GENETIC VARIATION IN F_7 GENERATION OF *Brassica napus* L.

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CERTIFICATE

This is to certify that thesis entitled, ***"Genetic variation in F_7 generation 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* ***SHANZIDA SULTANA****, Registration No.* ***10-03898*** *under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

Dated: June, 2016
Place: Dhaka, Bangladesh

(Prof. Dr. Md. Sarowar Hossain)
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ABSTRACT

A field experiment was conducted with 50 F_7genotypes of *Brassica napus* L. at the experimental field of Sher-e-Bangla Agricultural University, Dhaka to study the correlation, path coefficient and genetic diversity in F_7 generation during November 2015 to March 2016. The genotypes were found significantly different for all the characters studied. Comparatively phenotypic variances were higher than the genotypic variances for all the characters studied. The high GCV value was observed for number of secondary branches per plant (39.05) per plant. Days to 50% flowering, days to 80% maturity and thousand seed weight, primary branches per plant and seed yield per plant showed broad base heritability. The significant positive correlation with seed yield per plant was found in plant height (0.950**), the number primary branches per plant (0.977**), number of secondary branches per plant (0.665**), number of siliqua per plant (0.950**), No. of seeds per siliqua (0.947**) and thousand seed weight (0.974**).Path co-efficient analysis revealed that days to 50% flowering, days to 80% maturity, number of secondary branch, siliqua length and thousand seed weight had the negative direct effect on yield per plant whereas plant height and siliqua per plant had the positive direct effect on yield per plant. The genotypes were grouped into six clusters. The highest inter cluster distance (113.901) was observed between cluster I and IV and the maximum intra cluster distance (7.44) was found in cluster II. Considering group distance and other agronomic performance genotypes G7, G37 and G50 might be suggested for future hybridization program.

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SOME COMMONLY USED ABBREVIATION

FULL WORD	ABBREVIATION
Agro-Ecological Zone	AEZ
Agricultural	Agril.
And others	*et al.*
Accessions	ACC
Agronomy	Agron.
Analysis of Varience	ANOVA
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Biological	Biol.
Centimeter	cm
Co-efficient of Variation	CV
Ecology	Ecol.
Etcetera	etc.
Environmental Varience	δ^2_e
Figure	Fig
Food and Agricultural Organization	FAO
Genotype	G
Genetic Advance	GA
Genotypic Co-efficient of Variation	GCV
Genotypic Varience	δ^2_g
Gram	g
Heritability in broadsense	h^2b
Journal	J.
Kilogram	Kg
Meter	M
Mean sum of square	MSS
Murate of Potash	MP
Number	No.
Percent	%
Phenotypic Co-efficient of Variation	PCV
Phenotypic variance	δ^2_p
Randomized Complete Block Design	RCBD
Replication	R
Research	Res
Science	*Sci.*
Sher-e-Bangla Agricultural University	SAU

CHAPTER I

INTRODUCTION

Brassica napus L. (genome AACC, 2n=38) is commonly known as Rapeseed. Rapeseed is an important oil seed crop belonging to the family Brassicaceae. *Brassica* is a wide genus of cross pollinated oil crops and also an important genus of plant kingdom consisting of over 3200 species with high diverse morphology. Scientific interest of rapeseed has increased lately for the production of biodiesel to industrial lubricants and hydraulic oils, tensides for detergent, soap production and in manufacturing biodegradable plastics. The primary centre of origin for *Brassica napus* is near the Himalayan region and the secondary centre of origin is located in the European-Mediterranean area and Asia (Downy and Robelen, 1989). Major producing regions are China, the Indian subcontinent, Canada and Northern Europe (Ram and Hari, 1998).

Various species of *Brassica* are grown in Bangladesh. The genomic constitutions of the three diploid elemental species of *Brassica* are AA for *Brassica campestris*, BB for *Brassica nigra*, CC for *Brassica olerecea* having diploid chromosome number of 20, 16 and 18 respectively. Apart from this, the species *Brassica juncea* (AABB), *Brassica carinata* (BBCC) and *Brassica napus*(AACC) are the amphidiploids. Approximately, 70% of the total cultivated mustard in Bangladesh is the variety of either *Brassica rapa* or *Brassica napus. Brassica napus* L (AACC, 2n=38) is said the rape seed group of *Brassica.*

Brassica oil crops are the most important group of species that supply major edible oil in Bangladesh (BBS, 2011a). Mustard and rapeseed seeds contain 40%-45% oil, 25% protein (BBS, 2011b). Rape seed and mustard is the third highest source of edible oils supply in the world after soybean and palm. 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.

It occupies the 1st position in respect of area and production among the oil crops grown in Bangladesh. In Bangladesh, 252238.13 ha of land was under rapeseed cultivation (which is 77.71% of total oilseed cultivating area) during 2014-15 which produced about 246494 tons of seed and average yield was 0.977 ton per ha (BBS, 2015a). Bangladesh is deficit in edible oil, which costs valuable foreign currency for importing seeds and oil. Annually country is producing about 832638.72 tons of edible rapeseed oil as which is very low against the requirement (BBS, 2015b). Bangladesh imports 89970.08 tons of edible oil to meet up the annul requirement of the country in the year of 2014-15, which costs 3718457000 Tk. (BBS, 2015c).

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 the 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, 1995). 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 study the genetic variability in F_7 generation for selection of desired plant types.
- To study the interrelationships of yield contributing characters among themselves and with seed yield and their direct and indirect effects,
- To assess the contribution of different traits towards divergence, and
- To select promising genotypes considering early maturity, high yielding plants.

CHAPTER II
REVIEW OF LITERATURE

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

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

2.1. Genetic variability, heritability and genetic advance

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

Begum (2015), conducted an experiment by using some backcross generations to study genetic variability. The result revealed that seed yield per plant exhibits the highest value of heritability while days to 50% flowering exhibits the lowest value of heritability. High heritability with high genetic advance in percent of mean was observed for number of primary branches per plant, number of secondary

branches per plant, number of siliqua per plant, number of seed per siliqua, thousand seed weight and seed yield per plant.

Siddika (2015) carried out an experiment by using F_2 generation of some advanced *Brassica napus* L. lines. The result revealed that days to first flowering, plant height, length of siliqua, number of seeds per siliqua, thousand seeds weight, exhibited low genotypic and phenotypic co-efficient of variation. Number of primary branches per plant, number of secondary branches per plant, yield per plant and number of siliqua per plant showed moderate genotypic and phenotypic coefficient of variation. Days to first flowering, number of secondary branches per plant and 1000 seed weight showed high heritability with high genetic advance and genetic advance in percentage of mean.

A study was undertaken by Billal (2015) to evaluate some indigenous rapeseed genotypes for adaptability and yield traits in the agro-climatic condition of Mansehra. These genotypes were evaluated in randomized complete block design with three replications. Heritabilities (broad sense) were moderate to high in magnitude for all traits. 1000-seed weight exhibited significant ($p \leq 0.01$) differences validating the presence of genetic variation among the tested accessions. Greater variability among the accessions for 1000-seed weight was observed.

An experiment was carried out by Shakera (2014) and the result revealed that among twenty F_3 and F_4 progenies for most of the characters wide range of variation observed. In case of days to Plant height and number of siliqua per plant showed higher influence of environment for the expression of these characters. Number of secondary branches per plant, number of siliqua per plant, and yield per plant showed high genotypic and phenotypic coefficient of variation. Days to 50% flowering, days to maturity, plant height and siliqua length exhibited low genotypic and phenotypic coefficient of variation.

Parvin (2015) carried out an experiment by using BC_1F_4 materials of some advanced line of *Brassica napus* L. The result revealed that plant height (cm) and number of siliqua per plant moderate difference between genotypic and phenotypic variance where days 1st flowering, number of primary branches per plant, number of secondary branches per plant, siliqua length (cm), number of seeds per siliqua, 1000 seed weight (g) and yield per plant showed minimum difference between genotypic and phenotypic variance which indicated low environmental influence on these traits. Days to first flowering, number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua, thousand seed weight exhibited low genotypic and phenotypic co-efficient of variation. Plant height and siliqua length (cm) showed moderate genotypic and phenotypic coefficient of variation. Plant height (cm), number of primary branches per plant, siliqua length (cm), number of seeds per siliqua, 1000 seed weight (g) and yield per plant showed high heritability with high genetic advance and genetic advance in percentage of mean.

An experiment was carried out by Nabi (2014) the result showed that seed yield per plant exhibits the highest value of heritability while thousand seed weight exhibits the lowest value of heritability. High heritability with high genetic advance in percent of mean was observed for number of siliqua per plant, plant height, seed per siliqua and siliqua length indicating that these traits were under additive gene control and selection for genetic improvement for these traits would be effective. High heritability with moderate genetic advance in percent of mean was observed for primary branch and secondary branch indicating medium possibility of selecting genotypes. High heritability with low genetic advance in percent of mean was observed for day to 50% flowering and 80% maturity also observed in this experiment.

Helal *et al*. (2014) conducted an experiment to study Genetic variability, correlation of yield and yield contributing characters and coefficient of variance in

rapeseed or mustard. The results revealed that varieties produced the highest seed yields and 15% variation at genotypic and phenotypic level.

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

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

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

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.

A field experiment was conducted by Mili (2014) using 66 F_5 genotypes of *Brassica napus* L. to study the genetic diversity, variability. The genotypes were found significantly variable for most of the characters. Comparatively phenotypic variances were higher than the genotypic variances for all the characters studied. Also PCV were higher than the GCV for all the characters studied. Number of secondary branch, thousand seed weight, number of primary branch, number of siliqua per plant and seed yield per plant showed high broad base heritability.

Khan *et al.* (2013) evaluated thirty F_7 segregating lines and two parents of *Brassica rapa* to study variability, heritability and genetic advance. The result revealed that except thousand seed weight, significant variation was presented among all the genotypes for all the characters. Highest genotypic, phenotypic and environmental variances were observed in plant height while lowest one was in length of siliquae followed by thousand grain weight. Thousand seed weight, number of secondary branches per plant, seeds per siliquae, and siliquae length showed high heritability along with low genetic advance in percent of mean but moderate heritability with high genetic advance found in number of siliquae per plant. Considering important performances, the genotypes G-15, G-19, G-1, G-3, G-4, G-10, G-18, G21, and G-24 were found suitable for future breeding program.

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

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

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.

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

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*.

Genetic variability was studied by Ahlawat*et al.* (2006) for 12 characters in 19 genotypes of Indian mustard *(Brassica juncea* (L) czern & coss.). Estimate high phenotypic coefficient of variation than genotypic coefficient of variation were used for the characters numbers of primary and secondary branches, number of siliquae per plant and yield per plant, which indicated the presence of considerable amount of variation. Heritability and genetic advance were high for 1000-seed weight, number of siliquae per plant and plant height. Number of siliquae per plant and plant height had moderately high heritability with high genetic advance indicating that additive gene effects were important for these characters and selection pressure could be applied on them for yield improvement. Number of primary branches per plant and oil content had low heritability indicating that these traits were under the influence of environmental factors.

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

Katiyar *et al.* (1974); observed high genetic co-efficient of variation for days to first flowering, plant height (cm) and seed yield per plant (g) where as low values were observed for other characters like days to maturity and number of primary

branches per plant, while observing on genetic variability and genetic advance of seed yield and its components in Indian mustard.

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

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

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

2.2 Correlation among different characters

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

In an experiment undertaken by Sultana (2016) by using F_4 generations of Brassica napus revealed that significant positive correlation with seed yield per plant with all most all the characters except days to 50% flowering which was

positive but non-significant and days to maturity (non-significant negative) with seed yield per plant.

Correlation coefficients among the characters were studied by Begum (2015) to determine the association between yield and yield components of some backcross generations of *Brassica napus* L. In general, most of the characters showed the genotypic correlation co-efficient were higher than the corresponding phenotypic correlation co-efficient suggesting a strong inherent association between the characters under study and suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values.

Siddika (2015) observed correlation revealed that yield per plant had significant positive association with plant height, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, 1000 seeds weight both genotypic and phenotypic level. A significant genotypic positive correlation also observed for days to first flowering and length of siliqua.

Rameeh (2015) studied 36 rapeseed (*Brassica napus* L.) genotypes including four checks and 32 advanced lines and found that pods per plant, seeds per plant and 1000- seed weight traits were positively correlated with seed yield.

In an experiment by Parvin (2015) which showed that number of primary branches per plant, secondary branches per plant, siliqua per plant, siliqua length, number of seeds per siliqua, and 1000 seed weight (g) had significant positive correlation with number of secondary branches per plant, number of siliquae per plant, 1000 seed weight at genotypic level where Number of primary branches per plant, secondary branches per plant, siliqua per plant, number of seeds per siliqua, and 1000 seed weight (g) had significant association with number of secondary branches per plant, number of siliquae per plant, 1000 seed weight at genotypic level at phenotypic level. A significant genotypic positive correlation also observed for days to first flowering and length of siliqua.

Bilal *et al*. (2015) evaluated 23 genotypes of rapeseed to study the correlation between the yield and yield contributing characters. Positive significant correlation was observed between days to maturity and yield per plant (r = 0.279) as well as with 1000-seed weight (r = 0.057). Negative significant correlation was observed between plant height and pods per plant and 1000-seed weight. Number of pods per plant revealed positive significant correlation with 1000-seed weight and positive correlation with pod length, number of seeds per pod, yield per plant.

Another study on correlation by Shakera (2014) revealed that yield per plant had significant positive association with plant height, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, thousand seed weight (Both genotypic & phenotypic level).

An experiment was carried out by Hussain (2014) by using advanced lines of *Brassica rapa.* 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 thousand seed weight, no. of siliqua per plant, no. of primary branches per plant. In addition, there were non-significant positive correlation with no. of secondary branches per plant siliqua length.

Halder *et al*. (2014) conducted an experiment by using 14 genotypes including 11 advanced lines and 3 check varieties to study the correlation and observed that days to first flowering showed positive non-significant relationship with yield but high positive significant correlation with the days to 50% and 80% flowering. Highly significant negative correlation was found with number of secondary branches per plant and siliqua length.

Nabi (2014) studied correlation coefficients among the characters by using F_3 generation of some *Brassica napus* lines to determine the association between yield and yield components. In general, most of the characters showed the genotypic correlation co-efficient were higher than the corresponding phenotypic

correlation co-efficient suggesting a strong inherent association between the characters under study and suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values.

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

A research was conducted by Mili (2014) using 66 F5 genotypes of *Brassica napus* L. to study correlation and path coefficient analysis. The significant positive correlation with seed yield per plant was found in number of siliqua per plant,siliqua length, number of seed per siliqua and thousand seed weight.

A research was conducted by Lodhi *e.t a.l* (2014) using ninety diverse genotypes of Indian mustard (*Brassica juncea* Czern & Coss) were evaluated for fifteen quantitative traits. Seed yield/ plant was found to be positively and significantly correlated with number of primary branches/plant, number of secondary branches/ plant, primary branch angle, main shoot length, siliqua length, and number of seeds/ siliqua and non-significant with days to maturity; seed yield/plant had negative association with oil content.

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.

Esmaeeli Azadgoleh *et al.* (2009) mentioned positively significant correlation of seed yield with number of pod per plant, number of pods in sub branches and number of seeds per pod. An experiment was conducted by Basalma (2008) in Ankara conditions using 25 winter oil seed rape cultivars. Correlation analysis showed a high positive and statistically significant correlation between branches per plant, the number of pods on the main stem and plant height during two years. Plant height indicated negative correlation with seed yield, thousand seed weight and oil ratio.

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

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

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

Parveen (2007) conducted an experiment with F_2 population of *Brassica rapa* to study the correlation and observed that yield per plant had non-significant positive association with plant height, number of secondary branches per plant, number of seeds per siliqua and number of siliquae per plant, days to 50% flowering and length of siliqua.

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

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

The significant and positive correlation of seed yield per plant with plant height and 1000 seed weight, but high negative and significant correlations with seeds per siliqua, at both the genotypic and phenotypic levels were observed by Uddin *et al.* (2005). Seeds per siliqua, 1000 seed weight had high positive direct effects on seed yield per plant. Days to maturity and plant height had considerable negative direct effects on seed yield per plant.

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

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

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 (g) and oil percent were positively associated with seed yield.

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

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

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.

2.3 Path co-efficient analysis

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

Path co-efficient analysis by Sultana (2016) revealed that days to 50% flowering, number of secondary branch, number of siliqua per plant, number of seed per siliqua, and thousand seed weight had the positive direct effect on yield per plant whereas days to 80% maturity, plant height, number of primary branch and siliqua length had the negative direct effect on yield per plant.

Path co-efficient analysis experiment carried out by Siddika (2015) with using F_2 seggregating generation of some advanced lines of *Brassica napus* L. revealed that days to number of primary branches per plant, number of siliquae per plant, siliqua length, seeds per siliqua and thousand seed weight had the positive direct effect on yield per plant and days to first flowering, plant height and number of secondary branches per plant had the negative direct effect on yield per plant.

Begum (2015) observed that path co-efficient analysis revealed number of primary branch, number of secondary branch, number of siliqua per plant, number of seed per siliqua, and thousand seed weight had the positive direct effect on yield per plant whereas days to 50% flowering, days to 80% maturity, plant height and siliqua length had the negative direct effect on yield per plant.

In an experiment undertaken by Shakera (2014) by using some advanced lines of *Brassica rapa* revealed that days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, number of seeds per siliqua and thousand seed 92 weight had the positive direct effect on yield per plant. Siliqua length had the negative direct effect on yield per plant.

Parvin (2015) conducted an experiment which path coefficient analysis revealed that plant height, number of primary branches per plant, number of secondary branches per plant , number of siliquae per plant , siliqua length , number of seeds per siliqua and thousand seed weight had the positive direct effect on yield per plant and days to first flowering had the negative direct effect on yield per plant.

Hussain (2014) conducted an experiment by using advanced lines of *Brassica rapa* which result revealed that plant height, no. of primary branches per plant, no. of siliqua per plant, siliqua length, thousand seed weight showed positive direct effect with yield per plant. Days to 50% flowering, days to 80% maturity, no. of secondary branches per plant, no of seed per siliqua showed negative direct effect on yield per plant. Beside these days to 50% flowering, days to 80% maturity, no. of secondary branches per plant, no of seed per siliqua showed negative direct effect on yield per plant.

Path coefficient analysis revealed that number primary branches per plant, number of secondary branches per plant, plant height, days to 50% flowering, days to 80% maturity and thousand seed weight had the positive direct effect on yield per plant. This result was observed by Nabi (2014).

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

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

Afrin (2009) conducted a field experiment with 22 *Brassica napus* L. advanced lines to study path coefficient. Path coefficient analysis showed that the plant height had maximum positive direct effect on seed yield followed by number of

siliqua per plant and siliqua length and negative direct effect on number of secondary branches per plant and number of seeds per siliqua. Plant height, number of primary branches per plant and number of siliqua per plant were the most important contributors to seed yield per plant which could be taken in consideration for future hybridization program.

The path co-efficient analysis by Hosen (2008) exhibited that thousand seed weight had the highest positive direct effect followed by days to 50% flowering, length of siliqua, number of primary branches per plant, number of secondary branches per plant, days to maturity and number of seeds per siliqua while working with five parental genotypes of *Brassica rapa* and their ten F3 progenies including reciprocals.

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

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

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

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

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

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

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

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

2.4 Genetic diversity analysis

Diversity is the basis of crop improvement. If there were no diversity in nature no improvement would possible. But during continuous selection process for better quality and productivity, the gene pool of the selected final varieties has been made narrow down due to eliminating of genes for undesirable traits for example, declining amount of erucic acid in oil and glucosinolates in seeds. Due to which the differences at genetic level in *Brassica napus* L. has been made very limited which were so much important for many other promising characters.

Genetic diversity among *Brassica napus* genotypes was studied by Sultana (2016) which performed through Principal Component Analysis (PCA) and Cluster Analysis. The 62 genotypes fell into five distant clusters. The cluster IV

comprised the maximum number (19) of genotypes followed by same in cluster cluster III (18). The cluster I and V comprised 10 and 9 genotypes respectively. The lowest number of genotypes was present in cluster II. The highest inter-cluster distance (10.309) was observed between the cluster I and IV, if involved in hybridization may produce a wide spectrum of segregating population. The lowest inter-cluster distance (3.513) was observed between the cluster III and IV.

Rameeh (2015) carried out an experiment to study genetic diversity of twenty one rapeseed genotypes. These genotypes were evaluated based on randomized complete block design with three replications. On the basis of cluster analysis, the genotypes were classified in three groups and the group with high seed yield had high mean values of plant height, days to maturity and pods per plant. All the genotypes were classified in three groups with different mean values of the traits. The high seed yield genotypes with high mean value of pods on main axis and pods per plant were classified in group1 (C1). Group 1 (C1) and group 2(C2) had 1545.56 and 2160.55 kg per ha of seed yield.

In an another experiment Iqbal *et al.* (2014) studied different genotypes to determine the genetic variability and diversity among different mustard genotypes and reported that all the characters demonstrated high heritability (□80%) irrespective of any genotypes. The genotypes were grouped into four clusters by using Euclidean distance following Ward's method. The cluster III had higher intra cluster distance and the maximum inter cluster distance was observed between genotypes of clusters I and IV followed by clusters III and IV.

Khan (2014) used 211 genotypes of *Brassica napus* to study the genetic diversity. The recorded data were analyzed through two complementary methods, i.e., cluster analysis and principal component analysis. Through cluster analysis all the genotypes were divided into five main groups. It was found that 7 out of 21 principal components with an eigenvalue of ≥ 1.0 accounted for 69.99% of the overall differences found among 211 genotypes of *Brassica napus* L. The contribution of first three PCs in overall PCs was 26.96%, 10.00% and 8.9%, respectively.

An experiment was conducted by using 45 Indian mustard genotypes of different origin from India to study the extent of diversity for utilization in breeding program. To measure the genetic diversity among the genotypes D^2 analysis was used. The 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%) (Pandey *et al*., 2013).

Twenty four rapeseed genotypes including 2 cultivars and 22 advanced lines were studied by Rameeh (2013). The results revealed that factor analysis exhibited four factors including sink factor (pod per plant, pods length and seed yield), fixed capital factor (phenological traits), secondary fixed capital factor (duration of flowering), and metric factor (plant height). On the basis of cluster analysis, the genotypes were classified in four groups, and the group with high seed yield had high mean value of pods per plant.

Zare and Sharafzadeh (2012) evaluated 8 genotypes of rapeseed to determine the genetic divergence. The genotypes were grouped into four clusters. Based on the results, Modena and Sarigol, which had the highest grain yield, were located in a major cluster and Okapi, which had the lowest grain yield, was located in a single cluster else. SLM046, RGS003 and Hyola308 cultivars, which had lower grain yield, were placed in the third cluster that was partitioned into two small clusters. The fourth cluster included Licord and Zarfam cultivars also had high grain yield.

A field experiment was conducted by Zaman *et al.* (2010) which comprised eighteen advanced lines of mustard 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 inter cluster distance was observed between the cluster III and II followed by III and I and the lowest between cluster IV and III. Days to

50% flowering (81.94%), days to maturity (8.24%), plant height (5.82%), branches per plant (1.91%) and siliquae per plant (1.17%) contributed maximum towards the total divergence which suggested that these characters were highly responsible for genetic divergence in the present materials. The genotypes from cluster I had dwarf plant along with earliness in days to 50% flowering, days to maturity and maximum number of primary branches per plant.

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

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

CHAPTER III

MATERIALS AND METHODS

3.1 Experimental site:

The research work was conducted at the experimental farm of the Department of the Genetics and Plant Breeding, Sher-e-Bangla Agricultural University (SAU), Dhaka-1207, Bangladesh. The time period of the experiment was November 2015 to February 2016. The soil of the experimental plot was clay loam with medium high with medium fertility level. The general climatic feature of the experimental site was subtropical climatic weather having wet summer and dry winter.

3.2 Soil and climate

The experimental site was situated in the subtropical zone. The soil of the experimental site belongs to Agroecological region of "Madhupur Tract" (AEZ No. 28). The soil was clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH was 5.47 to 5.63 and organic carbon content is 0.82% (Appendix II). The records of air temperature, humidity and rainfall during the period of experiment were noted from the weather station, Sher-e-Bangla Agricultural University, Dhaka 1207(Appendix III).

3.3 Experimental materials:

The healthy seeds of 45 advanced line of F_7 of *Brassica napus* L. collected from the Dept. of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, which were used as experimental materials. The materials used in that experiment is shown in Table 1.

3.4 Methods

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

3.4.1 Land preparation

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

Table 1. Materials used for experiment

Genotype	F_7 Generations	Source
G1	Nap 2066 × Nap 205, P1	SAU
G2	Nap 9906 × Nap 205, P3	SAU
G3	Nap 9908 × Nap 9906, P3	SAU
G4	Nap 108 × Nap 205	SAU
G5	Nap 9908 × Nap 2066, P2	SAU
G6	Nap 9906 × Nap 205, P4	SAU
G7	Nap 2066 × Nap 205, P4	SAU
G8	Nap 9906 × Nap 9901, P2	SAU
G9	Nap 9908 × Nap 9906, P2	SAU
G10	Nap 2051 × Nap 0130, P2	SAU
G11	Nap 9906 × Nap 205, P1	SAU
G12	Nap 9906 × Nap 205, P2	SAU
G13	Nap 2066 × Nap 205, P3	SAU
G14	Nap 2066 × Nap 205, P2	SAU
G15	Nap 9908 × Nap 9906, P4	SAU
G16	Nap 9908 × Nap 0130, P4	SAU
G17	Nap 2051 × Nap 0130, P1	SAU
G18	Nap 9905 × Nap 9901, P2	SAU
G19	Nap 9908 × Nap 9901, P3	SAU
G20	Nap 2066 × Nap 0130, P1	SAU
G21	Nap 108 × Nap 2066, P3	SAU
G22	Nap 2066 × Nap 0130, P2	SAU
G23	Nap 108 × Nap 2066, P4	SAU
G24	Nap 108 × Nap 0130, P1	SAU
G25	Nap 9905 × Nap 205, P2	SAU
G26	Nap 9905 × Nap 9908, P1	SAU
G27	Nap 108 × Nap 0139, P3	SAU
G28	Nap 108 × Nap 0130, P2	SAU
G29	Nap 9901 × Nap 0130, P2	SAU
G30	Nap 9905 × Nap 9906, P2	SAU
G31	Nap 9906 × Nap 2066, P2	SAU

G32	Nap 9905 ✕ Nap 0130, P1	SAU
G33	Nap 2051 ✕ Nap 0130, P3	SAU
G34	Nap 9906 ✕ Nap 2066, P3	SAU
G35	Nap 108 ✕ Nap 2066, P2	SAU
G36	Nap 108 ✕ Nap 2066, P1	SAU
G37	Nap 9905 ✕ Nap 108, P1	SAU
G38	Nap 9908 ✕ Nap 0130, P2	SAU
G39	Nap 9905 ✕ Nap 9906, P1	SAU
G40	Nap 9901 ✕ Nap 2066, P2	SAU
G41	Nap 9906 ✕ Nap 9901, P1	SAU
G42	Nap 9908 ✕ Nap 2066, P1	SAU
G43	Nap 9901 ✕ Nap 2055, P1	SAU
G44	Nap 9908 ✕ Nap 9901, P4	SAU
G45	Nap 9901 ✕ Nap 0130, P1	SAU
G46	Nap 9908 ✕ Nap 9906, P1	SAU
G47	Nap 9905 ✕ Nap 108, P3	SAU
G48	Nap 9908 ✕ Nap 9901, P1	SAU
G49	Nap 9908 ✕ Nap 0130, P5	SAU
G50	Nap 9906 ✕ Nap 2066, P1	SAU

3.4.2 Application of manure and fertilizer

The crop was fertilized at the rate of 10 tons of Cowdung, The fertilizers like urea, triple super phosphate, muriate of potash, gypsum and zinc sulphate were applied in quantities of 270,170,100,150 and 5kg/ha, respectively, along with 10ton/ha of cow dung. The half amount of urea, total amount of Cowdung, TSP, MP, Gypsum, Zinc Oxide and Boron was applied during final land preparation. The rest amount of urea was applied as top dressing after 25 days of sowing.

3.4.3 Experimental design and layout

Field lay out was done after final land preparation. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The total area of the experiment was $30m \times 10m = 300m^2$. Each replication size was $56m \times 3.5m$, and the distance between replication to replication was 1m. The spacing between lines to line was 30cm. Seeds were sown in lines in the experimental plots on 14 November, 2015. The seeds were placed at about 1.5 cm depth in

the soil. After sowing the seeds were covered with soil carefully so that no clods were on the seeds.

3.4.4 Intercultural operations

Intercultural operations, such as weeding, thinning, irrigation, pest management, etc. were done uniformly in all the plots. Irrigation was given with cane after sowing of seeds to bring proper moisture condition of the soil to ensure uniform germination of the seeds. A good drainage system was maintained for immediate release of rainwater from the experimental plot during the growing period. The first weeding was done after 14 days of sowing. At the same time, 1st thinning was done and another after 7 days of1st thinning for maintaining a distance of 10 cm from plant to plant in rows of 30 cm apart. The critical weed free period for *Brassica* is 15 to30 days after sowing. Second weeding was done after 30 days of sowing. Aphid infection was found in the crop during the siliqua development stage. To control aphids Malathion-57 EC @ 2ml/liter of water was applied. The insecticide was applied in the afternoon.

3.4.5 Crop harvesting

Harvesting was done from about 90 days after sowing (DAS) depending upon the maturity. When 80% of the plants showed symptoms of maturity i.e. straw color of siliqua, leaves, stems desirable seed color in the mature siliqua, the crop was assessed to attain maturity. Fifteen plants were selected at random F_7 progenies in each replication. The plants were harvested by uprooting and then they were tagged properly. Data were recorded on different parameters from these plants. A pictorial view of experimental field at flowering and harvesting stage is presented in Plate 1 & 2.

3.4.6 Data collection

For studying different genetic parameters and inter-relationships, ten characters were taken into consideration. A pictorial view of observation and data collection is presented in Plate 3. The data were recorded on fifteen selected plants for each cross and ten selected plants for each parent on the following traits-

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

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

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

Plate 1. Photograph showing research field during observation at flowering stage.

Plate 2. Photograph showing experimental field at maturity stage.

Plate 3. Photograph showing data collection after harvesting different rapeseed genotypes.

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

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

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

vii. **Siliquae length (cm):** This measurement was taken in centimeter (cm) from the base to the tip of a siliqua of the five representative siliquae. **Number of seeds per siliqua:** Well filled seeds were counted from five siliquae which was considered as the number of seeds per siliqua.

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

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

3.5 Statistical analysis

The data were analyzed for different components. Phenotypic and genotypic variance was estimated by the formula used by Johnson *et al.* (1955). Heritability and genetic advance were measured using the formula given by Singh and Chaudhury (1985) and Allard (1960). Genotypic and phenotypic co-efficient of variation were calculated by the formula of Burton (1952). Simple correlation coefficient was obtained using the formula suggested by Clarke (1973)., Singh and Chaudhury (1985) and path coefficient analysis was done following the method outlined by Dewey and Lu (1995).

i) 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**, Where, $\delta^2 p = \delta^2 g + \delta^2 e$

c. $\bar{x}$ = Population mean

iii) 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 = Penotypic variance

iv) 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.

d. **v) Estimation of genetic advance in percentage of mean**

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

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

vi) Estimation of simple correlation co-efficient:

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

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

Where, $\sum$ = Summation

x and y are the two variables correlated

N = Number of observation

vii) Path co-efficient analysis:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

riy = Correlation of the character with yield.

viii) Estimation of Genetic Diversity

a. Principal Component Analysis (PCA)

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

b. Principal Coordinate Analysis (PCO)

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

c. Canonical Vector Analysis (CVA)

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

d. Average Intra-cluster Distances

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

e. Clustering

To divide the genotypes of the study into some number of mutually exclusive groups clustering were done using non-hierarchical classification. Starting from some initial classification of the genotypes into required groups, the algorithm repeatedly transfers genotypes from one group to another so long as such transfers improve the criterion, the algorithm switches to a second stage which examine the effect of swapping two genotypes of different classes and so on.

CHAPTER IV
RESULTS AND DISCUSSIONS

The results of the present investigation of genetic analysis that means genetic variability, associations of characters, path coefficient analysis and diversity studies of *Brassica napus* presented and discussed here under the following sections.

4.1. Mean, Range and Analysis of Variance

Days to 50% flowering differed significantly in all the genotypes ranging from 37.67to 51.33with mean value of 44.22 (Table 2). The CV value of days to 50% flowering was observed 1.44%. The maximum days to 50% flowering was observed in genotype G25 (51.33) and the lowest found in the genotype G3 (37.67) (Appendix 4).

Days to 80% maturity were varied significantly among the 50 genotypes. The value of days to 80%maturity varied from 75.00 to 93.00with mean a value of87.37 (Table 2). The maximum days to 80% maturity (93.00) was found in G11 whereas the minimum (75.00) from G3 (Appendix 4). According to the study the maximum days to 80%maturity was found in G11mustard genotypes. High days to 80%maturityshown late maturity and in contrary the lowest days to 80%maturityshowed early maturity of a variety and it was essential for release early maturing variety.

Plant height varied from 83.33 cm to 126.09 cm with average of 101.48 cm (Table 2). The coefficient of variation of this trait was 9.46%. The maximum plant height was observed by the genotype G25 (126.09 cm) and the minimum in G29 (83.33 cm) (Appendix 4). Plate 4 showing variation between the highest and the lowest plant height of *Brassica* genotypes from the result of the experiment it was observed that primary branches per plant were varied significantly among the 50 mustard genotypes.

Table 2. Range, Mean, CV (%) and standard deviation of 50 rapeseedgenotypes

Parameters	Range		Mean	CV (%)	SD	SE
	Min	Max				
Days to 50% flowering	37.67	51.33	44.22	1.44	0.64	0.24
Days to 80% maturity	75.00	93.00	87.37	0.51	0.45	0.17
Plant height (cm)	83.33	126.09	101.48	9.46	9.60	3.63
Primary branches per plant	2.37	7.10	3.35	12.48	0.42	0.16
Secondary branches per plant	0.87	5.37	2.14	26.00	0.56	0.21
Siliqua per plant	72.87	190.97	116.31	13.18	15.32	5.79
Siliqua length (cm)	5.85	11.30	7.46	7.62	0.57	0.21
Seeds per siliqua	14.09	30.45	21.29	12.33	2.62	0.99
1000 seed weight (g)	2.14	4.52	3.49	5.35	0.19	0.07
seed yield per plant (g)	5.45	11.77	8.34	10.42	0.87	0.33

CV (%) = coefficient of variation, SD = standard deviation and SE = standard error

G25 (126.09 cm) G29 (83.33 cm)

Plate 4. Photograph showing variation between the highest G25(Nap9905 X Nap205, P2) and the lowest G29(Nap9901 X Nap0130, P2) plant height of *Brassica napus* L. genotypes.

The ranges of primary branches per plant were from 2.37 to 7.10 with the mean value of 3.35 (Table 2).The maximum primary branches per plant (7.10) was found in G50whereas the minimum (2.37) from G2 (Appendix 4). According to the study G50 mustard genotype has the highest primary branches per plant. Plate 5 showing variation between the maximum and the minimum no. of primary branches of *Brassica* genotypes.

The genotype G37 recorded the maximum secondary branches per plant (5.37) while the minimum was observed by the genotype G1 (0.87) (Table 2). Plate 6 showing variation between the highest and the lowest no. of secondary branches of *Brassica* genotypes.

Siliqua per plant was observed from 72.87 to 190.97 with the mean of 116.31. The maximum siliqua per plant was found in the genotype G50 (190.97) while the minimum was observed in G12 (72.87). Plate 7 showing variation between the maximum and the minimum no. of siliqua per plant of *Brassica* genotypes.

Siliqua length was ranged from 5.85 cm to 11.30 cm with the mean value of 7.46 cm. The maximum siliqua per plant was observed in the genotype G2 (11.30 cm) while the minimum was observed in the genotype G31 (5.31 cm). Plate 8 showing variation between the maximum and the minimum siliqualengtht of *Brassica* genotypes.

Seeds per siliqua ranged were observed from 14.09 to 30.45 with the average of 21.29. The coefficient of variation was 12.33%. The maximum seeds per siliqua was found by the genotype G26 (30.45) and the minimum was observed from the genotype G31 (14.09) (Appendix 4).

1000 seed weight was observed from 2.14 g to 4.52 g with the mean value of 3.49 g. The maximum 1000 seed weight was observed in the genotype G25 (4.52 g) and the minimum was observed in the genotype G12 (2.14). Plate 9 showing variation between the maximum and the minimum thousand seed weight of *Brassica* genotypes.Yield per plant was observed from 5.45 g to 11.77 g with average of 8.34 g. The maximum was observed in G25 (11.77 g) while the minimum was observed in G12 (5.45 g).

G50(7.10) G2(2.37)

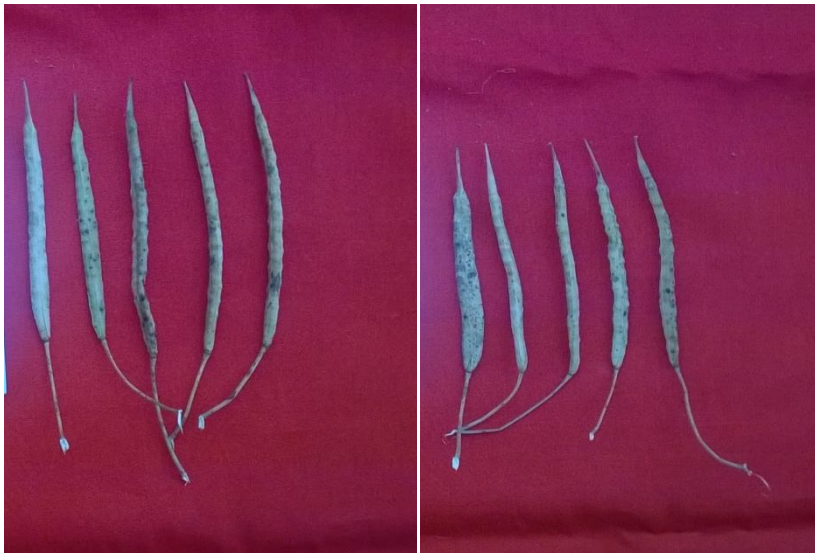
Plate 5. Photograph showing variation between the highest G50(Nap9906 X Nap2066, P1) and the lowest G2(Nap9906 X Nap205, P3) no. of primary branches of *Brassica napus* L. genotypes.

G37 G1

Plate 6. Photograph showing variation between the highest G37(Nap9905 X Nap108, P1) and the lowest G1(Nap2066 X Nap205, P1) no. of secondary branches of *Brassica napus* L. genotypes.

G50 (190.97) G12 (72.87)

Plate 7. Photograph showing variation between the highest G50(Nap9906 X Nap2066, P1) and the lowest G12(Nap9906 X Nap205, P2) no. of siliqua per plant of *Brassica napus* L. genotypes.



G2 (11.30 cm) G31 (5.31 cm)

Plate 8. Photograph showing variation between the highest G2 (Nap9906 X Nap205, P3 and the lowest G31(Nap9906 X Nap2066, P2) siliqua length of *Brassica napus* L. genotypes.

G25 (4.52 g) G12(2.14 g)

Plate 9. Photograph showing variation between the highest G25 (Nap9905 X Nap205, P2) and the lowest G12(Nap9906 X Nap205, P2) TSW of*Brassica napus* L. genotypes.

Analysis of variance (ANOVA)

The results of the analysis of variance (Table 3) of ten morphological traits revealed that the mean square due to accession were highly significant for all traits ($p<0.01$) indicating the presence of sufficient genetic variability in the accessions and considerable scope for their improvement.

4.2. Estimates of Genetic Parameters

The development of suitable plant type is of great importance for all the crops through planned design programme. Genetic variability Estimates including genotypic variance (σ^2_g) phenotypic variance (σ^2_p) environmental variance (σ^2_e) phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (Hb %), genetic advance (GA) and genetic advance as percent mean (GAM) were summarized in Table 4.

4.2.1. Estimates of Variance Components

The variance components include genotypic variance, environmental variance and phenotypic variance which are presented in (Table 4) and discussed here. The highest environmental variance observed (234.85) was in siliqua per plant which indicated that environmental component in total variation was high. The highest genotypic variance and phenotypic variance were 652.10 and 417.25, respectively; indicated the presence of high variation for this trait. The lowest environmental, genotypic and phenotypic variances were also 0.03, 0.31 and 0.35, respectively for 1000 seed weight this indicated the presence of low variation for this trait. All of the above results showed the potential of variation that existed in different traits.

Table 3.Analysis of variance for different characters in rapeseed genotypes

Characters/Variety	Mean sum of square		
	Replication (r-1) = 2	Genotype (g-1) = 49	Error (r-1)(g-1) = 98
Days to 50% Flowering	0.38	30.10**	0.41
Days to 80% Maturity	0.51	50.62**	0.20
Plant height (cm)	4.47	227.09**	20.46
Primary branches per plant	0.39	2.07**	0.17
Secondary branches per plant	0.16	2.41**	0.31
Siliqua per plant	236.71	1486.60**	234.85
Siliqua length (cm)	0.11	2.27**	0.32
Seeds per siliqua	14.59	34.27**	6.88
1000 seed weight (g)	1.49	0.97**	0.03
seed yield per plant (g)	11.10	7.49**	0.76

** Denote Significant at 1% level of probability

Table 4. Estimation of genetic parameters in ten characters of 50 rapeseedgenotypes

Parameters	$\sigma^2 p$	$\sigma^2 g$	$\sigma^2 e$	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
Days to 50% Flowering	10.31	9.90	0.41	7.26	7.11	1.44	96.05	6.35	14.36
Days to 80% Maturity	17.01	16.81	0.20	4.72	4.69	0.51	98.82	8.39	9.61
Plant height (cm)	158.31	66.24	92.06	12.40	8.02	9.46	41.84	10.85	10.69
Primary branches per plant	0.81	0.63	0.17	26.85	23.78	12.48	78.41	1.45	43.37
Secondary branches per plant	1.01	0.70	0.31	46.91	39.05	26.00	69.29	1.43	66.96
Siliqua per plant	652.10	417.25	234.85	21.96	17.56	13.18	63.99	33.66	28.94
Siliqua length (cm)	0.97	0.65	0.32	13.23	10.81	7.62	66.79	1.36	18.20
Seeds per siliqua	16.01	9.13	6.88	18.80	14.19	12.33	57.00	4.70	22.07
1000 seed weight (g)	0.35	0.31	0.03	16.87	16.00	5.35	89.95	1.09	31.27
seed yield per plant (g)	3.00	2.25	0.76	20.77	17.97	10.42	74.84	2.67	32.02

$\sigma^2 p$ = Phenotypic variance, $\sigma^2 g$ = Genotypic variance and σ^2 e = Environmental variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation.

4.2.2. Estimates of Genotypic and Phenotypic Coefficient of Variation

The highest phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were 46.91 and 39.05, respectively both of which were recorded for secondary branched per plant.In this case, the PCV values were more than GCV values. This indicated that the environmental effect was medium for the expression of these characters. The magnitudes of phenotypic and genotypic coefficient of variation were days to 80% maturity 4.72 and 4.69, respectively. In these cases, the PCV values were higher than GCV values across the environment. This indicated the presence of environmental influence on these characters (Sharma *et al*., 2009).

High to moderate GCV and PCV values were shown by all the characters except days to 50% flowering and days to 80% maturity that showed low GCV and PCV values. The present result revealed that higher PCV and GCV were recorded for primary branches per plant (26.85% and 23.78%), secondary branches per plant (46.91% and 39.05%), siliqua per plant (21.96% and 17.56%) and seed yield per plant (20.77% and 17.97%)(Table 4).

Phenotypic co-efficient of variation (PCV) agreed closely with the genotypic co-efficient of variation (GCV).The difference between PCV and GCV values was low indicating the low effects of environment in these characters. The difference in genotypic coefficient of variation and phenotypic coefficient of variation values were closer indicates that there was a minimum influence of environment on these characters. In general, phenotypic coefficient of variation values were higher than their corresponding genotypic coefficient variation values in all of the characters, (Figure 1).

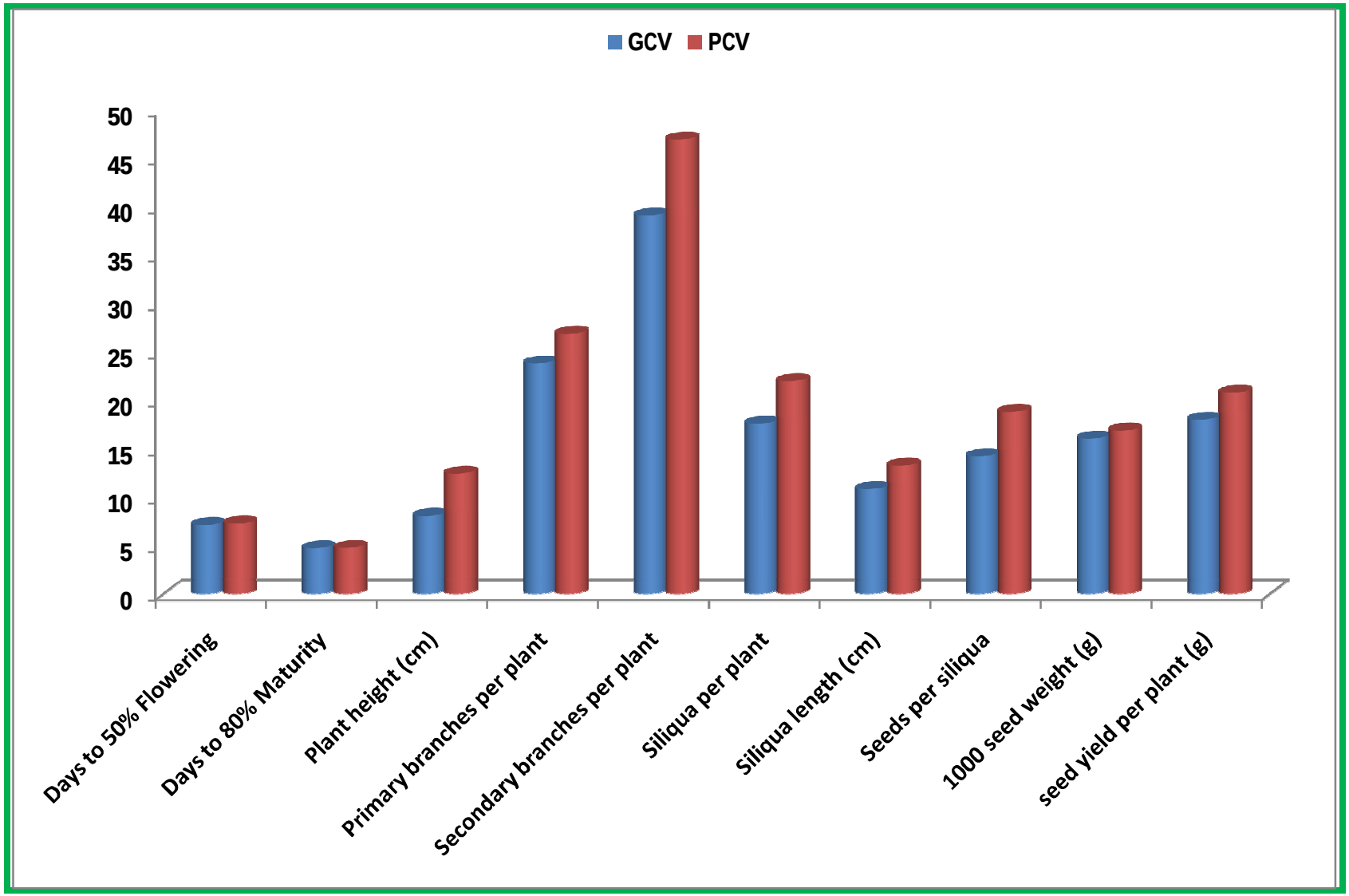


Figure 1. Genotypic and phenotypic variability in rapeseed

4.2.3. Estimates of Heritability and Genetic Advance

Broad sense heritability values were higher (more than 63%) for all the characters except plant height and seeds per siliqua, (Table 4 and Figure 2). Broad sense heritability ranged from 41.84% (plant height) to 98.82 % (days to 80% maturity). These broad sense heritability values were likely to be over estimated as in this calculation it was not possible to exclude variation due to different genetic components and their interactions.

The present estimation of high heritability was observed in days to 50% flowering (96.05), days to 80% maturity (98.82), primary branches per plant (78.41), secondary branches per plant (69.29), siliqua per plant (63.99), siliqua length (66.79), 1000 weight (89.95) and seed yield per plant (74.84). The heritability of the highest magnitude was noticed for days to 80% maturity (98.82). Thus, it indicated that larger proportion of phenotypic variance has been attributed to genotypic variance and reliable selection could be made on the basis of phenotypic expression. High estimated of heritability in broad sense indicated that substantial improvement can be made using standard selection procedures. In general, characters which exhibited high heritability suggested that the selection would be more effective whereas characters showing low heritability indicate that the selection would be affected by environmental factors. Based on the observation, in the present study, it can be surly concluded that selection of genotype based on days to 50% flowering, days to 80% maturity, primary branches per plant, secondary branches per plant, siliqua per plant, siliqua length, 1000 weight and seed yield per plantwould be more satisfactory.

The heritability estimates were, therefore, to be considered with these limitations in view. However, genetic advance (GA) expressed as percentage of mean was high (>20%) for the characters like primary branches per plant, secondary branches per plant, siliqua per plant, seeds per siliqua, 1000 seed weight and seed yield per plant.Moderate genetic advance as percent of mean was shown by days to 50% flowering and plant height.

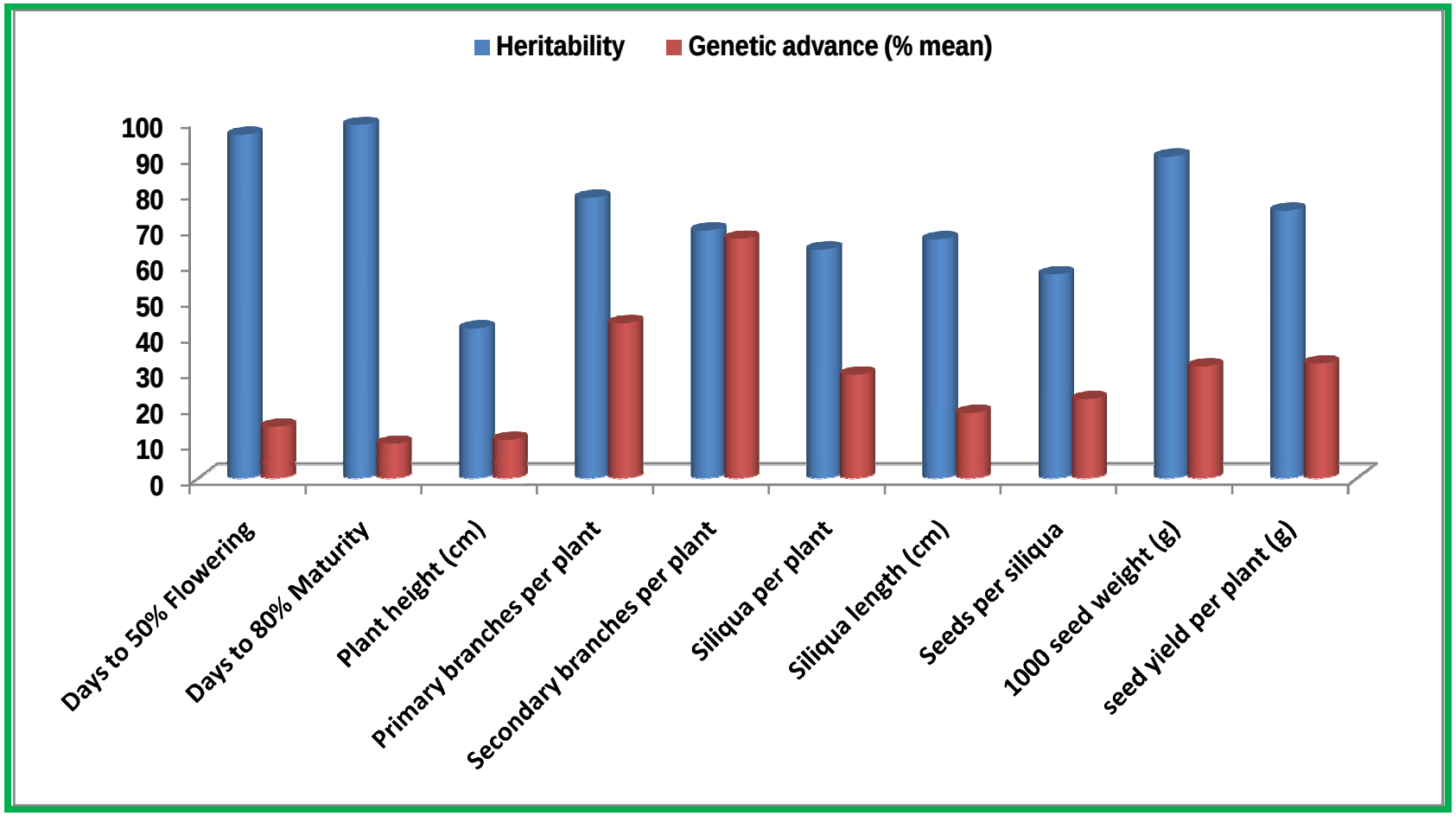


Figure 2. Heritability and genetic advance over mean in rapeseed

The estimate of genetic advance as percent of mean was the highest (66.96%) for secondary branches per plant and lowest (9.61%) for days to 80% maturity. Most of the traits studied had high genetic advance as percent of mean though it was moderate for plant height (10.69%) and low for days to 80% maturity (9.61%). Begum (2015) revealed that seed yield per plant exhibits the highest value of heritability while days to 50% flowering exhibits the lowest value of heritability. According to Johnson *et al*. (1955) high heritability estimates along with the high genetic advance is usually more helpful in predicting gain under selection than heritability estimates alone. The estimates of heritability accompanied by estimates of genetic advance as percent of means are more meaningful from the point of expected genetic gain. Genetic advance is the measure of improvement that can be achieved by practicing selection in a population.

The present study revealed high heritability coupled with high expected genetic advance as percent of means were observed in case of primary branches per plant (78.41 and 43.37), secondary branches per plant (69.29 and 66.96), siliqua per plant (63.99 and 28.94), 1000 seed weight (89.95 and 31.27) and seed yield per plant (74.84 and 32.02)respectively indicating good response to selection for these characters.These findings were supported by the researcher Begum (2015), Siddika(2015) and Nabi(2014). High heritability and high genetic advance for the above mentioned characters revealed that such characters are controlled additive gene action and selection based on these characters will be effective. The low heritability is being exhibited due to high environmental effects. Low heritability accompanied with low genetic advance for none of the character found. High heritability along with moderate genetic advance was observed for siliqua length (66.79% and 18.20%) indicating that these traits are amenable for selection, which may be attributed to both non-additive and additive gene effects and these traits can be improved through hybridization and use of hybrid vigour.

Correlation coefficient

Relationship between physiological and yield contributing characters was studied through analysis of correlation between them. The correlation coefficients between all the ten characters were presented in genotypic and phenotypic level in Table 5 and Table 6.The genotypic and phenotypic correlation of seed yield per plant with different characters was presented in Figure 3. Seed yield per plant was significant and positive correlation with plant height (0.950** and 0.254**), primary branches per plant (0.977** and 0.239**), secondary branches per plant (0.665** and 0.432**), siliqua per plant (0.950** and 0.315**), seeds per siliqua (0.947** and 0.143), 1000 seed weight (0.974** and 0.305**) at both genotypic and phenotypic level. These results were supported by the finding of Sultana (2016), Begum (2015), Siddika (2015) and Rameeh (2015) in mustard. Days to 80% maturity (-0.860** and -0.262**) was significantly and negatively correlated with seed yield per plant at both level indicating that seed yield per plant would be increased with the decrease of those characters. Similar results were obtained by Sirohi *et al.* (2004). Chowdhary *et al.* (1987), Srivastava and Singh (2002) observed positive significant correlation of seed yield with number of secondary branches.

Study of correlation at yield component levels exhibited that days to 50% flowering was positively and significantly correlated with days to 80% maturity (0.698** and 0.684**), plant height (0.382** and 0.322**), primary branches per plant (0.323** and 0.285**), secondary branches per plant (0.205* and 0.172*), siliqua per plant (0.496** and 0.402**) and 1000 seed weight (0.226** and 0.209*) at both genotypic and phenotypic level. Association studies of days to 80% maturity was observed positive and significant correlation with plant height (0.229** and 0.208*), primary branches per plant (0.232** and 0.206*), secondary braches per plant (0.256** and 0.218**), siliqua per plant (0.354** and 0.279**), siliqua length (0.232** and 0.201*) and 1000 seed weight (0.234** and 0.225**) at both level. Kumar *et al.* (1984) recorded positive and significant correlation between plant height and days to maturity which was supported with the findings.

Table 5. Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of rapeseed

	D50F	D80M	PH	PBP	SBP	SPP	SL	SPS	TSW	SYP
D50F	1									
D80M	0.698**	1								
PH	0.382**	0.229**	1							
PBP	0.323**	0.232**	0.372**	1						
SBP	0.205*	0.256**	0.265**	0.657**						
SPP	0.496**	0.354**	0.718**	0.740**	0.591**	1				
SL	0.000	0.232**	0.177*	-0.116	-0.052	0.125	1			
SPS	-0.035	0.018	0.374**	0.006	0.071	0.260**	0.557**	1		
TSW	0.226**	0.234**	0.454**	0.169*	0.328**	0.625**	0.196*	0.029	1	
SYP	0.048	-0.860**	0.950**	0.977**	0.665**	0.950**	-0.040	0.947**	0.974**	1

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

D50F = days to 50% Flowering, D80M = days to 80% Maturity, PH = plant height (cm), PBP = primary branches per plant, SBP = secondary branches per plant, SPP = siliqua per plant, SL = Siliqua length (cm), SPS = Seeds per siliqua, TSW = 1000 seed weight (g) and SYP = seed yield per plant (g).

Table 6. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of rapeseed

	D50F	D80M	PH	PBP	SBP	SPP	SL	SPS	TSW	SYP
D50F	1									
D80M	0.684**	1								
PH	0.322**	0.208*	1							
PBP	0.285**	0.206*	0.343**	1						
SBP	0.172*	0.218**	0.196*	0.491**	1					
SPP	0.402**	0.279**	0.600**	0.652**	0.536**	1				
SL	0.002	0.201*	0.179*	-0.084	-0.032	0.124	1			
SPS	-0.024	0.008	0.314**	0.021	0.010	0.220**	0.461**	1		
TSW	0.209*	0.225**	0.376**	0.137	0.244**	0.459**	0.152	0.036	1	
SYP	-0.001	-0.262**	0.254**	0.239**	0.432**	0.315**	-0.044	0.143	0.305**	1

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

D50F = days to 50% Flowering, D80M = days to 80% Maturity, PH = plant height (cm), PBP = primary branches per plant, SBP = secondary branches per plant, SPP = siliqua per plant, SL = Siliqua length (cm), SPS = Seeds per siliqua, TSW = 1000 seed weight (g) and SYP = seed yield per plant (g).

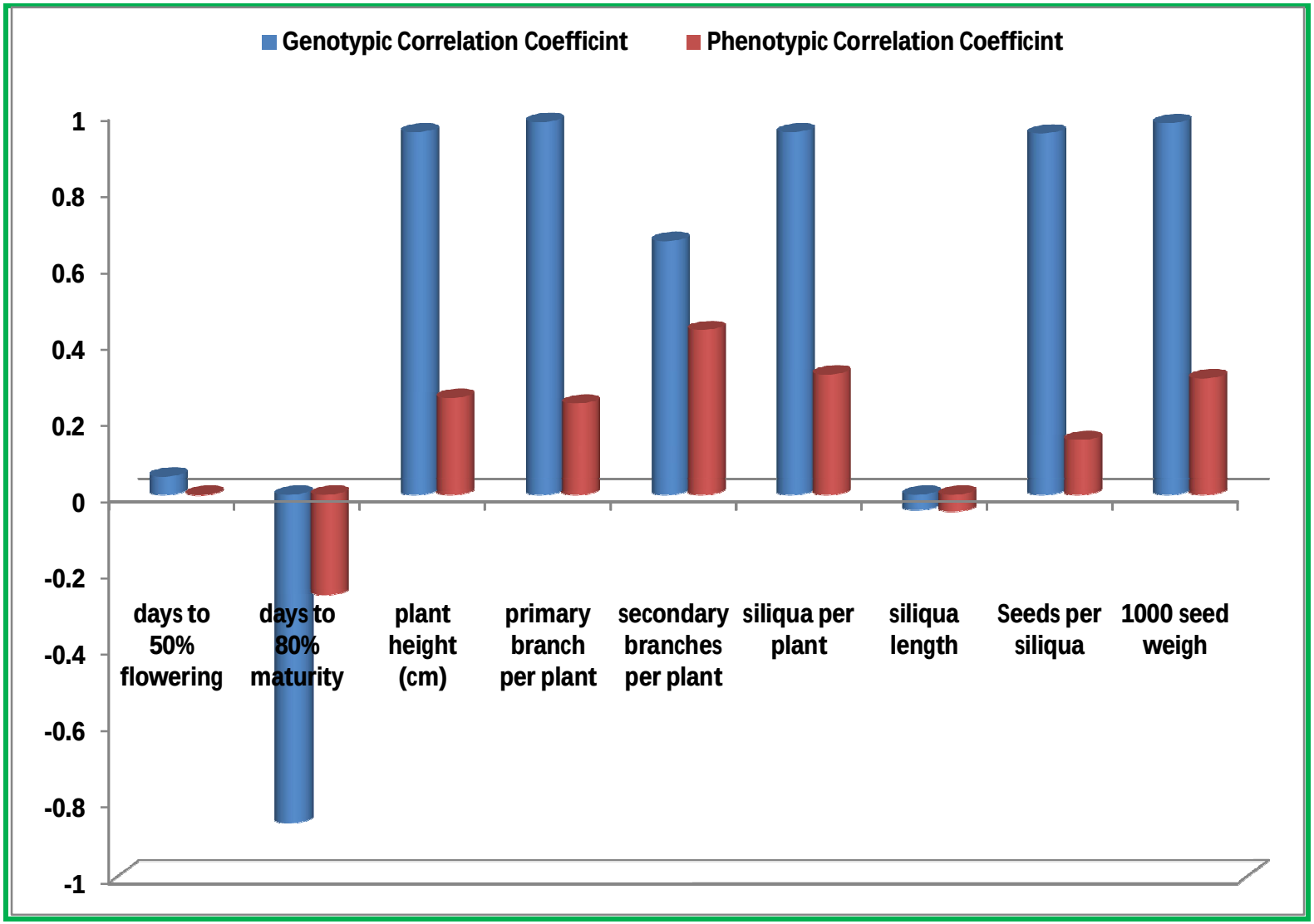


Figure 3. Genotypic and Phenotypic Correlation Coefficientofthirteen characters with seed yield in rapeseed

1000 seeds weight showed positive correlation with days to maturity.This is in conformity with the findings of Srivastava and Singh (2002).

Plant height showed positive and significant correlation with primary branches per plant (0.372** and 0.343**), secondary branches per plant (0.265** and 0.196*), siliqua per plant (0.718** and 0.600**), siliqua length (0.177* and 0.179*), seeds per siliqua (0.374** and 0.314**) and 1000 seed weight (0.454** and 0.376**) at both level. Similar associations for plant height with siliqua length (Basalma, 2008, Esmaeeli-Azadgoleh *et al*. 2009) and plant height with seeds per siliqua (Esmaeeli-Azadgoleh *et al*. 2009) were reported earlier.

Primary branches per plant showed positive and significant correlation with secondary branches per plant (0.657** and 0.491**), number of siliqua per plant (0.740** and 0.652**) and 1000 seed weight (0.169* and 0.137) at both levels.Similar observation was also made by Chowdhary*et al.* (1987), Kumar *et al.* (1984), Srivastava and Singh (2002).Secondary branches per plant showed positive and significant correlation with number of siliqua per plant (0.591** and 0.536**) and 1000 seed weight (0.328** and 0.244**). Siliqua per plant showed positively significant with seeds per siliqua (0.260** and 0.220**) and 1000 seed weight (0.625** and 0.459**). Siliqua length showed positive and significant correlation with number of seeds per siliqua (0.557** and 0.461**) and 1000 seed weight (0.196* and 0.152). According to Kachroo and Kumar (2009), 1000 seed weight showed positive correlation with seed yield.

Regression and Partial correlation

Analysis of variance (ANOVA) revealed that the regression was good fit for the data estimated (Table 7).Partial correlation analysis (Table 8) indicated that 1000 seed weight and siliqua per plant was significantly correlated with seed yield per plant and indicated that 1000 seed weight contributed over 48% and siliqua per plant contributed over 37% to total seed yield. The significance of partial regression coefficients was also tested. Linear regression analysis of yield on the basis of all yield components is given in Table 8. Yield showed a significant linear regression coefficient with 1000 seed weight and siliqua per plant. The selection of best regression equation done through backward elimination procedure revealed that 1000 seed weight and siliqua per plant were the most effective variables contributing to the seed yield.

Table 7. Analysis of Variance for regression

Source of Variation	DF	Sum of Squares	Mean Squares	F-Calculated	Significance
Regression	9	85.497	9.500	14.057	0.000
Error	39	26.356	0.676		
Total	48	111.853			

R-square value: 0.764
Adjusted R Square:0.710

Table8.Partial correlation and linear regression coefficients of yield contributing attributes on yield of rapeseed genotypes

Attributes	Partial correlation	Linear regression Coefficients (beta)	t-test for significance (for beta)
Days to 50% Flowering	0.067	0.050	0.418
Days to 80% Maturity	-0.055	-0.040	-0.342
Plant height (cm)	0.205	0.140	1.307
Primary branches per plant	-0.170	-0.121	-1.079
Secondary branches per plant	0.266	0.175	1.724
Siliqua per plant	0.379*	0.417	2.559*
Siliqua length (cm)	0.207	0.132	1.319
Seeds per siliqua	-0.155	-0.101	-0.980
1000 seed weight (g)	0.485**	0.388	3.462**

*** = Significant at 0.1%. ** = Significant at 1%.

Path analysis

As such from existing agro climatic situation basedperformed using correlation coefficient to determine direct and indirect influence considering ten characters. Seed yield being the complex outcome of different characters was considered as the resultant variable and other characters as causal variable. Estimates of direct and indirect effects of ten yield contributing characters are shown in Table 9. Among the characters that have positive direct effect on seed yield per plant, number of siliqua per plant (9.535) and plant height (0.834) had high positive direct effects on seed yield per plant. These results were agreed with findings of Sultana (2016), Siddika (2015), Begum (2015) and Parvin (2015). The genotypic correlation of number of siliqua per plant, number of seeds per siliqua and plant height with seed yield per plant was also high. Such high correlation with seed yield per plant was mainly due to the high positive direct effect of siliqua per plant and considerable positive indirect effects were number of siliqua per plant and plant height. Similar results were in accordance with studies of Dastidar and Patra (2004). Both correlation and path co-efficient studies revealed for number of siliquae per plant and plant height were the most important components for getting higher yield. Recent breeding research also emphasized on giving importance of these characters. Therefore, the present study suggested that number of siliqua per plant, plant height, secondary branches per plant and 1000 seeds weight should be included owing to importance in selecting the genotypes for higher seed yield in mustard.

Table 9. Partitioning of genotypic correlations into direct (bold) and indirect effects of ten important characters by path analysis of rapeseed

	Direct effect	Indirect effect via									Genotypic correlation with yield
		D50F	D80M	PH	PBP	SBP	SPP	SL	SPS	TSW	
D50F	-2.571	-	-0.480	0.319	-0.955	-0.297	4.729	0.000	0.03	-0.73	0.048
D80M	-0.688	-1.795	-	0.191	-0.686	-0.371	3.375	-0.113	-0.02	-0.75	-0.860**
PH	0.834	-0.982	-0.158	-	-1.100	-0.384	6.846	-0.086	-0.35	-1.46	0.950**
PBP	-2.956	-0.830	-0.160	0.310	-	-0.952	7.056	0.056	-0.01	-0.54	0.977**
SBP	-1.449	-0.527	-0.176	0.221	-1.942	-	5.635	0.025	-0.07	-1.06	0.665**
SPP	9.535	-1.275	-0.244	0.599	-2.187	-0.856	-	-0.061	-0.24	-2.02	0.950**
SL	-0.487	0.000	-0.160	0.148	0.343	0.075	1.192	-	-0.52	-0.63	-0.04
SPS	-0.94	0.09	-0.01	0.31	-0.02	-0.10	2.48	-0.27	-	-0.09	0.947**
TSW	-3.22	-0.58	-0.16	0.38	-0.50	-0.48	5.96	-0.10	-0.03	-	0.974**

Residual effect: **0.204**** = Significant at 1%. * = Significant at 5%.

D50F = days to 50% Flowering, D80M = days to 80% Maturity, PH = plant height (cm), PBP = primary branches per plant, SBP = secondary branches per plant, SPP = siliqua per plant, SL = Siliqua length (cm), SPS = Seeds per siliqua, TSW = 1000 seed weight (g) and SYP = seed yield per plant (g).

Genetic divergence

Information of the naturally occurring diversity in a population helps to identify diverse groups of genotypes that can be used for hybridization program. The interest of breeders in the use of measurements of genetic diversity dissimilarity as parameters of the indication of parental lines to be used in crosses is based on the biometric relationship between the heterosis manifested in hybrids and the divergence in the gene frequencies of parents . More efforts have been devoted to the study of genetic divergence after proof was obtained for the existence of significant correlation between parental diversity and hybrid performance in different crops.

Assemblage and assessment of divergence in the germplasm is essential to know the spectrum of diversity. In the present investigation, 50 genotypes of mustard were considered for the assessments of genetic diversity by multivariate analysis as per Mahalanobis' (1936) concept of generalize distance (D^2) considering ten important quantitative characters. Using Euclidean distance following Ward's method, the genotypes were grouped into six clusters (Table 10). Sultana (2016) got five clusters from 62 genotypes. Khan (2014) obtained 5clusters. Hence, there is a lot of scope for exchange of genes among genotypes within these clusters.

Cluster Analysis

50 genotypes of *Brassica napus* L. were grouped into six different clusters by applying non-hierarchical cluster using covariance matrix (Table 10). The results were more or less confirmatory with the cluster pattern of the genotypes obtained through Dendogram (Figure 4). Nath *et al.* (2003) reported five clusters and Rameeh (2013) reported 4 clusters in mustard. Cluster II contained the maximum number of 17 genotypes followed by cluster V, cluster VI and cluster III having sixteen, seven and five genotypes, respectively and cluster I having four and cluster IV having only one genotype (Table 10 and Figure 4). Sultana (2016) reported that cluster IV comprised the maximum number (19) ofgenotypes followed by cluster III (18). Zaman *et al.*(2010) found that cluster I contained the highest number of genotypes (6) and the cluster III contained the lowest

(3).Mahmud *et al.* (2008)recorded variable number of genotypes in different clusters. In the present study cluster I contained the 8% genotypes. Cluster II was composed of the 34% genotypes. Cluster III was constituted of 10% genotypes. On the other hand, cluster IV represented 2% genotypes namely G50, cluster V included 32% and cluster VI 14% genotypes included.

In many cases, the same cluster included genotypes from different ecogeographic region indicating the geographic distribution and genetic divergence did not follow the similar trend. This finding was in agreement with the findings of other researcher, Rawhat and Anand (1981), Gupta *et al.* (1991) and Mitra and Saini (1998) reported the non-correspondence of genetic and geographic diversity.

Table 10. Distribution of fifty genotypes in different clusters

Cluster no.	Genotypes	No. of populations	percent
I	G1, G2, G12, G31	4	8
II	G6, G9, G10, G11, G13, G14, G21, G26, G27, G32, G33, G38, G39, G40, G41, G46, G47	17	34
III	G3, G18, G20, G36, G49	5	10
IV	G50	1	2
V	G5, G8, G15, G17, G19, G22, G23, G24, G28, G29, G30, G34, G35, G43, G44, G48,	16	32
VI	G4, G7, G16, G25, G37, G42, G45	7	14
	Total	50	100

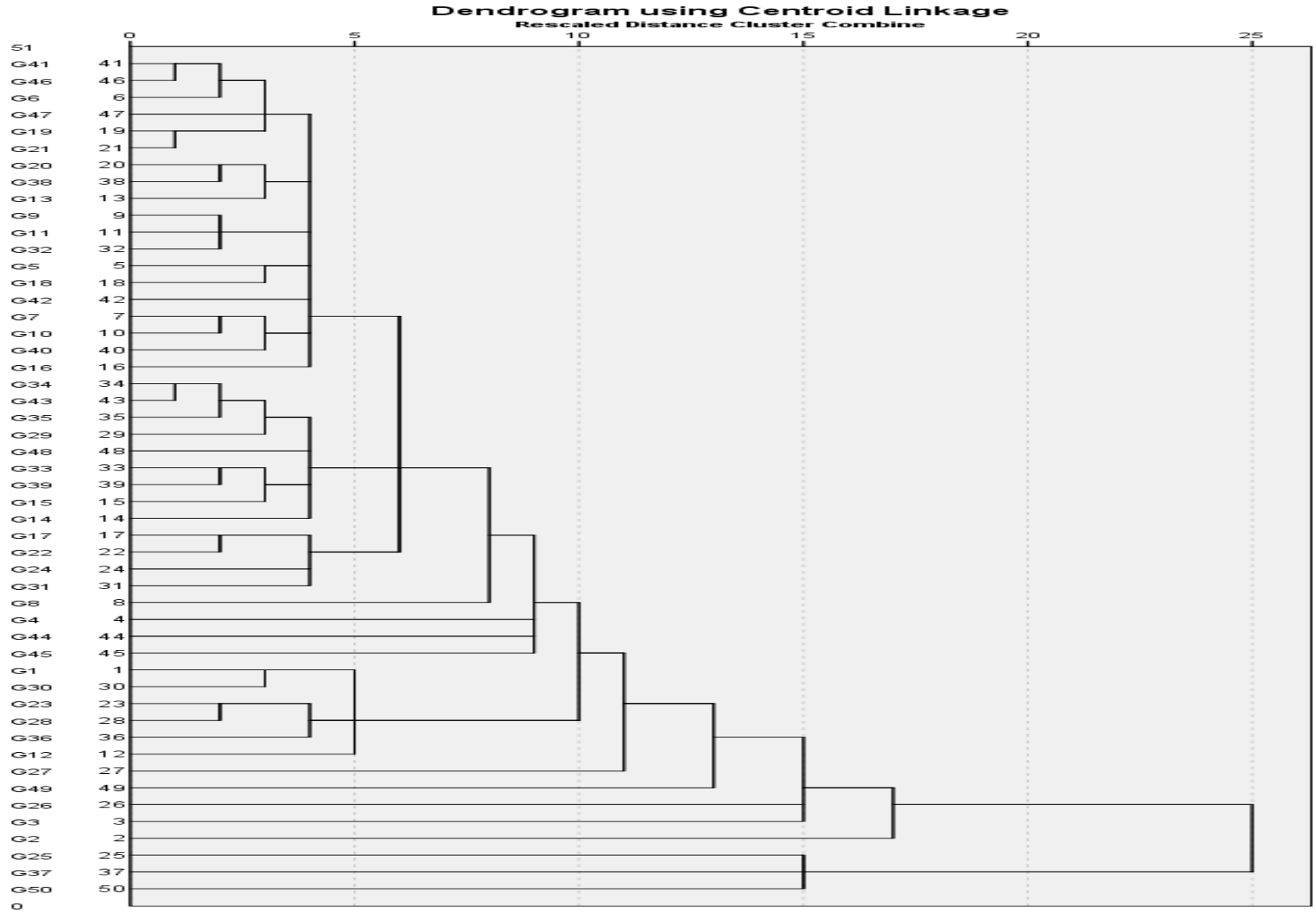


Fig 4.Dendrogram showing different clusters of 50 genotype

Principal Component Analysis (PCA)

PCA is a statistical method which attempts to describe the total variation in multivariate sample using fewer variables than in the original data set. In the end, the analysis results in the identification of the major attributes those are responsible for the observed variation within a given collection. Principal component analysis was carried out with 50 genotypes of *Brassica napus* L. The computed eigen values for the ten variables subjected to principal component analysis, together with the corresponding proportion and cumulative explained variances are given in Table 12. The first principal component accounted for 41.21 % of the total variation while principal components two and three accounted for 16.286 % and 12.874%, respectively (Table 11). Zaman *et al.* (2010) found that first three axes accounted for 94.00% of the total variation whereas the first principal components accounted for 81.94%. However, Khan (2014) reported that first three principal components accounted for 70.27% of the total variation where the first principal components accounted for 28.65%.

Scree plot is a useful visual aid to determine an appropriate number of principal components. The magnitude of an eigen values versus its number with the eigen values ordered from largest to smallest. To determine the appropriate number of components, we look for an elbow (bend) in the scree plot. The number of components is taken to be the point at which the remaining eigenvalues are relatively small and all about the same size. In this case, it appears without any other evidence, that three sample principal components effectively summarized the total sample variance (Figure 5). The first three principal axes accounted for 70.367% of the total variation among the characters describing 50 genotypes of *Brassica napus* L.

Table 11. Eigen values and yield percent contribution of ten characters of 50genotypes

Principal component axes	Eigen values	Percent variation	Cumulative % of Percent variation
I	4.121	41.207	41.207
II	1.629	16.286	57.493
III	1.287	12.874	70.367
IV	0.984	9.837	80.204
V	0.739	7.390	87.594
VI	0.414	4.138	91.731
VII	0.307	3.073	94.804
VIII	0.248	2.478	97.281
IX	0.167	1.671	98.953
X	0.105	1.047	100.000

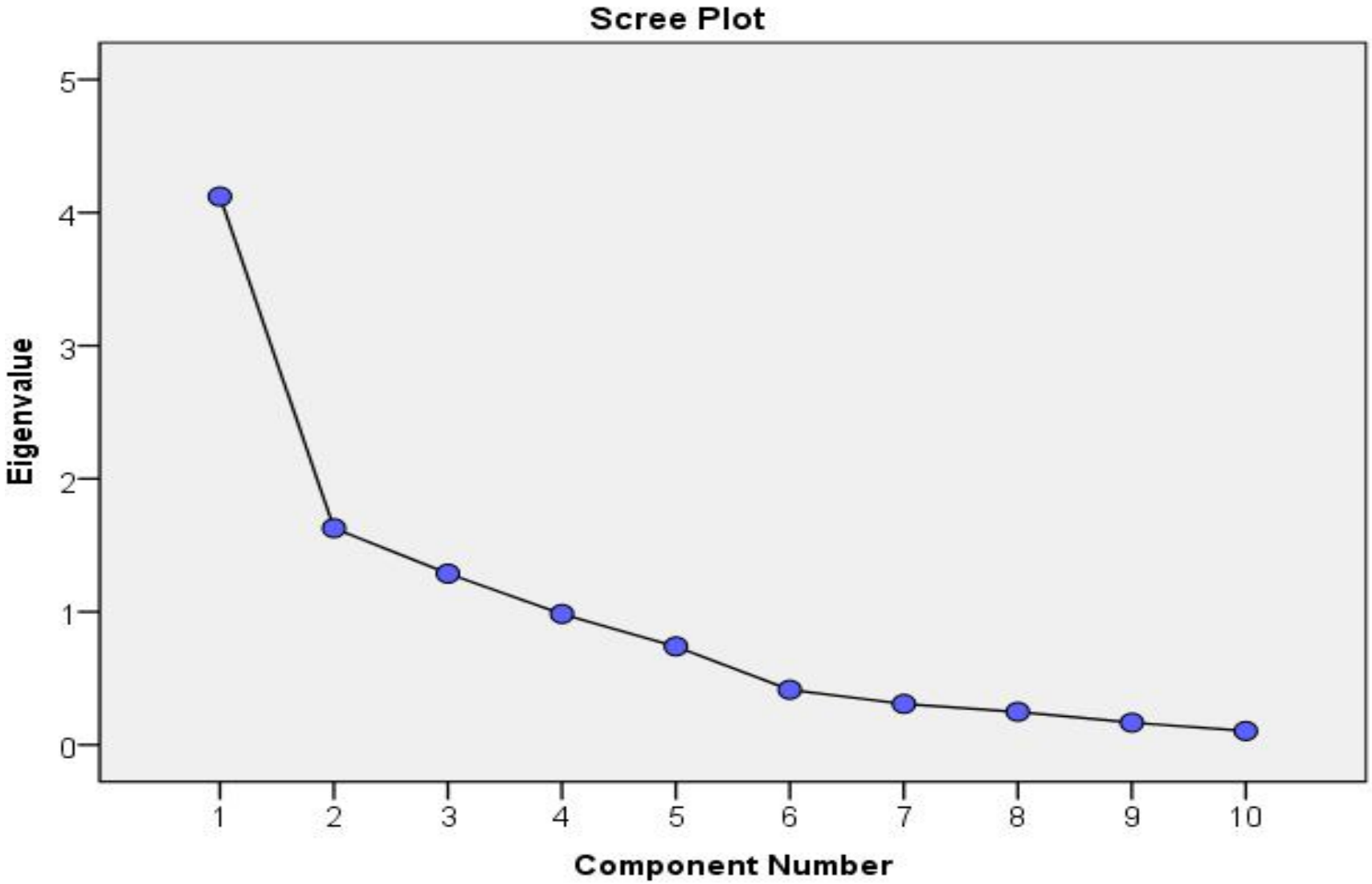


Fig 5.Graphical representation of scree plot by using eigen values of component axes

Contribution of characters towards divergence of the genotypes,the factor loadings of characters from PCA retained three components identified the major characters responsible for maximum variability (Table 12). The first principal component (PC1) can be consider as the component of siliqua per plant (0.901), seed yield per plant (0.818), primary branches per plant (0.758), secondary branches per plant (0.743), plant height (0.636) and 1000 seed weight (0.604). Principal component II (PC2) on the other hand indicated the importance of days to maturity (0.906) and days to 50% flowering (0.874). The characters associated with the principal component III (PC3) were siliqua length (0.840) and seeds per siliqua (0.799) for high loadings.

Table 12.Factors loadings for component character traits in principal component 1-3.

	Component		
	PCA1	PCA2	PCA3
SPP	0.901	0.228	0.160
SYP	0.818	0.226	0.258
PBP	0.758	0.103	-0.246
SBP	0.743	0.003	-0.181
PH	0.636	0.184	0.395
TSW	0.604	0.162	0.250
DM	0.144	0.906	0.002
DF	0.266	0.874	0.001
SL	0.005	0.138	0.840
SPS	0.127	-0.120	0.799

D50F = days to 50% Flowering, D80M = days to 80% Maturity, PH = plant height (cm), PBP = primary branches per plant, SBP = secondary branches per plant, SPP = siliqua per plant, SL = Siliqua length (cm), SPS = Seeds per siliqua, TSW = 1000 seed weight (g) and SYP = seed yield per plant (g).

Canonical Variate Analysis (CVA)

CVA was done to compute the inter-cluster distances. The values of inter-cluster distance (D2) are presented in Table 13. In this experiment, the inter-cluster distances were higher than the intra-cluster distances which indicated considerable range of genetic diversity among the genotypes of different groups. Mahmud *et al.*(2011) and Zahan *et al.*(2008) also reported similar result in Brassica. The highest inter-cluster distance was observed between cluster I and IV (113.901), followed by those of between cluster III and IV (96.083), cluster IV and V (89.330), cluster II and IV (71.587) and cluster I and VI (71.499). The maximum values of inter-cluster distance indicated that the genotypes belonging to cluster Iwere far away from those of cluster IV. In contrast, the lowest inter-cluster distance was observed between cluster III and V (14.760) followed by those of cluster II and V (19.131), I and III (20.135) (Table 14). However, genotypes from clusters I and IV if involved in hybridization may produce a wide spectrum of segregating population. Choudhary and Joshi (2001) reported that the derivatives selected from cross of diverse parents revealed greater diversity. Khan (2000) and Dhillon *et al.* (1990) also mentioned that maximum inter-cluster distance of parents gave desirable segregants for the development of high yielding varieties with quality. The genotypes of cluster III and V were genetically closed.

The intra cluster distance of cluster II had 7.44containing 17 genotypes which was the highest value that indicated the highest amount of genetic divergence within the group.

Thus, hybridization among genotypes drawn from these widely divergent clusters with high yield potential would likely to produce heterotic combinations and wide variability in segregating generations. Therefore it could be concluded that the genotypes present in combination of those clusters could be utilized for successful breeding programme.

Table 13.Intra (Bold) and inter cluster distances (D^2) for 50 genotypes

Cluster	I	II	III	IV	V	VI
I	**4.66**	42.478	20.135	113.901	25.366	71.499
II		**7.44**	24.973	71.587	19.131	29.100
III			**3.45**	96.083	14.760	53.599
IV				**0.00**	89.330	42.737
V					**5.33**	47.236
VI						**4.76**

Table 14. The nearest and farthest clusters from each cluster between D^2 values in rapeseed

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	I	III (20.135)	IV (113.901)
2	II	V (19.131)	IV (71.587)
3	III	V (14.760)	IV (96.083)
4	IV	VI (42.737)	I (113.901)
5	V	III (14.760)	IV (89.330)
6	VI	II (29.100)	I (71.499)

Cluster Mean

The mean values of each cluster for ten characters are presented in Table 15. There was wide range of variation in the cluster mean values for all the characters. The mean values of all characters for the respective clusters were categorized into high and low value. The present study revealed that clustersIV possessing high mean values for most of the desirable traits that means seven traits were desired to be crossed with cluster I which possessed low mean values for seven traits. This finding was strongly supported with identification of similar cluster combinations from interpretation of intercluster distance made in the present study and thereby the expected progenies inculcate traits in a positive direction and further selection would be more effective.

The genotypes from cluster IV earned the highest cluster mean values for number of primary branches per plant (7.10), number of secondary branches per plant (3.90), number of siliquae per plant (190.97), seed yield per plant (11.67 g), plant height (119.97 cm), days to 50% flowering (50.33) and days to 80% maturity (92.33), indicating high yielder and late maturing genotypes under this cluster. On the other hand, Cluster I produced the lowest mean values for days to 80% maturity (86.00), plant height (92.13), primary branches per plant (2.68), secondary branches per plant (1.36), siliqua per plant (81.17), 1000 seed weight (2.72) and seed yield per plant (6.62), indicating early maturing and low yielder genotypes constituted this cluster. If parents from cluster I and IV are involved in hybridization program then the highest heterosis in respect of yield, earliness, tallness, higher number of branches, seeds and siliquae per plant might be obtained. Srivastav and Singh (2000) reported that cluster III had the highest number of primary and secondary branches and the highest mean value for seed yield per plant and cultivars in cluster V with 1000-grain weight supported this result. Cluster V showed better performance in case of early flowering (42.69) and early maturity (86.02 days), On the other hand the genotypes included in cluster VIhighest mean for seeds per siliqua (23.53) and 1000 seed weight (3.99).

Table 15. Cluster mean for ten yield and yield related characters in 50rapeseedgenotypes

Characters	I	II	III	IV	V	VI
Days to 50% Flowering	43.58	45.00	43.67	50.33 H	42.69 L	45.71
Days to 80% Maturity	86.00 L	88.43	86.60	92.33 H	86.02 L	88.48
Plant height (cm)	92.13 L	104.64	104.72	119.97 H	93.84	111.61
Primary branches per plant	2.68 L	3.35	2.71	7.10 H	3.23	3.91
Secondary branches per plant	1.36 L	1.92	1.73	3.90 H	2.18	3.07
Siliqua per plant	81.17 L	121.54	96.74	190.97 H	106.38	149.68
Siliqua length (cm)	8.24	7.56	7.21	7.44	7.01	7.96
Seeds per siliqua	20.45	21.89	21.82	22.26	19.65 L	23.53 H
1000 seed weight (g)	2.72 L	3.74	3.23	3.44	3.27	3.99 H
seed yield per plant (g)	6.62 L	9.02	7.35	11.67 H	7.34	10.19

L = Lowest value
H = Highest value

Selection of genotypes as parent for hybridization program

Selection of genetically diverge parents is the prime task for any plant breeding activities. Considering magnitude of genetic distance, contribution of different characters towards the total divergence, magnitude of cluster means for different characters and field performance the genotypes G1 and G31 from cluster I; genotype G50 from cluster IV, genotypesG15, G35, G34, G43 from cluster V andgenotypes would be considered as better parents for release as open pollinated variety or further use in future hybridization program.

Table 16. Saline features of selected genotypes under clusters

Cluster No.	Genotypes	Main features
I	G1 G31	Early maturing Short plant statue Small seeded Low yielder
IV	G50	Late maturing Tall plant Highest branches per plant Highest siliqua per plant Highest yield
V	G15 G35 G34 G43	Early flowering and maturity
VI	G4 G7 G37	Highest seed per siliqua **Coarse** seeded High yielder

CHAPTER V
SUMMARY AND CONCLUSION

The present investigation was carried out to study genetic variability, character association, path analysis and genetic diversity on seed yield and related traits in mustard to identify the superior genotypes on yield and other desirable attributes. The experimental material consisting of 50 genotypes of mustard were raised in RCBD Design with three replications at Experimental Farm, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka during Rabi season 2015-16. The data was recorded on seed yield per plant and various other morphological traits viz., days to 50% flowering, days to 80% maturity, plant height, primary branches per plant, secondary branches per plant, siliqua per plant, siliqua length, seeds per siliqua and 1000 seed weight. The maximum days to 50% flowering was observed in genotype G25 (51.33)and the lowest found in the genotype G3. The maximum days to 80% maturity (93.00) was found in G11 whereas the minimum (75.00) from G3. The maximum plant height was observed by the genotype G25 (126.09 cm) and the minimum in G29 (83.33 cm). The maximum primary branches per plant (7.10) was found in G50whereas the minimum (2.37) from G2. The genotype G37 recorded the maximum secondary branches per plant (5.37) while the minimum was noticed by the genotype G1 (0.87). The maximum siliqua per plant was found in the genotype G50 (190.97) while the minimum was observed in G12 (72.87). The maximum seeds per siliqua was found by the genotype G26 (30.45) and the minimum was recorded from the genotype G31 (14.09). The maximum 1000 seed weight was observed in the genotype G25 (4.52 g) and the minimum was exhibited in the genotype G12 (2.14). The maximum seed yield per plant was observed in G25 (11.77 g) while the minimum in G12 (5.45 g).

Analysis of variance indicated significant differences among all the traits studied suggesting prevalence of wide range of genetic variability and scope of selection for these traits.

The highest genotypic variance and phenotypic variance were 652.10 and 417.25 respectively in siliqua per plant indicated the presence of high variation for this trait. The lowest environmental, genotypic and phenotypic variances were also 0.03, 0.31 and 0.35, respectively for 1000 seed weight indicated the presence of low variation for this trait. The highest phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were 46.91 and 39.05 respectively both of which were recorded for secondary branched per plant. The present result revealed that, higher PCV and GCV were recorded for primary branches per plant (26.85% and 23.78%), secondary branches per plant (46.91% and 39.05%), siliqua per plant (21.96% and 17.56%) and seed yield per plant (20.77% and 17.97%). The present study revealed high heritability coupled with high expected genetic advance as percent of means were observed in case of primary branches per plant (78.41 and 43.37), secondary branches per plant (69.29 and 66.96), siliqua per plant (63.99 and 28.94), 1000 seed weight (89.95 and 31.27) and seed yield per plant (74.84 and 32.02), respectively indicating good response to selection for these characters.

Seed yield per plant was significant and positive correlation with plant height (0.950** and 0.254**), primary branches per plant (0.977** and 0.239**), secondary branches per plant (0.665** and 0.432**), siliqua per plant (0.950** and 0.315**), seeds per siliqua (0.947** and 0.143), 1000 seed weight (0.974** and 0.305**) at both genotypic and phenotypic level. Days to 80% maturity (-0.860** and -0.262**) was significantly and negatively correlated with seed yield per plant at both level indicating that seed yield per plant would be increased with the decrease of those characters. Siliqua per plant showed positively significant with seeds per siliqua (0.260** and 0.220**) and 1000 seed weight (0.625** and 0.459**).

Partial correlation analysis (Table 8) indicated that 1000 seed weight and siliqua per plant was significantly correlated with seed yield per plant and indicated that 1000 seed weight contributed over 48% and siliqua per plant contributed over 37% to total seed yield. Yield showed a significant linear regression coefficient with 1000 seed weight and siliqua per plant. Number of siliqua per plant (9.535) and plant height (0.834) had high positive direct effects on seed yield per plant.

By genetic divergence analysis the 50 genotypes were grouped into six clusters. Cluster II contained the maximum number of 17 genotypes followed by cluster V (16). The first principal component accounted for 41.207 % of the total variation while principal components two and three accounted for 16.286 % and 12.874%, respectively. The first three principal axes accounted for 70.367% of the total variation among the characters describing 50 genotypes of *Brassica napus* L. The first principal component (PC1) can be considered for siliqua per plant (0.901), seed yield per plant (0.818), primary branches per plant (0.758), secondary branches per plant (0.743), plant height (0.636) and 1000 seed weight (0.604). PC2 importance for days to maturity (0.906) and days to 50% flowering (0.874) and PC3 was important for siliqua length (0.840) and seeds per siliqua (0.799) for high loadings. The highest inter-cluster distance was observed between cluster I and IV (113.901), followed by those of between cluster III and IV (96.083), cluster IV and V (89.330). The lowest inter-cluster distance was observed between cluster III and V (14.760). The intra cluster distance of cluster II had 7.44containing 17 genotypes which was the highest value that indicated the highest amount of genetic divergence within the group.

The present study revealed that clusters IV possessing high mean values for most of the desirable traits that means seven traits are desired to be crossed with cluster I which possessed low mean values for seven traits.

CONCLUSIONS

Best performing genotypes viz., G50, G7 and G37 were found for high yielder. G50 was totally different from other genotypes. The results of the present experiment revealed that the variability which existed among the selected mustard genotypes were much wider. Crossing program should be taken between cluster I and cluster IV; cluster IV and cluster V genotypes. It would produce more diversed lines for future early variety release. Among these cultivars, the superior genotypes may be used in future breeding program to develop short duration cultivar of mustard. This variability may be used for the selection of superior and short duration genotypes for commercial cultivation and at the farmer's level as well as for breeding new genotypes of mustard in our country.

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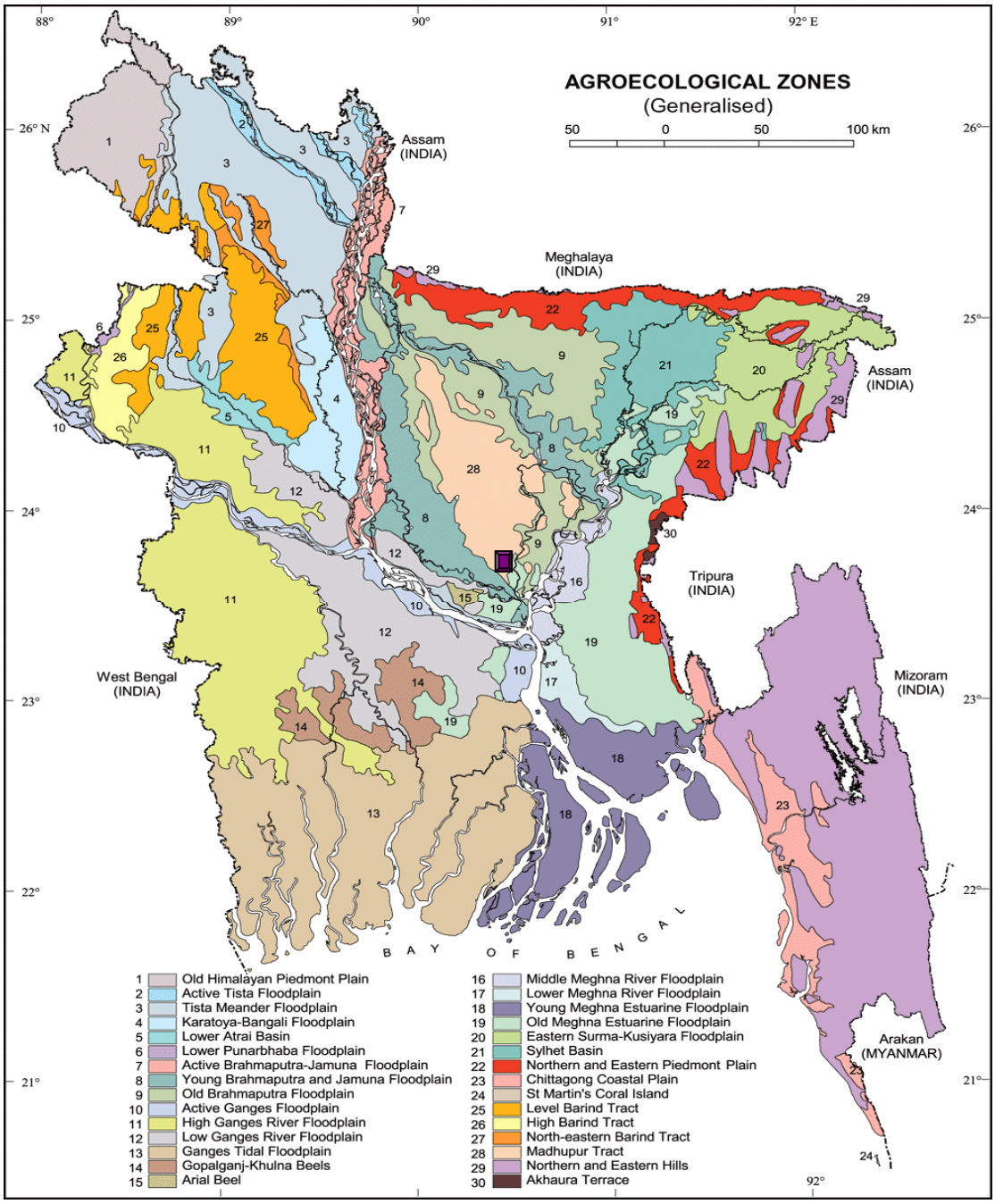
APPENDICES

Appendix I. Map showing the experimental site under the study



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

A. Physical composition of the soil

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

B. Chemical composition of the soil

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

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

Appendix III. Monthly average temperature, relative humidity and total rainfall and sunshine of the experimental site during the period from November, 2015 to February, 2016.

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
November, 2015	34.7	18.0	77	227	**5.8**
December, 2015	32.4	16.3	69	0	**7.9**
January, 2016	29.1	13.0	79	0	**3.9**
February, 2016	**28.1**	**11.1**	**72**	**1**	**5.7**

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

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

Genotype	50F	DM	PH	NPB	NSB	NSP	SL	NSS	TSW	SYP
G1	43.33	78.33	92.35	2.60	O.87	81.73	7.53	18.90	2.20	6.58
G2	42.33	90.67	94.10	2.37	1.30	83.07	11.30	24.35	3.03	6.73
G3	37.67	75.00	107.85	2.50	1.30	97.53	7.33	20.50	3.18	8.22
G4	44.00	84.33	118.73	4.17	2.43	156.10	7.22	22.60	3.98	10.12
G5	41.33	88.67	97.99	2.60	3.83	106.47	7.15	22.82	3.12	9.07
G6	43.00	90.00	105.70	3.60	2.10	116.97	8.03	22.39	3.24	8.95
G7	46.67	89.67	101.73	3.20	2.00	146.80	7.98	23.40	4.20	10.96
G8	41.00	88.33	92.37	2.68	2.26	76.47	8.38	23.33	3.73	10.11
G9	43.67	91.67	105.67	3.23	1.70	125.87	7.90	25.93	3.81	8.70
G10	46.67	87.67	105.53	3.10	2.27	130.87	7.17	21.25	3.90	10.76
G11	45.33	93.00	108.80	3.30	0.93	109.93	8.64	24.60	3.68	8.28
G12	40.67	86.00	89.53	2.63	1.13	72.87	8.26	24.45	2.14	5.54
G13	43.67	82.00	112.60	3.06	3.29	117.03	8.01	23.31	3.61	9.82
G14	41.33	86.00	115.02	2.74	2.60	98.57	7.65	21.73	3.48	8.69
G15	41.00	87.00	97.22	3.58	2.71	99.17	6.37	15.87	3.96	7.03
G16	41.00	78.00	97.37	2.46	2.12	94.66	7.72	21.00	3.50	9.67
G17	42.00	86.67	115.03	2.71	3.10	106.53	7.58	20.43	3.74	6.84
G18	39.00	82.00	105.63	3.66	2.73	91.53	7.38	19.33	3.94	9.11
G19	39.00	82.00	88.83	2.63	1.89	111.09	7.98	23.17	3.40	7.69
G20	42.00	77.00	103.03	2.47	1.31	78.92	7.22	19.27	3.49	7.70
G21	38.00	82.00	113.72	2.56	2.32	93.46	7.09	16.73	3.54	8.13
G22	42.00	81.00	90.71	2.63	1.06	57.90	8.20	22.29	3.56	7.74
G23	41.00	84.00	114.06	3.19	1.98	86.53	6.92	18.98	3.19	6.76
G24	42.00	75.00	104.97	2.65	1.58	74.37	8.19	23.67	2.94	8.78
G25	51.33	91.00	126.09	3.70	2.83	155.87	8.50	22.55	4.52	11.77
G26	41.00	84.00	103.03	2.93	1.41	59.93	8.70	21.43	3.41	9.25
G27	42.00	82.00	107.60	2.09	1.24	64.99	7.29	19.87	3.34	10.22
G28	44.00	89.00	98.60	2.60	1.33	79.09	8.35	21.43	3.14	6.11
G29	41.67	84.00	83.33	3.93	1.97	109.47	7.10	21.97	3.38	6.71
G30	42.00	76.00	99.02	2.92	1.89	64.59	7.25	19.34	3.67	5.91
G31	44.67	80.00	102.03	2.38	1.89	85.00	8.01	24.66	3.13	7,71
G32	43.00	79.00	112.72	2.49	1.72	83.27	7.23	25.63	2.91	7.78
G33	45.00	81.00	110.87	2.60	1.68	63.22	8.52	23.11	3.67	8.82
G34	38.67	82.00	105.30	2.89	1.31	71.93	8.05	22.29	2.94	6.75
G35	40.33	84.00	97.33	2.60	1.83	105.60	6.45	24.41	3.23	6.85
G36	39.00	79.00	99.87	2.43	1.90	73.47	7.28	18.56	3.52	5.88
G37	46.00	88.00	108.43	4.67	5.37	166.37	8.32	24.37	4.37	10.70
G38	42.00	78.80	95.59	2.88	2.26	81.98	7.82	22.10	3.49	9.34
G39	41.00	79.33	103.20	3.47	2.40	117.37	6.97	21.37	4.11	8.48
G40	42.00	81.00	98.75	2.87	2.58	94.73	8.45	22.53	3.21	9.78

Appendix IV. Continued

G41	44.00	88.00	110.57	3.97	1.67	119.77	6.80	20.93	4.18	8.73
G42	44.33	86.67	107.07	2.90	2.70	137.37	8.10	26.27	3.21	9.74
G43	41.67	88.00	91.90	2.67	1.63	99.00	7.42	19.28	3.44	6.76
G44	48.33	90.33	92.00	2.48	3.23	108.20	6.59	19.65	3.42	6.53
G45	46.67	91.67	108.33	5.17	3.34	149.50	7.15	22.97	2.69	8.31
G46	44.00	87.33	105.97	3.83	2.07	122.33	6.49	21.75	3.22	8.54
G47	46.00	89.00	109.83	4.10	3.17	128.27	7.13	18.20	3.33	9.11
G48	40.33	79.33	90.60	3.40	2.40	103.37	7.39	24.90	3.41	7.74
G49	49.67	91.00	109.90	2.83	0.97	92.57	6.61	21.16	2.61	5.84
G50	50.33	92.33	119.97	7.10	3.90	190.97	7.44	22.26	3.44	11.67
MIN	37.67	75.00	83.33	2.37	0.87	72.87	5.85	14.09	2.14	5.45
MAX	51.33	93.00	126.09	7.10	5.37	190.97	11.30	30.45	4.52	11.77
MEAN	44.22	87.37	101.48	3.35	2.14	116.31	7.46	21.29	3.49	8.34

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