GENETIC DIVERSITY AND CHARACTER ASSOCIATION OF *Brassica napus* L.

THESIS BY

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CERTIFICATE

This is to certify that thesis entitled, "Genetic Diversity And Character Association 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 ELORA PARVIN, Registration No. 08-03083 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: December, 2014
Place: Dhaka, Bangladesh

_____
(Dr. Firoz Mahmud)
Professor
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DEDICATED

TO

MY PARENTS

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December 2014, *The Author*

SAU, Dhaka

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ABSTRACT

A field experiment was conducted with 40 genotypes of *Brassica napus* L. at the experimental field of Sher-e-Bangla Agricultural University, Dhaka to study the genetic diversity and characters association during November 2013 to March 2014. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Analysis of variance for each trait showed significance differences among the genotypes. The first two components with eigen value were greater than other components. The highest inter cluster distance was observed between cluster II and V and the maximum intra cluster distance was found in cluster I. Comparatively phenotypic variances were higher than the genotypic variances for all the characters studied. Number of siliqua per plant (99.986) exhibited the highest value of heritability and number of primary branches per plant (26.459) exhibited the lowest value of heritability. Correlation coefficients among the characters were studied to determine the association between yield and yield components. The significant positive correlation with seed yield per plant was found in days to 1st flowering, days to 80% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant and siliqua per plant. Path co-efficient analysis revealed that days to 1st flowering, days to 50% flowering, days to 80% flowering, days to maturity, number of secondary branches per plant, number of siliquae per plant, and thousand-seed weight (gm) had the positive direct effect on yield per plant. Considering group distance and other agronomic performance genotypes G5 (Nap-0837), G2 (Nap-0733-1), G37 (Nap-2066), G31 (Nap-9901), G40 (Nap-108) and G11 (BARI- 8) might be suggested for future hybridization program.

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SOME COMMONLY USED ABBREVIATIONS

Abbreviation	Full word
%	Percent
ºC	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
gm	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

SOME COMMONLY USED ABBREVIATIONS (cont'd)

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

INTERODUCTION

Brassica oil is the world's third most important sources of edible vegetable oils. *Brassica* is an important genus of plant kingdom consisting of over 3200 species with high diverse morphology. It is originated in either the Mediterranean area or northern Europe. Scientific interest in rapeseed and its economic importance has lately increased largely due to the use of the high-grade oil for food purposes and as a source for the production of biodiesel.

In Bangladesh various species of *Brassica* are grown. The genomic constitutions of the three diploid elemental species of *Brassica* are AA for *Brassica campestris*, BB for *Brassica nigra* and CC for *Brassica oleracea* having diploid chromosome number of 20, 16 and 18 respectively. On the other hand the species *Brassica juncea* (AABB), *Brassica carinata* (BBCC) and *Brassica napus* (AACC) are the amphidiploids. Approximately, 70% of the total cultivated mustard in Bangladesh which is the variety of either *Brassica rapa* or *Brassica napus*.

Brassica oil crops are the most important group of species that supply major edible oils in Bangladesh (BBS, 2013). Mustard and rapeseed seeds contain 42% oil, 25% protein (Khaleque, 1985). Rapeseed and mustard is the third highest source of edible oils supply in the world after soybean and palm (FAO, 2012). The mustard oil is used not only for edible purpose but also is used in hair dressing, body massaging and in different types of pickles preparation. The oil cake contains proteins of high biological value and applicable quantities of calcium and phosphorus. It is used as a very good animal feed as well as organic manure for various crops.

Per capita consumption of edible oil is one of the lowest in the world (11g/head/day) which is one fifth of the recommended requirement for a balanced diet (FAO, 2011**).** About 70% of requirement of oil has been imported every year by spending huge amount of foreign currency involving Tk. 2951 core (BBS, 2011**).** In Bangladesh the seed yield of mustard/rapeseed is about 740kg/ha, which is very low in comparison to other developed countries (2400kg/ha) (FAO, 2011).

A plant breeding program can be divided into three steps viz. building up a gene pool of variable germplasm, selection of individual from the gene pool and utilization of selected individual to evolve a superior variety (Chauhan and Singh, 1985). The knowledge of genetic variability present in the population, heritability of economically important characters and correlation coefficients of those characters is very important before launching an effective breeding program.

There is plenty of scope to increase yield per unit of area through breeding superior varieties. Information on genetic variability and character association is a prerequisite for initiating a successful breeding program aiming to develop high yielding varieties. Determination of correlation co-efficient between the characters has a considerable importance in selecting breeding materials. The path co-efficient analysis has been found to give more specific information on the direct and indirect influence of each of the component characters upon seed yield (Behl *et al.,* 1992). Path-coefficient technique splits the correlations, 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).

Variability and genetic diversity are the fundamental law of plant breeding which is major tool being used in parent selection for efficient hybridization program (Khaleque, 1985). Genetic diversity is one of the criteria of parent selection. Inclusion of more diverse parents (within a limit) in hybridization is supposed to increase the chance of obtaining maximum heterosis and give broad spectrum of variability in segregating generations.

If a plant breeding program is to be advanced more rapidly and efficiently, knowledge of inter-relationships between yield and yield contributing characters are necessary. Thus, determination of correlation coefficient between characters has a considerable importance in selection practices. Because it helps in the construction of selection indices and also permits for the prediction of correlated responses. The correlation and path co-efficient analysis would provide a true picture of genetic association between different traits. Path co-efficient analysis has been found to give more specific measures on the direct and

indirect influence of each of the component characters upon seed yield (Gupta *et al.,* 1987; Chauhan and Singh, 1985). Therefore, it is expected that the path co-efficient analysis may provide more reliable assessment for selecting superior plant types for improvement of yield.

Keeping in mind the available genetic diversity and widely practiced breeding programs for developing variety for any trait, the present study was undertaken to achieve the following objectives:

- To determine the genetic variability and diversity among different *brassica napus* genotypes,
- To study the correlation co-efficient and the path co-efficient pattern of different characters and
- To select the better genotype based on performance of individual character as well as characters together.

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 genetic diversity, 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
- Relationship between yield and yield contributing characters
- Genetic divergence among *Brassica napus* genotypes

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.

High heritability and genetic advance for number of siliquae 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).

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).

Siliqua length is another important character for the development of fruits in oil seed crops like mustard and rapeseed. 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.

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).

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 per siliqua in oleiferous *Brassica* materials of diverse genetic base was observed by 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.

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).

Nanda *et al.,* (1995) observed that days to 1st flowering varied 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), Yadava (1983) and Thakral (1982) found significant variations for this character while working with different genotypes of *Brassica napus*.

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 the 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.

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).

Thousand seed weight is a very important character of rapeseed 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.

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

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 per plant, number of seed per 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*.

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), Chauhan and Singh (1985) and Sharma (1988) among different genotypes of *B. napus*, *B. rapa* and *B. juncea*.

Hosen (2008) conducted a study by using five parental genotype of *Brassica rapa* and their ten F_2 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 intergenotypic 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.

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 the maximum broad sense heritability get genetic advance seed yield followed.

Zebarjadi *et al.,* (2011) carried out an experiment to study some traits and to estimate genetic parameters in 16 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 oil percentage, whereas low genetic advance was observed for thousand kernel weight.

Abideen *et al.,* (2013) carried out 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.

2.2 Correlation among different characters

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*.

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.

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.

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 siliquae 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.

Gosh and Mukhopadhyay (1994) studied Tori-7 (*B. campestris var. toria*) for evaluation of seed yield and five 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.

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.

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 1000 seed weight, but high negative and significant correlations with seeds per siliqua at both genotypic and phenotypic levels.

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.

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 siliqua per plant. The number of seeds per siliqua had the greatest influence and number of siliquae per plant had the smallest effect on yield.

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.

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.

Malik *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 siliquae per plant showed significant negative correlation with number of seeds per siliqua and 1000 seed weight.

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 two varieties. Results revealed that number of primary branches per plant, number of secondary branches per plant, 1000 seed weight (gm) and oil percent were positively associated with seed yield.

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.

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 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, 1000 seed weight and oil ratio.

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.

2.3 Path co-efficient analysis

When more characters are involved in correlation study it becomes difficult to as certain 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.

Dhillor *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.,* (1997) also found negative direct effect of the trait 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.

Yadava *et al.,* (1993) when studied path co-efficient analysis of six yield components of 25 diverse varieties of Indian mustard and observed that number of siliquae per plant had the highest positive direct effect on seed yield.

Uddin *et al.,* (1995) studied path analysis in 13 Indian mustard (*B. juncea*) and observed that seeds per siliqua and 1000 seed weight had high positive direct effect on seed yield per plant.

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.

Shalini *et al.,* (2000) studied path analysis of Indian mustard germplasm and observed that number of siliquae per plant 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.

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.

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.

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 siliquae per plant and number of primary and secondary branches per plant.

2.4 Relationship between yield and yield contributing characters

Correlation coefficient analysis helps to determine the nature and degree of relationship between any two measurable characters. It resolves the complex relations between the events into simple form of association. But measure of correlation does not consider dependence of one variable over the other. Direct contribution of each component to the yield and the indirect effects it has through its association with other components cannot be differentiated from mere correlation studies. Path coefficient analysis fulfills this study. It was first developed and described by Wright (1921) as a tool in genetic analysis which partition the association of the components on yield and indirect effects of the characters on yield through other components. The association between the various characters in a rapeseed and mustard and the direct and indirect effects of a variable over the dependent variable has been studied by a number of investigators are reviewed here.

Ali *et al*., (1995) investigated the association between distance and mid-parent heterosis and they found that the correlation between genetic distance and heterosis was positive and highly significant for seed yield, siliqua per plant and seeds per siliqua. They estimated genetic distance among canola (rape) cultivars through multivariate analysis. They analysed 30 cultivars from various sources and clustered into three distinct clusters based upon five morphological characteristics and yield components (crown diameter, branches/plant, siliqua/plant, seeds/siliqua and yield/plant). Two cultivars from each cluster were selected as parents and 15 partial diallel inter and intracluster crosses were made between the six selected parents and evaluated at two locations in Michigan, USA in 1990-91.

Wang *et al*., (1999) analysed heterosis and combining abilities of 20 reciprocal cross combinations of five double low rape (*Brassica napus*) cultivars (lines) showing high seed yield. Positive mean heterosis varied among crosses. The positive mean heterosis number of siliquae per plant was 17.6% was highest, followed by number of seed per siliqua and 1000-seed weight.

Zhang *et al.,* (2000) crossed three double low cytoplasmically male sterile (CMS) and five double low restorer lines of *brassica napus* and they analyzed resulting 15 hybrids for eight yield components. In this experiment they found that the CMS F_1 had significant heterosis, particularly for yield, but that predicted for the F_2 was lower. They also suggested that the major yield components, total number of siliqua per plant had the highest heterosis and would be of more value in a breeding program than trying to increase number of seed per siliqua or 1000-seed weight.

Tyagi *et al*., (2001) evaluated 45 hybrids of Indian mustard obtained from crossing 10 cultivars for seed yield and yield components. The relative heterosis was desirable for plant height, number of primary and secondary branches per plant, seeds per siliqua, number of siliquae on main shoots, biological and seed yield, and oil content. Heterobeltiosis was desirable for primary and secondary branches per plant; siliquae on main shoots, and seed yields. Standard heterosis was desirable for the number of primary branches per plant and secondary branches per plant, siliqua length, and seeds per siliqua, number of siliquae on main shoots, biological and seed yields and oil content. The mean level of heterosis was highest for biological yield. The highest standard heterosis (206.14%) and heterobeltiosis (240.56%) for seed yield per plant was recorded in the cross BIO 772 × Rohini. This cross was the best heterotic combination for all the three types of heterosis for seed yield.

Gupta *et al.,* (2002) studied 18 lines rapeseed reported significant correlationship between plant height, number of siliqua on the main raceme and number of seed per siliqua, while plant height was significantly correlated with number of siliqua on the main raceme. In, general genotypic correlations were greater than phenotypic or environmental correlations. Seed yield was positively correlated with number of siliqua on the main raceme and 1000-seed weight.

Choudhary *et al.,* (2003) studied correlation and path coefficient analysis in 28 genotypes of Indian mustard including three controls (Varuna, Kranti and Pusabold). The observations were recorded for seed yield per plant and 11 quantitative characters viz., days to 1^{st} flowering, days to maturity, length of main axis, primary branches per plant, secondary branches per plant, number of siliqua per plant, siliqua length, number of seeds per siliqua,

1000-seed weight and reaction to *Alternaria* black spot on leaf and on siliquae. All the characters had highly significant and positive correlation with seed yield per plant, except for reaction to *Alternaria* black spot on both leaf and siliqua and days to 1st flowering.

Ramesh *et al.,* (2003) have studied eight genotypes of rape, including six cultivars (Shiralee, Regent, Ceres, PF7045/91, Darmor and Falcon) and two breeding lines (Yanter x Tower (BL 1) and Cobra x A.W. (BL2)) to determine the genetic parameters for number of pods per main axis (NPM), number of pods per plant (NPP), length of pod (LOP), number of seeds per pods, 1000-seed weight, seed yield, and total glucosinolate. Analysis of variance revealed significant general (a) and specific (b) combining ability mean squares for all traits except for 1000-seed weight, which indicated the importance of additive and no additive genetic effects. For 1000-seed weight, only the general combining ability mean square was statistically significant.

Mahak *et al.,* (2004) have studied genetic variability, heritability, genetic advance and correlation for eight quantitative characters (days to flowering, days to maturity, plant height, number of primary branches, length of main raceme, seed yield per plant, 1000-seed weight and oil content) in 21 hybrids of Indian mustard and their seven parents (Varuna, Pusa Bold, Basanti, Maya, NDR-850I, RH 30 and Kanti) grown during Rabi 2002/03 in Kanpur, Uttar Pradesh, India. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all characters. High heritability coupled with high genetic advance as percentage of mean was observed for days to flowering, followed by 1000-seed weight, days to maturity and plant height. Seed yield per plant showed positive correlation with number of primary branches, length of main raceme, 1000 seed weight and oil content.

An experiment was conducted by Poonam and Singh (2004) in 40 Indian mustard germplasms to determine the correlation and path coefficient values between yield and yield attributing character. Path coefficient analysis of seed yield per plot with different correlated characters was partitioned into direct and indirect effects. Plant height had the highest positive direct effect (0.836) followed by number of seeds per siliqua (0.791). The number of primary branches per plant, siliqua per plant and days to maturity had low but negative direct effects on seed yield.

Sudan *et al*., (2004) studied path analysis in Indian mustard. Path analysis indicated that number of primary branches was the most important character with the highest direct effect on seed yield. Other characters i.e. days to flowering, 1000 seed weight and number of seeds per siliqua had high positive effect on yield via other character suggesting the scope of their simultaneous improvement through selection.

Yadava *et al.,* (2004) estimated number of seeds per siliqua which was significantly and positively correlated with yield. Multiple correlation analysis showed that only seeds per siliqua and 1000-seed weight had a direct effect on yield. Seed yield was positively associated with days to flowering and plant height.

Goswami *et al.,* (2005) conducted experiment on variability studies for number of secondary branches, siliquae on main shoot, seeds per siliqua, 1000-seed weight and seed-yield per plant. Results showed that the coefficient of variation of pods per plant, filled grains per pod and 1000-grain weight on yield per plant were significant or very significant. So, there is considerable variability for the above character studied.

Goswami and Behl (2006) studied 43 genotypes of Indian mustard using D^2 statistics. They recorded data for plant height, primary branches, secondary branches, main shoot length, number of siliquae on main shoot, siliqua length, seeds per siliqua, 1000-seed weight, seed yield per plant and oil content. Days to 50% flowering, the genotypes were grouped into six and 15 clusters. The intracluster distances were almost equal and relatively lower than the inter-cluster distances.

Khan *et al.,* (2006) reported that the correlation for some quantitative traits relating to yield and quality were studied in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during 2002-2003. The 11 accessions of *Brassica napes* L. along with DGL as a standard variety were studied. The results indicated that a wide range of genetic variation existed among all the characters under study except 1000-grain weight. Correlation

analysis revealed that seed yield per plant was positively and significantly correlated with number of primary branches (0.4015), siliqua per plant (0.505), seeds per siliqua (0.79648), siliqua length (0.37037) and seed yield per plot (0.40931). However, it was negatively and non-significantly associated with number of secondary branches (-0.36663) and protein contents (-0.1372) at genotypic level. It was also found that indirect selection for number of seeds per siliqua would be effective in improving the seed yield per plant in present breeding material.

A study was conducted by Tusar *et al.,* (2006) to assess the nature and extent of variability of 11 yield related characters of five mustard genotypes. Phenotypic correlation studies indicated that seed yield per hectare was positively and significantly associated with plant height, total dry matter production and husk weight. The number of siliqua 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. Path coefficient analysis revealed that the number of siliqua per plant had the greatest direct contribution on seed yield followed by the number of seeds per siliqua and 1000-seed weight while indirect via number of siliqua per plant and 1000-seed weight. Although plant height and husk weight had a total positive correlation with seed yield, their direct effect on yield was negative. The number of seeds per siliqua showed very high positive direct effect on yield, but its correlation with yield was non-significant and negative.

Yadava *et al.,* (2006) observed 16 genotypes of rapeseed and estimated that genotypic and phenotypic correlation coefficient among seed yield per plant. It was observed that 1000 seed weight, days to flowering, seeds per siliqua and plant height were the most important yield related characters and positively correlated with yield.

Kumar *et al.,* (2009) studied 12 yield related trails in 15 genotypes of *B. napus* and *B. campestris*. For most characters studied, genotypic correlation coefficient were higher in magnitude them than this correspond phenotypic correlation coefficients. Seed yield was positively correlated with plant height and 1000 seed weight.

Jeromela *et al.,* (2011) conducted an experiment to assess genotype by environment interaction for seed yield per plant in rapeseed cultivars grown in Northern Serbia by the AMMI (additive main effects and multiplicative interaction) model and found significant interaction between genotype and environment. Seed yield per plant of the tested cultivars were found varied from 1.82 to 19.47 g throughout the seven seasons, with an average of 7.41 g. In the variance analysis, 72.49% of the total yield variation was explained by environment, 7.71% by differences between genotypes, and 19.09% by genotype by environment interaction.

Rameeh (2011) have studied eight genotypes of rape, including six cultivars (Shiralee, Regent, Ceres, PF7045/91, Darmor and Falcon) and two breeding lines (Yaster X Tower (BL I) and Cobra X A.W. (BL2) to determine the genetic parameter for number of siliqua per main axis, number of siliqua per plant, length of siliqua, number of seeds per siliqua, 1000-seed weight, seed yield. Analysis of variance revealed significant general (a) and specific (b) combining ability. For 1000-seed weight, only the general combining ability mean square was statistically significant.

In order to determine the most important traits affecting grain yield in Canola and identify the quantity of direct and indirect effects on grain yield, an experiment was conducted with 10 Canola varieties in a RCBD design with three replications by Khayat *et al*., (2012). The evaluation of correlation co-efficients illustrated that the total dry matter, harvest index, 1000- grain weight, the number of grains per pod, number of pods per plant, plant height; days to maturity and flowering period trait had a positive significant correlation with grain yield. Stepwise regression and path analysis indicated that, the number of pods per plant had the highest direct effect on grain yield. In addition, total dry matter, 1000- grain weight, and flowering and days to maturity also had a high direct effect on grain yield.

2.5 Genetic divergence among mustard genotypes

D^2 statistic developed by Mahalanobis (1936) provides a measure of magnitude of divergence between biological populations and relative contribution of each component character to the total divergence Nair and Mukherjee (1960). Mahalanobis D^2 statistic is

more reliable in selection of potential parent for hybridization program using these D^2 values cluster are formed. A summary of literature reviewed on mustard and other allied species are in presented below:

Peter and Rai (1995) studied genetic divergence using the D^2 statistics and canonical analysis among 25 genotypes of *Brassica napus*. They reported that genetic and geographical divergence was highly related with the genotypes. The genotypes were grouped into six clusters of which cluster I was the largest accommodating among these genotypes. The cluster VI had large genetic distance from the remaining clusters.Singh *et al.,* (1997) studied genetic divergence through D^2 statistic with 50 genotypes of *B. napus* growing in 12 environments based on 13 characters. They searched the clustering pattern and inter - intra cluster distances. On the basis of stability, high yield and divergence among the genotypes, nine crosses were recommended as suitable for use in breeding program.

Khulbe and Pan (1999) reported that siliqua per plant, siliqua length, seeds per siliqua, 1000 seed weight were positively associated with grain yield. Analysis of variance revealed that siliqua per plant, siliqua length, 1000 seed weight and seeds per siliqua were the major characters influencing grain yield.

Ali *et al.,* (2003) conducted experiment on 25 winter type rapeseed cultivars introduced from diverse sources of the world were studied for variability of seed yield and yield components. Significant differences among genotypes for most of the traits indicated that there was sufficient variability available to have an effective selection. Genotypic and phenotypic variances were the highest for pods per plant followed by plant height, whereas the maximum genotypic and phenotypic co-efficients of variability were found in seed yield per plant and pods per plant, respectively.

Kumar *et al.,* (2003) noted that the generation of mean analysis was carried out in six crosses of Indian mustard *(Brassica juncea)* to identify gene effects for plant height, primary and secondary branches per plant and seed yield. Both additive and non-additive gene effects were found for plant height with the latter being more important. For seed yield and

primary and secondary branches additive gene effects were more important than non-additive gene effects. Among the epistatic interactions identified, additive x additive and dominance x dominance interactions were important for plant height, whereas for number of branches and seed yield these interactions were significant in one or two crosses only. To improve these traits, crossing followed by delayed selection to obtain transgressive segregates and reciprocal recurrent selection could be utilized to exploit both types of gene effects.

Aunwinithul *et al.,* (2004) studied 33 genetically diverse genotypes of Indian mustard or diversity. The genotypes were grouped into eight different clusters. The cluster III was the biggest with 11 genotypes followed by cluster-I with nine genotypes, cluster V and VI consisted of four and three genotypes respectively. The cluster II and VII both had two genotypes each and similarly, cluster IV and VIII included one genotype each.

Goswami *et al.,* (2005) conducted experiment on variability studies for number of secondary branches per plant, siliquae on main shoot, seed per siliqua, 1000-seed weight and seed-yield per plant. Results showed that the coefficient of variation of pods per plant.

Kardam *et al., (2005)* noted that the nature and magnitude of variability for 10 characters in 200 progenies of Indian mustard *(B. juncea)* obtained from six crosses were studied during Rabi 2002-03 in Jobner, Rajasthan, India. Phenotypic coefficients of variation were higher in magnitude compared to genotypic coefficients of variation for most of the characters. Seed yield per plant was significantly associated with plant height, primary branches per plant, and number of siliquae per plant, number of seeds per siliqua and 1000-seed weight. The number of siliquae per plant had the highest direct contribution to seed yield, followed by primary branches per plant, 1000-seed weight, number of siliquae on main shoot and number of seeds per siliqua.

Singh *et al.,* (2005) conducted experiment on response of selection in generation for main shoot length, seeds per siliqua, seed mass and seed yield were studied in *Brassica* species. Observations were recorded on individual plant basis in one generation of three crosses of

Indian mustard *(B. juncea L.)* for each trait. Five plants with high and five with low values were selected for each trait. On the other hand a bulk was constituted by taking one seed from each plant in each cross. These selected plant- as well as the constructed bulks were raised to advance from generation to generation, comparisons were made between high and low selections for each trait as well as between high selection and bulk. It was observed that differences between high and low selection were non-significant for all traits except seed mass. On the other hand mean values under bulk were comparable to that of high selection group for each trait. Bulk was advised to be followed in early generation. Transgressive segregants were more frequent for main shoot length: seeds per siliqua and seed yield than for seed mass.

Massimo *et al.,* (2006) conducting experiment for determination of good combiners in *Brassica napus L.* genotypes, a study was conducted 8x8 diallel during 2004-05 and 2005-06. Analysis of variance revealed highly significant differences ($p<=0.01$) for all traits. Components of combining ability analysis exhibited that, GCA was highly significant ($p<=0.01$) for number of seeds per plant, while significant ($p<=0.05$) for number of pods per plant and pod length whereas non-significant for 1000 seed weight and seed yield per plant.

Baradaran *et al.,* (2007) noted that the field studies were conducted in Iran to determine the correlations between traits and its analysis and the cause and effect relationships in 15 rape cultivars. Results of the analysis of variance showed significant differences between yield and number of pods per plant, harvest index, oil percent, stem diameter, number of secondary branches per plant and biological yield at the 1% level in the cultivar. Based on stepwise regression, seed yield was considered as a dependent variable and the number of pods per plant, number of grains per pod. 1000-grain weight, number of nodes per stem and oil percent as independent variables. The highest determination coefficient was obtained for number of pods per plant. Therefore, the most important traits of the selection index for grain yield improvement were the number pods per plant, number of grains per pod, 1000-grain weight and number of nodes per stem.

Vivek *et al.,* (2007) studied the genetic diversity in 81 true breeding advanced generation cultivars of Indian mustard based on yield and yield components. They are followed by

cluster analysis and showed that out cluster XII, which was most diverse, had very high seed yield and number of siliquae per plant. Cluster VII also represented entries with high seed yield, number of siliquae per plant and highest number of seed per siliqua. Cluster XI with the lowest number of days to maturity could be considered as a good source for earliness.

Hossain *et al.,* (2008) studied the genetic divergence using D^2 statistic in 40 genotypes of rapeseed. The genotypes differed significantly for 10 yield and yield contributing characters and they grouped then into nine clusters. They observed that there was no close correspondence between geographical distribution and genetic divergence. A number of siliqua on the main raceme, seeds per siliqua and harvest index were the major contribution to genetic divergence and cluster IV and these genotypes were suggested for use in heterosis breeding.

Zaman *et al.,* (2010) conducted a field experiment 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 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 siliqua per plant (1.17%) contributed the maximum towards the total divergence which suggested that these characters were highly responsible for genetic divergence in the present materials.

Pandey *et al.,* (2013) conducted an experiment with 45 Indian mustard genotypes of different origin from India for evaluated for the extent of diversity for utilization in breeding program. D^2 analysis was conducted to measure the genetic diversity among the genotypes. The 45 genotypes were grouped in eight clusters using Tocher's method. Intra-cluster distance was maximum for cluster VI followed by cluster III. The maximum inter-cluster distance was found between cluster II and III indicating high genetic divergence among genotypes of these groups. The maximum contribution towards the divergence was accountable to 1000-grain weight (46.87%) followed by seed yield per plant (20.91%) and number of siliqua on main raceme (8.38%). Evaluation of germplasm through genetic

divergence which quantifies variation among genotypes on the basis of a group of characters (yield and yield contributing) helps in identification of promising parental materials for crop improvement. Germplasm collection was also valuable gene pools providing diverse genetic material that may be applied for the improvement of cultivars and advanced agronomic productivity. An assessment of genetic and genomic diversity within these collections can be used to assign lines and populations to diverse groups, to study the evolutionary history of wild relatives, to verify pedigrees and fill in the gaps in incomplete pedigree or selection history, to monitor changes in allele frequencies in cultivars or populations.

CHAPTER III

MATERIALS AND METHODS

To conduct the experiment 40 selected cultivars were used as lines and these were done among parents in Rabi season 2013-2014. In 2013-2014 Rabi seasons, the lines were grown in the experimental farm.

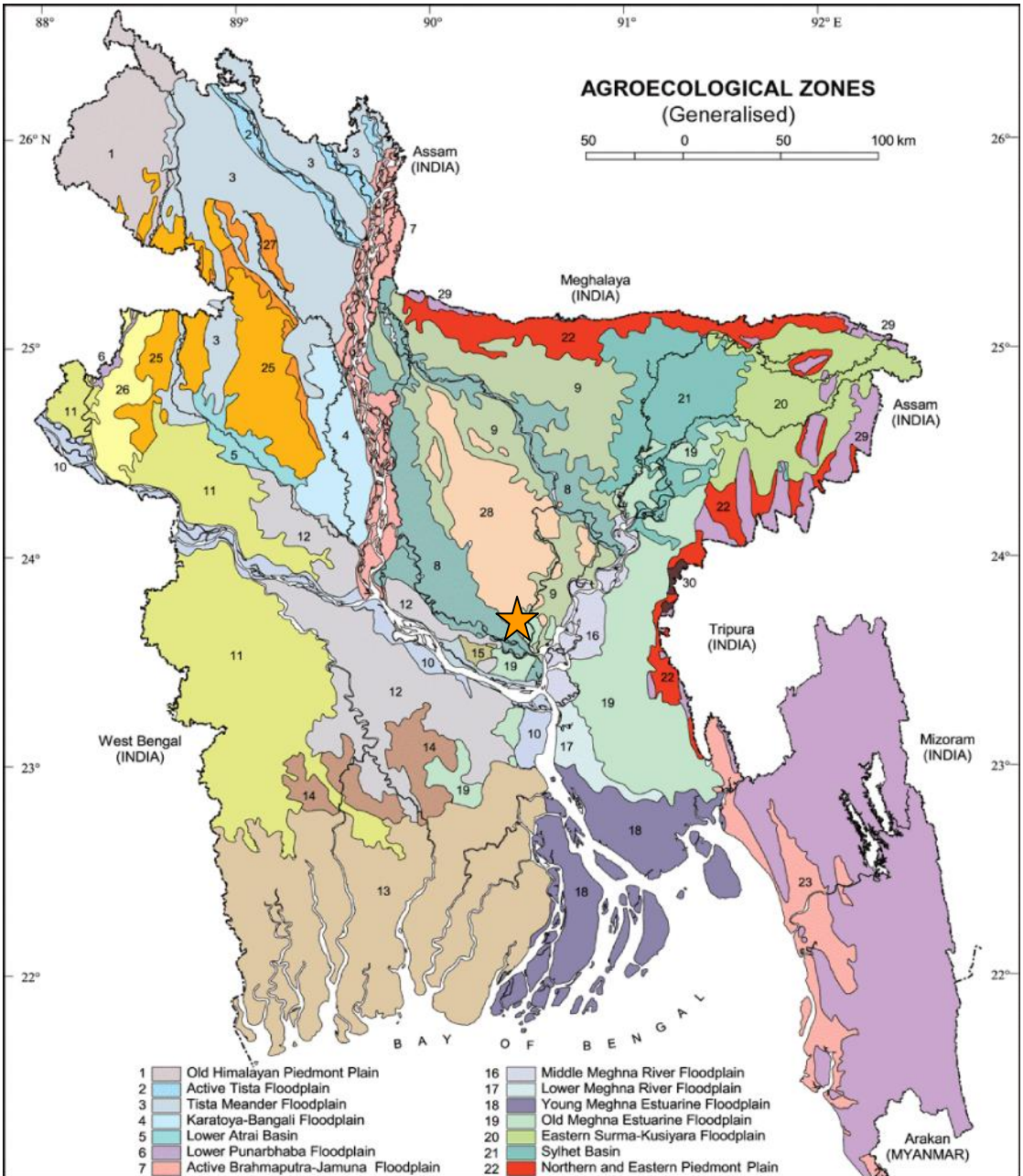
3.1 Experimental site and duration

The research work was conducted at the experimental farm of Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University (SAU), Dhaka-1207, Bangladesh, during the period from November 2013 to March 2014. The soil of the experimental plots were clay loam, land was medium high with medium fertility level. The site was situated in the subtropical climatic zone, wet summer and dry winter is the general climatic feature of this region (Figure 1). During the Rabi season the rainfall generally is scant and temperature moderate with short day length. Meterogical data on rainfall, temperature, relative humidity from November 2013 to April 2014 were obtained from the Department of Metrological Centre, Dhaka-1212, Bangladesh.

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 I). The records of air temperature, humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix II).



The experimental site under study

Figure 1: Location of the experimental field.

3.3 Plant Materials

40 lines were collected from the Bangladesh Agricultural Research institute, Gazipur-1701. These 40 lines were grown in the experimental farm of Sher-e-Bangla Agricultural University during the winter season of 2013 to 2014 are presented in Table 1.

3.4 Methods

3.4.1 Land preparation and fertilizer application

The land was ploughed well by power tiller followed by laddering. The stubbles and weeds were removed carefully. Chemical fertilizers were applied at the rate of 220-140-80-150-5 kg/ha of urea, Triple Super Phosphate (TSP), Muriate of Potash (MP), Gypsum and Zinc sulphate respectively. Cowdung was applied at the rate of five ton per hectare. The whole amount of TSP, MP, Gupsum, Zinc sulphate and 50% urea were applied as basal dose. The remaining 50% urea was applied as top dressing at flower initiation stage.

3.4.2 Experimental design and layout

The seeds of 40 lines were grown in Randomized Complete Block Design (RCBD) with three replications. Each plot consisted of single row of 3 m length spaced 40 cm apart and 10 cm between plants. The seeds were sown in separate line in the experimental field on 15 November 2013 by hand uniformly. The seeds were sown at a soil depth of 2.5 cm to 3.5 cm. After sowing the seeds were covered with soil carefully so that no clods were on the seeds. Seed germination started after three days of sowing on 18 November, 2013. Treatment was distributed in the experimental unit through randomization by using the random number.

3.4.3 Sowing of seeds

Seeds of 40 lines were grown in separate line in the experimental field on 15 November, 2013. The row spacing was 30 cm having plant spacing 15 cm within the row. The seedlings emerged with in four days.

Plate 1. Photograph showing the sowing the seeds *Brassica napus L.* in the experimental plot

Table 1. List of the 40 *Brassica napus L.* genotypes used in the experiment with their sources

Genotype No.	Name/Acc No.	Source
G1.	Nap-0717-2	BARI
G2.	Nap-0733-1	BARI
G3.	Nap-0762	BARI
G4.	Nap-08-4	BARI
G5.	Nap-0837	BARI
G6.	Nap-0865	BARI
G7.	Nap-0869	BARI
G8.	Nap-0876	BARI
G9.	Nap-0885	BARI
G10.	Nap-205	BARI
G11.	BARI-8	BARI

Genotype No.	Name/Acc No.	Source
G12.	BARI-13	BARI
G13.	Nap-10007	BARI
G14.	Nap-10009	BARI
G15.	Nap-10015	BARI
G16.	Nap-10017	BARI
G17.	Nap-10019	BARI
G18.	Nap-10020	BARI
G19.	Nap-1005	BARI
G20.	Nap-1007	BARI
G21.	Nap-10014	BARI
G22.	Nap-10012	BARI
G23.	Nap-0130	BARI
G24.	Nap-2012	BARI
G25.	Nap-2013	BARI
G26.	Nap-2022	BARI
G27.	Nap-9906	BARI
G28.	Nap-9908	BARI
G29.	Nap-248	BARI
G30.	Nap-2001	BARI
G31.	Nap-9901	BARI
G32.	Nap-9904	BARI
G33.	Nap-9905	BARI
G34.	Nap-2057	BARI
G35.	Nap-2037	BARI
G36.	Nap-206	BARI

Genotype No.	Name/Acc No.	Source
G37.	Nap-2066	BARI
G38.	Nap-179	BARI
G39.	Nap-94006	BARI
G40.	Nap-108	BARI

3.4.5 Irrigation and drainage

One post sowing irrigation was given by sprinkler after sowing of seeds to bring proper moisture condition of 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.

3.4.6 Intercultural operation, Insect and disease control

Necessary intercultural operations were done during the crop period to ensure normal growth and development of the plants. Thinning and 1st weeding were done after 15 days of sowing. Top-dressing, weeding and necessary thinning were done after 25 days of sowing. Malataf was sprayed two times one just before flowering and the other of the middle of flowering for protecting the crop from the attack of aphids and Rovral-50 WP was sprayed @ 20-g/10 L water first one at the time of siliquae setting of fruiting and second one after 15 days of 1st spraying to control *Alternaria* leaf spot. No remarkable disease attack was observed.

3.4.7 Harvesting of sample plants

When 80% of the plants showed symptoms of maturity i.e. straw color of siliqua, leaves, stem and desirable seed color in the matured siliqua, the crop was assessed to attain maturity. At maturity, 10 plants were selected at random from the middle row of each plot.

The sample plants were harvested by uprooting and then they were tagged properly. Data were recorded from these 10 plants.

3.4.8 Data recorded

3.4.8.1 Days to 1st flowering: Days to 1st flowering was counted when the 1st flowering plants had at least one open flower in each line. Flowering stage was shown in Plate 3.

Plate 2. Photograph showing a field view of the experimental site at SAU farm (Rabi 2013)

Plate 3. Photograph showing a field view of the experimental site in days to 1st flowering at SAU farm

3.4.8.2 Days to 50% flowering: Days to 50% flowering was counted when the 50% plants had at least one open flower in each lines. Flowering stage was shown in plate 4.

3.4.8.3 Days to 80% flowering: Days to 80% flowering was counted when near about 80% plants had at least one open flower of each lines. Flowering stage was shown in plate 5.

3.4.8.4 Days to maturity: Number of days required from sowing to siliquae maturity of 80% plants of each row.

3.4.8.5 Plant height: During harvesting the plant height was measured in cm from the ground level of the plant to the top of the plant. It was the longest inflorescence of the tallest raceme.

3.4.8.6 Number of primary branches per plant: Mean numbers of branches originated from the main stem from 10 randomly selected plants from each line at maturity.

3.4.8.7 Number of secondary branches per plant: Number of branches originated from the primary branch from 10 randomly selected plants from each line at maturity.

3.4.8.8 Number of siliquae per plant: Mean number of siliqua obtained from 10 randomly selected plants from line at maturity.

3.4.8.9 Length of siliqua: 10 siliquae was selected at random from every selected plant to measure the length of siliqua. The measurement was in cm. Distance between the end of the peduncle to the starting point of the beak was considered as siliqua length.

3.4.8.10 Number of seeds per siliqua: All siliqua from the sample plants was collected and 10 siliqua was randomly selected. Seeds obtained from them, were counted and average numbers of seeds per siliqua was recorded.

Plate 4. Photograph showing a field view of the experimental site in days to 50% flowering at SAU farm

Plate 5. Photograph showing a field view of the experimental site in days to 80% flowering at SAU farm

Side view

Close view

Plate 6: Photograph showing a field view at early flowering stage (side and close view)

3.4.8.11 Thousand-seed weight (g): Weight in grams of 1000-seed was recorded from 10 randomly selected plants of line.

3.4.8.12 Seed yield per plant (g): Mean seed weight in grams of 10 randomly selected plants from each line after harvest.

3.4.9 Statistical analysis

Genetic diversity was estimated following Mahalanobis's (1936) generalized distance (D^2). Selection of parents in hybridization program based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1977) reported that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a successful hybridization program. Statistical analysis such as Mahalanobis D^2 and Canonical Variate Analysis (CVA), which quantify the differences among several quantitative traits are efficient method of evaluating genetic diversity.Mean data of each quantitative character were subjected to both univariate and multivariate analysis. For univariate analysis of variance, analysis was done individually and least of significance was done by F- Test Pense and Shukhatme (1978). Mean, range, co-efficient of variation (CV) and correlation was estimated using MSTAT computer program. Multivariate analysis viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CLU) and Canonical

Variate Analysis (CVA) were done by using GENSTAT, R, PLABSTAT, Basica STAT, MSTAT and Excel program.

3.4.9.1 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,** $¢^2 p = ¢^2 g + ¢^2 e$

Where, $¢^2 g$ = Genotypic variance,

$¢^2 g$ = Environmental variance = Mean square of error

3.4.9.2 Estimation of genotypic and phenotypic co-efficient of variation:

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

$$GCV = \frac{\delta_g \times 100}{\bar{x}}$$

$$PCV = \frac{\delta_p \times 100}{\bar{x}}$$

Where, GCV = Genotypic co-efficient of variation

PCV = Phenotypic co-efficient of variation

δ_g = Genotypic standard deviation

δ_p = Phenotypic standard deviation

$\bar{x}$ = Population mean

3.4.9.3 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 = Phenotypic variance

3.4.9.4 Estimation of genetic advance:

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

$$GA = \frac{\delta^2_g}{\delta^2_p} . K . \delta_p$$

Where, GA = Genetic advance

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.

3.4.9.5 Estimation of genetic advance in percentage of mean:

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

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

3.4.9.6 Estimation of simple correlation co-efficient:

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

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

Where, $\sum$ = Summation

x and y are the two variables correlated

N = Number of observation

3.4.9.7 Path co-efficient analysis:

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1995) 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.

3.4.9.8 Estimation of Genetic Diversity

3.4.9.8.1Principal 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.

3.4.9.8.2 Canonical Vector Analysis (CVA)

Canonical Variate Analysis complementary to D^2 statistic is a sort of multivariate analysis where canonical vectors and roots representing different axes of differentiation and the amount of variation accounted for by each of such axes respectively and derived. Canonical Variate Analysis computed linear combination of original variability that maximized the ratio between ground and within group variations, there by giving functions of the original variables that could be used to discriminate between the groups. Thus in this analysis, a series of orthogonal transformation sequentially maximized the ratio of the groups to within group variations.

3.4.9.8.3 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 (PCA). The formula was used 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^2) within cluster.

3.4.9.8.4 Clustering

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

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CHAPTER IV

RESULTS AND DISCUSSION

The present study was conducted with a view to determine the variability among 40 materials of *Brassica napus L.*genotypes and also to study the correlation and path co-efficient for seed yield and different yield contributing characters. An experiment was conducted with 40 materials named Nap-0733-1, Nap-0762, Nap-08-4, Nap-0837, Nap-2013, Nap-2057, Nap-2037, Nap-179, Nap-0865, Nap-0869, Nap-0876, Nap-0885, Nap-205, Nap-10009, Nap-10015, Nap-10012, Nap-0717-2, Nap-10019, Nap-1005, Nap-9906, BARI-8, BARI-13, Nap-10007,Nap-10017, Nap-10020, Nap-1007, Nap-10014, Nap-0130, Nap-2012, Nap-2022, Nap-9908, Nap-248, Nap-2001, Nap-9901, Nap-9904, Nap-9905, Nap-206, Nap-2066, Nap-94006 and Nap-108. The data were recorded on different characters such as days to 1st flowering, days to 50% flowering, days to 80% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, length of siliqua (cm), number of seeds per siliqua, 1000 seed weight (gm) and seed yield per plant (gm). The data were statistically analyzed and thus obtained results are described below under the following heads:

- Mean performance
- Variability study in *Brassica napus*
- Heritability and genetic advance
- Correlation coefficient of characters
- Path coefficient analysis
- Genetic diversity analysis

4.1 Mean performance

Mean performance of 12 agronomic and yield related traits of lines were presented in Table 2. In the study significant variations were observed for most of the characters among 40 materials of *Brassica napus L.*

4.1.1 Days to 1st flowering

Considerable variations were observed among 40 materials for days to 1st flowering. In case of days to 1st flowering for line, it was ranged from 28.33 to 66.33 days. The days to 1st flowering were observed lowest (28.33 days) in Nap-10009 and highest (66.33 days) was observed in Nap-0837 (Table 2). The days to 1st flowering were observed in varieties 37.33 days in BARI-8 and 39.33 days in BARI-13 (Table 2). Singh *et al.,* (2005) obtained earliness on YSK-S501 × SS-2 in *B. campestris/rapa*. Singh *et al.,* (1997) observed earliness in PR-1108 × BJ-1235 in *Brassica juncea* L.

4.1.2 Days to 50% flowering

Considerable variations were observed among 40 materials for days to 50% flowering. In case of days to 50% flowering for line, it was ranged from 30.33 to 69.00 days. The days to 50% flowering were observed lowest (30.33 days) in Nap-10009 and highest (69.00 days) was observed in Nap-0837 (Table 2). The days to days to 50% flowering were observed in varieties 39.33 days in BARI-8 and 41.33 days in BARI-13 (Table 2). Singh *et al.,* (2005) obtained earliness on YSK-S501 × SS-2 in *B. campestris/rapa*. Singh *et al.,* (1997) observed earliness in PR-1108 × BJ-1235 in *Brassica juncea* L.

4.1.3 Days to 80% flowering

Considerable variations were observed among 40 materials for days to 80% flowering. In case of days to 80% flowering for parent, it was ranged from 33 to 72 days. The days to 80% flowering were observed the lowest (33.00 days) in Nap-10009 and the highest (72.00 days) observed in Nap-0837 (Table 2). The days to days to 50% flowering were observed in varieties 42.00 days in BARI-8 and 44.00 days in BARI-13 (Table 2). Singh *et al.,* (2005) obtained earliness on YSK-S501 × SS-2 in *B. campestris/rapa*. Singh *et al.,* (1997) observed earliness in PR-1108 × BJ-1235 in *Brassica juncea* L.

4.1.4 Days to maturity

Considering earliness, the minimum days to maturity was observed in Nap-10009 (82.67 days) and the maximum days (112.33 days) to maturity were observed in Nap- 0837 (Table 2). The varieties the days to maturity were observed in 87.29 days in BARI Sharisha 8 and 90.00 days in BARI Sharisha13 (Table 2).

Table 2: Mean performance for 12 different characters in 40 lines of *Brassica napus L.*

Genotype	Days to 1st flowering	Days to 50% flowering	Days to 80% flowering	Days to maturity	Plant height(cm)	Number of primary branches per plant	Number of secondary branches per plant	Number of siliquae per plant	Length of siliqua (cm)	Number of seeds per siliqua	Thousand-seed weight (gm)	Seed yield per plant (gm)
Nap-0717-2	33.33	35.33	38	85.52	86.14	2.95	3.6	97.94	7.21	22.97	3.01	11.23
Nap-0733-1	50.33	52.33	55	96.22	111.33	4.31	4.32	146.44	7.13	21.75	3.4	10.87
Nap-0762	56.33	58.33	61	104.57	120.22	3.84	3.95	138.76	7.79	22.43	2.91	9.51
Nap-08-4	60.33	62.33	65	107.67	104.16	2.91	3.38	128.34	7.31	24.32	3.73	11.83
Nap-0837	66.33	69	72	112.33	99.21	3.67	4.3	124.72	6.93	21.57	2.88	11.35
Nap-0865	30.33	32.33	35	85	96.77	3.19	3.15	164.8	7.76	20.04	3.68	12.75
Nap-0869	31.33	33.33	36	87.52	87.45	3.33	4.97	153.84	7.63	23.95	3.18	12.56
Nap-0876	32.33	34.33	37	86.19	101.03	2.75	3.83	160.48	8.06	21.63	3.71	13.25
Nap-0885	34.33	36.33	39	85.57	82.11	3	3.37	145.93	7.5	21.71	3.46	11.78
Nap-205	36.33	38.33	41	86.86	82.98	2.7	3.2	166.78	6.38	22.36	3.52	13.23
BARI-8	37.33	39.33	42	87.29	79.57	3.28	4.13	172.01	7.68	23.33	4.19	14.29
BARI-13	39.33	41.33	44	90	91.44	3.58	3.71	173.48	6.63	23.98	3.73	12.89
Nap-10007	45.33	47.33	50	95.67	90.53	3.35	3.51	156.48	7.23	24.17	3.29	8.58
Nap-10009	28.33	30.33	33	82.67	89.07	2.71	4.5	166.38	7.52	20.62	2.84	11.76

Nap-10015	29.33	31.33	34	83.33	87.22	3	4.38	145.68	7.29	19.45	3.35	12.21
Nap-10017	35.33	37.33	40	86.33	91.3	3.08	3.71	185.03	7.44	22.58	4.09	13.33
Nap-10019	41.33	43.33	46	90.33	100.93	3.12	3.48	138.72	7.82	23.84	3.72	10.89
Nap-10020	42.33	44.33	47	88.33	100.7	3.03	4.44	187.42	8.63	21	3.38	11.26
Nap-1005	43.33	45.33	48	91	95.85	3.08	4.4	145.47	7.73	24.37	3.47	12.45
Nap-1007	44.33	46.33	49	90.67	93.67	3.18	4	158.69	7.56	22.55	3.19	10.38
Nap-10014	46.33	48.33	51	90.67	94.76	3.08	4.28	165.83	7.99	18.24	3.62	12.19
Nap-10012	38.33	40.33	43	86.67	96.47	3.08	4.25	155.97	7.3	24.36	2.9	11.28
Nap-0130	47.33	49.33	52	93.33	100.69	3.6	5.17	178.04	7.86	21.86	3.55	10.78
Nap-2012	48.33	50.33	53	95	90.33	3.03	4.49	181.25	7.52	25.84	3.63	13.28
Nap-2013	49.33	51.33	54	95.33	103.53	3.03	5.33	148.4	7.95	24.42	3.7	11.53
Nap-2022	61.33	63.33	66	105	106.23	3.05	4.34	167.95	7.02	19.29	3.21	11.9

Table 2 (Cont'd)

Genotype	Days to 1st flowering	Days to 50% flowering	Days to 80% flowering	Days to maturity	Plant height(cm)	Number of primary branches per plant	Number of secondary branches per plant	Number of siliquae per plant	Length of siliqua (cm)	Number of seeds per siliqua	Thousand-seed weight (gm)	Seed yield per plant (gm)
Nap-9906	40.33	42.33	45	86.67	111.85	3.33	4.25	138.85	7.71	25.91	3.66	11.28

Nap-9908	51.33	53.33	56	97.67	120.99	3.59	5.31	178.63	7.42	23.58	3.81	11.54
Nap-248	52.33	54.33	57	98.67	119.02	3.16	4.48	190.66	6.63	21.81	4.04	12.78
Nap-2001	53.33	55.33	58	97.67	129.16	3.4	4.14	182.87	8.09	23.47	3.22	10.76
Nap-9901	55.33	57.33	60	100.67	136.62	3.19	4.03	197.82	7.37	24.36	3.5	11.58
Nap-9904	57.33	59.33	62	102.67	126.15	3.34	4.13	190.6	7.67	23.18	3.38	11.26
Nap-9905	58.33	60.33	63	104.33	116.83	4	5.21	172.64	7.7	22.91	3.72	12.25
Nap-2057	59.33	61.33	64	106	115.94	3.43	4.28	156.64	7.34	23.12	3.13	13.56
Nap-2037	62.33	64.33	67	108.67	106.69	3.53	4.08	162.41	8.01	22.62	3.77	13.01
Nap-206	54.33	56.33	59	95.67	108.79	3.32	3.83	169.6	7.48	20.73	3.57	11.25
Nap-2066	63.33	66.67	69	110.67	103.61	3.87	6.85	197.25	7.34	24.06	3.62	11.56
Nap-179	64	67	70	110.33	102.84	3.21	4	163.83	7.42	23.68	3.59	12.11
Nap-94006	66	67.33	71.33	111	107.31	3.14	4.04	182.02	6.97	23.08	3.72	10.71
Nap-108	63	64.33	66.67	107.33	130.23	3.91	6.64	165.3	8.69	26.37	3.01	12.89
Mean	47.73	49.77	52.48	95.68	102.99	3.28	4.29	162.6	7.52	22.79	3.48	11.85
Minimum	28.33	30.33	33	82.67	79.57	2.7	3.15	97.94	6.38	18.24	2.84	8.58
Maximum	66.33	69	72	112.33	136.62	4.31	6.85	197.82	8.69	26.37	4.19	14.29
Median	47.83	49.83	52.5	95.17	100.98	3.19	4.2	165.05	7.51	23.03	3.54	11.77
SD	11.54	11.6	11.66	9.1	14.16	0.36	0.78	21.02	0.47	1.79	0.33	1.13

Variance	133.14	134.64	135.97	82.73	200.41	0.13	0.61	441.8	0.22	3.22	0.11	1.28
SE Mean	1.82	1.83	1.84	1.44	2.24	0.06	0.12	3.32	0.07	0.28	0.05	0.18
C.V.	24.18	23.31	22.22	9.51	13.75	10.94	18.29	12.93	6.3	7.87	9.59	9.56

Chowdhury *et al.,* (2004) observed earliness in M-27 × Din-2 in *Brassica rapa* L. Singh *et al*., (2005) obtained earliness in SS-3 × SS-1 in *Brassica campestris* L.

4.1.5 Plant height (cm)

In this study, the highest plant height was observed in Nap-9901 (136.62 cm) whereas the minimum plant height was observed in BARI-8 (79.57 cm). Plant height observed in the varieties 91.44 cm in BARI-13 (Table 2). Chowdhury *et al.,* (2004) observed dwarfness in PT-303 × Tori-7 in *Brassica rapa* L. Nair *et al.,* (2005) observed significant variance for this trait in *Brassica juncea* L. Tyagi *et al.,* (2001) observed the highest variation in plant height among parents and their hybrid. These findings were closed resemblance to the reports of Chowdhury *et al*., (1993) and Yadava *et al*., (1993).

4.1.6 Number of primary branches per plant

Among the 40 materials the highest number of primary branches/plant was observed in Nap-0733-1(4.31) where as the minimum number of primary branches/plant was observed in Nap-205 (2.7) (Table 2). Number of primary branches per plant observed in the genotypes 3.28 in BARI-8 and 3.58 in BARI-13 (Table 2). Number of primary branches per plant showed little differences. The value indicating the apparent variation not only due to genotypes but also due to the large influence of environment (Table 2). Chowdhury *et al*., (2004) found more primary branches in Sampad× Tori-7 in *Brassica rapa* L. Singh *et al.,* (2005) obtained maximum number of primary branches per plant in YSK-8501 × SS-1 in *Brassica campestris* L. Chowdhary *et al.,* (1993) found significant differences for number of primary branches per plant. Similar results were obtained by Rashid (2007), Siddikee (2006) and Kumar *et al.,* (1996). Negative associations were found by Vershney *et al.,* (1986).

4.1.7 Number of secondary branches per plant

For the number of secondary branches per plant, parents showed at a range from 3.15 to 6.85. However, the parent Nap-0865 (3.15) flowered with the lowest time but the parent Nap-2066 (6.85) took the highest duration (Table 2). Number of secondary branches per plant observed in the genotypes 4.13 in BARI-8 and 3.71 in BARI-13 (Table 2). Chowdhury *et*

al., (2004) found maximum secondary branches in Sampad× Din-2 in *Brassica rapa* L. Singh and Murty (1980) observed more secondary branches per plant in YSC-68× SS-2 in *Brassica campestris* L. These findings are closing similar to the reports of Chowdhary *et al.,* (1993) and Mahmud (2008).

4.1.8 Number of siliqua per plant

Number of siliqua per plant were varied from 97.94 to 197.82.The number of siliqua per plant was observed the highest in Nap-9901 (197.82) followed by Nap-2066 (197.25). Whereas the minimum number of siliquae per plant observed in Nap-0717-2 (97.94) (Table 2). Number of siliqua per plant observed in the varieties 172.01 in BARI-8 and 173.48 in BARI-13 (Table 2).These combinations could be selected for the future breeding program to obtain desirable higher number of siliqua per plant. Chowdhury *et al.,* (2004) found the maximum siliquae in Sampad× Din-2 in *Brassica rapa* L. Singh and Murty (1980) observed more siliquae per plant in YSP-842 × SS-3 in *Brassica campestris* L.

4.1.9 Length of siliqua (cm)

Siliqua length of parent ranged from 6.38 to 8.69 cm. Length of siliqua was observed the highest in Nap-108(8.69cm) followed by Nap-10020 (8.63 cm) whereas the minimum length of pod was observed in Nap-205 (6.38cm) (Table 2). The varieties length of siliqua was observed 6.63 cm in BARI-13 and 7.68 cm in BARI-8 (Table 2). Huq (2006) showed BINAsar-6 × Tori 7 was not good for improving the trait in *Brassica rapa* L. Labowitz (1989) studied *Brassica campestris* population for pod length and observed high genetic variation on this trait. Olsson (1990) found high genetic variability for this trait.

4.1.10 Number of seeds per siliqua

Number of seeds per siliqua varied from 18.24 to 26.37. The number of seeds per siliqua was observed the highest in Nap-108(26.37). Nap-9906 (25.91) was found the second highest for number of seeds per siliqua. Whereas the minimum number of seeds per siliqua observed in Nap-10014 (18.24) (Table 2). The number of seeds per siliqua observed 23.33 in BARI-8 and 23.98 in BARI-13 (Table 2). Chowdhury *et al.,* (2004) found the highest seeds per siliqua in

Dhali× Sampad in *Brassica rapa* L. Singh *et al.,* (2005) obtained more seeds per siliquae in YSP-842 × YSK-8501 in *Brassica campestris* L.

4.1.11 Thousand seed weight (gm)

Thousand seed weight in *B. napus* varied with some extent i.e. from 2.84 to 4.19 gm in line. Thousand seed weight was found maximum in BARI-8 (4.19gm) where as the minimum thousand seed weight was found in Nap-10009 (2.84gm) (Table 2). Thousand seed weight observed in the varieties 3.73g in BARI-13 (Table 2). Singh *et al.,* (2005) observed more seed weight per plant in YSC-68 × SS-2 in *Brassica campestris* L. Chowdhury *et al.,* (2004) obtained the highest seed weight in Dhali× Sampad in *Brassica rapa* L.

4.1.12 Seed yield per plant (gm)

Seed yield per plant was found at diversely in different genotypes including lines. Seed yield of the genotypes varied from 8.58 to 14.29gm in lines. Yield is the most outstanding character and all the research work and objectives are dependent on yield. The highest amount of yield per plant was observed in BARI-8 (14.29 gm) followed by Nap-2057 (13.56 gm) (Table 2). Whereas the minimum yield per plant was observed in Nap-10007 (8.58 gm) (Table 2). The yield per plant of the varieties were 12.89 in BARI-13. Huq (2006) obtained the highest seed yield in Agroni× Tori 7, Agroni× BARIsar-6 and Shafal× BARIsar-6 in *Brassica rapa* L. Chowdhury *et al.,* (2004) obtained the highest seed yield in M-27 × Din-2 in *Brassica rapa*L. Singh *et al.,* (2005) observed more seed yield per plant in YSP-842 × YSK-8501 in *Brassica campestris* L.

4.2 Variability study in *Brassica napus*

Significant variations were observed for most of the characters among 40 materials of *Brassica napus*. The values of mean, CV%, phenotypic variances, genotypic variances, phenotypic coefficient of variation and genotypic coefficient of variation for different yield related characters were shown in Table 3.

4.2.1 Days to 1st flowering

Considerable variations were observed among 40 materials for days to 1st flowering. Phenotypic and genotypic variance for days to 1st flowering was observed as 137.274 and 131.066, 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 (24.546) was higher than the genotypic

Table 3. Estimation of genetic parameters in 12 characters of 40 genotypes in *Brassica napus L.*

Characters	Mean	CV%	$\pm^0$g	$\pm^0$ p	GCV	PCV	% Heritabiliy	GA	GA in % mean
Days to 1st flowering	47.733	24.348	131.066	137.274	23.984	24.546	95.478	23.044	13.705
Days to 50% flowering	49.775	23.486	132.498	138.890	23.126	23.677	95.398	23.160	13.774
Days to 80% flowering	52.475	22.237	134.740	138.432	22.121	22.422	97.333	23.591	14.031
Days to maturity	95.675	9.5739	80.174	85.249	9.359	9.650	94.047	17.888	10.639
Plant height(cm)	103.01	13.647	199.525	200.958	13.713	13.762	99.287	28.994	17.244
Number of primary branches per plant	3.2838	21.117	0.153	0.580	11.930	23.193	26.459	0.415	0.247
Number of secondary branches per plant	4.2864	19.042	0.584	0.676	17.832	19.182	86.422	1.464	0.871
Number of siliquae per plant	162.60	12.818	441.777	441.837	12.926	12.927	99.986	43.295	25.749
Length of siliqua (cm)	7.5428	7.2489	0.181	0.302	5.640	7.286	59.934	0.678	0.404
Number of seeds per siliqua	22.788	7.8599	3.192	3.262	7.840	7.925	97.872	3.641	2.166
Thousand-seed weight (gm)	3.4770	10.256	0.102	0.129	9.194	10.325	79.298	0.586	0.349
Seed yield per plant (gm)	11.823	11.507	0.918	1.866	8.105	11.555	49.197	1.385	0.823

CV (%) = Coefficient of Variation, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance, GCV = Genotypic Coefficient of Variation, PCV = Phenotypic Coefficient of Variation and GA= Genetic Advance.

coefficient of variation (23.984) which suggested that environment had a significant role on the expression of this trait (Table 3). 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).

4.2.2 Days to 50% flowering

Considerable variations were observed among 40 materials for days to 50% flowering. Phenotypic and genotypic variance for days to 50% flowering was observed as 138.89 and 132.498, 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 (23.677) was higher than the genotypic coefficient of variation (23.126) (Table 3), which suggested that environment had a significant role on the expression of this trait. High genotypic and phenotypic co-efficient of variation was recorded by Lekh *et al.,* (1998).

4.2.3 Days to 80% flowering

Considerable variations were observed among 40 materials for days to 80% flowering. Phenotypic and genotypic variance for days to 80% flowering was observed as 138.432 and 134.74, 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 (22.422) was higher than the genotypic coefficient of variation (22.121) (Table 3), which suggested that environment had a significant role on the expression of this trait. High genotypic and phenotypic co-efficient of variation was recorded by Lekh *et al.,* (1998).

4.2.4 Days to maturity

Phenotypic and genotypic variance for days to maturity was observed 85.249 and 80.174, 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 (9.65%) was higher than the genotypic coefficient of variation (9.359%) (Table

3), which suggested that environment had a significant 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).

4.2.5 Plant height (cm)

Phenotypic variance and genotypic variance were observed as 200.958 and 199.525, 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 (13.762%) and GCV (13.713%) also indicated presence of considerable variability among the genotypes for this trait (Table 3). The highest variation in plant height among parents and their hybrid was observed by Tyagi *et al.,* (2001).

4.2.6 Number of primary branches per plant

Phenotypic variance and genotypic variance were observed as 0.58 and 0.153, respectively. Relatively large differences between them indicating large environmental influences on these character and relatively high difference between PCV (23.193%) and GCV (11.93%) value indicating the apparent variation not only due to genotypes but also due to the large influence of environment (Table 3). Chowdhury *et al.,* (1993) also found significant differences for number of primary branches per plant.

4.2.7 Number of secondary branches per plant

Phenotypic variance and genotypic variance were observed as 0.676 and 0.584, respectively. Higher estimate of PCV (19.182%) and GCV (17.832%) values indicated presence of considerable variability among the genotypes for this trait (Table 3). 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.,* (1993) found significant differences for number of secondary branches per plant.

4.2.8 Number of siliqua per plant

Number of siliqua per plant showed the highest phenotypic variance (441.837) and genotypic variance (441.777) with large environmental influence and the difference between the PCV (12.927%) and GCV (12.926%) indicated existence of adequate variation among the genotype (Table 3). High genetic variation was also found by Kudla (1993).

4.2.9 Length of siliqua (cm)

Length of siliqua showed phenotypic variance (0.302) and genotypic variance (0.181) with little difference between them indicating that they were less responsive to environmental factors for their phenotypic expression and relatively medium PCV (7.286%) and GCV (5.64%) indicating that the genotype has moderate variation for this trait (Table 3). 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 Olsson (1990).

4.2.10 Number of seeds per siliqua

The phenotypic and genotypic variances for this trait were 3.262 and 3.192 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 7.925% and 7.84% respectively for number of seeds per siliqua which indicating that medium variation existed among different genotypes (Table 3). Similar variability was also recorded by Kumar and Singh (1994).

4.2.11 Thousand seed weight (g)

Thousand seed weight showed very low genotypic (0.102) and phenotypic (0.129) variance with high differences indicating that they were high responsive to environmental factors. The phenotypic co-efficient of variation (10.325%) and genotypic coefficient of variation (9.194%) were close to each other (Table 3). 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.

4.2.12 Yield per plant (gm)

The phenotypic variances and genotypic variances for this trait were 1.866 and 0.918 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 values of GCV and PCV were 8.105% and 11.555% indicating that the genotype has considerable variation for this trait (Table 3). Similar variability was also found by Khera and Singh (1988).

4.3. Heritability and genetic advance

4.3.1 Days to 1st flowering

Days to 1st flowering exhibited high heritability (95.478%) with low genetic advance (23.044) and genetic advance in percentage of mean (13.705%) indicated that this trait was controlled by non-additive gene (Table 3). This results support the reports of Malik *et al.,* (2000).

4.3.2 Days to 50% flowering

Days to 50% flowering exhibited high heritability (95.398%) with low genetic advance (23.16) and genetic advance in percentage of mean (13.774%) indicated that this trait was controlled by non-additive gene (Table 3).This results supported the reports of Malik *et al.,* (1995).

4.3.3 Days to 80% flowering

Days to 80% flowering exhibited high heritability (97.333%) with low genetic advance (23.591) and genetic advance in percentage of mean (14.031%) indicated that this trait was controlled by non-additive gene (Table 3).This results supported the reports of Malik *et al.,* (2000).

4.3.4 Days to maturity

Days to maturity shows high heritability (94.047%) with low genetic advance (17.888) and genetic advance in percentage of mean (10.639%) indicated that this trait was controlled by non-additive gene and medium possibility of selecting genotypes that would mature earlier (Table 3). In some of the crosses the frequency of the segregating plants showing reduced maturity was comparatively higher than the other crosses. Low heritability coupled with low genetic advance for this trait was also observed by Sharma (1994).

4.3.5 Plant height (cm)

Plant height shows high heritability 99.287% with moderately high genetic advance of 28.994 and genetic advance in percentage of mean of 17.244% (Table 3), 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 (Table 3). 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 3.

4.3.6 Number of primary branches per plant

Number of primary branches per plant exhibited low heritability 26.459 with low genetic advance of 0.415 and genetic advance in percentage of mean of 0.247%, which revealed that this trait was controlled by non-additive gene (Table 3). As a whole, the low 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.,* (1997). Yadava *et al.,* (1993) found high heritability and genetic advance for number of primary branches per plant.

4.3.7 Number of secondary branches per plant

Number of secondary branches per plant exhibited moderately high heritability (86.422%) with low genetic advance 1.464 and genetic advance in percentage of mean (0.871%), such results revealed that this trait was controlled by non-additive gene (Table 3). As a whole, the moderately high heritability and the consequent low genetic advance indicated the lower possibility of selecting genotypes.

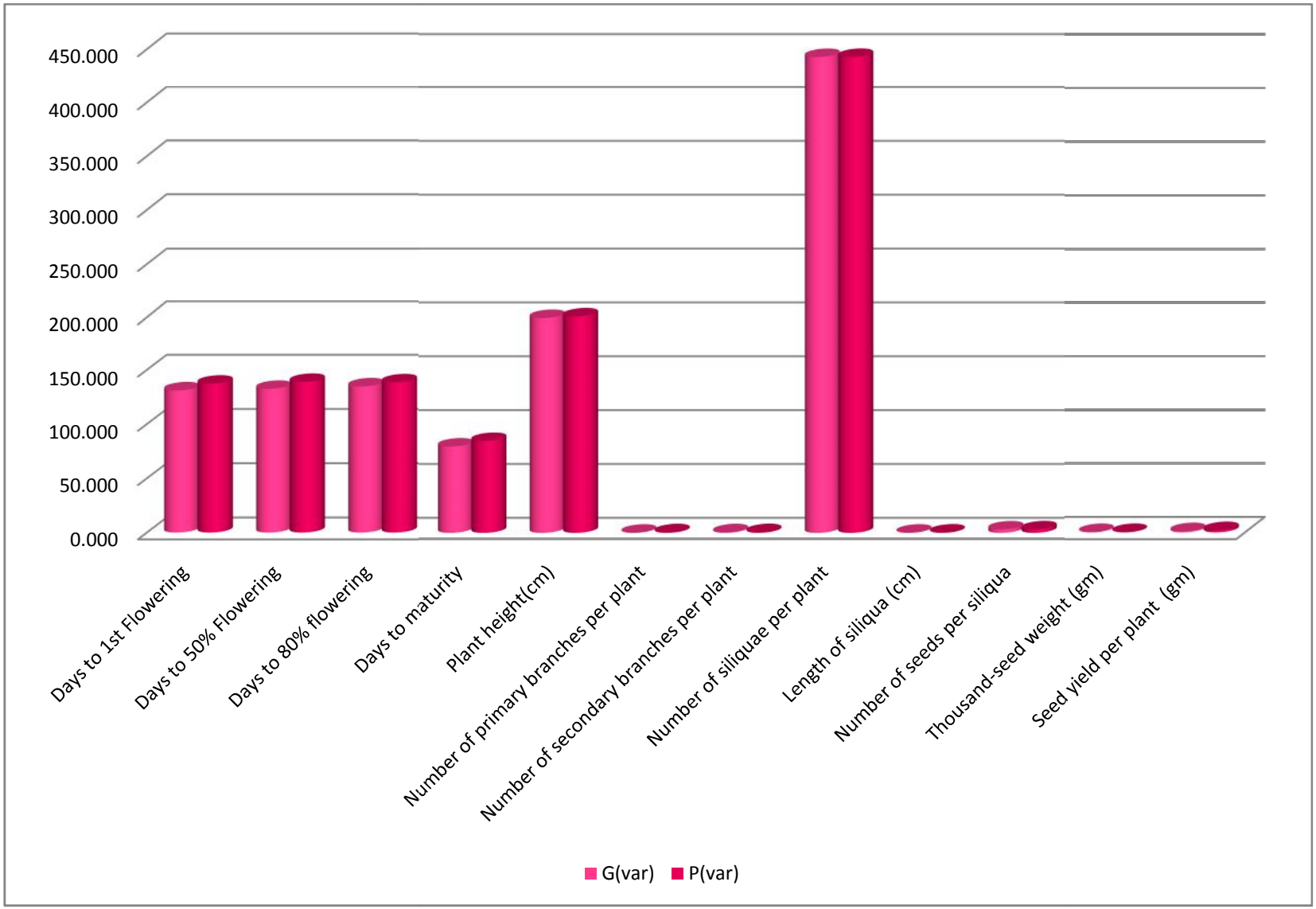

450.000
400.000
350.000
300.000
250.000
200.000
150.000
100.000
50.000
0.000
Days to 1st Flowering
Days to 50% Flowering
Days to 80% flowering
Days to maturity
Plant height(cm)
Number of primary branches per plant
Number of secondary branches per plant
Number of siliquae per plant
Length of siliqua (cm)
Number of seeds per siliqua
Thousand-seed weight (gm)
Seed yield per plant (gm)
G(var)
P(var)

Figure 2. Genotypic and phenotypic coefficient of variation in *Brassica napus L.*

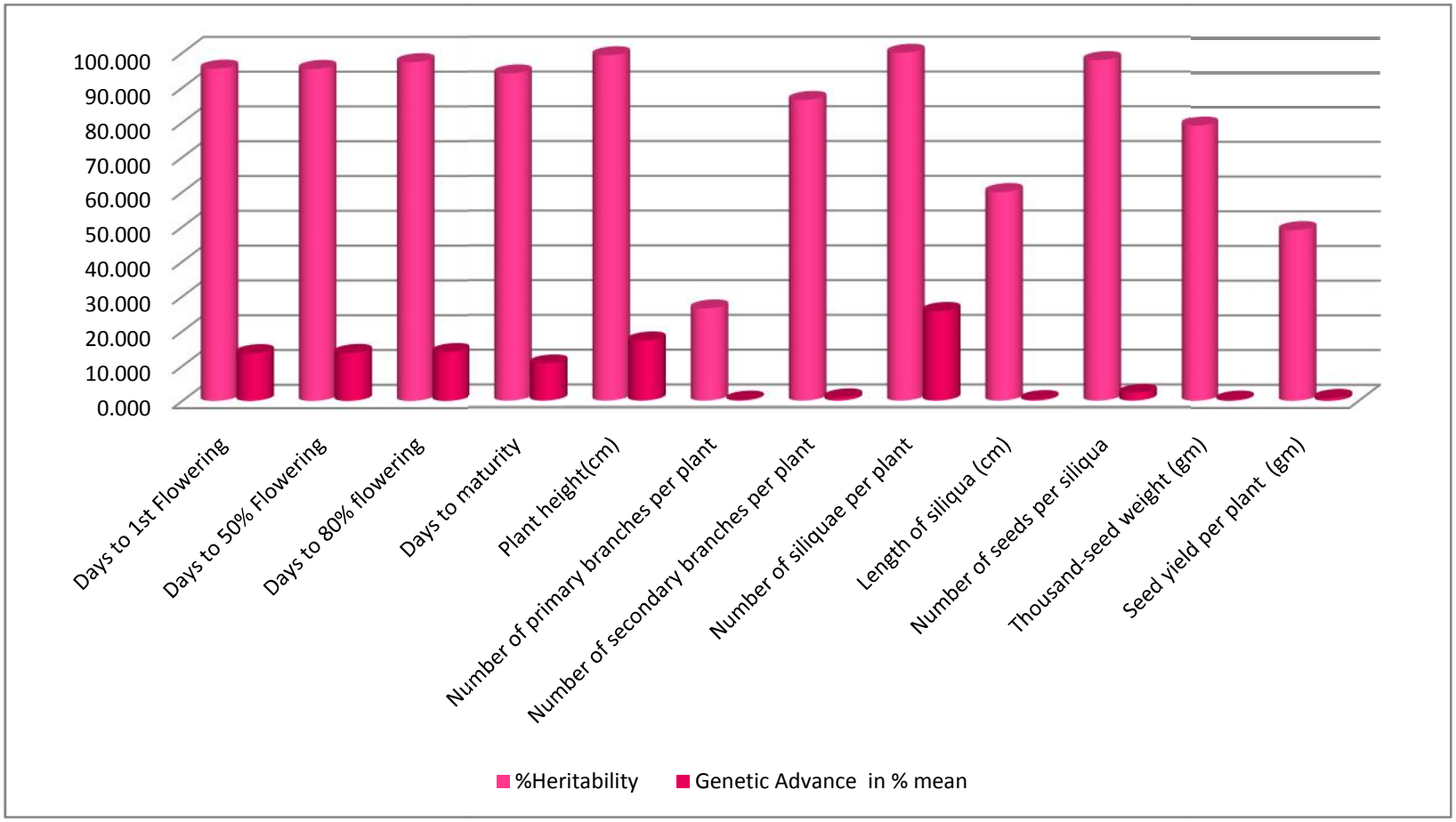


Figure 3. Heritability and genetic advance over mean in *Brassica napus L.*

Moderately high heritability coupled with low genetic advance was also found by Singh *et al.,* (1997). 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.

4.3.8 Number of siliqua per plant

Number of siliqua per plant exhibited very high heritability 99.986% with high genetic advance 43.295 and genetic advance in percentage of mean 25.749%. These results revealed the possibility of predominance of additive gene action in the inheritance of this trait (Table 3). 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.,* (2008) reported that the number of siliqua per plant were highly heritable coupled with high genetic advance.

4.3.9 Siliqua length

Siliqua length showed high heritability (59.934%) with low genetic advance (0.678) and low genetic advance in percentage of mean 0.404% indicated that this trait was controlled by non-additive gene (Table 3). High heritability for this trait was observed by Chaudhury *et al.,* (1990). Similar results were also found by Kwon *et al.,* (1989) and Rao (1977).

4.3.10 Number of seeds per siliqua

Number of seeds per siliqua showed high heritability 97.872% coupled with high genetic advance 3.641 and high genetic advance in percentage of mean 2.166%, indicated that this trait was controlled by additive gene and selection for this character would be effective (Table 3). High heritability coupled with high genetic advance for this trait was also observed by Singh (2004).

4.3.11 Thousand seed weight

Thousand seed weight exhibited high heritability 79.197% with low genetic advance 0.586 and genetic advance in percentage of mean 0.349%, revealed that this trait was controlled

by non-additive gene (Table 3). 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.,* (1997) reported the high heritability and genetic advance for thousand seed weight.

4.3.12 Seed yield per plant

Seed yield per plant showed high heritability 49.197% with high genetic advance (1.385) and moderately high genetic advance in percentage of mean 0.823% indicated this trait was controlled by additive gene and selection for this character would be effective (Table 3). 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 (2004) while working with 22 genotypes of *Brassica napus*.

4.4 Correlation coefficient of characters

Seed yield is a complex product being influenced by several quantitative traits. Some of these traits are highly associated with seed yield. The analysis of the relationship among those traits and their association with seed yield is very much essential to establish selection criteria. Breeders always look for genetic variation among traits to select desirable type. Correlation co-efficient between pairs of trait for 40 materials of *B. napus* are shown in Table 4 & 5.

4.4.1 Days to 1st flowering

Days to 1st flowering showed highly significant and positive correlation with days to maturity (G = 0.383, P = 0250) indicated that if days to 1st flowering increased then days to maturity also increased. It also exhibited insignificant and positive interaction with number of seed per siliqua (G = 0.117, P = 0.082), plant height (cm) (G = 0.116, P = -0.009) and number of secondary branches per plant (G = 0.123, P = 0.082). However, it had insignificant and negative interaction with number of thousand-seed weight (gm) (G = -0.055, P = -0.011) (Table 4 & 5). 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 1st flowering had insignificant and positive interaction with yield per plant.

4.4.2 Days to 50% flowering

Days to 50% flowering showed highly insignificant and negative correlation with days to maturity (G = -0.092, P = -0.041) indicated that if days to 50% flowering increased then days to maturity also increased. It also exhibited insignificant and positive interaction with number of number of secondary branches per plant (G = 0.083, P = 0.012) and seed yield per plant (gm) (G = 0.281, P = 0.164). However, it had insignificant and negative interaction with number of thousand-seed weight (gm) (G = -0.321, P = -0.034) (Table 4 & 5). 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 50% flowering had insignificant and positive interaction with yield per plant.

4.4.3 Days to 80% flowering

Days to 80% flowering showed highly significant and positive correlation with days to maturity (G = 0.738, P = 0.091) indicated that if days to 80% flowering increased then days to maturity also increased. It also exhibited insignificant and positive interaction with number of number of siliqua per plant (G = 0.482, P = 0.047). However, it had significant and negative interaction with number of thousand-seed weight (gm) (G = -0.612, P = 0.053) (Table 4 & 5). 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 80% flowering had insignificant and positive interaction with yield per plant.

4.4.4 Days to maturity

Days to maturity showed significant and positive correlation with number of seeds per siliqua (G= 0.102, P= 0.033) and siliqua length (G = 0.497, P = 0.087). It had insignificant and positive correlation with yield per plant (G 0.13, P = 0.279). However, it had insignificant and negative interaction with thousand seed weight (G =-0.723, P = -0.165) (Table 8 & 9).

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.

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

Characters	Days to 50% flowering	Days to 80% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Number of siliquae per plant	Length of siliqua (cm)	Number of seeds per siliqua	Thousand-seed weight (gm)	Seed yield per plant (gm)
Days to 1st flowering	0.383**	-0.712**	-0.322**	0.116	0.092	0.123	0.117	-0.125	0.293**	-0.055	-0.214**
Days to 50% flowering		-0.092	-0.215**	-0.207*	-0.011	0.083	-0.107	0.237**	-0.018	-0.321**	0.281**
Days to 80% flowering			0.738**	-0.339	-0.525**	-0.643**	-0.259	-0.325**	0.482**	-0.612**	-0.595**
Days to maturity				0.302**	0.912**	0.976**	-0.593**	0.497**	0.102	-0.723	0.13
Plant height(cm)					0.082	0.176	0.940**	0.618**	-0.415*	0.09	-0.590**
Number of primary branches per plant						0.597*	-0.364	0.151	-0.165	0.813**	0.443*
Number of secondary branches per plant							0.606*	-0.114	0.223	-0.473*	0.064

Number of siliquae per plant								0.885**	0.950**	-0.277	0.564**
Length of siliqua (cm)									-0.260	0.293	0.195
Number of seeds per siliqua										-0.314	0.312
Thousand-seed weight (gm)											0.237
Seed yield per plant (gm)											0.342

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

Table 5. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of *Brassica napus L.*

Characters	**Days to 50% flowering**	**Days to 80% flowering**	**Days to maturity**	**Plant height (cm)**	**Number of primary branches per plant**	**Number of secondary branches per plant**	**Number of siliquae per plant**	**Length of siliqua (cm)**	**Number of seeds per siliqua**	**Thousand-seed weight (gm)**	**Seed yield per plant (gm)**
Days to 1st flowering	0.250**	0.043	-0.127	-0.009	0.076	0.087	0.082	-0.043	0.106	-0.011	-0.069

Days to 50% flowering		-0.041	0.014	-0.06	-0.122	0.012	-0.09	-1.906**	0.043	-0.034	0.164
Days to 80% flowering			0.091	-0.07	-0.358	-0.426*	0.047	-0.292	-0.402*	0.053	0.212*
Days to maturity				0.104	-0.1	-0.015	0.097	0.087	0.033	-0.165	0.279
Plant height(cm)					0.139	0.037	0.267	0.138	-0.266	0.073	-0.252
Number of primary branches per plant						0.472*	-0.009	0.490*	-0.064	0.441*	0.533**
Number of secondary branches per plant							0.433*	0.431*	0.145	0.036	0.397
Number of siliquae per plant								0.626**	0.287	0.137	0.648*
Length of siliqua (cm)									-0.185	0.315	0.126
Number of seeds per siliqua										0.069	0.258
Thousand-seed weight (gm)											0.162
Seed yield per plant (gm)											0.405

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

4.4.5 Plant height (cm)

Plant height showed highly insignificant and positive interaction with number of primary branches (G = 0.082, P = 0.139), number of secondary branches (G = 0.176, P= 0.037), number of siliqua per plant (G = 0.940, P = 0.267) and thousand-seed weight (gm) (G = 0.09, P = 0.073) (Table 4 & 5). 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. However, it had insignificant and negative interaction with number of seeds per siliqua (G = -0.415, P = -0.266) (Table 4 & 5). Insignificant association of these traits indicated that the association between these traits were 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 Verma and Sachan (2000). 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.

4.4.6 Number of primary branches per plant

Number of primary branches per plant showed positive and significant interaction with number of secondary branch (G = 0.816, P = 0.597), thousand-seed weight (gm) (G = 0.813, P = 0.441) and seed yield per plant (gm) (G = 0.443, P = 0.533). 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. However, it had insignificant and negative interaction was found in number of seeds per siliqua (G = -0.165, P =- 0.064) (Table 4 & 5). Insignificant association of these traits indicated that the association between these traits were largely influenced by environmental factors. Similar results were obtained by Rashid (2007).

4.4.7 Number of secondary branches per plant

Number of secondary branch showed highly significant and positive interaction with number of siliqua per plant (G = 606, P = 433) that the traits were governed by same gene and simultaneous improvement would be effective and branching was an important contributor

to yield , independent of its association with plant size. It had significant and positive correlation with number of seed per siliqua (G = 0.223, P = 0.145) (Table 4 & 5). Indicated that if number of secondary branches increased the number of seed per siliqua and decreased the siliqua length. These findings are showing similar to the reports of Chowdhary *et al.,* (2004).

4.4.8 Number of siliqua per plant

Siliqua per plant showed significant and positive correlation with length of siliqua (cm) (G = 0.885, P = 0.626) and yield per plant (G = 0.564, P = 0.648). Malik *et al.,*(2000) reported positive correlation between siliqua per plant and seed yield. Whereas the insignificant and positive interaction was found in number of seed per siliqua (G = 0.950, P = 0.287) (Table 4 & 5). Insignificant association of these traits indicated that the association between these traits were largely influenced by environmental factors. Tyagi *et al.,* (2001) reported that number of seed per siliqua had positive and insignificant effect on seed yield per plant.

4.4.9 Siliqua length (cm)

Siliqua length showed insignificant and negative correlation with number of seeds per siliqua (G=-0.260, P=-0.185) indicated that the traits were governed by same gene and simultaneous improvement would be effective. It also showed insignificant and positive correlation with yield per plant (G=0.195, P=0.126) (Table 4 & 5). Indicated that if siliqua length increased then yield per plant decreased. Nasim *et al.,* (1994) reported that seed yield per plant was significantly and negatively with siliqua length.

4.4.10 Number of seeds per siliqua

Number of seeds per siliqua showed insignificant and positive interaction with thousand seed weight (G = -0.314, P 0.069). 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. However, it had insignificant and positive interaction with yield per plant (G = 0.312, P = 0.258) (Table 4 & 5). Insignificant association of these traits indicated that the association between these traits is 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.

4.4.11 Thousand seed weight

Thousand seed weight showed insignificant and positive interaction with yield per plant (G=0.237, P=0.162) (Table 4 & 5). Insignificant association of these traits indicated that the association between these traits were largely influenced by environmental factors. Saini and Kumar (1995) and Olsson (1990) found positive associations which supported the results. Tuncturk and Ciftci (2007) reported positive correlation between seed yield with 1000-seed weight which did not support the present findings.

4.5 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 1st flowering, days to 50% flowering, days to 80% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, length of siliqua (cm), number of seeds per siliqua and thousand-seed weight (gm) were causal (independent) variables. Estimation of direct and indirect effect of path co-efficient analysis for *Brassica napus* is presented in Table 6.

4.5.1 Days to 1st flowering

Path co-efficient analysis revealed that, days to 1st flowering had positive direct effect (0.2717) on yield per plant. Days to 50% flowering (0.4193), days to 80% flowering (0.9135), days to maturity (0.2494), number of secondary branches per plant (0.0727), number of siliqua per plant (0.0187) and length of siliqua (cm) (0.0011) had positive direct effect on yield per plant. Plant height (cm) (-0.1367), number of primary branches (-0.1367), and

number of seeds per siliqua (-0.0142) and thousand-seed weight (gm) (-0.0110) had negative direct effect on yield per plant (Table 6). Chauhan and Singh (1995) revealed that days to 50% flowering had positive direct effect on yield per plant.

Table 6. Path coefficient analysis showing Direct (Diagonal) and indirect effects of different characters on yield of *Brassica napus* L.

Characters	Days to 1st flowering	Days to 50% flowering	Days to 80% flowering	Days to maturity	Plant height(cm)	Number of primary branches per plant	Number of secondary branches per plant	Number of siliquae per plant	Length of siliqua (cm)	Number of seeds per siliqua	Thousand-seed weight (gm)	Genotypic correlation with yield
Days to 1st flowering	**0.2717**	0.4193	0.9135	0.2494	-0.1367	-0.1400	0.0727	0.0187	0.0011	-0.0142	-0.0110	0.1825
Days to 50% flowering	0.2686	**0.4225**	0.9175	0.2511	-0.1352	-0.1403	0.0733	0.0187	0.0015	-0.0140	-0.0108	0.1823
Days to 80% flowering	0.2682	0.4208	**0.9210**	0.2517	-0.1344	-0.1388	0.0718	0.0186	0.0019	-0.0139	-0.0100	0.1849
Days to maturity	0.0470	0.2049	0.4669	**0.2842**	-0.1244	-0.1396	0.0705	0.0140	0.0048	0.0150	-0.0231	0.3435**
Plant height(cm)	0.3524	0.3893	0.3978	0.7560	**-0.2113**	-0.1318	0.0688	0.0302	-0.0178	-0.0164	0.0282	0.3065**
Number of primary branches per plant	-0.1583	-0.2440	-0.9318	0.6439	0.1000	**-0.2784**	0.1019	0.0078	-0.0074	0.0140	-0.0342	0.2901*
Number of secondary branches per plant	0.7099	0.9878	0.2224	0.4382	0.0703	0.1373	**0.2067**	0.0282	-0.0240	-0.0187	0.0401	0.3581**
Number of siliquae per plant	0.6764	0.7041	0.6101	0.1945	0.0691	-0.0235	0.0633	**0.0922**	-0.0044	0.0010	0.1723	0.4966**
Length of siliqua (cm)	-0.1255	-0.1722	-0.4713	-0.0840	-0.0507	-0.0280	0.0671	0.0055	**-0.0740**	-0.0063	0.0286	0.0255
Number of seeds	0.6927	0.7055	0.5819	0.2787	-0.0500	-0.0563	0.0556	-0.0013	-0.0067	**-0.0693**	0.0254	0.0075

per siliqua												
Thousand-seed weight (gm)	0.2058	0.2054	0.4030	-0.0668	0.0134	0.0215	-0.0186	0.0358	0.0048	-0.0040	**0.4440**	0.4219

Residual Effect (R) = 0.2729

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

4.5.2 Days to 50% flowering

Path co-efficient analysis revealed that, days to 50% flowering had positive direct effect (0.4225) on yield per plant. Days to 1st flowering (0.2686), days to 80% flowering (0.9175), days to maturity (0.2511), number of secondary branches per plant (0.0733), number of siliqua per plant (0.0187) and length of siliqua (cm) (0.0015), had positive direct effect on yield per plant, plant height(cm) (-0.1352), number of primary branches (-0.1403), number of seeds per siliqua (-0.0140) and thousand-seed weight (gm) (-0.0108) had negative direct effect on yield per plant (Table 6). Chauhan and Singh (1995) revealed that days to 50% flowering had positive direct effect on yield per plant.

4.5.3 Days to 80% flowering

Path co-efficient analysis revealed that, days to 80% flowering had positive direct effect (0.9210) on yield per plant. Days to 1st flowering (0.2682), days to 50% flowering (0.4208), days to maturity (0.2517), number of secondary branches per plant (0.0718), number of siliqua per plant (0.0186) and length of siliqua (cm) (0.0019) had positive direct effect on yield per plant. Plant height (cm) (-0.1344), number of primary branches (-0.1388), number of seeds per siliqua (-0.0139) and thousand-seed weight (gm) (-0.0100) had negative direct effect on yield per plant (Table 6). Chauhan and Singh (1995) revealed that days to 80% flowering had positive direct effect on yield per plant.

4.5.4 Days to maturity

Path co-efficient analysis revealed that, days to maturity had positive direct effect (0.2842) on yield per plant. This trait had positive indirect effect through days to 1st flowering (0.0470), days to 50% flowering (0.2049), days to 80% flowering (0.4669), number of secondary branches per plant (0.0705), number of siliqua per plant (0.0140), length of siliqua (cm) (0.0048) and number of seeds per siliqua (0.0150). On the other hand, days to maturity had negative indirect effect via plant height (cm) (-0.1244), number of primary branches (-0.1396) and thousand-seed weight (gm) (-0.0231) (Table 6). Rashid (2007) revealed that days to maturity had positive direct effect on yield.

4.5.5 Plant height

Path analysis revealed that plant height had negative direct effect (-0.2113) on yield per plant. It had positive indirect effect on days to 1st flowering (0.3524), days to 50% flowering (0.3893), days to 80% flowering (0.3978), days to maturity (0.7560), number of secondary branches (0.0688), number of siliqua per plant (0.0302) and thousand-seed weight (gm) (0.0282) (Table 6). Varshney (1986) worked with several strains of *Brassica rapa* and observed that plant height had the negative direct effect on yield. On the other hand, plant height had negative indirect effect via number of primary branches per plant (-0.1318), length of siliqua (cm) (-0.0178) and number of seeds per siliqua (-0.0164) (Table 6). 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.

4.5.6 Number of primary branches per plant

Number of primary branches per plant had the negative direct effect on yield per plant (-0.2784). This trait had positive indirect effect on days to maturity (0.6439), Plant height (cm) (0.1000), number of secondary branches per plant (0.1019), number of siliqua per plant (0.0078) and number of seeds per siliqua (0.0140) . On the other hand, plant height had negative indirect effect via 1st flowering (-0.1583), days to 50% flowering (-0.2440), days to 80% flowering (-0.9318), length of siliqua (cm) (-0.0074) and thousand-seed weight (gm) (-0.0342) (Table 6). Mahla *et al.,* (2003) and Singh *et al.,*(2001) reported that number of primary branches per plant had direct positive effect on seed yield.

4.5.7 Number of secondary branches per plant

Path co-efficient analysis revealed that number of secondary branches had positive direct effect (0.2067) on yield per plant. It had positive indirect effect via days to 1st flowering (0.7099), days to 50% flowering (0.9878), days to 80% flowering (0.2224), days to maturity (0.4382), plant height(cm) (0.0703), number of primary branches (0.1373), number of siliqua per plant (0.0282) and thousand-seed weight (gm) (0.0401). On the other hand, plant height had negative indirect effect via length of siliqua (cm) (-0.0240) and number of seeds per

siliqua (-0.0187) (Table 6). 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.

4.5.8 Number of siliqua per plant

Path co-efficient analysis revealed that number of siliqua per plant had the positive direct effect (0.0922) on seed yield followed by positive indirect effect on via days to 1st flowering (0.6764), days to 50% flowering (0.7041), days to 80% flowering (0.6101), days to maturity (0.1945), plant height(cm) (0.0691), number of secondary branch (0.0633), number of seeds per siliqua (0.0010) and thousand-seed weight (gm) (0.1723). This trait had negative indirect effect on yield via number of primary branches (-0.0235), length of siliqua (cm) (-0.0044) (Table 6). This trait had significant positive genotypic correlation 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.

4.5.9 Length of siliqua

Path analysis revealed that length of siliqua had direct negative effect (-0.0740) on yield per plant. This trait had also indirect positive effect on number of secondary branch (0.0671), number of siliqua per plant (0.0055) and thousand-seed weight (gm) (0.0286). On the other hand, length of siliqua showed indirect negative effect on days to 1st flowering (-0.1255), days to 50% flowering (-0.1722), days to 80% flowering (-0.4713), days to maturity (-0.0840), plant height (cm) (-0.0507), number of primary branches (-0.0280) and number of seeds per siliqua (-0.0063) (Table 6). Hence, selection should be practiced for this trait which had longer siliqua in order to improve seed yield. Han (1990) and Singh *et al.,* (1985) reported that siliqua length had negative direct effect on yield per plant.

4.5.10 Number of seeds per siliqua

Path analysis revealed that number of seeds per siliqua had direct negative effect (-0.0693) on yield per plant. This trait had also indirect positive effect on days to 1st flowering (0.6927),

days to 50% flowering (0.7055), days to 80% flowering (0.5819), days to maturity (0.2787), number of secondary branches per plant (0.0556) and thousand seed weight (0.0254). On the other hand, this trait showed indirect negative effect on plant height (cm) (-0.0500), number of primary branches per plant (-0.0563), number of siliqua per plant (-0.0013) and length of siliqua (cm) (-0.0013) (Table 6). The negative direct effect was mainly counter balanced by indirect positive effect of different characters. 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.

4.5.11 Thousand seed weight

Thousand seed weight had positive direct effect on yield per plant (0.4440) and positive indirect effect on plant height (0.0282), number of secondary branch (0.0401), number of siliqua per plant (0.1723), siliqua length (0.0286) and number of seed per siliqua (0.0254) (Table 11).On the other hand, this trait showed negative indirect effect on days to 1st flowering (-0.0110), days to 50% flowering (-0.0108), days to 80% flowering (-0.0100), days to maturity (-0.0231) and number of primary branches per plant (-0.0342) (Table 6). Siddikee (2006) reported that thousand seed weight had the highest positive direct effect on seed yield per plant. Kudla (1993) reported that thousand seed weight had positive direct effect on seed yield.

4.6 Genetic diversity of the *Brassica napus L.*

Genetic diversity was analyzed using GENSTAT software program. Genetic diversity analysis involves several steps i.e. estimation of distance between the varieties, clustering and analysis of inter-cluster distance. Therefore, more than one multivariate technique was required to represent the results more clearly and it was obvious from the results of many researchers Rameeh (2011) *Brassica napus L.* multivariate techniques were used.

4.6.1 Construction of scatter diagram

Based on the values of principal component scores 2 and 1 obtained from the principal component analysis, a two dimensional scatter diagram (Z_1-Z_2) using component score 1 as

X-axis and component score 2 as Y-axis was constructed, which has been presented in Figure 4. The position of the genotypes in the scatter diagram was apparently distributed into five groups, which indicated that there existed considerable diversity among the genotypes.

4.6.2 Principal Component Analysis (PCA)

D^2 analysis through non-hierarchical clustering had taken care of simultaneous variation in all the characters under study. The distribution of genotypes in different clusters of the D^2 analysis has followed similar trend of the Z_1 and Z_2 vectors of the principal component analysis. The D^2 and principal component analysis were found to be alternative methods in giving the information regarding the contribution of characters towards divergence of rapeseed and mustard.

Generally genetic diversity is associated with geographical diversity but the former is not necessarily directly related with geographical distribution. The genotype within the same cluster although formed specific clusters were collected or originated from different places which indicated the geographical distribution and genetic divergence did not follow the same trend. In the present study pattern of clustering revealed that genotypes originating from the same country did not form a single cluster. The genotypes originating from different countries were grouped in the same cluster. This indicated that geographic diversity was not related to genetic diversity, which might be due to continuous exchange of genetic materials among the countries of the world.

Principal components were computed from the correlation matrix and genotype scores obtained from first components and succeeding components with latent roots greater than the unity contribution of the different morphological characters towards divergence were discussed from the latent vectors of the first two principal component. The Principal Component Analysis yielded Eigen values of each principal component axes with the first axes totally accounting for the variation among the genotypes, while three of these with Eigen values above unity accounted for 42.77%. The first two principal axes accounted for 57.07% of the total variation among the 12 characters describing 40 lines (Table 7). Based on principal component axes I and II, a two dimensional chart (Z_1-Z_2) of the cultivars are

presented in Figure 4. The scattered diagram revealed that apparently there were mainly five clusters.

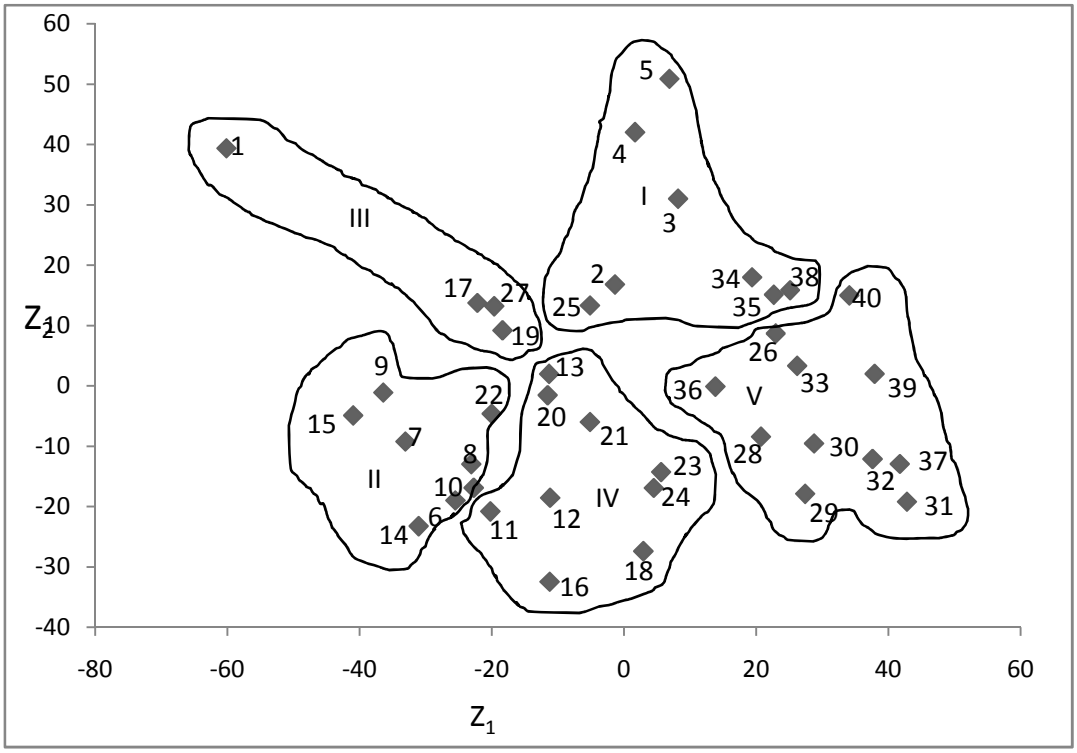


Figure 4. Scattered distribution of 40 *Brassica napus L.* genotypes on principal component score superimposed with clustering

In vector I (Z_I) obtained from PCA, the important characters responsible for genetic divergence in the axis of differentiation were days to 50% flowering (5.132), plant height (0.756), secondary branches per plant (0.578) and siliqua per plant (0.429). In vector II (Z_2), the second axis of differentiation, primary branches per plant (0.711), number of seeds per siliqua (0.031), siliqua per plant (0.429) and thousand seeds weight were important because all these characters had positive signs. On the other hand days to maturity, primary branches per plant, siliqua length, seed per siliqua, thousand seed weight and seed yield per plant in the first axis of differentiation and days to maturity, siliqua length and seed yield per plant in the second axis of differentiation had a minor role in the genetic divergence because they had positive signs. Leaf length and siliqua per plant in both the vectors had positive signs, which indicated they were the important component characters having higher contribution to the genetic divergence among the materials studied.But factorial discriminate and Mahalanobis's D^2 distance methods required collecting data plant by plant, while the PCA method required taking data by plots.

Among five clusters, cluster I was composed of eight lines; G2, G3, G4, G5, G25, G34, G35 and G38 (Table 8). From the clustering mean value (Table 9), it was observed that cluster I composed of days to 1st flowering (58.54 days), days to 50% flowering (60.75 days), days to 80% flowering (63.50 days), days to maturity (105.14 days), plant height (107.99 cm), number of primary branch per plant (3.49), number of secondary branch per plant (4.20), siliqua per plant (146.19), siliqua per length (7.49 cm), seed per siliqua (22.99), thousand seed weight (3.39 gm) and seed weight per plant (11.72 gm) (Table 8). Here the highest mean for siliqua per plant (146.19) followed by plant height (107.99 cm) and days to maturity (105.14 days). Cluster II was composed of eight lines; G6, G7, G8, G9, G10, G14, G15 and G22 (Table 8). These genotypes produced the highest mean for siliqua per plant (157.48) (Table 9). Cluster III was constituted of four lines; G1, G17, G19, and G27 (Table 8). The genotypes of this cluster produced the highest mean for siliqua per plant (130.25) and the lowest value for number of primary branches per plant (3.12).

Table 7. Eigen values and percentage of variation in respect of 12 characters in *Brassica napus L.*

Principal component axis	Eigen values	% of total variation accounted for	Cumulative percent
I	5.132	42.77	42.77
II	1.716	14.3	57.07
III	1.452	12.1	69.17
IV	0.965	8.04	

			77.21
V	0.756	6.3	83.51
VI	0.711	5.93	89.44
VII	0.578	4.81	94.25
VIII	0.429	3.58	97.83
IX	0.228	1.9	99.73
X	0.031	0.26	99.99
XI	0	0	99.99
XII	0	0	99.99

Table 8. Distribution of 40 *Brassica napus L.* genotypes in five different clusters

Cluster	Total no. of line	Genotype Number	Genotype Designation
I	8	G2, G3, G4, G5, G25, G34, G35, G38	Nap-0733-1, Nap-0762, Nap-08-4, Nap-0837, Nap-2013, Nap-2057, Nap-2037, Nap-179
II	8	G6,G7, G8, G9, G10, G14, G15, G22	Nap-0865, Nap-0869, Nap-0876, Nap-0885, Nap-205, Nap-10009, Nap-10015, Nap-10012
III	4	G1, G17, G19, G27	Nap-0717-2, Nap-10019, Nap-1005, Nap-9906
IV	9	G11, G12, G13, G16, G18, G20, G21, G23, G24	BARI-8, BARI-13, Nap-10007,Nap-10017, Nap-10020, Nap-1007, Nap-10014, Nap-0130, Nap-2012
V	11	G26, G28, G29, G30, G31, G32, G33, G36, G37, G39, G40	Nap-2022, Nap-9908, Nap-248, Nap-2001, Nap-9901, Nap-9904, Nap-9905, Nap-206, Nap-2066, Nap-94006, Nap-108

Cluster IV constituted of nine genotypes lines; G11, G12, G13, G16, G18, G20, G21, G23 and G24 (Table 8). The line produced the highest mean for siliqua per plant (173.14) and the lowest value for number of primary branches per plant (3.25) (Table 9). Cluster V constituted of 11 genotypes; line G26, G28, G29, G30, G31, G32, G33, G36, G37, G39 and G40 (Table 8). The genotypes of this cluster produced the highest mean values for siliqua per plant (181.39) (Table 9). Jagadev *et al*., (1991) showed the maximum genetic distance in between cluster III and IV suggesting wide diversity in rapeseed and mustard.

4.6.3 Canonical Variety Analysis

Canonical Variety Analysis was performed to compute the inter-cluster Mahalanobis's values. Statistical distances represent the index of genetic diversity among the clusters. The average intra and inter-cluster distance (D^2) values were presented in Table 10. Results indicated that the highest inter-cluster distance was observed between II and V (8.145), followed by between I and II (7.767), III and V (7.434). The lowest inter-cluster distance was observed between the cluster II and IV (3.917) followed by I and V (3.958), II and III (5.308) suggesting a close relationship among these clusters (Table 10). The inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups (Table 10).

Rameeh (2011) obtained larger inter-cluster distances than the intra-cluster distances in a multivariate analysis. Uddin (1994) obtained larger inter-cluster distances in the multivariate analysis in mustard. Khan (2000) reported similar results in raya. Lower intra-cluster

distances in all the eight clusters indicated the genotypes within the same cluster were closely related. Srivastav *et al.,* (2000) reported the lowest intra-cluster D^2 value in Indian mustard.

However, the maximum inter-cluster distance was recorded between cluster II and V (8.145) followed by between I and II (7.767), III and V (7.434) (Table 10). Genotypes from these clusters if involved in hybridization might produce a wide range of segregating population, as genetic variation was very distinct among these groups. The inter-cluster divergence varied from 0.304 to 0.420 maximum being from cluster

Table 9. Cluster means for 12 characters of 40 *Brassica napus L.* lines

Characters	Cluster				
	I	II	III	IV	V
Days to 1st flowering	58.54	32.58	39.58	42.89	57.82
Days to 50% flowering	60.75	34.58	41.58	44.89	59.82
Days to 80% flowering	63.50	37.25	44.25	47.56	62.55
Days to maturity	105.14	85.48	88.38	90.81	102.85
Plant height (cm)	107.99	90.39	98.69	92.55	118.63
No. of primary branch/plant	3.49	2.97	3.12	3.25	3.45
No. of secondary branch/plant	4.20	3.96	3.93	4.16	4.82
Siliqua/Plant	146.19	157.48	130.25	173.14	181.39
Siliqua/length (cm)	7.49	7.43	7.62	7.62	7.49

Seed/Siliqua	22.99	21.76	24.27	22.62	22.99
Seed weight (1000) gm	3.39	3.33	3.46	3.63	3.53
Weight of plant seed (gm)	11.72	12.35	11.46	11.89	11.68

Table 10. Average intra and inter-cluster distances (D^2) for 40 *Brassica napus L.*

lines

Cluster	**I**	**II**	**III**	**IV**	**V**
I	**0.420**	7.767	5.331	6.563	3.958
II		**0.384**	5.308	3.917	8.145
III			**0.414**	5.728	7.434
IV				**0.398**	6.116
V					**0.304**

*Bold figures denotes intra-cluster distance

V which comprised of 11 cultivars of diverse origin, while the minimum distance was observed in cluster III which comprised only four lines (Table 10).Similar results were obtained by Anand and Rawat (1984) in brown mustard. Verma and schan (2000) observed

no parallelism between geographic and genetic diversity. Gupta *et al.,* (1987) showed no correlation between geographic and genetic diversity. Mitra and Saini (1998) reported no evidence for any correlation between genetic divergence and geographic diversity. Chatterjee and Khare (1991) studied a negative relationship between geographic and genetic diversity. Results obtained from different multivariate techniques were superimposed in Figure 4 from which it might be concluded that all the techniques gave more or less similar results and one technique supplemented and confirmed the results of another one. The clustering pattern of the lines revealed that varieties/lines originating from the same places did not form a single cluster because of direct selection pressure.It has been observed that geographic diversity is not always related to genetic diversity and therefore, it is not adequate as an index of genetic diversity. Verma and Sachan (2000) studied that genetic drift and selection in different environment could cause greater diversity than geographic distance.

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

4.6.4 Non – hierarchical clustering

The computation from co-variance matrix gave non-hierarchical clustering among 40 genotypes. By application of non- hierarchical clustering using covariance matrix, the 40 *Brassica napus L.* genotypes were grouped into five different clusters. These results confirmed the clustering pattern of the lines according to the Principal Component Analysis. So, the results obtained through PCA were confirmed by non-hierarchical clustering. Compositions of different clusters with their corresponding lines included in cluster were presented in Table 8. Cluster V had maximum 11 lines followed by cluster I, II, IV, and III,

which had eight, eight, nine and four genotype respectively. Cluster III composed of five lines; G1, G17, G19, G27. Verma and Sachan (2000) reported 12 clusters; Gupta *et al.,* (1991) five clusters; Khan (2000) seven clusters and Srivastav and Singh (2002) six clusters in rapeseed and mustard. These results confirmed the clustering pattern of the genotypes according to the principal component analysis.

From the clustering mean value (Table 9), observed that cluster I produced the highest mean for days to 1st flowering (58.54 days), days to 50% flowering (60.75 days), days to 80% flowering (63.50 days), days to maturity (105.14 days), plant height (107.99 cm), number of primary branch per plant (3.49), number of secondary branch per plant (3.49), siliqua per plant (146.19), siliqua per length (7.49 cm), seed per siliqua (22.99), thousand seed weight (3.39 gm) and seed weight per plant (11.72 gm). Photograph showing seed, siliqua and plant of the different genotypes of this cluster has been presented in Plate 7-9. Verma and Sachan (2000) studied 20 genotypes of *Brassica napus L.* for the yield contributing characters and indicated that fruits/plant, secondary branches/plant and plant height are important traits for the selection of superior genotypes.

Cluster II was composed of eight lines; G6, G7, G8, G9, G10, G14, G15 and G22. These genotypes produced the highest mean for seed weight per plant (12.35 gm). Photograph showing seed, siliqua and plant of the different genotypes of this cluster has been presented in Plate 10-12.

Cluster III was constituted of four lines; G1, G17, G19, and G27. The genotypes of this cluster produced the highest mean for siliqua per length (7.62 cm), seed per siliqua (24.27) and lowest value for number of secondary branch per plant (3.93) and siliqua per plant (130.25). Photograph showing seed, siliqua and plant of the different genotypes of this cluster had been presented in Plate 13-15.

Cluster IV constituted of nine genotypes, lines; G11, G12, G13, G16, G18, G20, G21, G23 and G24. The line produced the highest mean for siliqua per length (7.62 cm), yield per plant

(11.89 gm) and lowest value for plant height (92.55 cm). Photograph showing seed, siliqua and plant of the different genotypes of this cluster has been presented in Plate 16-18.

Cluster V constituted of 11 genotypes, lines; G26, G28, G29, G30, G31, G32, G33, G36, G37, G39 and G40. The genotypes of this cluster produced the highest mean values for plant height (118.63 cm), number of secondary branch per plant (4.82), siliqua per plant (181.39). Photograph showing seed, siliqua and plant of the different genotypes of this cluster has been presented in Plate 19-21.

From the claster mean value it was observed that all the cluster mean values were more or less similar. The maximum range of variability was observed for yield (11.46 g to 12.35 g) among all the characters in five clusters. Cluster II included mainly early flowering and early maturing genotypes with high yield. To develop high yielding varieties/lines, genotypes of this group could be used in hybridization program.


Nap-0733-1


Nap-0762


Nap-08-4


Nap-0837


Nap-2013


Nap-2057


Nap-2037


Nap-179

Plate 7. Photograph showing seed type of the different genotypes of cluster I

Plate 8 (a). Photograph showing siliqua type of the different genotypes of cluster I

Plate 8 (b). Photograph showing siliqua type of the different genotypes of cluster I

Plate 9 (a). Photograph showing plant type of the different genotypes

of cluster I

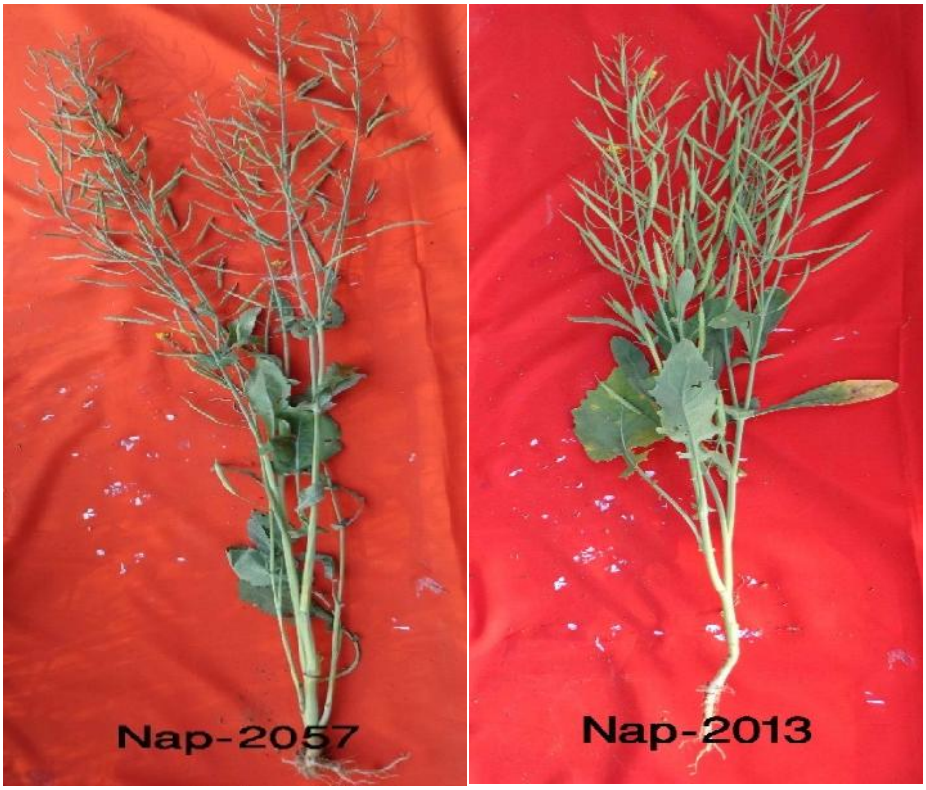


Plate 9 (b). Photograph showing plant type of the different genotypes of cluster I

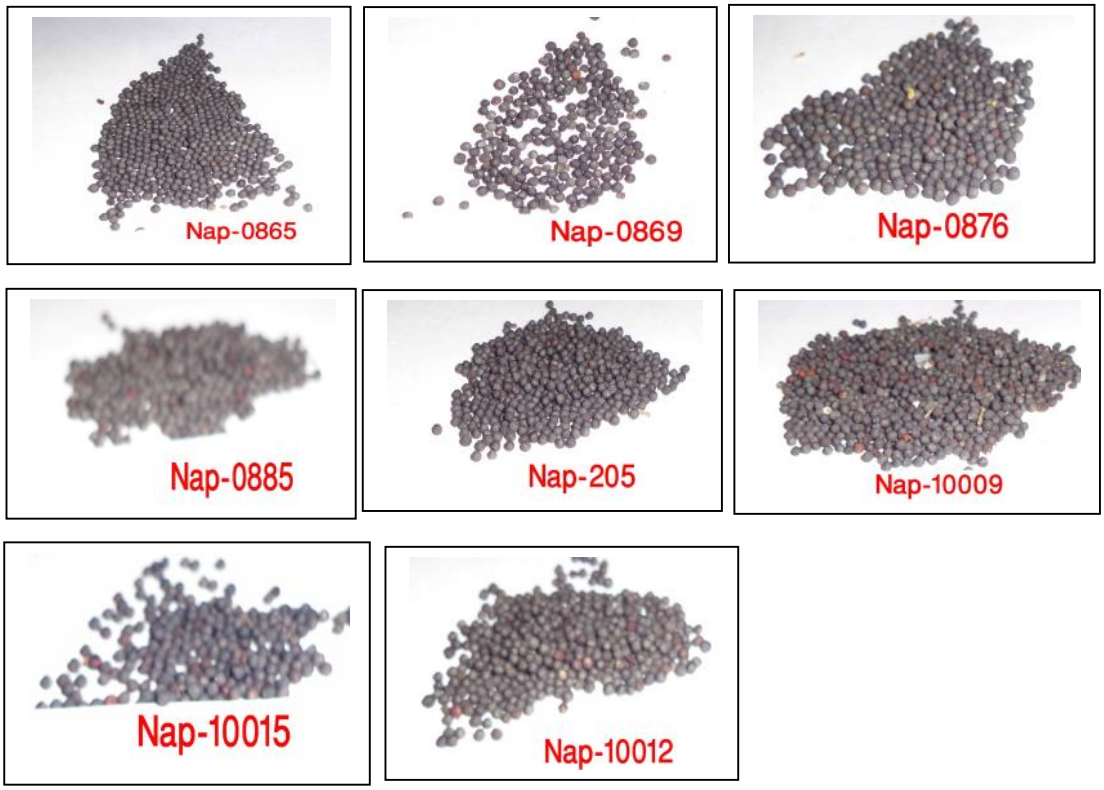


Plate 10. Photograph showing seed type of the different genotypes of cluster II

Plate 11 (a). Photograph showing siliqua type of the different genotypes of cluster II


Nap-10015


Nap-205


Nap-10012


Nap-10009

Plate 11 (b). Photograph showing siliqua type of the different genotypes of cluster II

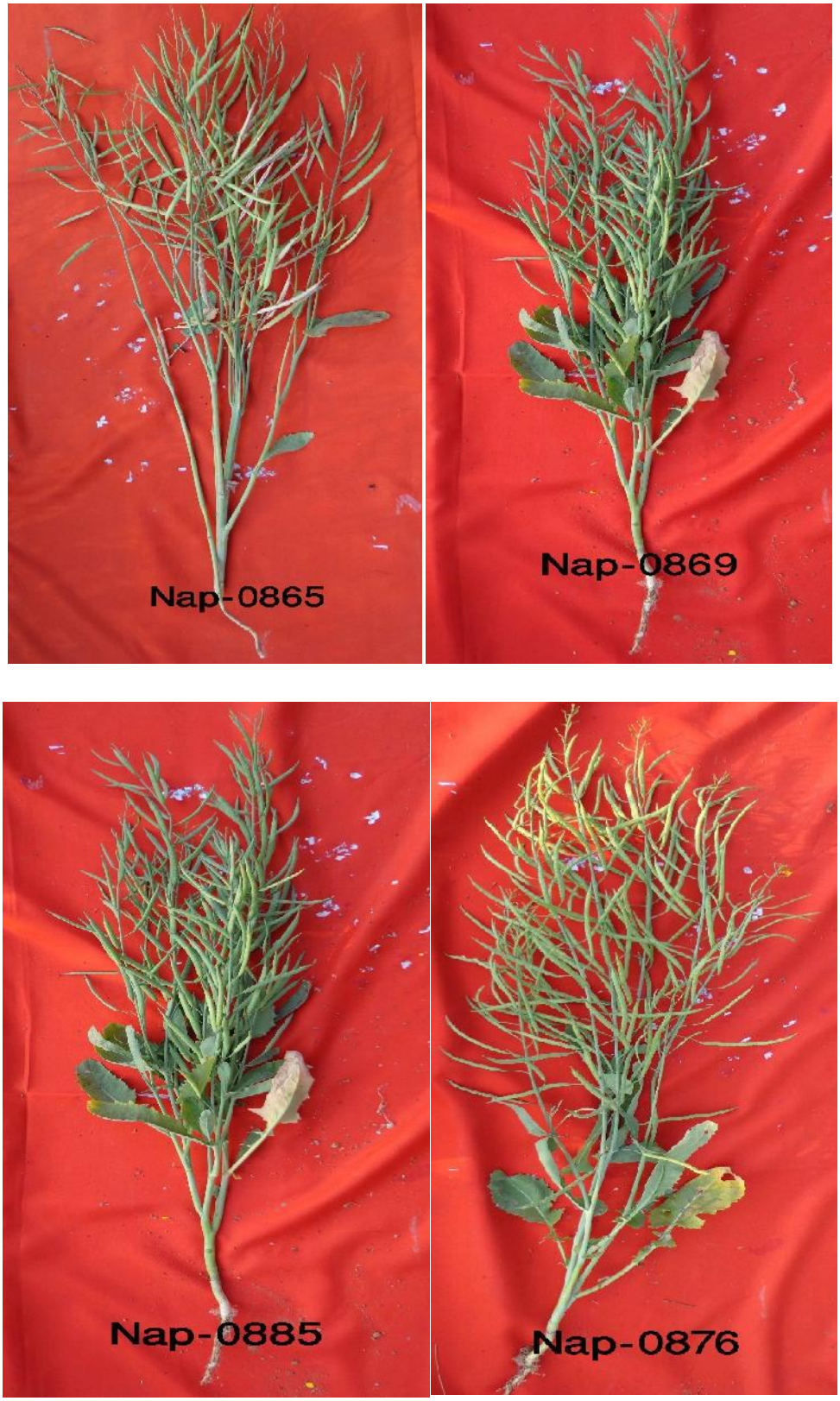


Plate 12(a). Photograph showing plant type of the different genotypes of cluster II


Nap-10009


Nap-205


Nap-10015


Nap-10012

Plate 12(b). Photograph showing plant type of the different genotypes of cluster II

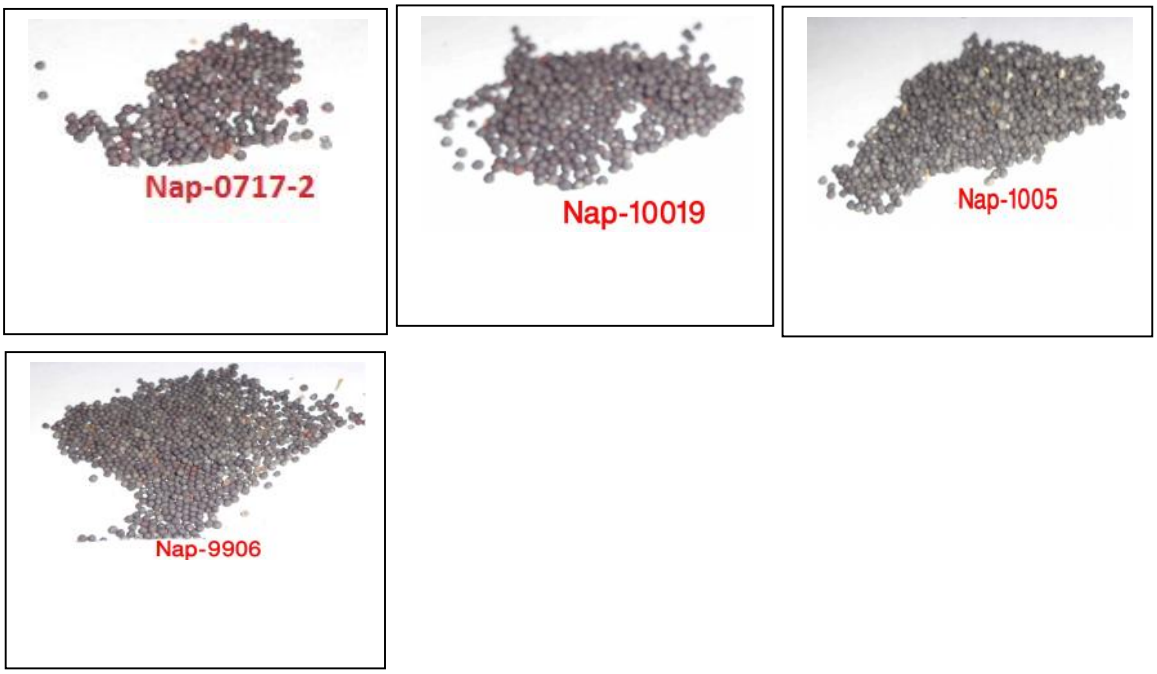


Plate 13. Photograph showing seed type of the different genotypes of cluster III


Nap-0717-2


Nap-10019

Plate 14. Photograph showing siliqua type of the different genotypes of cluster III

Plate 15 (a). Photograph showing plant type of the different genotypes of cluster III

Plate 15(b). Photograph showing plant type of the different genotypes of cluster III

Plate 16. Photograph showing seed type of the genotype of cluster IV


BARI-8
BARI-13

Plate 17(a). Photograph showing siliqua type of the genotype of cluster IV

Plate 17(b). Photograph showing siliqua type of the genotype of cluster IV


BARI-8
BARI-13

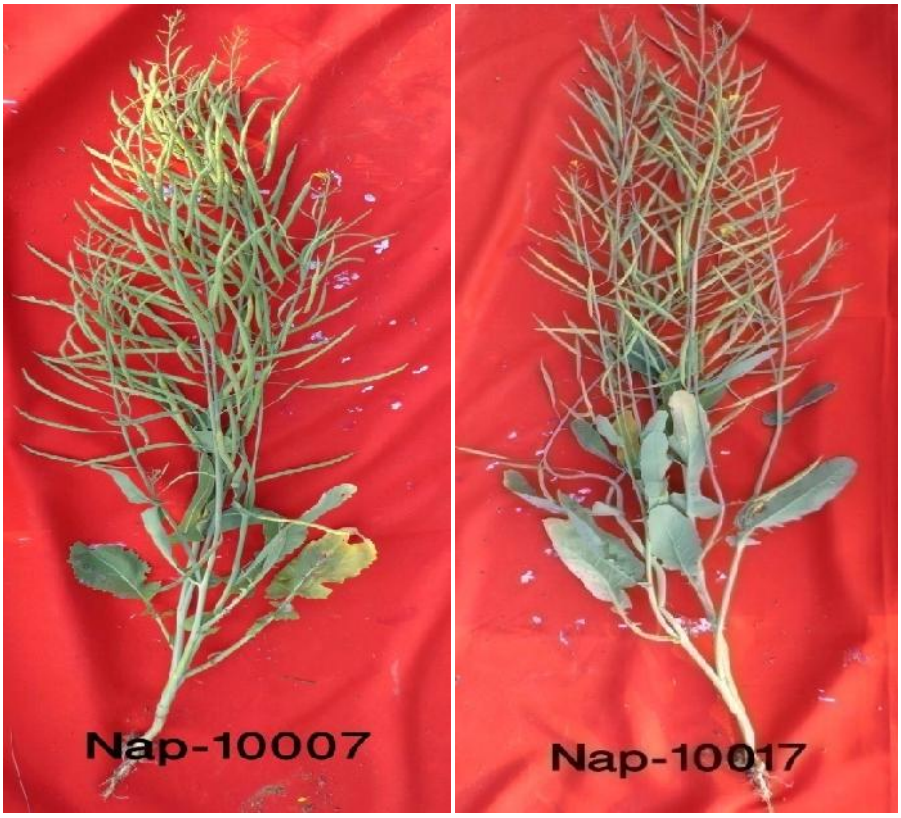
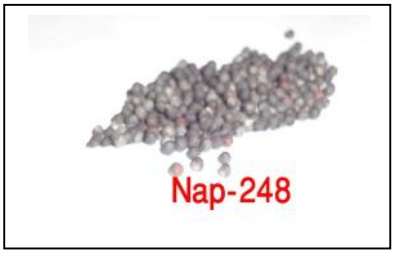


Plate 18(a). Photograph showing plant type of the genotype of cluster IV

Plate 18(b). Photograph showing plant type of the genotype of cluster IV


Nap-2022


Nap-9908


Nap-248


Nap-2001

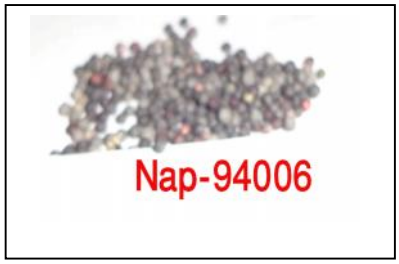

Nap-9901


Nap-9904


Nap-9905


Nap-206


Nap-2066


Nap-94006

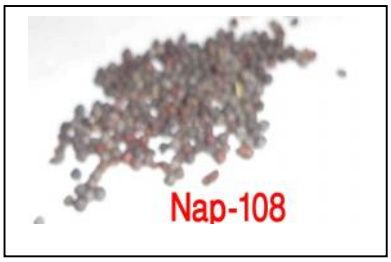

Nap-108

Plate 19. Photograph showing seed ype of the different genotypes of cluster V

Plate 20(a). Photograph showing siliqua type of the different genotypes of cluster V

Plate 20(b). Photograph showing siliqua type of the different genotypes of cluster V


Nap-248


Nap-2022


Nap-9908


Nap-9901


Nap-9904


Nap-2001

Plate 21(a). Photograph showing plant type of the genotype of cluster V

Plate 21(b). Photograph showing plant type of the genotype of cluster V

4.7 Selection of genotypes for future hybridization

Genotypically distant parents are able to produce higher heterosis (Rameeh, 2011) Results of the present studies indicated significant variation among the genotypes for all the characters studied. Number of siliqua per plant, siliqua length and seed weight per plant contributed the maximum towards yield improvement. 40 *Brassica napus L.* genotypes formed five different clusters. PCA and Cluster analysis gave similar results. Generally, diversity was influenced by the morphological characters, but not by the distribution of the genotypes, which indicated the importance of consumer preference and growers suitability. Considering diversity pattern and other agronomic performance lines G5 (Nap-0837), G2 (Nap-0733-1), G37 (Nap-2066), G31 (Nap-9901), G40 (Nap-108) and G11 (BARI- 8) could be considered suitable genotypes for efficient hybridization in future. Involving of such diverse lines in crossing program could produce desirable segregants. So, more or less divergent genotypes are recommended to use as parents in future hybridization program.

CHAPTER V

SUMMARY AND CONCLUSION

The experiment was conducted with 40 *Brassica napus L.* genotypes in the experimental farm of Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh, during the period from November 2013 to March 2014. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Data on various yield attributing characters such as, days to 1st flowering, days to 50% flowering, days to 80% flowering, days to 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 (gm) and seed yield per plant (gm) were recorded.

The analysis of variance showed significant differences among the genotypes for all the characters.From the mean performance it was observed that the days to 1st flowering, days to 50% flowering, days to 80% flowering and days to maturity were observed the lowest in Nap-10009 and the highest was observed in Nap-0837. The highest plant height was observed in Nap-9901 (136.62 cm) whereas the minimum plant height was observed in BARI-8 (79.57 cm). The highest number of primary branches per plant was observed in Nap-0733-1(4.31) whereas the minimum number of primary branches per plant was observed in Nap-205 (2.7). The number of siliquae per plant was observed the highest in Nap-9901 (197.82) whereas the minimum number of siliquae per plant was observed in Nap-0717-2 (97.94). Length of siliqua was resulted the highest in Nap-108 (8.69 cm) whereas the minimum length of siliqua was observed in Nap-205 (6.38cm). The number of seeds per siliqua was observed the highest in Nap-108 (26.37) whereas the minimum number of seeds per siliqua was observed in Nap-10014 (18.24). Thousand seed weight was found the maximum in BARI- 8 (4.19gm) where as the minimum thousand seed weight was found in Nap-10009 (2.84gm). Yield is the most outstanding character and all the research work and objectives are dependent on yield. The highest amount of yield per plant was observed in BARI-8 (14.29 gm) whereas the minimum yield per plant observed in Nap-1007 (8.58 gm).

Number of siliqua per plant (99.986) exhibited the highest value of heritability while number of primary branches per plant (26.459) exhibited the lowest value of heritability. High

heritability with high genetic advance in percent of mean was observed for number of siliqua per plant and plant height (cm) indicating that these traits were under additive gene control and selection for genetic improvement for these traits would be effective. 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 maturity, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant and seed yield per plant showed higher influence of environment for the expression of these characters. On the other hand, days to 1st flowering, days to 50% flowering, days to 80% flowering, plant height, number of seeds per siliqua, siliqua length and 1000-seed weight showed least difference phenotypic and genotypic variance suggesting additive gene action for the expression of the characters.

Correlation co-efficients among the characters were studied to determine the association between yield and yield components. The significant positive correlation with seed yield per plant were found in days to 1st flowering (G = 0.383), days to 80% flowering (G = 0.738), days to maturity (G= 0.102), number of primary branches per plant (G = 0.816), number of secondary branch (G = 606) and siliqua per plant (G = 0.885). In addition, there were non-significant positive correlation with seed yield per plant was also found in plant height (G = 0.082), number of seeds per siliqua (G = -0.314) and thousand seed weight (G=0.237).

Path co-efficient analysis revealed that days to 1st flowering, days to 50% flowering, days to 80% flowering, days to maturity, number of secondary branches per plant, number of siliqua per plant, and thousand-seed weight (gm) had the positive direct effect on yield per plant, whereas, number of primary branches per plant, plant height, length of siliqua and number of seeds per siliqua had the negative direct effect on yield per plant. The path coefficient studies indicated that plant height, number of primary branches per plant, number of secondary 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.

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 two components with eigen value were greater than unity

contributed a total of 42.77% variation towards the divergence. As per PCA, D^2 and Cluster Analysis, the genotypes were grouped into five different clusters. Cluster I, II, III, IV and V composed of eight, eight, four, nine, and 11 lines respectively. The highest inter-cluster distance was observed between clusters II and V 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 .

Results of the present studies indicated significant variation among the genotypes for all the characters studied. Number of siliqua per plant, siliqua length and seed weight per plant contributed maximum towards yield improvement. 40 *Brassica napus L.* genotypes formed five different clusters. Generally, diversity was influenced by the morphological characters, but not by the distribution of the genotypes, which indicated the importance of consumer preference and growers suitability. Considering diversity pattern and other agronomic performance lines G5 (Nap-0837), G2 (Nap-0733-1), G37 (Nap-2066), G31 (Nap-9901), G40 (Nap-108) and G11 (BARI- 8) could be considered suitable genotypes for efficient hybridization in future. Involving of such diverse. So, divergent genotypes are recommended to use as parents in future hybridization program.

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APPENDICES

Appendix I: 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 II: Monthly average temperature, relative humidity and total rainfall and Sunshine of the experimental site during the period from November, 2013 to April, 2014

Month	**Air temperature (ºc)**		**Relative humidity (%)**	**Rainfall (mm) (total)**	**Sunshine (hr)**
	Maximum	**Minimum**			
November, 2013	34.8	18.0	77	227	**5.8**
December, 2013	32.3	16.3	69	0	**7.9**
January, 2014	29.0	13.0	79	0	**3.9**
February, 2014	28.1	11.1	72	1	**5.7**

March, 2014	33.9	12.2	55	1	**8.7**
April, 2014	**34.6**	**16.5**	**67**	**45**	**7.3**

Source: Bangladesh Meteorological Department (Climate & Weather Division),

Agargoan, Dhaka – 1207.

Apendix III : Principal component score for 40 *Brassica napus L.* genotypes

Genotype no.	Z_1	Z_2
G1.	-60.13	39.37
G2.	-1.38	16.82
G3.	8.17	31.02
G4.	1.66	42.05
G5.	6.85	50.88
G6.	-25.51	-18.96
G7.	-33.06	-9.21
G8.	-23.1	-12.95
G9.	-36.41	-1.1
G10.	-22.74	-16.87
G11.	-20.22	-20.79
G12.	-11.18	-18.53
G13.	-11.35	2
G14.	-31.07	-23.23
G15.	-40.96	-4.89
G16.	-11.26	-32.43
G17.	-22.19	13.76
G18.	2.91	-27.38
G19.	-18.38	9.21
G20.	-11.56	-1.53
G21.	-5.16	-5.98
G22.	-20.02	-4.61
G23.	5.61	-14.26
G24.	4.48	-16.9

G25.	-5.16	13.33
G26.	22.93	8.7
G27.	-19.65	13.21
G28.	20.71	-8.4
G29.	27.38	-17.87
G30.	28.73	-9.52
G31.	42.77	-19.17
G32.	37.57	-12.1
G33.	26.17	3.34
G34.	19.36	18.01
G35.	22.64	15.12
G36.	13.81	-0.1
G37.	41.7	-12.92
G38.	25.11	15.87
G39.	37.88	2.01
G40.	34.06	15.01

Apendix IV : Analysis of variance for 12 characters of *Brassica napus L.*

Source	DF	Mean sum of square											
		DFF	D50F	D80F	DM	PH	NPB	NSB	NSP	LS	NSS	TSW	Yield
Replication	3	4.075	6.342	8.563	9.524	4.879	0.667	0.201	0.08	0.535	0.896	0.294	0.102
Genotypes	40	403.8**	342.1**	312.7**	247.9**	601.2**	0.4**	1.8**	325.4**	0.6**	9.6**	0.3**	3.7**
Error	78	6.451	4.376	3.786	5.011	1.340	0.523	0.089	0.06	0.11	0.048	0.019	0.969

*= Significant at 5 % level of probability, **= Significant at 1 % level of probability, DF= Degrees of freedom, DFF = Days to first flowering, D50F = Days to 50% flowering, D80F = Days to 80% flowering, DM = Days to maturity, PH= Plant height, NPB =No. of primary branches/plant, NSB = No. of secondary branches/plant, NSP = No. of siliquae/plant, LS = Length of siliqua, NSS = No. of seed/siliqua, TSW = Thousand seed weight.