GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN F_5 POPULATION OF *Brassica napus* L.

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CERTIFICATE

This is to certify that thesis entitled, ***"Genetic variability and character association in F_5 population of Brassica napus L."*** *submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of* ***MASTER OF SCIENCE in GENETICS AND PLANT BREEDING,*** *embodies the result of a piece of bona fide research work carried out by* ***SAYEDA MOSAMMAD SALWA KHATUN MILI,*** *Registration No.* ***08-03163*** *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, 2014
Place: Dhaka, Bangladesh

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TO

MY BELOVED PARENTS

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BY

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ABSTRACT

A field experiment was conducted with 66 F_5 genotypes of *Brassica napus* L. at the experimental field of Sher-e-Bangla Agricultural University, Dhaka to study the genetic diversity, variability, correlation and path coefficient analysis during November 2013 to February 2014. The genotypes were found significantly variable for most of the characters. Comparatively phenotypic variances were higher than the genotypic variances for all the characters studied. Also PCV were higher than the GCV for all the characters studied. Number of secondary branch, thousand seed weight, number of primary branch, number of siliqua per plant and seed yield per plant showed high broad base heritability. The significant positive correlation with seed yield per plant was found in number of siliqua per plant, siliqua length, number of seed per siliqua and thousand seed weight. Path coefficient analysis revealed that 50% flowering, number of siliqua per plant, number of seed per siliqua and thousand seed weight had the positive direct effect on yield per plant. The genotypes were grouped into six clusters. The highest inter cluster distance was observed between cluster IV and VI and the maximum intra cluster distance was found in cluster V. Considering group distance and other agronomic performance genotypes G12, G14, G15, G16, G17, G22 and G24 might be suggested for future hybridization program.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

LIST OF ABBREVIATED TERMS

Abbreviation	Full word
%	Percent
°C	Degree Celsius
@	At the rate
σ^2 p	Phenotopic variance
σ^2 g	Genotypic variance
σ^2 e	Environmental variance
h^2 b	Heritability in broad sense
AEZ	Agro-Ecological Zone
Agric.	Agriculture
Agril.	Agricultural
Agron.	Agronomy
Anova	Analysis of variance
BARI	Bangladesh Agricultural Research Institute
BBS	Bangladesh Bureau of Statistics
BD	Bangladesh
CN	Centi-meter
CV%	Percentage of Coefficient of Variation
cv.	Cultivars
Df	Degrees of Freedom
et al.	And others
etc.	Etcetera
F_3	The third generation of a cross between two dissimilar homozygous parents
FAO	Food and Agricultural Organization
g	Gram
G	Genotype
GA	Genetic Advance
GCV	Genotypic coefficient of variation
HI	Harvest Index
IARI	Indian Agricultural Research Institute
ICARDA	International Center for Agricultural Research in Dry Areas
J.	Journal
Kg	Kilogram
m	Meter

(Continued...)

Abbreviation	Full word
MS	Mean sum of square
MP	Murate Potash
MOA	Ministry of Agriculture
m^2	Square meter
PCV	Phenotypic coefficient of variation
RCBD	Randomized Complete Block Design
SAU	Sher-e-Bangla Agricultural University
TSP	Triple Super Phosphate

CHAPTER I
INTRODUCTION

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INTRODUCTION

Rapeseed is a major oilseed crop in Bangladesh. It contributes a lion share to the total edible oil production in the country. *Brassica* belonging to the family Brassicaceae is a wide genus of cross pollinated oil crops and also an important genus of plant kingdom consisting of over 3200 species with high diverse morphology. *Brassica* have taproot system, with succulent, straight and cylindrical stem. The leaves are pinnati-divided. The inflorescence is racemose and flowering is determinate beginning at the lowest bud on the main raceme and blooming continues for two-three weeks. Stigma is receptive for about six days.

The primary centre of origin for *Brassica napus* is near the Himalayan region and the secondary centre of origin is located in the European- Mediterranean area and Asia (Downy and Robelen, 1989). Major producing regions are China, the Indian subcontinent, Canada and Northern Europe (Ram and Hari, 1998).

The genus *Brassica* has generally been divided in to three groups namely- rape seed, mustard and cole. The rape seed group includes the diploid *Brassica napus* L, rape (AACC, 2n=38) while the mustard groups include species like *Brassica juncea* Czern Coss; *Brassica nigra* Koch and *Brassica carinata* Braun (Yarnell, 1956). Rapeseed (*Brassica napus* L., genome AACC, 2n = 38) is a relatively young species that originated in a limited geographic region through spontaneous hybridisations between turnip rape (*B. rapa* L., AA, 2n = 20) and cabbage (*B. oleracea* L., CC, 2n = 18) genotypes (Kimber and McGregor 1995), resulting in an amphidiploid genome comprising the full chromosome complements of its two progenitors. The species is divided into two subspecies, namely *B. napus* ssp. *napobrassica* (swedes) and *B. napus* ssp. *napus*, which includes winter and spring oilseed, fodder and vegetable forms. The latter include the distinct leaf rapes (*B. napus* ssp. *napus* var *pabularia*), which used to be common as a winter-annual vegetable (Snowdon *et al.* 2006). Rapeseed cultivars are classified as winter or spring types according to their vernalisation requirement in order to induce flowering. Winter cultivars are usually

higher yielding than spring cultivars, but they can only be grown profitably in areas where they regularly survive the winter (Butruille *et al.* 1999). Oilseed rape is cultivated predominantly as winter or semi-winter forms in Europe and Asia, respectively, whereas spring-sown canola types are more suited to the climatic conditions in Canada, northern Europe and Australia (Friedt *et al.* 2007).

Today oilseed rape (*B. napus* ssp. *napus*) is the most important source of vegetable oil in Europe and the second most important oilseed crop in the world after soybean (data from FAOstat: http://faostat.fao.org/). It is not only a high energy food but also a carrier for fat soluble vitamins (A, D, E and K) in the body. The seeds of modern varieties typically contain 40 to 45% oil, which provides a raw material for many other products ranging from rapeseed methyl ester (biodiesel) to industrial lubricants and hydraulic oils, tensides for detergent and soap production and biodegradable plastics (Friedt *et al.* 2007). After oil extraction the residual meal, which contains 38-44% of high quality protein, is used in livestock feed mixtures. However the nutritional value of rapeseed meal is compromised by the presence of glucosinolates, a group of secondary compounds typical for crucifer plant species. Leaf glucosinolates play an important role in interactions with insect pests and pathogens. On the other hand, high intakes of seed meal glucosinolates and their degradation products in livestock feeds can cause problems of palatability and are associated with goitrogenic, liver and kidney abnormalities (Walker and Booth 2001). In contrast to soybean meal, rapeseed meal is not widely used for human consumption (Snowdon *et al.* 2006).

Brassica, accounting for over 16% of the world's edible oil supply (Anonymous, 2005). It occupies the 1st position in respect of area and production among the oil crops grown in Bangladesh. In Bangladesh, 252238.13 ha of land was under rapeseed cultivation during 2010-11 which produced about 246494 tons of seed and average yield was 0.977 ton/ha (BBS, 2011b). Bangladesh is deficit in edible oil, which costs valuable foreign currency for importing seeds and oil. Annually country is producing about 832638.72 tons of edible rapeseed oil as which is very low against the requirement (BBS, 2011a). Bangladesh imports 89970.08 tons of edible oil to meet up the annul requirement of the country in the year of 2010-11, which costs 3718457000 Tk. (BBS, 2011c). The main reasons behind these are the use of low yielding local indigenous cultivars, unavailability of locally developed hybrids and low management

practices. Also this crop is mostly grown under residual soil moisture in winter season by following poor cultural practices; the average yield is quite low than in the developed countries (Hasanuzzaman and karim, 2007). The area for rapeseed and mustard is reduced from 784730 acres in 2000-01 to 578028 acres in 2008-09. There is 26.32% reduction in area for this crop (Bhuiyan, 2012). For increasing the yield of rape seed expansion of cultivated area is needed. There is a limited scope for horizontal expansion of its cultivation. So, for increasing rapeseed production its yield must be increased per unit area. Therefore, high yielding and short duration rapeseed varieties should be developed to fit into the existing cropping pattern (T-amon-mustard-Boro).

One of the main objectives of any breeding program is to produce high-yielding and better-quality lines for release as cultivars to farmers. The prerequisite to achieve this goal is to find sufficient amount of variability, in which desired lines are to be selected for further manipulation to achieve the target. Analysis of variability among the traits and the association of a particular character in relation to other traits contributing to yield of a crop would be of great importance in planning a successful breeding program (Mary and Gopalan 2006). Development of high-yielding cultivars requires a thorough knowledge of the existing genetic variation for yield and its components. The observed variability is a combined estimate of genetic and environmental causes, of which only the former one is heritable. However, estimates of heritability alone do not provide an idea about the expected gain in the next generation, but have to be considered in conjunction with estimates of genetic advance, the change in mean value among successive generations (Shukla *et al.*, 2006). Seed yield is a complex character that can be determined by several components reflecting positive or negative effects upon this trait, whereas it is important to examine the contribution of each of the various components in order to give more attention to those having the greatest influence on seed yield (Marjanovic-Jeromela *et al.*, 2007). Determination of correlation coefficients is an important statistical procedure to evaluate breeding programs for high yield, as well as to examine direct and indirect contributions to yield variables (Ali *et al.*, 2003). Path-coefficient technique splits the correlation coefficients into direct and indirect effects via alternative characters or pathways and thus permits a critical examination of components that influence a given correlation and can be helpful in formulating an

efficient selection strategy (Sabaghnia *et al.*, 2010). Therefore, correlation in combination with the path coefficient analysis quantifies the direct and indirect contribution of one character upon another (Dewey and Lu, 1959).

Genetic diversity refers to sum total of genetic variations found in a species or population. It is a prerequisite for the development of improved cultivars with wider adaptability and broad genetic base. Diversity analysis greatly helps the breeder in identification and proper choice of parents for specific breeding objectives. To realize heterosis, genetically divergent parents are generally considered to be useful. In such crosses more variability could be expected in the resulting segregating progenies (Joseph *et al.*, 1999). Precise information about the extent of genetic divergence on characters used for discrimination among the population is crucial in any crop improvement program, because selection of plants based on genetic divergence has become successful in several crops (Ananda and Rawat 1984; De *et al.*, 1988).

Keeping these in mind, this research was undertaken with following objectives:

Objectives:

- To study the variability of important quantitative characters in F_5 generation,
- To study the interrelationships of yield contributing characters among themselves and with seed yield; and their direct and indirect effects,
- To assess the contribution of different traits towards divergence, and
- To select promising genotypes considering early maturity and high yield.

CHAPTER II
REVIEW OF LITERATURE

CHAPTER II

REVIEW OF LITERATURE

Extensive researches on *Brassica* breeding have been performed in many countries for its improvement in respect of yield and yield contributing characters. A large number of literatures are available on variability, correlation and path analysis of yield and yield contributing characters of *Brassica* grown under a particular environment. An attempt has been made here to summarize the findings of this study relevant to the present investigation. The whole review has been divided into following sections, namely -

- Genetic variability, heritability and genetic advance
- Correlation among different characters
- Path co-efficient analysis
- Genetic Diversity analysis

2.1. Genetic variability, heritability and genetic advance

Genetic variability is a prerequisite for initiating a successful breeding program aiming to develop high-yielding varieties. Large numbers of literatures concerning the variability in the *Brassica* spp. are available. These literatures are outlined here.

Helal *et al.* (2014) conducted an experiment to study Genetic variability, correlation of yield and yield contributing characters and coefficient of variance in rapeseed or mustard. The results revealed that varieties produced the highest seed yields and 15% variation at genotypic and phenotypic level.

Abideen *et al.* (2013) conducted an experiment to study the genetic variability and correlation among different traits in *Brassica napus*. Results revealed that highly significant differences among the genotypes for most of the traits. Non significant differences were observed among the genotypes for primary branches and pods.

Rameeh (2013) evaluated twenty four rapeseed genotypes including two cultivars and 22 advanced lines, were based on randomized complete block design with three replications. Significant genotypes effects were exhibited for phenological traits, plant

height, yield components and seed yield, indicating significant genetic differences among the genotypes. High broad sense heritability were estimated for phenological traits, pods on main axis and seed yield, signifying selection gain for improving these traits. Duration of flowering and pods on main axis had high value of genetic coefficient of variation.

Belete *et al.* (2012) undertaken an investigation to estimate various genetic parameters for some agronomic traits of introduced Ethiopian mustard (*Brassica carinata* A. Brun) genotypes. The experiment was laid out in randomized complete block design with three replications at Holetta Research Center, Ethiopia. Analysis of variance showed significance difference among the genotypes for traits studied except plant height and seed yield. Phenotypic coefficient of variation and genotypic coefficient of variation ranged from 1.2-10.2% and 1.9-6.8%, respectively. The highest heritability values was shown by oil content (99.8%) followed by days to flowering (96.5%) and days to maturity (89.1%). High heritability along with high genetic advance (as percent of mean) was recorded for days to flowering and oil content. Days to flowering, days to maturity and oil content are important traits to be considered for further variety development program.

Zebarjadi *et al.* (2011) conducted an experiment to study some traits and to estimate genetic parameters in sixteen rapeseed genotypes in two conditions (irrigation and non-irrigation). Statistical analysis showed significant differences among the genotypes based on the data for 13 different characters, including chlorophyll content (SPAD), sugar solution (SS), stem size (SS), plant height, oil percent, oil yield etc. In stress condition heritability was maximum for oil percentage, whereas low genetic advance was observed for thousand kernel weight.

Alam (2010) was conducted a research by using 26 F_4 populations of some inter-varietal crosses of *Brassica rapa* to study the magnitude of variations in different characters heritability, genetic advance. There were significant variations in number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, days to 50% flowering, length of siliqua, number of seeds per siliqua, 1000-seed weight and yield per plant. Plant height, length of siliqua, number of siliquae per plant, days to 50% flowering showed low difference between

genotypic and phenotypic coefficient of variation. Plant height, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant showed high heritability coupled with high genetic advance and very high genetic advance in percentage of mean. However length of siliqua showed low heritability.

Ara (2010) conducted a field experiment by using eight F_2 and eight F_4 populations generated through inter-varietal crosses, along with three check variety of *Brassica rapa* to study the variation. From the values of mean, range and CV (%) of seed yield and yield contributing characters it was confirmed that there were considerable variation present among all the genotypes used in the experiment. The values of phenotypic variances were higher than corresponding genotypic variances. Days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, length of siliqua, seeds per siliqua, 1000-seed weight and yield per plant showed least difference between phenotypic and genotypic variances. The value of GCV and PCV indicated that there was least variation present among most of the characters. The days to maturity, length of siliqua, seeds per siliqua and 1000-seed weight showed high heritability with low genetic advance and genetic advance in percentage of mean. Low to medium heritability of siliqua length was observed by Kakroo and Kumar (1991), Sharma (1984) and Yadava *et al.* (1996).

Aytac and Kinaci (2009) conducted an experiment with 10 winter rapeseed genotypes for variation, genetic and phenotypic correlations and broad sense heritability for seed yield, yield and quality characters for 2 years. They observed maximum broad sense heritability get genetic advance seed yield followed.

Sheikh *et al.* (2009) studied the induction of genetic variability in Ethiopian mustard (*Brassica carinata*) for quality traits through interspecific hybridization. The result revealed that interspecific hybridization was used to enhance the spectrum of genetic variability in mustard for oil and meal quality traits from quality lines of *Brassica juncea*.

Aytac *et al.* (2008) reported highest genotypic and phenotypic variances for seed yield per plant followed by seed yield and high heritability of seed yield per plant, seed

yield, pods per main stem coupled with high genetic advance revealed that additive gene effects are important in determining these characters and could be improved through mass selection.

Hosen (2008) conducted a study by using 5 parental genotype of *Brassica rapa* and their ten F_3 progenies including reciprocals. There are large numbers of variations present among all the genotypes used in the experiment. The plant height, days to 50% flowering, and number of siliquae per plant showed high heritability with high genetic advance and genetic advance in percentage of mean.

An experiment was carried out by Mahmud (2008) with 58 genotypes of *Brassica rapa* to study inter genotypic variability. Significant variation was observed among all the genotypes for all the characters studied except thousand seed weight. High GCV value was observed for number of secondary branches per plant. High heritability values along with high genetic advance in percentage of mean were obtained for days to 50% flowering, seed per siliqua and siliqua length.

According to Tyagi *et al.* (2001) variation was the highest in parents and their hybrids for plant height. The seed yield per plant exhibited the highest co-efficient of variation (41.1%). Significant genetic variability was observed for this character by many workers like Andarhennadi *et al.* (1991), Malik *et al.* (1995), Kumar and Singh (1994), Yadava *et al.* (1993), Lebowitz (1989), Chaturvedi *et al.* (1988), Gupta *et al.* (1987) and Chauhan and Singh (1995) among different genotypes of *B. napus*, *B. rapa* and *B. juncea*.

Nanda *et al.* (1995) observed that days to first flowering varied both by genotypes and date of sowing, while working with 65 strains of *B. napus*, *B. juncea*, *B. carinata* and *B. rapa*. Many other researchers like Kumar and Singh (1994), Kumar *et al.* (1996), Kachroo and Kumar (1991), Andrahernnadi (1991), Lebowitz (1989), Biswas (1989), Singh *et al.* (1987), Chaudhury and Singh (1985), Yadava (1983) and Thakral (1982) found significant variations for this character while working with different genotypes of *Brassica napus*.

Dominance gene action was important in the expression of days to flowering was found by Jain *et al.* (1988). Significant genetic variability in days to 50% flowering in *B. napus* and *B. rapa* was observed by Singh *et al.* (1991).

Chandola *et al.* (1977) worked on 30 varieties of *B. campestris* and reported that the varietal differences were highly significant for plant height, due to varieties and growing conditions. They also found highly significant varietal differences for yield and six other yield components.

Katiyar *et al.* (1974) observed high genetic co-efficient of variation for days to first flowering, plant height (cm) and seed yield per plant (g) where as low values were observed for other characters like days to maturity and number of primary branches per plant, while observing on genetic variability and genetic advance of seed yield and its components in Indian mustard.

The highest genotypic co-efficient of variation was calculated for secondary branches. High genotypic and phenotypic co-efficient of variation was recorded for days to 50% flowering among 10 genotypes for each of *Brassica campestris*, *Brassica carinata* and *Brassica napus* and 24 genotypes of *Brassica juncea* by Lekh *et al.* (1998).

Generally high number of seeds per siliqua is desirable. On the variability of this trait a good number of literatures are available. Significant variability in number of seeds/siliqua in oleiferous *Brassica* materials of diverse genetic base was observed by Kudla (1993) and Kumar and Singh (1994). Similar significant variability in the genotypes of *Brassica napus*, *B. campestris* and *B. juncea* were studied by them. Bhardwaj and Singh (1969) observed GCV value of 35.85% in case of *Brassica campestris* genotypes.

High co-efficient of variation for thousand seed weight, pod length and number of seeds per pod for both genotypic and phenotypic level was found by Masood *et al.* (1999) while working with seven genotypes of *Brassica campestris* and standard cultivar of *Brassica napus* to study genetic variability.

Higher seed yield is the result of higher number of siliqua. Large variation is involved for this trait. High genetic variation in number of siliqua was observed by Yin (1989) while working with 8 cultivars of *Brassica napus*. Kumar *et al.* (1996) also observed and reported similar results of high variation for this trait.

Singh *et al.* (1987) observed variable results of GCV (25.41%) and PCV (29.15%) in *Brassica campestris* for siliquae number higher and the seed yield, GCV was reported

to be also as 18.85% by Yadava (1973) and Bhardwaj and Singh (1969) reported 97.3% of GCV. Number of siliquae per plant is one of the most important traits of *Brassica spp*. This trait has high variation and a considerable part of which appeared to be environmental. High genetic variation was found by Kudla (1993). Similar results was also found by Andraherinadi *et al.* (1991), Biswas (1989), Jain *et al.* (1988), Chowdhury *et al.* (1987) and Alam *et al.* (1986).

Siliqua length is another important character for the development of fruits in oil seed crops like mustard and rape seed. Peduncle, beak as well as siliqua length varies due to difference in genotypes. High genetic variability was found by Olsson (1990) for this character. Lebowitz (1989) found similar results while working with *B. rapa* for siliqua length. Thurling (1983) reported that selection for increased siliqua length is an effective strategy for yield improvement through raising seed weight per siliqua.

Thousand seed weight is a very important character of rape seed and mustard, where highest consideration is on the seed yield. This character has been found to vary widely from genotypes to genotypes and from environment to environment. A good number of literatures are available on the variability of this trait.

According to Kumar and Singh (1994) in *B. juncea*, Kudla (1993) in rapeseed, Andarhennadi *et al.* (1991) in brown mustard, Biswas (1989) in *Brassica campestris*, Lebowitz (1989) in *B. rapa*, Yin (1989) in *B. rapa* and Chowdhury *et al.* (1987) in *B. rapa* found different degrees of significant variations among the genotypes for thousand seed weight.

In every breeding program yield is the important character among various traits for oil crops. It is a complex trait which is influenced by various factors of production. A good number of literatures are available on the variability of this trait. High variability in different genotypes of *B. rapa* was reported by Sharma *et al.* (1994). Thakral (1982) also reported significant genetic variability in genotypes of *B. napus*. Similar high variability in different genotypes of *B. napus* was found by Khera and Singh (1988).

High degrees of variation for seed yield per plant in *B. rapa* was observed by Yin (1989) and Kudla (1993) in *B. napus* and Kumar *et al.* (1996) in *B. juncea*. Bhardwaj and Singh (1969) found GCV value of 96.99% among different strains of *B. rapa*.

Yadava (1973) found 48.76% GCV value among 29 strains of *B. juncea*. While Singh *et al.* (1987) found GCV and PCV values of 44.04% and 46.9% in *Brassica juncea*.

High heritability coupled with high genetic advance for seed yield per plant, number of secondary branches per plant, siliqua per plant, 1000 seed weight (g) and number of primary branches per plant was observed by Sheikh *et al.* (1999) while working with 24 genotypes of toria.

Lekh *et al.* (1998) carried out an experiment with 24 genotypes of *B. juncea* and 10 genotypes each of *B. campestris*, *B. carinata* and *B. napus* and observed highest genetic advance and high genotypic and phenotypic co-efficient of variation for days to 50% flowering and high heritability for other yield contributing characters.

Both additive and dominance genetic components were important for seed yield and yield components in *B. campestris var. toria*, and higher heritability for days to maturity and thousand seed weight while studied 8x8 diallel analysis (excluding reciprocals) was reported by Yadava *et al.* (1993).

Malik *et al.* (2000) observed very high broad sense heritability (h^2_b>90%) for number of primary branches per plant, days to 50% flowering and oil content while working with different strains of *B. napus*. They also observed low heritability (h^2_1, 50%) for plant height, number of siliqua/plant, number of seeds siliqua and seed yield. But high heritability for all these characters were found by Lodhi *et al.* (1979) while working with 55 genotypes of *B. napus*, *B. rapa* and *B. juncea*.

High heritability and genetic advance for number of siliqua per plant in *B. rapa* and *B. juncea* were observed by Varshney *et al.* (1986), but they found high heritability and genetic advance for plant height in all the three species. High narrow sense heritability and genetic advance for days to flowering and plant height were reported by Diwakar and Singh (1993) while working with segregating populations of yellow seeded Indian mustard (*B. juncea* L. Czern and Coss).

High heritability and genetic advance for number of seeds per siliqua and seed yield per plant was reported by Singh (1986) while working with 22 genotypes of *B. napus*, *B. campestris* and *B. juncea*.

Low heritability for yield per plant was observed by Malik *et al.* (1995), Kumar *et al.* (1988) and Yadava *et al.* (1993). Chen *et al.* (1983) and Wan and Hu (1983) found high heritability and genetic advance for days to flowering, number of primary branches per plant and plant height.

Kwon *et al.* (1989) and Rao (1977) reported high heritability (h > 90%) for siliqua length, but Kachroo and Kumar (1991), Sharma (1988) and Yadava *et al.* (1978) reported low to medium for this trait.

Singh *et al.* (1987) studied 179 genotypes of Indian mustard and found high heritability for seed yield per plant and oil content and the lowest heritability for number of primary branches per plant. In a study of variability and correlations in some varieties of brown sarson, reported high heritability for siliqua length, number of seeds per siliqua and thousand seed weight was observed by Chaudhury *et al.* (1990).

Plant height and number of seeds per siliqua were highly heritable where as siliqua length, number of primary branches per plant were less heritable was observed by Labana *et al.* (1980) while working with 104 mutants of Indian mustard *B. juncea* L. Czern and Coss. Chandola (1977) observed high genetic advance for plant height while working with 30 varieties of *B. rapa*.

Paul *et al.* (1976) found in his study that a good genetic advance was expected from a selection index comprising seed yield, number of seeds per siliqua, number of primary branches per plant and number of siliquae per plant.

Katiyar *et al.* (1974) reported heritability in the broad sense was associated with high genetic advance for number of siliquae on the main shoot and seed yield per plant while working with *B. campestris L. var. sarson*. In a study of genetic variability, heritability and genetic advance of Indian mustard Katiyar *et al.* (1974) reported high heritability for days to flowering, plant height, number of primary branches and seed yield per plant, moderate for days to maturity and low for the number of secondary branches. He also reported low genetic advance for number of primary branches and high values for days to flowering, plant height and seed yield per plant.

According to Yadava (1973) high heritability in the broad sense and genetic advance for days in maturity, plant height and number of node on the main shoot among the nine traits studied in 29 varieties. The most important feature in winter rape plant selection for seed yield and number of branches was reported by Teresa (1987).

According to Knott (1972) and Seitzer and Evans (1978), selection for yield in early segregating generations was effective in developing high yielding cultivars of self pollinated crops. Selection for bold seed size from F_2 to F_5 generations was highly effective was observed by Gupta and Labana (1985) in Indian mustard.

Chatterjee and Bhattacharyya (1986) found higher efficiency with index selection than selection based on yield alone. The efficiency increased with an increase in the number of characters in the index. The index comprising plant height, thousand seed weight and yield per plant was considered effective from the practical point of view.

2.2 Correlation among different characters

Analysis of correlation among different traits is important in breeding program. A good number of literatures are available on correlation among characters of *Brassica sp.* Some of these literatures are reviewed here:

Helal *et al.* (2014) conducted an experiment to study Genetic variability, correlation of yield and yield contributing characters and coefficient of variance in rapeseed or mustard. Correlation between seed yield and yield contributing characters showed significant and positively correlated with number of siliqua/plant, 1000 seed weight, straw yield, plant height, biological yield and harvest index. Correlation coefficient analysis of yield attributes had the highest and positive association with seed yield.

Rameeh (2012) aimed at finding out the planting date effect on yield associated traits and also determining the variations of correlations among the traits in different planting dates of rapeseed genotypes. Significant planting dates and genotypes effect for phonological traits, yield components, seed yield and oil percentage revealed significant differences of planting dates genotypes for these traits. The variation of correlation between duration of flowering and pods per plant was less than the correlation of duration of flowering to other traits in different planting dates.

Rameeh (2011) reported that thirty-six rapeseed genotypes including four cultivars and 32 advanced lines were evaluated in randomized complete block design with three replications. Siliquae per plant had significant positive correlation (0.80**) with seed yield. So any change for this trait will have considerable effect on seed yield.

A research was conducted by Alam (2010) using 26 F_4 populations of some inter-varietal crosses of *Brassica rapa* to study the correlation between pairs of different characters. Correlation study revealed that yield per plant had significant positive association with plant height, number of primary branches per plant, number of siliquae per plant, number of seeds per siliqua and siliqua length.

Ara (2010) conducted a field experiment by using eight F_2 & eight F_4 populations generated through inter-varietal crosses, along with three check variety of *Brassica rapa* to study correlation between pairs of different characters. Yield per plant had significant and highest positive correlation with length of siliqua, seeds per siliqua and 1000-seed weight.

Esmaeeli Azadgoleh *et al.* (2009) mentioned positively significant correlation of seed yield with number of pod per plant, number of pods in sub branches and number of seeds per pod.

An experiment was conducted by Basalma (2008) in Ankara conditions using 25 winter oil seed rape cultivars. Correlation analysis showed a high positive and statistically significant correlation between branches per plant, the number of pods on the main stem and plant height during two years. Plant height indicated negative correlation with seed yield, thousand seed weight and oil ratio.

Rashid (2007) carried out an experiment with 40 oleiferous *Brassica* species to estimate correlation and observed that, highly significant positive association of yield per plant with number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua and number of siliquae per plant.

An experiment was conducted by Parveen (2007) with F_2 population of *Brassica rapa* to study the correlation and observed that yield per plant had non-significant positive association with plant height, number of secondary branches per plant, number of

seeds per siliqua and number of siliquae per plant, days to 50% flowering and length of siliqua.

An experiment on oleiferous *Brassica campestris* L. was conducted by Siddikee (2006) to study the correlation analysis. The results revealed that yield per plant had highest significant positive correlation with number of siliquae per plant.

Tusar *et al.* (2006) studied phenotypic correlation and observed that seed yield per plant was positively and significantly associated with plant height, total dry matter production and husk weight. The number of siliquae per plant, 1000-seed weight, crop growth rate during 60-75 days after sowing and number of branches per plant were also positively associated with seed yield.

Zahan (2006) studied correlation and reported that yield per plant had highly significant positive association with plant height, length of siliqua, siliquae per plant and seed per siliqua but insignificant negative association with days to 50% flowering and days to maturity.

Mahak *et al.* (2004) conducted an experiment and studied correlation for eight quantitative characters. Seed yield per plant showed positive correlation with number of primary branches, length of main raceme, 1000-seed weight and oil content. Selection should be applied on these traits to improve seed yield in Indian mustard. Afroz *et al.* (2004) also studied correlation and found seed yield per plant had significant and positive correlation with number of primary branches per plant and number of siliquae per plant.

A field experiment was conducted to determine the genetic potential of *Brassica* accessions. Result revealed that eight accessions were sown in randomized complete block design in four replications. Plant height, number of primary branches, number of secondary branches, number of pods per plant and seed index were found positively correlated with seed yield. So, the emphasis should be given during experimentation for improvement of plant height, number of primary branches, number of secondary branches, number of pods per plant and seed index for improvement in yield of seed in *Brassica* (Khan and Khan, 2003).

Pankaj *et al.* (2002) studied four parental cultivars and the F_4 progenies of resultant crosses for correlation between yield and yield component traits. The genetic correlation was higher than the phenotypic correlation for the majority of the characters. The number of siliquae per plant, which had the strongest positive and significant correlation with yield per plant at both levels, was positively associated with the number of seeds per siliqua and test weight at both levels. The number of seeds per siliqua was positively associated with siliqua length and yield per plant at both levels.

Srivastava and Singh (2002) studied correlation in Indian mustard [*Brassica juncea* L. Czern and Coss] for 10 characters was conducted with 24 strains of Indian mustard along with 2 varieties. Results revealed that number of primary branches per plant, number of secondary branches per plant, 1000 seed weight (g) and oil percent were positively associated with seed yield.

Shalini *et al.* (2000) evaluated 81 genotypes of Indian mustard for the magnitude of association between their quantitative characters of secondary branches, plant height, number of siliquae and seeds per siliquae were highly associated with seed yield.

Malek *et al.* (2000) studied correlation analysis and reported that days to maturity showed insignificant correlation with seed yield at both genotypic and phenotypic levels. He also reported that number of branches per plant and number of siliqua per plant showed significant negative correlation with number of seeds per siliqua and 1000 seed weight.

Khulbe and Pant (1999) carried out a study of correlation in 8 Indian mustard (*Brassica juncea*) parents and their 28 F_1 hybrids and revealed that the number of siliqua per plant, length of siliqua, number of seeds per siliqua, thousand seed weight and harvest index were positively associated with seed yield.

The number of siliquae per plant, number of seeds per siliqua and plant height was significantly positively correlated with seed yield was observed by Masood *et al.* (1999) while studied seven genotypes of *B. campestris* and standard cultivar of *B. napus* to calculate correlation co-efficient.

Thakaral *et al.* (1999) studied correlation co-efficient on seed yield and yield contributing characters in eight Indian mustard (*Brassica juncea*) parents and their 28 F_1 hybrids grown at Hisar. The data indicated that higher seed yield could be obtained by selecting for increased plant height.

According to Kumar *et al.* (1999) genotypic correlation co-efficient were higher in magnitude than corresponding phenotypic correlation co-efficient for most characters. The plant height, siliquae on main shoot, siliquae per plant and thousand seed weight were positively correlated with seed yield. Gurdial and Hardip (1998) carried out an experiment with gobhi sarson (*B. nigra*) and reported that dwarf plant gave higher yield.

Zajac *et al.* (1998) studied phenotypic correlation between yield and its component and reported that strong positive correlation occurred between seeds per siliqua and actual yield. Positive but a weaker correlation was observed between seed yield and siliquae per plant. The number of seeds per siliqua had the greatest influence and siliquae number per plant had the smallest effect on yield.

Das *et al.* (1998) carried out an experiment with 8 genotypes of Indian mustard (*B. juncea*) and reported that the length of siliqua, seeds per siliqua had high positive genotypic correlation with seed yield per plant. The number of siliqua par plant, seed weight per plant and thousand seed weight were positively correlated with seed yield per plant were observed by Dileep *et al.* (1997).

Tyagi *et al.* (1996) carried out and experiment with six yield components in three cultivars of mustard and observed that plant height, siliqua per plant, siliqua length, seed weight, and seeds per siliqua had positive and significant effects on seed yield per plant.

Kumar *et al.* (1996) studied 12 genotypes of *B. juncea* for correlation analysis and found flowering time and plant height negatively correlated with number of primary branches per plant.

Uddin *et al.* (1995) while studied correlation analysis in 13 Indian mustard (*B. juncea*) and reported that seed yield per plant had high positive arid significant correlations

with plant height and thousand seed weight, but high negative and significant correlations with seeds per siliqua at both genotypic and phenotypic levels.

Arthamwar *et al.* (1995) studied correlation and regression in *B. juncea*. Results revealed that weight of siliqua per plant showed the highest correlation with seed yield followed by number of siliqua per plant, number of seeds per siliqua and thousand seed weight.

Nanda *et al.* (1995) studied correlation analysis with 65 strains of *B. juncea*, *B. rapa* and *B. napus* and observed that positive association between yield and siliqua filling period. Similar results also found by Olsson (1990) in *B. napus*. He also observed positive correlation between siliqua density and yield.

Nasim *et al.* (1994) studied correlation analysis in *B. rapa* and found 1000 seed weight was significantly and positively correlated with seed yield per plant and number of siliqua per plant but significantly and negatively correlated with siliqua length and number of seeds per siliqua.

Gosh and Mukhopadhyay (1994) studied Tori-7 (*B. campestris var. toria*) for evaluation of seed yield and 5 seed yield contributing characters and found that plant height, siliqua per plant, seeds per siliqua and thousand seed weight was significant and positively correlated with seed yield.

Ahmed (1993) worked with eight cv. of *B. campestris* and *B. juncea* for study of nature and degree of interrelationship among yield components and observed that siliqua length, number of siliqua per plant, number of seeds per siliqua and seed weight per siliqua was positively and linearly associated with seed yield per plant. He also observed that seed oil content was positively correlated with seed weight, but negatively correlated with number of seeds per siliqua.

Zaman *et al.* (1992) studied several yield contributing traits of Swedish advanced rape lines and reported that number of seeds per siliqua negatively correlated with siliqua per plant.

Reddy (1991) studied correlation analysis in Indian mustard (*B. juncea*) and reported that positive and significant correlation between seed yield and number of primary

branches per plant, number of secondary branches per plant, siliqua per plant and seeds per siliqua.

Swain (1990) studied correlations of yield components in 15 genotypes of brown sarson (*B. campestris var. dichotoma*) and found that number of siliqua per plant was the most important characters to yield.

Chaudhury *et al.* (1990) observed seed yield was positively correlated with siliqua length when evaluated seven of *B. juncea*, two of *B. carinata* cultivars and one cultivar each of *B. campestris* and *B. tournefortii*.

Chay and Thurling (1989) studied the inheritance of siliqua length among several lines of *B. napus* and reported that the siliqua length when increased there was an increase in the number of seeds per siliqua and thousand seed weight. The siliqua length was positively correlated with both number of seeds per siliqua and thousand seed weight was observed by Singh *et al.* (1987) in *B. rapa*, Chowdhury *et al.* (1987), Lebowitz (1989) and Lodhi *et al.* (1979) in *B. juncea*.

Singh *et al.* (1987) observed number of primary branches per plant negatively correlated with siliqua length and 1000 seed weight, but positively correlated with number of siliqua per plant.

In *B. juncea* Chowdhury *et al.* (1987) and Yadava *et al.* (1978) observed thousand seed weight positively associated with days to 50% flowering and days to 80% maturity, but negative correlation was observed by Singh *et al.* (1987) and Shivhare *et al.* (1975).

Chowdhury *et al.* (1987) and Yadava *et al.* (1978) also reported that thousand seed weight negatively correlated with plant height, number of primary branches per plant and number of siliquae per plant.

Das *et al.* (1984) observed thousand seed weight had high significant genotypic and phenotypic correlation with seed yield.

Srivastava *et al.* (1983) observed in *B. juncea* the number of primary branches per plant and secondary branches per plant, plant height and days to maturity showed significant positive association with the seed yield per plant. The number of primary

branches showed positive and significant association with the number of secondary branches per plant, plant height and days to maturity. Plant height showed positive and significant correlation with the number of secondary branches and days to maturity.

Labana *et al.* (1980) observed plant height negatively correlated with siliqua length and seeds per siliqua. Chowdhury *et al.* (1987) studied 179 genotypes of Indian mustard and observed positive correlation of plant height with number of siliqua per plant, number of primary branches per plant and seeds per siliqua. Positive association of plant height with these three traits in eight strains of yellow sarson was also found by Banerzee *et al.* (1968).

Labana *et al.* (1980) also found that number of primary branches per plant was negatively correlated with plant height and siliqua length. Shivahare *et al.* (1975) observed days to flowering were positively correlated with primary branches per plant and plant height.

Increasing the number of branches is a means of increasing yield, since the number of primary and secondary branches have a significant positive correlation with seed yield (Katiyar and Singh, 1974).

Banerjee (1968) reported significant correlation between number of siliqua per plant and number of seeds per siliqua in yellow sarson. But negative genotypic correlation between number of siliqua per plant and number of seeds per siliqua in brown sarson and toria varieties was observed by Tak (1976) when studied with *B. rapa*.

Ramanujam and Rai (1963) observed significant positive correlations between yield and all the yield components in *B. rapa cv. yellow sarson*. Zuberi and Ahmed (1973) observed similar results in *B. rapa cv. toria*. Campbell and Kondra (1978) observed positive correlation between yield and the yield components in rape seed (*B. napus*). However, Campbell and Kondra (1978) observed negative correlation between yield and the yield components.

2.3 Path co-efficient analysis

When more characters are involved in correlation study it becomes difficult to ascertain the traits which really contribute towards the yield. The path analysis under such situation helps to determine the direct and indirect contribution of these traits towards the yield.

Helal *et al.* (2014) conducted an experiment to study Genetic variability, correlation of yield and yield contributing characters and coefficient of variance in rapeseed or mustard. Path coefficient analysis of different yield contributing characters showed biological yield contributed maximum to seed yield with the highest correlation.

A research was conducted by Alam (2010) using 26 F_4 populations of some inter-varietal crosses of *Brassica rapa* to study the direct and indirect effect of different characters on seed yield. Path co-efficient analysis revealed that plant height, number of primary branches per plant, number of siliquae per plant, seeds per siliqua and siliqua length had the positive direct effect on yield per plant, days to 50% flowering, number of secondary branches per plant and 1000-seed weight had the negative effect on yield per plant.

Afrin (2009) conducted a field experiment with 22 *Brassica napus* L. advanced lines to study path coefficient. Path coefficient analysis showed that the plant height had maximum positive direct effect on seed yield followed by number of siliqua per plant and siliqua length and negative direct effect on number of secondary branches per plant and number of seeds per siliqua. Plant height, number of primary branches per plant and number of siliqua per plant were the most important contributors to seed yield per plant which could be taken in consideration for future hybridization program.

The path co-efficient analysis by Hosen (2008) exhibited that thousand seed weight had the highest positive direct effect followed by days to 50% flowering, length of siliqua, number of primary branches per plant, number of secondary branches per plant, days to maturity and number of seeds per siliqua while working with five parental genotypes of *Brassica rapa* and their ten F_3 progenies including reciprocals.

An experiment was conducted by Parveen (2007) with F_2 population of *Brassica rapa* to study the path analysis and observed that number of seeds per siliqua showed highest direct effect on yield per plant.

Rashid (2007) carried out an experiment with 40 oleiferous *Brassica* species to estimate path analysis and observed that yield per plant had the highest direct effect on days to maturity, number of seeds per siliqua, number of siliqua per plant and number of primary and secondary branches per plant.

Siddikee (2006) conducted and experiment on oleiferous *Brassica campestris L.* to study the path analysis and revealed that thousand seed weight had the highest positive direct effect on seed yield per plant.

Srivastava and Singh (2002) reported that number of primary branches per plant, number of secondary branches per plant and 1000 seed weight had strong direct effect on seed yield while working with Indian mustard (*B. juncea* L.). Results suggested that number of primary branches and 1000 seed weight were vital selection criteria for improvement in productivity of Indian mustard.

Shalini *et al.* (2000) studied path analysis of Indian mustard germplasm and observed that number of siliqua had the highest direct effect on seed yield followed by 1000 seed weight, number of primary branches per plant and plant height. Most of the characters had an indirect effect on seed yield.

Khulbe and Pant (1999) studied path co-efficient analysis in eight Indian mustard (*B. juncea*) parents and their 28 F_1 hybrids. The results revealed that harvest index, siliqua length, seeds per siliqua, siliqua per plant, thousand seed and days to initial flowering were the major traits influencing seed yield.

The number of seeds per siliqua exerted the highest effect on seed yield was observed by Masood *et al.* (1999) when they studied seven genotypes of *B. campestris* and standard cultivar of *B. napus*.

Sheikh *et al.* (1999) worked with 24 diverse genotypes of toria for assess the direct and indirect effect of seven quantitative and developmental traits on seed yield. Results revealed that thousand seed weight and siliqua per plant had highly positive direct effect on seed yield.

Yadava *et al.* (1996) when studied path co-efficient analysis of six yield components of 25 diverse varieties of Indian mustard and observed that number of siliqua per plant had the highest positive direct effect on seed yield.

Chauhan and Singh (1995) found high positive direct effect of days to 50% flowering, plant height, primary branches per plant, siliquae per plant and seeds per siliqua on seed yield while working with several strains of *B. juncea*.

Uddin *et al.* (1995) studied path analysis in 13 Indian mustard (*B. juncea*) and observed that seeds per siliqua and thousand seed weight had high positive direct effect on seed yield per plant. Chauhan and Singh (1995) observed that plant height, siliqua per plant and seeds per siliqua had high positive direct effect on seed yield.

Kachroo and Kumar (1991) studied several strains of *B. juncea* and found that thousand seed weight had positive direct effect, but days to 50% flowering and primary branches had negative indirect effect via seeds per siliqua on seed yield. Kumar *et al.* (1988) found the indirect positive effect of days to 50% flowering on seed yield.

Han (1990) studied *B. napus* and observed negative direct effect of number of siliquae per plant, siliqua length and positive direct effect of seeds per siliqua and plant height on seed yield. Dhillor *et al.* (1990) observed the highest positive direct effect on seed yield per plant. Kudla (1993) reported that 1000 seed weight had positive direct effect on seed yield.

Chaudhary *et al.* (1990) observed that days to 50% flowering and plant height indirectly contributed to plant yield.

Dhillon *et al.* (1990) reported that the plant height had the highest positive direct effect on seed yield per plant in *B. juncea*, but Singh *et al.* (1978) also found negative direct effect of the trait on seed yield.

Chowdhury *et al.* (1987) worked with 42 strains of mustard and observed that siliqua length had highest positive direct effect and number of primary branches per plant had the highest negative direct effect on seed yield. On the other hand, Gupta *et al.* (1987) observed that primary branching and thousand seed weight had the direct effect on seed yield.

Varshney (1986) worked with several strains of *B. rapa* and observed that plant height, siliqua per plant and thousand seed weight had the negative direct effect on yield.

Kumar *et al.* (1984) also worked with *B. juncea* and found negative indirect effect of days to flowering via plant height and siliqua length, but negative direct effect of these traits was observed by Singh *et al.* (1978). But many scientists like Singh *et al.* (1985) in *B. juncea*, Chen *et al.* (1983) in *B. napus* and Srivastava *et al.* (1983) in *B. juncea* observed that plant height, days to maturity, siliqua per plant, seeds per siliqua and thousand seed weight had positive direct and indirect effect on seed yield.

2.4 Genetic Diversity analysis

Genetic diversity plays an important role in plant breeding to identify lines of diverse origin for better heterosis. A good number of literatures are available on genetic diversity of *Brassica sp.* Some of these literatures are reviewed here:

Iqbal *et al.* (2014) studied to determine the genetic variability and diversity among different mustard genotypes. All the characters demonstrated high heritability (>80%) irrespective of any genotypes. Plant height, number of seeds siliqua^{-1}, number of siliqua plant^{-1} and length of siliqua were significantly correlated with seed yield per plant suggesting that genotypes with high partitioning efficiency gave increase in seed yield plant^{-1}. Among the characters, number of siliqua plant^{-1}, number of seeds siliqua-1and 1000 seeds weight had high positive direct effects on grain yield plant^{-1} so those characters should be included owing to importance in selecting the genotypes for higher seed yield in mustard. Using Euclidean distance following Ward's method, the genotypes were grouped into four clusters. The cluster III had higher intra cluster distance and the maximum inter cluster distance was observed between genotypes of clusters I and IV followed by clusters III and IV.

Rameeh (2013) evaluated twenty four rapeseed genotypes including 2 cultivars and 22 advanced lines, were based on randomized complete block design with three replications. The results of factor analysis exhibited four factors including sink factor (pod per plant, pods length and seed yield), fixed capital factor (phenological traits),

secondary fixed capital factor (duration of flowering), and metric factor (plant height). On the basis of cluster analysis, the genotypes were classified in four groups, and the group with high seed yield had high mean value of pods per plant.

Mahmud *et al.* (2011) reported that fifty five advanced line of *Brassica rapa* along with three commercially cultivated varieties as check were evaluated to study the genetic divergence through Mahalanobis D^2 statistics in respect of 10 different morphological characters. As per principal component analysis (PCA), D^2 and cluster analysis, the genotypes were grouped into six different clusters. Relationship was not found between genetic divergence and geographic distribution of the genotypes. Cluster II and cluster III had the maximum (13) and cluster IV had the minimum (6) number of genotypes. The inter cluster distance in most of the cases was larger than the intra cluster distance. The highest inter cluster distance was observed between cluster III and VI (19.52) and that of the lowest between cluster II and IV (3.02). Highest intra-cluster distance was observed in cluster VI (0.67). Plant height, number of secondary branches per plant and seeds per siliqua contributed maximum towards the total divergence. Considering diversity pattern, genetic status and other agronomic performances, line 39 and line 44 from cluster I; line 42 from cluster II; line 2, line 43 and line 45 from cluster V; line 50, line 52, line 54 and line 58 from cluster VI- might be selected as suitable parents in future hybridization program.

Zaman *et al.* (2010) a field experiment was conducted comprising eighteen advanced lines of mustard in a randomized block design with three replication for estimation of divergence among advanced lines of mustard. The genotypes were grouped into four clusters. Cluster I contained the highest number of genotypes (6) and the cluster III contained the lowest (3). The inter-cluster distances in all cases were larger than the intra-cluster distance which indicated that wider diversity was present among the genotypes of distant grouped. The highest intra cluster distance was observed in cluster II and the lowest in I. The highest inter cluster distance was observed between the cluster III and II followed by III and I and the lowest between cluster IV and III. Days to 50% flowering (81.94%), days to maturity (8.24%), plant height (5.82%), branches per plant (1.91%) and siliquae per plant (1.17%) contributed maximum towards the total divergence which suggested that these characters were highly responsible for genetic divergence in the present materials. But the highest cluster

means for primary branches per plant and maximum seeds per siliquae with minimum seed yield per plant were obtained from the cluster II. The genotypes from cluster I had dwarf plant along with earliness in days to 50% flowering, days to maturity and maximum number of primary branches per plant. Therefore, the genotypes from cluster I and III could be utilized in the hybridization program for getting desirable transgressive segregants and high heterotic response due to getting maximum yield along with short duration.

Afrin (2009) used different multivariate analysis techniques to classify 22 *Brassica napus* genotypes. The genotypes were grouped into four clusters. The highest inter-cluster distance was observed between clusters II and IV whereas the maximum intra-cluster distance was found in cluster II. Therefore, the genotypes belonging to cluster I and cluster II, cluster II and cluster III and cluster III and cluster IV have been selected for future hybridization program. The PCA gives Eigen values of principal component axes of coordination of genotypes with the first three axes accounted for 68.927% of total variation whereas the first principal components accounted for 28.695%. The role of number of secondary branches per plant and number of siliqua per plant in both the vectors were important components for genetic divergence in these materials. Considering group distance and other agronomic performance the inter-genotypic crosses between G1 and G2, G2 and G6; G6 and G7; G6 and G8 and G7 and G8 might be suggested for future hybridization program.

The genetic diversity of 22 rapeseed (*Brassica napus*) advanced genotypes was studied by Mahmud *et al.* (2008) using principal component analysis non-hierarchical clustering and canonical vector analysis. The genotypes were grouped into four clusters. Cluster II contained the maximum number of genotypes (9) and cluster III contained the lowest (2). The highest inter cluster distance was found between cluster I and cluster III and the lowest between cluster I and cluster II. The highest intra-cluster distance was noticed for cluster III and the lowest for cluster II. Cluster I had the highest mean values for siliqua length and thousand seed weight. Cluster III had the lowest cluster mean values for the number of days to 50% flowering and the number of days to maturity with moderate seed yield. Crosses between genotypes

belonging to cluster II with those of cluster I and cluster IV might therefore produce high heterosis in yield as well as earliness.

The D^2 analysis allowed the 36 genotyped/variety of linseed to be identified into five distinct clusters by Begum *et al.* (2007). The cluster I included 11 genotypes that had medium mean values for 1000-seed weight (g) and seed yield/plant. The cluster II contained six genotypes, which had the highest mean values for number of seeds/capsule, number of branches/plant and seed yield/plant. They also showed the highest mean value for plant height. It is also related with medium mean values for rest of the characters. The cluster IV included three genotypes having the highest mean values for number of capsules/plant and days to maturity. The cluster V included single genotype, which had the lowest mean values for days to maturity and plant height. The highest inter cluster distance was observed among clusters V, IV and II, while the lowest between III and I. The highest intra cluster distance was observed in cluster III that revealed maximum variability within the clusters. In this study, two traits such as number of branches/plant and number of seeds/capsule contributed the maximum towards divergence in the existing germplasm.

Goswami *et al.* (2006) reported the moderate genetic diversity between parents had the good general combining ability (GCA) effect and high specific combining ability (SCA) and high mean values in F_2, had the highest frequency of transgressive segregates in F_2 and the magnitude of transgression were high in Indian Mustard.

Nath *et al.* (2003) conducted and experiment with varieties, inter-variety and inter-species hybrids of *Brassica* oil crop to determine genetic divergence. The divergence study indicated that parent, inter-variety and inter-species hybrids almost clearly form five groups indicating that they are divergent and might be of value for future breeding program. Based on the study on genetic divergence of the *Brassica*, the varieties having the performance and located in the distant clusters could be utilized for hybridization program to develop desired high yielding varieties.

Choudhary and Joshi (2001) determined genetic diversity among the 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 through multivariate

analysis (D^2 statistic). The genetic distances calculated among different *Brassica* species revealed that *B. tournefortii* had maximum diversity with *B. juncea* followed by *B. napus*, *B. rapa* var. toria and *B. rapa* var. yellow sarson. 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. The characters, namely, plant height, secondary branches per plant, days to flowering and 1000-seed weight was contributed maximum towards genetic divergence.

Islam and Islam (2000) reported the genetic diversity in rapeseed and mustard using D^2 analysis of 42 genotypes. The genotypes were grouped into four clusters. The inter-cluster distances were larger than the intra-cluster distances. The characters contributed maximum in divergence analysis is days to 50% flowering, plant height, primary branches/plant and number of siliquae/plant.

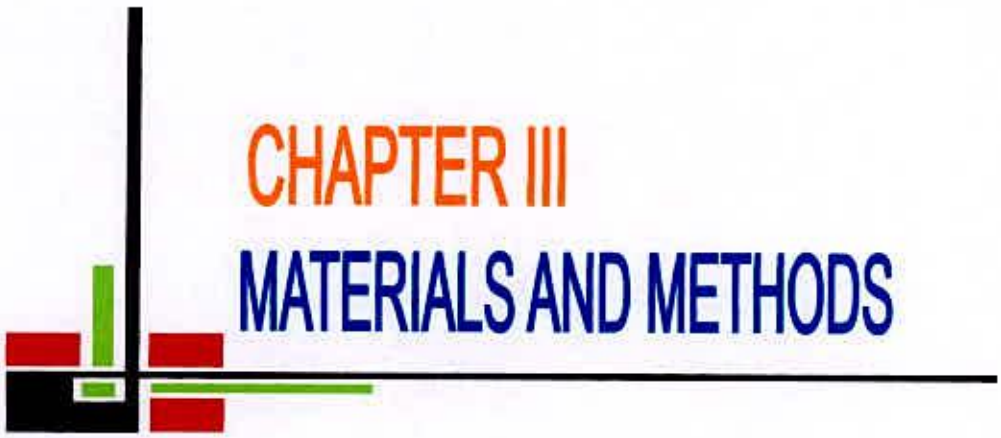
Genetic divergence was studied by Dhillon *et al.* (1999) for seed yield and six important yield components in Indian mustard (*Brassica juncea* Czern & Coss) and found 8 clusters. Cluster I comprising of 24 genotypes, whereas clusters VI, VII and VIII comprised of one genotype of each. Seed yield per plant showed maximum divergence followed by number of siliqua on main shoot and minimum by number of primary branches per plant. The inter cluster distance was maximum between clusters V and VIII (713.86) followed by clusters V and III (454.63).

Uddin (1994) conducted an experiment on genetic divergence among 34 genotypes of mustard were estimated using D^2 and principal component analysis. The inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups. Thirty one toria genotypes were grown in 12 artificially created environments in order to study genetic divergence by Singh and Gupta (1984). D^2 estimates based on 12 characters were used in obtaining the clustering pattern and inter- and intra-cluster distances. Out of 31 genotypes, on the basis of stability, high yield and divergence six genotypes were found to be suitable for use in a breeding program.

Nadaf *et al.* (1986) conducted multivariate analysis using Mahalanobis D^2 statistic to group 83 genotypes on the basis of yield/plant and six other agronomic characters of

bunch groundnut. They reported 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.

A study of genetic divergence using Mahalanobis D^2 statistic was conducted by Rawhat and Anad (1981) on 27 strains of Indian brown mustard (*Brassica juncea* L. Czern and Coss) for seven characters related to yield and fitness. The various strains were grouped in seven clusters on three diverse lines. Parallel variation was observed between clusters III, IV and VII on one line, and I, II and V on the other, with cluster VI diverging from the rest. The geographical diversity of strains was found not to be related with the genetic diversity. The characters that contributed maximally to divergence were days to flowering, plant height and 1000-seed weight in that order.



CHAPTER III

MATERIALS AND METHODS

CHAPTER III

MATERIALS AND METHODS

3.1 Experimental site:

The experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka – 1207 during November 2013 to February 2014. The location of the experimental site was situated at 230 74' N latitude and 900 35' E longitude with an elevation of 8.6 meter from the sea level. Photograph showing experimental sites (Appendix 1).

3.2 Soil and Climate:

The experimental site was situated in the subtropical zone. The soil of the experimental site belongs to Agroecological region of "Madhupur Tract" (AEZ No. 28). The soil was clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH was 5.47 to 5.63 and organic carbon content is 0.82% (Appendix II). The records of air temperature, humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix III).

3.3 Experimental materials:

The healthy seeds of sixty six F_5 of *Brassica napus* collected from the Dept. of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, which were used as experimental materials. The materials used in that experiment is shown in Table 1.

3.4 Methods

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

3.4.1 Land preparation

The experimental plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about good tilth. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly.

Table 1. Materials used for the experiment

Gentypes	F5 Populations	Source
G1	Nap 108 × Nap 9901, P_1	SAU
G2	Nap 108 × Nap 9901, P_2	SAU
G3	Nap 108 × Nap 9901, P_3	SAU
G4	Nap 108 × Nap 9901, P_4	SAU
G5	Nap 9901× Nap 0130, P_1	SAU
G6	Nap 9901× Nap 0130, P_2	SAU
G7	Nap 9905 × Nap 108, P_1	SAU
G8	Nap 9905 × Nap 108, P_2	SAU
G9	Nap 9905 × Nap 108, P_3	SAU
G10	Nap 9905 × Nap 205, P_1	SAU
G11	Nap 9905 × Nap 205, P_2	SAU
G12	Nap 9906 × Nap 2066, P_1	SAU
G13	Nap 9906 × Nap 2066, P_2	SAU
G14	Nap 9906 × Nap 2066, P_3	SAU
G15	Nap 205× Nap 0130, P_1	SAU
G16	Nap 205× Nap 0130, P_2	SAU
G17	Nap 205× Nap 0130, P_3	SAU
G18	Nap 205× Nap 0130, P_4	SAU
G19	Nap 9905 × Nap 0130, P_1	SAU
G20	Nap 9905 × Nap 0130, P_2	SAU
G21	Nap 9908 × Nap 0130, P_1	SAU
G22	Nap 9908 × Nap 0130, P_2	SAU
G23	Nap 9908 × Nap 0130, P_3	SAU
G24	Nap 9908 × Nap 0130, P_4	SAU
G25	Nap 9908 × Nap 0130, P_5	SAU
G26	Nap 9905 × Nap 9908, P_1	SAU
G27	Nap 9905 × Nap 9906, P_1	SAU
G28	Nap 9905 × Nap 9906, P_2	SAU
G29	Nap 108 × Nap 2066, P_1	SAU
G30	Nap 108 × Nap 2066, P_2	SAU
G31	Nap 108 × Nap 2066, P_3	SAU
G32	Nap 108 × Nap 2066, P_4	SAU
G33	Nap 2066 × Nap 0130, P_1	SAU

G34	Nap 2066 × Nap 0130, P_2	SAU
G35	Nap 9906 × Nap 0130, P_1	SAU
G36	Nap 9906 × Nap 0130, P_2	SAU
G37	Nap 108 × Nap 0130, P_1	SAU
G38	Nap 108 × Nap 0130, P_2	SAU
G39	Nap 108 × Nap 0130, P_3	SAU
G40	Nap 9901 × Nap 205, P_1	SAU
G41	Nap 9901 × Nap 205, P_2	SAU
G42	Nap 9906 × Nap 9901, P_1	SAU
G43	Nap 9906 × Nap 9901, P_2	SAU
G44	Nap 9908 × Nap 2066, P_1	SAU
G45	Nap 9908 × Nap 2066, P_2	SAU
G46	Nap 9908 × Nap 9901, P_1	SAU
G47	Nap 9908 × Nap 9901, P_2	SAU
G48	Nap 9908 × Nap 9901, P_3	SAU
G49	Nap 9908 × Nap 9901, P_4	SAU
G50	Nap 9905 × Nap 9901, P_1	SAU
G51	Nap 9905 × Nap 9901, P_2	SAU
G52	Nap 9901 × Nap 2066, P_1	SAU
G53	Nap 9901 × Nap 2066, P_2	SAU
G54	Nap 9908 × Nap 9906, P_1	SAU
G55	Nap 9908 × Nap 9906, P_2	SAU
G56	Nap 9908 × Nap 9906, P_3	SAU
G57	Nap 9908 × Nap 9906, P_4	SAU
G58	Nap 9906 × Nap 205, P_1	SAU
G59	Nap 9906 × Nap 205, P_2	SAU
G60	Nap 9906 × Nap 205, P_3	SAU
G61	Nap 9906 × Nap 205, P_4	SAU
G62	Nap 2066 × Nap 205, P_1	SAU
G63	Nap 2066 × Nap 205, P_2	SAU
G64	Nap 2066 × Nap 205, P_3	SAU
G65	Nap 2066 × Nap 205, P_4	SAU
G66	Nap 108 × Nap 205, P_1	SAU

3.4.2 Application of manure and fertilizer

The crop was fertilized at the rate of 10 tons of Cowdung, 250 kg Urea, 175 kg Triple Super Phosphate (TSP), 85 kg Muriate of Potash (MP), 250 kg Gypsum, 3 kg Zinc Oxide and Boron 1 kg per hectare. The half amount of urea, total amount of Cowdung, TSP, MP, Gypsum, Zinc Oxide and Boron was applied during final land preparation. The rest amount of urea was applied as top dressing after 25 days of sowing.

3.4.3 Experimental design and layout

Field lay out was done after final land preparation. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The total area of the experiment was 56m × 14m = 784m^2. Each replication size was 56m × 3.5m, and the distance between replication to replication was 1m. The spacing between lines to line was 30cm. Seeds were sown in lines in the experimental plots on 11 November, 2013. 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. A pictorial view of experimental field at flowering stage is presented in Plate 1.

3.4.4 Intercultural operations

Intercultural operations, such as weeding, thinning, irrigation, pest management, etc. were done uniformly in all the plots. Irrigation was given with cane after sowing of seeds to bring proper moisture condition of the soil to ensure uniform germination of the seeds. A good drainage system was maintained for immediate release of rainwater from the experimental plot during the growing period. The first weeding was done after 15 days of sowing. At the same time, thinning was done for maintaining a distance of 10 cm from plant to plant in rows of 30 cm. apart. Second weeding was done after 35 days of sowing. Aphid infection was found in the crop during the siliqua development stage. To control aphids Malathion-57 EC @ 2ml/liter of water was applied. The insecticide was applied in the afternoon.

Plate 1: Photograph showing the experimental field at SAU during flowering stage.

Plate 2. Photograph showing the experimental field at SAU during maturity stage.

3.4.5 Crop harvesting

Harvesting was done from 16th to 22nd February, 2014 depending upon the maturity. When 80% of the plants showed symptoms of maturity i.e. straw color of siliqua, leaves, stems desirable seed color in the mature siliqua, the crop was assessed to attain maturity. Fifteen plants were selected at random F_5 progenies in each replication. The plants were harvested by uprooting and then they were tagged properly. Data were recorded on different parameters from these plants. A pictorial view of experimental field at maturity stage is presented in Plate 2.

3.4.6 Data collection

For studying different genetic parameters and inter-relationships, ten characters were taken into consideration. The data were recorded on ten selected plants for each cross and ten selected plants for each parent on the following traits-

i. **Days to 50% flowering:** Days to 50% flowering were recorded from sowing date to the date of 50% flowering of every entry.

ii. **Days to 80% maturity:** The data were recorded from the date of sowing to siliquae maturity of 80% plants of each entry.

iii. **Plant height (cm):** It was measured in centimeter (cm) from the base of the plant to the tip of the longest inflorescence. Data were taken after harvesting.

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

v. **Number of secondary branches per plant:** The total number of branches arisen from the primary branch of a plant was counted as the number of secondary branches per plant.

vi. **Number of siliquae per plant:** Total number of siliquae of each plant was counted and considered as the number of siliquae/plant.

vii. **Siliqua length (cm):** This measurement was taken in centimeter (cm) from the base to the tip of a siliqua without beak of the ten representative siliquae..

viii. **Number of seeds per siliqua:** Well filled seeds were counted from ten representative siliquae, which was considered as the number of seeds per siliqua.

ix. **1000 seed weight (g):** Weight in grams of randomly counted thousand seeds of each entry was recorded.

x. **Seed yield/plant (g):** All the seeds produced by a representative plant was weighed in g and considered as the seed yield/plant.

3.4.7 Statistical analysis

All the collected data of the study were used to statistical analysis for each character, analysis of variance (ANOVA), mean, range were calculated by using MSTATC software program and then 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). Genotypic and phenotypic correlation coefficient was obtained using the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956); and path co-efficient analysis was done following the method outlined by Dewey and Lu (1959). Multivariate analysis viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) were done by using GENSTAT software.

Estimation of genotypic and phenotypic variances:

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

a. **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,

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

i) 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

δ_g = Genotypic standard deviation

δ_p = Phenotypic standard deviation

$\bar{x}$ = Population mean

ii) Estimation of heritability:

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

$$h^2_b(\%) = \frac{\delta^2_g}{\delta^2_p} \times 100$$

Where, h^2_b = Heritability in broad sense

δ^2_g = Genotypic variance

δ^2_p = Genotypic variance

iii) 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

δ^2_g = Genotypic variance

δ^2_p = Phenotypic variance

δ_p = Phenotypic standard deviation

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

iv) 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).

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

v) Estimation of simple correlation co-efficient:

Simple correlation co-efficient (r) was estimated with the following formula (Clarke, 1973; Singh and Chaudhary, 1985).

$$r = \frac{\sum xy - \frac{\sum x \cdot \sum y}{N}}{\sqrt{\left[\left\{\sum x^2 - \frac{(\sum x)^2}{N}\right\}\left\{\sum y^2 - \frac{(\sum y)^2}{N}\right\}\right]}}$$

Where, $\sum$ = Summation

x and y are the two variables correlated

N = Number of observation

vi) Path co-efficient analysis:

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985) and Dabholkar (1992), using simple correlation values. In path analysis, correlation co-efficient is partitioned into direct and indirect independent variables on the dependent variable.

In order to estimate direct & indirect effect of the correlated characters, say x1, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

$$r_{yx1} = P_{yx1} + P_{yx2}r_{x1x2} + P_{yx3}r_{x1x3}$$

$$r_{yx2} = P_{yx1}r_{x1x2} + P_{yx2} + P_{yx3}r_{x2x3}$$

$$r_{yx3} = P_{yx1}r_{x1x3} + P_{yx2}r_{x2x3} + P_{yx3}$$

Where, r's denotes simple correlation co-efficient and P's denote path co-efficient (Unknown). P's in the above equations may be conveniently solved by arranging them in matrix from.

Total correlation, say between x1 and y is thus partitioned as follows:

P_{yx1} = The direct effect of x1 on y.

$P_{yx2}r_{x1x2}$ = The indirect effect of x1 via x2 on y.

$P_{yx3}r_{x1x3}$ = The indirect effect of x1 via x3 on y.

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

$$P^2_{RY} = 1 - \sum P_{iy} \cdot riy$$

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

P_{iy} = Direct effect of the character on yield

Riy = Correlation of the character with yield.

vii) Estimation of Genetic Diversity

a. Principal Component Analysis (PCA)

Principal component analysis, one of the multivariate techniques, is used to examine the interrelationship among several characters and can be done from the sum of squares and product matrix for the characters. Therefore, principal component were computed from the correlation matrix and genotype scores obtained from the first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than the 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.

b. 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).

c. Canonical Vector Analysis (CVA)

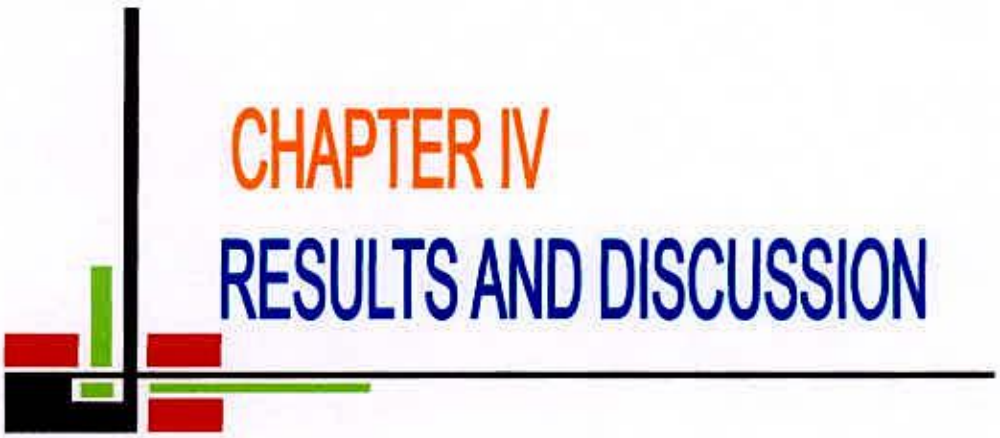
The canonical vector analysis compute a linear combination of original variabilities that maximize the ratio in between group to within group variation to be finding out and thereby giving functions of the original variabilities that can be used to discriminate between groups. Finally, a series of orthogonal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

d. Average Intra-cluster Distances

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 genotype included in the cluster. The square root of the average D^2 values represents the distances (D) within cluster.

e. Clustering

To divide the genotypes of the study into some number of mutually exclusive groups clustering were 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 criterion, the algorithm switches to a second stage which examine the effect of swapping two genotypes of different classes and so on.



CHAPTER IV

RESULTS AND DISCUSSION

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The present study was conducted with a view to determine the variability among sixty six F_5 materials of *Brassica napus* genotypes and also to study the correlation and path co-efficient for seed yield and different yield contributing characters. The data were recorded on different characters such as days to 50% flowering, days to maturity, plant height (cm), no. of primary branches per plant, no. of secondary branches per plant, no. of siliqua per plant, no. of seeds per siliqua, siliqua length (cm) thousand seed weight (g) and seed yield per plant (g). The data were statistically analyzed and thus obtained results are described below under the following heads:

- Variability study in *Brassica napus* L.
- Correlation coefficient of characters
- Path coefficient analysis
- Genetic diversity analysis

4.1 Variability study in *Brassica napus*

4.1.1 Variability among the sixty six F_5 materials for *Brassica napus*

Significant variations were observed for most of the characters among sixty six F_5 materials of *Brassica napus*. Table 2a and table 2b showed the values of mean, range CV%, phenotypic variances, genotypic variances, phenotypic coefficient of variation and genotypic coefficient of variation for different yield related characters.

4.1.1.1 Plant height (cm)

In this study the highest plant height was observed in G19 (Nap-9905 × Nap-0130, P_1) (118.43cm) (Plate 3) where as the minimum plant height was observed in G1 (Nap-108 × Nap-9901) (83.63cm) (Plate 3) (Table 2a). Phenotypic variance and genotypic variance were observed as 67.04 and 60.89, respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait. The estimates of PCV (7.85%) and GCV (7.48%) also indicated presence of variability among the genotypes for this trait (Table 2b). The highest variation in plant height among parents and their hybrid was observed by Tyagi *et al.* (2001).

Table 2a. Estimation of genetic parameters in ten characters of 66 genotypes in *Brassica napus* L.

Parameters	Min	Max	Mean	MS	CV(%)	$\sigma^2 g$	$\sigma^2 e$	$\sigma^2 P$
50F	36.00	46.00	41.34	11.664**	2.23	5.41	0.85	6.26
DM	65.00	72.00	68.44	9.254**	1.23	4.27	0.71	4.98
PH	83.63	118.43	104.34	127.93**	2.38	60.89	6.15	67.04
NPB	2.28	5.11	3.53	0.987**	4.36	0.48	0.02	0.51
NSB	0.70	4.90	1.68	0.906**	6.41	0.45	0.01	0.46
NSP	88.73	214.57	136.08	1101.598**	4.59	531.27	39.05	570.33
SL	6.88	9.29	8.01	0.558**	1.8	0.27	0.02	0.29
NSS	16.86	27.60	21.6	11.512**	3.03	5.54	0.43	5.97
TSW	1.81	4.36	3.44	0.642**	2.98	0.32	0.01	0.33
SYP	4.05	10.30	7.02	3.673**	2.07	1.83	0.02	1.85

**, * Correlation is significant at the 0.01 and 0.05 level, respectively.

50F = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), NPB=Number of Primary Branches per plant, NSB=Number of secondary branches per plant, NSP=Number of Siliqua per plant, NSS=Number of seed per silique, SL=Siliqua length, TSW = Thousand Seed Weight (g), SYP=Seed yield per plant, MS = mean sum of square, CV (%) = Coefficient of Variation, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance and σ^2 e = Environmental variance.

Table 2b. Estimation of genetic parameters in ten characters of 66 genotypes in *Brassica napus* L.

Parameters	GCV	ECV	PCV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
50F	5.62	2.23	6.05	86.37	4.45	10.77
DM	3.02	1.23	3.26	85.72	3.94	5.76
PH	7.48	2.38	7.85	90.83	15.32	14.68
NPB	19.66	4.36	20.13	95.31	1.4	39.53
NSB	39.8	6.41	40.31	97.47	1.36	80.94
NSP	16.94	4.59	17.55	93.15	45.83	33.68
SL	6.47	1.8	6.72	92.85	1.03	12.84
NSS	10.9	3.03	11.31	92.85	4.67	21.63
TSW	16.33	2.98	16.6	96.78	1.14	33.1
SYP	19.25	2.07	19.36	98.85	2.77	39.42

50F = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), NPB=Number of Primary Branches per plant, NSB=Number of secondery branches per plant, NSP=Number of Siliqua per plant, NSS=Number of seed per silique, SL=Siliqua length, TSW = Thousand Seed Weight (g), SYP=Seed yield per plant, GCV = Genotypic Coefficient of Variation, PCV = Phenotypic Coefficient of Variation and ECV = Environmental Coefficient of Variation.

Plate 3 . Photograph showing variation between highest G19 (Nap-9905 × Nap0130, P_1) and lowest plant height G1 (Nap-108 × Nap-9901, P_1) of *Brassica rapa* genotypes

4.1.1.2 Number of primary branches per plant

Among the 66 F_5 populations the highest number of primary branches per plant was observed in G42 (Nap 9906× Nap 9901, P_1) (5.11) (Plate 4) where as the minimum number of primary branches/plant was observed in G28 (Nap 9905× Nap 9906, P_2) (2.28) (Plate 4 and Table 2a). Phenotypic variance and genotypic variance were observed as 0.51 and 0.48, respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait. Relatively large differences between them indicating large environmental influences on these character and relatively low difference between PCV (20.13%) and GCV (19.66%) value indicating the apparent variation not only due to genotypes but also due to the influence of environment (Table 2b). Chowdhury *et al.* (1987) also found significant differences for number of primary branches per plant.

4.1.1.3 Number of secondary branches per plant

Among the 66 F_5 populations the highest number of secondary branches/plant was observed in G58 (Nap 9906 × Nap 205, P_1) (4.90) (Plate 5) whereas the minimum number of secondary branches/plant was observed in G51 (Nap 9905 × Nap 9901, P_2) (0.70) (Plate 5 and Table 2a). Phenotypic variance and genotypic variance were observed as 0.46 and 0.45, respectively. Higher estimate of PCV (40.31%) and GCV (39.80%) values indicated presence of considerable variability among the genotypes for this trait (Table 2b). Lekh *et al.* (1998) found highest genotypic coefficient of variation for number of secondary branches while working on 24 genotypes of *Brassica napus*. Chowdhury *et al.* (1987) found significant differences for number of secondary branches per plant. Genotypic and phenotypic variability in mustard are shown in Figure 1.

Plate 4. Photograph showing variation between highest G42 (Nap 9906× Nap 9901, P_1) and lowest G28 (Nap 9905× Nap 9906, P_2) primary branch of *Brassica rapa* genotypes

Plate 5. Photograph showing variation between highest G58 (Nap 9906 × Nap 205, P_1) and lowest G51 (Nap 9905 × Nap 9901, P_2) secondary branch of *Brassica rapa* genotypes

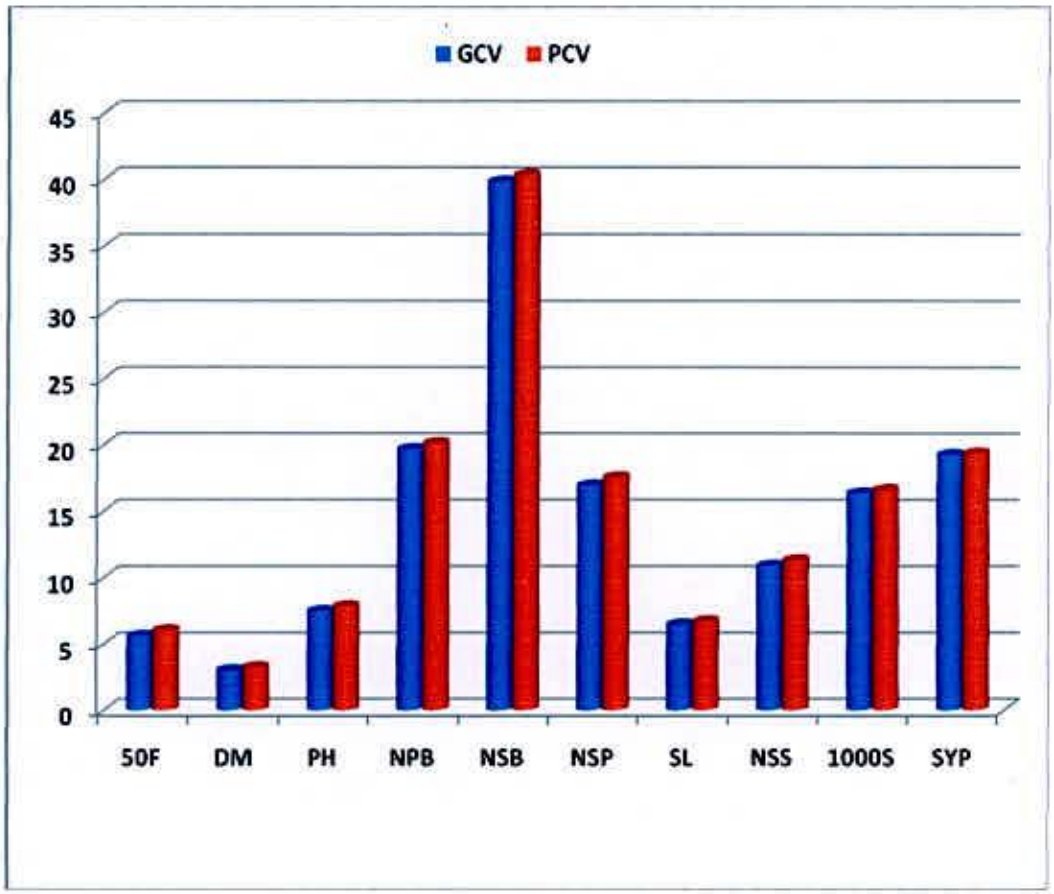


Fig. 1. Genotypic and phenotypic coefficient of variation in *Brassica napus* L.

4.1.1.4 Days to 50% flowering

Considerable variations were observed among 66 F_5 populations for days to 50% flowering. The days to 50% flowering were observed the lowest (36 days) in G38 (Nap 108 × Nap 0130, P_2) and highest (46 days) was observed in G55 (Nap-9908 × Nap-9906, P_2); G56 (Nap 9908 x Nap 9906, P_3) (Table 2a and plate 6).

Phenotypic and genotypic variance for days to 50% flowering was observed as 6.26 and 5.41, respectively with moderate differences between them, suggested moderate influence of environment on the expression of the genes controlling this trait. The phenotypic coefficient of variation (6.05%) was higher than the genotypic coefficient of variation (5.62%) (Table 2b), which suggested that environment has a significant role on the expression of this trait. High genotypic and phenotypic co-efficient of variation was recorded by Lekh *et al.* (1998).

Significant genetic variability in days to 50% flowering in *B. napus* was also observed by Singh *et al.* (1991).

4.1.1.5 Days to maturity

The highest days to maturity was observed in G1 (Nap 108 × Nap 9901, P_1); G55 (Nap 9908 × Nap 9906, P_2); G56 (Nap 9908 × 9906, P_3), G61 (Nap 9906 × Nap 205, P_4); G65 (Nap 2066 × Nap 205, P_4), G66 (Nap 108 × Nap 205,P_1) (72 days) and the minimum days to maturity was observed in G12 (Nap 9906 × Nap 2066, P_1); G14 (Nap 9906 × Nap 2066, P_3); G15 (Nap 205× Nap 0130, P_1); G16 (Nap 205× Nap 0130, P_2); G22 (Nap 9908 × Nap 0130, P_2); G24 (Nap 9908 × Nap 0130, P_4); 65 days (Table 2a). Phenotypic and genotypic variance for days to maturity was observed 4.98 and 4.27, respectively with moderate differences between them, suggested moderate influence of environment on the expression of the genes controlling this trait. The phenotypic coefficient of variation (3.26%) was moderately higher than the genotypic coefficient of variation (3.02%) (Table 2b), which suggested that environment has a role on the expression of this trait. Higher genotypic variances indicated the better transmissibility of a character from parent to the offspring. Similar result for this trait was also observed by Katiyar *et al.* (1974).

Plate 6. Photograph showing variation between highest and lowest flowering variation in between G38 (Nap 108 × Nap 0130, P_2) & G55 (Nap-9908 × Nap-9906, P_2); G56 (Nap 9908 x Nap 9906, P_3)

4.1.1.6 Number of siliqua per plant

The number of siliqua per plant was observed the highest in G57 (Nap 9908 × Nap 9906, P_4) (214.57) (Plate 7) and the lowest in G66 (Nap 108 × Nap 205, P_1) (88.73) (Plate 7). Number of siliqua per plant showed the highest phenotypic variance (570.33) and genotypic variance (531.27) with large environmental influence and the difference between the PCV (17.55%) and GCV (16.94%) indicated existence of adequate variation among the genotype (Table 2b). High genetic variation was also found by Kudla (1993).

4.1.1.7 Length of siliqua (cm)

Length of siliqua was observed the highest in G27 (Nap 9905 × Nap 9906, P_1) (9.29 cm) and the minimum length of pod was observed in G50 (Nap 9905 × Nap 9901, P_1) (6.88 cm) (Table 2a & plate 8). Length of siliqua showed phenotypic variance (0.29) and genotypic variance (0.27) with little difference between them indicating that they were less responsive to environmental factors for their phenotypic expression and relatively medium PCV (6.72%) and GCV (6.47%) indicating that the genotype has moderate variation for this trait (Table 2b). High co-efficient of variation for this trait for both genotypic and phenotypic variability was recorded by Masood *et al.* (1999). High genetic variability for this trait was also found by Olson (1990).

4.1.1.8 Number of seeds per siliqua

The number of seeds per siliqua was observed highest in G11 (Nap 9905 × Nap 205, P_2) (27.60). The minimum number of seeds per siliqua was observed in G1 (Nap 108 × Nap 9901, P_1) (16.86) (Table 2a). The phenotypic and genotypic variances for this trait were 5.97 and 5.54 respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait. The value of PCV and GCV were 11.31% and 10.9% respectively for number of seeds per siliqua which indicating that medium variation exists among different genotypes (Table 2b). Similar variability was also recorded by Kumar and Singh (1994).

Plate 7. Photograph showing variation between highest G57 (Nap 9908 × Nap 9906, P_4) and lowest G66 (Nap 108 × Nap 205, P_1) siliqua per plant of *Brassica rapa* genotypes

Plate 8. Photograph showing variation between highest G27 (Nap 9905 × Nap 9906, P_1) and lowest G50 (Nap 9905 × Nap 9901, P_1) siliqua length of *Brassica rapa* genotypes

4.1.1.9 Thousand seed weight (g)

Thousand seed weight was found maximum in G42 (Nap 9906 × Nap 9901, P_1) (4.36 g) where as the minimum thousand seed weight was found in G44 (Nap 9908 × Nap 2066, P_1) (1.81 g) (Table 2a and plate 9). Thousand seed weight showed very low genotypic (0.32) and phenotypic (0.33) variance with little differences indicating that they were low responsive to environmental factors. The phenotypic coefficient of variation (16.6%) and genotypic coefficient of variation (16.33%) were close to each other (Table 2b). There was a very little difference between phenotypic and genotypic co-efficient of variation, indicating minor environmental influence on this character. Significant variability for this trait was also found by Kumar and Singh (1994).

Masood *et al.* (1999) found high coefficient of variation for thousand seed weight while working with seven genotypes of *Brassica napus* to study genetic variability.

4.1.1.10 Yield per plant (g):

Yield per plant was found maximum in G17 (Nap 205 × Nap 0130, P_3) (10.30 g) when it was the minimum yield per plant was found in G44 (Nap 9908 × Nap 2066, P_1) (4.05g) (Table 2a). The phenotypic variances and genotypic variances for this trait were 1.85 and 1.83 respectively. The values are very close to each other indicated less environmental influences on this trait. The values of GCV and PCV were 19.25% and 19.36% indicating that the genotype has moderate variation for this trait (Table 2b). Similar variability was also found by Khera and Singh (1988).

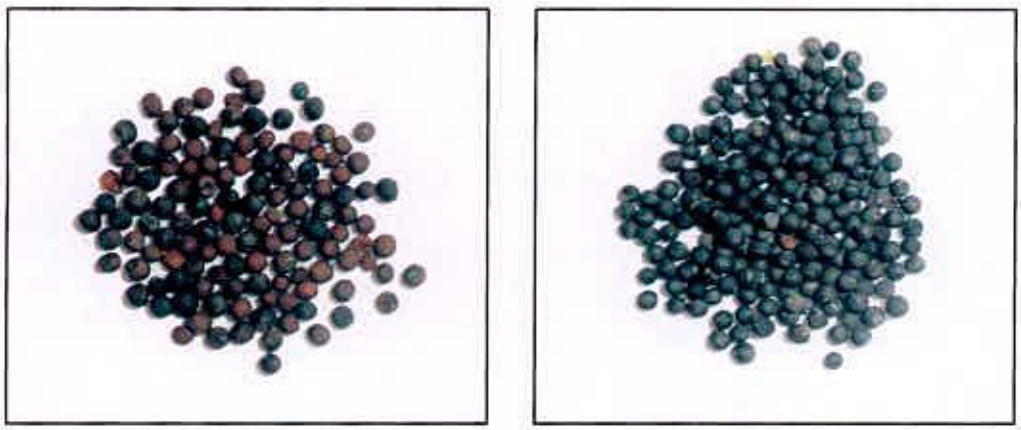


Plate 9. Photograph showing variation between highest G42 (Nap 9906 × Nap 9901, P_1) and lowest G44 (Nap 9908 × Nap 2066, P_1) genotypes of thousand seed weight of *Brassica rapa*

4.1.2 Heritability, genetic advance and selection

4.1.2.1 Plant height (cm)

Plant height of F_5 showed high heritability 90.83% with moderately high genetic advance of 15.32 and genetic advance in percentage of mean of 14.68% (Table 2b), revealed the possibility of predominance of additive gene action in the inheritance of this trait and indicating that this trait could be improved through selection process. High variability in plant height for *B. juncea*, *B. rapa* and *B. napus* was also observed by Varshney *et al.* (1986). Chandola (1977) observed high genetic advance for plant height while working with 30 varieties of *Brassica rapa.* Heritability and genetic advance in percentage of mean are shown in Figure 2.

4.1.2.2 Number of primary branches per plant

Number of primary branches per plant exhibited high heritability 95.31 with low genetic advance of 1.4 and genetic advance in percentage of mean of 39.53%, which revealed that this trait was controlled by non-additive gene. As a whole, the high heritability and the consequent low genetic advance indicated the lower possibility of selecting genotypes for this trait. However, some of the individual plants showed quite a reasonable lower primary branches which were selected for further study in the next generation. Low heritability coupled with low genetic advance was also found by Singh *et al.* (1987). Yadava *et al.* (1985) found high heritability and genetic advance for number of primary branches per plant.

4.1.2.3 Number of secondary branches per plant

Number of secondary branches per plant exhibited high heritability (97.47%) with low genetic advance 1.36 and genetic advance in percentage of mean (80.94%), such results revealed that this trait was controlled by non-additive gene. As a whole, the moderately high heritability and the consequent low genetic advance indicated the lower possibility of selecting genotypes. Moderately high heritability coupled with low genetic advance was also found by Singh *et al.* (1987). Sheikh *et al.* (1999) found high heritability coupled with high genetic advance for number of secondary branches per plant while working with 24 genotypes of toria.

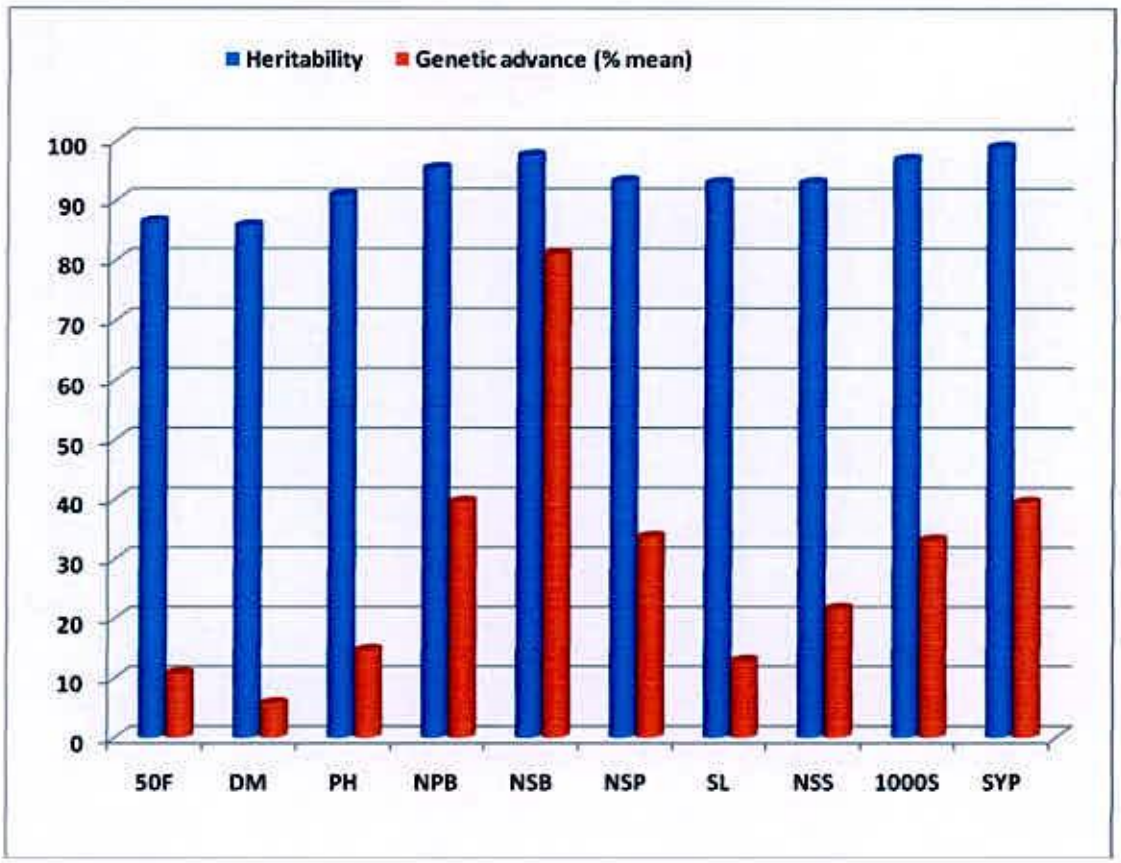


Fig. 2. Heritability and genetic advance over mean in *Brassica napus*.

4.1.2.4 Days to 50% flowering

Days to 50% flowering exhibited high heritability (86.37%) with low genetic advance (4.45) and genetic advance in percentage of mean (10.77%) indicated that this trait was controlled by non-additive gene. This results support the reports of Malik *et al.* (1995).

4.1.2.5 Days to maturity

Days to maturity showed high heritability (85.72%) with low genetic advance (3.94) and genetic advance in percentage of mean (5.76%) indicated that this trait was controlled by non-additive gene and medium possibility of selecting genotypes that would mature earlier. High heritability coupled with low genetic advance for this trait was also observed by Sharma (1984).

4.1.2.6 Number of siliqua per plant

Number of siliqua per plant exhibited high heritability 93.15% with high genetic advance 45.83 and genetic advance in percentage of mean 33.68%. These results revealed the possibility of predominance of additive gene action in the inheritance of this trait. This trait possessed high variation; it is high potential for effective selection for further genetic improvement of this character. High heritability coupled with high genetic advance for this trait was also observed by Sheikh *et al.* (1999). Mahmud *et al.* (2003) reported that the number of siliqua per plant were highly heritable coupled with high genetic advance. Akbar *et al.* (2007) also found higher GCV, higher heritability and genetic advance for this trait.

4.1.2.7 Siliqua length

Siliqua length showed high heritability (92.85%) with low genetic advance (1.03) and low genetic advance in percentage of mean 12.84% indicated that this trait was controlled by non-additive gene. High heritability for this trait was observed by Chaudhury *et al.* (1989). Similar results were also found by Kwon *et al.* (1989) and Rao (1977).

4.1.2.8 Number of seeds per siliqua

Number of seeds per siliqua showed high heritability 92.85% coupled with high genetic advance 4.67 and high genetic advance in percentage of mean 21.63%,

indicated that this trait was controlled by additive gene and selection for this character would be effective. High heritability coupled with high genetic advance for this trait was also observed by Singh (1986).

4.1.2.9 Thousand seed weight

Thousand seed weight exhibited high heritability 96.78% with high genetic advance 1.14 and genetic advance in percentage of mean 33.1%, revealed that this trait was controlled by additive gene and selection for this character would be effective. Johnson *et al.* (1955) reported that heritability estimates along with genetic group were more useful in prediction selection of the best individual. High heritability for this trait was also observed by Yadava *et al.* (1993). Singh *et al.* (2002) reported the high heritability and genetic advance for thousand seed weight.

4.1.2.10 Seed yield per plant

Seed yield per plant showed high heritability 98.85% with high genetic advance (2.77) and moderately high genetic advance in percentage of mean 39.42% indicated this trait was controlled by additive gene and selection for this character would be effective. High heritability coupled with high genetic advance for this trait was also observed by Sheikh *et al.* (1999). High heritability and genetic advance for seed yield per plant was reported by Singh (1986) while working with 22 genotypes of *Brassica napus*.

Significant variability was found in almost all the F_5 materials *Brassica napus* for most of the characters studied. The performance of the lines also compared with the one character variety, BS-13 as per objectives, selection was carried out among the 66 F_5 materials. Most promising 66 plants with short duration and high yield/plant were selected from the F_5 materials (Table 2a). There were large variations of the F_5 materials for siliqua per plant ranging from 88.73 to 214.57 siliqua. One plant from G42 (Nap 9906 × Nap 9901, P_1) (4.36 g) produced (4.36 g) thousand seed weight. One plant from G17 (Nap 205 × Nap 0130, P_3) produced exceptionally high yield/plant 10.30 g. (Table 2a).

4.2 Correlation coefficient

Yield is a complex product being influenced by several inter-dependable quantitative characters. Thus selection for yield may not be effective unless the other yield components influence it directly or indirectly are taken in to consideration. When selection pressure is exercised for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated characters. Hence knowledge regarding association of character with yield and among themselves provides guideline to the plant breeder for making improvement through selection vis-à-vis provide a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factors (Dewey and Lu 1959). Genotypic and phenotypic correlation co-efficient of different characters of 66 *Brassica napus* L. genotypes are shown in (Table 3 and table 4). Most of the characters showed the genotypic correlation co-efficient higher than the corresponding phenotypic correlation co-efficient suggesting a strong inherent association between the characters under study and consequently lower. Similar result was found by Pankaj *et al.* (2002). In few cases, phenotypic correlation co-efficient were higher than their corresponding genotypic correlation co-efficient suggesting that both environmental and genotypic correlation acted in the same direction and finally maximized their expression at phenotypic level.

4.2.1 Days to 50% flowering

Days to 50% flowering showed highly significant and positive correlation with days to maturity (G = 0.668, P = 0.640) indicated that if days to 50% flowering increased then days to maturity also increased. It also exhibited insignificant and positive interaction with plant height (G=0.087, P=0.080), number of secondary branch (G= 0.145, P=0.139) and number of siliqua per plant (G=0.103, P=0.091). However, it had insignificant and negative interaction with siliqua length (G = -0.245, P = -0.230), number of seed per siliqua (G= -0.169, P=0.160), thousand seed weight (G= -0.198, P= -0.192) and seed yield per plant (G= -0.034, P= -0.032) (Table 3 and table 4). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Parveen (2007) also revealed that days to 50% flowering had insignificant and positive interaction with yield per plant.

Table 3. Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different Genotype of *Brassica napus* L.

	DM	PH	NPB	NSB	NSP	SL	NSS	TSW	SYP
50F	0.668**	0.087	-0.027	0.145	0.103	-0.245	-0.169	-0.198	-0.034
DM		0.044	0.23	0.283*	0.126	-0.146	-0.171	-0.155	-0.123
PH			-0.500**	-0.152	0.390**	0.301*	0.246	-0.018	0.159
NPB				0.542**	0.233	-0.329**	-0.306*	0.017	-0.021
NSB					0.153	-0.259*	-0.244	-0.049	-0.093
NSP						0.178	0.069	-0.126	0.432**
SL							0.824**	0.028	0.380**
NSS								-0.131	0.380**
TSW									0.482**

** = Significant at 1%, * = Significant at 5%.

50F = Day to 50% flowering, DM = Day to maturity, PH = Plant Height (cm), NPB = Number of Primary Branches per plant, NSB = Number of secondary branches per plant, NSP = Number of Siliqua per plant, SL = Siliqua length (cm), NSS = Number of seed per silique, TSW = Thousand seed weight (g), SYP = Seed yield per plant (g)

Table 4. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of *Brassica napus* L.

	DM	PH	NPB	NSB	NSP	SL	NSS	TSW	SYP
50F	0.640**	0.080	-0.023	0.139	0.091	-0.230	-0.160	-0.192	-0.032
DM		0.044	0.209	0.272*	0.121	-0.138	-0.168	-0.156	-0.119
PH			-0.481**	-0.141	0.374**	0.294*	0.238	-0.021	0.158
NPB				0.534**	0.228	-0.319**	-0.297*	0.017	-0.018
NSB					0.150	-0.253*	-0.239	-0.051	-0.092
NSP						0.168	0.066	-0.116	0.425**
SL							0.790**	0.033	0.374**
NSS								-0.128	0.375**
TSW									0.483**

** = Significant at 1%; * = Significant at 5%.

50F = Day to 50% flowering, DM = Day to maturity, PH = Plant Height (cm), NPB = Number of Primary Branches per plant, NSB = Number of secondary branches per plant, NSP = Number of Siliqua per plant, SL = Siliqua length (cm), NSS = Number of seed per silique, TSW = Thousand seed weight (g), SYP = Seed yield per plant (g)

4.2.2 Days to maturity

Days to maturity showed significant and positive correlation with number of secondary branches (G= 0.283, P= 0.272). It had insignificant and positive correlation with plant height (G=0.044, P=0.044), number of primary branch (G= 0.23, P=0.209) and number of siliqua per plant (G=0.126, P=0.121).However, it had insignificant and negative interaction with siliqua length (G= -0.146, P= -0.138) number of seed per siliqua (G= -0.171, P=0.168), thousand seed weight (G= -0.155, P= -0.156) and seed yield per plant (G= -0.034, P= -0.032) (Table 3 and table 4). Insignificant association of these traits indicated that the association between these traits were largely influenced by environmental factors. Parveen (2007) also revealed that days to maturity had insignificant and positive interaction with yield per plant.

4.2.3 Plant height (cm)

Plant height showed highly significant and positive interaction with number of siliqua per plant (G = 0.390, P = 0.374) and siliqua length (G = 0.301, P = 0.294) whereas highly significant, but negative associations found in number of primary branches (G = -0.500, P = -0.481). Highly significant positive associations between plant height and other characters indicate that the traits were governed by same gene and simultaneous improvement would be effective. It had positive and insignificant interaction with number of seed per siliqua (G=0.246, P=0.238) and seed yield per plant (G=0.159, P=0.158. However, it had insignificant and negative interaction with Number of secondary branches (G = -0.152, P = -0.141), Thousand seed weight (G= -0.018, P= -0.021) (Table 3 and 4). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. These findings are showed resemblance to the reports of Parveen (2007). Shalini *et al.* (2000) also observed that plant height was highly associated with seed yield. Similar result was reported by Srivastava *et al.* (1983). Significant positive correlation between plant height and seed yield was found by Khan and Khan (2003). Chaudhary *et al.* (1990) found positive correlation of plant height with number of seed per siliqua, number of siliqua per plant. Basalma (2008) reported opposite result for this trait.

4.2.4 Number of primary branches per plant

Number of primary branches per plant showed positive and significant interaction with number of secondary branch (G = 0.542, P = 0.534) whereas significant, but negative found in siliqua length (G= -0.329, P= -0.319), number of seed per siliqua (G= -0.306, P= -0.297). These suggesting if number of primary branches increases then yield per plant also increases. Malik *et al.* (2000) reported similar result for number of primary branches and seed yield both at genotypic and phenotypic level. It had insignificant and positive correlation with number of seeds per siliqua (G = 0.233, P = 0.228) and thousand seed weight (G = 0.017, P = 0.017). However, it had insignificant and negative interaction was found in seed yield per plant (G = -0.021, P = -0.018) (Table 3 and table 4). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Similar results were obtained by Rashid (2007).

4.2.5 Number of secondary branches per plant

Number of secondary branch showed no significant and positive interaction with any character, but it had significant and neagtive correlation with siliqua length (G = -0.259, P = -0.253). However, it had insignificant and positive correlation with nsp (G= 0.153, P= 0.150) and also insignificant and negative interaction with Number of seed per siliqua (G = -0.244, P = -0.239), thousand seed weight (G = -0.049, P = -0.051) and seed yield per plant (G= -0.093, P= -0.092) (Table 3 and table 4). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. These findings are showing similar to the reports of Chowdhary *et al.* (1987).

4.2.6 Number of siliqua per plant

Siliqua per plant showed significant and positive correlation with seed yield per plant (G = 0.432, P = 0.425). Malik *et al.* (2000) reported positive correlation between siliqua per plant and seed yield. Whereas the insignificant and positive interaction was found in siliqua length (G = 0.178, P = 0.168), number of siliqua per seed (G = 0.069, P = 0.066). it had also insignificant and negative interaction with thousand seed weight (G= -0.126, P= -0.116) (Table 3 and table 4). Insignificant association of these traits indicated that the association between these traits is largely influenced by

environmental factors. Tyagi *et al.* (1996) reported that no. of seed per siliqua had positive and insignificant effect on seed yield per plant.

4.2.7 Siliqua length (cm)

Siliqua length showed highly significant and positive interaction with Number of seed per silique (G= 0.824, P= 0.790) and Seed yield per plant (G=0.380, P= 0.370) indicated that if siliqua length increased then yield per plant decreased. It also showed highly insignificant and positive correlation with yield per plant (G=0.028, P=0.033) (Table 3 and table 4) Nasim *et al.* (1994) reported that seed yield per plant was significantly and negatively with siliqua length.

4.2.8 Number of seeds per siliqua

Number of seeds per siliqua showed highly significant and positive interaction with Seed yield per plant (G = 0.380, P = 0.375). Highly significant positive associations between number of seeds per siliqua and seed length indicated that the traits were governed by same gene and simultaneous improvement would be effective. It had insignificant and negative interaction with thousand seed weight (G = -0.131, P = -0.128) (Table 3 and table 4). Insignificant association of these traits indicated that the association between these traits sis largely influenced by environmental factors. Nasim *et al.* (1994) reported that no. of seeds per siliqua had negative and significant effects on seed yield per plant. Ahmed (1993) also found similar results for this trait.

4.2.9 Thousand seed weight

Thousand seed weight showed highly significant and positive interaction with seed yield per plant (G=0.482, P=0.483) (Table 3 and table 4). Saini and Kumar (1995), Kakroo and Kumar (1991) and Olsson (1990) found positive associations which support the results. Tuncturk and Ciftci (2007) reported positive correlation between seed yield with 1000-seed weight which supports the present findings.

4.3 Path Co-efficient analysis

Association of character determined by correlation co-efficient may not provide an exact picture of the relative importance of direct and indirect influence of each of yield components on seed yield per hector. In order to find out a clear picture of the inter-relationship between seed yield per plant and other yield attributes, direct and indirect effects were worked out using path analysis at phenotypic level which also measured the relative importance of each component. Seed yield per plant was considered as a resultant (dependent) variable and days to 50% flowering, days to maturity, plant height, number of primary braches per plant, number of siliqua per plant, length of siliqua, number of seeds per siliqua and thousand seed weight were causal (independent) variables. Estimation of direct and indirect effect of path co-efficient analysis for *Brassica napus* is presented in Table 5.

4.3.1. Days to 50% flowering

Path co-efficient analysis revealed that, days to 50% flowering had positive direct effect (0.182) on yield per plant. This trait showed indirect positive effect on yield per plant through number of primary branch (0.005), number of siliqua per plant (0.065), siliqua length (0.054). On the hand, it showed indirect negative effect via days to maturity (-0.068) followed by plant height (-0.024), number of secondary branch (-0.002), number of seed per siliqua (-0.108), thousand seed weight (-0.134) finally it made negative correlation with seed yield (-0.034). (Table 5). Chauhan and Singh (1995) revealed that days to 50% flowering had positive direct effect on yield per plant.

4.3.2. Days to maturity

Path co-efficient analysis revealed that, days to maturity had negative direct effect (-0.102) on yield per plant. This trait had positive indirect effect through 50% flowering (0.122), number of siliqua per plant (0.084) and siliqua length (0.034). On the other hand, days to maturity had negative indirect effect via plant height (-0.011), number of primary branch (-0.036), number of secondary branch (-0.003), number of seed per siliqua (-0.108) and thousand seed weight (-0.101). Finally it made negative correlation with seed yield (-0.123) (Table 5). Rashid (2007) revealed that days to maturity had positive direct effect on yield. Alam *et al.* (1986), Singh *et al.* (1985) and Srivastava *et al.* (1983) observed that days to maturity had positive direct and indirect effect on seed yield.

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

Characters	Direct effect	Indirect effect									Genotypic correlation with yield
		50F	DM	PH	NPB	NSB	NSP	SL	NSS	TSW	
50F	0.182	-	-0.068	-0.024	0.005	-0.002	0.065	0.054	-0.108	-0.134	-0.034
DM	-0.102	0.122	-	-0.011	-0.036	-0.003	0.084	0.034	-0.108	-0.101	-0.123
PH	-0.263	0.016	-0.004	-	0.078	0.002	0.253	-0.067	0.158	-0.013	0.159
NPB	-0.156	-0.005	-0.023	0.131	-	-0.006	0.149	0.074	-0.196	0.013	-0.021
NSB	-0.012	0.025	-0.029	0.039	-0.084	-	-0.097	0.058	-0.152	-0.034	-0.093
NSP	0.648	0.018	-0.013	-0.103	-0.036	-0.002	-	-0.040	0.044	-0.087	0.432**
SL	-0.223	-0.044	0.015	-0.079	0.052	0.003	0.117	-	0.519	0.020	0.380**
NSS	0.633	-0.031	0.017	-0.066	0.048	0.003	0.045	-0.183	-	-0.087	0.380**
TSW	0.672	-0.036	0.015	0.005	-0.003	0.001	-0.084	-0.007	-0.082	-	0.482**

Residual effect: 0.274

**, * Correlation is significant at the 0.01 and 0.05 level, respectively.

50F = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), NPB=Number of Primary Branches per plant, NSB=Number of secondery branches per plant, NSP=Number of Siliqua per plant, NSS=Number of seed per silique, SL=Siliqua length, TGW = Thousand Grain Weight (g), SYP=Seed yeild per plant.

4.3.3. Plant height

Path analysis revealed that plant height had negative direct effect (-0.263) on yield per plant. It had positive indirect effect on 50% flowering (0.016), number of primary branch (0.078), number secondary branch (0.002), number of siliqua per plant (0.253) and number of seed per siliqua (0.158) (Table 5). Varshney (1986) worked with several strains of *Brassica rapa* and observed that plant height had the negative direct effect on yield. Plant height had negative indirect effect via days to maturity (-0.004), siliqua length (-0.067) and thousand seed weight per plant (-0.013) (Table 5). Plant height finally made significant positive correlation with seed yield (0.159). These results indicated that if plant height increases than seed yield also increases mostly through the positive indirect effect of plant height with other characters. Han (1990) and Singh (2004) also reported direct positive result for this character.

4.3.4. Number of primary branches per plant

Number of primary branches per plant had the negative direct effect on yield per plant (-0.156). This trait had positive indirect effect on plant height (0.131), number of siliqua per plant (0.149), siliqua length (0.074) and thousand seed weight (0.013). On the other hand, negative indirect effect was found on days to 50% flowering (-0.005), days to maturity (-0.023), number of secondary branch (-0.006) and number seed per siliqua (-0.196) (Table 5). Number of primary branches per plant finally makes negative correlation with seed yield (-0.021). Mahla *et al.* (2003) and Singh *et al.* (2001) reported that number of primary branches per plant had direct positive effect on seed yield. Gupta *et al.* (1987) observed that primary branching had the direct effect on seed yield.

4.3.5. Number of secondary branches per plant

Path co-efficient analysis revealed that number of secondary branches had negative direct effect (-0.012) on yield per plant. It had positive indirect effect via 50% flowering (0.025), plant height (0.039) and siliqua length (0.058) on seed yield per plant. On the other hand, days to maturity (-0.029), number of primary branch (-0.084), number siliqua per plant (-0.097), numer of seed per siliqua (-0.152) and thousand seed weight (-0.034) had negative indirect effect on yield per plant (Table 5). The genotypic correlation with seed yield was negative (-0.093). Yadava *et al.* (1996) found the number of secondary branch had the highest positive direct effect on

seed yield. Rashid (2007) observed that number of secondary branches per plant had the highest direct effect on seed yield per plant.

4.3.6. Number of siliqua per plant

Path co-efficient analysis revealed that number of siliqua per plant had the positive direct effect (0.648) on seed yield followed by positive indirect effect on days to 50% flowering (0.018) and number of seed per siliqua (0.044). This trait had negative indirect effect on yield via days to maturity (-0.013), plant height (-0.103), number of primary branch (-0.036), number secondary branch (-0.002), siliqua length (-0.040) and thousand seed weight (-0.087) (Table 5). Finally this trait had significant positive genotypic correlation (0.432) with yield per plant. Shalini *et al.* (2000) found the number of siliqua per plant had the highest direct effect on seed yield. Sheikh *et al.* (1999) revealed that siliqua per plant had highly positive direct effect on seed yield.

4.3.7. Siliqua length

Path analysis revealed that siliqua length had direct negative effect (-0.223) on yield per plant. This trait had also indirect positive effect on days to maturity (0.015), number of primary branch (0.052), number of secondary branch (0.003), number of siliqua per plant (0.117) number of seed per siliqua (0.519) and thousand seed weight (.020). On the other hand, length of siliqua showed indirect negative effect on 50% flowering (-0.044) and plant height (-0.079). (Table 5). The genotypic correlation with seed yield was positive and significant (0.380). Hence, selection should be practiced for this trait which had longer siliquae in order to improve seed yield. Han (1990) and Singh *et al.* (1978) reported that siliqua length had negative direct effect on yield per plant.

4.3.8. Number of seeds per siliqua

Path analysis revealed that number of seeds per siliqua had direct positive effect (0.633) on yield per plant. This trait had also indirect positive effect on days to maturity (0.017), number of primary branch (0.048), number of secondary branch (0.003) and number of siliqua per plant (0.045). On the other hand, this trait showed indirect negative effect on and 50% flowering (-0.031), plant height (-0.066), siliqua length (-0.183) and thousand seed weight (-0.087) Finally this trait had significant positive genotypic correlation (0.380) with yield per plant. (Table 5). Rashid (2007)

reported that number of seeds per siliqua had direct positive effect on yield per plant. Parveen (2007) also found similar results for this trait.

4.3.9 Thousand seed weight

Thousand seed weight had positive direct effect on yield per plant (0.672) and positive indirect effect on days to maturity (0.015), plant height (0.005) and number of secondary branch (0.001). (Table 5). On the other hand, this trait showed negative indirect effect on 50% flowering (-0.036), number of primary branch (-0.003), number of siliqua per plant (-0.084), siliqua length (-0.007), and number of seed per siliqua (-0.082) (Table 5). This trait had positive genotypic correlation with yield (0.482). Siddikee (2006) reported that thousand seed weight had the highest positive direct effect on seed yield per plant. Kachro and Kumar (1991) reported that thousand seed weight had positive direct effect on seed yield. Kudla (1993) reported that thousand seed weight had positive direct effect on seed yield.

4.4 Genetic Diversity Analysis

The genetic diversity of *Brassica napus* advanced lines are presented in Table 6 to 10 and Figure 3.

4.4.1 Principal Component Analysis (PCA)

Principal component analysis was carried out with 66 genotypes of *Brassica*. The computed eigen values for the 10 variables subjected to principal component analysis together with the corresponding proportion and cumulative explained variance are given in Table 6. Following the Proportion of Variance Criterion, three principal components were retained and these are the principal components whose cumulative explained variances were equal to or more than 99%. In summary, the principal component analysis resulted in the reduction of the 10 original variables to three independent linear combination, principal component of variables. These three principal components account for 78.16% of the total variation. The first principal component accounted for 36.15 % of the total variation while principal components two and three accounted for 27.21 % and 14.8 %, respectively (Table 6). Zaman *et al.*, (2010) reported that first three axes accounted for 94.00% of the total variation whereas the first principal components accounted for 81.94%. But Khan (2010) reported that first three principal components accounted for 70.27% of the total variation where the first principal components accounted for 28.65%.

Table 6. Eigen values and yield percent contribution of 10 characters of 66 Genotypes of *Brassica napus* L.

Characters	Eigen values	Percent variation	Cumulative % of Percent variation
Day to 50% flowering	4.145	36.15	36.15
Day to maturity	3.119	27.21	63.36
Plant height (cm)	1.696	14.8	78.16
Number of primary branches per plant	0.987	8.61	86.77
Number of secondary branches per plant	0.757	6.61	93.38
Number of siliqua per plant	0.345	3.01	96.39
Siliqua length (cm)	0.196	1.71	98.1
Number of seed per silique	0.135	1.18	99.28
Thousand seed weight (g)	0.057	0.49	99.77
Seed yield per plant (g)	0.026	0.23	100

4.4.2 Non-Hierarchical Clustering

Sixty six *Brassica napus* genotypes were grouped into six different clusters non-hierarchical clustering (Table 7). These results confirmed the clustering pattern of the genotypes obtained through principal component analysis. Mahmud *et al.* (2008) reported four clusters; Rawhat and Anad (1981) reported seven clusters; Nath *et al.* (2003) five clusters in *Brassica* species and Begum *et al.* (2007) reported five clusters in linseed. Cluster II had the highest number of (19) genotypes followed by III and IV which had 13 and 12 genotypes, respectively. On the other hand, Cluster V, I and VI had 9, 8 and 5 genotypes respectively (Table 7).

Cluster VI have G14 (Nap 9906 ×2066, P_3), G52 (Nap 9901 x Nap 2066, P_1), G54 (Nap 9908 x Nap 9906, P_1), G56 (Nap 9908 x Nap 9906, P_3), G57(Nap 9908 × Nap 9906, P_4) whereas cluster I composed of G2 (Nap 108 x Nap 9901,P_2), G3 (Nap 108 x Nap 9901,P_3), G5 (Nap 9901 x Nap 0130,P_1), G42(Nap 9906 x Nap 9901,P_1), G47(Nap 9908 x Nap 9901,P_2), G48 (Nap 9908 x Nap 9901,P_3), G49 (Nap 9908 x Nap 9901, P_4) and G55 (Nap 9908 × Nap 9906, P_2).

The genotypes from cluster VI earned the highest cluster mean value for day to 50% flowering (43.10), days to maturity (69.20), number of siliqua per plant (184.47) and seed yield per plant (7.74), but the lowest cluster mean for number of seeds per siliqua (20.77) and 1000-seed weight (3.16 g), indicates that this cluster could be used as a parent for higher yield. On the other hand Cluster I produced the highest mean for number of primary branch (4.61) and 1000-seed weight (3.62 g), early flowering (40.63 days), short plant height (92.62 cm), short siliqua length (7.76) and number of seed per siliqua (20.77).

The genotypes included in cluster II were highest mean value for plant height (109.67 cm), and number of seed per siliqua (22.49). Moreover, Cluster III had lower cluster mean for number of primary branch (3.23), number of secondary branch (1.51), siliqua length had higher cluster mean value (8.11), followed by cluster IV (36.67 days) suggested that this cluster composed of lowest number siliqua per plant (100.68) and seed yield (5.94). On the other hand, cluster V showed the early maturity plant (67.39), indicated the genotype of this cluster could be used for future hybridization program for early maturity plant. (Table 8).

Srivastav and Singh (2000) reported that cluster III had the highest number of primary, secondary branches and the highest mean seed yield per plant and cultivars in cluster V with 1000-grain weight.

Table 7. Distribution of genotypes in different clusters

Cluster no.	No. of Genotypes	No. of populations	Name of genotypes
I	G2, G3, G5, G42, G47, G48, G49, G55	8	Nap 108 × Nap 9901, P_2; Nap 108 × Nap 9901, P_3; Nap 9901× Nap 0130, P_1; Nap 9906 × Nap 9901, P_1; Nap 9908 × Nap 9901, P_2; Nap 9908 × Nap 9901, P_3; Nap 9908 × Nap 9901, P_4; Nap 9908 × Nap 9906, P_2
II	G6, G8, G10, G13, G16, G17, G19, G21, G23, G27, G28, G29, G30, G31, G36, G41, G43, G45, G60	19	Nap 9901× Nap 0130, P_2; Nap 9905 × Nap 108, P_2; Nap 9905 × Nap 205, P_1; Nap 9906 × Nap 2066, P_2; Nap 205× Nap 0130, P_2; Nap 205× Nap 0130, P_3; Nap 9905 × Nap 0130, P_1; Nap 9908 × Nap 0130, P_1; Nap 9908 × Nap 0130, P_3; Nap 9905 × Nap 9906, P_1; Nap 9905 × Nap 9906, P_2; Nap 108 × Nap 2066, P_1; Nap 108 × Nap 2066, P_2; Nap 108 × Nap 2066, P_3; Nap 9906 × Nap 0130, P_2; Nap 9901 × Nap 205, P_2; Nap 9906 × Nap 9901, P_2; Nap 9908 × Nap 2066, P_2; Nap 9906 × Nap 205, P_3
III	G4, G9, G11, G20, G25, G26, G33, G34, G40, G44, G53, G59, G61	13	Nap 108 × Nap 9901, P_4; Nap 9905 × Nap 108, P_3; Nap 9905 × Nap 205, P_2; Nap 9905 × Nap 0130, P_2; Nap 9908 × Nap 0130, P_5; Nap 9905 × Nap 9908, P_1; Nap 2066 × Nap 0130, P_1; Nap 2066 × Nap 0130, P_2; Nap 9901 × Nap 205, P_1; Nap 9908 × Nap 2066, P_1; Nap 9901 × Nap 2066, P_2; Nap 9906 × Nap 205, P_2; Nap 9906 × Nap 205, P_4
IV	G18, G22, G32, G35, G38, G39, G46, G58, G62, G63, G65, G66	12	Nap 205× Nap 0130, P_4; Nap 9908 × Nap 0130, P_2; Nap 108 × Nap 2066, P_4; Nap 9906 × Nap 0130, P_1; Nap 108 × Nap 0130, P_2; Nap 108 × Nap 0130, P_3; Nap 9908 × Nap 9901, P_1; Nap 9906 × Nap 205, P_1; Nap 2066 × Nap 205, P_1; Nap 2066 × Nap 205, P_2; Nap 2066 × Nap 205, P_4; Nap 108 × Nap 205, P_1
V	G1, G7, G12, G15, G24, G37, G50, G51, G64	9	Nap 108 × Nap 9901, P_1; Nap 9905 × Nap 108, P_1; Nap 9906 × Nap 2066, P_1; Nap 205× Nap 0130, P_1; Nap 9908 × Nap 0130, P_4; Nap 108 × Nap 0130, P_1; Nap 9905 × Nap 9901, P_1; Nap 9905 × Nap 9901, P_2; Nap 2066 × Nap 205, P_3
VI	G14, G52, G54, G56, G57	5	Nap 9906 × Nap 2066, P_3; Nap 9901 × Nap 2066, P_1; Nap 9908 × Nap 9906, P_1; Nap 9908 × Nap 9906, P_3; Nap 9908 × Nap 9906, P_4
	Total	66	

Table 8. Cluster mean values of 10 different characters of 66 genotypes

Characters	I	II	III	IV	V	VI
Days to 50% flowering	40.63	40.92	41.77	41.17	41.50	43.10
Days to maturity	68.75	68.42	68.92	68.21	67.39	69.20
Plant Height (cm)	92.62	109.67	109.49	101.81	97.21	108.36
Number of Primary Branches per plant	4.61	3.30	3.23	3.29	3.48	4.09
Number of secondary branches per plant	2.04	1.55	1.51	1.67	1.56	2.26
Number of Siliqua per plant	139.66	151.27	135.33	100.68	122.22	184.47
Siliqua length (cm)	7.76	8.23	8.11	7.82	7.94	7.89
Number of seed per silique	20.77	22.49	21.52	21.36	21.36	20.77
Thousand seed weight (g)	3.62	3.34	3.53	3.48	3.46	3.16
Seed yield per plant (g)	7.02	7.60	6.80	5.94	7.17	7.74

4.4.3 Canonical Variate Analysis (CVA)

Canonical Variate Analysis (CVA) was done to compute the inter-cluster distances. The intra and inter-cluster distance (D^2) values were shown in Table 9. In this experiment, the inter-cluster distances were higher than the intra-cluster distances thus indicating broader genetic diversity among the genotypes of different groups. Islam and Islam (2000) reported that the inter-cluster distances were larger than the intra-cluster distances. Uddin (1994) also reported similar result in mustard.

The highest inter-cluster distance was observed between clusters IV and VI (12.433), followed by between cluster V and VI (9.16), II and VI (7.555), III and VI (7.465), I and VI (7.059), I and VI (6.535), II and VI (5.07), II and V (4.655) and I and VI (4.124). In contrast, the lowest inter-cluster distance was observed between cluster I and VI (3.98), followed by IV and VI (3.49), I and VI (3.109), III and VI (2.775), and II and VI (2.424) (Figure 3). However, the maximum inter-cluster distance was observed between the clusters IV and VI (12.433) indicating genotypes from these two clusters, if involved in hybridization may produce a wide spectrum of segregating population. Dhillon *et al.* (1999) mentioned that maximum inter-cluster distance gave desirable segregants for the development of high yielding varieties with quality of oil for seed yield. On the other hand, the maximum intra-cluster distance was found in cluster V (1.0331), which contained of 9 genotypes, while the minimum distance was found in cluster IV (0.3786) that comprises 12 genotypes. The different multivariate analysis was superimposed in Figure 3 from which it could be concluded that different multivariate techniques supplemented and confirmed one another. According to scatter diagram all the genotypes were apparently distributed into six clusters. It is assumed that the maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. Furthermore, for a practical plant breeder, the objective is to achieve high-level production in addition to high heterosis. In the present study the maximum distance existence between cluster IV and VI. Goswami *et al.* (2006) found moderate genetic diversity between parents had the good general combining ability effect and high specific combining ability as well as high mean values in F_2 in Indian mustard.

Table 9. Intra (Bold) and inter cluster distances (D^2) for 66 genotypes

Cluster	I	II	III	IV	V	VI
I	**0.6423**	4.124	3.98	6.535	3.109	7.059
II		**0.4299**	2.424	7.555	4.655	5.07
III			**0.5522**	5.18	2.775	7.465
IV				**0.3786**	3.49	12.433
V					**1.0331**	9.16
VI						**0.9163**

Table 10. Relative contributions of the ten characters of 66 varieties to the total divergence

Characters	Vector-1	Vector-2
Day to 50% flowering	0.0395	-0.0862
Day to maturity	-0.055	0.1139
Plant Height (cm)	0.0131	0.1728
Number of Primary Branches per plant	0.2527	-0.6676
Number of secondary branches per plant	0.0313	-0.0182
Number of Siliqua per plant	-0.1494	-0.0258
Siliqua length (cm)	0.0714	0.5112
Number of seed per silique	0.0413	-0.177
Thousand seed weight (g)	0.2454	-0.6723
Seed yield per plant (g)	-0.0586	0.1983

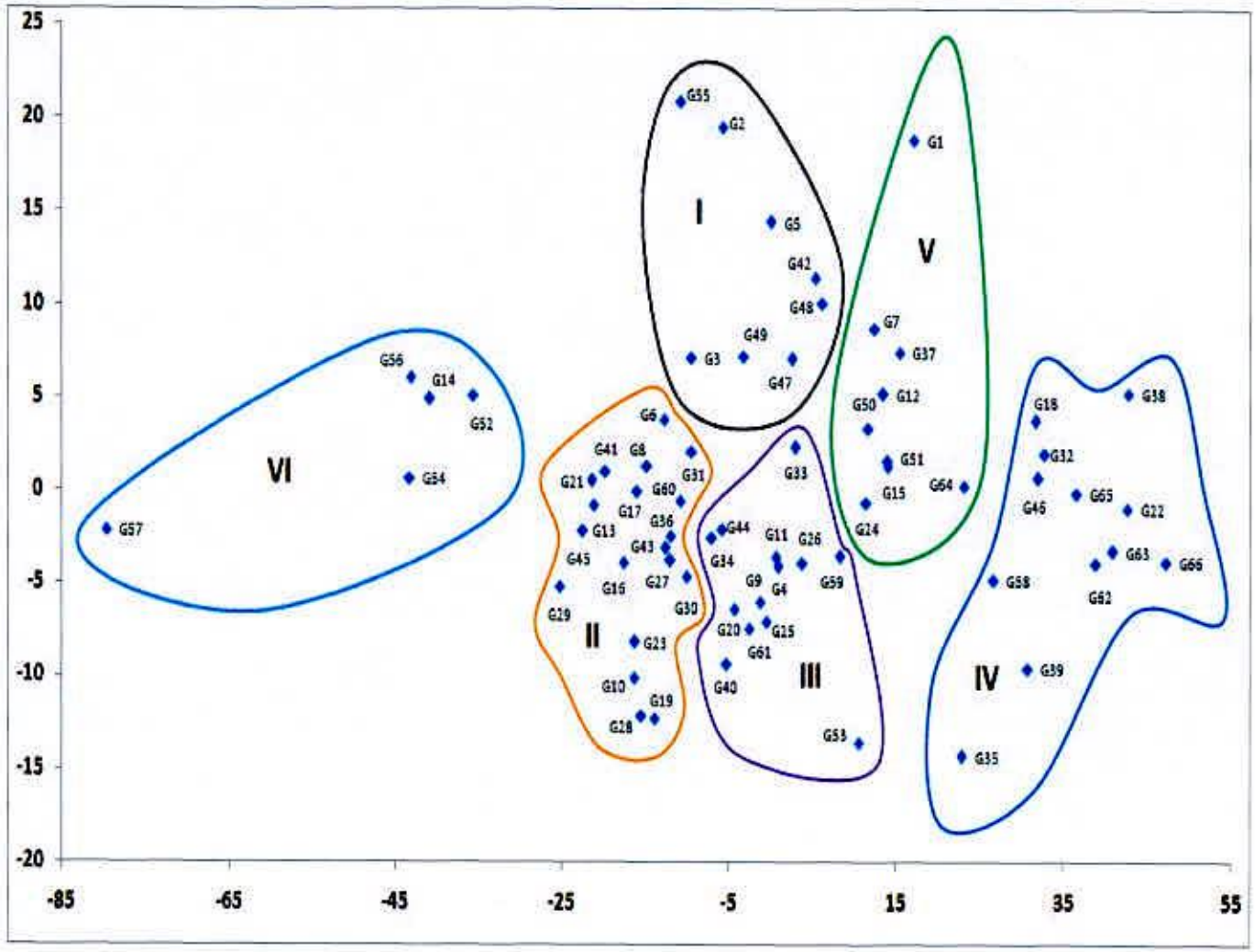


Fig. 3. Intra and inter cluster distances of 66 genotypes in *Brassica napus* L.

Keeping this in view, it appears that the crosses between genotypes from cluster IV with cluster VI might produce high level of segregating population. The crosses between the genotypes belonging cluster II with cluster IV, cluster II with cluster V, cluster II with cluster VI, and cluster V with cluster VI might produce high heterosis in respect of earliness and yield. So the genotypes belonging to these genotypes have been selected for future hybridization program.

4.4.4 Contribution of traits towards divergence of the genotypes

The latent vectors (Z_1 and Z_2) obtained from principal component analysis (PCA). The important characters responsible for genetic divergence in the axis of differentiation in vector I (Z_1) were number of primary branch (0.2527), thousand seed weight (0.2454), siliqua length (0.0714) and number of seed per siliqua (0.0413). In vector II (Z_2), siliqua length (0.5112), seed yield per plant (0.1983), plant height (0.1728) and days to maturity (0.1139) (Table 10).

The role of plant height and siliqua length in both the vectors was important components for genetic divergence in these materials. On the other hand, the role of number of siliqua per plant had a minor role in the genetic divergence. Islam and Islam (2000) reported days to 50% flowering, plant height, primary branches per plant and number of siliqua per plant contribute maximum in divergence in rapeseed and mustard. Begum *et al.* (2007) reported that branches per plant and number of number of seeds siliquae contributed the maximum towards divergence in the existing linseed germplasm. Choudhary and Joshi (2001) concluded that plant height, secondary branches per plant, days to flowering and 1000-seed weight contributed the maximum towards genetic divergence.

4.4.5 Selection of parents for future hybridization

Selection of genetically diverse parents is the prime task for any plant breeding activities. Therefore, considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotypes G12 (Nap 9906 × Nap 2066, P_1), G14 (Nap 9906 × Nap 2066, P_3), G15 (Nap 205× Nap 0130, P_1), G16 (Nap 205× Nap 0130, P_2), G22 (Nap 9908 × Nap 0130, P_2), G24 (Nap 9908 × Nap 0130, P_4) for short duration and early maturity and G17(Nap 205× Nap 0130, P_3) for higher seed yield. Therefore, considering group distance and agronomic performance the inter-genotypic crosses between G16 and G12, G16 and G15, G16 and G24, G16 and G14, G12 and G14, G15 and G14, G24 and G14, G17 and G22 might be suggested for future hybridization program.

CHAPTER V

SUMMARY AND CONCLUSION

CHAPTER-V

SUMMARY AND CONCLUSION

The present study was undertaken with 66 F_5 genotypes of *Brassica napus* L. at the Sher-e-Bangla Agricultural University Farm, Bangladesh during November 2013 to February 2014. Seeds were sown in the main field in Randomized Complete Block Design (RCBD) with three replications. Data on various yield attributing characters such as, days to 50% flowering, days to 80% maturity, plant height (cm), number of primary branch per plant, number of secondary branch per plant, number of siliqua per plant, siliqua length (cm), number of seeds per siliqua, 1000-seed weight (g) and seed yield per plant (g) were recorded.

From variability analysis of F_5 progenies, it was observed that significant variation exist among all the genotypes used for most of the characters studied. Plant height exhibited highest in G19 (Nap 9905 × Nap 0130, P_1) and lowest in G1 Nap 108 × Nap 9901, P_1). The highest number of primary branches per plant was recorded in G42 (Nap 9906 × Nap 9901, P_1) and lowest number was recorded in G28 (Nap 9905 × Nap 9906, P_2). The highest number of secondary branches per plant was observed in G58 (Nap 9906 × Nap 205, P_1). The minimum days to 50% flowering was found in G38 (Nap 108 × Nap 0130, P_2). The lowest days to maturity was observed in G12 (Nap 9906 × Nap 2066, P_1), G14 (Nap 9906 × Nap 2066, P_3), G15 (Nap 205× Nap 0130, P_1), G16 (Nap 205× Nap 0130, P_2), G22 (Nap 9908 × Nap 0130, P_2), G24 (Nap 9908 × Nap 0130, P_4).

The number of siliqua per plant showed highest in G57 (Nap 9908 × Nap 9906, P_4) and lowest in G66 (Nap 108 × Nap 205, P_1). The highest siliqua length was recorded in G27 (Nap 9905 × Nap 9906, P_1) and the lowest siliqua length was observed in G50 (Nap 9905 × Nap 9901, P_1). The number of seeds per siliqua was found highest in G11 (Nap 9905 × Nap 205, P_2) and the lowest in G1 (Nap 108 × Nap 9901, P_1). The seed yield per plant was the highest in G17 (Nap 205× Nap 0130, P_3) and the lowest observed in G44 (Nap 9908 × Nap 2066, P_1).

However, the phenotypic variance and phenotype coefficient of variation were higher than the corresponding genotypic variance and genotypic coefficient of variation for

all the characters under study. In case of days to Plant height and number of siliqua per plant showed higher influence of environment for the expression of these characters.

On the other hand, days to maturity, days to 50% flowering, number of primary branch, number of secondary branch, number of seeds per siliqua, siliqua length, 1000-seed weight and seed yield per plant showed least difference phenotypic and genotypic variance suggesting additive gene action for the expression of the characters.

Seed yield per plant (98.85) exhibits the highest value of heritability while days to maturity (85.72) exhibits the lowest value of heritability. High heritability with high genetic advance in percent of mean was observed for number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, number of seed per siliqua, thousand seed weight and seed yield per plant indicating that these traits were under additive gene control and selection for genetic improvement for these traits would be effective.

High heritability with moderate genetic advance was observed for days to 50% flowering, plant height and siliqua length indicating medium possibility of selecting genotypes. High heritability with low genetic advance in percent of mean was observed for days to maturity indicating that non-additive gene effects were involved for the expression of these characters and selection for such traits might not be rewarding.

Correlation coefficients among the characters were studied to determine the association between yield and yield components. In general, most of the characters showed the genotypic correlation co-efficient were higher than the corresponding phenotypic correlation co-efficient suggesting a strong inherent association between the characters under study and suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values.

In few cases, phenotypic correlation co-efficient were higher than their corresponding genotypic correlation co-efficient suggesting that both environmental and genotypic correlation in these cases act in the same direction and finally maximize their expression at phenotypic level. The significant positive correlation with seed yield per

plant were found in number of siliqua per plant (G=0.432, P=0.425), siliqua length (G=0.380, P=0.374), number of seed per siliqua (G=0.380, P=0.375) and thousand seed weight (G=0.482, P=0.483). In addition, there were non-significant positive correlation with seed yield per plant was also found in plant height (G=0.159, P=0.158).

Path co-efficient analysis revealed that days to 50% flowering, number of siliqua per plant, number of seed per siliqua, and thousand seed weight had the positive direct effect on yield per plant. Whereas, days to maturity, plant height, number of primary branch, number of secondary branch, and siliqua length had the negative direct effect on yield per plant.

The genotypic correlation of number of siliqua per plant and thousand seed weight with seed yield per plant was positive and considerably higher in magnitude. It is mainly due to high positive direct effect and positive indirect effects of others characters and selection would be effective for this trait. The path coefficient studies indicated that number of siliqua per plant siliqua length, number of seeds per siliqua and thousand seed weight were the most important contributors to seed yield per plant which could be taken in consideration for future hybridization program.

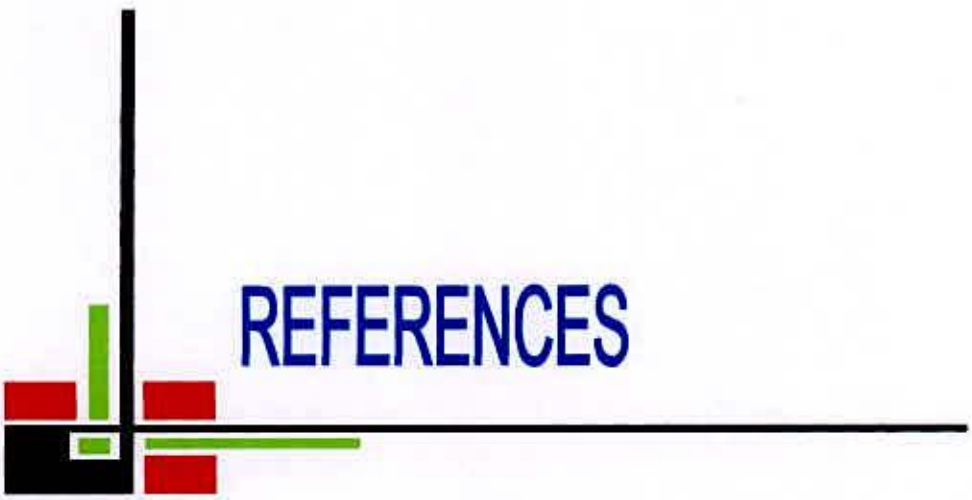
Genetic diversity among *Brassica napus* genotypes was performed through Principal Component Analysis (PCA), Cluster Analysis, Canonical Variate Analysis (CVA) using GENSTAT computer program. The first three principal component axes accounted for 78.16% variation towards the divergence. Among six clusters cluster II contained maximum number of genotypes (19) while cluster VI had only five genotypes. According to PCA, D^2 and cluster analysis, the genotypes grouped into six divergent clusters using Z_1 and Z_2 values obtained from principal component scores. The highest inter-cluster distance was observed between clusters IV and VI (12.433) indicating genotypes from these two clusters, if involved in hybridization may produce a wide spectrum of segregating population while the lowest inter-cluster distance was observed between cluster II and III (2.424).

On the other hand, the maximum intra-cluster distance was found in cluster V (1.0331), which contained of nine genotypes, whereas the minimum distance was found in cluster IV (0.3786) that comprises twelve genotypes. Therefore, it appears

that the crosses between genotypes from cluster IV with cluster VI might produce high level of segregating population. The crosses between the genotypes belonging cluster II with cluster IV, cluster II with cluster V, cluster II with cluster VI, and cluster V with cluster VI might produce high heterosis in respect of earliness and yield. So the genotypes belong to these genotypes have been selected for future hybridization program.

The role of plant height and siliqua length in both the vectors was important components for genetic divergence in these materials. On the other hand, the role of number of siliqua per plant had a minor role in the genetic divergence.

Considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotypes G12 (Nap 9906 × Nap 2066, P_1), G14 (Nap 9906 × Nap 2066, P_3), G15 (Nap 205× Nap 0130, P_1), G16 (Nap 205× Nap 0130, P_2), G22 (Nap 9908 × Nap 0130, P_2), G24 (Nap 9908 × Nap 0130, P_4) for short duration and early maturity and G17(Nap 205× Nap 0130, P_3) for higher seed yield. Therefore, considering group distance and agronomic performance the inter-genotypic crosses between G16 and G12, G16 and G15, G16 and G24, G16 and G14, G12 and G14, G15 and G14, G24 and G14, G17 and G22 might be suggested for future hybridization program.



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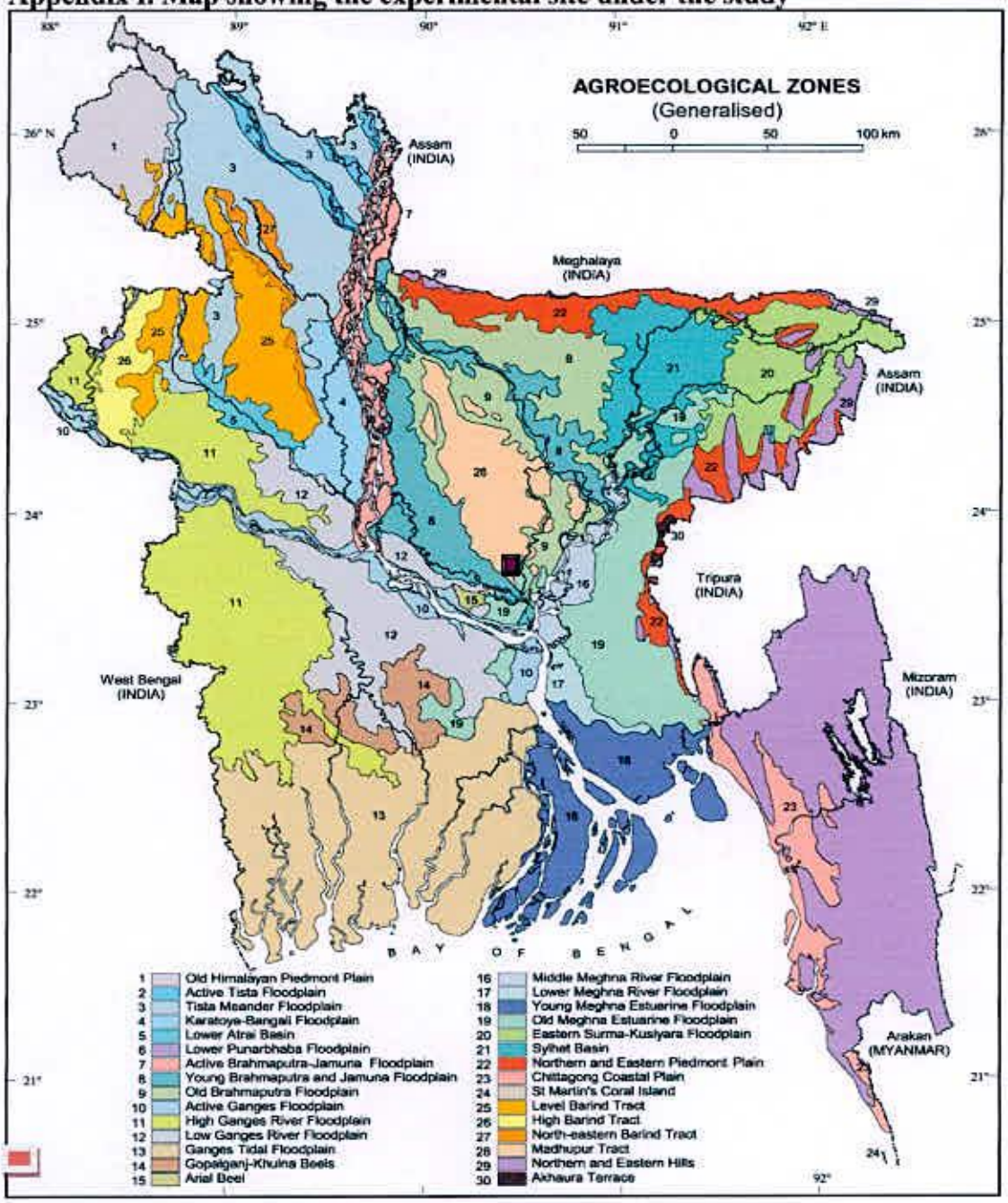
APPENDICES

Appendix I. Map showing the experimental site under the study



The experimental site under study

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

A. Physical composition of the soil

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

B. Chemical composition of the soil

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

Source: Central library, Sher-e-Bangla Agricultural University, Dhaka.

Appendix III. Monthly average Temperature, Relative Humidity and Total Rainfall and sunshine of the experimental site during the period from November, 2012 to february, 2013

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
November, 2012	34.8	18.0	77	227	5.8
December, 2012	32.3	16.3	69	0	7.9
January, 2013	29.0	13.0	79	0	3.9
February, 2013	28.1	11.1	72	1	5.7

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

Appendix IV. Mean performance of various growth parameter and yield components

Genotype	50F	DM	PH	NPB	NSB	NSP	SL	NSS	TSW	SYP
G1	45.50	72.00	83.63	4.63	1.75	121.75	7.64	16.86	3.36	5.90
G2	40.00	68.00	86.00	4.58	2.10	144.50	7.72	19.65	4.25	7.55
G3	40.00	67.50	98.42	4.66	1.96	146.50	8.22	24.60	3.68	7.80
G4	44.50	71.50	108.22	3.04	1.35	134.59	8.11	21.63	2.95	7.05
G5	42.50	69.00	89.73	4.65	2.13	138.08	8.53	25.44	2.81	8.85
G6	38.50	69.00	102.38	3.89	1.82	149.21	8.51	21.81	3.96	8.85
G7	42.00	65.50	94.00	2.58	2.17	125.02	7.33	20.34	3.55	7.25
G8	41.00	69.00	105.10	3.27	1.38	150.98	8.45	21.59	2.73	7.10
G9	43.00	69.00	110.58	3.75	1.50	136.46	8.76	20.56	4.20	6.85
G10	40.50	71.50	116.45	2.65	1.20	150.79	8.52	24.06	3.10	6.92
G11	39.00	67.50	107.43	3.75	1.73	134.95	8.66	27.60	3.46	8.85
G12	38.50	65.00	97.15	3.59	1.53	123.57	8.67	23.71	2.90	6.00
G13	40.50	69.00	107.90	3.45	1.60	156.93	8.35	24.09	2.92	6.10
G14	40.50	65.00	105.13	3.40	1.91	177.23	8.16	22.50	3.38	9.30
G15	38.50	65.00	101.09	3.05	1.20	122.43	8.30	21.68	4.05	8.10
G16	39.00	65.00	110.55	3.31	1.49	153.00	8.43	23.69	3.27	7.60
G17	42.50	67.50	106.50	3.23	0.90	151.87	8.16	22.71	4.07	10.30
G18	41.00	65.50	95.70	3.57	1.43	105.33	8.39	27.25	3.00	7.55
G19	43.50	66.00	118.43	2.66	0.97	148.07	8.37	21.78	3.76	8.50
G20	42.50	69.00	110.99	2.77	1.30	139.47	8.89	24.75	3.87	8.55
G21	44.00	69.00	106.68	2.85	1.65	157.34	8.11	22.74	4.08	8.25
G22	37.50	65.00	99.33	2.32	1.15	93.82	7.99	21.41	4.14	7.50
G23	41.00	68.50	114.50	3.37	1.80	151.00	9.09	24.43	4.26	8.40
G24	41.00	65.00	103.14	2.53	0.90	124.75	8.59	23.76	2.83	6.60
G25	40.00	65.50	111.36	2.76	0.95	135.63	8.18	22.61	4.03	6.90
G26	41.00	67.50	107.75	2.53	1.15	131.83	7.92	20.30	4.15	6.95
G27	43.00	71.50	109.28	3.12	1.64	147.46	9.29	27.42	2.05	6.35
G28	44.00	71.00	118.29	2.28	1.49	149.69	8.53	23.84	3.23	7.60
G29	40.00	67.50	112.85	2.77	1.35	160.35	8.13	23.75	3.33	8.60
G30	40.00	66.00	110.50	3.30	1.40	145.40	7.66	20.61	3.38	6.65
G31	40.00	67.50	103.61	4.50	1.42	145.79	7.89	22.88	3.24	7.35
G32	40.00	67.50	97.83	3.87	1.30	104.00	7.64	21.75	3.04	6.05
G33	40.00	68.50	101.61	3.18	1.16	133.49	8.53	21.60	4.06	7.30
G34	39.50	68.00	107.64	3.15	1.03	142.73	8.90	24.09	3.80	7.39
G35	37.50	65.50	115.35	2.93	1.20	111.53	8.57	21.98	4.29	7.00
G36	38.50	67.00	108.73	3.63	1.32	147.70	7.82	19.68	3.23	5.30
G37	38.50	67.50	94.56	3.29	1.33	121.91	8.42	24.47	3.32	7.11
G38	36.00	65.50	93.37	3.53	0.97	94.61	7.74	19.91	3.19	4.65

G39	42.00	70.50	109.40	2.70	1.03	104.38	8.02	22.82	3.88	6.55
G40	40.00	70.00	114.76	3.59	1.09	140.00	7.08	17.72	3.23	6.20
G41	41.00	67.50	106.53	4.21	3.29	155.82	7.11	17.69	3.55	7.85
G42	36.50	69.00	92.57	5.11	1.94	132.37	7.82	19.65	4.36	6.00
G43	41.50	69.50	109.15	3.05	1.20	148.08	8.18	21.97	2.82	7.65
G44	43.00	68.00	107.39	3.45	1.56	141.60	7.70	19.52	1.81	4.05
G45	38.00	67.00	109.82	3.65	1.65	158.13	7.68	20.56	2.87	5.90
G46	39.50	68.50	99.60	3.31	1.81	104.61	7.37	17.42	2.83	4.10
G47	40.50	69.50	97.01	3.93	1.77	134.61	7.59	21.54	2.91	5.55
G48	41.50	69.50	93.70	4.70	1.90	131.30	7.90	19.73	3.89	7.70
G49	38.00	65.50	98.03	4.75	2.38	140.34	7.24	18.57	3.87	7.10
G50	43.50	69.50	99.64	4.72	2.35	124.92	6.88	19.29	3.96	7.45
G51	42.50	67.00	100.84	3.32	0.70	122.47	8.05	20.44	3.51	8.11
G52	41.50	68.50	104.63	4.20	2.38	172.00	7.59	18.25	3.81	8.25
G53	45.00	68.50	116.38	2.46	1.58	123.75	7.38	20.19	2.98	4.81
G54	43.00	69.50	109.73	4.30	2.35	179.03	8.23	22.96	2.76	5.72
G55	46.00	72.00	85.50	4.51	2.15	149.59	7.09	16.95	3.17	5.61
G56	46.00	72.00	104.50	3.75	2.13	179.50	7.41	19.53	2.13	5.85
G57	44.50	71.00	117.80	4.78	2.52	214.57	8.05	20.63	3.73	9.57
G58	41.50	70.00	105.50	4.20	4.90	109.05	8.16	21.90	3.30	5.30
G59	41.00	71.00	107.00	3.65	3.65	127.30	8.02	19.11	3.52	6.35
G60	41.00	71.00	106.45	3.55	1.87	146.60	8.05	22.02	3.63	9.05
G61	44.50	72.00	112.26	3.96	1.63	137.46	7.30	20.09	3.82	7.20
G62	44.50	67.50	102.88	3.60	1.70	97.10	7.23	19.97	3.05	4.95
G63	44.00	69.00	101.99	3.00	1.65	95.15	7.46	19.40	4.03	5.35
G64	43.50	70.00	100.85	3.65	2.15	113.20	7.58	21.66	3.67	8.05
G65	45.50	72.00	99.30	2.83	1.00	99.82	7.74	20.96	4.07	7.70
G66	45.00	72.00	101.50	3.60	1.90	88.73	7.58	21.55	2.97	4.55
MEAN	41.34	68.44	104.34	3.53	1.68	136.08	8.01	21.60	3.44	7.02
MIN	36.00	65.00	83.63	2.28	0.70	88.73	6.88	16.86	1.81	4.05
MAX	46.00	72.00	118.43	5.11	4.90	214.57	9.29	27.60	4.36	10.30
LSD5	1.84	1.68	4.95	0.31	0.22	12.48	0.29	1.31	0.20	0.29

50F = Day to 50% flowering, DM = Day to maturity, PH = Plant Height (cm), NPB = Number of Primary Branches per plant, NSB = Number of secondary branches per plant, NSP = Number of Siliqua per plant, SL = Siliqua length (cm), NSS = Number of seed per silique, TSW = Thousand seed weight (g), SYP = Seed yield per plant (g)

Appendix V. Principal component score 1 & 2.

Genotype	Z_1	Z_2
G1	17.06	18.8
G2	-5.75	19.48
G3	-9.51	7.12
G4	0.87	-4.1
G5	-0.04	14.4
G6	-12.75	3.8
G7	12.43	8.69
G8	-14.86	1.31
G9	-1.26	-6.03
G10	-16.29	-10.12
G11	0.62	-3.66
G12	13.46	5.18
G13	-21.13	-0.8
G14	-40.85	4.89
G15	14.01	1.28
G16	-17.58	-3.93
G17	-16.01	-0.07
G18	31.62	3.74
G19	-13.86	-12.32
G20	-4.36	-6.42
G21	-21.43	0.49
G22	42.6	-0.98
G23	-16.24	-8.18
G24	11.42	-0.67
G25	-0.49	-7.11
G26	3.76	-3.91
G27	-12.04	-3.82
G28	-15.5	-12.14
G29	-25.24	-5.2
G30	-10.03	-4.68
G31	-9.51	2.04
G32	32.71	1.96
G33	2.95	2.3
G34	-7.05	-2.55

G35	22.83	-14.31
G36	-12.01	-2.51
G37	15.41	7.43
G38	42.73	5.21
G39	30.65	-9.57
G40	-5.29	-9.36
G41	-19.83	1.01
G42	5.39	11.4
G43	-12.58	-3.13
G44	-5.81	-2.09
G45	-22.51	-2.18
G46	31.93	0.65
G47	2.51	7.06
G48	6.2	10.04
G49	-3.25	7.2
G50	11.67	3.34
G51	13.95	1.59
G52	-35.6	5.06
G53	10.56	-13.57
G54	-43.28	0.61
G55	-10.75	20.84
G56	-43.04	6.05
G57	-79.69	-2.17
G58	26.59	-4.83
G59	8.32	-3.58
G60	-10.79	-0.62
G61	-2.53	-7.48
G62	38.83	-3.9
G63	40.87	-3.28
G64	23.07	0.24
G65	36.51	-0.14
G66	47.24	-3.83