first male flower bud opening.

The maximum genetic advance was observed in respect of number of seed per fruit (45.79) and followed by maximum value was 37.19 in respect of genetic advance for average fruit weight among thirteen characters of ridge gourd genotypes.

The maximum genetic advance in percent of mean (GAMP) was obtained for yield per plant (54.46%) and the lowest was for days to first male flower bud open (2.03%). The low heritability (8.05%) with genetic advance in percent of mean (2.03%) indicated additive gene action for character expression.

Multivariate analysis was carried out through principal component analysis (PCA), principal coordinate analysis (PCO), cluster analysis, and canonical vector analysis (CVA) using Genstat 5.13 software programme. The first four principal characters with eigen values were greater than unity contributed 87.94% variation toward divergence. As per as PCA, D^2 and cluster analysis using morphological traits, the genotypes were grouped into five different clusters. Cluster I, II, III, IV and V comprised 1, 4, 7, 5 and 8 genotypes, respectively.

The maximum cluster distance was observed between cluster I and III (35.77) followed by the distance between clusters I and II (27.27), I and IV (22.34), III and V (21.05). The lowest inter-cluster distance was observed between cluster II and IV (6.92) followed by IV and V (8.00), II and III (9.25).

The highest intra-cluster distance was identified in cluster II (0.915) and the lowest intra-cluster distance was observed in cluster I (0.00). Genotypes included in cluster I was suitable for number of primary branches (3.00), fruit length (28.80 cm), number of seed per fruit and hundred seed weight (12.00 g) both in cluster I & II and I & III. Cluster IV had the highest mean for fruit weight (137.47 g), number of fruits per plant (22.80), second highest fruit length (26.48 cm). Cluster V had second highest value for fruit circumference (12.52 cm), fruit weight (134.60 g), number of seed per fruit (164.87), number of fruit per plant (20.50) and ultimate second highest value for yield (2.78 kg).

Findings of the present study indicated significant variation among the genotypes for all the character studied. Diversity in general influenced by the morphological characters which indicated importance of consumer inclination and grower suitability. Considering diversity pattern and other field performances, the genotypes G1, G10, G15, G19 and G20 from cluster IV and cluster V comprises of G4, G5, G7, G14, G21, G22, G24 and G25 could be best choice as suitable parents for efficient hybridization programme. The inter genotypic crosses between G1 & G8; G1 & G9; G1 & G16; G9 & G25; G8 & G25; G1 & G10; G1 & G17; G17 & G25; G1 & G5 and G11 & G18 might be suitable choice for future hybridization programme.

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

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

ii. Selection procedure would be applied for desired characters such as lowest days to first male flower, first female flower, fruit length, fruit circumference, number of fruits per plant to develop high yielding varieties.

iii. Relatively higher value and lower differences between genotypic co-efficient of variation and phenotypic coefficient of variation of different yield contributing characters like average fruit weight, number of fruits per plant, yield per plant were observed which indicates high potentiality to select these traits in future which were less affected by environmental influence.

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

REFERENCES

Abusaleha and Dutta, O.P. (1989). Interrelationship of yield components in cucumber. *Veg. Sci.*, **15** (1):75-85.

Abusaleha and Dutta, O.P. (1990). Studies on variability, heritability and scope of improvement in cucumber. *Haryana J. Hort. Sci.*, **19** (3-4):349-352.

Ananthan, M. and Pappoah, C.M. (1997). Combining ability and correlation studies in cucumber (*Cucumis sativus* L.). *South Indian Hort.*, **45** (1&2): 57-58.

Anonymous. (1991). Basat Barite Sabji Utpadan (in Bengali). BARI, Gazipur, Bangladesh. P. 239.

Ashok, P. and Rajan, S. (2002). Principal component analysis of growth, yield and seed characters of snake gourd (*Trichosanthes anguina* L.). *Veg. Sci.*, **29**(2):137-141.

Badade, D.S., Warade, S.D. and Gaikwad, S.K. (2001). Genetic divergence in bottle gourd. *J. Maharashtra Agril. Univ.*, **26**(2):137-139.

Banik, B.R. (2003). In heritance pattern in snake gourd (*Trichosanthes anguina* L.). Ph, D Thesis. Department of Genetics and Plant Breeding. Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur. pp. 1-60.

BBS. (2008). Monthly Statistical Bulletin, Bangladesh (August). Bangladesh Bureau of Statistics Division, Ministry of Planning, Government of the People's Republic of Bangladesh. pp. 63-67.

Belaj, A., Satovic, Z., Rallo, L. and Trusillo. (2002). Genetic diversity and relationship in olive (*Olea europea* L.) germplasm collection as determined by RAPD.*Theor. Appl. Genet.*, **105**(4): 638-644.

Bhatt, G.M. (1973). Significant of path co-efficient analysis determining the nature of character association. *Euphytica*, **22**: 338-343.

Burton, G.W. (1952). Quantitative inheritance in Grasses. Proc. 6th. Int. Grassland. Cong., 1: 277-283.

Chen, J.F., Staub, J., Adelberg, J., Lewis, S. and Kunkle, B. (2002). Synthesis and preliminary characterization of a new species in *Cucumis*. *Euphytica*, **123**(3): 315-322.

Choer, E., Kharakwal, H.B. and Silva, J.B. (2000). Genetic divergence evaluation in accessions of *Cucurbita spp*. through multivariate analysis. *Agropecuaria clima Temperado*. 3(2): 213-219. [Cited from CAB Abst., 2000/08-2002/07].

Choudhary, M.L. and Mandal, G. (1987). Correlation and path analysis in cucumber (*Cucumis sativus* L.). *Haryana J. Hort. Science*, **16** (3&4): 269-273.

Choudhury, B. (1967). Vegetables. National book Trusti, New Delhi, India. 155-157.

Choudhury, B.D., Bhat, P.N. and Singh, V.P. (1975). Genetic diversity in cluster beans. *Indian J. Agric Sci*., **45**: 530-535.

Chowdhury, D. and Sharma, K.C. (2002). Studies on variability, heritability, genetic advance and correlation in ridge gourd (*Luffa acutangula* Roxb.). *Hort. J.*, **15**(3): 53-58.

Comstock, R. E. and Robinson, H. F. (1952). Genetic parameters their estimation and significance. Proc. of 6th Int. Grassland Cong. 1:128-291.

Crossa, J., Hernandez, C.M., Bretting, P., Eberhart, S.A. and Taba, C. (1993). Statistical genetic consideration for maintaining germplasm collections. *Theor. Appl. Genet.*, **86**: 673-678.

Digby, P., Galway, N. and Lane, P. (1989). GENSTAT 5: A Second Course. Oxford Science. Oxford Science Publications, Oxford. p. 103-108.

Dora, D.K., (2001). Genetic divergence in pointed gourd (*Trichosanthes dioica* Roxb.). *Veg. Sci.*, **28**(2): 170-171.

Dora, D.K., Acharya, G.C., Das, S. and Behera, T.K. (2003). Numerical taxonomic approach better alternative for clustering of pointed gourd. *Orissa J. Hort.*, **31**(2): 76-79.

Dora, D.K., Behera, T.K., Acharya, G.C., Das, S., Mahapatra, P. and Mishra, B. (2003). Genetic variability and character association in pointed gourd (*Trichosanthes dioica* Roxb.). *Indian J. Hort.*, **60**(2): 163-166.

Gaur, P., Gupta, C. and Kishore, H. (1978). Studies on genetic divergence in potato. *Euphytica*, **27**:361-368.

Gomez, K.A. and Gomez, A.A. (1984). Statistical Procedure for Agricultural Research. John Wiley and Sons Inc., New York. pp. 67-215.

Griffing, B. and Lindstone, E.W. (1954). A study of combining abilities of corn inbreeds having varying proportion of corn germplasm. *Agron. J.*, **46**(4): 454-460.

Guffar, A. (2008). Characterization and genetic diversity of sponge gourd (*Luffa cylindrica* L.). M. Sc. Thesis. Dept. Genet. and Plant Breed., SAU, Dhaka.

Habib, S.H., Khaleda Akter, Basher, M.K. and Khalequzzaman, M. (2007). Multivariate analysis of divergence in advanced line and local rice accessions. *Bangladesh J. Agril. Res.* **32**(1): 29-36.

Harhsawardhan, C. and Ram, H.H. (2003). Genetic diversity studies in musk melon. *Ann. Agril. Res.*, **24**(2): 345-349.

Hazra, P., Ghosh, R. and Nath, S. (2003). Identification of important yield components in pointed gourd (*T. anguina* Roxb). *Crop Res. Hisar.*, **25**(2): 244-252.

Hossain, M.S. (1996). Floral biology of ridge gourd. M. Sc. Thesis. Dept. Genet. And Plant Breed., IPSA, Salna, Gazipur.

Islam, M.N. (1993). Studies on heterosis and combining ability in bottle gourd. M. Sc. Thesis, Dept. Genet. & Plant Breed., BSMRAU, Gazipur.

Jain, S.K., Qualets, C.O., Bhatt, G.M. and Wu, K.K. (1975). Geographical patterns of phenotypic diversity in a world of collection of durum wheat. *Crop Sci.*, **15**: 700-704.

Johnson, H.W., Robinson, H.F. and Comstock, R.I. (1955). Estimates of genetic and environmental variabilaity in soybean. *Agron J.*, **47**(2): 314-318.

Joseph, S. (1978). Genetic variability and correlation studies in snake gourd (*Trichosanthes anguina* L.) M. Sc. Thesis. Kerala Agricultural University. Trissur, Kerala, India. 120p.

Joshi, A.B. and Dhawan, N.L. (1966). Genetic improvement of yield with special reference to self –fertlization. *Crop Ind. J. Genet. Pl. Breed.* **26** A**:** 101-113.

Kabir, M. E. (2007). Genetic variability, correlation and path analysis of pointed gourd (*Trichosanthes dioica* Roxb.) M. Sc. Thesis. Dept. of Horticulture and Post Harvest Technology. Sher-e-Bangla Agricultural University. Abstract.

Kadam, P.Y. and Kale, R.I. (1987). Genetic variability in ridge gourd. *J. Maharashtra Agril. Univ.*, **12**(2): 242-243.

Karuppaiah, P., Kavitha, R. and Senthilkumar, P. (2005). Divergent analysis in ridge gourd (Luffa acutangula). India: Palani Paramount Publications.

Khan, A.S.M.R., Rabbani, M.G., Siddique, M.A. and Hossain, M.I. (2008). Study on genetic diversity of pointed gourd using morphological characters. *Bangladesh J. Agril. Res.* **33(3)**:607-616.

Kumaran, S.S., Natarajan, S. and Thamburoj, S. (1998). Correlation and path analysis studies in pumpkin (*Cucurbita moschata* poir.). *South Indian Hort.*, **46** (3&6): 138-142.

Li, J.W., Sun, S.R. and Rer, Y. H. (1997). Study on genetic correlation, path analysis of the main agronomic characters of cucumber. *Acta Agril. Univ., Henamensis.* **31(3):** 244-247.

Lush, J.L. (1943). Animal Breeding Plans. Iowa State Press, Ames, Iowa, p. 437.

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

Mannan, M.A. (1992). Studies on variability, genetic parameters and correlation in bitter gourd. M. Sc. Thesis. Dept. Genet. and Plant Breed., BAU, Mymensingh. pp 28-65.

Masud, M.A.T., Habib, A.K.M.A., Ahmed, S.U. and Hossain, S.M.M. (2001). Genetic diversity in sponge gourd (*Luffa cylindrica*). *Bangladesh J. Plant. Breed. Genet.*, **14**(2): 37-41.

Mathew, S.M., Gopalakrishan, P.K. and Peter, K.V. (1986). Genetic distance among five botanical varieties of *Cucumis melo. Agric. Res. J.*, Kerala, **24**(2): 195-196.

Mathew, S.S. and Khader, K.M.A. (1999). Genetic studies in snake gourd (*Trichosanthes anguina* L.). *J. Trop. Agril.*, **37**(1-2): 71-72.

Mondal, S.N., Rashid, A., Inove, K., Hossain, A.K.M.A. and Hossain, M.A. (1989). Genetic variability, correlation and path co-efficient analysis in watermelon. *Bangladesh J. Plant Breed. Genet.*, **2**(1): 31-35.

More T.A. and Seshodri. (2002). Studies on genetic divergence in muskmelon (*Cucumis melo* L.) *J. Maharashtra Agril. Univ.*, **27**(2): 127-131.

Murty, B.R. and Arunachalam, I.J. (1966). The nature of genetic divergence in relation to breeding system in crop plants. *Indian J. Genet.* **26**:188-198.

Nourish, M. J. (1993). SPSS for Windows-Professionals Statistics. Release 6.0 SPSS Inc. 444N, Michigan Avenue, Chicago, Illinoise, 6061.

Patil, R.M. (1988). Studies on relative performance of different genotypes of cucumber (*Cucumis sativus* L.). J. Res. Birsa. Agril. Univ., **49** (1): 62-69.

Prasad, U.S.R.K., Singh, D.P. and Singh, R.P. (1993). Biological divergence in the land races of Indian Cucumber (*C. sativus*). *Indian J. Hort.*, **50** (1): 63-65.

Prasad, L., Gautam, N.C. and Singh, S.P. (1988). Studies on genetic variability and character association in watermelon (*Citrullus lanatus*). *Veg. Sci.*, **15** (1): 86-94.

Quamruzzaman, A.K.M., Rahman, M.H., Md. Nurul Islam, Rahman, S.M.L. and Sarker, B.C. (2008). Genetic diversity in land races of ridge gourd. *Bangladesh Res. Pub. J.*, **1** (1): 5-12.

Rahman, A.F.M.H. (1988). Kumra Jatio Shabji-O Ful (in Bangla). Dhashiri Printing and Publishing Co., Dhaka, pp.179-81.

Rahman, M.M., Rasul, M.G., Islam, M.S., Sultana, N. and Hossain, M.A. (2000). Genetic divergence in chilli (*Capsicum annum* L.). *Bangladesh J. Plant Breed. Genet.*, **13**(2): 07-11.

Rahman, M.M., Dey, S.K. and Wazuddin, M. (1991). Study of yield and yield components and vine characters of some cucurbit genotypes, *BAU Res. Prog.*, **5**: 75-85.

Rahman, M.M., Dey, S.K. and Wazuddin, M. (1990). Yield, yield components and plant characters of several bitter gourds, ribbed gourd, bottle gourd and sweet gourd genotype. *BAU Res. Progress*, **4**: 117-127.

Rajendran, P.C. (1985). Crop improvement in watermelon. Ph.D. Thesis. Tamil Nadu Agril. Univ. Tamil Nadu, India. pp. 75-90.

Rajput, J.C., Palve, S.B. and Jamadagni, B.M. (1991). Correlation and path analysis studies in cucumber (*Cucumis* sativus L.). *Maharashtra J. Hort.*, **5**(2): 52-55.

Ram, D., Raj, M., Verma, A. and Singh, Y. (2006). Genetic variability and association analysis in *Luffa* sp. *Indian J. Hort.*, **63**(3) [Cited from Abst., http://www.indianjournals.com]

Ram, D., Kallo, G. and Singh, M. (2001). Cluster analysis in pointed gourd (*Trichosanthes dioica* Roxb.). *Veg. Sci.*, **28**(1): 67-68.

Ramos, S.S.R., Queiroz, M.A., Casali, V.W.D. and Cruz, C.D. (2000). Genetic diversity of squash germplasm from northeast of Brazil. *Horticulture Brasileira*, **18**(3): 195-199. [Cited from CAB Abst., 2000/08-2002/07]

Rao, B.N., Rao, P.V. and Reddy, B.M.M. (2000). Correlation and path analysis in segregating population of ridge gourd. *Crop Res. Hisar*, **20**(2): 338-342.

Rao, C.R. (1952). Advanced Statistical Methods in Biometrical Research. John Wiley and Sons. New York. pp. 45-110.

Raseed, M.M., Nabi, S.A., Rasul, M.G. and Mian, M.A. (2002). Genetic divergence in pumpkin (*Cucurbita moschata*). *Bangladesh J. Plant. Breed. Genet.*, **15**(1): 39-41.

Rashid, M.M. (2000). Genetic divergence in pumpkin. M.S. Thesis, Dept. Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur, p 85.

Rastogi, K.B., Arya, D. and Deep, D. 1990. A note on interrelatiohip between yield and important plant characters of cucumber (*Cucumis sativus* L.). *Veg. Sci.*, **17**(1): 102-104.

Reddy, K.S. and Rao, M.R. (1984). Studies on heritability, genetic advance and character association in ribbed gourd. *South Indian Hort.*, **32**(2): 97-100.

Rumaran, S., Walterajan, S. and Suraj, S.T. (1997). Genetic variability in pumpkin. South Indian Hort., **45** (1&2): 10-12.

Sahni, G.P., Singh, P.K. and Saha, B.C. (1987). Genotypic and phenotypic variability in ridge gourd. *Indian J. Agril. Sci.*, **57**(9): 666-668.

Sanwal S.K., Yadav, R.K., Singh, P.K. and Rai, N. (2008). Variability and genetic diversity studies in indigenous chow-chow genotypes of northeast India. *Indian J. Hort.* **65**(2) [Cited from Abst., http://www.indianjournals.com]

Sarkar, S.K., Marity, T.K. and Som, N.G. (1999). Correlation and path coefficient studies in pointed gourd (*Trichosanthes dioica* Roxb.). *Indian J. Hort.*, **56**(3): 252-255.

Schwartz, D. (1960). Genetic studies on mutant enzymes in maize: synthesis of hybrid enzymes by heterozygotes. Proc. Nat. Acad. Sci., **46**: 1210-1215.

Seshadri, V.S., More, T.A. and Nishimura, S. (2002). Indian landrace in *Cucumis melo. Acta. Hort.*, **588** (2): 187-193.

Shah, S.R. and Kale, P.N.)2002). Yield component association analysis in ridge gourd. *J. Maharashtra Agril. Univ.*, **27**(2): 197-198.

Sharma, A., Vidyasagar, K. and Pathania, N.K. (2000). Studies on combining ability for earliness and marketable fruit yield in cucumber (*Cucumis sativus* L.). *Himachal. J. Agril. Res.*, **26**(1 & 2): 54-61.

Sharma, R.R. and Nath, P. (1971). A comparative study on sex-expression and sex ratio in common melons. *Madras Agril. J.*, **58**(7): 578-586.

Shinde, S.J., Nilangekar, R.G., Barkule, S.R., Hingole, D.G., Kadam, A.S. and Sukase, K.A. (2003). Studies on fruit characteristics of different ridge gourd genotypes. *J. Soils Crops*, **13**(1): 52-55.

Sidhu, A.S. and Gautam, N.C. (1985). Genetic divergence and hybrid performance in water melon. *Indian J. Agril. Sci.*, **55**: 459-461.

Singh, D.K. and Ram, H.H. (2003). Correlation among fruit characters in the indigenous germplasm lines of musk melon. Prog. Hort., **35**(1): 69-72.

Singh, N.K. and Singh, R.K. (1988). Correlation and path co-efficient analysis in water melon. *Veg. Sci.*, **15**(1): 95-100.

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

Singh, R.V., Verman, T.S. and Thakur, P.C. (2002). Characters association in cucumber. *Haryana J. Hort. Sci.*, **31** (1&2): 91-93.

Singh, R.P., Mohan, J. and Singh, D. (2002). Studies on genetic variability and heritability in ridge gourd. *Agril. Sci. Digest.*, **22**(4): 279-280.

Singh, V.P., Singh, K. and Jaiswal, R.C. (1986). Genetic variability and correlation studies in pointed gourd (*T. dioica* Roxb.). *Narendra Deva J. Agric. Res.*, **1**(2): 120-124.

Swamy, K.R.M., Dutta, O.P., Ramchander, P.R. and Wahi, S.D. (1984). Interrelationship among yield and other quantitative characters in muskmelon (*Cucumis melo* L.). *South Indian Hort.*, **32**(6): 334-339.

Sych, Z.D. (1990). Results of watermelon breeding material. Ovoshchevodstvo-i-Bakhchevodstvo, **35**: 67-69. [Cited from CAB Abstract].

Upadhya, M.R. and Murty, B.R. (1970). Genetic diversity in relation to geographical distribution in pear millet. *J. Plant Breed. Genet.*, **75** (3 &4): 125-128.

Varalaksmi, B., Reddy, Y.N. and Reddy, B.M. (1994). Genetic divergence in ridge gourd (*Luffa acutangula* Roxb.). *J. Genet. Breed.*, **48**(2): 131-134.

Varghese, P. (1991). Heterosis in snake gourd (*Trichosanthes andguina* L.). M.S. Thesis, Kerala Agricultural University. Kerala, India. pp. 37-60.

Vijay, O.P. 1987. Genetic variability, correlation and path analysis in muskmelon (*Cucumis melon* L.). Indian J. Hort., **44** (3&4): 233-238.

Yawalkar, K.S. (1985). Vegetable Crops of India. 3rd ed. Agric. Horticultural Publishing House. Nagpur., pp. 166-170.

Zaman, A.K.M., Masud, Q.M.A.T. and Rashid, M. A. (2004). Regional Yield Trial of Sponge gourd. HRC Annual Report. Horticulture Research Centre, BARI, Joydebpur, Gazipur. P.39.

APPENDICES

Appendix I. Monthly average temperature, relative humidity, total rainfall and sunshine (hours/day) of the experimental site during the period from (February, 08 to October, 08)

Month	Average Temperature ^{0}C		RH%	Average Rainfall (mm)	Sunshine (hours/Month)
	Maximum	**Minimum**			
February	26.10	15.20	57	56	329.15
March	31.70	22.00	64	45	372.67
April	34.50	24.50	59	91	381.23
May	34.70	24.90	67	206	411.85
June	32.40	26.30	78	446	407.20
July	31.80	26.40	82	476	416.45
August	32.10	26.50	79	318	400.90
September	31.00	27.15	79	257	368.03
October	30.70	24.46	79	163	259.07

Source: BBS (2008)

Appendix II. Nutrient contents in ridge gourd

Constituents	Per 100 g of edible portion	Constituents	Per 100 g of edible portion
Moisture	95.2 g	Protein	0.5 g
Fat	0.1 g	Minerals	0.3 g
Fibre	0.5 g	Carbohydrate	3.0 g
Calcium	40 mg	Magnesium	11 mg
Phosphorus	40 mg	Iron	1.6 mg
Oxalic acid	27 mg	Sodium	2.9 mg
Potassium	50 mg	Copper	0.16 mg
Sulphur	13 mg	Chlorine	7 mg
Vitamin A	56 IU	Thiamine	0.07 mg
Riboflavin	0.01 mg	Nicotinic acid	0.2 mg
Vitamin C	5.0 mg	-	-

(Source: Choudhury, B 1967)