GENETIC DIVERSITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS IN SESAME (*Sesamum indicum* L.)

BY

SHAHNEWAZ BEGUM

REGISTRATION NO. 04-01285

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

MASTER OF SCIENCE

IN

GENETICS AND PLANT BREEDING

SEMESTER: JANUARY- JUNE, 2009

Approved by:

(Dr. Md. Sarowar Hossain)	**(Dr. Firoz Mahmud)**
Professor	Associate Professor
Supervisor	Co-supervisor

(Dr. Firoz Mahmud)
Chairman
Examination Committee

Dr. Md. Sarowar Hossain
Professor
Department of Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Dhaka-1207, Bangladesh

Phone: +8802 9144270-9, Ext. 315 (offi.ce)
Mob: +8801552499169, Fax: +88029112649
E-mail: sarowar2001@rediffmail.com

CERTIFICATE

This is to certify that thesis entitled, ***"Genetic Diversity, Correlation and Path Coefficient Analysis in Sesame (Sesamum indicum L.)"*** *submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of* ***MASTER OF SCIENCE*** *in* ***GENETICS AND PLANT BREEDING****, embodies the result of a piece of bonafide research work carried out by Shahnewaz Begum, Registration No.* ***04-01285*** *under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

Dated: June, 2009
Place: Dhaka, Bangladesh

(Dr. Md. Sarowar Hossain)
Professor
Supervisor


Dedicated to
my
Beloved Parents

ACKNOWLEDGEMENTS

All praises to Almightly and Kindfull trust on to "Omnipotent Creator" for his never-ending blessing, it is a great pleasure to express profound thankfulness to my respected parents, who entiled much hardship inspiring for prosecuting my studies, thereby receiving proper education.

I would like to express my heartiest respect, my deep sense of gratitude and sincere, profound appreciation to my supervisor, ***Prof. Dr. Md. Sarowar Hossain****, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for his sincere guidance, scholastic supervision, constructive criticism and constant inspiration throughout the course and in preparation of the manuscript of the thesis.*

I would like to express my heartiest respect and profound appreciation to my Co-supervisor, ***Dr. Firoz Mahmud, Associate professor and Chairman,*** *Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for his utmost cooperation and constructive suggestions to conduct the research work as well as preparation of the thesis.*

I am grateful to ***prof. Dr. Md. Shah-E-Alam****, Honorable Vice Chancellor, Sher-e-Bangla Agricultural University, Dhaka for providing me with all possible help during my studies.*

It is great pleasure for me to express my sense of gratitude to the honorable minister of Science, Information and Communication Technology of People's Republic of Bangladesh for give me opportunity of M.S. study under the National Science, Information and Communication Technology Scholarship.

I am highly grateful to my honorable teachers ***professor. Dr. Md. Shahidur Rashid Bhuiyan, Professor Abu Akbar Mia, Dr. Naheed Zeba, Associate professor*** *and* ***Md. Kazi Kamrul Huda, Assistant professor****, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for providing me information by which my experiment was successful.*

I express my sincere respect to all the teachers of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for providing the facilities to conduct the experiment and for their valuable advice and sympathetic consideration in connection with the study.

I am pleasure to all stuffs and workers of Genetics and Plant Breeding Department and all farm labors and stuffs of Sher-e-Bangla Agricultural University, Dhaka for their valuable and sincere help in carrying out the research work.

I would like to thank Asmaul Husna who has helped me with technical support to prepare this thesis paper. I also thank all of my roommates and friends especially Milee, Rumi, Kotha, Maliha, Deepty, Shormi, Shuva,Ratna, Munni, Sheuli and senior sister (Mumtaz Parvin, Arzo) to help me in my research work.

Mere diction is not enough to express my profound gratitude and deepest appreciation to my father (Md. Ayub), mother (Nasima Begum), brother (Md. Kamrul Hasan), cousin (Rakib, Pahim, Lata, Niha, Nitu, Eva, Mim, Binti) and friends for their ever ending prayer, encouragement, sacrifice and dedicated efforts to educate me to this level.

June, 2009 ***The Author***
SAU, Dhaka

GENETIC DIVERSITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS IN SESAME (*Sesamum indicum* L.)

By

SHAHNEWAZ BEGUM

ABSTRACT

Fifty genotypes of sesame (*Sesamum indicum* L.) were studied in a field experiment conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, during November 2008 to February 2009. The objectives of the study were to measure the variability among the genotypes for yield and yield contributing characters, estimate genetic parameters, association among the characters and their contribution to yield. There was a great deal of significant variation for all the characters among the genotypes. Considering genetic parameters high genotypic co-efficient of variation (GCV) was observed for yield per plant, no. of capsules per plant & no. of seeds per capsule where as low genotypic co-efficient of variation (GCV) was observed days to 80% maturity and length of capsule. In all cases, phenotypic variances were higher than the genotypic variances except days to 80% maturity and length of capsules. Higher heritability with low genetic advance in percent of mean was observed in days to 80% maturity which indicated that non-additive gene effect was involved for the expression of this character and selection for such trait might not be rewarding. High heritability with high genetic advance was observed for number of capsule per plant and yield per plant indicated that these traits were under additive gene control and selection for genetic improvement for this trait would be effective. Correlation studies revealed that highest significant association of yield per plant and 1000-seeds weight at both genotypic and phenotypic level. Path co-efficient analysis revealed that number of capsules per plant showed maximum direct positive contribution on yield per plant. Highest intra-cluster distance was found in cluster in cluster IV and lowest in cluster V among five clusters. The highest inter cluster distance was observed between cluster I and II and lowest between cluster III & V. Considering genetic diversity and other agronomic performance the genotypes G5, G9, G32 from cluster I, G49 from cluster II and G29 from cluster V might be selected as suitable parents for future hybridization program.

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

LIST OF ABBREVIATED TERMS

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

Chapter I

Introduction

CHAPTER I

INTRODUCTION

Sesame (*sesamum indicum* L.), locally known as 'Til' is one of the oldest cultivated oil crops. It is an ancient oil crop grown in Indo-Pak sub-continent since over 5000 years ago (Bisht *et al.*, 1998). It is regarded as the queen of oil crops by users because of the quality of its oil and for its resistance to oxidation and rancidity even when stored at high ambient air temperature.

Sesame is originated from Africa and later it is spread through West Asia to India, China and Japan. The *Sesamum* belongs to the family pedaliaceae. Sesame is basically a crop of the tropics and sub tropics. Its main distribution is between 25^0 S and 25^0 N latitude, but it can be grown well up to 40^0 N latitude in China, Russia, USA, 30^0 S in Australia and 50^0 S latitude in South America. The important countries in the world, which grow sesame, India, China, Philippines, Burma, Korea, Thailand, Sri Lanka and Pakistan etc. Based on antiquity, diverse forms of cultivated sesame and occurrence of wild species India is now considered as the basic centre of origin (Balasurbramanian and Palaniappan, 1999).

India is the world's major sesame producer with a third of the world acreage and approximately a quarter of the total production (Balasurbramanian and Palaniappan, 1999). In Bangladesh it ranks third in terms of area and fifth in terms of production among the oil crops (BBS, 2001). The national average seed yield is 616 kg per hectare (FAO, 1998).

Sesame is the sixth most important oilseed crop in the world with an area of 7.78 million ha and a total production of 3.15 million ton and an average yield of 405 kg/ha (FAO, 2002). More than 50 percent of the world area under sesame is in Asia, followed by 30 Percent in Africa. The average yield per ha

varies from 121 kg in Egypt to 158 kg in Sudan (FAO, 2002). Oil content of sesame ranges from 34.4 to 59.8 % while protein content varies from 19 to 30 % (Ashri, 1998). The oil is mainly used for cooking and is also used for manufacturing margarine, cosmetics and toiletries. Sesame oil can be used to absorb the fragment essence of scented flowers. In the perfumeries it is used as laxative. The meal is mainly used as livestock and poultry feed.

Sesame produces an excellent crop with a rainfall of 500 to 600 mm (Balasurbramanian and Palaniappan, 1999). It is fairly a drought resistant crop capable to withstand a higher degree of water stress. The seedling stage, however, is susceptible to moisture shortage. Sesame is highly sensitive to water logging. It is a short day plant and requires a minimum of 10 hours light per day (Balasurbramanian and Palaniappan, 1999). The crop responses strongly to environmental variation performing best when temperature is high throughout the entire growing season (Yermanos, 1980 and Beech, 1981). Generally sandy clay loam or sandy loam soils with a p^H range of 5.3 to 8.0 are good for sesame cultivation. Sesame seed germination is positively correlated with soil tilth. Finer the tilth, maximum is the germination and establishment.

Although sesame is one of the major oil crops in our country but improvement is very slow due to lack of genotypes resources, improved research programme, discontinuous and short duration research project, limited international cooperation, limited exchange of know-how and materials and low price of the output. In Bangladesh the total production of oil crops can meet only 30% of the country's demand. The rest amount is imported at the cost of huge foreign exchange. There is no scope to increase oil crop cultivation in winter season due to the extensive and intensive cultivation of area under boro rice and wheat. It is possible to increase oil crop production by cultivating improved varieties of summer oil crops like sesame. T-6 and BARI TIL-2 are two recommended verities of sesame available in Bangladesh, which have low seed

yield, susceptible to disease and pest, indeterminate growth habit and asynchronous ripening of capsule. Thus the development of high yielding variety(s) of sesame with desirable traits is necessary to increase the production of oil per unit area to meet the demand of edible oil as well as to save foreign exchange. Study of diverse genotypes of a crop is necessary to assess their performances, which help to develop a new variety in suitable scale. It is important to understand the usable variability existing among them. Choice of genetically diverge parents for hybridization under trangressive breeding programme is also dependent upon this classification. Before attempting hybridization it is necessary to identify the compatible parents, because success of any hybridization depends on the high cross compatibility of the parents along with other desirable agronomic characters.

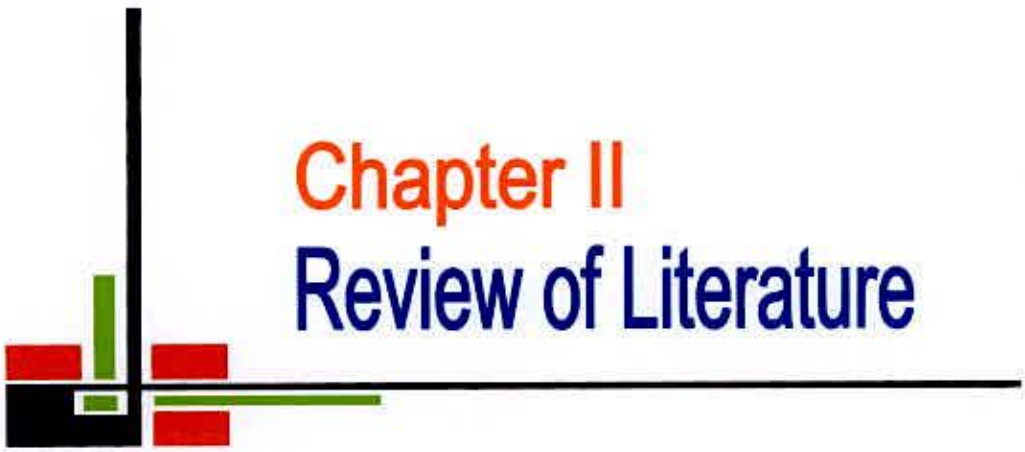
The variability among different genotypes of a species is known as genetic diversity. It arises either due to geographical separation or due to genetic barriers to cross ability. Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display a great heterosis than those between closely related strains (Singh, 1983) which permits to select the genetically divergent parents to obtain the desirable recombination of the segregating generations.

Hybridization is one of the major tools for the improvement of a crop. Before hybridization genetic diversity of the existing varieties need to be known. It is well established that the greater the genetic diversity the higher the chance of getting better hybrid or recombinant. It is a major tool being used in parent selection for efficient hybridization program (Bhatt, 1973; Khanna and Chaudhary, 1974; Chandra, 1977). Moreover, evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomooka, 1991). Multivariate analysis with D^2 technique measures the amount of genetic diversity in a given population in respect of several characters (Naidu and Satanarayana, 1991). It is one of the potent

techniques for measuring the genetic divergence both in intra and inter cluster level. If a plant breeding program is to be advanced more rapidly and efficiently, knowledge of inter-relationships between yield contributing characters is necessary. Thus, determination of correlation between characters has a considerable importance in selection practices, since it helps in the construction of selection indices and also permits for the prediction of correlated response.

With conceiving the above scheme in mind, the present research work has been undertaken in order to fulfilling the following objectives:

i. To categories the various germplasms of sesame under different group based on genetic diversity
ii. To analyze the genetic diversity of the genotypes in respect of different characters
iii. To assess the contribution of different traits towards divergence and
iv. To screen out the suitable genotypes for future breeding program.



Chapter II
Review of Literature

CHAPTER II

REVIEW OF LITERATURE

Sesame *(Sesamum indicum* L.) is the summer leading oil crop in Bangladesh (BBS, 2001). Investigation on sesame in its major growing countries like in Bangladesh is limited and in developed countries it is a minor crop with little interest. As a result information on its diversity is limited. However, information available in these aspects of sesame has been reviewed and present in this section.

2.1 Morphological diversity

Study of morphological diversity is usually based on a set of descriptors. The descriptors list of sesame was published by International Board for Plant Genetic Resource (IBPGR) secretariat, Rome, Italy in 1981 (Anon. 1981). The IBPGR has now renamed as international Plant Genetic Resource Institute (IPGRI). Cultivated sesame is rich in morphological diversity.

Uddin and Mitra (1994) observed a range of 27-64 seeds per capsule in their study including 27 diverse genotypes of sesame. Alvaran (1993) and Begum (1997) also observed wide range of variability for this trait.

Bisht *et al.* (1998) reported a wide range of variation existed among 3129 sesame genotypes in respect of plant height, branching pattern, stem pubescence, corolla pubescence, capsule pubescence, flower color, flowers per leaf axil, capsule shape, capsule size, number of capsules per leaf axil, number of locules in the capsule, capsules per plant, seeds per capsule, seed weight and yield per plant.

El-Hifny *et al.* (1988) found significant differences among genotypes for plant height, height to first capsule, capsule length and yield per plant.

Ashri (1998) reported it is desirable to produce flower in the nodes near to the soil surface, which reduces biomass and facilitates harvest.

Shadakshari *et al.* (1995) evaluated 225 sesame genotypes and observed a wide range of variability for nodes to first flower, total number of capsules, capsules length, seed yield per plant, number of locules per capsule, total number of branches, days to 50% flower and days to maturity.

VanRheenen (1981d) expressed non-branching types could produce well if planted in high densities.

Lee *et al.* (1989) reported a uniculm tall variety of sesame "Jinjuggae" produced three capsules per leaf axil, white seeds, 10% more capsules per plant, higher seed oil content and more seed yield.

Main and Yadav (1996) reported that under medium to high input condition uniculm type is desirable while under low input moderately branched at lower nodes to compensate for poor stands.

Kobayashi (1981) reported opposite phylotaxy produced higher number of capsules per plant than alternate or spiral ones. He obtained an increase in seed yield per plant form plants with short internodes as compared with the original ones.

VanRheenen (1981a) reported the frequency of occurrence of capsule length as 55.2% short, 28.2% intermediate and 16.4% long from the data of 67 cultivars obtained from 11 countries of the world.

VanRheenen (1981b) stated as multi-locular cultivar had somewhat shorter capsules of wider diameter with 1.7 times more seeds of smaller size and 62% higher seed yield per capsule by weight than four locular cultivar. However in

his another study he concluded that the character multi-locular capsule is undesirable from yield point of view on the basis of the result obtained from the study of 11 generations of transfer this trait into a four locular variety.

Beech (1981) reported seed color ranges from white through cream and brown to black. He also reported black seeded cultivars tend to give higher seed yield than the others. Uzo and Ojiake (1981) described the seed color of sesame as white, brown, pure white, light brown , chocolate, brown white, dull white and black brown.

Ashri (1998) reported that acute leaf angle permits maximum sunlight penetration than horizontal or droopy leaf. He also reported, deep taproot penetration with a well distributed secondary root system provides opportunity for maximum exploitation of soil moisture.

Desai, (1981) reported deep taproot enable the genotype to be drought resistance capable of withstanding a higher degree of water-stress. Late type have heavily branched roots while early type have short roots.
Tepora (1993) reported a range of oil % in sesame seed as 34.4-59.8 % with mean 50% and in another study a range of 34.34-54.9 % with a normal value of 40 %.

Raheja *et al.* (1989) estimated oil % in 70 sesame genotypes in India with a range of 46.2-56.8. Liu *et al.* (1992) in a collection of 410 sesame germplasm estimated mean oil % of 53.1. Amin and Kothari (1989) reported seeds of 14 sesame cultivars contained 33.18-42.34% oil.

Tashiro *et al.* (1991) studied oil content in 42 strains of *Sesamum indicum* and found strains with white seed had 55.0% which was 7.2 % more than those of strains with black seed.

Desai (1981) observed sort duration varieties have much higher harvest index than the long durated ones.

Beech (1981) reported majority of the cultivars suffers from severe seed shattering under farmer's condition.

Ashri (1998) reported fast vigorous seed germination and seedling emergence, with strong hypocotyls elongation assure better emergence.

Mponda *et al.* (1997) evaluated seven seedling and five agronomic characters in 50 sesame genotypes (*sesamum indicum*) and observed higher genetic variances for cotyledon length. They suggested variety with rapid seedling growth, early maturity and three quadricarpellate capsules per leaf axil had the potentiality for improvement in yield.

2.2 Genetic diversity

Genetic divergence means the nature and degree of variability existing among the genotypes under studies, which are measured by range, mean, standard deviation, variance, standard error, coefficient of variation etc. Genetic diversity analysis is mainly based on multivariate techniques. During last decades different multivariate techniques have been developed through the development of computer program. However literature related to efficient multivariate techniques for diversity analysis is reviewed in the following paragraphs.

Nair and Mukharjee (1960) estimated degree of divergence between biological populations and relevant contribution of different components to the total divergence by D^2 statistic in teak. They were the pioneers to use the D^2 statistic as a measure of genetic divergence in the field of the plant breeding.

Patil (1993) reported selection of parents in hybridization programme based on Mahalanobis's D^2 statistic is more reliable as the requisite knowledge of

parents in respect of a mass of characteristics is available prior to crossing. Genetic diversity is not always related to geographical diversity.

Thangavelu and Rajasekaran (1983) reported limited diversity and no relationship between geographical diversity in sesame.

Anitha and Dorairaj (1990) grouped eight parents and 56 hybrids into 15 clusters based on D^2 analysis. They observed highest values for seed yield, oil content, number of primary branches and harvest index in the genotypes of Cluster V and the plant attributes number of seeds per capsule, total capsules per plant and days to flowering were important in the study of genetic divergence.

Mahapatra *et al.* (1993) evaluated 29 *Sesamum indicum* L. varieties from 11 Indian states for seven yield components using D^2 and canonical analysis. They observed 29 varieties were grouped into nine clusters, which did not show any relationship of genetic diversity with geographical origin.

Patil (1993) studied 100 sesame genotypes and observed considerable amount of genetic diversity in the material representing diverse geographical regions revealed no relation between geographical diversity and genetic diversity.

Patil and Sheriff (1994) used the Mahalanobis D^2 statistic in the analysis of genetic diversity for 16 yield related traits in 100 varieties of sesame (*Sesamum indicum* L.). They stated analysis of variance showed significant inter-varietals differences in all the traits and on the basis of genetic distance, varieties were grouped into 14 clusters and distribution of genotypes in the different clusters was not in accordance with the geographical origin.

Uddin *et al.* (1994) performed multivariate analysis including 41 genotypes in sesame and grouped them into four clusters based on principal component and

cluster analysis. Their study revealed greater inter-cluster distances than intra-cluster distances.

Uddin and Chowdhury (1994) studied 27 genotypes in sesame and performed multivariate analysis grouping the genotypes into four clusters. They reported inter-cluster distances were greater than the intra- cluster distances and no relation between geographical diversity and genetic diversity.

WenXing *et al.* (1994) carried out principal component analysis in 31 sesame (*Sesamum indicum* L.) varieties and chosen 11 varieties as parents for use in a breeding programme. They estimated genetic distance using cluster analysis and stated that the 31 varieties were divided into 14 groups. They also reported effects on genetic diversity were more beneficial if crossing was carried out between genotypes belonging to different groups if their genetic distance (D^2) was greater than 12.5.

Main and Bahl (1989) reported parental clusters separated by medium D^2 values exhibited significant positive heterosis for pods per plant seeds per pod and seed yield per plant in chickpea.

Ganesh and Thangavelu (1995) employed Mahalanobis D^2 analysis to study the genetic diversity in sesame and grouped 50 sesame genotypes into four clusters. They reported inter-cluster distances were greater than the intra-cluster distances and the clustering pattern. They observed that the geographical diversity was not related to the genetic diversity. They also stated crossing between divergent parents usually produced greater heterotic effect than those between closely related ones.

Manivannan and Nadarajan (1996) measured plant height, number of branches, capsules per plant and seed yield in 52 sesame (*Sesamum indicum* L.) genotypes and observed cluster analysis grouped the genotypes into six groups,

of which clusters II, V and VI were the most divergent from the others. They informed plant height was the major contributor to genetic divergence followed by number of branches, seed yield and capsules per plant.

Swain and Dikshit (1997) analyzed data on 13 quantitative characters in 40 genotypes of *Sesamum indicum* L. collected from different states of India using Mahalanobis' D^2 statistic and observed the genotypes were grouped into 14 clusters with no relationship between geographic origin and genetic diversity. They stated seed oil content made the largest contribution to total divergence, followed by 1000-seed weight, capsule length and days to flowering.

Paramasivam (1980) classified 100 sesame genotypes into seven diverse clusters bases on principal component analysis and cluster analysis.

2.3 Path Co-efficient Analysis

Path analysis is a standardized partial regression analysis which splits the correlation coefficient into the measures of direct and indirect effects that specify the contribution of a particular character to seed yield. This analysis has been used by many plant breeders as an essential tool in determining the characters that contribute appreciably to yield variation. This also can be utilized as important selection component for improvement of yield.

Using this analysis, some researchers found component characters that directly and indirectly affect seed yield.

Dixit (1975) and Shukla (1983) reported that days to 50 percent flowering and plant height had negative direct effects on seed yield.

Govinda (1982) observed high positive direct effect of plant height on seed yield.

Reddy and Stephen (1987) also recorded high direct effect of plant height on seed yield in both parents and hybrids.

Thangavelu (1980) reported the greatest positive direct effect of the number of capsules per plant on seed yield. Further, he found that other characters had indirect effects on yield via the number of capsules per plant.
Thangavelu and Rajasekaran (1984) observed high positive direct effect of the total number of capsules per plant on seed yield followed by 1000-seed weight and plant height.

Yadava *et al.* (1980) were found the number of capsules per plant had direct effect on seed yield followed by days to 50% flowering and 1000-seed weight. When indirect effects were considered, the number of capsules had high indirect effect also.

Tepora *et al.* (1983) reported that the number of capsules per plant gave the highest positive direct effect on seed yield followed by plant height, number of seeds per capsules, 1000-seed weight and dry matter production. In, maturity and harvest index were observed to have negligible positive direct effects on seed yield. Furthermore, recent researches found more characters that direct affected seed yield.

Reddy (1986) found out that capsule length, plant height, days to maturity and 1000-seed weight had considerable direct effects on seed yield.
Vadhani *et al.* (1992) reported that capsule number had maximum direct influence on highest seed yield. He also noticed that almost all the other component characters contributed towards yield through this character.
Salas (1995) reported that the number of capsules per plant, total dry matter and maturity had high positive direct effects on seed yield and high total contributions to the determination in yield.

Kadir *et al.* (1996) reported that seed yield along with eight yield components were used to estimate genetic parameters, association and path analysis in 17

genotypes of sesame. The highest PCV and GCV were observed in 1000 seed weight followed by seed yield and primary branches per plant and the lowest PCV and GCV were for days to maturity. They also observed that days to 50% flowering, branches per plant, capsules per plant, seeds per plant and 1000-seed weight had the positive and significant association with seed yield both at phenotypic and genotypic levels.

Jalal and Biswa (1994) observed that capsules per plant, branches per plant and seeds per capsules per plant contributed more towards seed yield per plant when other characters remained constant. Seed yield per plant had the highest multiple correlation coefficients together with capsules per plant and seeds per capsule.

The above mentioned literatures indicated that the number of capsules per plant had the highest direct influence on the yield. It can also have the highest indirect influence via other characters. Large direct effects on seed yield were also recorded in plant height, number of seeds per capsules, flowering, maturity and total dry matter. The high direct effects of the different component characters on seed yield suggest that these characters can be used as selections indices for yield improvement.

2.4 Heritability

The heritability of a component character is one of its most important properties. It expresses the proportion of the total variance that is attributable to the average effects of genes. This is what determines the degree of resemblance between parents and offsprings. Its predictive role expresses the reliability of the phenotypic value as a guide to the breeding value. Only the phenotypic values of individuals can be directly measured but it is the breeding value that determines their influence on the next generation (Falconer, 1977).

Studies have shown the effect of high heritability to progenies in sesame. According to Jones (1986), a high heritability estimate shows that superior parents tend to give the best progenies while poor parents generally yield poor progenies.

Pathak and Dixit (1986; 1992) observed high heritability for days to 50% flower, days to maturity and plant height. Moreover, high heritability for capsule number and seed yield were reported by Paramasivam and Prasad (1981), Thangavelu and Rajasekaran (1982), and Chandramony and Nayar (1985).

Salas (1995) averred that the high heritability (h^2_b) estimates for number of capsules (86.85%), maturity (95.12%) and total dry matter (62.15) can give considerable gain in yield with the use of these three characters as selection indices.

2.5 Genotypic and phenotypic coefficient of variation and Genetic advance

Genotypic and phenotypic coefficient of variation (GCV & PCV) is useful to the plant breeders in the assessment of genetic variability present in a character in a population. Burton (1952) suggested that high GCV together with high heritability estimates gives the best picture of the extent of gain to be expected by selection. While the estimation of genetic advance shows the extent of genetic gain that can be expected through selection in the character to be improved upon.

Wright (1921; 1935) suggested that only additive effect of genes contributes toward genetic advancement.

High GCV and PCV were observed by Pathak and Dixit ((1992) for plant height and capsules number.

Pathak and Dixit (1986) found that plant height and capsule number had higher magnitude of genetic advance as percentage of mean, whereas capsule length and seeds per capsules revealed low genetic advance. Moderately higher genetic advance were observed in days to flowering and maturity.

On the other hand according to Khidir and Gizouli (1974) capsules per plant showed high genetic advance.

Kumari and Balasubramanian (1993) recorded that number of capsules per plant and total dry weight per plant had high amount of genetic variation coupled with high heritability and genetic advance.

Chapter III

Materials and Methods

CHAPTER III

MATERIALS AND METHODS

The research work was conducted in the experimental field of Genetics and Plant Breeding of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh during the period from November 2008 to February 2009. The materials and methods of this experiment are presented in this chapter under the following headings-

3.1 Experimental Site

The location of the experimental site is $23^0 74'$ N latitude and $90^0 35'$ E longitude with an elevation of 8.2 meter from sea level.

3.2 Characteristics of Soil

The soil of the experimental area was loamy belonging to the Madhupur Tract (UNDP, 1988) under AEZ 28 (Appendix III). The selected plot was medium high land.

3.3 Weather condition of the Experimental Site

The geographihcal situation of the experimental site was under the subtropical climate, characterized by three distinct seasons, Rabi season from November to February and Kharif 1 from March to June and Kharif 2 from July to October (Edris *et al.*, 1979). Details of the metrological data of air temperature, relative humidity, rainfalls and sunshine during the period of the experiment was collected from the Weather Station of Bangladesh, Sher-e-Bangla Nagar, presented in (Appendix II).

3.4 Planting Materials

In this research work, the seeds of *Sesamum indicum* were used. The purity and germination percentage were leveled as around 100% and above 90%

respectively. The source of all the genotypes used in this experiment was Bangladesh Agricultural Research Institute (BARI), Joydebpur, Gazipur. The names of genotypes are presented in Table 1.

3.5 Layout of the Experiment

Field layout was done after final land preparation. The materials were laid out in Randomized Complete Block Design (RCBD) with three replications. The plot size was 28.50 m × 2 m. Block to block distance one meter, row to row distance 30 cm, plant to plant distance was 10 cm. Seeds were sown in lines in the experimental plots on 14 November, 2008. The seeds were placed at about one cm depth in the soil.

3.6 Preparation of the Main Field

The plot selected for the experiment was opened in the first week of November 2008 with power tiller and was exposed to the sun for a week, after one week the land was harrowed, ploughed and cross ploughed several times by laddering to obtain a good tilth. Weeds and stubbles were removed and finally obtained a desirable tilth of soil for sowing of sesame seeds.

3.7 Application of Fertilizers

The fertilizers N, P, K and Gypsum in form of urea, TSP, MP and Gypsum respectively were applied. The entire amount of TSP, MP and Gypsum were applied before sowing as basal dose. Urea was applied in two equal installments at basal dose and before flowering respectively. The dose and method of application of fertilizer are shown in Table 2.

3.8 Sowing of Seeds in the Field

The sesame seeds were sown in lines each having a line to line distance of 30 cm under direct sowing in the well prepared plot on 14 November 2008.

Table 1. Name of *Sesamum indicum* genotypes used in the experiment

Sl. NO.	Genotypes	Sources of Genotypes	Sl. No.	Genotypes	Sources of Genotypes
G1	BD-6961	BARI	G26	BD-6992	BARI
G2	BD-6962	BARI	G27	BD-6993	BARI
G3	BD-6963	BARI	G28	BD-6994	BARI
G4	BD-6964	BARI	G29	BD-6996	BARI
G5	BD-6960	BARI	G30	BD-6997	BARI
G6	BD6979	BARI	G31	BD-6999	BARI
G7	BD-6980	BARI	G32	BD-7000	BARI
G8	BD-6981	BARI	G33	BD-7001	BARI
G9	BD-6982	BARI	G34	BD-7003	BARI
G10	BD-6983	BARI	G35	BD-7004	BARI
G11	BD-6984	BARI	G36	BD-7005	BARI
G12	BD-6985	BARI	G37	BD-7006	BARI
G13	BD-6986	BARI	G38	BD-7007	BARI
G14	BD-6987	BARI	G39	BD-7008	BARI
G15	BD-6988	BARI	G40	BD-7009	BARI
G16	BD-6989	BARI	G41	BD-7010	BARI
G17	BD-6990	BARI	G42	BD-7011	BARI
G18	BD-6966	BARI	G43	BD-7012	BARI
G19	BD-6968	BARI	G44	BD-7013	BARI
G20	BD-6969	BARI	G45	BD-7014	BARI
G21	BD-6970	BARI	G46	BD-7015	BARI
G22	BD-6971	BARI	G47	BD-7016	BARI
G23	BD-6974	BARI	G48	BD-7017	BARI
G24	BD-6978	BARI	G49	BD-7018	BARI
G25	BD-6991	BARI	G50	BD-7019	BARI

NB: BARI-Bangladesh Agricultural Research Institute

Table 2. Dose and methods of application of fertilizers in sesame field

Fertilizers	Dose (Kg/ha)	Application (%)	
		Basal	Before Flowering
Urea	6	3	3
TSP	9	9	–
MP	3	3	–
Gypsum	6	6	–

3.9 After Care

When the seedling started to emerge in the beds it was always kept under careful observation. After emergence of seedling, various intercultural operations were accomplished for better growth and development of the sesame seedlings.

3.9.1 Irrigation

Light over head irrigation was provided with a watering can to the plots once immediately after germination and continued for three times for proper growth and development of the plants.

3.9.2 Thinning and Gap filling

The seedling were first thinned from all of the plots at seven days after emergence and second thinning was carried out after seven days from first thinning for maintaining a distance of 10 cm from plant to plant in the experimental plots.

3.9.3 Weeding

Weeding was done to keep the plots free from weeds, easy aeration of soil which ultimately ensured better growth and development. The newly emerged weeds were uprooted carefully after complete emergence of sesame seedlings and whenever necessary. Breaking the crust of the soil, when needed.

3.9.4 Top dressing

After basal dose, the remaining dose of urea was top dressed before flowering.

3.10 Plant protection

The crop was protected from the attack of aphids by spraying Malathion-57 EC @ 2 ml/liter of water. The insecticide was applied for the first time before one week of flower initiations and it was applied for another two times at an interval of 15 days. The insecticide was applied in the evening.

3.11 Harvesting, threshing and cleaning

The crop was harvested depending upon the maturity of each genotype. Harvesting was done manually. Enough care was taken for harvesting, threshing and also cleaning of sesame seeds.

3.12 Data recording

3.12.1 Days to 50% flowering

Difference between the date of sowing to the date of flowering of a genotype was counted as days to 50 % flowering. Days to 50% flowering was recorded when 50% flowers of a genotype were at the flowering stage.

3.12.2 Days to 80% maturity

Maturities of the crops of 50 genotypes were recorded considering the maturity symptom such as color of the capsule turned from greenish to yellowish colored and leaves were dropped.

3.12.3 Plant height (cm)

The height of plant was recorded in centimeter (cm). Data were recorded as the average of ten plants selected at random from the each line of 50 genotypes of each plot after harvest. The height was measured from the ground level to the tip of the growing point.

3.12.4 Number of primary branches per plant

The total number of primary branches arisen from the main stem of a plant was counted as the number of primary branches per plant.

3.12.5 Number of capsules per plant

Total number of capsules of the randomly selected 10 plants from each line was recorded and then average number of capsules per plant was estimated.

3.12.6 Length of capsules (cm)

For this character measurement was taken in cm from the base to the tip of a capsule from the five representative capsules from each line of 50 genotypes for three replication and average data was recorded.

3.12.7 Width of the capsule (cm)

Width of the capsule was measured in five fruits of each genotype for three replication in cm and average data was recorded.

3.12.8 Number of seeds per capsule

Ten capsules from each line of 50 genotypes were selected randomly and number of seeds was counted and the average number of seed per capsule was determined.

3.12.9 1000- seed weight (g)

One thousand seeds were counted randomly from the total seeds of cleaned harvested seed for each genotype and then weighted in grams.

3.12.10 Yield per plant (g)

Seed weight per plant was measured from the randomly selected plants and then average was designated as yield per plant. A picture of field view of the experimental field is presented in Plate no 1.

3.13 Statistical analysis

Mean data of the characters were subjected to multivariate analysis. Univariate analysis of the individual character was done for all characters under study using the mean values (Singh and Chaudhury, 1985) and was estimated using MSTAT-C computer programme. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV %) were also estimated using MSTAT-C. Multivariate analysis was done by computer using GENSTAT 513 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).

3.13.1 .1 Estimation of genotypic and phenotypic variances

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

Plate 1. Field View of the experimental field

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

Where,

GMS = Genotypic mean sum of squares

EMS = Error mean sum of squares

r = number of replications

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

Where,

σ^2_g = Genotypic variance

EMS = Error mean sum of square

3.13.1.2 Estimation of genotypic and phenotypic correlation co-efficient

For calculating the genotypic and phenotypic correlation co-efficient for all possible combinations the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956) were adopted.

The genotypic co-variance component between two traits and have the phenotypic co-variance component were derived in the same way as for the corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows:

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

Where,

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

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

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

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

Where,

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

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

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

3.13.1.3 Estimation of genotypic and phenotypic co-efficient of variation

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

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

Where,

σ^2_g = Genotypic variance

$\bar{x}$ = Population mean

Similarly,

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

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

Where,

σ^2_{ph} = Phenotypic variance

$\bar{x}$ = Population mean

3.13.1.4 Estimation of heritability

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

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

Where,

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.13.1.5 Estimation of genetic advance

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

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

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

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

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.13.1.6 Estimation of genetic advance in percentage of mean

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

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

3.13.2 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:

3.13.2.1 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.

3.13.2.2 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 maximum distance between each pair of the n points using similarity matrix (Digby *et al.*, 1989)

3.13.2.3 Cluster analysis (CA)

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

3.13.2.4 Canonical Vector analysis (CVA)

Canonical vector analysis (CVA) finds linear combination of original variability 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.

3.13.2.5 Calculation of D^2 values

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

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

Where,

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

x = Number of characters.

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

3.13.2.6 Computation of average intra-cluster distances

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

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

Where,

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

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

3.13.2.7 Computation of average inter-cluster distances

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

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

Where,

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

n_i = Number of populations in cluster i

n_j = Number of populations in cluster j

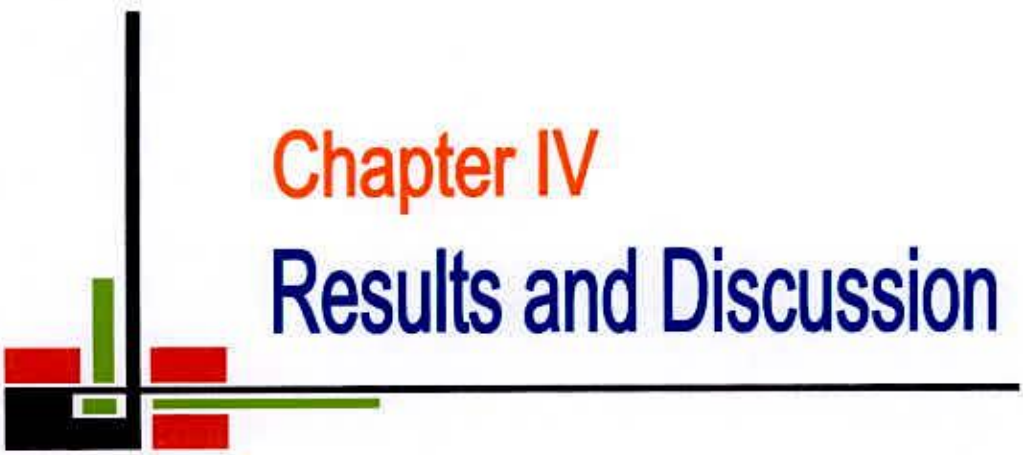
3.13.2.8 Cluster diagram

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

3.13.2.9 Selection of genotypes 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. Genotypes or lines were selected for efficient hybridization programme according to Singh and Chaudhury (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 parents
ii. Selection of particular genotypes from the selected clusters
iii. Relative contribution of the characters to the total divergence
iv. Other important characters of the genotypes performance



Chapter IV
Results and Discussion

CHAPTER IV

RESULTS AND DISCUSSION

In this chapter the results obtained from the study are presented and discussed. The data pertaining to 50 sesame genotypes as well as yield and its contributing characters were computed and statistically analyzed and the results thus obtained are discussed below under the following heads:

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

analysis

4.1 GENETIC PARAMETERS

The analysis of variances among the genotypes studied here were (probability is 0.01) highly significant. The mean sum of square, mean, range, variance components, genotypic and phenotypic coefficients of variations, heritability, genetic advance and genetic advance in percent of mean (GAPM) are presented in (Table 3). The results are discussed character wise as follows:

4.1.1 Days to 50% flowering

Mean sum of square for days to 50% flowering was highly significant (Table 3) indicating existence of considerable difference for this trait. The maximum days to 50% flowering were found 61 days and the minimum was recorded 32 days with mean value 42.47 days (Appendix IV). The genotypic variance was 68.01 and phenotypic variance was 74.59. The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes controlling this trait. The difference between genotypic co-efficient of variation (19.30) and phenotypic co-efficient

Table 3: Genetic parameters of yield and yield contributing characters of 50 sesame genotypes

Parameter	Days to 50% flowering	Days to 80% Maturity	Plant height (cm)	No. of primary branches / plant	No. of capsule/ plant	Length of capsule (cm)	Width of capsule (cm)	No. of seeds / capsule	1000 seeds weight (g)	Yield/plant (g)
MS value	210.62**	184.33**	171.09**	1.47**	358.73**	0.08**	0.02**	281.62**	12.38**	198.69**
Gen. var	68.01	60.28	55.61	0.47	19.11	0.03	0.01	93.63	4.13	65.81
Env. var	6.58	3.49	4.27	0.05	1.38	0.00	0.00	0.73	0.12	1.66
Phe. var	74.59	63.77	59.88	0.52	120.49	0.03	0.01	94.36	4.25	67.47
GCV	19.30	7.60	11.73	16.30	29.87	9.35	13.62	23.48	20.86	51.53
PCV	20.21	1.82	12.17	17.16	30.04	9.16	14.17	23.57	21.16	52.18
ECV	6.00	1.83	3.25	5.38	3.21	2.23	3.92	2.08	3.54	8.19
Herit.	91.18	94.53	92.67	90.18	98.86	94.61	92.35	99.22	97.20	97.54
G Ad.	20.79	19.93	18.97	1.12	28.65	0.42	0.21	25.45	5.29	21.15
GAPM	48.65	19.50	29.84	40.86	78.40	24.00	34.55	61.74	54.30	134.36
%CV	6.00	1.83	3.25	5.38	3.21	2.23	3.92	2.08	3.55	8.21
Mean	42.74	102.18	63.59	4.22	36.54	1.77	0.61	41.22	9.72	16.52
SE	0.70	0.65	0.63	0.06	0.89	0.01	0.01	0.79	0.17	0.67

Here ** indicates significant at 1% level of probability, MS= Mean Sum, Gen. Var.= Genotypic variance, Env. Var.= Environmental Variance, Phe. Var.= Phenotypic variance, GCV= Genotypic coefficient of variance, PCV= Phenotypic Coefficient of variance, ECV= Environmental coefficient of variance, Herit.= Heritability, G Ad=Genetic Advance, GAPM= Genetic Advance Percent Mean, CV= Coefficient of variation, SE= Standard Error

of variation (20.21) was minimum. Heritability estimated for this trait was high (91.18%) with high genetic advance (20.79) and high genetic advance in percent of mean (48.65), indicated that selection for this character would be effective. Pathak and Dixit (1986; 1992) observed high heritability and moderately higher genetic advance for days to 50% flowering.

4.1.2 Days to 80% maturity

Mean sum of square for days to 80% maturity was highly significant (Table 3), indicating existence of wide range of variation among the sesame genotypes for this trait. The maximum days to 80% maturity was found 119.67 days and minimum was recorded 92.00 days with mean value 102.18 days (Appendix IV). The genotypic variance was 60.28 and phenotypic variance was 63.77. The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation (7.60) was higher than the phenotypic co-efficient of variation (1.82). Heritability for this trait was estimated very high (94.53%) and genetic advance (19.93) and genetic advance in percent of mean (19.50) was found moderately high, indicated that selection for this character would be effective. Pathak and Dixit (1986; 1992) observed high heritability and moderately higher genetic advance for days to 80% maturity. Salas reported high heritability (95.12%) for days to 80% maturity.

4.1.3 Plant height (cm)

Mean sum of square for plant height was highly significant (Table 3) indicating existence of wide range of variation among the sesame genotypes for this trait. The maximum plant height was found 78.18 cm and minimum was recorded 47.57 cm with the mean value 63.59 cm (appendix IV). The genotypic variance was 55.61 and phenotypic variance was 59.88. The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes

controlling this trait. The genotypic co-efficient of variation was 11.73 and phenotypic co-efficient of variation was 12.17. Heritability (92.67%) estimates for this trait was high, genotypic advance (18.97) and genotypic advance in percent of mean (29.84) was found moderately high, indicated that selection for this character would be effective. High heritability was observed by Pathak and Dixit (1986; 1992) for plant height. Pathak and Dixit (1986) found that plant height had higher magnitude of genetic advance in percent of mean. Photograph showing variation of plant height and number of primary branches in different genotypes of sesame in Plate 2.

4.1.4 Number of primary branches per plant

Mean sum of square for number of primary branches per plant was highly significant (Table 3), indicating existence of wide range of variation among the sesame genotypes for this trait. The maximum number of primary branches per plant was found 5.47 and the minimum was recorded 2.37 with mean value 4.22 (Appendix IV). The genotypic variance was 0.47 and phenotypic variance was 0.52. Genotypic co-efficient of variation (16.30) and phenotypic co-efficient of variation (17.16) were close to each other indicating less environmental influence in case of number of primary branches per plant. Heritability estimates for this trait was high (90.18%) with low genotypic advance (1.12) and genotypic advance in percent of mean (40.86) was found moderately high. Reddy (1986) found similar results in sesame. Tepora *et al.* (1983) reported the high heritability and high genetic advance in percent of mean for number of primary branches per plant.

4.1.5 Number of capsules per plant

Mean sum of square for number of capsules per plant was highly significant (Table 3) indicating existence of considerable difference among the sesame genotypes for this trait. The maximum numbers of capsules per plant were

Plate 2. Showing variation in plant height and number of primary branches in different Sesame genotypes

found 65.03 and the minimum was recorded 18.73 with mean value 36.54 (Appendix IV). The genotypic variance was 19.11 and phenotypic variance was 120.49. The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation was 29.87 and phenotypic co-efficient of variation was 30.04. Heritability estimates for this trait was very high (98.86%) with high genetic advance (28.86) and genetic advance in percent of mean (78.40) was also found high, indicated that selection for this character would be effective. High genotypic co-efficient of variation and phenotypic co-efficient of variation were observed by Pathak and Dixit (1992) for number of capsules per plant. Pathak and Dixit (1986) found that number of capsule had higher magnitude of genetic advance in percent of mean. High heritability for number of capsules was reported by Paramasivam and Prasad (1981), Thangavelu and Rajasekharan (1982) and Chandramony and Nayar (1985).

4.1.6 Length of capsule (cm)

Mean sum of square for length of capsule (cm) was highly significant (Table 3) indicating existence of considerable difference among the sesame genotypes for this trait. The maximum capsule length was found 2.14 cm and the minimum was recorded 1.45 cm with mean value 1.77 cm (Appendix IV). The genotypic variance and phenotypic variance was same (0.03). The genotypic co-efficient of variation (9.35) and phenotypic co-efficient of variation (9.16) were close to each other indicating less environmental influence in case of length of capsule. Heritability estimates for this trait was high (94.61%) with low genotypic advance (0.42) and genotypic advance in percent of mean (24.00) was found moderately high. Reddy (1986) found similar results in sesame. Pathak and Dixit (1986) found that capsule length revealed low genetic advance. El-Hifny *et al.* (1988) found significant differences among genotypes for capsule length. Photograph showing variation of length of capsule in different Sesame genotypes in Plate 3.

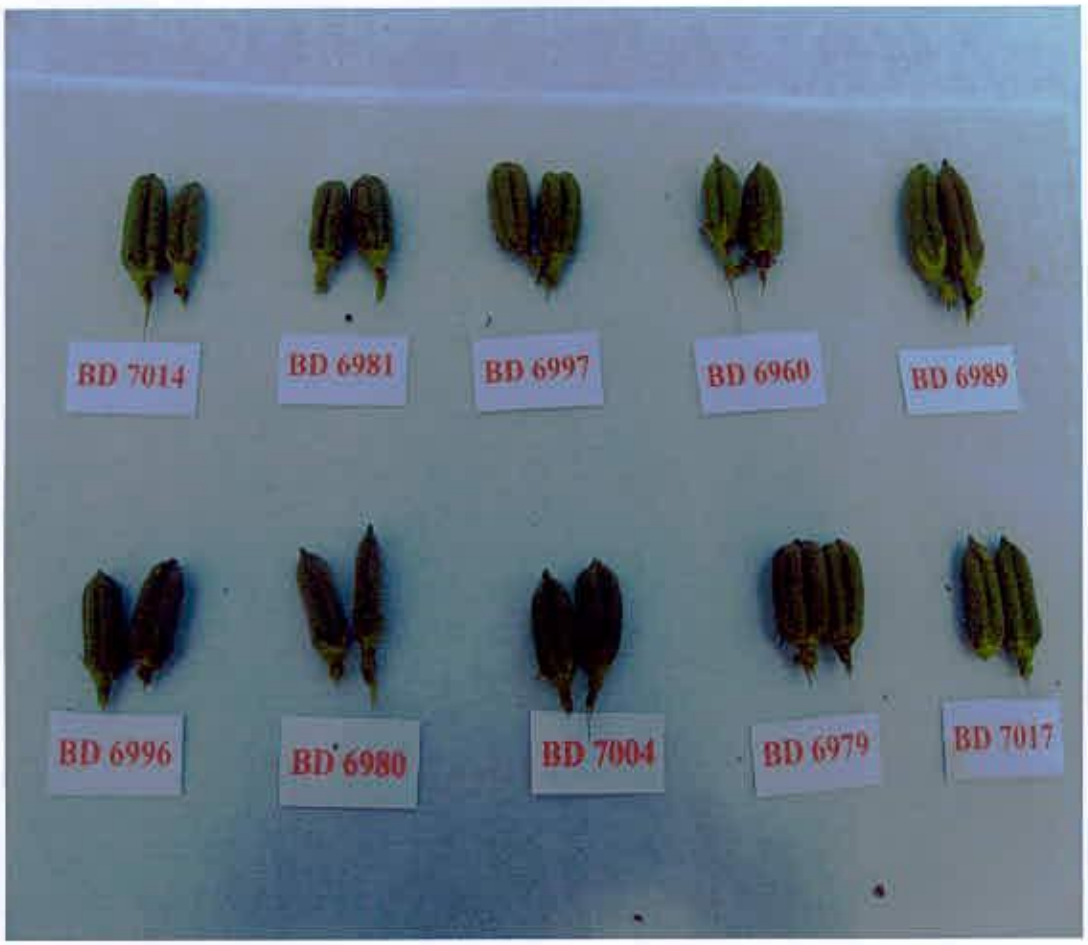


Plate 3. Showing variation of length of capsule in different Sesame genotypes

4.1.7 Width of capsule (cm)

Mean sum of square for width of capsule was highly significant (Table 3) indicating existence of considerable difference among the sesame genotypes for this trait. The maximum capsule width was found 0.77 cm and the minimum was recorded 0.44 cm with mean value 0.61 cm (Appendix IV). The genotypic variance and phenotypic variance was same (0.01). Genotypic co-efficient of variation (13.62) and phenotypic co-efficient of variation (14.17) were close to each other indicating less environmental influence in case of width of capsule. Heritability estimates for this trait was high (92.35%) with low genotypic advance (0.21) and genotypic advance in percent of mean (34.55) was found moderately high.

4.1.8 Number of seeds per capsule

Mean sum of square for number of seeds per capsule was highly significant (Table 3) indicating existence of considerable difference among the sesame genotypes for this trait. The maximum number of seeds per capsule was found 63.00 and the minimum was recorded 19.03 with mean value 41.22 (Appendix IV). The genotypic variance was 93.63 and phenotypic variance was 94.36. Genotypic co-efficient of variation (23.48) and phenotypic co-efficient of variation (23.57) were close to each other indicating less environmental influence in case of number of seeds per capsule. Heritability estimates for this trait was very high (99.22%), genotypic advance (25.45) and genotypic advance in percent of mean (61.74) was also found high, indicated that selection for this character would be effective. Reddy (1986) found similar results in sesame. Tepora *et al.* (1983) reported the high genotypic as well as phenotypic co-efficient of variations for number of seeds per capsule in sesame.

4.1.9 1000-seeds weight (g)

Mean sum of square for 1000-seeds weight was highly significant (Table 3) indicating existence of considerable difference among the sesame genotypes

for this trait. The maximum 1000-seeds weight was found 17.08 g and the minimum was recorded 6.12 g with mean value 9.72 g (Appendix IV). The genotypic variance was 4.13 and phenotypic variance was 4.25. The genotypic co-efficient of variation (20.86) and phenotypic co-efficient of variation (21.16) were close to each other indicating less environmental influence in case of 1000-seeds weight. Heritability estimates for this trait was high (97.20%) with low genotypic advance (5.29) and genotypic advance in percent of mean (54.30) was found moderately high. Kadir *et al.* (1996) reported the highest genotypic as well as phenotypic co-efficient of variations were observed for 1000-seeds weight in sesame.

4.1.10 Yield per plant (g)

Mean sum of square for yield per plant was highly significant (Table 3) indicating existence of considerable difference among the sesame genotypes for this trait. The maximum yield per plant was found 35.17 g and the minimum was recorded 10.08 g with mean value 16.52 g (Appendix IV). The genotypic variance was 65.81 and phenotypic variance was 67.47. The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation was 51.53 and phenotypic co-efficient of variation was 52.18. Heritability estimates for this trait was high (97.54%), genotypic advance (21.15) and genotypic advance in percent of mean (134.36) was also found high, indicated that selection for this character would be effective. High heritability for yield per plant was reported by Paramasivam and Prasad (1981), Thangavelu and Rajasekaran (1982) and Chandramony and Nayar (1985). El-Hifny *et al.* (1988) found significant differences among genotypes for yield per plant.

4.2 CORRELATION CO-EFFICIENT

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

Results of genotypic and phenotypic correlation co-efficient of 10 yield and its contributing traits of sesame were estimated and shown in Table 4 which discussed character wise as follows:

4.2.1 Days to 50% flowering

Days to 50% flowering found to display highly significant positive relationships with days to 80% maturity and plant height at both genotypic and phenotypic level (Table 4). It also showed significant positive relationship with width of capsule at both genotypic and phenotypic level. Highly significant positive association between days to 50% flowering and days to 80% maturity indicates that the traits are governed by same gene and simultaneous improvement would be effective. This character showed insignificant positive correlation with number of primary branches per plant and yield per plant at both genotypic and phenotypic level. This character also showed insignificant negative correlation with number of capsule per plant, length of capsule, number of seeds per capsule and 1000 seeds weight at both genotypic and

Table 4: Genotypic and phenotypic correlation of ten yield contributing characters of 50 sesame genotypes

Character	correlation	Days to 50% flowering	Days to 80% Maturity	Plant Height (cm)	No. of primary branches/ plant	No. of capsule/ plant	Length of capsule (cm)	Width of capsule (cm)	No. of seeds/ capsule	1000 seeds weight (g)
Days to 80% Maturity	G	0.941**	-							
	P	0.912**	-							
Plant Height(cm)	G	0.212**	0.219**	-						
	P	0.201**	0.205**	-						
No. of primary branches/ plant	G	0.012	0.002	0.065	-					
	P	0.007	-0.003	0.059	-					
No. of capsule/ plant	G	-0.046	-0.056	0.296**	0.324**	-				
	P	-0.045	-0.053	0.289**	0.303**	-				
Length of capsule (cm)	G	-0.116	-0.191**	-0.069	-0.081	0.198**	-			
	P	-0.106	-0.177**	-0.068	-0.082	0.191**	-			
Width of capsule (cm)	G	0.165*	0.251**	-0.05	0.155*	0.231**	0.081	-		
	P	0.143*	0.233**	-0.046	0.164*	0.222**	0.059	-		
No. of seeds/capsule	G	-0.095	-0.068	0.023	0.091	0.190**	0.394**	0.308**	-	
	P	-0.093	-0.070	0.022	0.084	0.187**	0.377**	0.293**	-	
1000 seeds weight (g)	G	-0.019	-0.083	-0.02	0.268**	0.227**	0.275**	0.148*	0.006	-
	P	-0.004	-0.081	-0.017	0.248**	0.222**	0.262**	0.147*	0.004	-
Yield/plant (g)	G	0.013	0.005	0.148*	0.349**	0.661**	0.301**	0.228**	0.324**	0.478**
	P	0.011	0.005	0.150*	0.328**	0.652**	0.276**	0.226**	0.323**	0.465**

Here, * indicates significant at 5% level of significance, ** indicates significant at 1% level of significance, G= Genotypic, P= Phenotypic

phenotypic level. Mahapatra *et al.* (1993) reported almost similar result in different genotypes of sesame. Plate 4a is showing variation of flower and plate 4b is showing variation of inflorescences in different genotypes of sesame.

4.2.2 Days to 80% maturity

The character showed highly significant positive relationship with plant height and width of capsule (Table 4). Highly significant positive association between days to 80% maturity and plant height indicates that the traits are governed by same gene and simultaneous improvement would be effective. The character showed highly significant negative association with length of capsule. The character reflected insignificant positive relationship with number of primary branches per plant at genotypic level and with yield per plant at both genotypic and phenotypic level. It also showed insignificant negative correlation with number of primary branches per plant at phenotypic level and with number of capsules per plant, number of seeds per Capsules, 1000 seeds weight at both genotypic and phenotypic level. Insignificant association of these traits indicated that these traits are largely influenced by environmental factors.

4.2.3 Plant height

The character showed highly significant positive relationship with number of capsule per plant and significant positive relationship with yield per plant at both genotypic and phenotypic level (Table 4). It indicated that increasing plant height caused to increase number of capsule per plant and yield per plant. The character showed insignificant positive relationship with number of primary branches per plant and number of seeds per capsule at both genotypic and phenotypic level. It also showed insignificant negative correlation with length of capsule, width of capsule and 1000 seeds weight at both genotypic and phenotypic level. Insignificant association of these traits indicated that the association among these traits is largely influenced by environmental factors. Dikshit (1992) reported almost similar result for plant height.

Plate 4a. Showing Variation of flower in different genotypes of sesame

Plate 4b. Showing variation of inflorescences in different genotypes of sesame

4.2.4 Number of primary branches per plant

Number of primary branches per plant showed highly significant positive correlation with number of capsule per plant, 1000seeds weight, yield per plant and significant positive relation with width of capsule at both genotypic and phenotypic level (Table 4). Highly significant positive correlation between two traits indicated the traits are governed by same gene and simultaneous improvement would be effective. The character showed insignificant positive relationship with number of seeds per capsule at both genotypic and phenotypic level. It also showed insignificant negative relationship with length of capsule at both genotypic and phenotypic level. Ganesh and Thangavelu (1995) reported similar result for number of primary branches per plant.

4.2.5 Number capsules per plant

Number capsules per plant showed highly significant positive correlation with length of capsule, width of capsule, number of seeds per capsule, 1000 seeds weight and yield per plant at both genotypic and phenotypic level (Table 4). Highly significant positive relationship between number of capsule per plant and length of capsule indicated that the traits are governed by same gene and simultaneous improvement would be effective. Paramasivam and Prasad (1981) reported similar result.

4.2.6 Length of capsule

Length of capsule showed highly significant positive correlation with number of seeds per capsule, 1000 seeds weight and yield per plant at both genotypic and phenotypic level (Table 4). It also showed insignificant positive relationship with width of capsule at both genotypic and phenotypic level. Highly significant positive correlation between length of capsule and number of seeds per capsule indicates that the traits are governed by same gene and simultaneous improvement would be effective. The result revealed that with

increase length of capsule would have increase yield per plant. This result is similar with the findings of Ganesh and Thangavelu (1995).

4.2.7 Width of capsule (cm)

Width of capsule showed highly significant positive correlation with number of seeds per capsule and yield per plant at both genotypic and phenotypic level (Table 4). It also showed significant positive relationship with 1000 seeds weight at both genotypic and phenotypic level. Significant positive correlation between two traits indicates that both traits are governed by same gene and simultaneous improvement would be effective. Yadava *et al.* (1980) reported positive and significant association was observed between seed yield and capsule length and width.

4.2.8 Number of seeds per capsule

Number of seeds per capsule showed highly significant positive correlation with yield per plant and positive insignificant relationship with 1000 seeds weight at both genotypic and phenotypic level (Table 4). Highly significant positive relation between number of seeds per capsule and yield per plant indicated that these traits are governed by same gene and simultaneous improvement would be effective. Yadava *et al.* (1980) reported similar result.

4.2.9 1000-seed weight (g)

The trait, 1000-seeds weight showed highly significant positive correlation with yield per plant at both genotypic and phenotypic level (Table 4). It indicates that if 1000-seeds weight increase yield per plants will also increase. Yadava *et al.* (1980) reported similar result.

4.3 PATH CO-EFFICIENT ANALYSIS

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

4.3.1 Days to 50% flowering

Days to 50% flowering showed the negative direct effect (-0.160) on yield (Table 5). The character also showed the maximum positive indirect effect through days to 80% maturity (0. 251) and followed by number of primary branches per plant (0.001). The character produced the negative indirect effect on yield via plant height (-0.008), number of capsule per plant (-0.025), length of capsule (-0.006), width of capsule (-0.012), no. of seeds per capsule (-0.021) and 1000-seeds weight (-0.006) which finally made insignificant positive correlation between days to 50% flowering and yield per plant (0.013). Dixit (1975) and Shukla (1983) reported that days to 50% flowering had negative direct effects on seed yield.

4.3.2 Days to 80% maturity

Days to 80% maturity showed a positive direct effect (0.267) on yield (Table 5). This character also showed the highest negative indirect effect on days to 50% flowering (-0.151) and followed by number of capsule per plant (-0.031), 1000 seeds weigh (-0.029), width of capsule (-0.019), number of seeds per capsule (-0.015), length of capsule (0.011) and Plant height (-0.009) which cumulatively possessed insignificant positive genetic correlation between days to 80% maturity and yield per plant yield (0.005). Salas (1995) reported that days to 80% maturity had high positive direct effects on seed yield. Reedy (1986) also found out that days to maturity had considerable direct effects on seed yield.

Table 5. Direct (bold) and indirect effect of 50 Sesame genotypes

Character	Days to 50% flowering	Days to 80% maturity	Plant height (cm)	No. of primary branches/ plant	No. of capsule/ plant	Length of capsule (cm)	Width of capsule (cm)	No. of seeds/ capsule	1000 seeds weight (g)	Genetic Correlation With yield
Days to 50% flowering	**-0.160**	0.251	-0.008	0.001	-0.025	-0.006	-0.012	-0.021	-0.006	0.013
Days to 80% maturity	-0.151	**0.267**	-0.009	0.000	-0.031	-0.011	-0.019	-0.015	-0.029	0.005
Plant height (cm)	-0.034	0.059	**-0.039**	0.005	0.160	-0.004	0.004	0.005	-0.007	0.148*
No. of primary branches/ plant	-0.002	0.001	-0.003	**0.080**	0.176	-0.004	-0.012	0.020	0.093	0.349**
No. of capsule/ plant	0.007	-0.015	-0.012	0.026	**0.541**	0.011	-0.017	0.041	0.079	0.661**
Length of capsule (cm)	0.019	-0.051	0.003	-0.007	0.107	**0.055**	-0.006	0.086	0.095	0.301**
Width of capsule (cm)	-0.026	0.067	0.002	0.012	0.125	0.004	**-0.075**	0.067	0.051	0.228**
No. of seeds/capsule	0.015	-0.018	-0.001	0.007	0.103	0.022	-0.023	**0.218**	0.002	0.324**
1000 seeds weight (g)	0.003	-0.022	0.001	0.022	0.123	0.015	-0.011	0.001	**0.347**	0.478**
									Residual effect	0.621

4.3.3 Plant height (cm)

Plant height showed the negative direct effect (-0.039) on yield (Table 5). The character also showed the positive indirect effect through number of capsule per plant (0.160) followed by days to 80% maturity (0.059), number of primary branches per plant (0.005), number of seeds per capsule (0.005) and width of capsule (0.004) . On the other hand, the character produced the negative indirect effect on yield via days to 50 % flowering (-0.034), 1000-seed weight (-0.007) and length of capsule (-0.004) which cumulatively possessed significant positive genetic correlation between plant height and yield per plant (0.148). Dixit (1975) and Shukla (1983) reported that plant height had negative direct effects on seed yield. Figure 1 showing path diagram of yield and its contributing traits in different genotypes of sesame.

4.3.4 Number of primary branches per plant

Number of primary branches per plant showed positive direct effect (0.080) on yield (Table 5). This character also showed the highest positive indirect effect through number of capsule per plant (0.176) followed by 1000-seed weight (0.093), number of seeds per capsule (0.020) and days to 80% maturity (0.001). The character also produced the negative indirect effect on yield via width of capsule (-0.012), length of capsule (-0.004), plant height (-0.003) and days to 50% flowering (-0.001). The cumulative effects of these characters produced highly significant positive genotypic correlation between number of primary branches per plant and yield per plant (0.349).

4.3.5 Number of capsule per plant

Number of capsule per plant showed a highest positive direct effect (0.541) on yield (Table 5). This character also showed some positive indirect effect through 1000-seed weight (0.079), number of seeds per capsule (0.041), number of primary branches per plant (0.026), length of capsule (0.011) and days to 50% flowering. The character also produced the negative indirect effect on yield via plant height (-0.012), days to 80% maturity (-0.015) and

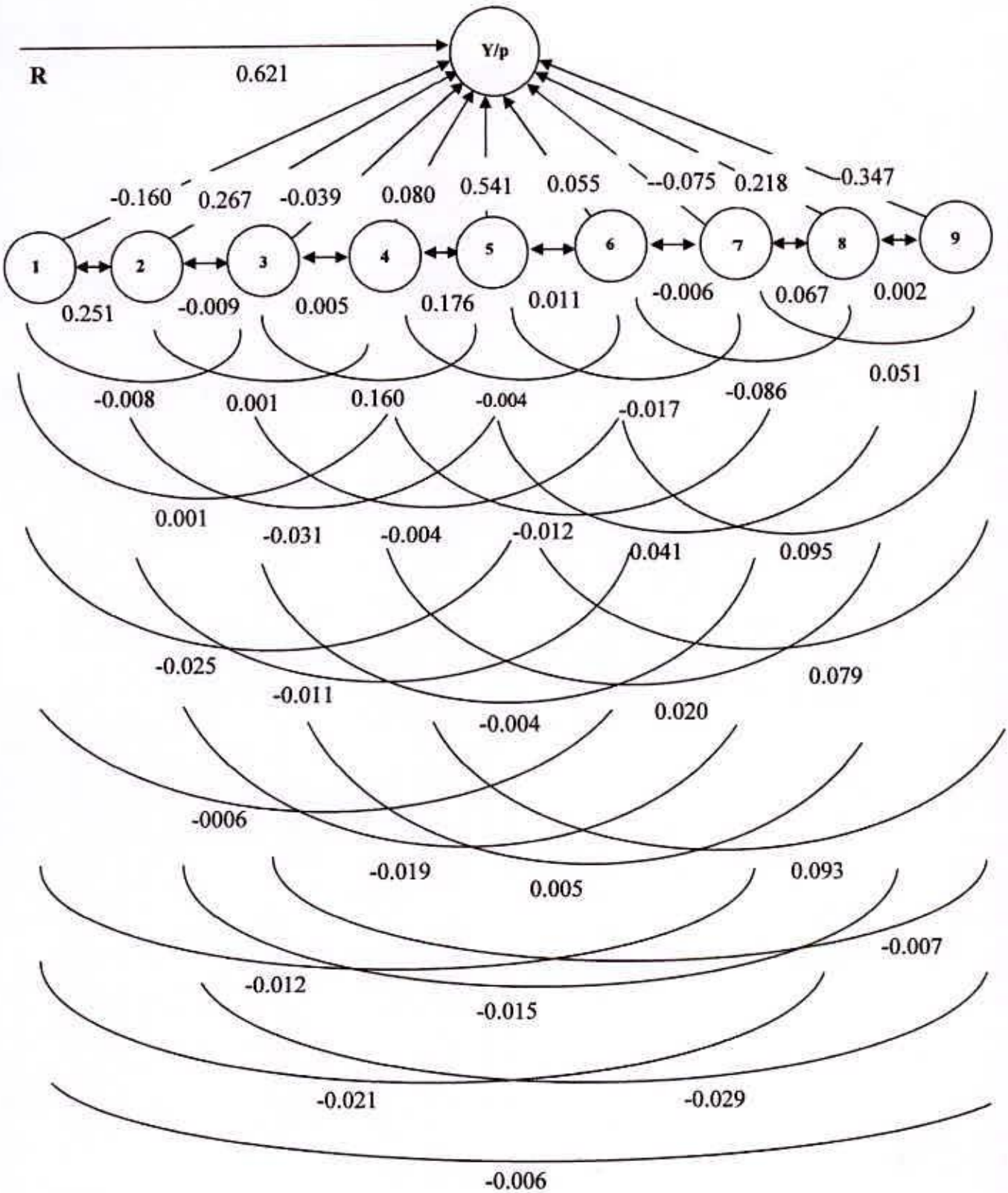


Fig. 1 Path diagram of yield contributing characters in different genotypes of Sesame.

1= Days to 50% flowering, 2= Days to 80% maturity, 3= Plant height, 4=No. of primary branches /plant, 5=No. capsules/ plant, 6= length of capsule, 7= width of capsule, 8= No. seeds /capsule, 9 = 1000-seeds weight, y/p= yield / plant, R= residual effect = 0.621

width of capsule (-0.017). The cumulative effects of these characters produced a highly significant positive genotypic correlation between number of capsule per plant and yield per plant (0.661). Thangavelu (1980) reported the greatest positive direct effect of the number of capsules per plant on seed yield. Tepora *et al.* (1983) also reported same result.

4.3.6 Length of capsule (cm)

Length of capsule showed the positive direct effect (0.055) on yield (Table 5). This character exhibited some positive indirect effect through number of capsule per plant (0.107) followed by 1000-seed weight (0.095), number of seeds per capsule (0.086), days to 50% flowering (0.019) and plant height (0.003). But the character also produced some negative indirect effect through days to 80% maturity (-0.051) and number of primary branches per plant (-0.007). These characters finally made highly significant positive correlation between length of capsule and yield per plant (0.301). Reedy (1986) found out that capsule length had considerable direct effects on seed yield.

4.3.7 Width of capsule (cm)

Width of capsule showed negatively direct effect (-0.075) on yield (Table 5). This character, however, showed positive indirect effect through days to 80% maturity (0.067), plant height (0.002), no. primary branches per plant (0.012), number of capsule per plant (0.125), length of capsule (0.004), number of seeds per capsule (0.067) and 1000-seed weight (0.051). The only negative indirect effect via days to 50% flowering (-0.026) was observed. Those were cumulatively produced highly significant positive genotypic correlation between width of capsule and yield per plant (0.228).

4.3.8 Number of seed per capsule (cm)

Number of seed per capsule showed a positive direct effect (0.218) on yield (Table 5). This character also showed positive indirect effect through days to 50% flowering (-0.015), number of primary branches per plant (0.007),

number of capsule per plant (0.103), length of capsule (0.022), and 1000-seed weight (0.002). The negative indirect effects were also observed via days to 80% maturity (-0.018), plant height (-0.001) and width of capsule (-0.023) which were contributed to result highly significant positive genotypic correlation with yield per plant (0.324).

4.3.9 1000-seed weight (g)

1000-seed weight showed a positive direct effect (0.347) on yield (Table 5). This character showed positive indirect effect through days to 50% flowering (0.003), plant height (0.001), number of primary branches per plant (0.022), number of capsule per plant (0.123), length of capsule (0.015), number of seeds per capsule (0.001). This character also showed negative indirect effect through days to 80% maturity (-0.022) and width of capsule (-0.011) and finally made highly significant positive genotypic correlation with yield per plant (0.478). Reedy (1986) found out that 1000 seed weight had considerable direct effects on seed yield.

4.4 MULTIVARIATE ANALYSIS

4.4.1 Principal component analysis (PCA)

Principal component analysis was carried out with 50 genotypes of sesame. First three Eigen values for three principal coordination axes of genotypes accounted for 70.83 % variation (Table 6). A two dimensional scattered diagram (Fig. 2) was developed on the basis of the principal component score; Z_1 and Z_2 score (Appendix V).

4.4.2 Principal coordinates analysis (PCO)

The results obtained from principal coordinate analysis showed that the highest inter genotypic distance was observed between genotypes G37 - G49 (1.678) followed by G32 - G37 (1.609) and the lowest distance was observed between genotypes G33 - G34 (0.195) followed by the distance (0.245) between

Table 6: Eigen values and percentage of variation for corresponding 10 component characters in 50 genotypes of Sesame

Character	Eigen value	% variation	Cumulative variation
Days to 50% flowering	7.051	41.47	41.47
Days to 80% Maturity	2.88	16.94	58.41
Plant height (cm)	2.112	12.42	70.83
Number of primary branches per plant	1.824	10.73	81.56
Number of capsule per plant	1.565	9.21	90.77
Length of capsule (cm)	0.762	4.48	95.25
Width of capsule (cm)	0.556	3.27	98.52
Number of seeds per capsule	0.129	0.76	99.28
1000 seeds weight (g)	0.099	0.58	99.86
Yield per plant (g)	0.023	0.14	100

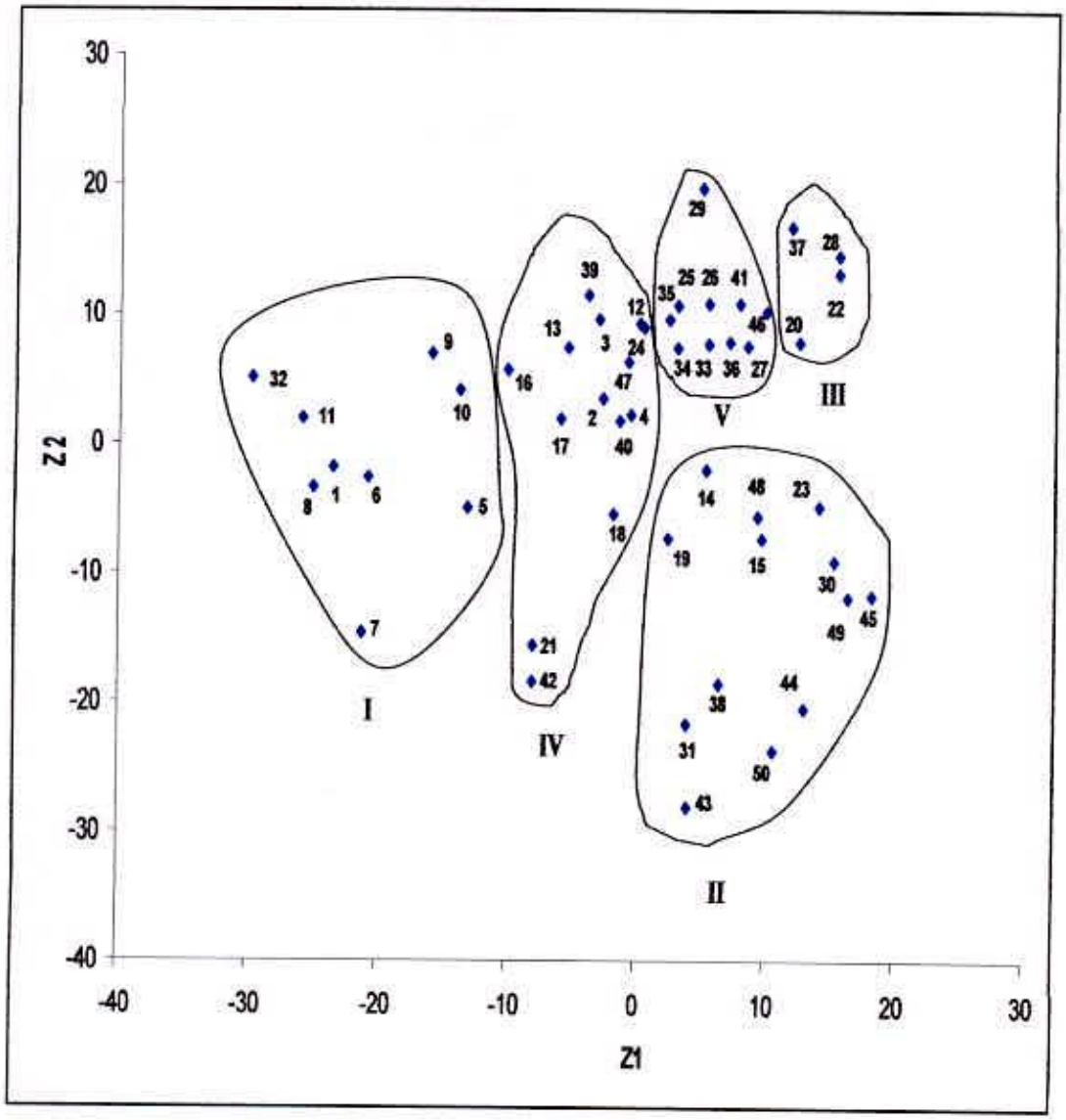


Fig. 2 Scattered distributions of 50 genotypes of Sesame based on their principal component scores superimposed with clusters

genotypes G12 - G35 (Table 7). The difference between the highest and the lowest inter genotypic distance indicated the moderate variability among the 50 genotypes of sesame. The highest intra-cluster distance was recorded in cluster IV (0.913) containing 14 genotypes (BD6962, BD6963, BD-6964, BD-6985, BD-6986, BD-6989, BD-6990, BD-6966, BD-6970, BD-6978, BD-7008, BD-7009, BD-7011, BD-7016). The lowest intra-cluster distance was observed in cluster V (0.469) having ten genotype viz. BD-6991, BD-6992, BD-7015, BD-6996, BD-7001, BD-7003, BD-7004, BD-7005, BD-7010 and BD-6993. It favored to decide that intra-group diversity was the highest in cluster IV and the lowest in cluster V. Cluster II having 13 genotypes viz. BD-6987, BD-6988, BD-6968, BD-6974, BD-6997, BD-7019, BD-7007, BD-7012, BD-7013, BD-7014, BD-7017, BD-7018, BD-6999 and had an intra-cluster distance 0.713. Cluster I having nine genotypes viz. BD-6961, BD-6960, BD-6979, BD-6980, BD-6981, BD-6982, BD-6983, BD-6984, BD-7000 and had an intra-cluster distance 0.638 and cluster III having only four genotypes viz. BD-6969, BD-6971, BD-6994, BD-7006 and had an intra-cluster distance 0.657 (Table 8 and 10).

4.4.3 Non-hierarchical clustering

The computations from covariance matrix gave non-hierarchical clustering among 50 genotypes of sesame and grouped them into five clusters. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. So the results obtained through PCA were confirmed by non-hierarchical clustering. Table 8 represents the clusters occupied by 50 genotypes of sesame. It explains that's cluster IV contained the highest number of genotypes 14, cluster II constitute by 13 genotypes, cluster I constitute by nine genotypes, cluster V constitute by ten genotypes and cluster III constitute by four genotypes. Cluster IV was composed of BD-6962, BD-6963, BD-6964, BD-6985, BD-6986, BD-6989, BD-6990, BD-6966, BD-6970, BD-6978, BD-7008, BD-7009, BD-7011, BD-7016.

Table 7. Ten highest and ten lowest inter genotypic distance among 50 Sesame genotypes

Sl No.	Genotypic combination	Distance
A. 10 highest genotypic distances		
1	G37 - G49	1.678
2	G32 - G37	1.609
3	G11 - G49	1.508
4	G8 - G22	1.489
5	G8 - G20	1.473
6	G7 - G22	1.447
7	G36 - G49	1.446
8	G32 - G44	1.422
9	G7 - G20	1.416
10	G32 - G46	1.411
B. 10 lowest genotypic distances		
1	G33 - G34	0.195
2	G12 - G35	0.245
3	G3 - G39	0.251
4	G7 - G8	0.258
5	G3 - G4	0.296
6	G12 -G41	0.296
7	G35 - G41	0.301
8	G6 - G16	0.316
9	G34 - G40	0.318
10	G25 - G36	0.326

The genotypes of cluster IV are collected from Plant Genetic Resource Centre, BARI, Gazipur. Cluster mean for 10 traits are presented in (Table 9). This cluster was unable to lead in respect of the highest cluster. Cluster II was formed by 13 genotypes viz. BD-6987, BD-6988, BD-6968, BD-6974, BD-6997, BD-7019, BD-7007, BD-7012, BD-7013, BD-7014, BD-7017, BD-7018, BD-6999 were collected from Plant Genetic Resource Centre, BARI, Gazipur. This cluster was able to lead in respect of the highest cluster mean value for two characters. Among 10 characters the highest cluster mean value was achieved for eight characters viz. plant height (68.08), number primary branches per plant (4.67), number of capsule per plant (52.47), length of capsule (1.9), width of capsule (0.64), number of seeds per capsule (50.95), 1000-seeds weight (10.8) and yield (24.75) which was belongs to the cluster I. Similarly, cluster II showed the highest cluster mean value for only two characters viz. days to 50% flowering (54.24) and days to 80% maturity (112.10). Genotypes BD-6969, BD-6971, BD-6994, BD-7006 established cluster III. These are collected from Plant Genetic Resources Centre, Bangladesh Agricultural Research Institute, Gazipur, Considering other clusters viz. cluster III, IV and V were produced no highest cluster mean value across the characters studied.

4.4.4 Canonical variate analysis

The highest inter-cluster distance was observed (Table 10 or Figure 3) between cluster I and cluster II (6.763) followed by between clusters I and cluster IV (6.693) and between cluster II and cluster IV (5.874). Similarly, the lowest inter-cluster distance was observed between the cluster III and cluster IV (1.451). Moderate or intermediate distance was found between cluster I and cluster III (4.918). On the other, the highest intra-cluster distance was found in cluster IV (0.913) followed by cluster II (0.713). The lowest intra-cluster distance was also observed in cluster V (0.469). The inter cluster distances were found much higher than the intra cluster distances suggesting wider genetic diversity existed among the genotypes of different groups.

Table 8. Distribution of 50 Sesame genotypes in five clusters

Cluster	No. of genotypes	Designation
I	9	BD-6961, BD-6960, BD-6979, BD-6980, BD-6981, BD-6982, BD-6983, BD-6984, BD-7000,
II	13	BD-6987, BD-6988, BD-6968, BD-6974, BD-6997, BD-7019, BD-7007, BD-7012, BD-7013, BD-7014, BD-7017, BD-7018, BD-6999
III	4	BD-6969, BD-6971, BD-6994, BD-7006
IV	14	BD-6962, BD-6963, BD-6964, BD-6985, BD-6986, BD-6989, BD-6990, BD-6966, BD-6970, BD-6978, BD-7008, BD-7009, BD-7011, BD-7016
V	10	BD-6991, BD-6992, BD-7015, BD-6996, BD-7001, BD-7003, BD-7004, BD-7005, BD-7010, BD-6993

Table 9. Cluster mean for 10 characters of 50 Sesame genotypes

Character	Cluster				
	I	II	III	IV	V
Days to 50% flowering	40.11	54.24	35.83	39.63	36.91
Days to 80% maturity	100.33	112.1	95.75	99.52	97
Plant height (cm)	68.08	64.76	56.05	61.55	62.99
No. of primary branches/ plant	4.67	4.21	3.66	4.18	4.13
Number of capsule per plant	52.47	34.02	20.38	34.02	35.04
Length of capsule (cm)	1.90	1.72	1.76	1.68	1.80
Width of capsule (cm)	0.64	0.63	0.54	0.60	0.60
Number of seeds per capsule	50.95	40.67	49.63	26.52	42.55
1000 seeds weight (g)	10.8	9.9	8.82	9.68	9.19
Yield per plant (g)	24.75	14.65	12.08	15.37	14.4

Table 10. Average intra (bold) and inter cluster distances (D^2) for 50 Sesame genotypes

Cluster	I	II	III	IV	V
I	**0.638**				
II	6.763	**0.713**			
III	4.918	3.758	**0.657**		
IV	6.693	5.874	2.58	**0.913**	
V	4.149	5.086	1.451	2.561	**0.469**

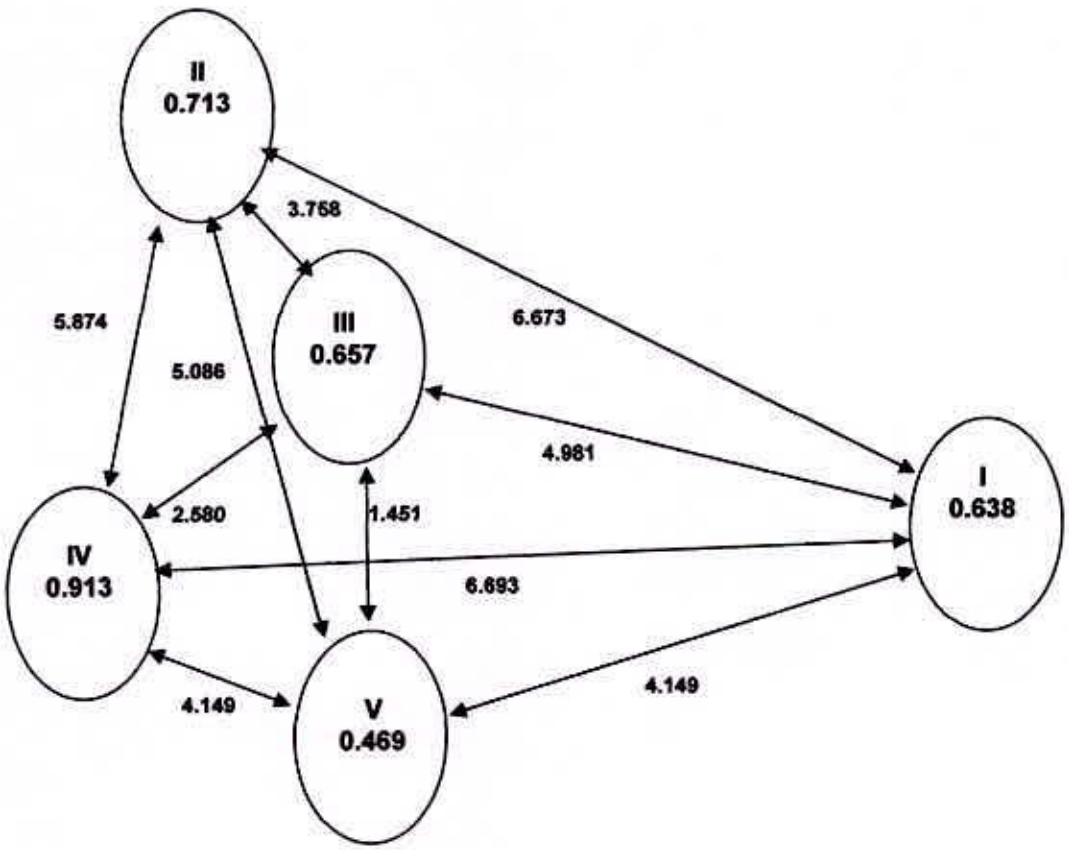


Fig. 3 Diagram showing intra and inter-cluster distances of 50 genotypes of Sesame

Results of different multivariate analysis were superimposed in Figure 2 from which it may be concluded from the above results that different multivariate techniques supplemented and confirmed one another.

A two-dimensional scatter diagram was constructed using component I as X – axis and component II as Y- axis, reflecting in the relative position. The genotypes were apparently distributed into five clusters. It was also revealed that the genotypes of cluster IV were more diverse from the genotypes of cluster V. It is assumed that maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. However, for a practical plant breeder, the objective is not only high heterosis but also to achieve high level production. In the present study the maximum distance existence between clusters I & II. But considering the yield and duration crosses involving cluster I and II may exhibit high heterosis for yield. Main and Bahl (1989) reported that the parents separated by D^2 Values of moderate magnitude generally showed higher heterosis.

4.4.5 Contribution of characters towards divergence of the genotypes

The values of Vector I and Vector II are presented in Table 11. Vector I obtained from PCA expressed that days to 50% flowering (0.3237), no. of seeds per capsules (0.0258) and 1000-seed weight (0.1731) were major characters that contribute to the genetic divergence. It was the reflection of first axis of differentiation. In vector II width of capsule (6.7709) showed its important role toward genetic divergence. Negative values in both vectors days to 80% maturity, plant height, number primary branches per plant, number of capsule per plant, length of capsule had lower contribution towards the divergence.

Table 11. Latent vectors for 10 principal component characters of 50 sesame genotypes

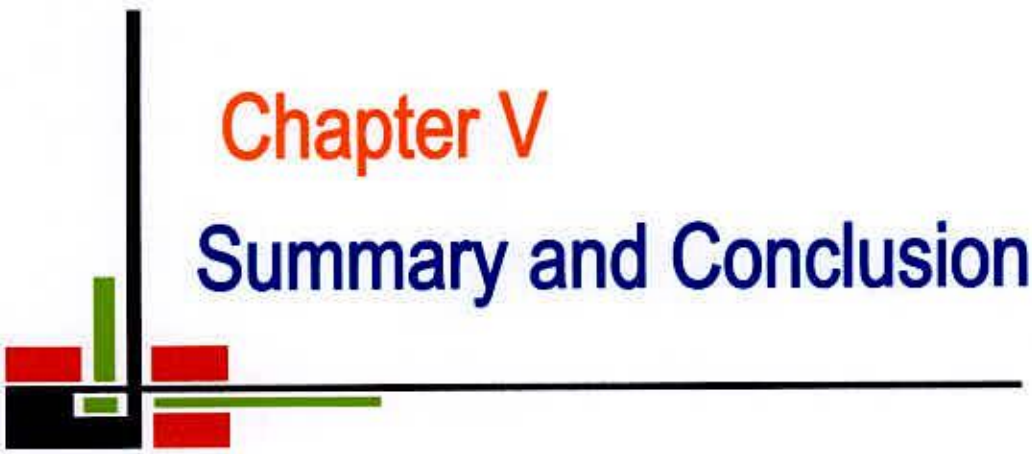
Character	Vector I	Vector II
Days to 50% flowering	0.3237	-0.0446
Days to 80% maturity	-0.6990	-0.0977
Plant height (cm)	-0.0539	-0.0244
Number of primary branches per plant	-0.0664	-0.1046
Number of capsule per plant	-0.0349	-0.0769
Length of capsule (cm)	-3.4915	-0.2753
Width of capsule (cm)	-2.3776	6.7709
Number of seeds per capsule	0.0258	-0.175
1000 seeds weight (g)	0.1731	-0.201
Yield per plant (g)	-0.1659	-0.0175

4.4.6 Selection of genotypes as parent for hybridization programme

Among the inter cluster distance, distance between I and II (6.763) were the highest and other clusters were more or less intermediate distance. Inter mediate diverse parents have the more chance to contribute heterosis in the subsequent generations. To select cluster to obtain more heterotic genotype four pairs of clusters to be considered for this purpose, they are I & II, I & III, I & IV and II & V. Cluster I had the highest cluster mean for plant height (68.08), number primary branches per plant (4.67), number of capsule per plant (52.47), length of capsule (1.9), width of capsule (0.64), number of seeds per capsule (50.95), 1000-seeds weight (10.8) and yield / plant (24.75). Cluster I comprised with the genotypes BD-6961, BD-6960, BD-6979, BD-6980, BD-6981, BD-6982, BD-6983, BD-6984, BD-7000. Similarly, cluster II showed the highest cluster mean value for only two characters viz. days to 50% flowering (54.24) and days to 80% maturity (112.10). The cluster II comprised with the genotypes BD-6987, BD-6988, BD-6968, BD-6974, BD-6997, BD-7019, BD-7007, BD-7012, BD-7013, BD-7014, BD-7017, BD-7018, BD-6999. Hybridization between the genotypes of cluster I and cluster II will manifest maximum heterosis and create wide genetic variability.

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 G5, G9, G32 from cluster I, G49 from cluster II and G29 from cluster V would be suitable for highest yield per plant for future hybridization programme.

It assumed that highest heterosis would be manifested 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 G5 & G29, G5 & G49, G9 & G49, G9 & G29, G32 & G49, G32 & G29, G29 & G49 might be suitable choice for future hybridization programme.



Chapter V

Summary and Conclusion

CHAPTER V

SUMMARY AND CONCLUSION

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

The field experiment was laid out in Randomized Complete Block Design (RCBD) with three (3) replications. Data on different characters were recorded and analyzed statistically. The analysis of variance of all the traits was computed and significant differences were found among the accessions in respect of different characters studied. The maximum value in respect of days to 50% flowering (61days) was observed in G43 and minimum days to 50% flowering (32 days) were recorded in G29. Genotype number G43 the maximum value (119.67days) to 80% maturity and lowest days to 80% maturity (92days) was recorded in G29. In respect of plant height genotype G5 recorded the highest value (78.18 cm) and genotype G37 conducted the lowest value (47.57 days). Genotype no. G11 is the highest number of primary branch (5.47) and genotype no. G50 is the lowest numbers of primary branch (2.37) were counted. In case of no. of capsules per plant the highest value (65.03) was recorded in G32 and the lowest value was (18.73) recorded in G46. In respect of capsule length, longest capsule (2.14 cm) was observed in G19 and the genotype no. G28 had the smallest length (1.45 cm). In case of width of capsule the highest value (.79 cm) was observed in G42 and the lowest value (.44 cm) was observed in G31. Genotype no. G9 is the highest number of seeds per capsule (63.10) and genotype no. G49 is the lowest number of seeds per capsule (19.03). In case of 1000 seeds weight, the highest value (17.08 g) was

observed in G6 and the lowest value (6.12 g) was observed in G11. The highest average yield per plant (35.47 g) was in G49 and the lowest yield per plant (10.08 g) was recorded in G37. The phenotypic variance was higher than the corresponding genotypic variance in all the characters expect first days to 80% maturity indicates greater influence of environment on the expression of these characters. The highest estimated heritability among ten yield contributing characters 99.22%, 98.86%, 97.54% and 94.61% was in number of seeds per capsule, number of capsules per plant, yield per plant and length of capsule respectively. The lowest heritability was 91.18% in first day to 50% flowering. The maximum genetic advance was observed in respect of no. of capsules per plant (28.65) and followed by maximum value was 25.45 in respect of genetic advance for no. of seeds per capsule among ten characters of sesame genotypes. The maximum genetic advance in percent of mean (GAMP) was obtained for yield per plant (134.36%) and the lowest was for day to 80% maturity (19.50%).

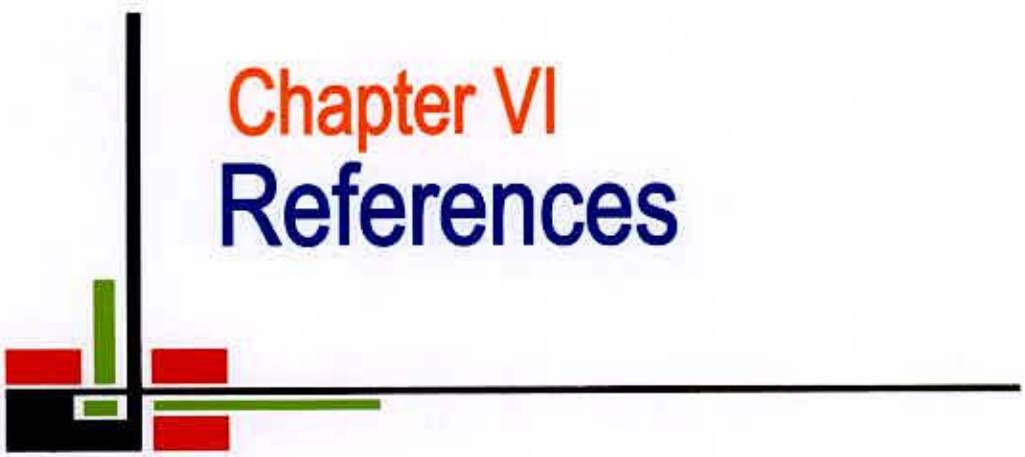
Multivariate analysis was carried out through principle component analysis (PCA), principle coordinate analysis (PCO), cluster analysis and canonical vector analysis (CVA) using GENSTAT 513 software program. The first three principle characters with Eigen values accounted for 70.83% variation toward divergence. As per PCA, D^2 and cluster analysis using the genotypes were grouped into five clusters. Cluster I, II, III, IV, V comprised 9, 13, 4, 14 & 10 respectively. The maximum cluster distance was observed between I & II (6.763) followed by the distance between clusters I & IV (6.693), II & IV (5.874), II & V (5.086). The lowest inter-cluster distance was observed between cluster III & IV (1.451) followed by IV & V (2.561).

The highest intra-cluster distance was identified in cluster IV (.913) and the lowest intra-cluster distance was observed in cluster V. Genotypes included in cluster I were suitable for yield per plant (24.75gm), number of seeds per capsule (50.95), number of capsule per plant (52.47), Plant height (68.08 cm),

days to 80% maturity (100.33), cluster II, had the highest mean for first day to 50% flowering.

Findings of the present study indicated significant variation among the genotypes for all the characters studied. Considering diversity pattern and other field performances, the genotypes G5, G9 G32 from cluster I, genotype G49 from cluster II and genotype G29 from cluster V may be considered as suitable parents for efficient hybridization programme. The inter genotypic crosses between G5 & G29, G5 & G49, G9 & G29 G9 & G49, G32 & G29, G32 & G49, G29 & G49 might be suitable choice for future hybridization programme. The result of the present study revealed that a wide variability exists among the collected sesame genotypes. In addition, there was also genotypic variability of different yield contributing characters with yield of sesame. From the findings of the present study, the following conclusions could be drawn:

i. Wide range of genetic diversity existed among the sesame genotypes. That variability could be used for future breeding programme of sesame in Bangladesh.
ii. Selection procedure would be applied for desired characters such as days to 50% flowering, day to 80% maturity and no. of capsule per plant, no. of seeds per plant, length and width of capsule 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 no. of capsule per plant, no. of seeds per plant, yield per plant .
iv. Further collection of sesame germplasm would be continued for getting more variability and desired traits in sesame.



Chapter VI
References

CHAPTER VI

REFERENCES

Alvaran, P. J. (1993). Selection indices for high yield in sesame (*Sesamum indicum* L.). MS Dissertation. Central Luzon State University, Muoz,Nueva Ecija, Phillipines. P.100.

Amin, D. and Kothari, I. L. (1989). Seed composition of some new varieties of sesame. *J. Oil Technologist's Assoc.* India. **21** (1): 15-16.

Anitha, N. and Dorairaj, M. S. (1990). Genetic divergence and hybrid performance in sesame. *Journal Oilseeds Res.* 7(1): 63-71.

Anonymous. (1981). Descriptiors for sesame. AGP:IBPGR/80/71. IBPGR Secretariat, Rome, Italy. P.19.

Ashri, A. (1998). Sesame Breeding. **In**: Janick, J. (Ed), Plant Breeding Reviews. John Wiley and Sons, Inc. P.179-228.

Balasurbramanian, T. N. and Palaniappan, S. P.(1999). Sesame. **In**: Rathore, P.S. (Ed.), Techniques and management of field crop production. Agrobios, Jodhpur, India. P.178-196.

BBS. (2001). Yearbook of agricultural statistics of Bangladesh, (1999). Bangladesh Bureau of Statistics. Ministry of planning, Govt. of the people's republic of Bangladesh, Dhaka. P.31.

Beech, D. F. (1981). Sesame an agronomic approach to yield improvement. **In**: Ashri, A. (Ed.), Sesame: status and improvement. FAO plant protection paper. No. 29: P.121-127.

Begum, H. (1997). Biometrical studied on sesame (*Sesamum indicum* L.) under rice-based cropping system. Ph. D. Dissertatiopn. Faculty of Institute of Graduate Studies, Central Luzon State University, Munoz, Nueva Ecija, Phillipines. P.88.

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

Bisht, I. S., Mahajan, R.K., Loknathn, T. R. and Agrawal, R. C. (1998). Diversity ion Indian sesame collection and stratification of germplasm accessions in different diversity groups. Genetic resources and crop evolution. **45**(4): 325-335.

Burton, C. W. (1952). Quantitative inheritance in pearl millet, *Pennisetum glaucum. Agron. J.*, **43**:409-17.

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

Chandra, S. (1977). Comparison of Mahalanobis's method and meterrglyph technique in the study of genetic divergence in *Linum usitatissimum* L. germplasm collection. *Euphytica*. 26: 141-148.

Chandramony, D. and Nayar, N. K. (1985). Genetic variability in *sesamum*. *Indian J. Agric. Sci.* **55** (12):769-70.

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

Desai, N. D. (1981). Integrating breeding objectives and agricultural practices for Indian conditions. **In**: Sesame: status and improvement. Ashri, A. (Ed.). FAO plant production and protection paper. 29: P.118-119.

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

Dikshit, U. N. (1992). Genetic analysis in sesamum. **In**: Genetic divergence, heterosis and nature of gene action. Ph. D. Dissertation. Orissa Unversity of Agriculture and Technology, Bhubaneswar, India. P.31-50

Dixit, R. K. (1975). Path analysis for some quantitative traits in sesame (*Sesamum orientate* L.) Plant Science 7:9-12.

Edris, K. M., Islam, A. T. M. T., Chowddhury, M. S. and Haque, A. K. M. M. (1979). Detailed soil Survey of Bangladesh Agricultural University Farm, Mymensingh, Dept. Soil Survey, Govt. People's Republic of Bangladesh. P.118.

El-Hifny, M.Z., Mahdy, E. E., Bakheit, B. R., Guirguis, N. R. and El-Shimy. A. (1988). Evaluation of some cultivars and promising strains of sesame (*Sesamum indicum* L.). Assiut *J. Agril Sci.* **19**(4):35-50.

Falconer, D. S. (1977). Introduction to quantitative genetics. Longman group limited. P. 365.

FAO. (1998). FAO production Year Book, Food and Agricultural Organization of United Nations. Rome, Italy.52:108.

FAO. (2002). Production Year Book, Food and Agricultural Organization of the united Nations, Rome, Italy. 42:190-193.

Ganesh, S. K. and Thangavelu, S. (1995). Genetic divergence in sesame (*Sesamum indicum*). *Madraj Aric. J.*, **82**(4):263-265.

Govinda, R. (1982). Genetic variability, correlation and divergence in *Sesamum indicum* L.

Hanson, C. H., Robinson, H. F. and Comstock, R. E. (1956). Biometrical studies of yield in Segregation population of Korean Lespedza. *Agron J.*, 48: 268 -272.

Jalal, M. and Biswa, N. M. (1994). Variability of some quantitative characters in sesame (*Sesamum indicum* L.). *Bangladesh J. Agri.* 19: 17-22.

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.

Jones, A. (1986). Sweet potato heritability estimates and their use in plant breeding. *Hort. Science* 21: 14-17.

Kadir, M., Biswas, B. K., Podder, P., Alam, M. S. and Adhikary, S. K. (1996). Genetic parameters, character association and path analysis in sesame. *Bangladesh J. Agril. Res.* **21** (1): 37-43.

Khanna, K. R. and Chaudhary, R. C. (1974). The nature of gene action and combining ability for some vegetative characters in tomato. *Euphytica.* 23: 159-165.

Khidir, O. M. and Gizouli O. H. D, L. (1974). Estimates of genetic and environmental variability in sesame. Experimental Agriculture 10:105-12.

Kobayashi, T. (1981). The type and classification of cultivated sesame based on genetic characters. **In**: Ashri, A. (Ed.). FAO plant production and protection paper. No. 29: 86-88.

Kumari, A. N. and Balasubramanian, M. (1993). Genetic variability in soybean. *Madras Agric. J.* **80**(8): 429-433.

Lee, J. I., Lee, B. H., Seong, N. S., Kang, C. H., Lee, S. T. and Park, R. K. (1989). A new sesame varity for second-cropping "Jinjuggae". Res Reports of Rural Development Administration, Upland and Industtrial Crops. **31**(3):29-33.

Liu, J. R., Zheng, Y. Z. and Xu, R. Q. (1992). Analysis of the nutrient quality of seed and screening for prominent germplasm in sesame. Oil crops of China.1:24-26.

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

Mahapatra, K. C, Biswal, A. K. and Satpathy, D. (1993). Relationship of F_2 segegation pattern with genetic divergence of parenys in sesame. *Indian J. Genet. Pl. Breed.* **53** (4): 372-380.

Main, M. A. K. and Bahl, P. N. (1989). Genetic divergence and Hybrid performance in chickpea. *Indian J. Genet.* **49** (1): 119-124.

Manivannan, A. and Nadarajan, N. (1996). Genetic divergence in Sesame. *Madras Agril J.* **83** (12): 789-790.

Main, M. A. K. and Yadav, L. N. (1996). The nature of genetic divergence in sesame. *Indian J. Genet.* **26** (1): 188-198.

Miller, P. J., Williams, J. C., Robinson, H. F. and Comstock, R. E. (1958). Estimation of genotypic and environmental variance and co-variance in upland cotton and their implications in selection . *Agron. J.* **50** (2): 126 – 131.

Mponda, O. K. K., Morse, S., Gibbon, S., Arthur, A. E. (1997). Genetic studies on seedling vigour in sesame. Ann. Applied Biol. **131** (1):161-170.

Naidu, N. V. and Satanarayana, A. (1991). Studies on the genetic divergence over environments in Mungbeab *Vigna radiata* (L) Wilczek. *Indian J. Genet.* **51**(4): 454-460.

Nair, K. R. and Mukharjee, H. K. (1960). Classification of natural and plantation teak (*Tetona grandis*) grown at different location of India and Burma with respect to its mechanical and physiological properties. Sankhya.28:1-20.

Nandpuri, B.S., Singh, S. And Lal, T. (1973). Studies on the genetic variability and correlation of some economic characters in tomato. *J. Res.* 10: 316-21.of Bangladesh, Dhaka. P.131.

Paramasivam, K. (1980). Genetic analysis of yield and yield components in F_2 and F_3 generations of sesame (*Sesamum indicum* L.). Unpublished M. S. (Ag.) Thesis. Tamil Nadu Agricultural University. P.40-51.

Paramasivam, K. and Prasad, M. N. (1981). Studies on variability and heritability in segregating populations of sesame (*Sesamum indicum* L.) crosses. *Madras Agric. J.* **68**(1):1-6.

Pathak, H. C. and Dixit, S. K. (1986). Genetic variability, correlation and path coefficient analysis for components of seed yield in single stemmed sesame (*Sesamum indicum* L.). In Tropical oilseeds Abstracts. **12**(10):101.

Pathak, H. C. and Dixit, S. K . (1992). Genetic variability and inter-relations studies in black seeded sesame. *Madras Agric. J.* **79**(1): 94-100.

Patil, R. R. (1993). Multivariatee analysis in sesame (*Sesamum indicum* L.) M.Sc. thesis. Dept. of Gn. Pl. Breed. Univ. Agril. Sci. Bengalore, India. P.4-82.

Patil, R. R. and Sheriff, R. A. (1994). Genetic divergence in (*Sesamum indicum* L.). Mysore *J. Agril. Sci.*. **28**(2):106-110.

Raheja, R. K., Ahuja, K. L., Batta, S. K., Labana, K. S. and Chaurasia, B. D. (1989). Evaluation if some promising Indian genotypes of sesame for oil content and component fatty acids. Annals Biol. Ludhiana, India. 5(1):33-38.

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

Reddy, O. U. K. and Stephen, D. (1987). Variability character association and genetic divergence of sesame yield components in *Sesamum indicum* L.M.S. (Ag.) Thesis. Tamil Nadu Agricultural University, Caimbatore.

Reddy, O. U. K. (1986). Studies on Variability character association and genetic divergence in *Sesamum indicum* L. Unpublished M.S. (Ag.) Thesis. Tamil Nadu Agricultural University, Caimbatore. P.94.

Salas, I. C. M. (1995). Characters associated with high yield in sesame (*Sesamum indicum* L.). Unpublished M. S. (Crop Science) Thesis. Central Luzon State University, Munoz, Nueva Ecija. P.95.

Shadakshari, Y. G., Virupakshappa. K., Shivashankar, G. (1995). Genetic variability studies in the germplasm collections of sesame (*Sesamum indicum* L.). *Mysore J. Agril. Sci.* **29**(2): 133-137.

Singh, P. (1983). Studies on genetic variability and diversity of rice. *Madras Agric. J.*, **70** (7): 436-440.

Shukla, G. P. (1983). Path coefficent analysis in sesame. *Indian J. Agri. Science* **53**(6): 407-408.

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

Swain, D. and Dikshit, U. N. (1997). Genetic divergence in rabi sesame (*Sesamum indicum* L.) *Indian J. Genet.* **53**(3):296-300.

Tashiro, T, Fukuda, Y. and Osawa, T. (1991). Oil contents of seeds and minor components in the oil of sesame, (*Sesamum indicum* L.), as affected by capsule position. *Japanese J. Crop Sci.* **60**(1):116-121.

Tepora, N. M. (1993). Progress of sesame research in the Philippines. Sesame and Safflower newletter No. 8. Published by institute of sustainable agriculture (IAS), CSIC apartado 4084 Cordoba, Spain. P.22-29.

Tepora, N. M., Delacruz, Q. D. and Alvaran, P. J. (1983). Selection for high yield in sesame Unpublished by 1982-1983 special projects Technical Report. Clsu. P.6.

Thangavelu, S. and Rajasekaran, S. (1982). Studies on genetic variability in sesame (*Sesamum indicum* L.). *Madras Agric. J.* **69**:780-783.

Thangavelu, S. and Rajasekaran, S. (1983). Correlation and path coefficient analysis in *sesamum*. *Madras Agric. J.* **70**(2):109-113.

Thangavelu, S. and Rajasekaran, S. (1984). Crop improvement strategies in sesame in Tamil Nadu (India). In Riley, K. W. (ED.). Proc. Of workshop on oilcrops. Cairo, Egypt. IDRC manuscript report 93c. P.115-122.

Thangavelu, S. (1980). Studies in variability, D^2 statistics and correlation in sesame (*Sesamum indicum* L.). Unpublished M.S. (Ag.) Thesis. Tamil Nadu Agricultural University, Madras. P.38-50.

Tomooka, N. (1991). Genetic diversity and landrace differentiation of mungbean, (*Vigna radiata* L.) Wilczekand evaluation of its wild relatives (The subgenus Ceratotropics) as breeding materials. Tech. Bull. Trop. Res. Center, Japan No. 28. Ministry of Agr. Forestry and Fisheries, Japan.1. P.20-22

Uddin, M. J. and Chowdhury, M. A. Z. (1994). Multivariate analysis in sesame (*Sesamum indicum* L.). *Bangladesh J. Plant. Breed. Genet.* 7(1): 37-41.

Uddin, M. S. and Mitra, B. N. (1994). Variability of some quantitative characters in sesame (*Sesamum indicum* L.). *Bangladesh J. AGRI.* **19**:17-22.

Uddin, M.J., Islam, M.S., Khaleque, M.A., Khatun, M.F. and Sheikh, M. H. R. (1994). Multivariate analysis in sesame (*Sesamum indicum* L.). Ann. Bangladeshh Agric. **8**(1): 19-23.

UNDP. (1988). Land Resources Appraisal of Bangladesh for Agricultural Development. Report 2: Agro-ecological Regions of Bangladesh, FAO, Rome. P. 212-577.

Uzo, J. O. and Ojiake, G. U. (1981). Breeding and selection method for sesame on the basis of major Nigerian sesame strains, F_1, hybrids and segregating generations. **In**: Ashri, A. (Ed.). FAO plant production and protection paper. No. 29: 108-112.

Vadhani, H. K., Kukadia, M. U. and Parmar, V. L. (1992). Correlation and path analysis in *Sesamum. GAU Rrs. J.* **18**(1): 31-34.

VanRheenen, H. A. (1981a). The desirability of long versus short capsules in sesame (*Sesamum indicum* L.).**In**: Ashri, A. (Ed.). FAO plant production and protection paper. No. 29: 103-109.

VanRheenen, H. A. (1981b). The desirability of multi-versus four-locular capsules in sesame (*Sesamum indicum* L.). **In**: Ashri, A. (Ed.). FAO plant production and protection paper. No. 29: 108-112.

VanRheenen, H. A. (1981d). Breeding objectives and assessment of principal commercial strains of sesame. **In**: Ashri, A. (Ed.). FAO plant production and protection paper. No. 29: 113-114.

WenXing, W., Wei, W. X., Zhang, H., Lu, F. Y. and Wei, S. L. (1994). Principal components analysis and genetic distance estimation and their application in sesame breeding programme. Accta Agricultural Boreali Sinica. 9(3): 29-33.

Wright, S. (1921). Correlation and causation. *Jouranl of Agricultural Research* **20**: 557-85.

Wright, S. (1935). The analysis of variance and correlation between relatives with respect to deviation from an optimum. Genetics, princeton 30: 243-56.

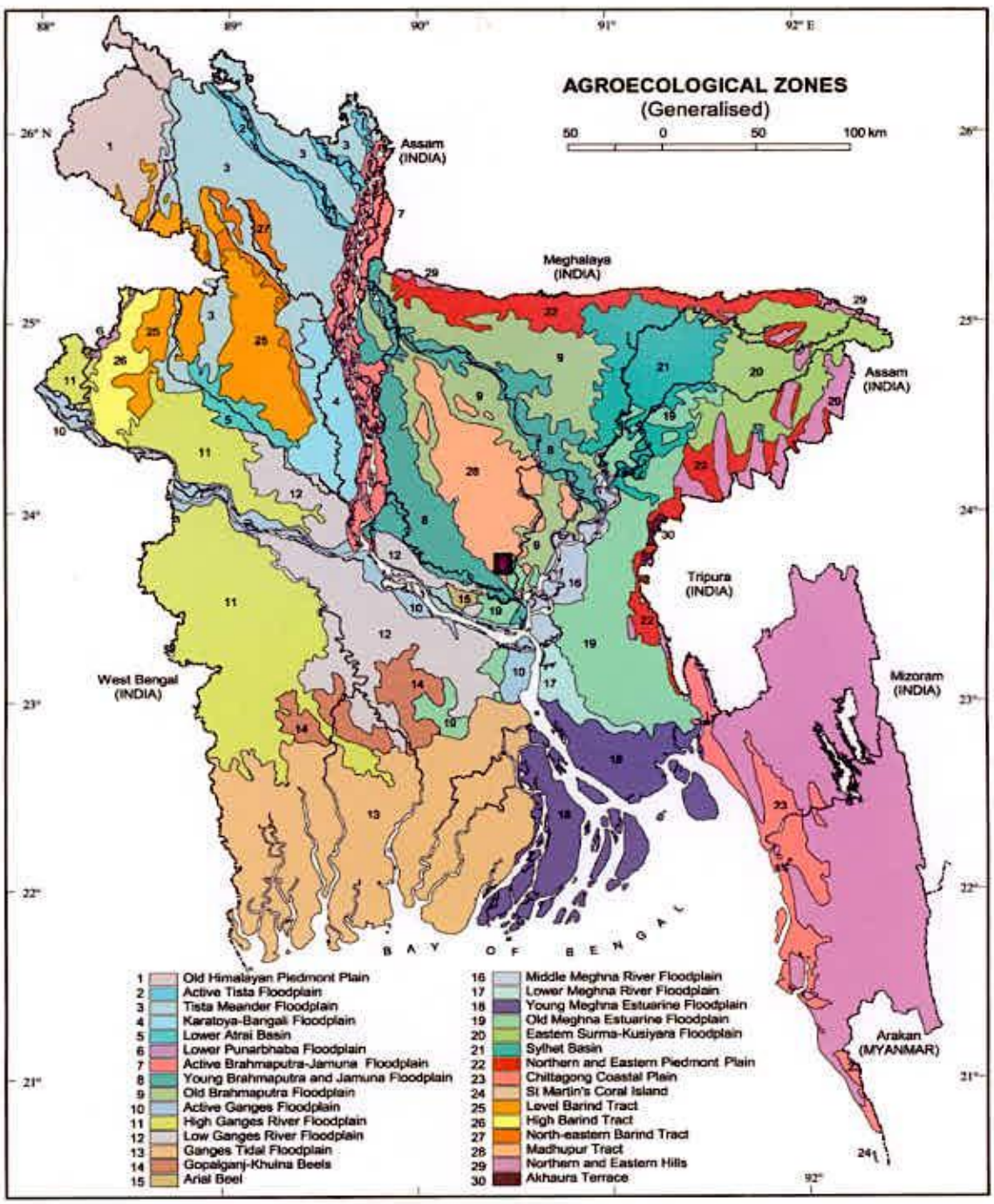
Yadava, T. P., Prakash, K. and Yadav, A. K. (1980). Asociation of yield and its components in *sesamum. Indian J.Agric. Sci.* **50**(4): 317-319.

Yermanos, D. M. (1980). Sesame. **In**: Fehr, W.R. and Hadley, H. H. (Eds.), Hybridization of crop plants. American Soc. Agron. Crop Sci. Soc. America, Madison. P. 549-563.


Appendices

APPENDICES

Appendix I. Map showing the experimental site under the study



Appendix II. Monthly average record of air temperature, rainfall, relative humidity, soil temperature and Sunshine of the experimental site during the period from October 2008 to September 2009

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximm	Minimum			
October, 2008	34.8	22.8	77	227	5.8
November, 2008	32.3	21.3	69	0	5.6
December, 2008	29.0	17.7	79	0	3.9
January, 2009	28.1	14.1	72	1	5.7
February, 2009	33.9	16.2	55	1	8.7
March, 2009	34.6	17.5	67	45	7.3
April, 2009	35.8	20.3	65	88	8.3
May, 2009	36.7	20.3	70	205	7.7
June, 2009	35.4	22.5	80	577	4.2
July, 2008	34.0	24.6	83	563	3.1
August, 2008	36.0	23.6	81	319	4.0
September, 2008	34.8	24.4	81	279	4.4

Source: Bangladesh Meteorological Department (Climate & Weather Division) Agargoan, Dhaka - 1212

Appendix III. Physical characteristics and chemical composition of soil of the experimental plot

Soil characteristics	Analytical results
Agrological Zone	Madhupur Tract
P^H	6.00 – 6.63
Organic matter	0.84
Total N (%)	0.46
Available phosphorous	21 ppm
Exchangeable K	0.41 meq / 100 g soil

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

Appendix IV: Mean performance of different parameters of 50 sesame genotypes

Parameters	Minimum	Mean	Maximum
Days to 50% flowering	61	42.47	32
Days to 80% maturity	119.67	102.18	92
Plant height (cm)	78.18	63.59	47.57
Number of primary branches per plant	5.47	4.22	2.37
Number of capsule per plant	65.03	36.54	18.73
Length of capsules (cm)	2.14	1.77	1.45
Width of the capsule (cm)	0.79	0.61	0.44
Number of seeds per capsule	63.10	41.22	19.03
1000 seed weight (g)	17.08	9.74	6.12
Yield per plant (g)	35.17	16.32	10.08

Appendix V. Principal component score 50 genotypes of Sesame

SL. No.	Genotype	Z1	Z2
1	BD-6961	-23.522	-1.947
2	BD-6962	-2.75	3.491
3	BD-6963	-3.032	9.547
4	BD-6964	-0.558	2.17
5	BD-6960	-13.179	-4.926
6	BD-6979	-20.782	-2.646
7	BD-6980	-21.293	-14.627
8	BD-6981	-25.016	-3.489
9	BD-6982	-15.937	6.854
10	BD-6983	-13.747	4.062
11	BD-6984	-25.884	1.797
12	BD-6985	0.432	8.947
13	BD-6986	-5.465	7.348
14	BD-6987	5.264	-2.045
15	BD-6988	9.65	-7.387
16	BD-6989	-10.039	5.563
17	BD-6990	-5.956	1.907
18	BD-6966	-1.82	-5.465
19	BD-6968	2.35	-7.388
20	BD-6969	12.453	7.843
21	BD-6970	-8.074	-15.56
22	BD-6971	15.513	13.155
23	BD-6974	14.053	-4.789
24	BD-6978	0.052	9.187
25	BD-6991	3.068	10.587
26	BD-6992	5.433	10.816
27	BD-6993	8.477	7.499
28	BD-6994	15.465	14.501
29	BD-6996	4.878	19.708
30	BD-6997	15.26	-8.994
31	BD-6999	3.855	-21.67
32	BD-7000	-29.853	4.928
33	BD-7001	5.386	7.72
34	BD-7003	2.995	7.319
35	BD-7004	2.404	9.48
36	BD-7005	7.018	7.84
37	BD-7006	11.835	16.713
38	BD-7007	6.346	-18.516
39	BD-7008	-3.878	11.435
40	BD-7009	-1.44	1.696
41	BD-7010	7.739	10.751
42	BD-7011	-8.088	-18.366
43	BD-7012	3.986	-28.087
44	BD-7013	12.948	-20.522
45	BD-7014	18.138	-11.786
46	BD-7015	9.803	10.22
47	BD-7016	-0.78	6.314
48	BD-7017	9.279	-5.568
49	BD-7018	16.381	-11.815
50	BD-7019	10.634	-23.811