INTER-GENOTYPIC VARIABILITY AND GENETIC DIVERSITY ANALYSIS IN F_4 LINES OF *BRASSICA RAPA*

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REGISTRATION NO. 07-02613

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, 2008

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CERTIFICATE

This is to certify that thesis entitled, **"INTER-GENOTYPIC VARIABILITY AND GENETIC DIVERSITY ANALYSIS IN F_4 LINES OF BRASSICA RAPA"** submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING,** embodies the result of a piece of bona fide research work carried out by **NASRIN JAHAN** Registration No. **07-02613** 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 2008
Place: Dhaka, Bangladesh

(Dr. Md. Shahidur Rashid Bhuiyan)
Supervisor

Dedicated to
My
Beloved Parents

LIST OF ABBREVIATED TERMS

FULL NAME	ABBREVIATION
Agro-Ecological Zone	AEZ
And others	*et. al.*
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Centimeter	cm
Co-efficient of Variation	CV
Days After Sowing	DAS
Degree Celsius	^{o}C
Degrees of freedom	d.f
Etcetera	etc.
Food and Agriculture Organization	FAO
Fourth generation of a cross between two dissimilar homozygous parent	F_4
Genetic Advance	GA
Genotypic Co-efficient of Variation	GCV
Genotypic Variance	δ^2_g
Hectare	ha
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
Sher-e-Bangla Agricultural University	SAU
Standard Error	SE
Square meter	m^2
Triple Super Phosphate	TSP
United Nations Development Program	UNDP

ACKNOWLEDGEMENTS

All praises to Almightly and Kindful 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 wish to express my earnest respect, sincere appreciation and enormous indebtedness to my reverend supervisor, Dr. Md. Shahidur Rashid Bhuiyan, Professor, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, for his continuous direction, constructive criticism, encouragement and valuable suggestions in carrying out the research work and preparation of this thesis.

I wish to express my gratitude and best regards to my respected Co-Supervisor, Dr. Md. Sarowar Hossain, Professor, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for his scholastic supervision, helpful commentary and unvarying inspiration throughout the research work and preparation of the thesis.

I am highly grateful to my honorable teachers Md. Firoz Mahmud (chairman), Kazi Md.Kamrul Huda (assistant Professor), Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, for their valuable teaching, direct and indirect advice, and encouragement and cooperation during the whole study period

I feel to expresses my heartfelt thanks to all the teachers of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for their valuable suggestions and encouragement during the period of the study

I thank to Md. Rakibul Hasan (auni), Mumtaz pervin, Sukti Rani Chowdhury for their help and inspiration in preparing my thesis.

I found no words to thanks my parents, my brother and sister for their unquantifiable love and continuous support, their sacrifice never ending affection, immense strength and untiring efforts for bringing my dream to proper shape. They were constant source of inspiration, zeal and enthusiasm in the critical moment of my studies.

June, 2008 ***The Author***

SAU, Dhaka

INTER-GENOTYPIC VARIABILITY AND GENETIC DIVERSITY ANALYSIS IN F_4 LINES OF *BRASSICA RAPA*

By

Nasrin Jahan

ABSTRACT

A field experiment was conducted in the experimental field of Genetics and Plant Breeding Department, Sher-e Bangla Agricultural University, Dhaka, Bangladesh, to study on inter-genotypic variability and genetic diversity in 10 F_4 lines obtained through intervarietal crosses along with 8 released varieties of *Brassica rapa* during November 2007 to March 2008. Significant variation was observed among all the genotypes for all the characters studied. Considering genetic parameters high genotypic co-efficient of variation (GCV) was observed for number of secondary branches/plant, siliquae/plant, yield/plant whereas days to maturity showed very low GCV. High heritability with low genetic advance in percent of mean was observed for days to maturity which indicated that non-additive gene effects were involved for the expression of this character and selection for such trait might not be rewarding. High heritability with moderate genetic advance in percent of mean was observed for plant height and days to 50% flowering indicating that this trait was under additive gene control and selection for genetic improvement for this trait would be effective. Different Multivariate analysis was performed to classify 18 genotypes. All the genotypes were grouped into four clusters. Principal Component Analysis, Principal Coordinate Analysis, Cluster Analysis, Canonical Variate Analysis gave similar results. Cluster IV was the largest cluster comprising of 7 genotypes and cluster II was the smallest cluster with 2 genotypes. Cluster II had the highest intra-cluster distance and Cluster I had the lowest intra cluster distance. Inter cluster distance was maximum (11.697) between clusters II and III. The results revealed that genotypes chosen for hybridization from clusters with highest distances would give high heterotic F_1 and broad spectrum of variability in segregating generations. The characters-number of primary branches/plant, number of secondary branches/plant and days to 50% flowering contributed maximum towards divergence. Considering cluster distance, inter genotypic distance and other agronomic performance G2 and G14 from cluster I; G18 from cluster II; G1, G9 and G12 from cluster III and G16 and G17 from cluster IV may be considered to be better parents for future uses in hybridization program.

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Chapter 1
Introduction

I. INTRODUCTION

The oleiferous *Brassica* symbolized by rapeseed and mustard is one of the leading oilseed crops in our country. *Brassica* is an important genus of plant kingdom consisting of over 3200 species with highly diverse morphology. In Bangladesh more than 134.875 thousand metric ton of local rape and mustard produced from total 392.900 thousand acre of cultivable land and about 540.005 thousand metric ton of hybrid rape and mustard produced from total 127.145 thousand acre of cultivable land in the year 2006-2007 (BBS, 2008). It is used as a condiment, salad, green manure and fodder crop and as a leaf and stem vegetable in the various mustard growing countries of the world. It is mainly self-pollinating crop, although on an average 7.5 to 30% out-crossing does occur under natural field conditions (Abraham, 1994; Rakow and Woods, 1987).

From nutritional point of view fats and oils in our diets are mostly needed for calories and vitamin absorbent. It produces highest amount of calories per unit in comparison with carbohydrate and protein diets. For human health, in a balanced diet 20-25% of calories should come from fats and oils. Although, oilseed crops play a vital role in human diet, the consumption rate of oil in our country is far below than that of balanced diet (6 g oil per day per capita against the optimum requirement of 37g per head per day, Rahman, 1981).

The genus *Brassica* has generally been divided into three groups namely, (i) the mustard (ii) the rapeseed and (iii) the cole. The genomic constitutions of the three elemental species of *Brassica* are as follows: 'AA' for *B. rapa*, 'BB' for *B. nigra* and 'CC' for *B. oleracea* having haploid chromosome

number 10, 8 and 9, respectively. The species *B. juncea* (AABB), *B. carinata* (BBCC) and *B. napus* (AACC) are the amphidiploids, and originated by combinations of the diploid elemental species. All these species have many cultivated varieties suited to different agro-climatic conditions. Meanwhile, about 25 mustard and rapeseed varieties have been released, among these, 15 from Bangladesh Agricultural Research Institute (BARI), 4 from Bangladesh Institute of Nuclear Agriculture (BINA), 3 from Bangladesh Agricultural University (BAU), 2 from Sher-e-Bangla Agricultural University (SAU) and 1 from Bangladesh Agricultural Development Corporation (BADC) but most of them are not popular to the farming community because of their long duration, low to moderate yield and susceptibility to severe biotic and abiotic stresses. Breeders in Bangladesh have released some improved varieties of mustard / rapeseed which require more than 110 days to mature. These varieties did not fit to the existing T.Amon-Mustard-Boro cropping pattern. Farmers are cultivating short duration Tori 7 variety though the yield of this variety is very low. This variety fits very well in the existing cropping pattern but we are deficient in short duration high yielding varieties. It is, therefore, needed to develop improved mustard and rapeseed varieties with high yield potential, shorter growth duration which could be fit into T.Amon–Mustard-Boro cropping pattern.

The F_4 materials were generated by crossing among the 5 varieties to develop high yielding short duration and yellow seeded materials for future release. The different promising F_4 lines obtained in 2006 would be used to compare them along with some check varieties. If these materials showed better performance in respect of yield and some yield contributing characters, individual promising materials will also be selected in 2008.

There is plenty of scope to increase yield per unit of area through breeding superior varieties. The production potential of rapeseed and mustard may be well exploited if the varieties can be identified with early maturity, rapid response to high fertility, large seed size and high oil content. The oil content of mustard in Bangladesh varies from 30 to 40 percent depending on the variety, climate and production condition (Rahman *et al.*,1993).

Genetic diversity arises either due to geographical separation or due to genetic barriers to crossability. Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display a greater heterosis than those between closely related strains (Singh, 1983) which permits to select the genetically divergent parents to obtain the desirable recombination in the segregating generations. Selection of parents based on genetic divergence has become successful in several crops (Ashana and Pandey, 1980; Ananda and Rawat, 1984; De *et al.*,1988).

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

1. To compare the yield potential and yield contributing characters of different promising F_4 lines,
2. To analyze the genetic variability of the genotypes in respect of different morphological characters,
3. To screen out the suitable genotypes for future breeding program.

Chapter 2
Review of Literature

II. REVIEW OF LITERATURE

Oleiferous *Brassica* is one of the common and most important oil crops of Bangladesh and as well as many countries of the world. In Bangladesh the average productivity of mustard is low in comparison to the developed countries. Identification of superior parents, promising cross combination and suitable breeding methodology are the important pre-requisites for development of high yielding genotypes. The crop has received much attention by the researchers on various aspects of its production and utilization for different consumer uses. Many studies on the variability, correlation, heritability and genetic advance have been carried out in many countries of the world. The work so far done in Bangladesh is not adequate and conclusive. Nevertheless, some of the important and informative works and research findings have been reviewed in this chapter under the following headings:

2.1 Variability

The representative varieties used in many different studies under certain agro ecological conditions of production have expressed different degrees of variation. Parts of these were genetic and part non-genetic. It is therefore, important to review the variabilities that have been found in different materials for some specific characters of interest. The improvement of a crop is dependent on the magnitude of genetic variability and the extent of heritability of desirable characters of the genotypes available. A critical review of genetic variability is therefore, a prerequisite for planning and evaluation of a breeding program.

Katiyar *et al.* (2004) carried out a study on variability for the seed yield in ninety intervarietal crosses of *Brassica campestris*. Existence of significant

variation among parents and crosses indicated the presence of adequate genetic variance between parents which reflected in differential performance of individual cross combinations.

Tyagi *et al.* (2001) evaluated forty-five hybrids of Indian mustard obtained from crossing 10 cultivars for seed yield and yield components. Variation was highest for plant height of parents and their hybrids. The seed yield per plant exhibited the highest coefficient of variation (41.1%).

Masood *et al.* (1999) studied seven genotypes of *Brassica campestris* and standard cultivar of *Brassica napus* to calculate genetic variability. The co-efficient of variation was high for thousand seed weight, pod length and number of seeds per pod for both genotypic and phenotypic variability.

Lekh *et al.* (1998) conducted an experiment with 24 genotypes of *Brassica juncea* and 10 genotypes each of *Brassica campestris*, *Brassica carianata* and *Brassica napus* during the rabi season of 1992-93 and 1993-94. The highest genotypic co-efficient of variation was calculated for secondary branches. High genotypic and phenotypic coefficient of variation was recorded for days to 50% flowering. Shen *et al.* (2002) tested 66 F_1 hybrids of *Brassica campestris* and significant differences were found between F1s and their parents for yield per plant and seed oil content.

Labana *et al.* (1987) studied 39 strains of Ethiopian mustard and found low genetic variation. When Varshney et al. (1986) found high variability in plant height working with a number of strains of *B. napus, B. juncea and B. rapa* . Genotypic Co-efficient of Variation (GCV) for plant height in different genotypes of *B. juncea* was found to be 10.96 by Singh *et al.* (1987), 9.3 by Labana *et al.* (1980), 31.38 by Yadava (1973), 21.16 in

brown sarson by Bhardwaj and Singh (1969), 12.32 in yellow sarson and 5.9 in toria by Tak and Patnaik (1977).

Plant height is an important character which is largely influenced by genotype, soil, water availability, temperature etc. But significant genetic variability was observed by many researchers like Kumar *et al.* (1996), Malik *et al.* (1995), Kumar and Singh (1994), Singh *et al.* (1991), Gupta and Labana (1989), Chauhan and Singh (1985) among different genotypes of *B. napus, B. campestries and B. juncea.*

Significant genetic variation for number of primary branches/plant was recorded by several researchers. Singh *et al.* (1989) studied this character under normal and stress conditions in 29 genotypes of *B. napus and B. rapa* and found significant variation among the genotypes. Similar result was reported earlier by Kumar and Singh (1994), Kakroo and Kumar (1991), Yin (1989), Biswas (1989), Jain *et al.* (1988), Labana *et al.* (1987), Gupta *et al.* (1987). GCV and PCV values of 14.44 and 24.43 were reported by Singh *et al.* (1987) in different strains of B. juncea. But, according to Tak and Patnaik (1977) these values were 33.2 and 57.1 in yellow sarson.

Usually higher the siliqua number higher is the seed yield. This trait has high variation and a considerable part of which appeared to be of environmental. Yin (1989) studied 8 cultivars of *Brassica napus* and observed high genetic variation in number of siliquae per plant. Similar results of high variation for this trait has also been observed and reported by Kumar et al. (1996). According to Tak and Patnaik (1977) genotypic co–efficient of variation (GCV %) and phenotypic co-efficient of variation (PCV %) of this trait in yellow sarson were as high as 55.4% and 53.2% respectively. The same values in Toria were 27.1% and 23.5%. Further

variable result of GCV and PCV for this character 25.41 and 29.15%, respectively was observed by Singh *et al.* (1987) in *Brassica campestris*. GCV was reported to be also as 18.85% by Yadava (1973) and 97.3% by Bhardwaj and Singh (1969). These review indicated that there exists sufficient variation in number of siliquae per plants and the same is variable with variable production conditions and genetic materials as used by different authors.

In general, high number of seeds per siliqua is desirable. A good number of literatures are available on the variability of this character. Kumar et al. (1996) reported the presence of significant variability in the genotypes of *Brassica napus, Brassica campestris and Brassica juncea* they studied. Similar significant variability in number of seeds per siliqua in oleiferous *Brassica* materials of diverse genetic base have also been observed by Kudla (1993) and Kumar and Singh (1994). In case of genotypes of *Brassica campestris* the value of GCV was 35.85% as observed by Bhardwaj and Singh (1969). According to Tak and Patnaik (1977) values of GCV and PCV were found to be 13.1% and 18.5% respectively in yellow sarson. While the value of the same for toria were 16.3% and 22.6%. Low values of GCV and PCV were also observed in *Brassica juncea* by Singh et al. (1987). According to them values were 6.46% and 9.5% for GCV and PCV respectively. Labana *et al.* (1987) also observed GCV and PCV of 9.82% and 15.96% respectively in genotypes of *Brassica juncea* for number of seeds per siliqua. These indicate that the genotypes of *Brassica juncea* are less variable than those of *Brassica campestris*.

Thousand seed weight is also an important trait of *Brassica* oil crops, where highest consideration is on the seed yield. This trait has been found to vary widely from genotypes to genotypes and from environment to environment

including macro and micro environments. A good number of literatures are available on the variability of this character. According to Chowdhury *et al.* (1987), Yin (1989), Labowitz (1989) and Biswas (1989) in *Brassica campestris*, Andrahennadi *et al.* (1991) in brown mustard, Kudla (1993) in sewede rape and Kumar and Singh (1994) in *Brassica juncea* reported different degrees of significant variations of thousand seed weight due to variable genotypes. In case of *Brassica campestris* (toria ecotypes), GCV and PCV, two important parameters of breeding values were found 11.8% and 18.9% respectively (Bhardwaj and Singh, 1969). The respective values of the same were 13.1% and 16.5% in brown sarson as reported by Tak and Patnaik (1977). Labowitz (1989) studied *Brassica campestris* population for siliqua length and observed high genetic variation in this trait.

Variability in consideration of days to 50% flowering, an important yield component, is very useful in selecting materials of short, medium or long duration crop. In general, early flowering genotype mature early and late flowering genotype delayed maturity. Several workers investigated the variability in respect of days to flowering. Nanda *et al.* (1995) reported from an experiment conducted with 65 strains of *Brassica napus, B. rapa, B. juncea* and *B. carinata* found days to 50% flowering varied by genotype. Singh *et al.* (1991) studied different morphological characters of 29 genotypes of *B. napus* and *B. rapa* grown under normal and stress conditions of *Brassica* production. They found the existence of significant genetic variability for days to 50% flowering. Kumar *et al.* (1996), Kumar and Singh (1994), Andrahennadi (1991), Biswas (1989), Singh *et al.* (1987), Chauhan and Singh (1985), Thurling (1983), Thakral (1982) and many other researchers worked with different genotypes of *Brassica.* In general, according to them, significant variations were observed in the character for days to 50% flowering.

Jain et al. (1988) in an experiment analysis of gene effects using means of six populations of a cross Varuna X YRT-3 of Indian mustard and observed that dominance gene action was important in the expression of days to flowering. Partial dominance was observed for this character by Kumar et al. (1991). It is evident from all these results that sufficient genetic variations exist for days to 50% flowering.

Days to maturity for any crop are most important criteria for assessment of variability. It is influenced by genotypes and various environmental factors. Significant genetic variation was found by several workers among different genotypes of rapeseed and mustard. Biswas (1989) found high GCV and PCV among 18 genotypes of *B. napus* while Sharma (1984) working with 46 genotypes of *B. juncea* and found low GCV and PCV values. Yadava (1973) found 7.6 GCV among 29 strains of *B. juncea,* while in yellow sarson Tak and Patnaik (1977) found this value as 4.5 and 1.8, respectively. Significant variation for days to maturity was also found by Kumar and Singh (1994), Singh *et al.* (1991), Grosse and Geisler (1988), Khera and Singh (1988), Gupta *et al.* (1987), Chauhan and Singh (1985) and many other researcher in their research work.

Yield is the most important trait for all crops in every breeding program. This is a complex trait influenced largely by a number of component characters and factors of production. A good number of research works have been conducted on this character. Significant genetic variability in genotypes belonging to toria ecotype of *Brassica campestris* was reported by Thakral (1982). Similar high variability in different genotypes of *Brassica campestris* was reported by Sharma (1994). Khera and Singh (1988) also reported significant variation in yield due to genotypes of

Brassica napus. A high degree of variation for seed yield per plant was reported by Yin (1989) in *Brassica campestris*, Kudla (1993) in *Brassica napus* and Kumar *et al.* (1996) in *Brassica juncea.* According to Bhardwaj and Singh (1969), the value of GCV was found to be 96.99% among different strains of brown sarson (*Brassica campestris*). This value appeared to be very high for yield as because 48.76% GCV was found by Yadava (1973) among 29 strains of *Brassica juncea.* While, Singh *et al.* (1987) observed GCV and PCV values of 44.04% and 46.9% in *Brassica juncea.* The same values were only 9.6% and 19.47% among different genotypes of *Brassica juncea* Labana *et al.* (1987). The comparative position of the genotypes of these two species indicates the presence of high variability due to difference in species and genotypes.

From the reviews above it is clear that a wide range of variability existed for different morphological characters among different genotypes of *Brassica* oil crops and it indicates the scope of utilization of these variability for further breeding programs.

2.2 Genetic Diversity

Cluster analysis showed a wide diversity of genotypes from the same geographical regions. An investigation was conducted by Malik *et al.* (1997) to determine the extent of diversity and relationships among the *B. juncea* germplasm from Pakistan using morphological characters and showed a comparatively low level of phenotypic variation amongst them and where genetically similar to the oilseed cultivars. However, the oilseed forms and vegetable cultivars were genetically distinct. They revealed that the evaluated germplasm appears to have a narrow genetic base which undergoes a high level of genetic erosion.

An investigation was carried out by Sen *et al.* (2002) to assess genetic divergence, morphological and quality attributes in 12 accessions of each of three *Brassica* species viz; *B. juncea, B. napus* and *B. carinata.* The inter species variation was higher than inter variety variability. The range of variation was highest in *B. juncea* followed by *B. napus* and *B. carinata*

Choudhary and Joshi (2001) studied genetic diversity among 88 entries including eighty F_4 derivatives i.e., 20 each selected from *Brassica* crosses viz., *B. juncea* × *B. napus, B. juncea* × *B. rapa var. toria, B. juncea* × *B. rapa var. yellow sarson and B. tournefortii* × *B. juncea,* and eight parent genotypes was assessed through multivariate analysis and reported significant differences among the family groups as well as within the family were recorded for the trait that were studied. The multivariate (D^2)analysis revealed enormous diversity among inter specific cross derivatives. They also calculated genetic distances among different *Brassica* species revealed that *B. tournefortii* had maximum diversity with *B. juncea* followed by *B. napus, B. rapa* varity toria and *B. rapa* variety yellow sarson. They reported that the derivatives selected from cross of diverse parents revealed greater diversity. The clustering pattern showed that many derivatives of the cross fell into the same cluster but in many cases in spite of common ancestry many descendants of the cross spread over different clusters. They also reported that the traits namely, plant height, secondary branches/plant, days to flowering and 1000 seed weight were contributed maximum towards genetic divergence.

Islam and Islam (2000) evaluated the genetic diversity in rapeseed and mustard using D^2 analysis of 42 genotypes. The genotypes were felt into four clusters. The inter cluster distances were larger than the intra cluster

distances. The characters contributed maximum in divergence analysis are days to 50% flowering, plant height, branches/plant and siliquae/plant.

The clustering and ordination methods used often cannot deal explicitly with the computational consequences of large data sets with incomplete information. However, it is shown that the ordination technique of principal component analysis and the mixture maximum likelihood method of clustering can be employed to achieve such analysis (Harch *et al.*, 1999). Genotypes within the cluster are having a smaller D^2 value among themselves than those from group belonging to two different clusters. On the other hand, the inter-cluster distance is the criterion used for selecting genotypes for parent for hybridization. The genotypes those in clusters with maximum inter cluster distance are genetically more divergent. Variation within the cluster is measured by inter-cluster distance.

Forty four genotypes of toria were evaluated by Mitra and Saini (1998) collected from different eco-geographical areas for yield and various components during rabi 1991-92. On the basis of D^2 analysis, the 43 genotypes were grouped into 7 clusters. No evidence was obtained for any correlation between genetic divergence and geographical diversity. Siliqua in the main shoot and seeds per siliqua were the major contributors to genetic divergence.

Nineteen genotypes (crosses and parents) of Indian mustard *(B. juncea)* grown at Ranchi during the winter season under rainfed conditions. Genotypes were grouped into 3 clusters based on D^2 analysis was studied by Mahto (1996).

Islam (1995) studied genetic divergence among 90 genotypes of groundnut using D^2 and principal components analysis and grouped the varieties into 5 clusters. The inter-cluster distances were larger than the intra-cluster distance suggesting wider genetic diversity among the genotypes of different groups.

Uddin (1994) reported from an experiment on genetic divergence among 34 genotypes of mustard were estimated using D^2 and principal component analysis. The genotypes felt into four clusters. The inter-cluster distance was larger than the intra-cluster distance suggesting wider genetic diversity among the genotypes of different groups. The intra-cluster values were lower in all the clusters.

Nineteen genotypes of rape mustard *(B. rapa)* were studied by Jagadev *et al.* (1991) which were grown during the winter season. They studied different characters and analyzed the variance using D^2 statistic. Genotypes were grouped into 5 clusters. Seed weight, days to maturity and seed yield were the largest contributors to D^2 values.

Sindhu *et al.* (1989) investigated diversity in 20 strains of black gram from different agro-ecological zones of India using Mahalanobis's D^2 statistic. They observed no parallelism between geographical and genetic diversity.

Reddy *et al.* (1987) conducted a study of genetic divergence of groundnut for pod yield/plant and 12 related characters by Mahalanobis's D2 statistics. The greatest inter cluster distance was observed between clusters I (with 10 to 11 varieties depending on years) and II (4 to 6 varieties) and between clusters I and IV.

Mahalanobis's D^2 statistic to group 83 genotypes on the basis of yield/plant and six other agronomic characters of bunch groundnut by Nadaf *et al.* (1986). They found nine clusters, which were not related to the grouping formed by geographical origin. They also observed that variation in pod yield accounted for 88% of the total variation between clusters but number of developed pods, days to 50% flowering and 1000 seed weight were important in accounting for divergence with clusters.

Shanmugam and Rangasamy (1982) observed that the characters yield per plant and pod per plant contributed considerably towards diversity in black gram. Again the same authors in 1982 assigned 45 genotypes of black gram often clusters by analyzing data on yield and nine yield components using Mahalanobis' D^2 statistic and stated that geographical diversity was not the only factor for determining genetic diversity. The clustering pattern more or less confirmed the canonical (vector) analysis. They found that yield per plant contributed most too genetic divergence.

2.3 Heritability and Genetic Advance

The variation of heritability can be estimated with greater degree of accuracy when heritability in conjunction with genetic advance as percentage of mean is studied. Johnson *et al.* (1995) suggested the necessity of estimating genetic advance along with heritability in order to draw a more reliable conclusion in a selection program. Many experiments have been conducted in the investigation of heritability and genetic advance on yield and yield components of mustard. The most relevant reviews are reviewed here.

Malik *et al.* (1995) observed very high broad sense heritability (>90%) for number of primary branches, days to 50% flowering and oil content while working with different strains of *B. napus*. They also found low heritability (<50%) for number of siliquae/plant, number of seeds/siliquae, plant height and yield. But Singh *et al.* (1991) found high heritability for all these characters. Li *et al.* (1990) also recorded similar high heritability results in studies with *B. napus*.

Varshney *et al.* (1986) found high heritability and high genetic advance for plant height when conducted an experiment of 45 genotypes of *B. napus, B. rapa* and *B. juncea* species; but high heritability and genetic advance for siliquae/plant only in B. *rapa.* Singh (1986) studied 22 genotypes of *B. napus, B. rapa and B. juncea* and reported high heritability and genetic advance in seed yield, 1000 seed weight and number of seeds/siliquae. Inheritance of seed oil content was studied by Han (1990) in 7 inbreeds of *B. napus,* crossed in a diallel fashion and reported high heritability (81.16%) for this trait. However, Yadava *et al.* (1985) reported low heritability for oil content in *B. juncea.* Wan and Hu (1983) observed high heritability and genetic advance for flowering time, number of primary branches/plant and plant height. Low heritability of yield was reported by many researchers like Malik *et al.* (1995), Kumar *et al.* (1988), Yadava *et al.* (1985), Chen *et al.* (1983); but Singh (1986) reported high heritability for this character.

In a study Sharma (1984) observed high heritability for plant height, days to flowering and low heritability for days to maturity when working with 46 genotypes of *B. juncea.* He also found low genetic advance for days to maturity and high genetic advance for yield/plant. In another study of Indian mustard Singh *et al.* (1987) observed high heritability (80-95%) for oil

content and yield/plant. The lowest heritability (34.9%) was recorded for number of primary branches per plant.

Labana *et al.* (1980) found that plant height and number of seeds/siliquae were highly heritability, whereas, number of primary branches and seed yield per plant were less heritable when working with 104 mutants of Indian mustard. The yield variation thus principally owed to the environmental influence, for which selection would not be much effective. The selection of the material would be more practicable for plant height and number of seed/siliquae. This confirmed the finding of Chaudhari and Prasad (1968). In the same experiment the genetic advance was highest for plant height (13.75%) followed by number of seeds/siliquae (12.43%) and seed yield/plant (9.75%). This offers scope for this improvement through selection. This is because high heritability and genetic advance together provide better indication of the amount of genetic progress that can result from selection of the best individuals.

Chandola *et al.* (1977), working with 30 varieties of *B. rapa* found high estimates of genetic advance for plant height. Paul *et al.* (1976) observed in one of experiment that a good genetic advance was expected from a selection index comprising seed yield, number of seeds/pod, number of siliquae/plant and number of primary branches per plant.

Thurling (1974) reported in the genotypes of *B. rapa* that the expected genetic advance in yield using a selection index technique based on simultaneous selection of several characters was significantly greater than that expected from selection for yield alone, and several indices including measurement of both yield components and vegetative characters were expected to promote a greater ratio of advance in yield than direct selection.

From the exceeding review it can be concluded that approximately all characters expected yield are high heritable in nature and the predictable genetic advance, being high for plant height, primary branches/plant, 1000 seed weight and yield, assortment is possible for high yield using number of characters in selection programs.

Chapter 3

materials & methods

III. MATERIALS AND METHODS

A field experiment was conducted in the experimental field of Genetics and Plant Breeding Field Laboratory of Sher-e Bangla Agricultural University, Dhaka, Bangladesh during the period from November 2007 to March 2008 to study on the inter genotypic variability and genetic divergence in oleiferous *Brassica* species. The materials and methods of this experiment are presented in this chapter under the following headings –

3.1 Experimental Site

The present piece of research work was conducted in the field of Genetics and Plant Breeding Department, Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka, Bangladesh. The location of the site is 23074/ N latitude and 90035/ 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 under AEZ 28. The soil of the experimental plots were clay loam, land was medium high with medium fertility level. The Physical and Chemical characteristics of initial soil in the experimental field are presented in Appendix I.

3.3 Weather Condition of the Experimental Site

The geographical situation of the experimental site was under the subtropical climate, characterized by three distinct seasons, the monsoon or rainy season from November to February and the pre-monsoon period or hot season from March to April and monsoon period from May to October.

(Edris *et. al.*, 1979). During the rabi season the rainfall generally is scant and temperature moderate with short day length. Meteorological data on rainfall, temperature, relative humidity from November 2007 to March 2008 were obtained from the Department of Meteorological centre, Dhaka-1207, Bangladesh (Appendix II). The experiment was conducted using ten F_4 lines along with their five parental materials and three check variety.

3.4 Planting materials used

Eighteen genotypes were used in the study. The seeds of 18 genotypes were collected from *Brassica* Breeding Project of Sher-e-Bangla Agricultural University (SAU), Dhaka-1207, Bangladesh. Descriptions of the genotypes are given in Table 1.

3.5 Methods

The following precise methods have been followed to carry out the experiment.

3.5.1 Preparation of the Main Field

The plot selected for the experiment was opened in the first week of November 2007 with a power tiller, and was exposed to the sun for a week. After one week the land was harrowed, ploughed and cross-ploughed several times followed by laddering to obtain a good tilth. Weeds and stubbles were removed, and finally obtained a desirable tilth of soil for sowing of *Brassica* seeds. The experimental plot was partitioned into the unit plots in accordance with the experimental design mentioned in 3.5.3.

Recommended doses of well-rotten cowdung manure and chemical fertilizers were mixed with the soil of each unit plot (Table 2).

Table 1. Sources of 18 *Brassica rapa* genotypes

Designation	Genotypes	Sources
G1	BARI sarisha-6	BARI
G2	SS-75	BARI
G3	F_6	SAU
G4	Tori-7	BARI
G5	BARI sarisha-9	BARI
G6	F_6×BARI sarisha-9	SAU
G7	BARI sarisha-9×F_6	SAU
G8	Tori-7×BARI sarisha-6	SAU
G9	BARIsarisha-6×Tori-7	SAU
G10	Tori-7×F_6	SAU
G11	F_6×Tori-7	SAU
G12	Tori-7×SS-75	SAU
G13	SS-75×Tori-7	SAU
G14	BARI sarisha-9×BARI sarisha-6	SAU
G15	BARI sarisha-6×BARI sarisha-9	SAU
G16	BARI sarisha-15	BARI
G17	Real Tori-7	Farmer's Field
G18	SAU sarisha-1	SAU

3.5.2 Application of Manure and Fertilizers

The fertilizers N, P, K, S and B in the form of urea, TSP, MP, Gypsum and borax, respectively were applied. The entire amount of TSP, MP, Gypsum, Zinc sulphate and borax was applied during the final preparation of land. Urea was applied in two equal installments at before sowing and before flowering. The dose and method of application of fertilizer are shown in Table 2.

Table 2. Dose and method of application of fertilizers in field

Fertilizers	Dose (kg/ha)	Application (%)	
		Basal	Before flowering
Urea	250	50	50
TSP	170	100	--
MP	85	100	--
Gypsum	150	100	--
Borax	60	100	--

Source: Krishi Projukti Hatboi, BARI, Joydebpur, Gazipur

3.5.3 Experimental design and layout

Field lay out was done after final land preparation. The seeds of parents and F_4 materials were laid out in a Randomized complete block design (RCBD) with three replications. The size of the unit plot was 5m×25m. A distance of 1.5 m from block to block, 30 cm from row to row and 10 cm from plant to plant was maintained. Seeds were sown in lines in the experimental plots on 11th November, 2007 by hand uniformly. The seeds were placed at about 1.5 cm depth in the soil. After sowing the seeds were covered with soil carefully so that no clods were on the seeds. Seed germination started after 3 days of sowing on 14th November 2007. Treatment was distributed in the

Plate 1a. Field view of experimental site

Plate 1b. Field view of experimental site (close view)

experimental unit through randomization by using the random number. Field view of the experimental plot is presented in (plate 1a and plate 1b).

3.5.4 After Care

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

3.5.4.1 Irrigation

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

3.5.4.2 Thinning and Gap Filling

The seedling were first thinned from all of the plots at 10 Days after sowing (DAS), 2nd thinning was carried out after 17 days for maintaining proper spacing of the experimental plots.

3.5.4.3 Weeding and Mulching

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

3.5.4.4 Top Dressing

After basal dose, the remaining doses of urea were top-dressed in 2 equal installments. The fertilizers were applied on both sides of plant rows and mixed well with the soil.

3.5.5 Plant Protection

Malathion 57 EC insecticide was applied after one month of seeds sowing at 12 days interval for 3 times with 1 ml in 2.5 liters water for protecting the crop from the attack of aphids and Rovral-50 WP was sprayed @ 20-g/10L water first one at the time of siliquae setting and second one after 15 days of 1st spraying to control *Alternaria* leaf spot. No remarkable disease attack was observed.

3.5.6 Harvesting

Harvesting was started from 5 February, 2008 depending upon the maturity of the plants. When 80% of the plants showed symptoms of maturity i.e.; straw colour of siliquae, leaves, stem and desirable seed colour in the matured siliquae, the crop was assessed to attain maturity. Ten plants were selected at random from each plot in each replication. The sample plants were harvested by uprooting and then they were tagged properly. Data were recorded from these plants.

3.5.7 Collection of data

For studying different genetic parameters and inter-relationships the ten characters were taken into consideration

3.5.8 Methods of collecting data

3.5.8.1 Days to 50% flowering

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

3.5.8.2 Days to maturity

Number of days required from sowing to siliquae maturity of 80% plants of each entry. Maturities of the crops of 18 genotypes were recorded considering the maturity symptom such as color changing of the plant from greenish to straw colored appearance.

3.5.8.3 Plant height

The height of plants was recorded in cm as the average of 10 plants selected at random from the inner rows of each plot after harvest. The height was measured from the ground level to the tip of the growing point of the main branch

3.5.8.4 Number of primary branches/plant

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

3.5.8.5 Number of secondary branches/plant

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

3.5.8.6 Number of siliquae/plant

The total numbers of siliquae of the randomly selected 10 plants of a plot were recorded and then average numbers of siliquae were estimated.

3.5.8.7 Length of siliquae

Distance between the ends of the peduncle to the starting point of the beak was recorded as siliquae length and was presented in centimeter (cm).

3.5.8.8 Number of seeds/siliquae

Ten siliquae from each plant were selected randomly and number of seeds was counted and the average number of seed per siliquae was determined.

3.5.8.9 1000 seed weight

One thousand seeds were counted from randomly selected plants of each plot and then weighted in grams.

3.5.8.10 Seed Yield/plant

Seed weight per plant was measured from the randomly selected plants and then average was designated as seed yield per plant.

3.5.9 Statistical analysis

The data obtained for different characters were statistically analyzed to find out the significance of the difference among the *Brassica* genotypes. The mean values of all the characters were evaluated and analysis of variance was performing by the 'F' test. The significance of the difference among the treatments means was estimated by the least significant difference (LSD) test at 5% level of probability (Gomez and Gomez, 1984). Correlation coefficient was estimated according to Singh and Chaudhury (1985).

3.5.10 Estimation of variability

The data were analyzed for different components. Phenotypic and genotypic variance was estimated by the formula used by Johnson *et al.* (1955). Heritability and genetic advance were measured using the formula given by Singh and Chaudhary (1985) and Allard (1960). Genotypic and phenotypic co-efficient of variation were calculated by the formula of Burton (1952).

3.5.10.1 Estimation of genotypic and phenotypic variances: Genotypic and phenotypic variances were estimated according to the formula of Johnson *et al.* (1955).

Genotypic variance, $\delta^2 g = \frac{MSG - MSE}{r}$

Where, MSG = Mean sum of square for genotypes

MSE = Mean sum of square for error, and

r = Number of replication

b. Phenotypic variance, $\delta^2 p = \delta^2 g + \delta^2 e$

Where, $\delta^2 g$ = Genotypic variance,

$\delta^2 e$ = Environmental variance = Mean square of error

3.5.10.2 Estimation of Genotypic and Phenotypic Co-efficient of variation: Genotypic and phenotypic co-efficient of variation were calculated by the following formula (Burton, 1952).

$$GCV = \frac{\delta g \times 100}{\bar{x}}$$

$$PCV = \frac{\delta p \times 100}{\bar{x}}$$

Where, GCV = Genotypic co-efficient of variation

PCV = Phenotypic co-efficient of variation

δg = Genotypic standard deviation

δp = Phenotypic standard deviation

$\bar{x}$ = Population mean

3.5.10.3 Estimation of heritability: Broad sense heritability was estimated by the formula suggested by Singh and Chaudhary (1985).

$$h^2b\ (\%) = \frac{\delta^2 g}{\delta^2 p} \times 100$$

Where, h^2b = Heritability in broad sense.

$\delta^2 g$ = Genotypic variance

$\delta^2 p$ = Phenotypic variance

3.5.10.4 Estimation of Genetic Advance: The following formula was used to estimate the expected genetic advance for different characters under selection as suggested by Allard (1960).

$$GA = \frac{\delta^2 g}{\delta^2 p} . K. \delta p$$

Where, GA = Genetic advance

$\delta^2 g$ = Genotypic variance

$\delta^2 p$ = Phenotypic variance

δp = Phenotypic standard deviation

K = Selection differential which is equal to 2.06 at 5% selection Intensity

3.5.10.5 Estimation of Genetic Advance in percentage of mean: Genetic advance in percentage of mean was calculated by the following formula given by Comstock and Robinson (1952).

$$\text{Genetic Advance in percentage of mean} = \frac{\text{Genetic advance}}{\bar{X}} \times 100$$

3.5.11 Estimation of Diversity

3.5.11.1 Principal Component Analysis (PCA)

Principal Component Analysis (PCA), one of the multivariate techniques, is used to examine the inter-relationship among several characters and can be done from sum of squares and product matrix for the characters. Therefore, Principal Component were computed from the correlation matrix and genotypes scores obtained from the first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity (Jager *et al.* 1983). Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.5.11.2 Principal Coordinate Analysis (PCO)

Principal coordinate analysis is equivalent to principal component analysis but it is used to calculate inter-unit distances. Through the use of all dimensions of P it gives the maximum distances between each pair of the n point using similarity matrix (Digby *et al.*, 1989).

3.5.11.3 Clustering

To divide the genotypes of the study into some number of mutually exclusive groups clustering was done using non-hierarchical classification. Starting from some initial classification of the genotypes into required groups, the algorithm repeatedly transfers genotypes from one group to another so long as such transfers improve the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm

switches to a second stage which examine the effect of swapping two genotypes of different classes and so on.

3.5.11.4 Canonical Variate Analysis (CVA)

Using canonical vector analysis a linear combination of original variabilities that maximize the ratio in between group to within group variation to be finding out and there by giving functions of the original variabilities that can be used to discriminate between groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing the ratio of the among groups to the within group variations.

3.5.11.5 Computation of Average Intra-cluster Distances

When the clusters were formed, the average intra-cluster distances for each cluster was calculated by taking possible D^2 values within the member of a cluster obtained from the Principal Coordinate Analysis (PCO). The formula used was D^2/n, where D^2 is the sum of distances between all possible combinations (n) of the genotypes included in the cluster. The square root of the average D^2 values represents the distances (D) within cluster.

3.5.11.6 Cluster Diagram

Cluster Diagram was drawn using the intra and inter cluster distance. It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

Chapter 4
Results & Discussions

IV. RESULTS AND DISCUSSION

The present experiment was conducted to determine the breeding values in respect of genotypic effects and comparative performances of different F_4 materials generated through intervarietal crosses along with their parent materials as well as three check varieties of *Brassica rapa*. The study was carried out to find out the phenotypic and genotypic variability, co-efficient of variation, heritability, genetic advance, genetic diversity among different genotypes to estimate the direct and indirect effect of yield contributing traits on yield. Ten characters such as plant height, number of primary branches per plant, number of secondary branches per plant, days to 50% flowering, days to maturity, number of siliquae per plant, length of siliqua, number of seeds per siliquae, thousand seed weight and seed yield per plant were studied of 18 genotypes of *Brassica rapa*.

4.1 Variability

The analysis of variance (ANOVA) of the data on different yield components and yield of *Brassica* are given in (Table 3). The mean values over three replications for the characters of all genotypes are presented in Table 4. Genotypic, phenotypic and environmental variance and genotypic, phenotypic and environmental coefficients of variation are presented in Table 5. Among the genotypes almost all characters showed highly significant variation indicating wide scope of selection for these characters. i.e. the data revealed substantial variability and thus high possibility of improvement in most of the traits. The variability in the present study indicated the potentiality of the materials generated through intervarietal crosses for selecting desirable segregants in the F_4 generation for the

development of new varieties. The phenotypic variance was partitioned into genotypic and environmental variances for clear understanding of the pattern of variations. In general environmental influences were minimal on yield and its component characters (Table 5).

4.1.1 Plant Height (cm)

The mean square due to genotype from the analysis of variance was found statistically significant at 1% level of probability for plant height (555.475**) indicating genotypic differences present among the genotypes used under the present study (Table 3). From the mean value it was found that the tallest genotype was G1(125 cm) which was statistically different with 16 other genotypes except G3 (119 cm) while the shortest genotype was G17 (65 cm) which was followed by G8 (88 cm) (Table 4).

The phenotypic variance (216.72) was considerably higher than the genotypic variance (169.38) and the phenotypic and genotypic co-efficient of variations were 14.49 % and 12.81 %, respectively (Table 5). The result indicated the existence of inherent variability among the population with possibility of high potential for selection. Highest phenotypic and genotypic variances and genotypic and phenotypic co-efficient of variations for plant height were also observed by Mishra and Yadav (1992), Uddin *et al.* (1995), Azad and Hamid (2000) and Venkatramana *et al.* (2001) in their study.

4.1.2 Number of Primary Branches/Plant

Analysis of variance of the data for number of primary branches/plant showed highly statistically significant difference among the genotype (Table 3). Maximum number of primary branches/plant was recorded in

Table 3. Analysis of variance of the data of 10 important characters of 18 *Brassica rapa* genotypes

Sources of variation	D.F	Mean Sum of Squares of characters									
		Plant height (cm)	Number of primary branches/ plant	Number of secondary branches /plant	Days to 50% flowering	Days to maturity	Number of siliquae/ plant	Length of siliqua (cm)	Number of seeds/ siliqua	Thousand seed weight (g)	Seed yield/plant (g)
Replication	2	30.525	0.020	1.074	7.167	6.907	565.729	0.151	3.245	0.095	1.404
Genotype	17	555.475**	3.721**	16.426**	61.020**	32.153**	6302.133**	0.584**	26.070**	0.422**	5.876**
Error	34	47.34	0.444	1.032	5.049	5.300	658.212	0.087	3.898	0.122	0.451
CV		6.77%	11.81%	15.99%	6.63%	2.49%	13.51%	7.62%	11.74%	11.56%	10.39%

** Denote significant at 1% level of probability

genotype G1 (8.07) which was significantly different from other genotypes and the genotypes G2 and G16 were statistically similar (both are 7.10) (Table 4). On the other hand the minimum number of primary branches/plant was recorded in the genotypes G17 (4.17) which was followed by G18 (4.20).

The phenotypic variance (1.54) was slightly higher than the genotypic variance (1.09) indicating less environmental influence on this characters (Table 5) and relatively moderate genotypic co-efficient (18.53%) and phenotypic co-efficient of variation (21.97%) which indicate that the genotype has high variability (Table 5). Chawdhury *et al.* (1987) found significant differences for number of primary branches per plant. Kuriakose and Joseph (1986), Alam *et al.* (1985) and Uddin *et al.* (1995) reported the similar results earlier

4.1.3 Number of Secondary Branches/Plant

In the present experiment analysis of variance of the data for number of secondary branches/plant showed highly significant difference among the genotypes included in the present experiment. The mean squares value (16.426**) regarding to number of secondary branches/plant (Table 3) indicated the presence of variability among the genotypes. Highest number of secondary branches/plant was recorded in genotype G9 (9.40) (Table 4) which was statistically similar with G7, G11, G12, G13.The lowest mean was observed in G18 (1.73) which was statistically different with 16 genotypes except G16 (Table 4). Number of secondary branches per plant showed low values and little differences between genotypic (5.13) and phenotypic (6.16) variance indicating that they had some short of interaction with environment and relatively high GCV (35.65%) and PCV (39.07%)

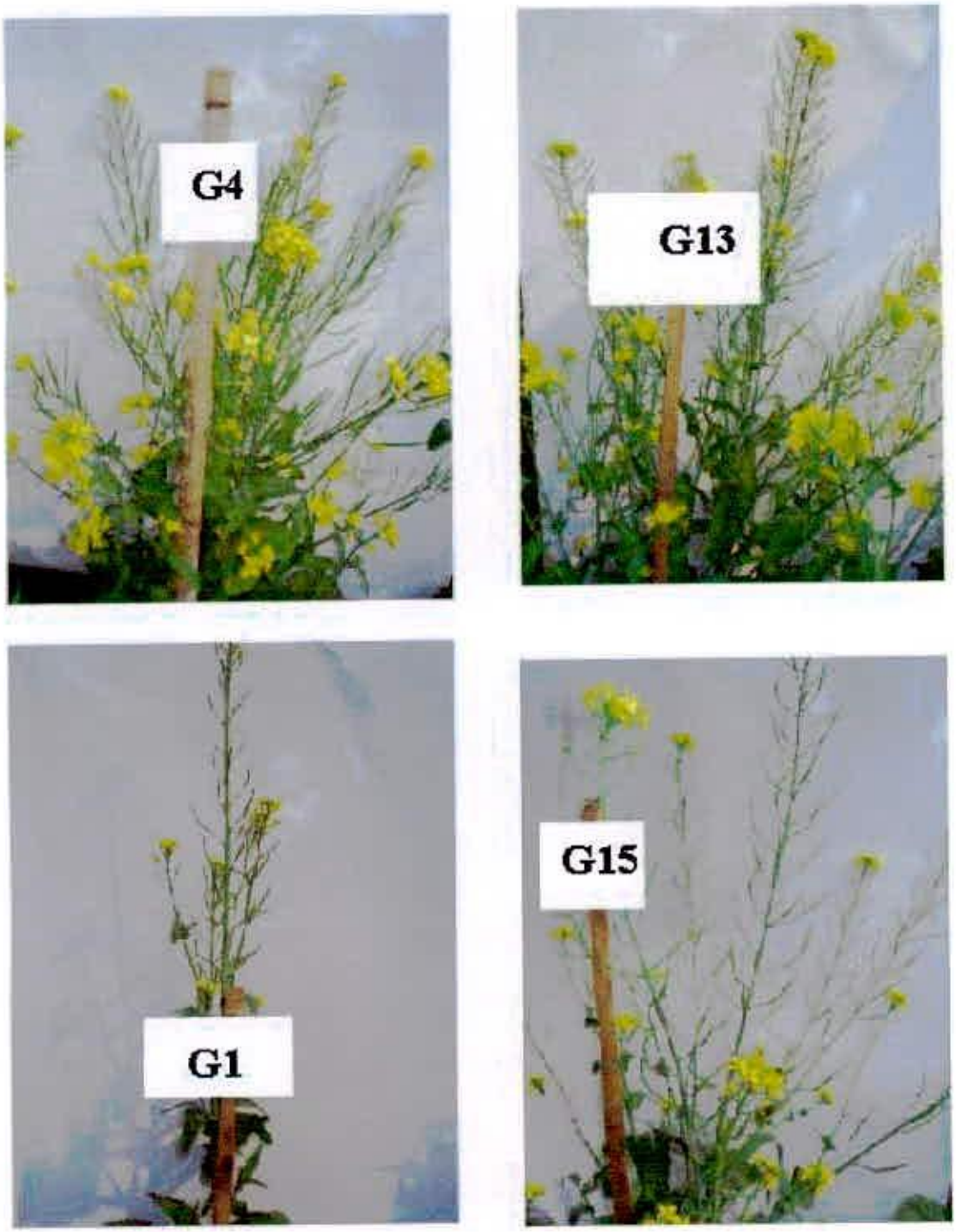

Plate 2. Genotypes G4, G13, G1 and G15 at flowering stage showing branching status.

Table 4. Mean performance of ten different characters of 18 genotypes of *Brassica rapa*

Designation	Plant height(cm)	No. of primary branches/ plant	No. of secondary branches/plant	Days to 50% flowering	Days to maturity	No. of Siliquae /plant	Siliquae length (cm)	No. of seeds/ Siliquae	1000 seed wt.(g)	yield/ plant (g)
G1	125 a	8.07a	3.43fg	40a	92c-e	235 a-c	4.13bc	21ab	2.93bc	8.97a
G2	115 a-c	7.10ab	5.80c-e	40a	99a	201b-f	3.36ef	17cd	3.79a	8.06ab
G3	119ab	6.07b-e	8.17ab	35bc	90ef	244ab	3.46d-f	12ef	2.94bc	6.44c-e
G4	92gh	5.47c-g	6.03c-e	31de	99a	143gh	3.88b-e	15c-f	2.63cd	6.00c-f
G5	95f-h	4.60gh	4.60ef	34b-d	91d-f	133h	3.73b-f	14d-f	3.01bc	4.22g
G6	102d-g	5.03e-h	6.67b-d	33c-e	95a-d	186d-g	4.00b-d	18bc	3.50ab	5.52ef
G7	99f-h	6.63bc	8.50a	32c-e	90ef	211a-e	3.90b-e	16c-e	3.06bc	8.66a
G8	88h	4.37gh	5.60de	29ef	96ab	172e-h	3.96b-d	16c-e	2.59cd	5.70d-f
G9	100e-h	5.87b-f	9.40a	30de	93b-e	228a-d	3.96b-d	15c-f	2.99bc	7.00bc
G10	105c-g	5.47c-g	6.17c-e	31c-e	92b-e	231a-d	3.68b-f	14d-f	2.98bc	6.92b-d
G11	96f-h	5.93b-e	8.77a	32c-e	91c-e	197b-f	3.84b-f	16c-e	2.63cd	5.94c-f
G12	107b-f	5.27d-h	9.13a	34b-e	91c-e	259a	3.30f	12f	2.70cd	5.40e-g
G13	99e-h	5.10e-h	8.77a	30de	90ef	220a-e	3.70b-f	18cd	2.82cd	8.24a
G14	112b-e	6.50b-d	6.13c-e	37ab	90ef	187c-g	4.26b	17cd	2.29d	5.01fg
G15	95f-h	4.60f-h	5.93c-e	31de	95ac	155f-h	3.75b-f	15e-f	3.00bc	5.59ef
G16	113a-d	7.10ab	1.83g	40a	86f	146gh	3.87b-f	22a	2.21d	8.01ab
G17	65 i	4.17h	7.70a-c	25f	91c-e	182d-g	3.64cf	15c-f	3.08bc	5.30e-g
G18	94f-h	4.20gh	1.73g	41a	90ef	79i	5.33a	21ab	2.98bc	5.34c-g
$LSD_{(0.05)}$	11.42	1.106	1.686	3.728	3.82	42.57	0.489	3.276	0.555	1.114

Note: Means separated by uncommon letters in order of alphabetic preferences are significantly different from each other at p = 0.05

Table 5. Estimation of genetic parameters for yield and yield contributing characters of 18 genotypes of *Brassica rapa*

Genetic parameters ▶ Characters ▼	σ^2_g	σ^2_p	σ^2_e	GCV (%)	PCV (%)	ECV (%)
Plant height	169.38	216.72	47.34	12.81	14.49	6.77
No. of Primary branches/plant	1.09	1.54	0.44	18.53	21.97	11.81
No. of secondary branches/plant	5.13	6.16	1.03	35.65	39.07	15.99
Days to 50% flowering	18.66	23.71	5.05	12.75	14.37	6.63
Days to maturity	8.95	14.25	5.30	3.23	4.08	2.49
Siliquae/plant	1881.31	2539.52	658.21	22.84	26.54	13.51
Siliqua length	0.17	0.25	0.09	10.51	12.98	7.61
No. of seeds/pod	7.39	11.29	3.90	16.16	19.98	11.74
1000 seed wt.	0.103	0.215	0.112	11.10	16.02	11.56
Seed Yield/plant	1.81	2.26	0.45	20.81	23.26	10.39

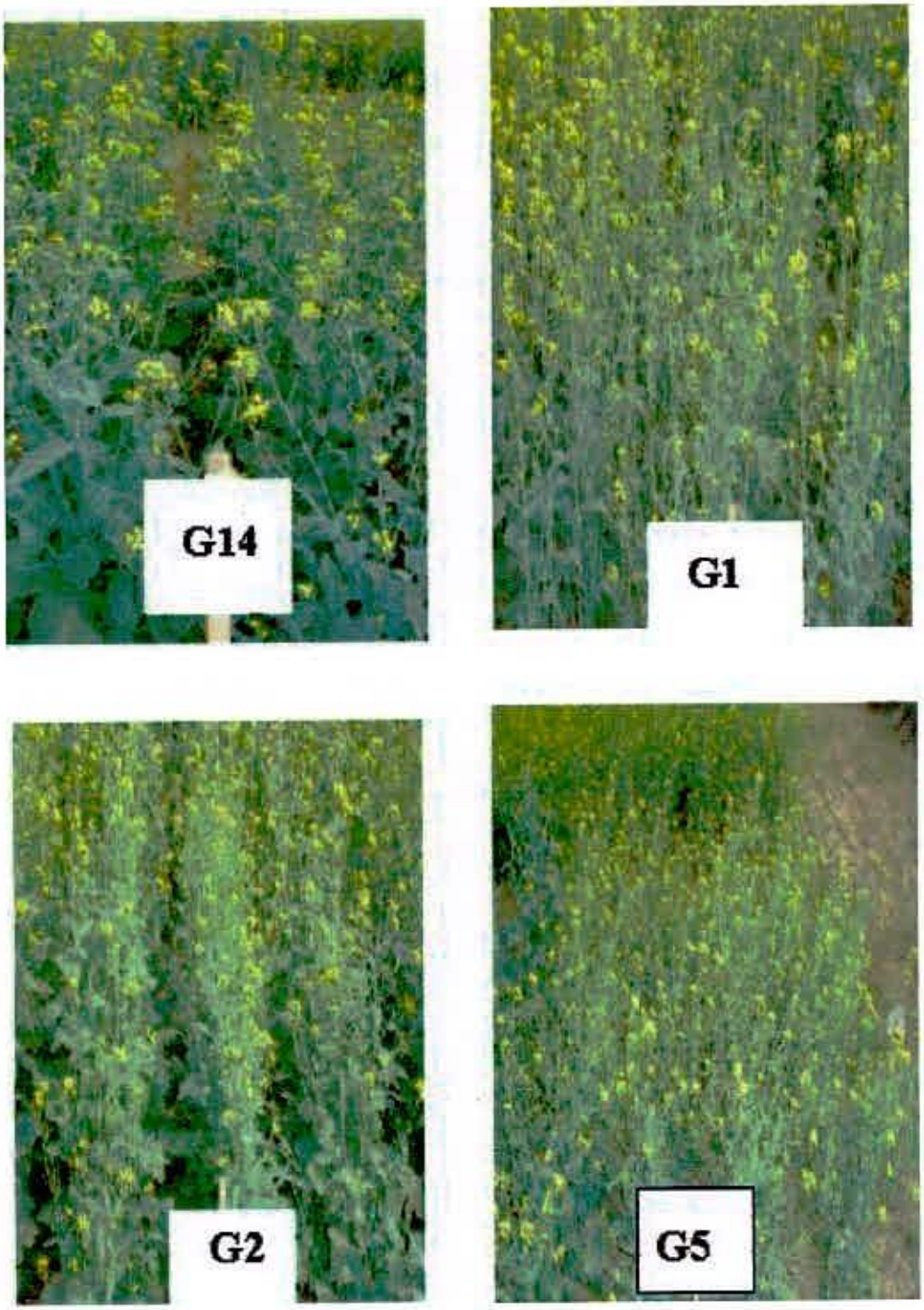

Plate 3. Photograph showing the genotypes G14, G1, G2 and G5 at flowering stage

which indicated that the genotype had high variability (Table 4). Lekh *et al.* (1998) reported similar results in their study.

4.1.4 Days to 50% Flowering

From the (Table 3) there were highly significant variations among the genotypes (61.020**) for days to 50% flowering. The days to 50% flowering was observed highest (41) in G18 which was statistically similar with G1, G2 and G16 but significantly different from other genotypes. The lowest value found in G17 (25) which was followed by G8 (Table 4).

Genotypic and phenotypic variance of days to 50% flowering was observed 18.66 and 23.71, respectively with high differences between them indicating large environmental influences on these character for their phenotypic expression and values of GCV and PCV were 12.75% and 14.37% respectively which indicate moderate variability present among the genotypes for this character (Table 6). Lekh *et al.* (1998) recorded highest GCV and PCV for days to 50% flowering. A field view of different days to 50% flowering of *Brassica* is presented in plate 4.

4.1.5 Days to Maturity

Significant difference was observed among all genotypes (32.153**) studied for this character (Table 3).The days to maturity was observed lowest in G16 (86) which was statistically significant and different from those of 17 other genotypes. The highest value was in G2 and G4, which was statistically significant and different from those of 16 other genotypes.

Genotypic and phenotypic variance of days to maturity was observed 8.95 and 14.25 respectively with high differences between them indicating that they were more responsive to environmental factors for their phenotypic

Plate 4. Photograph showing the different days to 50% flowering

Plate 5. Photograph showing the genotypes G4 at maturity stage

expression and values of GCV and PCV were 3.23% and 4.08%, respectively which indicated that the genotype has relatively less variation (Table 5). Higher genotypic variances indicate the better transmissibility of a character from parent to the offspring (Ushakumari *et al.* 1991).

4.1.6 Number of Siliquae/Plant

The mean square value due to genotype from the analysis of variance was found statistically significant at 1% level of probability for number of siliquae/plant among the genotypes used as experimental material under the present experiment (Table 3). From the mean value it was found that the highest number of siliquae/plant was recorded for the genotype G12 (259) which was closely followed by the genotype G3 (244) while the minimum number (79) was recorded for the genotype G18.

The phenotypic variance (2539.52) was considerably higher than the genotypic variance (1881.31) and the phenotypic and genotypic co-efficient of variations were 26.54% and 22.84%, respectively (Table 5). The result indicated the existence of inherent variability among the population with possibility of high potential for selection. Highest phenotypic and genotypic variances and genotypic and phenotypic co-efficient of variations for number of pod / plant were also observed by Mishra and Yadav (1992), Uddin *et al.* (1995), Azad and Hamid (2000) and Venkatramana *et al.* (2001)

4.1.7 Length of Siliqua (cm)

A significant variation was recorded among the genotypes in consideration of length of siliquae (Table 3). Maximum length of siliquae were recorded in G18 (5.33cm) genotypes followed by G14 (4.26cm). Minimum length of siliquae (3.30 cm) was recorded for the genotype G12 (Table 4)

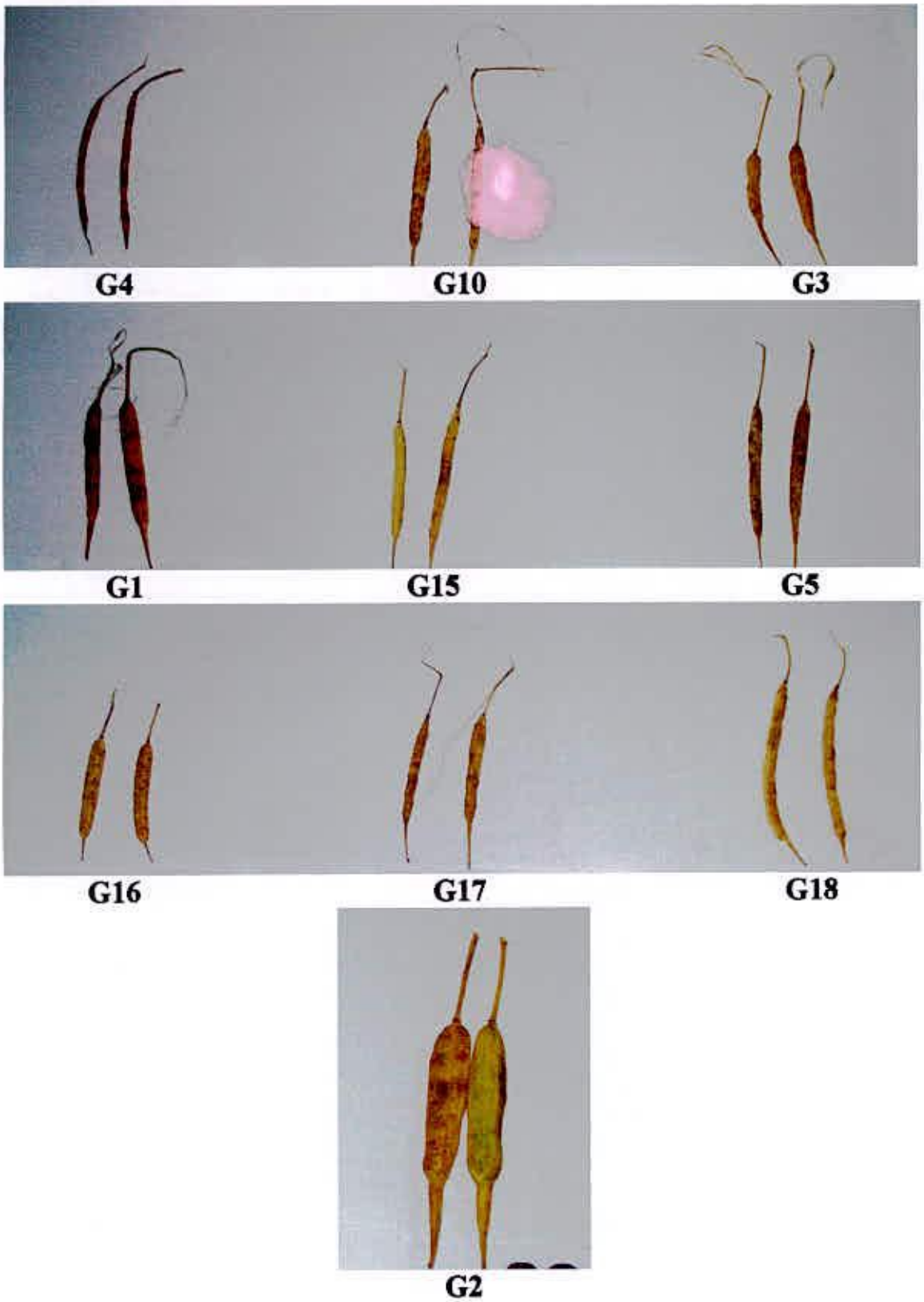

Plate 6. Photograph showing the length of siliqua in respect of different genotypes

Length of siliqua showed minimum amount of genotypic and phenotypic variance (0.17 and 0.25, respectively) with minimum difference between them indicating that they were less responsive to environmental factors for their phenotypic expression. According to Table 5, GCV and PCV of 10.51% and 12.98% respectively for length of siliqua which indicate that sufficient variation exist among different genotypes. Deshmukh *et al.* (1986) also reported phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation. (Plate 6 showing the length of siliqua in different genotypes).

4.1.8 Number of Seeds / Siliqua

The value of the analysis of variance of the data for the number of seeds/siliqua showed highly significant difference (26.070**) among the genotypes of *Brassica* used in the present experiment. The mean squares value regarding to the character indicated the presence of variability among the genotypes (Table 3). Maximum number of seed/siliquae was recorded in genotype G16 (22) which was followed by the genotypes G18 and G1 (21 and 21 respectively) and the minimum (12) was recorded in the genotypes G12 which was statistically different from other genotypes

The difference in magnitudes in between genotypic (7.49) and phenotypic (11.29) variances was relatively high for number of seeds per siliqua indicating large environmental influence on these characters (Table 5) and the moderate phenotypic and genotypic co-efficient of variations were 19.98% and 16.16%, respectively (Table 5) for this character of *Brassica* genotypes. The result indicated the existence of adequate variation among the population with possibility of high potential for the selection of low phenotypic co-efficient of variation regarding this which was earlier noticed by Prakash *et al.* (2000). Yogendra *et al.* (2002) also reported low

phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) for this character.

4.1.9 1000 Seed Weight (g)

The mean square due to genotype from the analysis of variance was found statistically significant at 1% level of probability for 1000 seed weight indicating genotypic differences among the genotypes used under the present experiment (Table 3). From the mean value it was found that the highest 1000 seed weight was recorded in the genotype G2 (3.79g) which was followed by G6 (3.50 g) while the lowest 1000 seed weight (2.21g) was in the G16 (Table 4).

The phenotypic variance (0.215) was considerably higher than the genotypic variance (0.103) and the phenotypic and genotypic co-efficient of variations were 16.02% and 11.10%, respectively for 1000 seed weight of *Brassica* genotypes (Table 5). The result indicated the existence of inherent variability among the population with possibility of high potential for selection. Highest phenotypic and genotypic variances and genotypic and phenotypic co-efficient of variations for 1000 seed weight were also observed by Mishra and Yadav (1992), Uddin *et al.* (1995), Azad and Hamid (2000) and Venkatramana *et al.* (2001).

4.1.10 Yield/Plant

In the present experiment, the genotype mean square for seed yield per plant was found significant 5.876** (Table 3). The DMRT test indicated the existence of both significant and insignificant differences in different means. The seed yield per plant was recorded highest in the G1 (8.79) which

G5

G13

G9

G2

G4

Plate 7. Photograph showing the genotypes G5, G13, G9, G2 and G4 at maturity stage

Table 6. Grand mean and range of yield and yield contributing characters of 18 genotypes of *Brassica rapa*

Identifier	Minimum	Maximum	Mean
Plant height	65.4	125.2	101.6
No. of primary branch/plant	4.167	8.067	5.641
No. of secondary branch/plant	1.733	9.400	6.354
Days to 50% flowering	25.33	41.33	33.89
Days to maturity	86.67	99.00	92.63
Siliquae/plant	79.6	259.6	189.9
Siliqua length (cm)	3.296	5.333	3.874
Seeds/pod	12.05	22.89	16.82
1000 seed wt.	2.213	3.787	2.896
Seed yield/plant	4.218	8.967	6.462

was statistically similar with the genotypes G7 and G13 and the lowest mean value (4.22) was in G5 (Table 4). Shen *et al.* (2002) observed significant differences between F_1s and their parents for yield per plant. Katiyar *et al.* (2004) found significant variation among parents and crosses indicated the presence of adequate genetic variance which reflected in differential performance of intervarietal cross combinations of *Brassica campestris*.

Seed yield per plant showed low values of genotypic (1.81) and phenotypic (2.26) variance with little differences indicating that they had some of interaction with environment and moderate GCV (20.81%) and PCV (23.26%) indicating that the genotype are considerably variable for this character (Table 5). Bhardwaj and Singh (1969) reported GCV of seed yield per plant was 96.99% in *Brassica campestris* and Singh (1987) reported values 44.04% and 46.9% of GCV and PCV respectively for *Brassica juncea*.

4.2 Heritability and Genetic Advance

Findings of the heritability, genetic advance and genetic advance in percentage of mean of individual character are discussed in this part of the thesis and the results related to this character are presented in Table 7

4.2.1 Plant Height

Plant height showed very high heritability (78.16%) together with high genetic advance (23.70%) and genetic advance in percentage of mean (23.33) which indicated that most likely the heritability was due to additive gene effects and selection may be effective which was also earlier reported by Singh and Singh (1999).

4.2.2 Number of Primary Branches/Plant

Number of primary branches/plant showed high heritability (71.10%) coupled with low genetic advance (1.82%) and genetic advance in percentage of mean (32.18). These findings revealed that it was indicative of non-additive gene action. The high heritability was being exhibited due to favorable influence of environment rather than genotypes and selection for such traits may not be rewarding which was also earlier reported by Islam and Rasul (1998), Singh and Singh (1999).

4.2.3 Number of Secondary Branches/Plant

High heritability (83.26%) coupled with low genetic advance (4.26%) and high genetic advance in percentage of mean (67.01) was calculated in respect of number of secondary branches/plant. These findings discovered the action of non-additive gene effect on the expression of this character as well as a scope of improvement through selection may not be rewarding which was also earlier reported by Kumar *et al.* (1998)

4.2.4 Days to 50% Flowering

Days of 50% flowering showed high heritability (78.70%) with genetic advance (7.89%) and genetic advance in percentage of mean (23.29) revealing that the character is governed by non-additive genes and heterosis breeding may be useful and also indicates that the character is least influenced by the environmental effects.

Table 7. Heritability, Genetic advance and Genetic advance in percent of means for yield and yield contributing characters of 18 genotypes of *Brassica rapa*

Genetic parameters ➤ / Characters ▼	Heritability h^2_b(%)	Genetic advance	GA in percent of means
		5%	5%
Plant height	78.16	23.70	23.33
No. of primary branches/plant	71.10	1.82	32.18
No. of secondary branches/plant	83.26	4.26	67.01
Days to 50% flowering	78.70	7.89	23.29
Days to maturity	62.81	4.88	5.27
Siliquae/plant	74.08	76.90	40.50
Siliquae length	65.57	0.68	17.53
No. of seeds/siliquae	65.47	4.53	26.94
1000 seed wt.	47.99	0.46	15.84
Seed yield/plant	80.04	2.48	38.35

4.2.5 Days to Maturity

The magnitude of heritability in broad sense (h^2b) of this character was high (62.81%) and low genetic advance (4.88%) and low genetic advance in percentage of mean (5.27). These findings indicative of non-additive gene action. The high heritability is being exhibited due to favorable influence of environment rather than genotypes and selection for such traits may not be rewarding. Similar findings were reported by Alam *et al.* (1985) and Hossain (1988).

4.2.6 Number of Siliquae/Plant

Number of siliquae/plant showed very high heritability (74.08%) coupled with very high genetic advance (76.90%) and very high genetic advance in percentage of mean (40.50). As this trait possessed high genetic advance, it was high potential for effective selection for further genetic improvement of this trait.

4.2.7 Length of Siliquae (cm)

Length of siliquae/plant showed very high heritability (65.57%) with very low genetic advance (0.68%) and genetic advance in percentage of mean (17.53) these findings exposed the action of non-additive gene effect on the expression of this character as well as a scope of improvement through selection.

4.2.8 Number of Seeds/Siliquae

The magnitude of heritability in broad sense (h^2b) of this trait was high (65.47%) and low genetic advance (4.53%) and genetic advance in percentage of mean (26.94). These results indicate non-additive genes

involvements in the expression of the character and this with limit scope of improvement by direct selection.

4.2.9 1000 Seed Weight (g)

High heritability (47.99%) associated with very low genetic advance (0.46%) and genetic advance in percentage of mean (15.84) was calculated in respect of 1000 seed weight of *Brassica* genotypes. These findings exposed the action of non-additive gene effect on the expression of this character as well as a scope of improvement through selection.

4.2.10 Seed yield/Plant (g)

High heritability (80.04%) coupled with low genetic advance (2.48%) and genetic advance in percentage of mean (38.35) was recorded in respect of yield/plant. These findings revealed that it is indicative of non-additive gene action. The high heritability is being exhibited due to favorable influence of environment rather than genotypes and selection for such traits may not be rewarding.

4.3 Diversity

The result of the genetic diversity of *Brassica* genotypes are presented in Table 8 to 13 and Figure 1 to 3.

4.3.1 Principle Component Analysis (PCA)

The principle component analysis produce Eigen values of principle component axes of coordination of genotypes with the first axes totally accounted for the variation among the genotypes, whereas three of these Eigen values above unity accounted for 74.30% (Table 8). The first two principal axes accounted for 61.28% of the total variation among the ten

characters describing 18 genotypes. On the basis of principal axes I and II, a two dimensional chart (Z_1-Z_2) of the genotypes are presented in Figure 1. The scatter diagram revealed that there were four apparent clusters. The genotypes were distantly located from each other (Figure 2).

4.3.2 Principal Coordinate Analysis (PCO)

Principal coordinate analysis was performed on auxiliary of principal component analysis. Inter genotypic distances obtained from Principal Coordinate Analysis showed that the highest distance (1.9795) was observed between the genotypes G6 & G18 followed by G7 & G18 (1.9318), G9 & G18 (1.9288), G3 & G18 (1.8886) and the lowest distance was observed between the genotypes G4 & G15 (0.2199) followed by G9 & G13 (0.2685), G3 & G12 (0.2745) and G7 & G13 (0.3318) (Table 9). By using these distances from distance matrix intra-cluster distances were calculated (Table 12). The highest intra-cluster distance was found in cluster II (1.057) composed of 2 genotypes followed by cluster IV (0.739) with 7 genotypes. The lowest intra-cluster distance was found in cluster I (0.630) composed of 3 genotypes, which is almost similar with cluster III (0.631). These result revealed that the genotypes in cluster II were distantly related, on the other hand the genotypes in cluster I were closely related.

4.3.3 Non-Hierarchical Clustering

Using co-variance matrix with the application of non-hierarchical clustering, the 18 genotypes were grouped into four clusters. These results confirmed the clustering pattern of the genotypes obtained through principal component analysis. Golakiya and Makne (1991) while assessing genetic diversity of 23 groundnut genotypes and grouped them into six clusters. Reddy and

Table 8. Eigen values and percentage of variation in respect of 10 characters in 18 *Brassica rapa* genotypes

Principal component axis	Eigen values	% of total variation accounted for	Cumulative percent
I	3.732	33.93	33.93
II	3.008	27.35	61.28
III	1.432	13.02	74.30
IV	1.065	9.68	83.98
V	0.672	6.11	90.09
VI	0.39	3.54	93.63
VII	0.318	2.90	96.53
VIII	0.138	1.25	97.78
IX	0.121	1.10	98.88
X	0.09	0.82	99.70

Table 9. Ten of each higher and lower inter-genotypic distance (D^2) between pair of *Brassica rapa* genotypes

10 higher value D^2 value	Genotypes combination	10 lower D^2 values	Genotypes combination
1.9795	G6 & G18	0.2199	G4 & G15
1.9318	G7 & G18	0.2685	G9 & G13
1.9288	G9 & G18	0.2745	G3 & G12
1.8886	G3 & G18	0.3318	G7 & G13
1.8666	G5 & G18	0.3327	G7 & G9
1.8585	G13 & G18	0.3356	G6 & G15
1.7518	G10 & G18	0.3360	G9 & G11
1.7481	G17 & G18	0.3561	G8 & G15
1.6097	G12 & G17	0.3582	G3 & G9
1.5926	G2 & G18	0.3736	G7 & G11

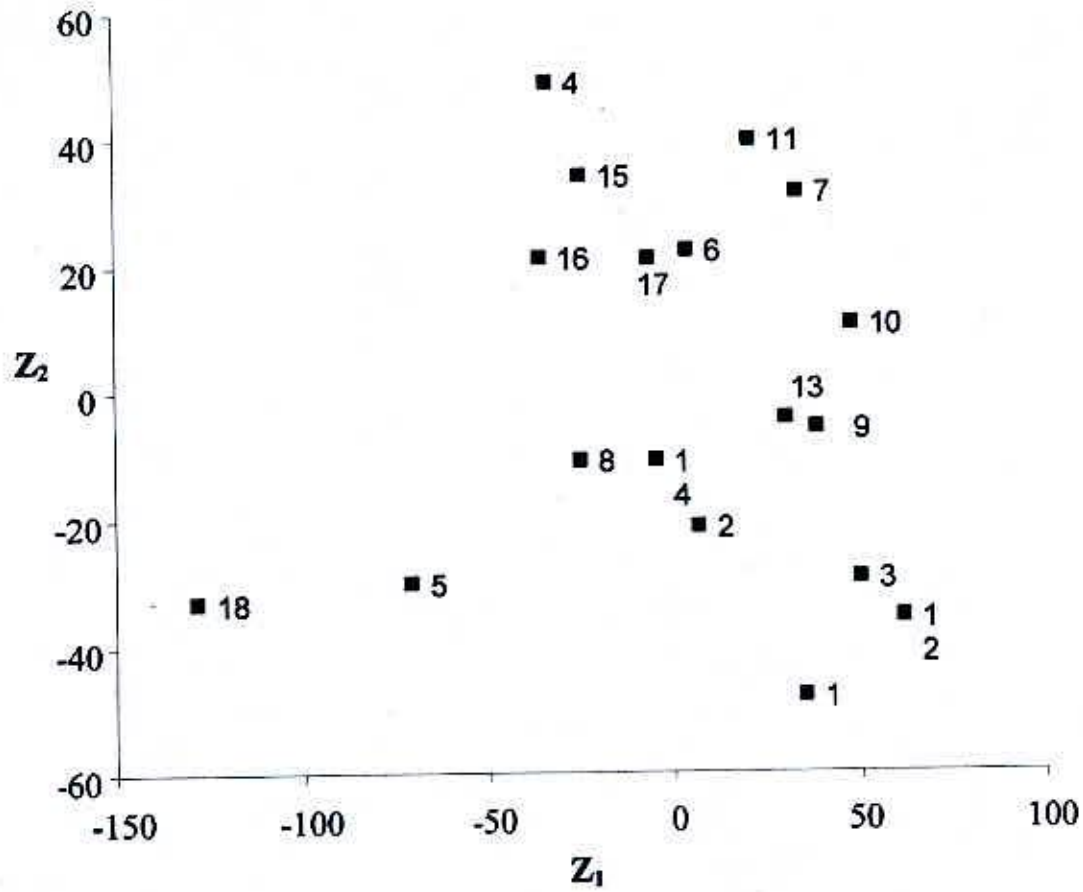

Figure 1: Scatter distribution of 18 *Brassica rapa* genotypes based on their principal component scores

Reddy (1987) reported on 48 genotypes of which were grouped into 11 clusters. On the other hand Baydar and Bayraktar (1994) reported 35 genotypes which were divided into 6 clusters of different genetic divergences. Badignnavar *et al.* (2002), Joel and Mylsamy (1998), Islam *et al.* (1995) were found the same results Compositions of different clusters with their corresponding genotypes in each cluster are presented in Table 6.

Cluster IV had maximum number of genotypes (7) followed by III, I and II which had 6, 3 and 2 genotypes, respectively (Table 10). Cluster I composed of 3 genotypes namely G2, G8 and G14. From the clustering mean values (Table 11), it was observed that the mean value of cluster I ranked first for number of primary branch (5.99) and days to maturity (95.33).

Cluster II was composed of 2 genotypes namely G5 and G18 (Table 10). Cluster II had the highest cluster mean for days to 50% flowering (37.83), siliquae length (4.53), seeds/ siliquae (18.22) and 1000 seed wt. (3.00) and the lowest for days to maturity (90.83), number of primary branch (4.40) and number of secondary branch (3.17) (Table11).

Cluster III constituted of six genotypes namely G1, G3, G9, G10, G12 and G13 (Table 10). This group possessed genotypes with the highest cluster mean for plant height (109.63), number of secondary branch (7.51), siliquae/plant (236.72) and seed yield/plant (7.16). This cluster contains tallest plant (Table 11).

Cluster IV had maximum number of (7) genotypes namely G4, G6, G7, G11, G15, G16 and G17 (Table 10). These group contained the second highest cluster mean for number of secondary branch (6.49), days to maturity (92.81), seed/siliquae (17.22) and seed yield/plant (6.43). The

maximum range of variability was observed for number of siliquae/plant (106.43-236.72) among all the characters in four clusters (Table 11).

4.3.4 Canonical Variate Analysis (CVA)

To compute the inter-cluster Mahalanobis's D^2 values canonical variate analysis was used. The Table 12 indicates the intra and inter-cluster distance (D^2) values. The inter-cluster distances were higher than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups. Singh *et al.* (1987) obtained larger inter-cluster distances than the intra-cluster distances in a multivariate analysis in mustard. Results indicated that the highest inter-cluster distance was observed between clusters II and III (11.697), followed by between cluster II and IV (9.812), I and II (8.721), III and IV (6.770) (Table 12). The lowest inter-cluster distance was observed between cluster I and III (3.619), followed by I and IV (3.941). However, the maximum inter-cluster distance was observed between the clusters II and III (11.697) maintaining more distance than other clusters. Genotypes from these two clusters, if involved in hybridization may produce a wide spectrum of segregating population.

Similar reports were also made by Singh *et al.*, (1996). Zhang *et al.*, (1987) reported that the greater genetic distances implying higher heterosis than those with similar genetic distances. The intra-cluster distance varied from 0.630-1.057. Result of different multivariate analysis were superimposed in Figure 3 from which it may be concluded from the above results that different multivariate techniques supplemented and confined one another.

Table 10. Distribution of 18 genotypes of *Brassica rapa* in four clusters

Cluster	Number of genotypes	Name of genotypes
I	3	G2, G8, G14
II	2	G5, G18
III	6	G1, G3, G9, G10, G12, G13
IV	7	G4, G6, G7, G11, G15, G16, G17

Table 11. Cluster means for 10 characters of 18 *Brassica rapa* genotypes

Characters	Cluster			
	I	II	III	IV
Plant height (cm)	105.64	94.75	109.63	94.91
Number of primary branches/plant	5.99	4.40	5.97	5.56
Number of secondary branches/plant	5.84	3.17	7.51	6.49
Days to 50% flowering	35.56	37.83	33.56	32.33
Days to maturity	95.33	90.83	91.67	92.81
Siliquae/plant	186.86	106.43	236.72	174.83
Siliqua length	3.86	4.53	3.70	3.84
Seeds/pod	17.18	18.22	15.71	17.22
1000 seed wt. (gm)	2.89	3.00	2.89	2.87
Yield/plant (gm)	6.26	4.78	7.16	6.43

A two-dimensional scatter diagram was constructed using component I in X-axis and component II in Y-axis, reflecting in the relative position (Figure 1). As per scatter diagram the genotypes were apparently distributed into four clusters. It was also revealed that the genotypes of cluster II was more diverse from the genotypes of cluster I. 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 existed between cluster II and cluster III (Figure 3). But considering duration and yield, crosses involving cluster II and cluster III 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. Keeping this in view, it appears that the crosses between the genotypes belonging cluster II with cluster IV and genotypes in cluster I with cluster II might produce high heterosis for yield as well as for earliness. Also the crosses between genotypes from cluster II with cluster I and IV might produce high level of segregating population. So the genotypes belonging to cluster I and cluster II, cluster II and cluster IV and cluster III and cluster IV have been selected for future hybridization program.

4.4 Contribution of Characters towards Divergence of the Genotypes

Contribution of characters towards divergence of the genotypes is presented in table 13. The vector-I (Z_1) obtained from PCA, the important characters responsible for genetic divergence in the axis of the differentiation were 1000 seed wt. (3.2986), number of primary branches (1.2725), number of secondary branches (0.2329) and days to 50% flowering (0.0216). In vector-II (Z_2), number of primary branches (0.4983), seeds/pod (0.4577),

Table 12. Average inter cluster distance (D^2) and Intra cluster distance (bold) for 18 *Brassica rapa* genotypes

Cluster	I	II	III	IV
I	**0.630**			
II	8.721	**1.057**		
III	3.619	11.697	**0.631**	
IV	3.941	9.812	6.770	**0.739**

Table 13. Latent Vectors for 10 characters of 18 *Brassica rapa* genotypes

Characters	Vectors 1	Vectors 2
Plant height	-0.0410	-0.1276
No.of primary branch/plant	1.2725	0.4983
No.of secondary branch/plant	0.2329	0.0004
Days to 50% flowering	0.0216	0.2696
Days to maturity	-0.3396	0.0868
Siliqua/plant	-0.0893	0.0013
Siliqua length	-0.1884	-1.9633
seed/pod	-0.2035	0.4577
1000 seed wt.	3.2986	-0.0089
Yield/plant	-0.6378	-0.6309

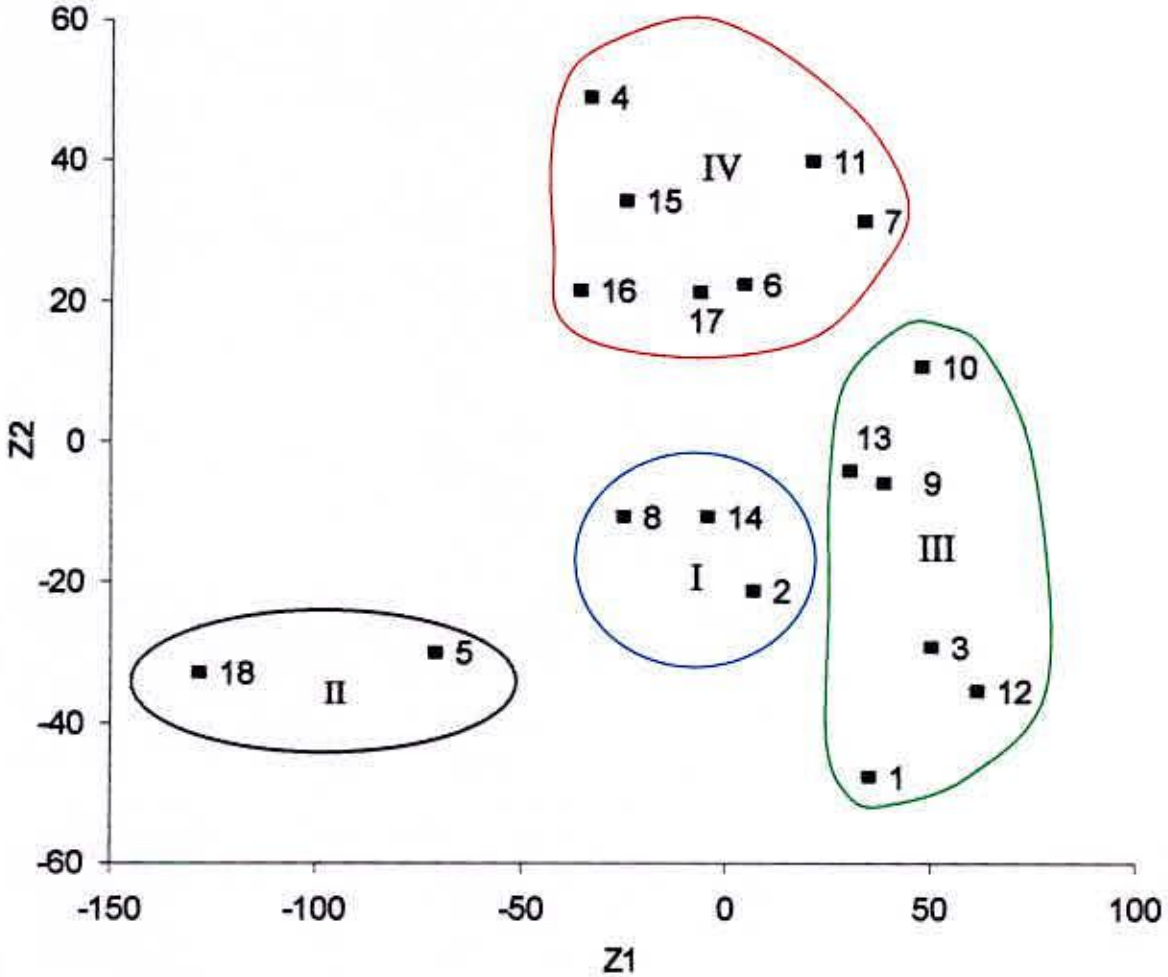

Figure 2: Scatter distribution of 18 *Brassica rapa* genotypes based on their principle component scores superimposed with clustering

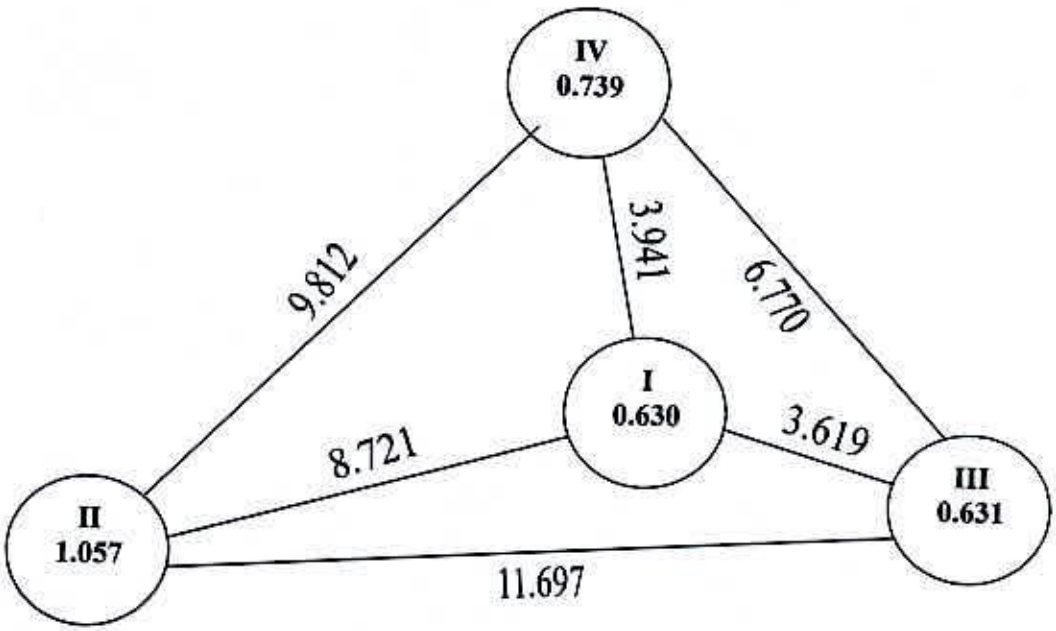

Figure 3: Diagram showing intra and inter cluster distances (D^2) of 18 *Brassica rapa* genotypes

days to 50% flowering (0.2696), days to maturity (0.0868), siliquae/plant (0.0013) and number of secondary branches/plant (0.0004) were important but plant height, days to maturity, siliquae/plant, siliquae length, seed/ siliquae and seed yield/plant played only a minor role in the first axis of differentiation. The role of number of primary branch, number of secondary branch and days to 50% flowering in both the vectors were important components for genetic divergence in these materials.

4.5 Comparison of Different Multivariate Techniques

The clustering pattern of D^2 analysis through non-hierarchical clustering has taken care of simultaneous variation in all the characters under study. The distribution of genotypes in different clusters of the D^2 analysis has followed more or less similar trend of the Z_1 (principle component score I) and Z_2 (principle component score II) vectors of the principle component analysis. The D^2 and principle component analysis were found to be alternative methods in giving the information regarding the contribution of characters towards divergence in mustard.

4.6 Selection of Parents for Future Hybridization

A higher heterosis could be produced from the crosses between genetically distant parents. Selection of genetically diverse parents with specific objectives is an important step for hybridization program. Considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotypes G2 for higher seed yield/plant and for highest 1000 seed wt; G8 for lower plant height, lower days to 50% flowering and G14 for lower days to maturity from cluster I; G18 for highest length of siliquae and lower days to maturity

from cluster II; G1 for highest number of primary branch and for highest yield/plant; G3 for higher number of siliquae/plant and G9 for lower days to 50% flowering, G12 for highest number of siliquae/plant from cluster III; G16 for lowest days to maturity and G17 for lowest days to 50% flowering and plant height from cluster IV were found promising. Therefore considering group distance and other agronomic performance genotypes G8, G9, G12 and the inter genotypic crosses between G2 and G17; G3 and G17; G1 and G17; G2 and GI; G1 and G16 may be suggested for future hybridization program to develop high yielding varieties with early maturity.

Chapter 5
Summary & Conclusion

V. SUMMARY AND CONCLUSION

Inter-genotypic variability and genetic diversity were studied in 10 F_4 lines obtained through inter varietal crosses along with 8 released varieties of *Brassica rapa* at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, during November 2007 to March 2008. Seeds are sown in the field in Randomized Complete Block Design (RCBD) with three replications. Data on Plant height (cm), number of primary branches/plant, number of secondary branches/plant, days to 50% flowering, days to maturity, number of Siliquae /plant, 1000 seed wt. (g), number of seeds/siliquae, Siliquae length (cm), seed yield/ plant (g) were recorded. The variation within F_4 materials of each cross was minimum but there were highly significant variations among the different crosses for almost all the characters studied.

The highest mean value was observed for number of siliquae/plant (189). This character also exhibited the highest range of variation (79.60-259.57) indicated that all the genotypes showed wide range of variation in respect of this character. The phenotypic variance was higher than the corresponding genotypic variance for all the characters. However, these differences were in case of plant height, days to 50% flowering, days to maturity, siliquae/plant, number of seeds/siliquae indicating greater influence on environment for the expression of these characters. Among these characters, number of primary branches/plant, number of secondary branches/plant, siliquae length, 1000 seed wt. and seed yield/plant showed least difference between phenotypic and genotypic variance, which indicated additive gene action for the expression of this characters. All these characters showed moderate to high

phenotypic and genotypic co-efficient of variation except days to maturity. Among the characters the highest genotypic co-efficient of variation was recorded in number of secondary branches/plant (35.65) followed by siliquae/plant (22.84), yield/plant (20.81), number of primary branches/plant (18.53), number of seeds/siliquae (16.16), Plant height (12.81) in order of merit.

Heritability in broad sense was moderate to high for all the characters studied and it ranged from 47.99 % to 83.26 % which indicated that selection based on phenotypic expression of any character for breeding could be effective. The genetic advance was moderate to high for almost all the characters except number of primary branches/plant, length of siliqua and thousand seed weight. Thus, the genotypes which performed well in various characters were due to genetic reasons and have a possibility for improvement through selection in the subsequent generations.

Multivariate analysis was performed through Principal Component Analysis, Principal Coordinate Analysis, Cluster Analysis, Canonical Variate Analysis using GENSTAT 513 software program. As per PCA, D^2 and cluster analysis, the genotypes grouped into four clusters. Four clusters were found from a scatter diagram formed by Z_1 and Z_2 values obtained from PCA. Inter genotypic distances obtained from Principal Coordinate Analysis showed that the highest distance (1.9795) was observed between the genotypes G6 & G18 and the lowest distance was observed between the genotypes G4 & G15 (0.2199) The highest intra-cluster distance was found in cluster II (1.057) which composed of 2 genotypes and the lowest in cluster I (0.630). The highest inter-cluster distance was observed between cluster II and cluster III (11.647) followed by cluster II and cluster IV

(9.812). The lowest inter-cluster distance observed between cluster I and III (3.691) followed by cluster I and cluster IV (3.941). Genotypes included in cluster I were important for seed yield/plant, days to 50% flowering and lowest plant height; cluster II for highest for length of siliquae; cluster III for siliquae/plant and cluster IV were found promising for days to maturity.

Considering cluster distance, inter genotypic distance and other agronomic performance G2 and G14 from cluster I; G18 from cluster II; G1, G9 and G12 from cluster III and G16 and G17 from cluster IV may be considered to be better parents for future uses in hybridization program to develop high yielding varieties with early maturity.


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Appendices

Appendix I. Physical and Chemical characteristics of initial soil in the experimental field

A. Physical composition of the soil

Soil separates	*(%)*	*Method employed*
Sand	36.90	Hydrometer method (Day, 1995)
Silt	26.40	-do-
Clay	36.66	-do-
Texture class	Silty clay loam	-do-

B. Chemical composition of the soil

Sl. No.	*Soil Characteristics*	*Analytical data*	*Method employed*
1.	Organic carbon (%)	0.82	Walkly and Black, 1947
2.	Total N (kg/ha)	1790.00	Bremner & Mulvaney, 1995
3.	Total S (ppm)	225.00	Bardsley and Lancster, 1965
4.	Total P (ppm)	840.00	Olsen and Sommers, 1982
5.	Available N (kg/ha)	54.00	Bremner, 1965
6.	Available P (kg/ha)	69.00	Olsen and Dean, 1965
7.	Exchangeable K (kg/ha)	89.50	Pratt, 1965
8.	Available S (ppm)	16.00	Hunter, 1984
9.	P^H (1:2.5 soil to water)	5.55	Jeckson, 1958
10.	CEC	11.23	Chapman, 1965

Source: Soil Resources Development Institute (SRDI), Khamarbari, Dhaka

Appendix II. Monthly average temperature, relative humidity and total rainfall of the experimental site during the period from November 2007 to April 2008

Year	Month	*Air temperature (^{0}C)		*Relative Humidity (%)	*Total Rainfall (mm)	*Sunshine (hr)
		Maximum	Minimum			
2007	November	31.8	16.8	67	111	5.7
	December	28.2	11.3	63	0	5.5
2008	January	29.0	10.5	61.5	23	5.6
	February	30.6	10.8	54.5	56	5.8
	March	34.6	16.5	61.5	45	5.8
	April	36.9	19.6	59.5	91	8.3

*Monthly average

Source: Bangladesh Meteorological Department (Climate division), Agargaon, Dhaka - 1207

Appendix III. Principal component scores for 18 *Brassica rapa* genotypes

Designation	Z_1	Z_2
G1	35.07	-47.86
G2	6.82	-21.32
G3	49.97	-29.37
G4	-33.35	48.93
G5	-70.92	-30.03
G6	4.09	22.27
G7	33.53	31.40
G8	-24.87	-10.82
G9	38.45	-5.87
G10	47.89	10.61
G11	21.07	39.69
G12	61.50	-35.57
G13	30.17	-4.30
G14	-4.54	-10.84
G15	-24.57	34.06
G16	-35.52	21.22
G17	-6.36	20.93
G18	-128.43	-33.12