GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS IN F_3 GENERATION OF *Brassica napus* L.

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CERTIFICATE

This is to certify that thesis entitled, **"GENETIC VARIABILITY, CORRELATION AND PATH ANALYSISININ F_3 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 **SANJIDA AHMED SHAWON**, **REGISTRATION NO. 10-03969,** 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.

Date: June, 2016
Place: Dhaka, Bangladesh

_____
Prof. Dr. Firoz Mahmud
Supervisor

DEDICATED
TO
MY FATHER & MOTHER

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ABSTRACT

An experiment was carried out with 69 genotypes of *Brassica napus* L. in the experimental farm, Sher-e-Bangla Agricultural University (SAU), Dhaka during November 2015 to February 2016 for estimation of character association and genetic diversity. Analysis of variance revealed significant differences among the genotypes for days to 50% flowering, days to 80% maturity, plant height, branches per plant, siliqua per plant, seeds per siliqua, thousand seeds weight and seed yield per plant. The phenotypic variance and phenotype coefficient of variation were higher than the corresponding genotypic variance and genotypic coefficient of variation. High heritability with high genetic advance in percent of mean was observed for secondary branches per plant, siliqua per plant, 1000-seed weight and seed yield per plant. The significant positive correlations of seed yield per plant were found with plant height, primary branches per plant, secondary branches per plant, siliqua per plant and 1000-seed weight in both genotypic and phenotypic level. Siliqua length, days to 50% flowering and days to 80% maturity was correlated negatively with seed yield per plant. Partial correlation was significant for 1000seed weight, siliqua per plant, plant height and primary branches per plant. Yield showed a significant linear regression coefficient with 1000-seed weight, siliqua per plant, plant height, and primary branches per plant. Path analysis revealed that plant height, primary branches per plant, siliqua per plant, seeds per siliqua and 1000 seeds weight had the positive direct effect on yield per plant. Sixty nine genotypes were grouped into six different clusters and the highest 26 genotypes included in the cluster III. Eigen values of principal component axes showed that three Eigen values above unity accounted for 58.004%. The present study revealed that the cluster V with high mean values for four traits were desired to be crossed with cluster I which possessed low mean values of three characters for getting high heterosis. Same cross between clusters V and II; V and IV. The highest inter-cluster distance was observed between clusters I and VI and the maximum intra-cluster distance was found in cluster V. The results of the present experiment revealed that identification of superior genotypes were G42, G33, G67, G2, G65, G5, G62, G28, G59, G64 and G69. They might be used as open pollinated varieties and parents in future hybridization program.

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ABBREVIATIONS

Full word	Abbreviation
Percent	%
Degree Celsius	^{0}C
At the rate	@
Phenotypic variance	σ^2_p
Genotypic variance	σ^2_g
Environmental variance	σ^2_e
Broad sense heritability	h^2_b
Agro Ecological Zone	AEZ
Agriculture	Agric.
Agricultural	Agril.
Agronomy	Agron.
Analysis of variance	ANOVA
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Bangladesh	BD
Centimeter	cm
Coefficient of Variation in percent	CV%
Cultivars	cv.
Degrees of freedom	Df
And others	*et al.*
Etcetera	etc.
The third generation of a cross between two dissimilar homozygous parents	F_3
Food and Agriculture Organization	FAO
Gram	g
Genotype	G
Genetic Advance	GA
Genotypic coefficient of variation	GCV
Harvest Index	HI
Indian Agricultural Research Institute	IARI
International Center for Agricultural Research in Dry Areas	ICARDA
Journal	J.
Kilogram	Kg
Meter	M

ABBREVIATIONS (*Continued*.)

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

CHAPTER I

INTRODUCTION

Brassica is a genus of plants in the mustard family (Brassicaceae). This family includes about 300 genus and about 3700 species. The members have a cosmopolitan distribution around the world. The members of the genus are collectively known as cruciferous vegetables, cabbages, or mustards. It comprises of several economically important species which yield edible roots, stems, leaves, buds, flowers and seeds condiment. Most of the species are used as oilseed crop and some as forage. Oilseed *Brassica* is commonly known as rapeseed and mustard and occupy an important position in the rainfed agriculture of our country. They provide the most concentrated source of energy and also help to absorb vitamins A, D, E and K. Its cultivation has increased dramatically during last decades. It is the second highest source of edible oils supply in the world after soybean (FAO, 2014).

Rapeseed is one of the most important oil and protein rich annual crops in the world. Oils and fats lipids extracted from vegetables are constituting an important component of human diet. Oils extracted from plant origin are nutritionally superior to that of animal origin. Therefore, vegetable oil has been always considered as a major component for food preparation. Bangladesh produces good number of oil seed crop like mustard, sesame, groundnut, linseed, niger, safflower, sunflower, soybean, castor etc. *Brassica* oil crops are the most important group of species that supply major edible oils in Bangladesh (BBS, 2013). Mustard and rapeseed seeds contain 42% oil, 25% protein (Khaleque, 1985). The mustard oil is used not only for edible purpose but also in different types of pickles preparation. The oil cake is used as a very good animal feed and organic manure for various field crops. It contains proteins of high biological value and applicable quantities of calcium and phosphorus.

Bangladesh required 0.30 million tons of oil equivalent to 0.85 million tons of oil seed for nourishing her people. At present, the oil seed production is about 0.26 million tons, which covers only 30% of the domestic need (BBS, 2011). About 70% of requirement of oil has been imported every year by spending huge amount of foreign currency involving Tk. 2951core (BBS, 2011). Per capita consumption of edible oil is the lowest in Bangladesh from the world (11g/head/day) which is one fifth of the recommended requirement for a balanced diet (FAO, 2014). The genomic constitutions of the three diploid elemental species of *Brassica* are AA for *Brassica campestris*, BB for *Brassica nigra* and CC for *Brassica oleracea* having diploid chromosome number of 20, 16 and 18 respectively. On the other hand the species *Brassica juncea* (AABB), *Brassica carinata* (BBCC) and *Brassica napus* (AACC) are the amphidiploids. Approximately, 70% of the total cultivated mustard in Bangladesh which is the variety of either *Brassica rapa* or *Brassica napus*. Among the oilseed crops *Brassica rapa*, *B. napus* and *B. juncea* is known as rapeseed, oilseed rape or canola (Khan *et al*., 2008). *B. rapa* and *B. napus* is referred as rapeseed where the rest one is known as mustard.

The seed yield of mustard/rapeseed in Bangladesh is about 740kg/ha, which is very low in comparison to other developed countries (2400 kg/ha) (FAO, 2014). On the other hand, Bangladesh produces soybean but no method for oil extraction from soybean available whereas Bangladesh has extraction mechanism available for mustard. So, giving emphasis on mustard can help us to save foreign currency.

Improvement of existing oilseed crops and introduction of a new oilseed need urgent attention to increase the domestic production that may reduce the huge shortage of oils. The most of the released mustard cultivars are generally long in duration and thus, did not fit well for cultivation in cropping pattern. If we can develop new lines which would be successfully cultivated between Aman and Boro rice rotation without affecting present cropping pattern, since after Aman rice harvest and before the transplantation of Boro rice 70-80 days are available for cultivating gap filling crop. So, it is urgent to analyze the genetic diversity and its

response for the selection of good mustard genotypes for increasing our cropping intensity.

Nature and magnitude information of variability present in the existing material and association among the various morphological characters is a pre-requisite for any breeding programme to be initiated by the local breeder for high yields. However, seed yield, a complex character is usually controlled by non-additive gene actions and it is not only influenced by a number of other morphological characters which are governed by a large number of genes, but also environment to a great extent. Thereby, the heritable variation creates difficulty in a selection programme. Therefore, it is necessary to partition the overall variability into heritable and non-heritable components which enables the breeders to adopt suitable breeding procedure for further improvement of genetic stocks.

Systematic plant breeding program can be divided into three steps viz. building up a gene pool of variable germplasm, selection of individual from the gene pool and utilization of selected individual to evolve a superior variety (Chauhan and Singh, 1985). The knowledge of genetic variability present in the population, heritability of economically important characters and correlation coefficients of those characters is very important before launching an effective breeding program. A plenty of scope is possible 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). Genetic diversity is the basic for genetic improvement. It is widely accepted that information about germplasm diversity and genetic relatedness among elite breeding material is a fundamental element in plant breeding (Mukhtar *et al*., 2002 and Khaleque, 1985).

Genetic diversity is very important factor for any hybridization program aiming at genetic improvement of yield especially in self pollinated crops (Joshi and Dhawan, 1966). Different methods have been used to assess genetic diversity. This can be obtained from pedigree analysis, morphological traits or using molecular markers. With the development of advanced biometrical method such as multivariate analysis (Rao, 1952) based on Mahalanobis' (1936) D^2 statistics and Ward's no-hierarchical squared Euclidean distance method have become possible to quantity magnitude of diversity among germplasm for their evaluation in respect of breeding program.

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

Objectives:

- To study the variability of important quantitative characters.
- To study the characters association of yield contributing characters among themselves and with yield; and their direct and indirect effects.
- To assess genetic diversity among the genotypes and
- To select promising genotypes considering high yield with early maturity.

CHAPTER II

REVIEW OF LITERATURE

Brassica species has received much attention by a large number of researchers on various aspects of its production and utilization. Brassica species is the most important oil crop of Bangladesh and many countries of the world too. Many studies on the genetic analysis that means variability, character association, path co-efficient analysis, genetic diversity have been carried out in many countries of the world. The review of literature concerning the studies presented under the following heads:

2.1 Genetic variability, heritability and genetic advance

Information on genetic variation, heritability and expected genetic advance of different characters of a set of mustard populations is important because these genetic parameters are reported to be influenced by growing environmental conditions. As a matter of fact different workers reported various magnitude of the extent of genetic variation, heritability and genetic advance for the same character. In the present study these genetic parameters were estimated in mustard and the information would be helpful for breeding programs.

Shaukat *et al*. (2015), evaluated eight *Brassica napus* genotypes to investigate genetic variability and heritability. They reported that analysis of variance showed highly significant differences ($P \leq 0.01$) among *Brassica napus* genotypes for primary branches per plant. The coefficient of variation for primary branches was 13.04%. High broad sense heritability estimates were observed for primary branches per plant (0.83), plant height (0.78), pods per main raceme (0.65), seeds per pod (0.61), 1000-seed weight (0.61), while moderate heritability values were recorded for pod length (0.57), pods per plant (0.55), and seed yield per plant (0.50).

Bilal *et al*. (2015), evaluated 23 genotypes of *Brassica napus*. The study was undertaken 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.

Rameeh (2015), reported that broad sense heritability estimates varied from 0.18 to 0.98 for pods length and days to end of flowering. High broad sense heritability was determined for phonological traits, plant height and seed yield demonstrating selection gain for improving these traits will be high. Pods on main axis and pods per plant had high value of genetic coefficient of variation.

Sharafi *et al*. (2015), studied 28 winter rapeseed cultivars to evaluate genetic variation. They reported that yield, number of branches per plant and plant height had the highest variation. Broad sense heritability estimates ranged from 6% to 87% for seed yield and pod length, respectively. These results showed that cultivars with higher number of pod per plant had higher seed production.

Walle *et al.* (2014), carried out a study with thirty six genotypes of Ethiopian mustard (*Brassica carinata*) and result revealed that there were significant difference in days to 50% flowering, plant height and primary branches per plant. GCV was lower than the PCV for all yield related characters studied. High heritability with high genetic advance was observed in plant height, number of secondary branches per plant and days to 80% maturity.

Mekonnen *et al.* (2014), evaluated thirty six genotypes of Ethiopian mustard, *Brassica carinata* to study variability. The GCV ranged from 4.3% to 44.14% and PCV from 8.3% to 91.7%. Comparatively high GCV estimates were observed for

number of pods per plant, primary and secondary branches per plant, seed yield per plot, and seed yield per hectare. The highest PCV was in primary branches per plant. Higher GCV and PCV for seed yield, number of pods per plant, primary and secondary branches which indicated that, it might provide better scope for improvement through selection. Besides these, higher heritability along with higher genetic advance was observed in days to maturity, days to flowering, grain-filling period, number of pods per plant, secondary branches per plant, plant height, seed yield/plot and hectare and lowest one was in primary branches per plant.

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

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. 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.

Ali *et al.* (2013), conducted an experiment with thirty lines of *Brassica carinata* and reported that PCV and GCV ranged from 4.92-48.24% and 3.2-38.1%, respectively. The highest heritability values were recorded for pod length (0.83) followed by pods on main raceme and the genetic advance as percent of mean was the highest for seed yield per plant and pods on main raceme. 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 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.

Rameeh (2011), conducted an experiment with thirty-six rapeseed genotypes including four cultivars and 32 advanced lines. He found that most variations among the genotypes were in seeds per siliqua and siliquae on main raceme with 18.0 and 25.3 per cent coefficient of variation, respectively. Heritability (bs) estimates were high for siliquae on main raceme, seeds per siliqua and siliquae per plant (0.70, 0.77 and 0.81, respectively).

Afrin *et al.* (2011), conducted an experiment in *Brassica napus* and studied heritability. The plant height showed highest value of broad sense heritability while the number of primary branches per plant, number of secondary branches per plant, siliqua length, number of seed per siliquae, number of siliqua per plant, thousand seed weight and seed yield per plant showed moderate broad sense heritability. Days to 80% maturity showed lowest heritability.

Alam (2010), conducted an experiment by using twenty six F_4 populations of *Brassica rapa* L. to study the variation among them. Higher phenotypic variation was present than the genotypic variation. High heritability with high genetic advance was found for plant height, number of primary branches per plant, number of secondary branches per plant and number of siliquae per plant.

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 two years. They observed the maximum broad sense heritability get genetic advance seed yield. A field experiment was conducted by Jahan (2008) to study on inter-genotypic variability

in 10 F_4 lines along with 8 varieties of *Brassica rapa*. Significant variation was observed among all genotypes for all the characters studied. High genotypic co-efficient of variation (GCV) was observed for secondary branches per plant, siliquae per plant, yield per plant. High heritability with low genetic advance in percent of mean was observed for days to maturity which indicated that non-additive gene effects were involved for the expression of this character and selection for such trait might not be rewarding. High heritability with moderate genetic advance in percent of mean was observed for plant height indicating that this trait was under additive gene control and selection for genetic improvement for this trait would be effective.

A study was conducted by Hosen (2008) using five parental genotypes of *Brassica rapa* and their ten F_3 progenies including reciprocals. The result revealed that there were large variations present among all the genotypes used in the experiment. Number of primary branches per plant, number of secondary branches per plant, length of siliqua, number of seeds per siliquae, thousand seed weight and yield per plant showed least difference between phenotypic and genotypic variances. The values of GCV and PCV indicated that there was considerable variation among all the characters except days to maturity. The plant height and number of siliquae per plant showed high heritability with high genetic advance and genetic advance in percentage of mean.

An experiment was carried out by Mahmud *et al.* (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 seed per siliqua and siliqua length. Parveen (2007), studied variability in F_2 progenies of the inter-varietal crosses of 17 *Brassica rapa* genotypes. The result revealed that there were significant variations among the different genotypes used in the experiment. Number of primary branches per plant

and secondary branches per plant showed high heritability coupled with high genetic advance and very high genetic advance in percentage.

Baradaran *et al.* (2007), reported results of the field studies in Iran to determine the variation in 15 rape cultivars. Results of the analysis of variance showed significant differences between yield and number of siliqua per plant, harvest index, oil percent. They noticed most important trails for high PCV and GCV for the number siliqua per plant and 1000-grain weight. Akbar *et al.* (2007); evaluated eight advanced lines and two check variety of *Brassica juncea* in Pakistan and studied variability, heritability and genetic advance of different yield components. The highest GCV was found in seed yield per plant followed by plant height, siliqua per plant and thousand grain weight while lowest GCV was in number of primary branches per plant. Highest heritability was found yield per plant followed by plant height, thousand grain weight, siliqua per plant and number of primary branches per plant. The maximum genetic advance was found in seed yield per plant followed by siliqua per plant, plant height, thousand grain weight and minimum in primary branches per plant.

Rashid (2007), studied variability of forty oleiferous *Brassica* species. High GCV (Genotypic Co-efficient of Variation) value was observed for plant height and number of siliqua per plant. Yadava *et al.* (2007); studied twelve genotypes of *B. napus* grown in 18 environments, where heritability estimates were high for number of days to first flowering and maturity, 1000-seed weight and plant height. These four characters showed relatively constant values over a range of environments. Yield showed a wide variation and estimated genetic advance showed wide variation for all characters except number of days to first flowering, plant height and 1000-seed weight.

Khan *et al.* (2006), studied variation for yield and yield contributing characters in rapeseed and reported significant variation for eleven accessions of *Brassica napus* L. They indicated that a wide range of genetic variation with high PCV and GCV

for seed yield, siliqua per plant, seeds per siliqua, siliqua length. Goswami *et al.* (2005); conducted an experiment on variability studies for number of secondary branches, siliqua on main raceme, seeds per siliqua, 1000-seed weight and seed yield per plant. Results showed that the coefficient of variation of siliqua per plant were significant. So, there was considerable variability for the above character studied.

Kardam and Singh (2005), studied the nature and magnitude of associations for 10 characters in progenies of Indian rapeseed obtained from six crosses during rabi 2002-03 in Rajasthan, India. PCV were higher in magnitude compared to GCV for most of the characters. Seed yield per plant was significantly and positively variable with plant height, number of seeds per siliqua and 1000-seed weight.

Uddin *et al.* (2005); evaluated variation for yield and yield contributing characters in rapeseed and reported significant variation from (*B. napus*) genotypes, for yield and yield components where considerable high genotypic and phenotypic coefficients of variation occurred for 1000 seed weight, seed yield per plant and siliqua per plant.

Yadava *et al*. (2004), estimated heritability in the broad sense and genetic advance which were high for plant height, maturity and siliqua number on the main raceme in 29 varieties of Indian rapeseed. Heritability and genetic advance were high for yield per plant, plant height and days to first flowering. Niraj and Srivastava (2004), studied on variability and character association in Indian mustard of 21 genotypes of *Brassica juncea*. RH-9704 and IGM-21 recorded the highest seed yield. Phenotypic coefficient of variation was high for oil yield per plant, seed yield per plant and seed weight. Heritability was high for test weight, days to flowering, days to maturity and plant height.

Mahak *et al.* (2004), studied heritability and genetic advance for days to flowering, days to maturity, plant height, number of siliqua per raceme, length of main raceme, seed yield per plant, 1000-seed weight and oil content. High heritability

coupled with high genetic advance as percentage of mean was observed for days to flowering, followed by 1000-seed weight, days to maturity and weight. Thakral (2004), worked on variation for yield and yield contributing characters in rapeseed and reported significant variation for 8 Indian rapeseed parental lines and their 28 F_1 hybrid. They noticed high PCV and GCV for plant height and seed yield characters.

Choudhary *et al.* (2003), studied variability in Indian mustard for 10 characters during rabi season in India. A wide range of variability was observed for all characters, except for primary branches per plant, siliqua length, number of seeds per siliqua and thousand seed weight. Genotypic and phenotypic coefficient of variability was recorded high for secondary branches per plant, seed yield per plant and number of siliqua per plant. High heritability coupled with high genetic advance as percentage of mean was observed for secondary branches per plant, seed yield per plant and number of siliquae per plant, indicating preponderance of additive gene action. Gupta *et al.*(2002); studied yield and seven yield components in 18 strains of *Brassica napus* for morphological and phenological yield characters. They reported high expected genetic advance and high heritability for plant height, 1000-seed weight and yield per plant, indicating additive gene effects for these characters. Number of siliqua per plant showed a high heritability estimate with low expected genetic advance indicating non-additive gene effects.

Tyagi *et al.* (2001), evaluated forty-five hybrids of Indian mustard obtained from crossing 10 cultivars for seed yield and yield components. Variation was highest for plant height of parents and their hybrids. The seed yield per plant exhibited the highest coefficient of variation (41.1%). An experiment was conducted for studies of genetic variability in 25 genotypes by Pant and Singh (2001). Analysis of variance revealed highly significant genotypic differences for all traits studied, except for days to flowering, number of primary branches and oil content. Seed yield per plant had the highest coefficient of genotypic and phenotypic variability. All traits showed high heritability, with the highest value estimated for seed yield

per plant. The estimates of genetic advance were comparatively low for oil content and days to flowering. The genotypic coefficient of variation and heritability estimates for oil content and days to flowering suggest that these traits cannot be improved effectively merely by selection.

Ghosh and Gulati (2001), studied genetic variability and association of yield components in Indian mustard for 36 genotypes. The genotypic and phenotypic coefficients of variability (GCV and PCV, respectively) were high in magnitude for all the characters except plant height. The differences between the PCV and GCV were narrow for all the characters studied, coupled with high heritability except plant height, indicating the usefulness of phenotypic selection in improving these traits. High heritability, coupled with high genetic advance was observed for number of primary branches, number of siliquae on main shoot, main shoot length and number of seeds per siliqua. This result suggests the importance of additive gene action for their inheritance and improvement could be brought about by phenotypic selection. Singh *et al.* (2001) studied different morpho-physiological characters of 29 genotypes of *B. napus* grown under normal and stress condition of production. They found the existence of significant genetic variability for days to 50% flowering.

An experiment was conducted by Shalini *et al.* (2000) to study variability in *Brassica juncea* L. Different genetic parameters was estimated to assess the magnitude of genetic variation in 81 diverse Indian mustard genotypes. The analysis of variance indicated the prevalence of sufficient genetic variation among the genotypes for all 10 characters studied. Genotypic coefficient of variation, estimates of variability, heritability values and genetic gain were moderate to high for 1000 seed weight, number of siliquae per plant and number of secondary branches per plant, indicating that the response to selection would be very high for these yield components. For the other characters, low coefficient of variation, medium to low heritability and low genetic gain were observed. Malik *et al.* (2000); observed very high broad sense heritability (h^2b>90%) for number of

primary branches per plant and oil content while working with different strains of *B. napus*. They also observed low heritability (50%) for plant height, number of siliqua per plant, number of seed per siliqua and seed yield. But high heritability for all these characters were found by Lodhi *et al.*(1979) while working with 55 genotypes of *B. napus*, *B. rapa* and *B. juncea*.

Thousand seed weight is a very important character of rapeseed and mustard, where highest consideration is on the seed yield. This character has been found to vary widely from genotypes to genotypes and from environment to environment. A good number of literatures are available on the variability of this trait. High heritability coupled with high genetic advance for seed yield per plant, number of secondary branches per plant, siliqua per plant, 1000 seed weight (gm) and number of primary branches per plant was observed by Sheikh *et al.* (1999) while working with 24 genotypes.

An experiment was conducted by Khulbe and Pan (1999) to estimates of variability, heritability and genetic advance for yield and its components in Indian mustard revealed maximum variability for seed yield. All the characters except oil content exhibited high heritability with high or moderate genetic advance, suggesting the role of additive gene action in conditioning the traits. Non-additive gene action appeared to influence the expression of days to maturity, while environment had a major influence on oil content. The use of pedigree selection or bi parental mating in advanced generations was advocated to achieve substantial gains.

2.2 Correlation among different characters

Correlation coefficient analysis helps to determine the nature and degree of relationship between any two measurable characters. It resolves the complex relations between the events into simple form of association. But measure of correlation does not consider dependence of one variable over the other. Direct contribution of each component to the yield and the indirect effects it has through

its association with other components cannot be differentiated from mere correlation studies. Path coefficient analysis fulfills this study. It was first developed and described by Wright (1921), as a tool in genetic analysis which partition the association of the components on yield and indirect effects of the characters on yield through other components.

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.

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.

Ejaz- Ul- Hasan *et al*. (2014), studied correlation between different traits of *Brassica napus* and found high and positively significant phenotypic correlation between plant height and seeds per plant. Uddin *et al*. (2013); conducted an experiment with seven parental and twenty one F_2 progenies of *Brassica rapa* to study correlation among different yield component and found that yield per plant had high significant positive correlation with number of primary branches per plant, number of secondary branches per plant and siliqua per plant at both phenotypically and genotypically and significant positive correlation at genotypically in days to flowering and days to maturity.

Maurya *et al.* (2012), carried out an experiment with one hundred genotypes of *Brassica juncea* and observed that a high positive correlation was presented between length of siliqua, seed yield, thousand grain weight and days to 50%

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

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

Rameeh (2011), conducted an experiment with thirty-six rapeseed genotypes including four cultivars and 32 advanced lines. He found that siliquae per plant had significant positive correlation (0.80**) with seed yield and also it had significant positive direct effect (0.85**) on seed yield. Afrin *et al.* (2011); studied on *Brassica napus* and found positive correlation with seed yield per plant in plant height, number of primary branches per plant and number of siliqua per plant. The highest significant positive correlation was found between days to 50% flowering and plant height.

Kumar *et al.* (2009), studied 12 yield related trails in 15 genotypes of *B. napus* and *B. campestris*. For most characters studied, genotypic correlation coefficient were higher in magnitude than this correspond phenotypic correlation coefficients. Seed yield was positively correlated with plant height and 1000 seed weight. In an experiment Mahmud *et al.* (2008); found highly significant positive association of seed yield per plant with number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant.

An experiment was conducted by Basalma (2008) in Ankara using 25 winter oil seed rape cultivars. Correlation analysis showed a high positive and statistically significant correlation between branches per plant, the number of pods on the main stem and plant height during two years. Plant height indicated negative correlation with seed yield, 1000 seed weight and oil ratio.

A study was conducted by Hosen (2008) using five parental genotypes of *Brassica rapa* and their ten F_3 progenies including reciprocals. He found yield per plant showed highest significant and positive correlation with days to maturity followed by number of seeds per siliquae, number of secondary branches per plant, length of siliqua and number of siliqua per plant. Rashid (2007), carried out an experiment with 40 oleiferous *Brassica* species to estimate correlation and observed that highly significant positive association of yield per plant with number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua and number of siliquae per plant.

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

Akbar *et al.* (2007), evaluated eight advanced lines and two check variety of *Brassica junea* in Pakistan and reported that siliqua per plant had strong positive correlation with the seed yield followed by plant height while non-significantly negative correlation with thousand grain weight. But significantly negative correlation was present in siliqua per plant and primary branches per plant.

An experiment on oleiferous *Brassica campestris* L. was conducted by Siddikee (2006) to study the correlation analysis. The results revealed that yield per plant had the highest significant positive correlation with number of siliquae per plant. A study was conducted by Tusar *et al.* (2006); to assess the nature and extent of variability of eleven yield related characters of five mustard genotypes. Phenotypic correlation studies indicated that seed yield per ha 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. Path coefficient analysis revealed that the number of siliquae per plant had the greatest direct contribution on seed yield followed by the number of seeds per siliqua and 1000-seed weight while indirect via number of siliquae per plant and 1000-seed weight. Although plant height and husk weight had a total positive correlation with seed yield, their direct effect on yield was negative. The number of seeds per siliqua showed very high positive direct effect on yield, but its correlation with yield was non-significant and negative.

Yadav *et al.* (2006), observed 16 genotypes of rapeseed and estimated genotypic and phenotypic correlation coefficient among seed yield per plant. It was observed that 1000 seed weight, days to flowering, seeds per siliqua and plant height were the most important yield related characters and positively correlated with yield. Zahan (2006), studied correlation and reported that yield per plant had highly significant positive association with plant height, length of siliqua, siliquae per plant and seed per siliquae but insignificant negative association with days to 50% flowering, days to maturity.

Uddin *et al.* (2005), observed 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. 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. Afroz *et al.* (2004); studied correlation and found seed yield per plant had significant and positive correlation with number of primary branches per plant and number of siliqua per plant.

An experiment was conducted by Poonam and Singh (2004) in forty Indian mustard germplasms to determine the correlation and path coefficient values between yield and yield attributing character. Path coefficient analysis of seed yield per plot with different correlated characters was partitioned into direct and indirect effects. Plant height had the highest positive direct effect (0.836) followed by number of seeds per siliqua (0.791). The number of primary branches per plant, siliqua per plant and days to maturity had low but negative direct effects on seed yield. Mahak *et al.* (2004); conducted an experiment and studied correlation for 8 quantitative characters. Seed yield per plant showed positive correlation with number of primary branches, length of main raceme, 1000-seed weight and oil content. Selection should be applied on these traits to improve seed yield in Indian mustard.

Sudan *et al.* (2004), made observations on ten morpho-agronomical characters in *B. juncae* which were studied for correlation and path coefficient analysis using 10 genetically diverse genotypes. Seed yield showed significant and positive correlation with number of primary branches per plant, number of secondary branches per plant and 1000 seed weight. Path analysis indicated that number of primary branches was the most important character with the highest direct effect on seed yield. Other characters, viz., days to maturity, 1000 seed weight and number of seeds per siliqua had high positive effect on yield via other characters suggesting the scope of their simultaneous improvement through selection. An experiment conducted by Niraj and Srivastava (2004), on character association studies in

Indian mustard of 21 genotypes of *Brassica juncea*. Seed yields were positively and significantly correlated with plant height and primary branches but negatively correlated with test weight.

Choudhary *et al.* (2003), studied correlation and path coefficient analysis in twenty eight genotypes of Indian mustard including three controls (Varuna, Kranti and Pusa bold). Observations were recorded for seed yield per plant and eleven quantitative characters viz., days to first flowering, days to maturity, length of main axis, primary branches per plant, secondary branches per plant, number of siliquae per plant, siliqua length, number of seeds per siliqua, 1000-seed weight and reaction to Alternaria black spot on leaf and on siliqua. All the characters had highly significant and positive correlation with seed yield per plant, except for reaction to Alternaria black spot on both leaf and siliqua and days to first flowering.

Pankaj *et al.* (2002), studied four parental cultivars and the 174 progenies of resultant crosses for correlation between yield and yield component traits. The genetic correlation was higher than the phenotypic correlation for the majority of the characters. The number of siliqua per plant, which had the strongest positive and significant correlation with yield per plant at both levels, was positively associated with the number of seeds per siliquae and test weight at both levels. The number seeds per siliquae were positively associated with siliqua length and yield per plant at both levels. Srivastava and Singh (2002), studied correlation in Indian mustard (*Brassica juncea* L.) for 10 characters with 24 strains along with two varieties. Results revealed that number of primary branches per plant, number of secondary branches per plant, 1000-seed weight (gm) and oil percent were positively associated with seed yield.

The association between the various characters in a rapeseed and mustard and the direct and indirect effects of a variable over the dependent variable has been studied by a number of investigators are reviewed here. Gupta *et al.* (2002); studied 18 lines rapeseed reported significant correlation between plant height, number of

siliqua per raceme and seed number per siliqua, while plant height was significantly correlated with number of siliqua per raceme. In general, genotypic correlations were greater than phenotypic or environmental correlations. Seed yield was positively correlated with number of siliqua per raceme and 1000-seed weight.

Badsra and Chaudhary (2001), studied correlation on 14 traits of 16 Indian mustard genotypes. Seed yield was positively correlated with stem diameter, number of siliquae per plant and oil content, while oil content was positively correlated with harvest index only. Among the characters only three were positively correlated with seed yield.

Association of yield components in Indian mustard among 12 yield components were studied in 36 genotypes selected from different geographical regions by Ghosh and Gulati (2001). Seed yield exhibited significant positive association with yield contributing traits like days to 50% flowering, days to maturity, plant height, number of secondary branches, number of siliquae on main shoot and oil content. Days to maturity showed insignificant correlation with seed yield at both genotypic and phenotypic levels. The number of branches per plant and number of siliquae per plant showed significant negative correlation with number of seeds per siliqua and 1000 seed weight was reported by Malik *et al*. (2000); while studied correlation analysis.

According to Kumar *et al.* (1999), genotypic correlation co-efficient were higher in magnitude than corresponding phenotypic correlation co-efficient for most characters. The plant height, siliquae on main shoot, siliquae per plant and thousand seed weight were positively correlated with seed yield. The number of siliquae per plant, number of seeds per siliqua and plant height was significantly positively correlated with seed yield was observed by Masood *et al.* (1999); while studied seven genotypes of *B. campestris* and standard cultivar of *B. napus* to calculate correlation co-efficient.

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

Nanda *et al.* (1995), studied correlation coefficient analysis with 65 strains of *B. juncea*, *B. rapa* and *B. napus* and found that positive correlation between yield and siliqua filling period. Relevant results also reported by Olsson (1990), in *B. napus*. He also found that positive association between siliqua density and yield. Uddin *et al.* (1995); while conducted experiment on association analysis in 13Indian mustard (*B. juncea*) and found that seed yield per plant had high significant and positive association with plant height and thousand seed weight, but high significant and negative association with seeds per siliqua at both genotypic and phenotypic levels.

Research studied on Tori-7 (*B. campestris var. toria*) for performance studies of seed yield and five yield contributing traits whose more contribution to seed yield and found that plant height, siliqua per plant, seeds per siliqua and 1000 seed weight was positively and significantly associated with seed yield(Gosh and Mukhopadhyay, 1994). Ahmed (1993), worked with eight cv. of *B. campestris* and *B. juncea* for examining the nature and degree of correlation among yield and yield components and observed that siliqua length, number of siliquae per plant, number of seeds per siliqua and seed weight per siliqua was linearly and positively correlated with seed yield per plant. He also revealed that seed oil content was positively associated with 1000 seed weight, but negatively associated with number of seeds per siliqua.

Zaman *et al.* (1992), studied several yield contributing traits of Swedish advanced rape lines and reported that number of seeds per siliqua negatively correlated with siliqua per plant. Reddy (1991), studied correlation analysis in Indian mustard (*B. juncea*) and reported that positive and significant correlation between seed yield and number of primary branches per plant, number of secondary branches per plant, siliqua per plant and seeds per siliqua. Chaudhury *et al*, (1990); observed seed yield was positively correlated with siliqua length when evaluated seven of *B. juncea*, two of *B. carinata* cultivars and one cultivar each of *B. campestris* and *B. tournefortii*.

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. The association between the various characters in a rapeseed and mustard and the direct and indirect effects of a variable over the dependent variable has been studied by a number of investigators are reviewed here.

Sharafi *et al.* (2015),were evaluated28 winter rapeseed cultivars and results showed that number of pods per plant, number of seeds per pod, and 1000-seed weight had positive direct effect on seed yield.

Ejaz-Ul-Hasan *et al.* (2014), conducted an experiment on *Brassica napus* and studied path coefficient. The result revealed that the highest direct positive effect of seeds per plant on yield and followed by days to maturity, days to flowering, seeds per siliquae, siliqua length and thousand seed weight while plant height had direct negative effect on the yield per plant. Mekonnen *et al.* (2014); conducted an experiment to study path co-efficient in *Brassica carinata* and found that days to maturity and secondary braches per plant had positive and direct genotypic correlation with seed yield.

Uddin *et al.* (2013), conducted an experiment with seven parental and twenty one F_2 progenies of *Brassica rapa* to study path coefficient and reported that days to 50% flowering, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, siliquae length, seed per siliquae and thousand seed weight showed direct positive association with seed yield per plant while the plant height and days to maturity had direct negative association. In order to determine the most important traits affecting grain yield in Canola and identify the quantity of direct and indirect effects on grain yield, an experiment was conducted with 10 Canola varieties in a RCBD design with three replications by Khayat *et al*. (2012). Stepwise regression and path analysis indicated that, the number of pods per plant had the highest direct effect on grain yield. In addition, total dry matter, 1000-grain weight, and flowering and days to maturity also had a high direct effect on grain yield.

Afrin *et al.* (2011), studied with *Brassica napus* to identify the path co-efficiant among the characters. The plant height was found the highest positive and direct effect on seed yield per plant followed by number of siliqua per plant and siliqua length. Alam (2010), studied path co-efficient analysis that revealed that plant height, number of primary branches per plant, number of siliqua per plant, seeds per siliquae and siliqua length had the direct positive effect on yield per plant while days to 50% flowering, number of secondary branches per plant and thousand seed weight had the negative direct effect on yield per plant. The path co-efficient analysis by Hosen (2008), exhibited that thousand seed weight had the highest positive direct effect followed by days to 50% flowering, length of siliqua, number of primary branches per plant, number of secondary branches per plant, days to maturity and number of seeds per siliqua while working with five parental genotypes of *Brassica rapa* and their ten F_3 progenies including reciprocals.

An experiment was carried out by Mahmud *et al.* (2008); with 58 genotypes of *Brassica rapa.* Path analysis showed that yield per plant had the highest direct effect on number of primary branches per plant, number of siliquae per plant,

number of secondary branches per plant and number of seeds per siliqua. Aytac *et al.* (2008); evaluated on six genotypes of spring rape seed and studied path coefficient and the result stated that plant height, number of siliqua per plant, seeds per siliquae had the highest and positive direct effect on yield per plant for all cultivars except cv. Star. 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 the highest direct effect on yield per plant.

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

By path analysis, Zahan (2006), reported that siliquae/plant had positive direct effect on yield/plant. And days to 50% flowering had negative direct effect on yield/plant. Khan *et al.* (2006); studied correlation for some quantitative traits relating to yield and quality. The results revealed that seed yield per plant was positively and significantly correlated with number of primary branches (0.4015), siliqua per plant (0.505), seeds per siliqua (0.79648), siliqua length (0.37037) and seed yield per plot (0.40931). However, it was negatively and non-significantly associated with number of secondary branches (-0.36663) and protein contents (-0.1372) at genotypic level. It was also found that indirect selection for number of seeds per siliqua would be effective in improving the seed yield per plant in present breeding material. 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.

Afroz *et al.* (2004); studied path coefficient analysis and found maximum direct positive effects by plant height followed by number of siliqua per plant, number of primary branches per plant, 1000-seed weight and number of siliqua shattering per plant on seed yield per plant.

An experiment was conducted by Poonam and Singh (2004) in 40 Indian mustard germplasms to determine the correlation and path coefficient values between yield and yield attributing character. Path coefficient analysis of seed yield per plot with different correlated characters was partitioned into direct and indirect effects. Plant height had the highest positive direct effect (0.836) followed by number of seeds per siliqua (0.791). The number of primary branches per plant, siliqua per plant and days to maturity had low but negative direct effects on seed yield. Sudan *et al.* (2004); studied path analysis in Indian mustard. Path analysis indicated that number of primary branches was the most important character with the highest direct effect on seed yield. Other characters i.e. days to flowering, 1000 seed weight and number of seeds per siliqua had high positive effect on yield via other character suggesting the scope of their simultaneous improvement through selection.

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

Research found that primary branches per plant, secondary branches per plant and 1000 seed weight had highest direct effect on seed yield while working with Indian mustard (*B. juncea* L.)(Srivastava and Singh, 2002).Earlier research was supported that 1000 seed weight and primary branches per plant were the vital selection criteria for improvement in productivity of Indian mustard. Studied on path analysis of mustard genotypes and found that siliquae per plant had the highest direct effect on seed yield which was followed by 1000 seed weight, primary branches per plant and plant height, that was reported by Shalini *et al.* (2000). Most of the characters were studied had an indirect effect on seed yield.

Sheikh *et al.* (1999), worked with many diverse mustard genotypes to assess the direct and indirect effect of quantitative and developmental traits on seed yield and revealed that 1000 seed weight and number of siliqua per plant had highly positive

direct effect on seed yield. Yadava *et al.* (1996) studied on path coefficient analysis on six yield components of twenty five diverse genotypes and found that the siliquae number per plant had the highest positive direct effect on seed yield. Path analysis was studied by Uddin *et al*. (1995) in thirteen Indian mustard (*B. juncea*) and found that seeds per siliqua and 1000 seed weight had high positive direct effect on seed yield per plant.

Kudla (1993),revealed that thousand seed weight had positive direct effect on seed yield. Research reported was published that the plant height had the highest positive direct effect on seed yield per plant in *B. juncea*(Dhillor *et al.*, 1990); but Singh *et al.* (1997); reported that negative direct effect of plant height on seed yield. Earlier research was studied that negative direct effect of number of siliquae per plant, siliqua length and positive direct effect of seeds per siliqua and plant height on seed yield (Han, 1990).

2.4 Genetic divergence among mustard genotypes

Evaluation of germplasm through genetic divergence which quantifies variation among genotypes on the basis of a group of characters (yield and yield contributing) helps in identification of promising parental materials for crop improvement. Germplasm collections are also valuable gene pools providing diverse genetic material that may be applied for the improvement of cultivars and advanced agronomic productivity. An assessment of genetic diversity within these collections can be used to assign lines and populations to diverse groups. D^2 statistic developed by Mahalanobis (1936), provides a measure of magnitude of divergence between biological populations and relative contribution of each component character to the total divergence (Nair and Mukherjee, 1960). Mahalanobis D^2 statistic is more reliable in selection of potential parent for hybridization programme using these D^2 values cluster are formed. A summary of literature reviewed on mustard and other allied species are in presented below.

Rameeh (2015), evaluated twenty one rapeseed genotypes 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.

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), studied 211 genotypes of *Brassica napus* to evaluate 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.

Pandey *et al.* (2013), conducted an experiment with 45 Indian mustard genotypes of different origin from India for evaluated for the extent of diversity for utilization in breeding program. D^2 analysis was conducted to measure the genetic diversity among the genotypes. The 45 genotypes were grouped into 8 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. Maximum

contribution towards the divergence was accountable to 1000-grain weight (46.87%) followed by seed yield per plant (20.91%) and number of silique on main raceme (8.38%).

Zaman *et al.* (2010), conducted a field experiment for estimation of divergence among 45 advanced lines of mustard. The genotypes were grouped into four clusters. Cluster I contained the highest number of genotypes (6) and cluster III contained the lowest (3). The highest intra cluster distance was observed in cluster II and the lowest in I. The highest inter cluster distance was observed between the cluster III and II followed by III and I; and the lowest between cluster IV and III. Days to 50% flowering (81.94%), days to maturity (8.24%), plant height (5.82 %), branches per plant (1.91%) and 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. Hossain *et al.* (2008); studied the genetic divergence using D^2 statistic in 40 genotypes of rapeseed. The genotypes differed significantly for 10 yield and yield contributing characters, and they grouped them into 9 clusters. They observed that there was no close correspondence between geographical distribution and genetic divergence. A Number of siliqua on the main raceme, seeds per siliqua and harvest index had major contribution to genetic divergence. The genotypes under cluster IV were suggested for use in heterosis breeding.

Vivek *et al.* (2007), studied the genetic diversity in 81 true breeding advanced generation cultivars of Indian mustard based on yield and yield components. They are followed by cluster analysis and showed that out cluster XII, which was most diverse, had very high seed yield and number of siliquae per plant. Cluster VII also represented entries with high seed yield, number of siliquae per plant and highest number of seed per siliqua. Cluster XI with the lowest number of days to maturity could be considered as a good source for earliness. Goswami and Behl (2006), studied 43 genotypes of Indian mustard using D^2 statistics. They recorded data for plant height, primary branches, secondary branches, main shoot length, number of

siliquae on main shoot, siliqua length, seeds per siliqua, 1000-seed weight, seed yield per plant and oil content. The genotypes were grouped into six clusters. The intra cluster distances were almost equal and relatively lower than the inter-cluster distances.

Aunwinithul *et al.* (2004); studied 33 genetically diverse genotypes of Indian mustard for diversity. The genotypes were grouped into eight different clusters. The cluster III was the biggest with 11 genotypes followed by cluster-I with 9 genotypes, cluster V and VI consisted of 4 and 3 genotypes respectively. The cluster II and VII both had two genotypes each and similarly, cluster IV and VIII included one genotype each.

Yadava *et al.* (2004), studied 50 lines of *B. napus* and reported that the lines were grouped into twelve clusters with maximum inter cluster distances between the clusters XII and IX (35.51), II and III (33.03) and XI and IX (31.21). The characters contributing to the maximum divergence were in descending order, oil content, days to flowering, plant height, siliqua length and siliqua number on the main raceme. Jagadev *et al*. (1999); studied on some 19 genotypes of rapeseed (*B. napus*). They studied yield and yield contributing characters grouped the genotypes into 5 clusters with clusters I comprising these genotypes, clusters II and 12 each and clusters IV and V one each.

Singh *et al.* (1997), studied genetic divergence through D^2 statistic with 50 genotypes of *B. napus* growing in 12 environments based on 13 characters. They searched the clustering pattern and their inter and intra cluster distances. On the basis of stability, high yield and divergence among the genotypes, nine crosses were recommended as suitable for use in breeding programme.

Peter and Rai (1995), studied genetic divergence using the D^2 statistics and canonical analysis among 25 genotypes of *Brassica napus*. They reported that genetic and geographical divergence was highly related with the genotypes. The

genotypes were grouped into six clusters of which cluster I was the largest accommodating among these genotypes. The cluster VI had large genetic distance from the remaining clusters.

CHAPTER III

MATERIALS AND METHODS

This chapter deals with the information on the subject of materials and methods that were used in conducting the experiment. It consists of a short explanation of locations of the experimental site, soil characteristics, climate, materials used in the experiment, layout and design of the experiment, land preparation, manuring and fertilizing, seeds sowing, intercultural practices, harvesting, data recording procedure and statistical analysis etc., which are presented as follows:

3.1 Experimental site

The experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka during November 2015 to February 2016. The location of the experimental site was situated at $23^0$74' N latitude and $90^0$35' E longitude with an elevation of 8.6 meter from the sea level. Map showing the experimental site (Appendix II).

3.2 Soil and Climate

The experimental site was situated in the subtropical zone. The soil of the experimental site belongs to the Agro-ecological zone of "The Modhupur Tract" (AEZ-28). The soil was clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The p^H ranges from 5.47 to 5.63 and organic carbon content is 0.82% (Appendix III). The records of air temperature, humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix IV).

3.3 Experimental materials

Good and healthy seeds of the selected sixty nine *Brassica napus* genotypes were collected from the Dept. of Genetics and Plant Breeding, Sher-e-Bangla

Agricultural University, Dhaka. They were used as research materials. The materials are shown in Table 1.

3.4 Methods

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

3.4.1 Land preparation

The research plot was prepared by implementing several ploughing and cross ploughing which was followed by laddering and harrowing with tractor and power tiller to ensure the good tilth. All weeds residues and other previous crop stubbles were significantly removed from the research field and leveled properly so that no up down places were remain in the field.

3.4.2 Application of manure and fertilizer

The experimental field was fertilized as the rate of 10 tons of cowdung, 250 Kg urea, 175 Kg triple super phosphate (TSP), 85 Kg murate of potash (MoP), 250 Kg gypsum, 3 Kg zinc oxide and 1 Kg boron per hectare. The fifty percent of total urea, total amount of cowdung, TSP, MoP, 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.

Table 1. Materials used for the experiment

Genotypes	Pedigree	Genotypes	Pedigree
G1	Nap248xNap2037	G36	Nap9905xNap9904
G2	Nap9908xNap2057	G37	B-13XNap2022
G3	Nap248xNap2012	G38	Nap205xNap2037
G4	Nap9905xNap2037	G39	Nap9908xNap206
G5	BS-13xNap2001	G40	Nap108xNap2037
G6	Nap9906xNap179	G41	Nap205xNap2037
G7	Nap248xNap206	G42	Nap9908xNap2022
G8	Nap9908xNap2037	G43	Nap9905xNap2066
G9	Nap298xNap2057	G44	B-13XNap2012
G10	Nap9908xNap2066	G45	Nap205xNap2022
G11	BS-13xNap2013	G46	Nap248xNap2022
G12	Nap9908xNap0130	G47	B-13XNap179
G13	Nap9905xNap206	G48	Nap205xNap2266
G14	BS-13xNap2066	G49	Nap9906xNap206
G15	Nap9906xNap9904	G50	Nap9908xNap2012
G16	Nap9908xNap179	G51	Nap248xNap0130
G17	Nap9908xNap9904	G52	Nap9906xNap0130
G18	Nap205xNap2013	G53	Nap9908xNap9901
G19	Nap9905xNap0130	G54	Nap248xNap94006
G20	Nap9908xNap2013	G55	Nap248xNap9904
G21	Nap108xNap206	G56	Nap9908xNap94006
G22	Nap9908xNap9901	G57	Nap248xNap9901
G23	Nap205xNap940061	G58	Nap9905xNap179
G24	Nap248xNap2001	G59	Nap205xNap 0130
G25	Nap9905xNap2001	G60	B-13xNap 0130
G26	Nap9905xNap2022	G61	Nap108xNap179
G27	Nap9906xNap94006	G62	B-13XNap2037
G28	Nap108xNap2022	G63	Nap248xNap2066
G29	Nap9905xNap94006	G64	Nap205xNap206
G30	Nap9908xNap2008	G65	Nap205xNap9901
G31	Nap205xNap179	G66	B-13XNap2057
G32	Nap9905xNap2054	G67	Nap9906xNap2022
G33	Nap108xNap2057	G68	Nap9905xNap9901
G34	BS-13XNap9901	G69	Nap9906xNap2012
G35	Nap248xNap179		

3.4.3 Experimental design and layout

After final land preparation field layout was done. The present experiment was carried out in Randomized Complete Block Design (RCBD) with three replications. Total area of experimental was 56 m x 14 m = 784 m^2. Land size was 56 m x 3.5 m of each replication, and the distance between replications was 1 m. The spacing between lines was 30 cm. All seeds were sown in line in experimental field on 14 November 2015. All selected seed of genotypes were sown about 1.5 cm depth in the soil. After sowing the seeds were covered with loose soil with awareness so that no clods were on the sown seeds. A pictorial view of experimental field at flowering stage is presented in Plate 1.

3.4.4 Intercultural operations

Weeding, thinning, irrigation, pest management, etc. were done uniformly in all the experimental plots. Irrigation was given first time with water cane after sowing seeds to get appropriate moisture condition of the experimental field soil to make sure uniform germination of the seeds. A good drainage system was maintained for immediate release of rainwater from the research plot in the time of crop growing period. A photograph of making irrigation and drainage channel was presented in Plate 2. The first weeding was done after 15 days of seed sown. At the same time, excess seedling uprooting e.g. thinning was done for maintaining a similar distance of 10 cm from plant to plant in rows of 30 cm apart (Plate 3). Second weeding was done after 35 days of seed sowing. Some insects like aphid generally sucking plant cell sap and infested crop during the siliqua development stage. To minimize the infested aphid, insecticide Malataf 57 EC under Malathion group was sprayed @ 2 ml/liter of water. A good condition of the experiment at flowering stage presented in Plate 4.

Plate 1. Experimental field showing different genotypes at flowering stage

Plate 2. Irrigation and drainage channel preparation in the experimental field of *Brassica*.

Plate 3.Thinning of excess seedling of *Brassica* in the experimental plot.

Plate 4. Showing the experimental field at flowering stage

3.4.5 Crop harvesting

The crop was harvested at90 days after sowing (DAS) on the basis of maturity. When the cultivated plants showed 80% morphological maturity symptoms like siliqua, leaves, and stem color as straw and desired seed color in the matured siliqua also straw, the planted crop was assumed to reach maturity. Fifteen plants from each replication were selected at randomly. The mature crops were harvested by uprooting and then they were tagged properly. Selected crop related characteristics were recorded from these plants from each replication according to accession.

3.4.6 Data collection

Ten different parameters numerical measurement were taken into consideration for studying different genetic parameters, correlation, path analysis and genetic diversity. Quantitative data were recorded on ten selected plants for each genotype for each replication on following parameters. The details of data recording are given below on individual plant basis.

Days to 50% flowering: Total days to 50% flower opening were taken from seed sowing date to the date of 50% flowering of every entry. It was measure in days.

Days to 80% maturity: Total days from seed sowing to 80% siliqua of plant were maturity were recorded as 80% maturity of each entry. It was measured in days.

Plant height: Plant height was recorded as distance from the base of the plant to the tip of the longest inflorescence. This quantitative trait was measured in centimeter (cm). This measurement was taken after harvesting.

Primary branches per plant: The total number of branches arisen from the main stem of a plant was counted as the primary branches per plant. This quantitative measurement was denoted in number.

Secondary branches per plant: The total number of branches arisen from all the primary branches of a plant was counted as the secondary branches per plant. This trait was expressed in number.

Siliquae per plant: Total number of siliquae of each plant were counted and considered as the siliquae per plant. It was mentioned in number.

Siliqua length: The distance from the base to the tip of a siliqua without beak of the ten representative siliquae. It was denoted in centimeter (cm).

Seeds per siliqua: Well filled seeds were counted from ten representative siliquae and then calculated average, which was considered as the seeds per siliqua. It was denoted in number.

1000 seed weight: Weight of randomly counted thousand seeds of each entry was recorded. It was measured in gram (g).

Seed yield per plant: Weight of filled seeds produced by 10 representative plants from each replication and then calculated average, which was considered as the seed yield per plant. It was denoted in gram (g).

3.4.7 Statistical analysis

Mean data of the characters were used to statistical analyze like analysis of variance (ANOVA), mean, range etc. were calculated by using MSTATC software program. Genotypic and phenotypic variance were estimated by the formula used by Johnson *et al*. (1955). Heritability and genetic advance were measured using the formula given by Singh and Chaudhary (1985) and Allard (1960). Genotypic and phenotypic coefficient of variation was calculated by the formula of Burton (1952). Genotypic and phenotypic correlation coefficient was obtained using the formula suggested by Miller *et al.* (1958), Johnson *et al*. (1955) and Hanson et al. (1956); path coefficient analysis was done following the method outlined by Dewey and Lu (1959). Multivariate analysis viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA) were done by using GENSTAT 5.13 and Microsoft Excel 2007 software.

3.4.7.1 Estimation of genotypic and phenotypic variances

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

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

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of square

r = number of replications

Phenotypic variance (σ^2_p)=$\sigma^2_g + \sigma^2_e$

Where,

σ^2_g = Genotypic variance,
σ^2_e = Error variance

3.4.7.2 Estimation of genotypic and phenotypic co-efficient of variation

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

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

Where,

σ^2_g = Genotypic variance

$\bar{x}$ = Population mean

Phenotypic co-efficient variation (PCV%) = $\sqrt{\frac{\pm^2_p}{\bar{x}}} \times 100$

Where,

σ^2_p = Phenotypic variance

$\bar{x}$ = Population mean

3.4.7.3 Estimation of heritability

Heritability in broad sense was estimated (Lush, 1943) by the following statistical formula that was suggested by Johnson *et al.* (1955).

Heritability, $h^2_b\% = \frac{\pm^2_g}{\pm^2_p} \times 100$

Where,

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

3.4.7.4 Estimation of genetic advance

The genetic advance for different traits under selection was calculated by using the statistical formula that was suggested by Lush (1943) and Johnson *et al.* (1955).

Genetic advance, $GA = K. h^2_b. \sigma_p$

Or Genetic advance, $GA = K. \frac{\pm^2_g}{\pm^2_p} . \pm_p$

Where,

K = Selection intensity, the value which is 2.06 at 5% selection intensity

σ_p = Phenotypic standard deviation

h^2_b= Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

3.4.7.5 Estimation of genetic advance mean's percentage

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

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

3.4.7.6 Estimation of genotypic and phenotypic correlation co-efficient

The calculation of genotypic and phenotypic correlation co-efficient for all possible combinations through the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956) were adopted. The genotypic co-variance component between two traits and the phenotypic co-variance component were derived in the same way as for the corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows:

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

Where,

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

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

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

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

Where,

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

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

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

3.4.7.7 Estimation of path co-efficient

It was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985), using phenotypic correlation coefficient values. In path analysis, correlation coefficients between yield and yield contributing characters were partitioned into direct and indirect effects on yield.

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

$P^2_{RY} = 1- (r_{1.y}P_{1.y} + r_{2.y}P_{2.y} +……..+ r_{i.y}P_{i.y})$

Where,

$P^2_{RY} = R^2$

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

$P_{1.y}$ = Direct effect of the i th character on yield y.

$r_{1.y}$ = Correlation of the i th character with yield y.

3.4.7.8 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance (D^2) statistic and its auxiliary analyses. The parents selection in hybridization programme based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) suggested that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a hybridization programme. Multivariate analysis viz. Principal Component analysis, Principal Coordinate analysis, Cluster analysis and Canonical Vector analysis (CVA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

3.4.7.8.1 Principal Component analysis (PCA)

Principal Component analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, Principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity. Contribution of the different morphological characters towards

divergence is discussed from the latent vectors of the first two principal components.

3.4.7.8.2 Principal Coordinate analysis (PCO)

Principal Coordinate analysis is equivalent to PCA but it is used to calculate inter unit distances. Through the use of all dimension of p it gives the minimum distance between each pair of the n points using similarity matrix (Digby *et al.*, 1989).

3.4.7.8.3 Cluster analysis (CA)

Cluster analysis divides the genotypes of a data set into some number of mutually exclusive groups. Clustering was done using non-hierarchical classification. In SPSS 20.0, the algorithm is used to search for optimal values of chosen criterion proceeds as follows. Starting from some initial classification of the genotypes into required number of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

3.4.7.8.4 Canonical Vector analysis (CVA)

Canonical vector analysis (CVA) finds linear combination of original variabilities that maximize the ratio of between group to within group variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing of the ratio of among groups to the within group variations. The canonical vector are based upon the roots and vectors of WB, where W is the pooled within groups covariance matrix and B is the among groups covariance matrix.

3.4.7.8.5 Calculation of D^2 values

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

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

Where,

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

x = Number of characters.

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

3.4.7.8.6 Computation of average intra-cluster distances

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

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

Where,

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

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

3.4.7.8.7 Computation of average inter-cluster distances

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

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

Where,

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

n_i= Number of populations in cluster i

n_j= Number of populations in cluster j

CHAPTER IV
RESULTS AND DISCUSSIONS

The present study was conducted to find out genetic variability, character association, path analysis and genetic diversity analysis in *Brassica napus genotypes* during Rabi season 2015-16. Results of the study are illustrated in the following sections.

4.1 Analysis of variance

Highly significant differences ($p \leq 0.01$)) was observed among the genotypes for all the characteristics, including days to 50% flowering, days to 80% maturity, plant height (cm), primary branches per plant, secondary branches per plant, siliqua per plant, siliqua length (cm), seeds per siliqua, 1000 seed weight (g) and seed yield per plant (g). The findings clearly denoted that existence of high variability for yield and yield contribution traits among the genotypes included. Therefore, a lot of scope was found by considering the majority of the traits for selection of the superior genotypes. The mean sum of squares of all the ten characters is presented in Table 2. Significant differences among the genotypes was observed by many researchers like Walle *et al.* (2014), Zebarjadi *et al.* (2011),Parveen (2007), Khan *et al.* (2006), Xu-Suqin *et al.* (2006), Rukhsana *et al.* (2005), Uddin *et al.* (2005), Thakra *et al.* (2004), Pant and Singh (2001) and Shalini *et al.* (2000).

Table 2. Analysis of variance for different characters in *Brassica napus* L.

Characters/Variety	Mean sum of square		
	Replication (r-1) = 2	Genotype (g-1) = 68	Error (r-1)(g-1) = 136
Days to 50% flowering	2.616	10.189**	3.984
Days to 80% maturity	190.174	30.939**	6.042
Plant height (cm)	0.940	168.853**	37.630
Primary branch per plant	0.937	0.419**	0.118
Secondary branches per plant	0.014	0.633**	0.149
Siliqua per plant	163.161	850.477**	183.205
Siliqua length (cm)	0.093	0.878**	0.265
Seeds per siliqua	0.391	9.213**	4.045
1000 seed weight (g)	0.040	0.478**	0.110
Seed yield per plant (g)	0.004	2.020**	0.454

** Significant at 1% level of probability

4.2 Genetic variability, heritability and genetic advance

The estimation of genetic parameters like genotypic and phenotypic variance, genotypic and phenotypic coefficients of variation (GCV & PCV), heritability (h^2b), genetic advance (GA) and genetic advance as per cent mean (GAPM) for all the traits were studied. The heritability (h^2b) estimates split the environmental pressure from the total variability and indicate the accurateness with which a genotype can be identified by its phenotypic expression, as a result making the selection more successful. It`s objectives to determine the relative amount of heritable portion of difference. The heritability in broad sense (h^2b) is the proportion of genotypic variance to the total variance; its significance has been emphasized by Johnson *et al.* (1955) in plants. The findings of genetic variability are presented in Table 3. The genotypic coefficient of variability and phenotypic coefficient of variability are depicted in Figure 1. A graphical representation of heritability in broad sense and genetic advance in percent of means are shown in Figure 2. The mean performance of *B. napus* genotypes for various growth traits and yield components are presented in Appendix 1.

4.2.1 Days to 50% flowering

The analysis of variance (ANOVA) revealed that significant variation was observed among all the genotypes (10.189**) studied for days to 50% flowering (Table 2). The ranged of days to 50% flowering was from 26.00 to 35.50 days. The lowest days to 50% flowering was observed in G7 (26.00 days) and highest was observed in G57(35.50 days) (Appendix 1). Phenotypic and genotypic variance for days to 50% flowering was shown as 7.09 and 3.10 (Table 3), respectively with more gap between them, suggested more influence of environment on the expression of the genes controlling this trait. The phenotypic coefficient of variation (8.63%) was higher than the genotypic coefficient of variation (5.71%), which suggested that environment had significant role on the expression of this trait. Sharma (1984) found low GCV and PCV values, while Tak and Patnaik (1977) found these values as 4.5% and 1.8% respectively but Biswas (1989) found high GCV and PCV for this trait.

Table 3. Estimation of genetic parameters for different characters in *Brassica napus* L.

Parameters	$\pm^2$p	$\pm^2$g	$\pm^2$ e	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
Days to 50% flowering	7.09	3.10	3.98	8.63	5.71	6.47	43.79	2.40	7.78
Days to 80% maturity	18.49	12.45	6.04	5.21	4.27	2.98	67.33	5.96	7.22
Plant height (cm)	103.24	65.61	37.63	9.28	7.40	5.61	63.55	13.30	12.15
Primary branches per plant	0.27	0.15	0.12	17.80	13.32	11.80	56.02	0.60	20.54
Secondary branches per plant	0.39	0.24	0.15	39.45	31.04	24.35	61.91	0.80	50.32
Siliqua per plant	516.84	333.64	183.20	22.61	18.16	13.46	64.55	30.23	30.06
Siliqua length (cm)	0.57	0.31	0.27	9.47	6.93	6.45	53.57	0.83	10.45
Seeds per siliqua	6.63	2.58	4.04	14.04	8.76	10.97	38.98	2.07	11.27
1000 seed weight (g)	0.29	0.18	0.11	13.77	10.91	8.41	62.70	0.70	17.79
Seed yield per plant (g)	1.24	0.78	0.45	24.85	19.77	15.05	63.31	1.45	32.41

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

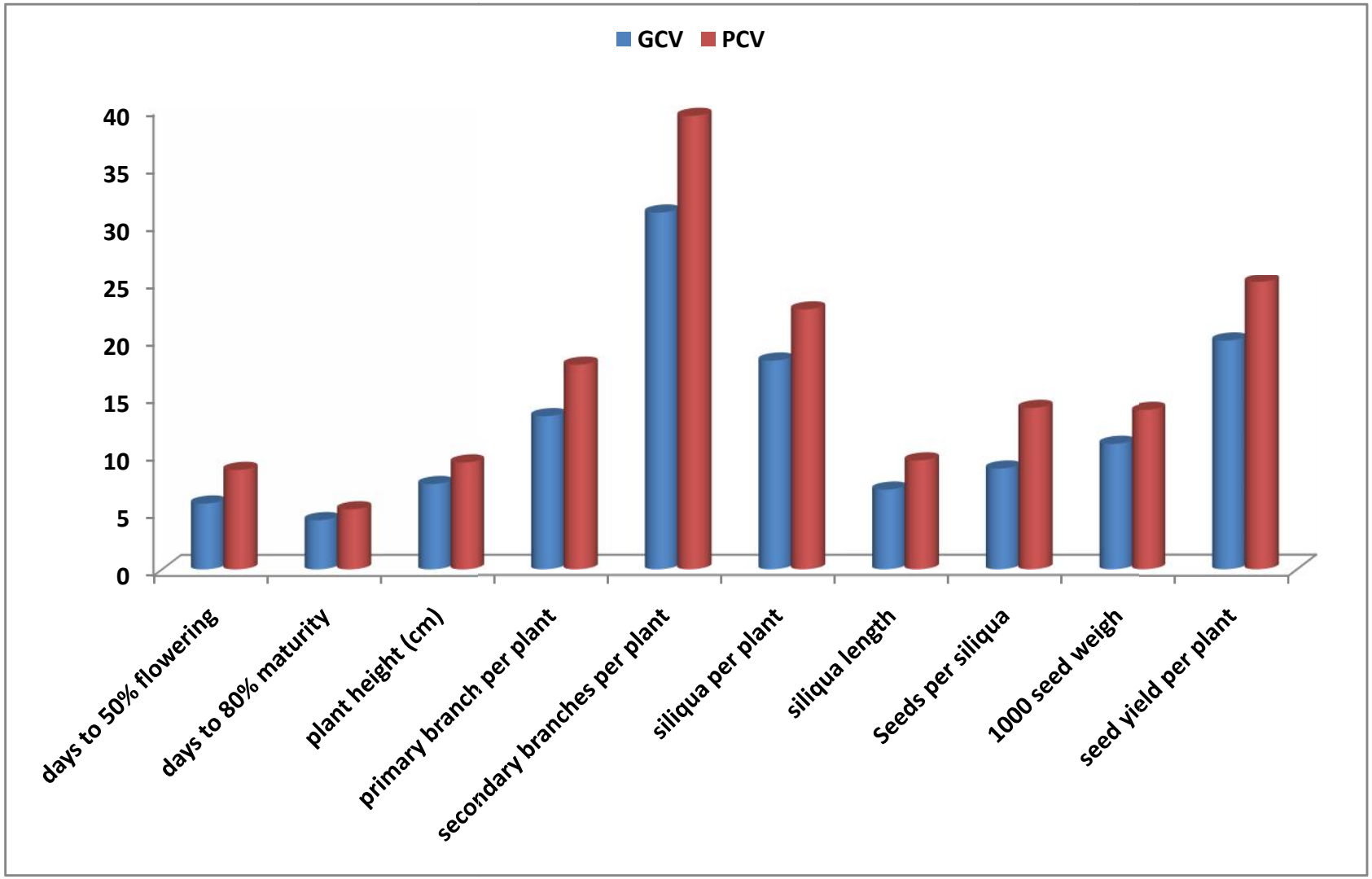


Figure 1.Genotypic and phenotypic variability in *Brassica napus* L.

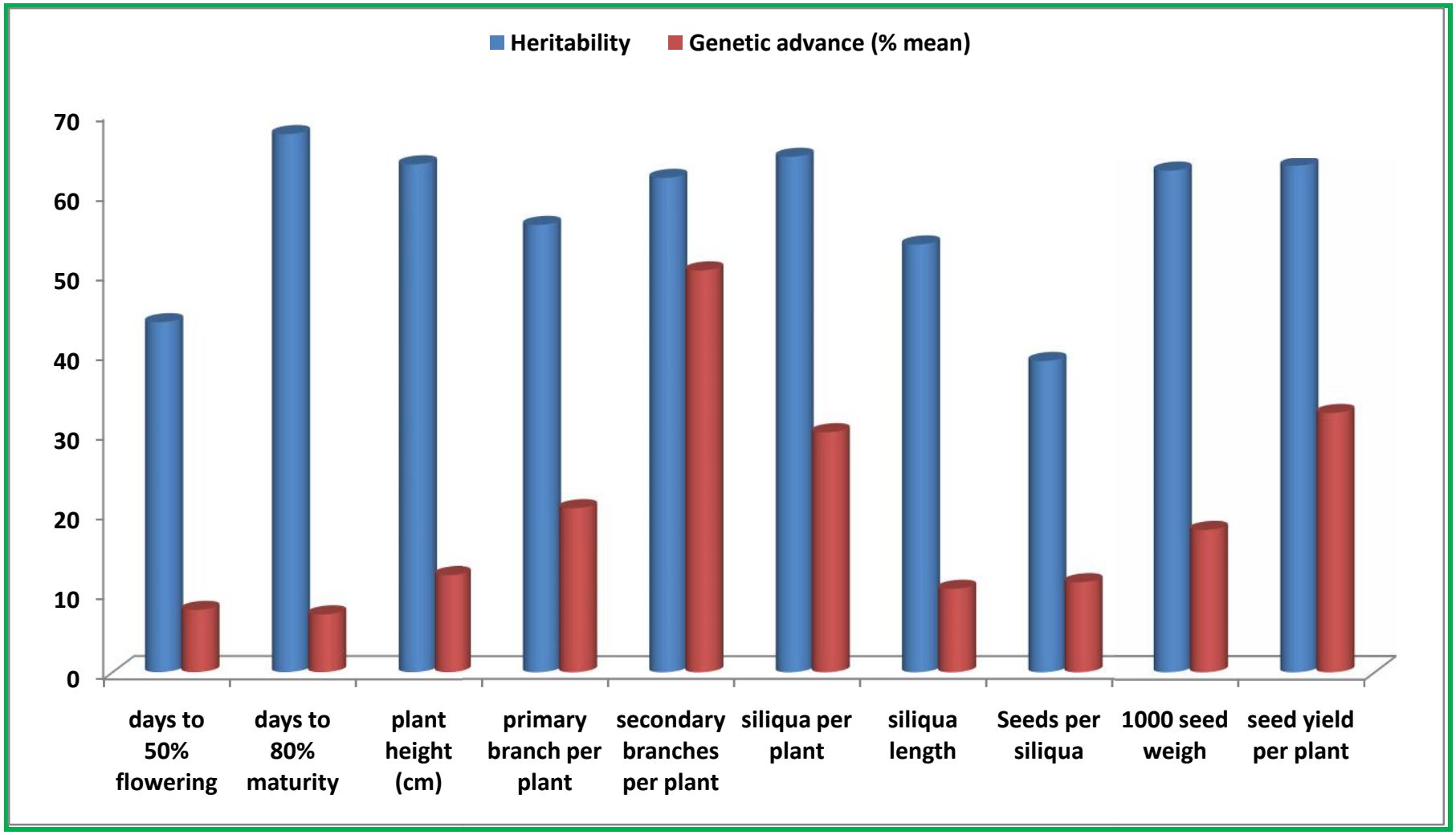


Figure 2. Heritability and genetic advance over mean in *Brassica napus* L.

Days to 50% flowering exhibited moderate heritability (43.79%), low genetic advance (2.40) with low genetic advance in percent of mean (7.78%) which revealed that the character was governed by both additive and non-additive gene action and this character was influenced by the environmental effect. It showed moderate possibility for the selection of this trait (Table 3). Saifullah (2010) also found high heritability (88.86%) and low genetic advance (2.06%). Aktar (2010) and Khan *et al*. (2012) supported the result.

4.2.2 Days to 80% maturity

The ANOVA (Table 2) represented that days to 80% maturity showed significant variations among the genotypes (30.939**) at the level of 1% probability. The highest days to 80% maturity was observed in G69 (89.50) and the lowest days to maturity was observed in G14 (76.00 days) (Appendix 1). Here G14 showed early maturity among all the studied genotypes. Phenotypic and genotypic variance for days to maturity were observed 18.49 and 12.45, respectively with high differences between them, suggested high influence of environment on the expression of the genes controlling this trait. The phenotypic coefficient of variation 5.21% was higher than the genotypic coefficient of variation (4.27%), which suggested that apparent variation not only due to genotypic effect but also due to environmental effect (Table 3). Naznin (2013) also found low difference between PCV (22.15) and GCV (19.74) in *B. rapa* L. Days to 80% maturity showed high heritability (67.33%) with low genetic advance (5.96) and genetic advance in percentage of mean (7.22%) indicated that this trait was controlled by additive and non-additive gene action and selection for such trait might moderately possible (Table 3). Naznin (2013) found high heritability (89.14%) with low genetic advance (8.69%) for the trait.

4.2.3 Plant height

Highly significant variations were observed among the genotypes (168.853**) at 1% level of probability (Table 2) for this trait. The highest plant height was observed in G58 (128.01 cm) whereas the minimum plant height was observed in G69 (83.51 cm)

(Appendix 1). High phenotypic variance (103.24) and genotypic variance (65.61) were observed (Table 3). The differences between phenotypic variance and genotypic variance was high revealed that high environmental effect on the expression of the genes controlling this trait. The lower PCV (9.28%) and GCV (7.40%) value for this trait. Low phenotypic coefficient of variation and genotypic coefficient of variation was found by Ghosh and Gulati (2001). The magnitude of heritability of this trait was high (63.55%) with moderate genetic advance (13.30) and genetic advance in percent of mean (12.15%). These findings were the indication of additive and non-additive gene action and selection for such trait was moderately effective. High heritability (92.48%) with moderate genetic advance (18.87) was found by Saifullah (2012) for the trait, where Naznin (2013) found high heritability (71.01%) with low genetic advance in percent of mean (9.49%) for this trait.

4.2.4 Primary branches per plant

Significant differences were observed among the genotypes for number of primary branches per plant (0.419**). Among the genotypes the highest number of primary branches per plant was observed in G21 (4.75) whereas the minimum number of primary branches/plant was observed in G43 (1.83). Low phenotypic variance (0.27) and genotypic variance (0.15) was observed on this trait. Relatively high difference between PCV (17.80%) and GCV (13.32%) value indicating the obvious variation not only due to genotypes but also due to the influence of environment. Hosen (2008) showed least difference between phenotypic and genotypic variances. Moderate heritability (56.02%) and very low genetic advance (0.60) and high genetic advance in percent of mean (20.54%) that determined the presence of additive and non-additive gene effect on the expression of this trait. Khan *et al.* (2012) found high heritability (60.17%) and high genetic advance (17.89%) for the trait

4.2.5 Secondary branches per plant

Secondary branches per plant showed highly significant differences (Table 2) among the genotypes (0.633**). Among the genotypes the highest secondary branches per plant was observed in G7 (2.90) whereas the minimum secondary branches per plant was observed in G16 (0.40). Difference between phenotypic variance (0.39) and genotypic variance (0.24) were low that means less environmental effect involved in this character (Table 3). High PCV (39.45%) and GCV (31.04%) values indicated presence of variability among the genotypes for this trait (Table 3). High GCV and PCV for this trait which indicated that, it might provide better scope for improvement through selection. Lekh *et al.* (1998) found the highest genotypic coefficient of variation for number of secondary branches while working on 24 genotypes of *Brassica napus*. Secondary branches per plant exhibited high heritability (61.91%) with high genetic advance in percentage of mean (50.32%). These findings revealed that the action of additive gene involved on the expression of this character as well as a scope of improvement through selection must be rewarding (Table 3). Akter (2010) supported the result as he also found high heritability (89.65%) and low genetic advance (3.50%). Moderately high heritability coupled with low genetic advance was also found by Singh *et al.* (1987).

4.2.6 Siliqua per plant

Highly significant variations were found for number of siliqua per plant (850.477**) among the genotypes, (Table 2). The highest siliqua per plant was observed in G59 (144.94) and the lowest in G12 (63.98). Siliqua per plant showed highly difference between phenotypic variance (516.84) and genotypic variance (333.64). The highest phenotypic variance and genotypic variance indicating large environmental influence, high genotypic variance indicating the better transmissibility of the character from parent to their offspring. The high PCV (22.61%) and moderate GCV (18.16%) was observed, which indicates that existence of adequate variation among the genotypes. High genetic variation was also found by Kudla (1993). Low GCV (20.19) and high PCV (33.81) was found by Khan *et al.* (2013). Siliqua per plant exhibited high

heritability (64.55%) with high genetic advance (30.23) and genetic advance in percentage of mean (30.06%). These results implied the possibility of predominance of additive gene action in the inheritance of this trait. Direct selection of this trait can improvement the genotypes. Khan *et al.* (2013) also found moderate heritability (35.65%) with high genetic advance (48.78%) which supports the trait.

4.2.7 Siliqua length (cm)

The analysis of variance (ANOVA) showed that there was highly significant differences among the genotypes for siliqua length (0.878**) at 1% level of significance (Table 2). Siliqua length was observed the highest in G65 (9.90 cm) and the minimum siliqua length was observed in G53 (6.30 cm). Phenotypic variance (0.57) and genotypic variance (0.31) with little difference between them indicating that they were less responsive to environmental factors for their phenotypic expression. Low PCV (9.47%) and GCV (6.93%) indicating that the genotypes have moderate variation for this trait (Table 3). Difference between PCV and GCV indicated high possibility of selecting this trait. High variation for this trait for both genotypic and phenotypic was recorded by Masood *et al.* (1999). Siliqua length showed moderate heritability (53.57%) with very low genetic advance (0.83) and moderate genetic advance in percent of mean (10.45%) indicated that environmental effect was more than the genotypic effect and due to non-additive gene action selection for further improvement of the trait might not be effective. Saifullah (2010) found the similar result for this trait.

4.2.8 Seeds per siliqua

Significant differences among the genotypes were (9.213**) observed for seeds per siliquae (Table 2).Seeds per siliqua was observed highest in G53 (22.74). The minimum number of seeds per siliqua was observed in G2 (12.97). The phenotypic and genotypic variances for this trait were 6.63 and 2.58, respectively (Table 3). The phenotypic variance appeared to be higher than the genotypic variance indicated influence of environment on the expression of the genes controlling this trait. The

value of PCV and GCV were 14.04% and 8.76%, respectively which indicating moderately environmental effect exists among different genotypes. Due to less difference between GCV and PCV this trait can be improved through the selection. Similar variability was also recorded by Kumar and Singh (1994). Seeds per siliquae showed moderate heritability (38.98%) with low genetic advance (2.07) and moderate genetic advance in percent of mean (11.27%). The character was governed by non-additive genes and moderate heritability was being exhibited due to favorable environment rather than genotypes and selection for this trait may not be effective. Saifullah (2010) also found high heritability (88.86%) and low genetic advance (2.06). Aktar (2010) and Khan *et al.* (2012) supported the result.

4.2.9 1000-seed weight (g)

The significant differences were observed among the genotypes for 1000 seed weight (0.478**) (Table 2). Thousand seed weight was found maximum in G49 (5.44 g) whereas the minimum thousand seed weight was found in G10 (2.58 g) (Appendix I). It is an important yield contributing character. It showed very low phenotypic variance (0.29) and genotypic variance (0.18) with little differences indicating that they were low responsive to environmental factors (Table 3). The moderate phenotypic coefficient of variation (13.77%) and genotypic coefficient of variation (10.91%) were close to each other (Table 3). There was moderate difference between phenotypic and genotypic co-efficient of variation, indicating environmental influence on this character was moderate. Khan *et al*. (2013) found large difference between GCV (3.67) and PCV (18.09) while Naznin (2013) found very low difference (PCV=9.85 and GCV=8.13) in *B. rapa*. in this trait. The heritability of this trait was high (62.70%) and low genetic advance (0.70) and moderate genetic advance in percent of mean (17.79%). These results indicated additive and non-additive genes involvement in the expression of the trait and moderate scope of improvement by direct selection on this trait. Low heritability (16.09%) with low genetic advance (0.16) was found by Akter (2010) and high heritability (65.03%) with low genetic advance (0.31%) was stated by Saifullah (2010) for the trait.

4.2.10 Seed yield per plant (g)

Seed yield per plant showed significant mean sum of squares (2.020**) due to different genotypes that suggested considerable range of variation for this trait (Table 2). Seed yield per plant was found maximum in G5 (7.06 g) and minimum was found in G46 (2.60 g) (Appendix I). The phenotypic variances and genotypic variances for this trait were 1.24 and 0.78, respectively (Table 3). The values are close to each other indicated less environmental influences on this trait. The high values of PCV and GCV were 24.85% and 19.77% (Table 3) indicating that the genotypes have high environmental variation for this trait. Highest GCV and PCV for seed yield per plant which indicated that, it might provide better scope for improvement through selection which was also reported by Mekonnen (2014). Naznin (2013) and Akter (2010) found more PCV for the trait. The estimates of heritability alone fail to indicate the response to selection (Johnson *et al.,* 1955). Therefore, the heritability estimates appears to be more meaningful when accompanied by estimates of genetic advance. The genetic advance as percent mean (GAM) was also estimated. High heritability (63.31%) coupled with low genetic advance (1.45) with high genetic advance in percent of mean (32.41%) indicated that low influence of genotypic materials and additive gene effect was present (Table 3). Highly possibility showed for the selection of this trait. Higher heritability along with highest genetic advance as percent of mean was observed in this character by Mekonnen (2014) attributed to additive gene actions. Naznin (2013) found high heritability (57.05%) with low genetic advance (0.99%) for the trait. Aytac and Kinaci (2009) observed highest heritability and genetic advance over mean was supported this results.

4.3 Association analysis

Seed yield is a complex product being influenced by several quantitative traits. Some of these traits are highly associated with seed yield. The analysis of the relationship among those traits and their association with seed yield is very much essential to establish selection criteria. Breeders always look for genetic variation among traits to select desirable type. It is evident that in most of the cases, the genotypic correlation

co-efficient were higher than the corresponding phenotypic correlation co-efficient. This indicated a strong inherent association between the characters studied and suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values. In few cases, however, phenotypic correlation co-efficient were same or higher than their corresponding genotypic correlation co-efficient suggesting that both environmental and genotypic correlation in these cases act in the same direction and finally maximize their expression at phenotypic level.

Relationship between yield and yield contributing characters was studied through analysis of correlation between them. The correlation coefficients between all the characters were presented in Table 4 and Table 5 for genotypic and phenotypic correlation coefficient, respectively.

In the present study out of 45 associations 23 associations were significant in genotypic level and 17 associations were significant in phenotypic level. Among the genotypic 23 significant associations, 14 associations were positively significant and the rest nine was negatively significant. From the phenotypic 17 significant associations, 12 were positively significant and rest five was negatively significant. The significant and positive association between the characters suggested additive genetic model thereby less affected by the environmental fluctuation. Besides, eight relationships were positive and non-significant at genotypic level and 13 relationships were positive and non significant in phenotypic level were observed. The positive and non-significant association referred information of inherent relation among the pairs of combination. While the negative and non-significant association referred a complex linked of relation among the pair of combinations.

Seed yield per plant was significant positive correlation with plant height (0.407^{**} and 0.393^{**}), primary branches per plant (0.457^{**} and 0.445^{**}), secondary branches per plant (0.311^{**} and 0.416^{**}), siliqua per plant (0.587^{**} and 0.626^{**}) and 1000 seeds

weight (0.286** and 0.262**) in both genotypic and phenotypic level (Table 4, Table 5 and Figure 3) suggesting that genotypes with high partitioning efficiency gave increase in seed yield per plant. Uddin *et al*. (2013) and Singh (2010) found high significant positive correlation of seed yield per plant with secondary branches per plant and siliqua per plant at both level supported this results. Maurya *et al.* (2012) and Khayat *et al.* (2012) reported seed yield per plant had significant positive correlation with plant height, siliqua length and 1000 seed weight. Mahmud *et al.* (2008) and Afrin *et al.* (2011) found positive correlation of seed yield per plant with plant height, primary branches per plant and siliqua per plant supported these results. Siliquae per plant had significant positive correlation with seed yield reported by Rameeh (2011). Siliqua length (-0.230**and -0.020)was negatively correlated with seed yield per plant indicating that seed yield per plant would be increased with the decreased of that character. Days to 50% flowering (-0.077 and -0.134) and days to 80% maturity (-0.155 and -0.027) were correlated negatively with seed yield per plant, indicated that seed yield per plant would be increased with the decreased of days to 50% flowering and days to 80% maturity. A schematic diagram of genotypic and phenotypic correlation coefficient of yield contributing traits with seed yield was presented in Figure 3.Study of correlation at yield components levels exhibited that days to 50% flowering showed negatively and significant correlation with days to maturity (-0.352**and -0.251**), siliqua per plant (-0.189* and -0.187*) at both levels. Days to maturity showed positively and significantly correlated with secondary branches per plant (0.171*) and seeds per siliqua (0.169*) at genotypic level.

Plant height showed positive and significant correlation with primary branches per plant (0.210* and 0.246**), secondary branches per plant (0.253** and 0.263**), siliqua per plant (0.592** and 0.529**) at both genotypic and phenotypic level and significant negative correlation with 1000 seed weight (-0.399** and -0.198*) at both levels. Plant height also showed positive and insignificant correlation with siliqua length (0.077 and 0.161) and seeds per siliqua (0.039 and 0.066) at both levels.

Primary branches showed positive and significant correlation with secondary branches per plant (0.690** and 0.620**), siliqua per plant (0.502** and 0.555**) at both level and negative significant correlation with seeds per siliqua (-0.188*) and 1000 seed weight (-0.219**) at genotypic level.

Secondary branches per plant showed positive and significant correlation with siliqua per plant (0.559** and 0.605**) at both level and positive correlation with siliqua length (0.156 and 0.161) and seeds per siliqua (0.113 and 0.064). Basalma (2008) reported significant positive correlation of branches per plant with siliqua per plant supported these findings. Siliqua per plant showed positive correlation with siliqua length (0.066) and seeds per siliqua (0.077) at phenotypic level. Siliqua length showed positive and significant correlation with seeds per siliqua (0.340** and 0.208*) and negative association with 000-seed weight (-0.182* and -0.088) at both levels. Seeds per siliqua showed negatively correlation with 1000 seeds weight (-0.323** and -0.198*) at both levels.

As such from existing agro climatic situation based on the present study it could be stressed that more emphasis should be given for plant height, primary and secondary branches per plant, siliqua per plant and thousand seeds weight as they showed very high to fair degree of positive association with seed yield at both genotypic and phenotypic levels.

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

	D50F	DM	PH	PBP	SBP	SPP	SL	SPS	TSW	YPP
D50F	1									
DM	-0.352**	1								
PH	-0.040	-0.024	1							
PBP	-0.117	0.076	0.210*	1						
SBP	-0.076	0.171*	0.253**	0.690**	1					
SPP	-0.189*	0.121	0.592**	0.502**	0.559**	1				
PL	-0.069	-0.117	0.077	-0.147	0.156	-0.107	1			
SPS	-0.153	0.169*	0.039	-0.188*	0.113	-0.014	0.340**	1		
TSW	0.024	0.014	-0.399**	-0.219**	-0.184*	-0.137	-0.182*	-0.323**	1	
YPP	-0.077	-0.155	0.407**	0.457**	0.311**	0.587**	-0.230**	-0.080	0.286**	1

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

D50F = days to 50% flowering, DM = 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 5. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of *Brassica napus* L.

	D50F	DM	PH	PBP	SBP	SPP	SL	SPS	TSW	YPP
D50F	1									
DM	-0.251**	1								
PH	-0.119	0.003	1							
PBP	-0.173*	0.095	0.246**	1						
SBP	-0.100	0.107	0.263**	0.620**	1					
SPP	-0.187*	0.092	0.529**	0.555**	0.605**	1				
PL	0.037	-0.016	0.161	0.011	0.161	0.066	1			
SPS	-0.051	0.026	0.066	-0.045	0.064	0.077	0.208*	1		
TSW	-0.007	-0.083	-0.198*	-0.104	-0.045	-0.031	-0.088	-0.198*	1	
YPP	-0.134	-0.027	0.393**	0.445**	0.416**	0.626**	-0.020	-0.018	0.262**	1

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

D50F = days to 50% flowering, DM = 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).

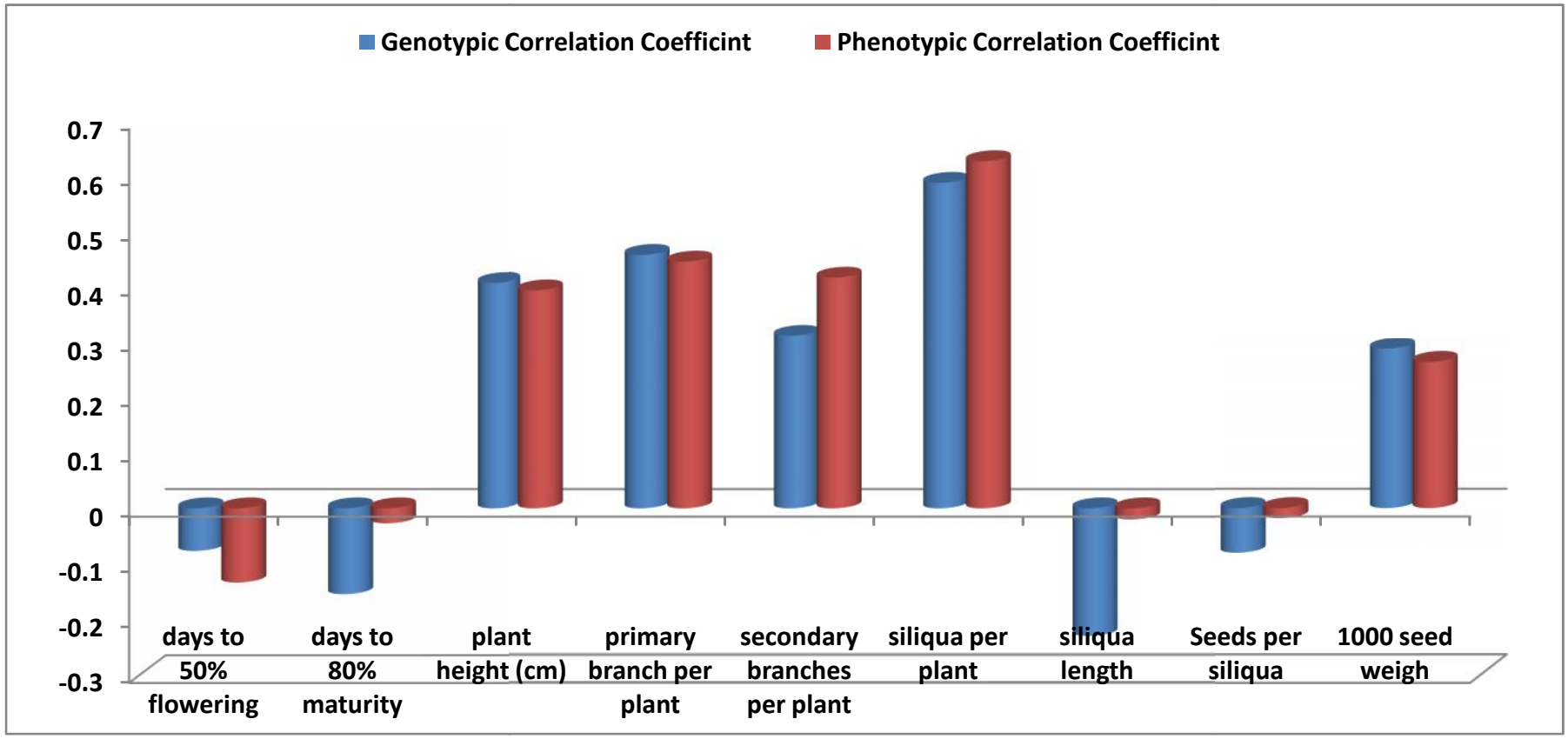


Figure 3. Genotypic and Phenotypic Correlation Coefficient of yield contributing traits with seed yield of *Brassica napus* L.

Regression and Partial correlation

Analysis of variance for regression was revealed that significant variation present among the genotypes (Table 6). Partial correlation was significant for 1000 seed weight ($P < 0.01$), siliqua per plant ($P < 0.01$), plant height ($P < 0.05$) and primary branches per plant ($P < 0.05$) (Table 7) indicated that 1000 seed weight contributed over 49% to total seed yield, siliqua per plant contributed over 34% and other two traits primary branches per plant and plant height was contributed 29% and 28% respectively. The significance of partial regression coefficients was also tested (Table 7). Linear regression analysis of yield on the basis of all yield components is given in Table 7. Yield showed a significant linear regression coefficient with 1000 seed weight, siliqua per plant, plant height, and primary branch per plant. The selection of best regression equation done through backward elimination procedure revealed that 1000 seed weight, siliqua per plant were the most effective variables contributing to the seed yield.

Table 6. Analysis of variance for regression

Source of variation	Sum of squares	df	Mean square	F	Sig.
Regression	39.379	9	4.375	8.814	0.000
Residual	29.288	59	0.496		
Total	68.667	68			

Table 7. Partial correlation and linear regression coefficients of yield contributing attributes on yield of *Brassica napus* L.

Attributes	Partial correlation	Linear regression coefficients (beta)	t-test for significance (for beta)
Days to 50% flowering	-0.018	-0.012	-0.136
Days to 80% maturity	-0.187	-0.131	-1.458
Plant height (cm)	0.288*	0.252	2.306*
Primary branch per plant	0.291*	0.283	2.334*
Secondary branches per plant	-0.028	-0.027	-0.217
Siliqua per plant	0.348**	0.373	2.855**
Siliqua length	-0.129	-0.092	-1.000
Seeds per siliqua	0.121	0.087	0.938
1000 seed weigh	0.495**	0.409	4.372**

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

4.4 Path coefficient analysis

Correlation co-efficient determines association of characters that might not provide an exact picture of the relative importance of direct and indirect influence of each yield components on seed yield of the plant. A clear picture of the interrelationship between seed yield and others yield contributing characters, direct and indirect effects of them can be worked out by using path analysis at genotypic level which also measures the relative importance of each component on yield (Wright, 1921 and modify by Dewey and Lu, 1957). Seed yield is considered as a resultant (dependent) variable and days to 50% flowering, days to 80% maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of siliquae, number of seeds per silique, length of silique and thousand seed weight were causal (independent) variable. Estimation of direct and indirect effect of path co-efficient analysis for *Brassica napus* are presented in Table 8. Residual effects of their independent variables, which have influenced on yield been denoted as R.

Among the characters that have positive direct effect on seed yield per plant were plant height (0.454), primary branches per plant (0.575), siliqua per plant (0.238), seeds per siliqua (0.35) and 1000 seeds weight (0.68). The genotypic and phenotypic correlation of plant height, siliqua per plant, siliqua length and thousand seeds weight with seed yield per plant was also high and positive. Such high positive correlation with seed yield per plant was mainly due to the high positive direct effect and considerable positive indirect effects of these characters. The path co-efficient analysis by Hosen (2008) and Siddikee (2006) exhibited that thousand seed weight had the highest positive direct effect that supported this findings. Uddin *et al.* (2013) and Alam (2010) reported primary branches per plant, siliqua per plant, siliquae length and thousand seed weight showed direct positive association with seed yield per plant that also supported present findings.

Table 8. Partitioning of genotypic correlations into direct and indirect effects of important characters by path analysis of *Brassica napus* L.

Characters	Direct effect	D50F	DM	PH	PBP	SBP	SPP	PL	SPS	TSW	Total Indirect Effect	Genotypic correlation with seed yield
D50F	-0.033	-	0.101	-0.018	-0.067	0.013	-0.045	0.011	-0.05	0.02	-0.043	-0.077
DM	-0.287	0.012	-	-0.011	0.044	-0.030	0.029	0.018	0.06	0.01	0.130	-0.155
PH	0.454	0.001	0.007	-	0.121	-0.045	0.141	-0.012	0.01	-0.27	-0.046	0.407**
PBP	0.575	0.004	-0.022	0.095	-	-0.122	0.119	0.023	-0.07	-0.15	-0.118	0.457**
SBP	-0.177	0.003	-0.049	0.115	0.397	-	0.133	-0.025	0.04	-0.13	0.488	0.311**
SPP	0.238	0.006	-0.035	0.269	0.289	-0.099	-	0.017	0.00	-0.09	0.348	0.587**
PL	-0.158	0.002	0.034	0.035	-0.085	-0.028	-0.025	-	0.12	-0.12	-0.071	-0.230**
SPS	0.35	0.01	-0.05	0.02	-0.11	-0.02	0.00	-0.05	-	-0.22	-0.432	-0.080
TSW	0.68	0.00	0.00	-0.18	-0.13	0.03	-0.03	0.03	-0.11	-	-0.397	0.286**

Residual effect (R): **0.217** ** = Significant at 1%. * = Significant at 5%.

D50F = days to 50% flowering, DM = 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).

Plant height showed positive direct effect on seed yield per plant where the correlation coefficient was also positive and significant. Plant height showed indirect positive effect through primary branches per plant (0.121), siliqua per plant (0.141) and days to maturity (0.007). Its negative indirect effect observed via 1000 seed weight (-0.27) and secondary branches per plant (-0.045).

Primary branches per plant showed positive direct effect on seed yield per plant where the correlation was also significant and positive with seed yield. Secondary branches (-0.177) showed negative direct effect on seed yield per plant where the correlation was significant and positive.

Siliqua per plant showed positive direct effect on seed yield per plant where the correlation was also significant and positive correlation with seed yield.

1000 seed weight showed highest positive direct effect on seed yield per plant as well as correlation also positive and significant with it. The residual effect was 0.217, indicating that the ten characters contributed 78.3 percent of variability in seed yield per plant studied in path analysis. The residual effect towards seed yield in this study may be due to several reasons such as may be other causal factors (characters) that not included in the analysis contribute more towards yield and sampling errors.

By studing correlation, regression and path co-efficient revealed that 1000 seed weight, siliquae per plant, primary branches per plant and plant height were the most important components for getting higher yield. Recent breeding research also emphasized giving importance of these characters. Therefore, the present study suggested that siliqua per plant and 1000-seed weight should be included owing to importance in selecting the genotypes for higher grain yield in *Brassica napus*.

4.5 Genetic diversity

The knowledge of available genetic diversity is an important factor for any heritable improvement and its nature and degree is useful for selecting desirable parents from a germplasm for the successful breeding programme. There is still much scope for improving of genetic architecture desirable for hybrid through heterosis breeding. Its magnitude in desirable direction is preferable. The success of hybridization depends upon the selection of suitable parental genotypes and performance of their cross combinations.

Genetic diversity was analyzed using GENSTAT 5.1 software program. Genetic diversity analysis involves several steps i.e. estimation of distance between the varieties, clustering and analysis of inter-cluster distance. Therefore, more than one multivariate technique was required to represent the results more clearly and it was obvious from the results of many researchers.

The amount of diversity available in the crop decides the success of any crop improvement programme with manifested objectives. Assemblage and assessment of divergence in the germplasm is essential to know the spectrum of diversity. In the present investigation, 69 genotypes of *Brassica napus* 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. Based on D^2-value, the genotypes were grouped into six clusters (Table 9).

Nonhierarchical clustering

With the application of covariance matrix for nonhierarchical clustering, 69 *Brassica napus* genotypes were grouped into six different clusters. It is stated that 37.68% genotypes were included in cluster III and it was followed by 31.88% in cluster I, 14.49% genotypes under cluster IV, 13.04% genotypes in cluster V and 1.45% in both cluster II and VI. The composition of clusters with different genotypes is presented in Table 9. The cluster III included 26 genotypes, which was the highest, followed by cluster I

with 22 genotypes, cluster IV with 10 genotypes and cluster V with 9 genotypes. Cluster II and VI contained only one genotype in each. Zaman *et al.* (2010) reported four clusters by 45 genotypes. The 45 genotypes were grouped in eight clusters using Tocher's method found by Pandey *et al.* (2013). Goswami and Behl (2006) reported with 43 genotypes and found six clusters by D^2 statistics. The cluster III was the biggest with 11 genotypes followed by cluster I with 9 genotypes reported by Aunwinithul *et al.* (2004).

Table 9. Distribution of different genotypes of *Brassica napus* L. in different clusters

Cluster no.	Name of genotypes	No. of populations	Percent
I	1, 12, 13, 15, 16, 30, 31, 33, 34, 42, 44, 45, 46, 47, 48, 49, 50, 51, 57, 66, 67, 68	22	31.88
II	2	1	1.45
III	3, 4, 7, 9, 11, 14, 17, 18, 19, 20, 22, 24, 26, 35, 38, 39, 40, 41, 43, 52, 53, 54, 55, 56, 60, 61	26	37.68
IV	5, 8, 10, 21, 29, 36, 37, 58, 62, 65	10	14.49
V	6, 23, 25, 27, 28, 32, 59, 63, 64	9	13.04
VI	69	1	1.45
	Total	69	100.00

Principal component analysis

Even though the ANOVA results confirmed the suitability of studied traits to expose the morphological differences *Andrographis Paniculata* accessions, a further step was taken to illustrate the effectiveness of each characteristic in the population's variation (Talei *et al.,* 2013). Principal components analysis is a powerful approach in germplasm collections that allows a better understanding on the structure of the entire collection. PCA makes it possible to identify the most suitable variables among the studied accessions (Iezzoni and Pritts 1999; Upadhyaya *et al.* 2006). Therefore, the most important outcome of the scree plot-based PCA was to ease detecting the principal components with an Eigen value greater than an arbitrary value K = 1. The illustrative feature of the scree plot-based PCA was mostly due to the simple and one-dimensional nature of the generated graphs. These principal components (PCs) can be utilized to calculate the morphological distances of the accessions in the future studies (Goodman, 1972 and Schut *et al*., 1997). The PCA gives Eigen values of principal component axes of coordination of genotypes with the first axes totally accounted for the variation among the genotypes, whereas three of these Eigen values above unity accounted for 58.004% (Table 10). The first two principal axes accounted for 45.253% of the total variation among the characters describing 69 genotypes of *Brassica napus* genotypes. Belete (2011) reported 91.4% variation contributed by first five principal components through principal component analysis in Ethiopian mustard. A dendrogram of the genotypes was shown six different clusters (Figure 4).

The component matrices of the quantitative-based PCA revealed three main principal components (Table 11). In PCA1, days to 50% flowering, days to 80% maturity, plant height and primary branches per plant with Eigen values of 2.959 caused 29.586% of the total variation in the quantitative data. In PCA 2,siliqua length and seeds per siliqua with Eigen values of 1.567 caused 45.253% of the total variation in the quantitative data. The PCA of the qualitative characteristics resulted in generating three PCs with the

Table 10. Eigen values and percent of total variation of different characters in *Brassica napus* L. genotype

Principal component axes	Eigen values	Percent of total variation	Cumulative variation
I	2.959	29.586	29.586
II	1.567	15.666	45.253
III	1.275	12.752	58.004
IV	0.989	9.889	67.893
V	0.922	9.220	77.113
VI	0.752	7.516	84.630
VII	0.687	6.873	91.502
VIII	0.350	3.501	95.004
IX	0.273	2.731	97.734
X	0.227	2.266	100.000

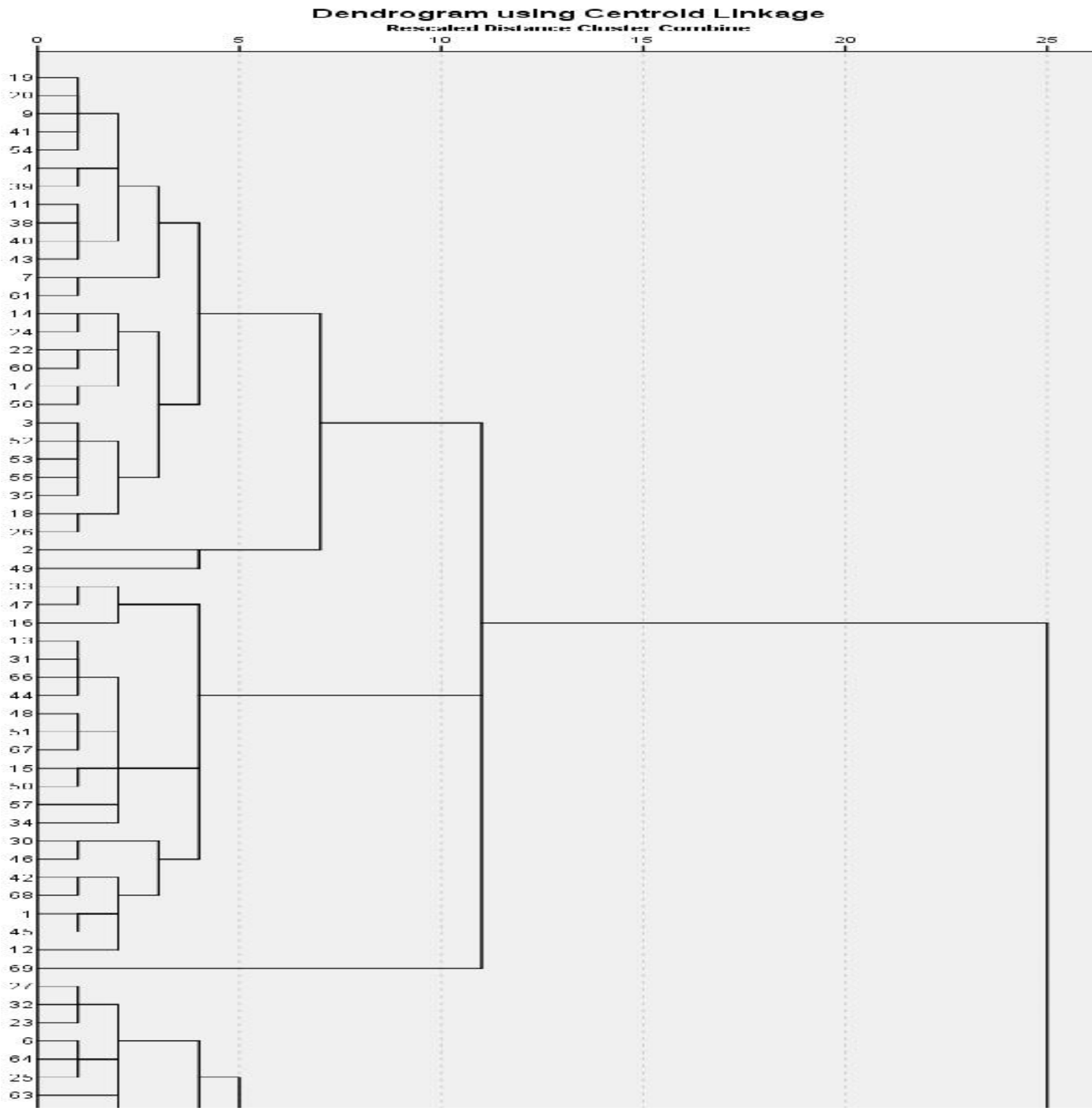


Figure 4. Dendrogram showing six different clusters of 69 genotypes

Eigen values of 2.959, 1.567 and 1.275, respectively served as the most effective PCs. These three PCs caused a total of 58.004% of qualitative variation in ten morphology characters of 69 accessions. These results indicate that days to 50% flowering, days to 80% maturity, plant height, primary branches per plant, siliqua length and seeds per siliqua could be suitable candidates to investigate the morphological variation of the species in future studies.

Cluster Mean

According to the cluster means (Table 12), Cluster I showed better performance in case of early flowering and maturity. Thus indicated that genotype of this cluster could be used for parent in future hybridization program for early maturity. The genotypes included in cluster II showed, early maturity, highest 1000 seed weight and seed yield per plant and lowest number of seeds per siliqua indicating the possibility of selection of high yield performing genotypes and it also coarse seeded cluster. The genotypes under Cluster III possessed, lower siliqua length, higher seeds per siliqua. The genotypes of cluster IV had the highest days to 50% flowering and the highest siliqua length. Genotypes under cluster V showed the highest plant height, siliqua per plant, primary branches per plant and seeds per siliqua; and the lowest days to flowering. Moreover, genotypes of cluster VI had late maturity, highest primary branches per plant; and the lowest plant height, siliqua length, 1000 seed weight and seed yield per plant. Pictorial view of genotypes of different clusters are presented in Plate 5, 6, 7 & 8.

Table 11. Factor analysis for different studied traits in *Brassica napus* L. cultivars

Characters	Component		
	PCA1	**PCA2**	**PCA3**
Days to 50% flowering	0.872	0.041	0.106
Days to 80% maturity	0.771	-0.316	-0.094
Plant height (cm)	0.753	-0.050	0.172
Primary branch per plant	0.745	0.152	0.150
Secondary branches per plant	0.627	0.315	-0.118
Siliqua per plant	-0.059	-0.717	-0.061
Siliqua length	-0.023	0.654	0.140
Seeds per siliqua	0.034	0.629	-0.158
1000 seed weigh	-0.005	0.040	0.827
Seed yield per plant	-0.149	0.002	-0.721
Eigen value	2.959	1.567	1.275
Cumulative%	29.586	45.253	58.004

Table 12. Cluster mean for yield and yield related characters in *Brassica napus* L. genotypes

Characters	I	II	III	IV	V	VI
Days to 50% flowering	31.12	31.00	30.85	31.55**	29.56*	30.50
Days to 80% maturity	81.74	79.25*	83.27	82.40	82.94	89.50**
Plant height (cm)	103.00	96.34	111.98	114.20	117.63**	83.51*
Primary branch per plant	2.61*	3.02	2.88	3.31	3.16	3.51**
Secondary branches per plant	1.22*	1.75	1.60	1.85	2.07**	1.57
Siliqua per plant	76.93*	108.70	100.20	119.94	134.70**	89.50
Siliqua length	7.95	7.94	7.94	8.17**	8.04	7.73*
Seeds per siliqua	18.19	14.74*	18.42	18.52	19.08**	18.33
1000 seed weigh	4.04	4.78**	3.87	3.69	3.98	3.64*
Seed yield per plant	3.86	5.57**	4.39	5.05	5.44	3.05*

** = Highest valus
* = Lowest value

The present study revealed that the cluster V with high mean values for four traits were desired to be crossed with cluster I which possessed low mean values of three characters for getting high heterosis. Same cross between clusters V and II; V and IV. This finding was strongly supported with identification of similar cluster combinations from interpretation of inter cluster distance made in the present study and thereby the expected progenies inculcate traits in a positive direction and further selection would be more effective.

Canonical Variate Analysis (CVA)

Canonical Variate Analysis (CVA) was done to compute the inter-cluster distances. The intra and inter-cluster distance (D^2) values were shown in Table 13. In this experiment, the inter-cluster distances were higher than the intra-cluster distances thus indicating broader genetic diversity among the genotypes of different groups. Islam and Islam (2000) reported that the inter cluster distances were higher than the intra-cluster distances. Uddin (1994) also reported similar result in mustard. The highest inter-cluster distance was observed between clusters I and VI (60.964), followed by the distance between clusters II and VI (50.538), I and V (43.928) and III and VI (36.254). In contrast, the lowest inter-cluster distance was observed between cluster III and IV (12.739), followed by I and II (14.455) (Table 14). However, the maximum inter-cluster distance was observed between the clusters I and VI (60.964) indicating that genotypes from these two clusters, if involved in hybridization, may produce a wide spectrum of segregating population. Dhillon *et al.* (1999) mentioned that maximum inter cluster distance gave desirable segregants for the development of high yielding varieties with quality of oil for seed yield. On the other hand, the maximum intra-cluster distance was found in cluster V (5.77), which contained of nine genotypes; while the minimum distance was found in cluster II & VI (0.00), whose were comprised of one genotype each. Intra cluster distance was maximum for cluster VI followed by cluster III found by Pandey *et al.* (2013). The intra cluster distances in all the four clusters were lower than the inter cluster distances and which indicated that genotypes within the same cluster were closely related. The inter cluster distances

Table 13. Intra (Bold) and inter cluster distances (D^2) for *Brassica napus* L. genotypes

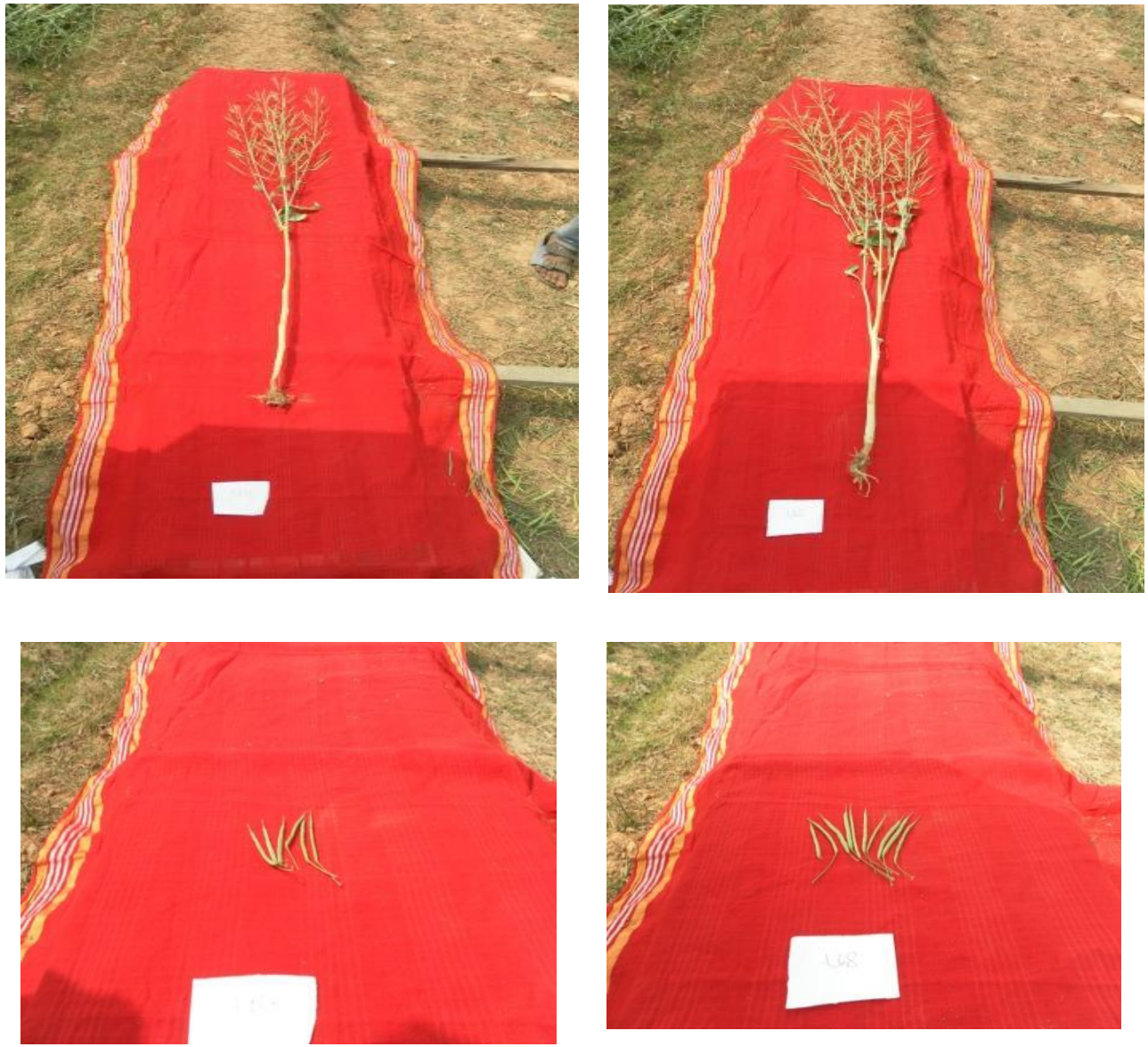
Cluster	I	II	III	IV	V	VI
I	**3.45**	14.455	25.069	32.171	43.928	60.964
II		**0.00**	18.137	20.281	34.143	50.538
III			**2.65**	12.739	19.165	36.254
IV				**4.76**	15.614	30.826
V					**5.77**	17.143
VI						**0.00**

Table 14.The nearest and farthest clusters from each cluster between D^2 values in *Brassica napus* L.

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	**I**	**II (**14.455)	**VI (**60.964)
2	**II**	**I (**14.455)	**VI (**50.538)
3	**III**	**IV (**12.739)	**VI (**36.254)
4	**IV**	**III (**12.739)	**I (**32.171)
5	**V**	**IV (**15.614)	**I (**43.928)
6	**VI**	**V (**17.143)	**I (**60.964)

G42 **G33** **G37**

Plate 5. Photographs of selected genotypes under Cluster I (plant in above and pod in under)



G2 **G69**

Plate 6. Photographs of genotype under cluster II (left) and Cluster VI (right)

G5 **G65**

Plate 7. Photographs of genotypes under cluster IV

G28 **G59**

Plate 8. Photographs of genotypes under cluster V

were larger than the intra cluster distances which indicated wider genetic diversity among the genotypes of different groups. Hence, there is a lot of scope for exchange of genes among genotype within these clusters.

4.5.8 Selection of parents

Cluster I genotypes for early maturing and medium yielder, where cluster II for coarse seeded, early maturing and high yielder. Genotypes under cluster IV denote high siliqua length and high yielder. Genotypes of cluster V possessed taller plant and more siliqua per plant. Cluster VI represented more primary branches per plant, late maturing, low yielder and small seeded (Table 15).

Considering diversity pattern and other agronomic performance genotypes G42, G33 and G67 were selected from cluster I, G2 from cluster II, genotypes G65, G5 and G62 from cluster IV, genotypes G28, G59 and G64 were from cluster V and genotype G69 from cluster VI could be considered as suitable genotypes for developing open pollinated varieties and further use for efficient hybridization in future. Involving of such diverse lines in inter cluster genotypes crossing program could produce desirable segregants. So, more divergent genotypes were recommended to use as parents in future hybridization program.

Table 15. Salient features of selected genotypes under different clusters

Cluster No.	Genotypes Code	Pedigree	Main feature
I	G42 G33 G67	Nap9908xNap2022 Nap108xNap2057 Nap9906xNap2022	Early maturity Medium yielder
II	G2	Nap9908xNap2057	Early maturity High yielder Coarse seeded
IV	G65 G5 G62	Nap205xNap9901 BS-13xNap2001 B-13XNap2037	High siliqua length High yielder
V	G28 G59 G64	Nap108xNap2022 Nap205xNap 0130 Nap205xNap206	Taller plant More siliqua per plant
VI	G69	Nap9906xNap2012	More primary branches per plant Late maturing Low yielder Small seeded

CHAPTER V

SUMMARY AND CONCLUSION

The experiment was carried out with the objective to assess the selection of superior genotypes from 69 *Brassica napus* L. genotypes through study the genetic analysis that mean variability, association, path analysis and morphological diversity among the genotypes for improvement of yield. The experiment was carried out at the experimental Farm of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh during the period from November 2015 to February 2016. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Data on different morphological characters were recorded time to time and analyzed statistically. The results of the studies have been summarized as follows:

The analysis of variance showed highly significant differences among the genotypes for all the characters. From the mean performance it was observed that the days to 50% flowering was observed the lowest in G7 and highest in G57. The highest days to 80% maturity was observed in G69 and the lowest days to maturity was observed in G14. Plant height was observed the highest in G58 whereas the minimum plant height was observed in G69. The highest primary branches per plant were observed in G21 whereas the lowest primary branches per plant were observed in G43. The genotype G7 was performed the highest secondary branches per plant and lowest by the genotype G16. The highest siliquae per plant was observed by the genotype G59 whereas the lowest siliquae per plant was observed by G12. Siliqua length was resulted the longest by G65 whereas the shortest siliqua length was observed by G53. Maximum seeds per siliqua were observed in G53 whereas the minimum seeds per siliqua were observed in G2. Thousand seed weight was found the maximum in G49 whereas the minimum thousand seed

weight was found in G10. Yield is the most outstanding character and all the research work and objectives are dependent on yield. The highest amount of yield per plant was observed in G5 whereas the lowest yield per plant observed in G46. Siliqua per plant (64.55) exhibited the highest value of heritability while seeds per siliqua (38.98) exhibited the lowest value of heritability. The phenotypic variance and phenotype coefficient of variation were higher than the corresponding genotypic variance and genotypic coefficient of variation for all the characters under study. In case of secondary branches per plant and seeds per siliqua showed higher influence of environment for the expression of these characters. On the other hand, days to 80% maturity , plant height (cm), siliqua length , 1000 seed weight and seed yield per plant showed least differences of phenotypic and genotypic variance suggesting additive gene action for the expression of these characters. High heritability with high genetic advance in percent of mean was observed for secondary branches per plant, siliqua per plant, 1000 seed weight and seed yield per plant indicating that these traits were under additive gene control and selection for genetic improvement for these traits would be effective.

Relationship between yield and yield contributing characters was studied through analysis of correlation between them. The significant positive correlations of seed yield per plant were found with plant height, primary branches per plant, secondary branches per plant, siliqua per plant and 1000 seeds weight in both genotypic and phenotypic level suggesting that genotypes with high partitioning efficiency gave increase in seed yield per plant. Siliqua length was negatively correlated with seed yield per plant indicating that seed yield per plant would be increased with the decreased of that character. Days to 50% flowering and days to 80% maturity were correlated negatively with seed yield per plant, indicated that seed yield per plant would be increased with the decreased of days to 50% flowering and days to 80% maturity.

Partial correlation was significant for 1000 seed weight, siliqua per plant, plant height and primary branches per plant indicated that 1000 seed weight contributed over 49% to total seed yield, siliqua per plant contributed over 34% and other two traits viz. primary branches per plant and plant height was contributed 29 and 28% respectively. Yield showed a significant linear regression coefficient with 1000 seed weight, siliqua per plant, plant height, and primary branch per plant. The selection of best regression equation revealed that 1000 seed weight, siliqua per plant were the most effective variables contributing to the seed yield.

The path coefficient analysis was performed using correlation coefficient to determine direct and indirect influence considering ten characters. It was revealed that plant height, primary branches per plant, siliqua per plant, seeds per siliqua and 1000-seed weight had the positive direct effect on yield per plant, whereas, days to maturity, secondary branches per plant and siliqua length had the negative direct effect on yield per plant. The path coefficient studies indicated that plant height, primary branches per plant, siliqua per plant, seeds per siliqua and 1000 seeds weight were the most important contributors to seed yield per plant which could be taken in consideration for future hybridization program. The residual effect was 0.217 indicating that the ten characters contributed 78.3 percent of variability in seed yield per plant studied in path analysis. The residual effect towards seed yield in this study may be due to other causal factors (characters) and sampling errors.

Genetic diversity among *Brassica napus* genotypes was performed through Principal Component Analysis (PCA), Cluster Analysis and Canonical Vector Analysis (CVA). All the 69 *Brassica napus* genotypes were grouped into six different clusters. The highest cluster III included 26 genotypes followed by cluster I with 22 genotypes, cluster IV with 10 genotypes and cluster V with 9 genotypes. Cluster II and VI contained one genotypes in each. Eigen values of

principal component axes showed that three Eigen values above unity accounted for 58.004%. The first two principal axes accounted for 45.253% variation describing 69 genotypes of *Brassica napus*. Cluster I showed better performance in case of early flowering and maturity. Cluster II showed the early flowering, early maturity, highest 1000 seed weight and seed yield per plant and lowest number of seeds per siliqua indicating the possibility of selection of high yield performing genotypes and it also coarse seeded cluster. Cluster III possessed late flowering, low siliqua length, high seeds per siliqua. The genotypes of cluster IV had late flowering and highest siliqua length. Cluster V showed highest plant height, siliqua per plant, primary branches per plant and seeds per siliqua; and early flowering. Genotypes of cluster VI had late maturity, highest primary branches per plant; and lowest plant height, siliqua length, 1000 seed weight and seed yield per plant.

The present study revealed that the cluster V with high mean values for four traits are desired to be crossed with cluster I which possessed low mean values of three characters for getting high heterosis. Same cross between clusters V and II; V and IV. The highest inter-cluster distance was observed between clusters I and VI (60.964) indicating that genotypes from these two clusters, if involved in hybridization, may produce a wide spectrum of segregating population and the lowest inter-cluster distance was observed between cluster III and IV (12.739). The maximum intra-cluster distance was found in cluster V (5.77), which contained of nine genotypes; while the minimum distance was found in cluster II & VI (0.00). In conclusion, the results of the present experiment revealed that the variability existed among the selected *Brassica napus* genotypes for all the characters studied but not much wide. Among the genotypes the superior genotypes were G42, G33, G67, G2, G65, G5, G62, G28, G59, G64 and G69. They might be used as open pollinated verities and parents in future hybridization program.

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APPENDICES

Appendix I. Mean performance of different characters of *Brassica napus L.* genotypes

Gen	D50F	DM	PH	PBP	SBP	SPP	SL	SPS	TSW	YPP
G1	32.50	80.50	98.45	2.74	1.74	68.68	8.90	19.04	3.80	3.22
G2	29.00	77.50	102.61	3.42	2.38	108.81	8.44	12.97	4.13	5.67
G3	30.50	88.50	103.68	2.90	2.23	90.65	8.61	17.29	3.79	3.28
G4	30.50	84.00	115.70	3.27	2.47	114.03	7.75	15.30	3.73	4.17
G5	34.50	79.00	122.30	3.20	1.62	116.73	8.10	19.08	3.93	7.06
G6	30.00	78.50	121.81	3.04	2.29	135.37	8.00	19.22	3.44	4.19
G7	26.00	88.50	125.35	3.20	2.90	108.50	9.51	22.12	3.70	4.66
G8	31.00	76.00	117.30	3.38	1.70	123.43	7.95	16.88	3.28	4.96
G9	33.00	81.00	113.99	2.64	2.02	103.60	8.26	18.03	4.43	4.05
G10	34.50	76.50	122.19	3.17	1.52	113.09	8.67	20.59	2.58	4.51
G11	28.50	89.00	114.22	2.59	1.04	100.32	7.35	19.71	3.86	4.76
G12	34.00	83.00	101.46	2.56	0.52	63.98	7.74	15.77	4.31	2.77
G13	29.50	86.50	105.24	2.59	1.62	80.06	8.62	20.74	3.44	3.52
G14	34.50	76.00	109.80	2.70	1.17	90.67	8.21	15.18	3.80	4.29
G15	30.50	80.00	95.68	2.07	0.67	79.20	8.83	21.59	3.25	2.80
G16	27.50	82.00	115.95	2.20	0.40	80.45	7.86	18.48	3.55	3.03
G17	30.50	80.50	119.94	2.52	1.11	94.05	8.12	15.77	3.62	3.94
G18	29.00	85.50	104.34	2.73	1.47	102.13	7.10	22.06	3.32	4.63
G19	31.50	83.00	113.27	2.71	1.65	105.95	7.89	18.95	4.31	3.91
G20	32.00	84.00	113.75	3.44	1.87	103.73	7.56	18.26	3.44	4.77
G21	33.00	82.50	107.28	4.75	2.77	121.45	6.69	15.15	3.63	4.77
G22	28.00	83.50	112.77	3.11	1.72	94.04	7.82	18.79	4.01	5.21
G23	27.50	87.50	113.61	2.74	1.87	133.21	7.70	18.00	3.97	4.48
G24	32.00	77.00	113.30	2.57	1.26	88.80	7.59	20.99	3.40	3.72
G25	32.00	76.50	118.77	3.20	1.98	135.14	8.67	21.31	3.86	4.80

Appendix I. (Contd.).

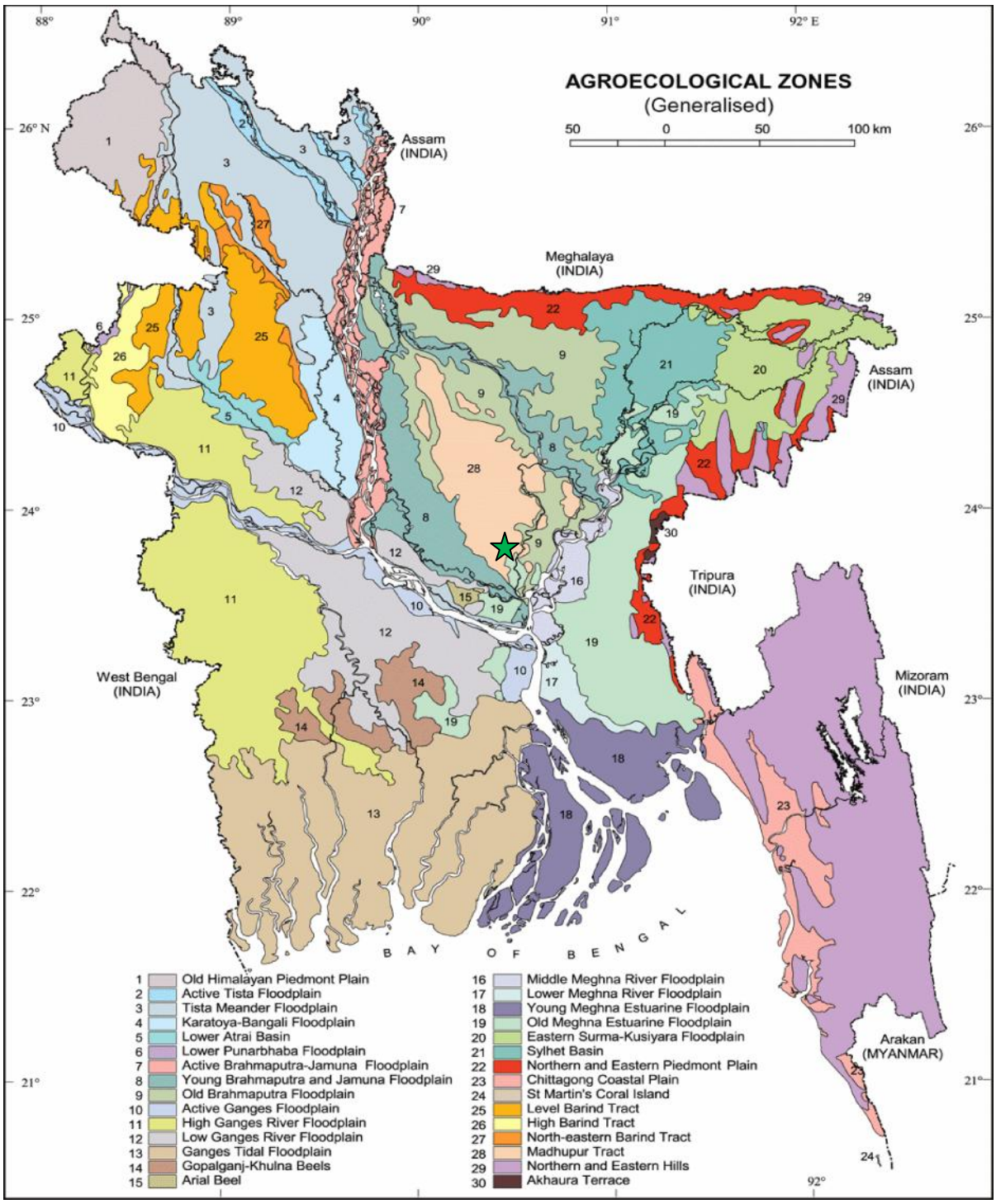
Gen	D50F	DM	PH	PBP	SBP	SPP	SL	SPS	TSW	YPP
G26	34.00	81.00	105.46	2.57	1.68	100.14	8.77	19.38	4.31	4.29
G27	28.50	85.00	114.27	2.97	1.90	127.50	8.48	19.55	4.23	5.99
G28	32.50	87.50	121.60	2.83	1.93	139.05	7.93	20.58	3.59	5.96
G29	28.50	80.50	102.40	3.25	2.15	125.00	8.95	20.51	3.95	4.45
G30	32.00	79.00	112.13	2.52	1.30	64.50	8.32	19.63	3.71	2.80
G31	31.00	82.50	103.35	2.94	1.60	80.65	8.33	19.86	3.45	4.19
G32	29.50	81.50	111.85	2.64	2.25	132.23	8.22	18.80	4.09	5.45
G33	34.00	77.50	114.37	2.56	1.19	79.72	8.40	15.78	4.37	4.03
G34	30.00	89.50	97.73	2.47	0.95	74.40	7.49	18.57	3.72	3.75
G35	33.00	80.50	101.20	2.61	1.58	91.50	8.85	21.60	4.23	3.43
G36	34.50	87.00	105.85	2.69	2.18	126.29	7.55	17.46	4.33	3.86
G37	26.00	88.50	111.39	3.39	1.18	118.29	8.32	16.94	4.20	4.18
G38	28.50	88.50	118.26	3.43	1.61	103.98	7.97	17.97	3.85	3.96
G39	30.50	83.50	115.39	3.21	2.07	110.03	7.73	16.53	3.63	5.96
G40	35.00	88.00	113.89	3.04	2.04	102.68	7.83	20.55	3.98	3.59
G41	30.50	77.50	109.70	3.10	1.94	105.17	7.92	18.10	3.62	4.68
G42	32.00	77.50	106.23	2.39	0.79	73.96	8.85	16.92	5.25	5.18
G43	32.00	85.50	116.64	1.83	0.62	101.72	6.95	13.62	3.75	3.95
G44	27.50	83.50	102.00	2.55	0.83	77.73	7.66	16.37	4.17	3.82
G45	30.00	78.50	93.60	2.48	1.00	68.83	8.54	21.01	4.22	2.89
G46	31.00	86.00	110.39	2.24	0.93	67.38	8.73	19.00	3.91	2.60
G47	34.00	81.00	110.28	2.75	1.23	83.66	7.95	18.11	4.63	5.24
G48	30.50	82.00	100.38	2.99	1.44	85.70	6.37	16.79	5.38	5.89
G49	33.00	81.00	90.06	2.62	1.12	108.59	7.44	16.51	5.44	5.47
G50	31.00	78.00	96.37	2.41	1.39	78.79	7.04	18.71	4.62	4.73

Appendix I. (Contd.).

Gen	D50F	DM	PH	PBP	SBP	SPP	SL	SPS	TSW	SYP
G51	30.00	78.50	98.20	2.81	1.97	84.47	7.64	16.97	3.92	3.95
G52	31.00	88.50	100.57	2.52	0.80	94.58	8.34	17.51	3.79	3.32
G53	30.50	82.50	106.46	2.92	1.39	93.24	6.30	22.74	3.57	4.36
G54	31.00	79.50	110.57	3.22	1.46	109.65	7.96	15.56	3.66	4.32
G55	30.50	83.50	105.51	2.98	1.37	93.62	8.07	17.46	4.40	4.23
G56	33.00	78.50	115.48	3.05	0.59	96.50	7.59	20.23	3.79	4.93
G57	35.50	83.50	92.13	2.68	2.22	79.30	7.68	16.56	3.91	4.00
G58	30.50	82.50	128.01	2.89	1.62	125.21	8.06	16.44	3.61	5.15
G59	26.50	86.00	112.20	3.80	1.93	144.94	7.21	17.13	4.44	5.73
G60	27.00	80.50	109.34	2.89	1.57	96.89	7.73	17.36	4.63	5.91
G61	29.50	87.00	123.00	3.31	2.05	109.20	8.66	17.81	4.13	5.85
G62	31.50	85.50	119.77	2.97	1.87	117.23	7.52	21.02	3.68	5.38
G63	31.50	85.00	121.64	3.29	1.87	131.83	7.83	17.93	4.41	6.64
G64	28.00	79.00	122.92	3.93	2.58	133.07	8.32	19.22	3.84	5.76
G65	31.50	86.00	105.57	3.43	1.90	112.66	9.90	21.14	3.74	6.25
G66	30.50	88.50	106.57	3.38	2.16	83.17	7.79	18.24	3.57	4.15
G67	28.50	78.50	99.00	2.64	1.10	89.07	6.84	20.03	4.35	4.83
G68	32.00	80.50	103.56	2.93	0.66	71.80	7.46	13.86	3.36	3.72
G69	30.50	89.50	83.51	3.51	1.57	89.50	7.73	18.33	3.64	3.05
Min	26.00	76.00	83.51	1.83	0.40	63.98	6.30	12.97	2.58	2.60
Max	35.50	89.50	128.01	4.75	2.90	144.94	9.90	22.74	5.44	7.06
Mean	30.86	82.61	109.44	2.91	1.59	100.57	7.99	18.34	3.93	4.48
CV%	6.47	2.98	5.61	11.80	24.35	13.46	6.45	10.97	8.41	15.05

D50F = days to 50% flowering, DM = days to 80% maturity, PH = plant height (cm), PBP = primary branch 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).

Appendix II. Map showing the experimental site under the study



★ **The experimental site under the study**

Appendix III: 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 IV. Monthly average temperature, relative humidity, 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**