GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS IN F_6 GENERATION OF RAPESEED (*Brassica napus* L.)

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CERTIFICATE

This is to certify that thesis entitled, **"Genetic variability, correlation and path analysis in F_6 generation of Rapeseed (*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 OMME KULSUM HIRA, Registration No. 09-03591 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: December 2015
Place: Dhaka, Bangladesh

(Prof. Dr. Firoz Mahmud)
Supervisor

DEDICATED
TO
MY BELOVED PARENTS,
HUSBAND & CHILDREN

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ABSTRACT

The experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka with 50 *Brassica napus* genotypes to study the genetic varibility, asoociation of correlation and diversity during November 2014 to February 2015. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Analysis of variance revealed significant differences among the genotypes for plant height, branches per plant, siliqua per plant, seeds per siliqua, thousand seeds weight and seed yield per plant. The significant positive correlations of seed yield per plant were found with plant height, secondary branches per plant, siliqua per plant, siliqua length and thousand seed weight in both genotypic and phenotypic level suggesting that genotypes with high partitioning efficiency to increase seed yield per plant. Path coefficient analysis revealed that the thousand seeds weight had the greatest direct contribution on seed yield. The genotypes were grouped into four clusters. Cluster III contained the highest 16 genotypes and the cluster IV contained the lowest (6). The highest inter-cluster distance was observed between clusters I and IV indicating genotypes from these two clusters were diverse, if involved in hybridization might produce a wide spectrum of segregating population while the lowest inter-cluster distance was observed between cluster II and III. Considering group distance, seed yield per plant and other agronomic performance genotypes G4 (9906 X 205 (P1)), G34 (9908 X 9906 (P3)), G5 (9905 X 9901 (P2)), G40 (9901 X 2055 (P2)), G9 (9901 X 2066 (P2)) and G7 (9906 X 205 (P2)) might be used as open pollinated verities and need to further performance and stability test; and could be used as parents in future hybridization program.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

SOME COMMONLY USED ABREVIATIONS

Full word	Abbreviation
Percent	%
Degree Celsius	^0C
At the rate	@
Phenotypic variance	σ^2_p
Genotypic variance	σ^2_g
Environmental variance	σ^2_e
Heritability in broad sense	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	CN
Percentage of Coefficient of Variation	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 Agricultural 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

SOME COMMONLY USED ABREVIATIONS (*Continued*...)

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

CHAPTER I
INTRODUCTION

Rapeseed and mustard is the second highest source of edible oils supply in the world. The genus *Brassica* is an important member of the cruciferae family consisting of over 3200 species with high diverse morphology. 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. In most of the regions of the world, 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.

Seed provides oil both for industrial and culinary purpose. Vegetable oils and fats lipids constitute an important component of human diet. Oils as 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, sunflower, soybean and 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 is used in hair dressing, body massaging and in different types of pickles preparation. The oil cake contains proteins of high biological value and applicable quantities of calcium and phosphorus. It is used as a very good animal feed as well as organic manure for various crops.

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, 2011**).**

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.

In Bangladesh the seed yield of mustard/rapeseed is about 740kg/ha, which is very low in comparison to other developed countries (2400 kg/ha) (FAO, 2011). 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.

Information on the nature and magnitude 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.

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

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

yield (Behl *et al.,* 1992). Path-coefficient technique splits the correlations, coefficients into direct and indirect effects via alternative characters or pathways and thus permits a critical examination of components that influence a given correlation and can be helpful in formulating an efficient selection strategy (Sabaghnia *et al.*, 2010).

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 in F_6 generation;
- To study the interrelationships of yield contributing characters among themselves and with yield; and their direct and indirect effects;
- To assess the contribution of different traits towards divergence; and
- To select promising genotypes considering high yield with early maturity.

CHAPTER II

REVIEW OF LITERATURE

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.

2.1 Origin and geographical distribution

Due to their agricultural importance, *Brassica* plants have been the subject of much scientific interest. Six particularly important species (*Brassica carinata*, *B. juncea*, *B. oleracea*, *B. napus*, *B. nigra* and *B. rapa*) are derived by combining the chromosomes from three earlier species, as described by the Triangle of U theory. But the edible oil is obtained from *B. napus*, *B. juncea* and *B. campestris*.

The genus is native in the wild in Western Europe , the Mediterranean and temperate regions of Asia. In addition to the cultivated species, which are grown worldwide, many of the wild species grow as weeds, especially in North America, South America, and Australia.

Brassica is the most important oil crops of Bangladesh and many countries of the world. The crops have received much attention by a large number of researchers on various aspects of its production and utilization. Identification of suitable parental lines on the basis of their genetic parameters, nature and magnitude of genetic variability and the correlation of different yield attributing characters is important for successful *Brassica* breeding programs. Yield in *Brassica* is associated with many yield contributing characters and in addition there are other characters plant height, primary and secondary branches, siliqua per plant, siliqua length, seeds per plant and thousand seeds

weight etc. which also contribute to *Brassica* yield. Reviewing the information and knowledge on performance of different genotypes, variation for genetic divergence, relationship between yield and yield contributing characters, heritability, genetic diversity based analysis in *Brassica* for yield and yield contributing characters is important for future breeding programme for developing high yielding varieties.

A large number of literatures are available on genetic diversity, variability, correlation and path analysis of yield and yield contributing characters of *Brassica* grown under a particular environment (latest to older from 2016 to 1999). An attempt has been made here to summarize the findings of this study relevant to the present investigation.

2.2 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.

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 braches 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 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 the all 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 junea* 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 is 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 day s 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. He 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 (h2b>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 biparental mating in advanced generations was advocated to achieve substantial gains.

2.3 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.

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. 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 them 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 F3 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 F2 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 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 that genotypic and phenotypic correlation coefficient among seed yield per plant. It was observed that 1000 seed weight, days to flowering, seeds per siliqua and plant height were the most important yield related characters and positively correlated with yield. 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 Pusabold). The 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. Czern and Coss] for 10 characters was conducted with 24 strains of Indian mustard along with two varieties. Results revealed that number of primary branches per plant, number of secondary branches per plant, 1000 seed weight (gm) and oil percent were positively associated with seed yield.

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 correlationship 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 3 characters 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 component and reported that strong positive correlation occurred between seeds per siliqua and actual yield. Positive but a weaker correlation was observed between seed yield and siliqua per plant. The number of seeds per siliqua had the greatest influence and number of siliquae per plant had the

smallest effect on yield. 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 analysis with 65 strains of *B. juncea, B. rapa* and *B. napus* and observed that positive association between yield and siliqua filling period. Similar results also found by Olsson (1990), in *B. napus*. He also observed positive correlation between siliqua density and yield. Uddin *et al.* (1995); while studied correlation analysis in 13 Indian mustard (*B. juncea*) and reported that seed yield per plant had high positive arid significant correlations with plant height and 1000 seed weight, but high negative and significant correlations with seeds per siliqua at both genotypic and phenotypic levels.

Gosh and Mukhopadhyay (1994), studied Tori-7 (*B. campestris var. toria*) for evaluation of seed yield and five seed yield contributing characters and found that plant height, siliqua per plant, seeds per siliqua and thousand seed weight was significant and positively correlated with seed yield. Ahmed (1993), worked with eight cv. of *B. campestris* and *B. juncea* for study of nature and degree of interrelationship among yield components and observed that siliqua length, number of siliquae per plant, number of seeds per siliqua and seed weight per siliqua was positively and linearly associated with seed yield per plant. He also observed that seed oil content was positively correlated with seed weight, but negatively correlated with number of seeds per siliqua.

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*.

2.4 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.

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

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 founded 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 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 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 indicated that a wide range of genetic variation existed among all the characters under study except 1000-grain weight. Correlation analysis revealed that seed yield per plant was positively and significantly correlated with number of primary branches (0.4015), siliqua per plant (0.505), seeds per siliqua (0.79648), siliqua length (0.37037) and seed yield per plot (0.40931). However, it was negatively and non-significantly associated with number of secondary branches (-0.36663) and protein contents (-0.1372) at genotypic level. It was also found that indirect selection for number of seeds per siliqua would be effective in improving the seed yield per plant in present breeding material. A study was conducted by Tusar *et al.* (2006); to assess the nature and extent of variability of 11 yield related characters of five mustard genotypes. Phenotypic correlation studies indicated

that seed yield per hectare was positively and significantly associated with plant height, total dry matter production and husk weight. The number of siliqua per plant, 1000-seed weight, crop growth rate during 60-75 days after sowing and number of branches per plant were also positively associated with seed yield. Path coefficient analysis revealed that the number of siliqua per plant had the greatest direct contribution on seed yield followed by the number of seeds per siliqua and 1000-seed weight while indirect via number of siliqua per plant and 1000-seed weight. Although plant height and husk weight had a total positive correlation with seed yield, their direct effect on yield was negative. The number of seeds per siliqua showed very high positive direct effect on yield, but its correlation with yield was non-significant and negative. 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.

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

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

Seed yield per plant showed positive correlation with number of primary branches, length of main raceme, 1000 seed weight and oil content. 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. Choudhary *et al.* (2003); studied correlation and path coefficient analysis in 28 genotypes of Indian mustard including three controls (Varuna, Kranti and Pusabold). The observations were recorded for seed yield per plant and 11 quantitative characters viz., days to 1st flowering, days to maturity, length of main axis, primary branches per plant, secondary branches per plant, number of siliqua per plant, siliqua length, number of seeds per siliqua, 1000-seed weight and reaction to *Alternaria* black spot on leaf and on siliquae. All

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

Gupta *et al.* (2002); studied 18 lines rapeseed reported significant correlationship between plant height, number of siliqua on the main raceme and number of seed per siliqua, while plant height was significantly correlated with number of siliqua on the main raceme. In general genotypic correlations were greater than phenotypic or environmental correlations. Seed yield was positively correlated with number of siliqua on the main raceme and 1000-seed weight. Srivastava and Singh (2002), reported that number of primary branches per plant, number of secondary branches per plant and 1000 seed weight had strong direct effect on seed yield while working with Indian mustard (*B. juncea* L.). Results suggested that number of primary branches and 1000 seed weight were vital selection criteria for improvement in productivity of Indian mustard. Shalini *et al.* (2000); studied path analysis of Indian mustard germplasm and observed that number of siliquae per plant had the highest direct effect on seed yield followed by 1000 seed weight, number of primary branches per plant and plant height. Most of the characters had an indirect effect on seed yield.

Sheikh *et al.* (1999); worked with 24 diverse genotypes of mustard for assess the direct and indirect effect of seven quantitative and developmental traits on seed yield. Results revealed that thousand seed weight and siliqua per plant had highly positive direct effect on seed yield. The number of siliquae per plant had the highest positive direct effect on seed yield was observed by Yadava *et al.* (1996); when studied path co-efficient analysis of 6 yield components of 25 diverse varieties of Indian mustard. Uddin *et al.* (1995); studied path analysis in 13 Indian mustard (*B. juncea*) and observed that seeds per siliqua and 1000 seed weight had high positive direct effect on seed yield per plant.

Kudla (1993) reported that 1000 seed weight had positive direct effect on seed yield. Yadava *et al.* (1993); when studied path co-efficient analysis of six yield components of 25 diverse varieties of Indian mustard and observed that number of siliquae per plant had the highest positive direct effect on seed yield. Dhillor *et al.* (1990); reported that the plant height had the highest positive direct effect on seed yield per plant in *B. juncea*, but Singh *et al.* (1997); also found negative direct effect of the trait on seed yield. Han (1990), studied *B. napus* and observed negative direct effect of number of siliquae per plant, siliqua length and positive direct effect of seeds per siliqua and plant height on seed yield. Dhillor *et al.*(1990); observed the highest positive direct effect on seed yield per plant.

2.5 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.

Pandey *et al.* (2013); conducted an experiment with 45 Indian mustard genotypes of different origin from India for evaluated for the extent of diversity for utilization in breeding program. D^2 analysis was conducted to measure the

genetic diversity among the genotypes. The 45 genotypes were grouped in 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 the cluster III contained the lowest (3). The highest intra cluster distance was observed in cluster II and the lowest in I. The highest inter cluster distance was observed between the cluster III and II followed by III and I and the lowest between cluster IV and III. Days to 50% flowering (81.94%), days to maturity (8.24%), plant height (5.82 %), branches per plant (1.91%) and 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 then 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 were the major contribution to genetic divergence and cluster IV and these genotypes 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.

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

Kardam and Singh (2005), noted that the nature and magnitude of variability for 10 characters in 200 progenies of Indian mustard *(B. juncea)* obtained from six crosses were studied during Rabi 2002-03 in Jobner, Rajasthan, India. Phenotypic coefficients of variation were higher in magnitude compared to genotypic coefficients of variation for most of the characters. Seed yield per plant was significantly associated with plant height, primary branches per plant, and number of siliquae per plant, number of seeds per siliqua and 1000-seed weight. The number of siliquae per plant had the highest direct contribution to seed yield, followed by primary branches per plant, 1000-seed weight, number of siliquae on main shoot and number of seeds per siliqua. 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. Khulbe and Pan (1999), reported that siliqua per plant, siliqua length, seeds per siliqua, 1000 seed weight were positively associated with grain yield. Analysis of variance revealed that siliqua per plant, siliqua length, 1000 seed weight and seeds per siliqua were the major characters influencing grain yield. 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 1112 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, transplanting of seedlings, 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-1207 during November 2014 to February 2015. 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. Photograph showing the experimental site (Appendix III).

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

3.3 Experimental materials

The healthy seeds of fifty F_6 of *Brassica napus* collected from the Dept. of Genetics and Plant Breeding, Sher-E-Bnalga Agricultural University, Dhaka-1207 which were used as experimental materials. The materials used in that experiment is shown in Table 1.

3.4 Methods

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

3.4.1 Land preparation

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

3.4.2 Application of manure and fertilizer

The crop was fertilized as the rate of 10 tons of cowdung, 250 Kg urea, 175 Kg triple super phosphate (TSP), 85 Kg murate of potash (MP), 250 Kg gypsum, 3 Kg zinc oxide and boron 1 Kg per hectare. The half amount of urea, total amount of cowdung, TSP, MP, gypsum, zinc oxide and boron was applied during final land preparation. The rest amount of urea was applied as top dressing after 25 days of sowing.

Table 1. Materials used for the experiment

Genotypes	F6 Populations	Genotypes	F6 Populations
G1	9905 X 108 (P1)	G26	108 X 2066 (P2)
G2	108 X 9901 (P2)	G27	108 X 2066 (P3)
G3	108 X 9901 (P1)	G28	9906 X 0130 (P1)
G4	9906 X 205 (P1)	G29	108 X 2066 (P1)
G5	9906 X 205 (P3)	G30	9905 X 9901 (P2)
G6	9908 X 9906 (P4)	G31	9908 X 9906 (P1)
G7	9906 X 205 (P2)	G32	9908 X 9901 (P2)
G8	9901 X 2066 (P1)	G33	9909 X 9901 (P1)
G9	9901 X 2066 (P2)	G34	9908 X 9906 (P3)
G10	9908 X 2066 (P1)	G35	9908 X 9906 (P2)
G11	9906 X 9901 (P2)	G36	9905 X 9906 (P2)
G12	9908 X 0130 (P2)	G37	108 X 103 (P2)
G13	9908 X 0091 (P3)	G38	108 X 2066 (P4)
G14	9906 X 9901 (P1)	G39	9901 X 2055 (P1)
G15	108 X 9901 (P3)	G40	9901 X 2055 (P2)
G16	9908 X 9901 (P1)	G41	108 X 130 (P1)
G17	9908 X 2066 (P2)	G42	9906 X 130 (P2)
G18	9908 X 9906 (P2)	G43	108 X 130 (P3)
G19	9908 X 9901 (P4)	G44	2066 X 130 (P1)
G20	9905 X 0130 (P1)	G45	9905 X 9906 (P1)
G21	9908 X 0130 (P4)	G46	9906 X 205 (P4)
G22	9905 X 0130 (P2)	G47	2066 X 205 (P1)
G23	9901 X 0130 (P1)	G48	9905 X 9908 (P1)
G24	9905 X 205 (P1)	G49	9908 X 130 (P3)
G25	9906 X 2066 (P3)	G50	205 X 130 (P2)

P1 = Plant 1, P2 = Plant 2, P3 = Plant 3 and P4 = Plant 4

3.4.3 Experimental design and layout

Field lay out was done after final land preparation. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Total experimental area was 56 m x 14 m = 784 m^2. Each replication size was 56 m x 3.5 m, and the distance between replications was 1 m. The spacing between lines was 30 cm. Seeds were sown in line in the experimental plots on 24 November 2014. The seeds were placed at about 1.5 cm depth in the soil. After sowing the seeds were covered with soil carefully so that no clods were on the seeds. A pictorial view of experimental field at flowering stage is presented in plate 1.

3.4.4 Intercultural operations

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

3.4.5 Crop harvesting

The crop was harvested in different dates according to maturity. Harvesting was started on 10th February 2015 and continued on 17th February 2015 depending upon the maturity. When 80% of the plants showed maturity symptoms like straw color of siliqua, leaves, stem and desirable seed color in

the matured siliqua, the crop was assessed to attain maturity. The harvesting wad done by my supervision and also present my research supervisor, the photograph shown in Plate 3. 15 plants were selected at randomly from F_6 progenies in each replication. The plants were harvested by uprooting and then they were tagged properly. Data were recorded on different parameters from these plants.

3.4.6 Data collection

Ten characters were taken into consideration for studying different genetic parameters, association and genetic diversity. 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.

Plant height: The distance from the base of the plant to the tip of the longest inflorescence. It was measured in centimeter (cm). This data were taken after harvesting.

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

Secondary branches per plant: The total number of branches arisen from all the primary branches of a plant were counted as the secondary branches per plant. It was denoted in number.

Plate 1. Experimental field showing different genotypes at flowering stage

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). Data collection and compilation photograph was shown in Plate 4.

Plate 2. Pest control by spraying pesticide in *Brassica napus* field.

Plate 3. Collecting data from experiment Field.

Plate 4. Harvesting of *Brassica napus* according to accession and maturity

Plate 5. Data collection and compilation in lab by technical assistance from supervisor.

3.4.7 Statistical analysis

Mean data of the characters were used to statistical analyze like analysis of variaancce (ANOVA), mean, range were calculated by using MSTATC software program. Genotypic and phenotypic variance was estimated by the formula used by Johnson *et al*. (1955). Heritability and genetic advance were measured using the formula given by Singh and Chaudhary (1985) and Allard (1960). genotypic and phenotypic coefficient of variation were calculated by the formula of Burton (1952). genotypic and phenotypic correlation coefficient was obtained using the formula suggested by Miller et al. (1958), Johnson et al. (1955) and Hanson et al. (1956); 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).

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

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of square

r = number of replications

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

Where,

σ^2_g = Genotypic variance

EMS = Error mean sum of square

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 %) = $\sqrt{\frac{\sigma^2_g}{\bar{x}}} \times 100$

Where,

σ^2_g = Genotypic variance

$\bar{x}$ = Population mean

Similarly, the phenotypic co-efficient of variation was calculated from the following formula.

Phenotypic co-efficient variation (PCV) = $\sqrt{\frac{\sigma^2_{ph}}{\bar{x}}} \times 100$

Where,

σ^2_p = Phenotypic variance

$\bar{x}$ = Population mean

3.4.7.3 Estimation of heritability

Broad sense heritability was estimated (Lush, 1943) by the following formula, suggested by Johnson *et al.* (1955).

Heritability, $h^2_b\% = \frac{\sigma^2 g}{\sigma^2 p} \times 100$

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 expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1943) and Johnson *et al.* (1955).

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

Or Genetic advance, $GA = K. \frac{\sigma^2 g}{\sigma^2 p} . \sigma_p$

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 have 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:

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

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

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

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 per hectare. In order to estimate direct and indirect effects of the

correlated characters, i. e. 1, 2, 3….and 8 on yield y, a set of simultaneous equations (eight equations in this example) is required to be formulated as shown below:

$r_{1.y} = P_{1.y} + r_{1.2} P_{2.y} + r_{1.3} P_{3.y} + r_{1.4} P_{4.y} + r_{1.5} P_{5.y} + r_{1.6} P_{6.y} + r_{1.7} P_{7.y} + r_{1.8} P_{8.y}$

$r_{2.y} = r_{1.2} P_{1.y} + P_{2.y} + r_{2.3} P_{3.y} + r_{2.4} P_{4.y} + r_{2.5} P_{5.y} + r_{2.6} P_{6.y} + r_{2.7} P_{7.y} + r_{2.8} P_{8.y}$

$r_{3.y} = r_{1.3} P_{1.y} + r_{2.3} P_{2.y} + P_{3.y} + r_{3.4} P_{4.y} + r_{3.5} P_{5.y} + r_{3.6} P_{6.y} + r_{3.7} P_{7.y} + r_{3.8} P_{8.y}$

$r_{4.y} = r_{1.4} P_{1.y} + r_{2.4} P_{2.y} + r_{3.4} P_{3.y} + P_{4.y} + r4_{1.5} P_{5.y} + r_{4.6} P_{6.y} + r_{4.7} P_{7.y} + r_{4.8} P_{8.y}$

$r_{5.y} = r_{1.5} P_{1.y} + r_{2.5} P_{2.y} + r_{3.5} P_{3.y} + r_{4.5} P_{4.y} + P_{5.y} + r_{5.6} P_{6.y} + r_{5.7} P_{7.y} + r_{5.8} P_{8.y}$

$r_{6.y} = r_{1.6} P_{1.y} + r_{2.6} P_{2.y} + r_{3.6} P_{3.y} + r_{4.6} P_{4.y} + r_{5.6} P_{5.y} + P_{6.y} + r_{6.7} P_{7.y} + r_{6.8} P_{8.y}$

$r_{7.y} = r_{1.7} P1.y + r_{2.7} P_{2.y} + r_{3.7} P_{3.y} + r_{4.7} P_{4.y} + r_{5.7} P_{5.y} + r_{6.7} P_{6.y} + P_{7.y} + r_{7.8} P_{8.yy}$

$r_{8.y} = r_{1.8} P_{1.y} + r_{2.8} P_{2.y} + r_{3.8} P_{3.y} + r_{4.8} P_{4.y} + r_{5.8} P_{5.y} + r_{6.8} P_{6.y} + r_{7.8} P_{7.y} + P_{8.y}$

Where,

r_{1y} = Genotypic correlation coefficients between y and I th character (y = Fruit yield)

P_{iy} = Path coefficient due to i th character (i= 1, 2, 3,….8)

1 = Plant height (cm)

2 = Primary branches per plant

3 = Secondary branches plant

4 = Silique per plant

5 = Silique length (cm)

6 = Seeds per siliqua

7 = Thousand seed weight (g)

8 = Seed yield per plant (g)

Total correlation, say between 1 and y i.e., r_{1y} is thus partitioned as follows:

$P_{1.y}$ = the direct effect of 1 on y

$r_{1.2} P_{2.y}$ = indirect effect of 1 via 2 on y

$r_{1.3} P_{3.y}$ = indirect effect of 1 via 3 on y

$r_{1.4} P_{4.y}$ = indirect effect of 1 via 4 on y

$r_{1.5} P_{5.y}$ = indirect effect of 1 via 5 on y

$r_{1.6}\ P_{6.y}$ = indirect effect of 1 via 6 on y

$r_{1.7}\ P_{7.y}$ = indirect effect of 1 via 7 on y

$r_{1.8}\ P_{8.y}$ = indirect effect of 1 via 8 on y

Where,

$P_{1.y,}\ P_{2.y,}\ P_{3.y.}$ ..…… $P_{8.y}$ = Path coefficient of the independent variables 1, 2, 3,….,8 on the dependent variable y, respectively.

$r_{1.y,}\ r_{2.y,}\ r_{3.y,}$ …., $r_{8.y}$ = Correlation coefficient of 1, 2, 3,…., 8 with y, respectively.

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 :

$P^2_{RY} = 1- (r_{1.y}P_{1.y} + r_{2.y}P_{2.y} +\text{……..}+ r_{8.y}P_{8.y})$

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 Genstat, 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

3.4.7.8.8 Cluster diagram

Using the values of intra and inter-cluster distances ($D = \sqrt{D^2}$), a cluster diagram was drawn as suggested by Singh and Chuadhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

CHAPTER IV
RESULTS AND DISCUSSIONS

The results of the present exploration of genetic variability, character association, path analysis and diversity studies in F_6 segregating generations of *Brassica napus* carried out during Rabi season 2014-15 are presented in the following sections.

4.1 Analysis of variance

The analysis of variance indicated highly significant amount of variability among the genotypes for all the characters studied *viz*., plant height (cm), primary branches per plant, secondary branches per plant, siliqua per plant, siliqua length (cm), seeds per siliqua, thousand seed weight (g) and seed yield per plant (g). The results clearly revealed that presence of high variability for yield and yield contribution characters among the genotypes studied. Therefore there is a lot of scope for selection for majority of the traits in the genotypes. The mean sum of squares of all the eight characters are presented in Table 2. Significant differences among the genotypes was observed by many researcher like Shalini *et al.* (2000), Pant and Singh (2001), Thakra *et al.* (2004), Rukhsana *et al.* (2005), Uddin *et al.* (2005), Khan *et al.* (2006), Xu-Suqin *et al.* (2006), Parveen (2007), Zebarjadi *et al.* (2011) and Walle *et al.* (2014).

4.2 Genetic variability, heritability and genetic advance

The success of crop improvement programme depends on the amount of genetic variability presented in the population. The extent of genetic variability can determine the speed and quantum of genetic improvement through selection or hybridization followed by selection. Phenotypic variance measures the magnitude of variability arising out of differences in phenotypic values while the genotypic variance measures the magnitude of variation due to difference within the genotypic values.

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

Source	Df	Mean sum of square							
		PH	**PBP**	**SBP**	**SP**	**SL**	**SPP**	**TSW**	**SYP**
Replication	2	372.99	2.34	4.63	5,365.13	0.06	4.33	2.36	5.26
Treatment	49	140.72**	2.24**	1.79**	1,554.31**	1.09**	27.26**	2.84**	14.72**
Error	98	38.86	0.31	0.55	278.57	0.41	3.37	0.02	0.09

** = Significant at the 0.01 level.

PH = plant height (cm), PBP = Primary branches per plant, SBP = secondary branches per plant, SP = siliqua per plant, SL = siliqua length (cm), SPP = seeds per per siliqua, TSW = thousand seed weight (g) and SYP = seed yield per plant (g).

The heritability estimates separate the environmental influence from the total variability and indicates the accuracy with which a genotype can be identified by its phenotypic performance, thus making the selection more effective. Its aim in determining the relative amount of heritable portion of variation. As such the heritability in broad sense is the proportion of genotypic variability to the total variability, its importance has been emphasized by Lush (1949) in animals and Johnson *et al.* (1995b) in plants.

The presence of narrow gap between PCV and GCV for all the characters expect secondary branches per plant under study, suggested that these traits studied had low environmental influence except secondary branches per plant. 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 per cent mean (GAM) was also estimated.

The estimates of mean, range, genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic advance as per cent mean for all the characters were studied and the results are presented in Table 3 and depicted in Figure 1 and 2. The mean performance of *Brassica napus* F_6 segregating genotypes for various growth characters and yield components are presented in Appendix 1.

4.2.1 Plant height (cm)

The grand mean plant height recorded was 113.94 cm. It ranged from 101.55 cm to 127.70 cm (Appendix 1). The analysis of variance revealed highly significant differences among the genotypes with respect to plant height. The maximum plant height (127.70 cm) was recorded by the G45 '9905 X 9906 (P1)' and the lowest plant height (101.55 cm) was recorded by G43 '108 X 130 (P3)'. The PCV and GCV were 7.49 and 5.11 per cent respectively. The estimate of heritability was moderate at 46.63 per cent with low genetic advance in percent of mean (7.19%) (Table 3).

Table 3. Estimation of genetic parameters in eight characters of 50 genotypes in *Brassica napus*

Parameters	**s^2 p**	**s^2g**	**s^2 e**	**PCV**	**GCV**	**ECV**	**Heritability**	**Genetic advance (5%)**	**Genetic advance (% mean)**
Plant height (cm)	72.82	33.95	38.86	7.49	5.11	5.47	46.63	8.20	7.19
Primary branches per plant	0.95	0.64	0.31	25.04	20.55	14.31	67.35	1.36	34.75
Secondary branches plant	0.97	0.41	0.55	27.72	18.16	20.94	42.94	0.87	24.52
Silique per plant	703.82	425.25	278.57	19.36	15.05	12.18	60.42	33.02	24.09
Siliqua length (cm)	0.64	0.22	0.42	10.41	6.14	8.40	34.84	0.58	7.47
Seeds per siliqua	11.34	7.96	3.38	15.89	13.32	8.67	70.22	4.87	22.99
Thousand seed weight (g)	0.96	0.94	0.02	20.62	20.44	2.72	98.26	1.98	41.73
Seed yield per plant (g)	4.97	4.87	0.10	43.64	43.20	6.14	98.02	4.50	88.11

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

4.2.2 Primary branches per plant

It ranged from 2.54 to 6.52 with a mean value of 3.91. Maximum number of primary branches were recorded in G19 '9908 X 9901 (P4)' and G48 '9905 X 9908 (P1)' genotype showed the minimum number of primary branches. The PCV and GCV observed were 25.04 and 20.55 per cent, respectively. Higher GCV and PCV for primary branches per plant which indicated that, it might provide better scope for improvement through selection also reported by Mekonnen (2014). GCV was lower than the PCV for this character and it was supported by Walle *et al.* (2014) findings. High heritability (bs) of 67.35 per cent coupled with high genetic advance over percentage of mean 34.75 per cent were noticed. The similar findings was found by Alam (2010).

4.2.3 Secondary branches per plant

The number of secondary branches per plant ranged from 2.06 to 5.10 with a mean of 3.55. The genotypic, phenotypic and environmental variances observed were 0.41, 0.97 and 0.55, respectively. The PCV and GCV were 27.72 and 18.16 respectively. The moderate heritability estimates of 42.94 per cent with an high expected genetic advance over mean of 24.52 per cent were recorded for this trait. Maximum number of secondary branches per plant was recorded in the G6, '9908 X 9906 (P4)' and minimum number in the G47, '2066 X 205 (P1)'.

4.2.4 Siliqua per plant

The number of siliqua per plant ranged from 93.04 to 191.68 with mean of 137.06. The minimum number of siliqua per plant was observed in G44, '2066 X 130 (P1)' while maximum number of siliqua per plant was found in the G30, '9905 X 9901 (P2)'. The coefficient of variability at phenotypic and genotypic level were 19.36 and 15.05 per cent respectively. The values for high heritability and high genetic gain over mean were 60.42 and 24.09 per cent, respectively. High heritability with high genetic advance was found by Alam (2010) for this trait that supported the results.

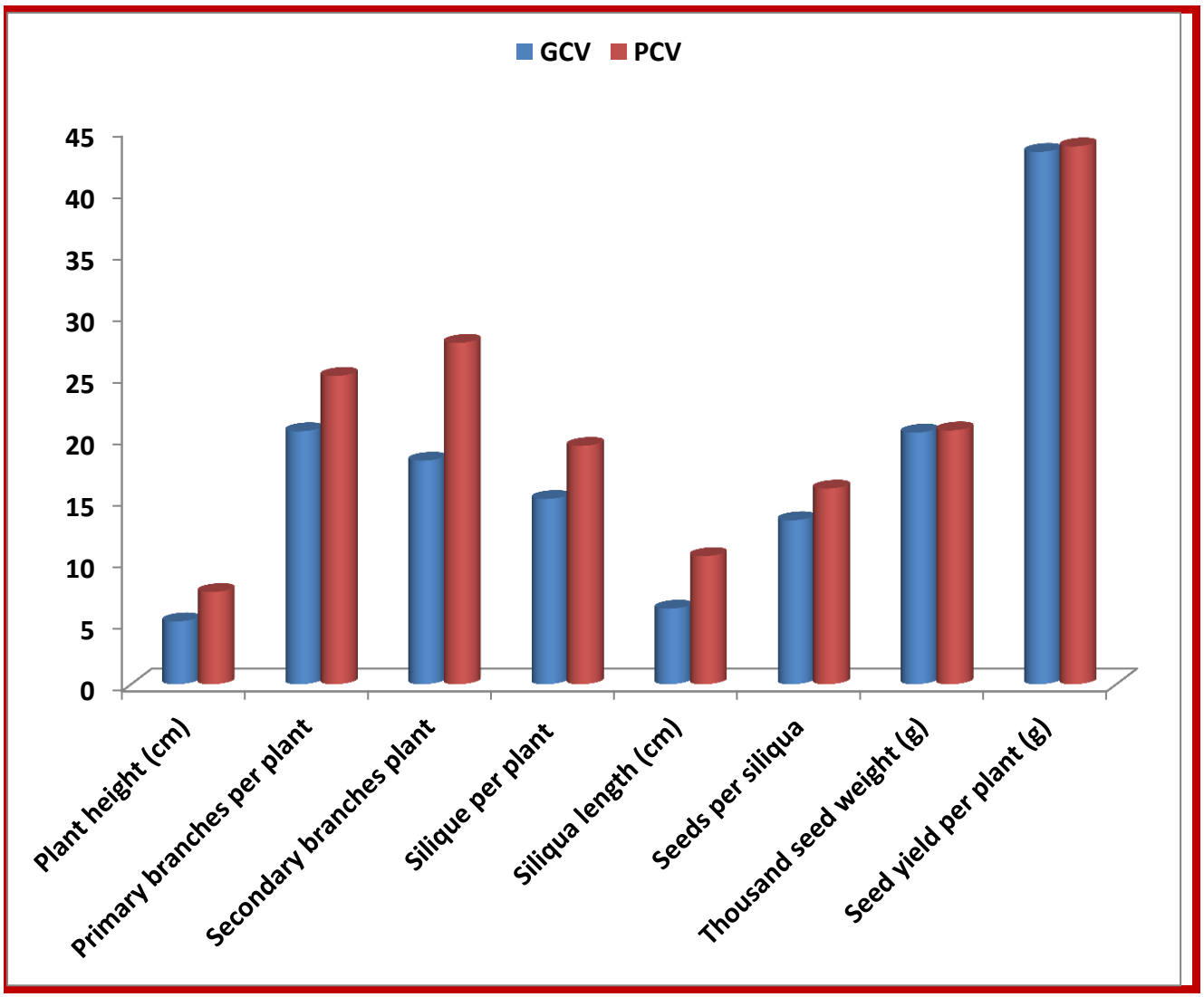


Figure 1. Genotypic and phenotypic variability in *Brassica napus*

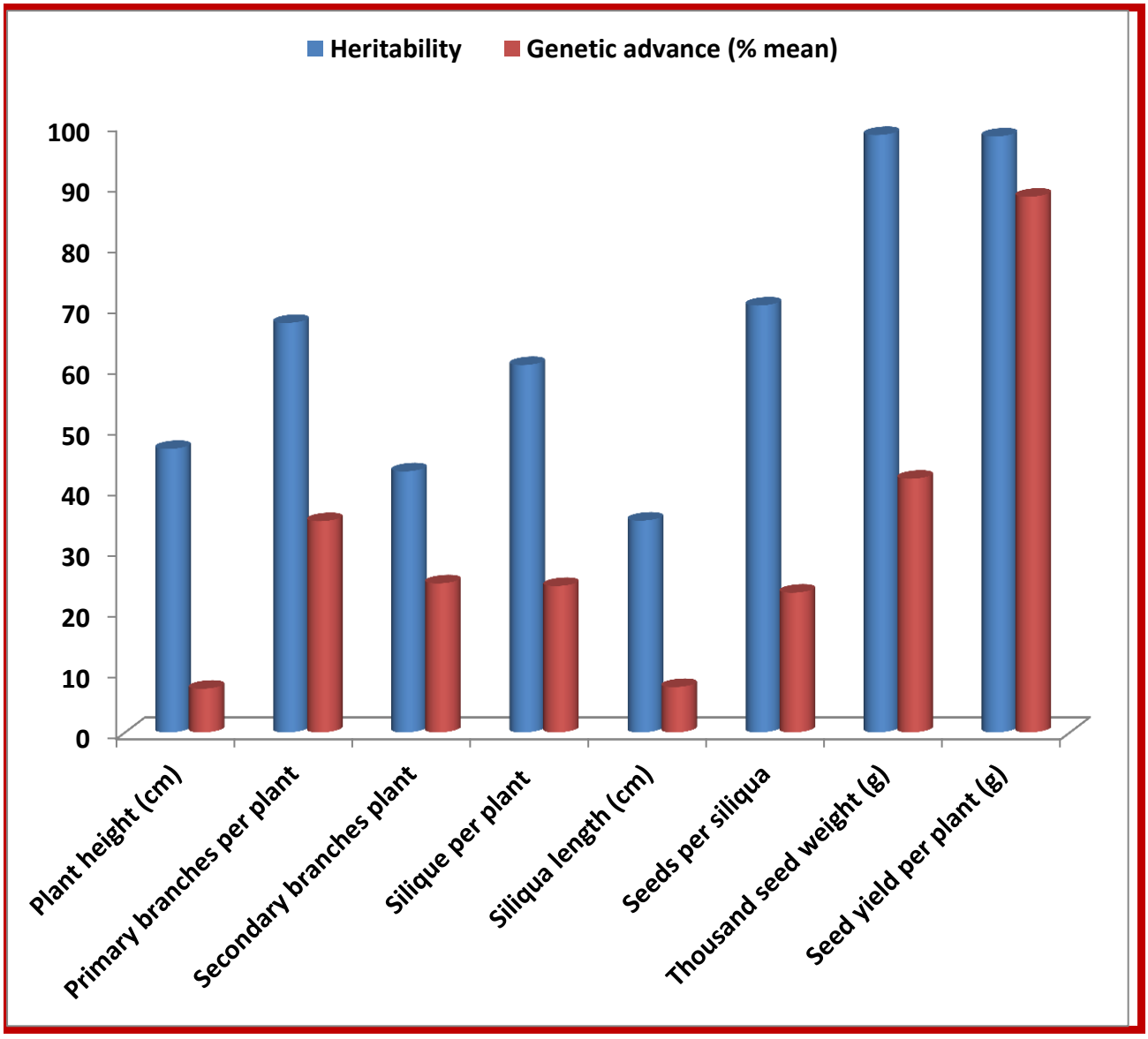


Figure 2. Heritability and genetic advance over mean in *Brassica napus*

4.2.5 Siliqua length (cm)

It ranged from 5.78 to 8.90 cm with a mean of 7.70 cm. The minimum siliqua length was recorded by the G13, '9908 X 0091 (P3)' and G36, '9905 X 9906 (P2)' showed the maximum siliqua length. The PCV and GCV obtained were 10.41 and 6.14 per cent respectively. The values of moderate heritability (34.84%) along with low genetic advance as per cent mean (7.47%) were observed for this trait.

4.2.6 Seeds per siliqua

Significant difference among genotypes for seeds per siliqua was noticed. It ranged from 13.97 to 28.26 with a mean of 21.19. Highest seeds per siliqua were recorded by the G25, '9906 X 2066 (P3)' while G41, '108 X 130 (P1)' showed the lowest seeds per siliqua. The PCV and GCV for this character were 15.89 and 13.32 per cent, respectively. It showed high heritability of 70.22 per cent along with high genetic advance over mean 22.99 per cent.

4.2.7 Thousand seed weight (g)

The mean thousand seed weight noticed was 4.75 g with a range from 3.30 g to 6.68 g. The line G44, '2066 X 130 (P1)' showed the minimum thousand seed weight and the maximum thousand seed weight was recorded in the G30, '9905 X 9901 (P2)'. The values 20.62 and 20.44 were noticed for PCV and GCV, respectively. Higher GCV and PCV for thousand seed weight which indicated that, it might provide better scope for improvement through selection. The highest heritability estimate was 98.26 per cent with high genetic advance over mean was 41.73 per cent.

4.2.8 Seed yield per plant (g)

The mean seed yield per plant was noticed 5.11 g with a range from 2.44 g to 10.82 g in the G16, '9908 X 9901 (P1)' and G40, '9901 X 2055 (P2)' respectively. Highest phenotypic coefficient of variability (43.64%) and genotype coefficient of variability (43.20%) was observed. 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). High heritability (98.02%) and genetic advance over mean (88.11%) were recorded. Higher heritability along with highest genetic advance was observed in this characters by Mekonnen (2014) attributed to additive gene actions. Aytac and Kinaci (2009) observed highest heritability and genetic advance over mean was supported this results.

4.3 Association analysis

Although variability estimates provide information on the extent improvement possible in different characters, but they do not throw light on the extent of nature of relationship prevalent between the characters. This could be obtained from association analysis that determines the direction of action of different characters. Based on this analysis, the traits that can be selected for improving the desired variables can be ascertained.

Yield, a complex character is predominantly governed by a large number of genes and is greatly influenced by environmental fluctuations. Therefore, selection based on yield alone is not effective. An improvement in yield can be brought by effecting indirect selection for yield contributing components, whose heritability are high and show a strong association with yield. The direct observable phenotypic correlation does not indicate the magnitude or direction of genetic correlation which presents a true genetic picture of relationship between the genes controlling the characters. In the present investigation, correlations between seed yield and its component characters were studied.

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

In the present study out of 28 associations 16 associations were significant in genotypic level and 14 associations were significant in phenotypic level. Among the genotypic 16 significant associations, 14 associations were positively significant and the rest two was negatively significant. From the phenotypic 14 significant associations, all were positively significant. The significant and positive association between the characters suggested additive genetic model thereby less affected by the environmental fluctuation. Besides, 12 relationships were positive and non-significant and five relationships were negative and non significant in genotypic level and seven relationships were positive and non-significant and seven relationships were negative 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, secondary branches per plant, siliqua per plant, siliqua length, and 1000 seeds weight in both genotypic and phenotypic level (Table 4 & Table 5) suggesting that genotypes with high partitioning efficiency gave increase in seed yield per plant. Only number of primary branches per plant was negatively correlated with seed yield per plant indicating that seed yield per plant would be increased with the decreased of that character. Uddin *et al*. (2013) and Singh (2010) found high significant positive correlation of 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 this results. Siliquae per plant had significant positive correlation with seed yield reported by Rameeh (2011).

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

Characters	Primary branches per plant	Secondary branches plant	Silique per plant	Siliqua length (cm)	Seeds per plant	Thousand seed weight (g)	Yield per plant (g)
Plant height (cm)	-0.285**	0.072	0.129	-0.002	0.245**	0.423**	0.298**
Primary branches per plant		0.547**	0.132	-0.204*	-0.080	-0.140	-0.026
Secondary branches plant			0.486**	0.081	0.043	0.308**	0.334**
Silique per plant				0.416**	0.195*	0.265**	0.532**
Siliqua length (cm)					0.246**	-0.020	0.208*
Seeds per siliqua						0.149	0.005
Thousand seed weight (g)							0.730**

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

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

Characters	Primary branches per plant	Secondary branches plant	Silique per plant	Siliqua length (cm)	Seeds per plant	Thousand seed weight (g)	Yield per plant (g)
Plant height (cm)	-0.086	0.221**	0.254**	-0.005	0.142	0.292**	0.198*
Primary branches per plant		0.472**	0.264**	-0.111	-0.082	-0.116	-0.034
Secondary branches plant			0.539**	0.101	0.052	0.179*	0.210**
Silique per plant				0.180*	0.132	0.209*	0.415**
Siliqua length (cm)					0.174*	-0.017	0.121
Seeds per siliqua						0.120	0.013
Thousand seed weight (g)							0.718**

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

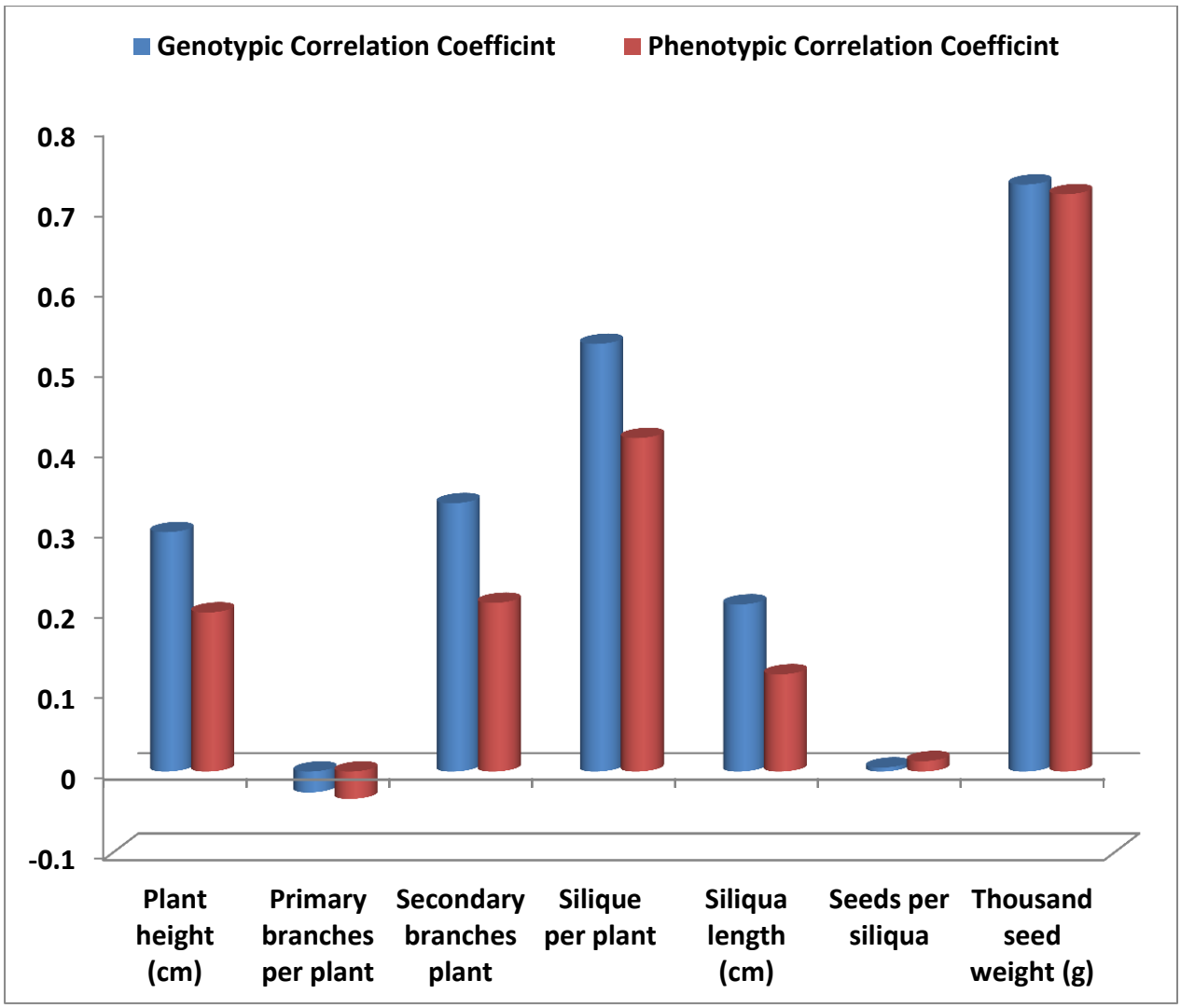


Figure 3. Genotypic and Phenotypic Correlation Coefficient for eight characters of *Brassica napus*.

Study of correlation at yield components levels exhibited that plant height showed positive and significant correlation with seeds per siliqua and thousand seeds weight at genotypic level and significant positive correlation with secondary branches per plant, siliqua per plant and thousand seeds weight. Plant height also showed positive and insignificant correlation with secondary branches per plant and siliqua per plant at genotypic level and primary branches per plant was negatively and significantly correlated with plant height at genotypic level.

Primary branches showed positive and significant correlation with secondary branches per plant at both level and positive significant correlation with siliqua per plant at phenotypic level. Negative correlation was observed of primary branches per plant with siliqua length, seeds per siliqua and 1000 seeds weight at both level.

Secondary branches per plant showed positive and significant correlation with siliqua per plant and thousand seeds weight at both level and positive correlation with siliqua length and seeds per siliqua. Basalma (2008) reported significant positive correlation of branches per plant with siliqua per plant supported this findings.

Siliqua per plant showed significant positive correlation with siliqua length and thouand seeds weight at both level and significant correlation with seeds per siliqua at genotypic level.

Siliqua length showed positive and significant correlation with seeds per siliqua and negative association with plant height and primary branches per plant at both level.

Seeds per siliqua showed positive correlation with 1000 seeds weight and secondary branches per plant at both level. 1000 seeds weight showed positive correlation with seeds per siliqua at both level.

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, 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 level.

4.4 Path coefficient analysis

The estimation of correlation coefficient indicates only the event and nature of association between yield and its attributes, but does not show the direct and indirect effects of different yield attributes on yield as such seed yield is dependent on several component characters which are mutually associated. These will in turn impair the true association existing between a component and seed yield and a change in any one component is likely to disturb the whole network of cause and effect. Thus each component has two paths of action viz., (1) the direct influence on seed yield (2) Indirect effects through components which are not revealed from the correlation studies. The path analysis was first suggested by Wright (1921) and later modified by Dewey and Lu (1957) provides an effective measure of direct and indirect causes of association and depicts the relative importance of each factor involved in contributing to the final product it seed yield.

The path coefficient analysis was performed using correlation coefficient to determine direct and indirect influence considering eight characters viz. plant height, primary branches per plant, secondary branches per plant, siliqua per plant, siliqua length, seeds per siliqua and 1000 seeds weight to seed yield per plant. Seed yield being the complex outcome of different characters, was considered as the resultant variable and other characters as causal variable. Estimates of direct and indirect effects of eight yield contributing characters are shown in Table 6.

Table 6. Partitioning of genotypic correlations into direct and indirect effects of eight important characters by path analysis of *Brassica napus*

Character	Direct effect	Indirect effect via							Genotypic correlation with yield
		Plant height (cm)	Primary branches per plant	Secondary branches plant	Silique per plant	Silique length (cm)	Seeds per plant	Thousand seed weight (g)	
Plant height (cm)	0.052	-	-0.038	-0.010	0.047	0.000	-0.051	0.300	0.298**
Primary branches per plant	0.135	-0.015	-	-0.078	0.048	-0.033	0.017	-0.099	-0.026
Secondary branches plant	-0.143	0.004	0.074	-	0.176	0.013	-0.009	0.218	0.334**
Silique per plant	0.363	0.007	0.018	-0.069	-	0.067	-0.040	0.188	0.532**
Siliqua length (cm)	0.161	0.000	-0.028	-0.012	0.151	-	-0.051	-0.014	0.208*
Seeds per siliqua	-0.207	0.013	-0.011	-0.006	0.071	0.040	-	0.106	0.005
Thousand seed weight (g)	0.709	0.022	-0.019	-0.044	0.096	-0.003	-0.031	-	0.730**

Residual effect: **0.292** ** = Significant at 1%. * = Significant at 5%.

Among the characters that have positive direct effect on seed yield per plant were plant height, primary branches per plant, siliqua per plant (0.363), siliqua length (0.161) and 1000 seeds weight (0.709). 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 supported this findings.

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 siliqua per plant and 1000 seeds weight. Its negative indirect effect observed via primary and secondary branches per plant and seeds per plant.

Primary branches per plant showed positive direct effect on seed yield per plant where the correlation was insignificant and negative at genotypic level. Secondary branches (-0.143) showed negative direct effect on seed yield per plant where the correlation was significant and positive.

The residual effect was 0.292, indicating that the eight characters contributed 70.8 percent of variability in seed yield per plant studied in path analysis. The residual effects 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.

Both correlation and path co-efficient studies revealed for siliquae per plant, siliqua length, thousand seeds weight 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 that siliqua per plant, and 1000 seeds 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.

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, 50 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 eight important quantitative characters. Based on D^2-value, the genotypes were grouped into four clusters (Table 7).

4.5.1 Nonhierarchical clustering

With the application of covariance matrix for nonhierarchical clustering, 50 *Brassica napus* genotypes were grouped into four different clusters. It is stated that 32% genotypes were included in cluster III and it was followed by 28% in clusters both I & II and the remaining were in cluster IV. The composition of clusters with different genotypes is presented in Table 7. The cluster III included 16 genotypes, which is the highest followed by cluster I & II whose are contained 14 genotypes each. Cluster IV contained six genotypes. Zaman *et al.* (2010) reported four cluster 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 cluster 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).

4.5.2 Principal component analysis

Eigen values of principal component axis, percent of total variation and cumulative variation accounted for them obtained from principal component analysis are presented in Table 8. The results showed that the first principal axis, plant height largely accounted for the variation among the genotypes which alone contributed 31.46% of the total variation among the genotypes. The first four characters of the principal component axes with eigen values above unity accounted for 78.86% of the total variation among the eight characters. The rest four characters contributed remaining 21.14% of total variation. Based on principal component scores I and II obtained from the principal component analysis, a two-dimensional scatter diagram (Z_1-Z_2) using component score 1 as X axis and component score 2 as Y axis was constructed, which has been presented in Figure 4.

4.5.3 Inter cluster distance

The average intra and inter cluster D^2 values are given in Table 9 and the nearest and farthest cluster from each cluster based on D^2 value is given in Table 10**.** It was observed that inter cluster distance were always higher than those of intra cluster distance. The maximum inter cluster distance was observed between genotypes of cluster I and IV **(**11.180) followed by clusters II and IV (8.297) and I and III (6.377). Thus, hybridization among genotypes drawn from these widely divergent clusters with high yield potential would likely to produce heterotic combinations and wide variability in segregating generations. Therefore it could be concluded that the genotypes present in combination of those clusters could be utilized for successful breeding programme.

Table 7. Distribution of fifty genotypes in different clusters

Cluster no.	No. of Genotypes	No. of populations
I	G2, G7, G8, G9, G10, G11, G12, G13, G20, G22, G33, G41, G44, G47	14
II	G1, G3, G14, G16, G23, G26, G27, G38, G39, G42, G43, G45, G46, G48	14
III	G5, G17, G19, G21, G24, G25, G28, G29, G31, G32, G34, G36, G37, G40, G49, G50	16
IV	G4, G6, G15, G18, G30, G35	6
Total		50

Table 8. Eigen values and yield percent contribution of eight characters of 50 genotype

Principal component axes	Eigen values	Percent variation	Cumulative % of Percent variation
I	2.51	31.46	31.46
II	1.60	20.00	51.46
III	1.23	15.38	66.84
IV	0.96	12.02	78.86
V	0.69	8.65	87.51
VI	0.47	5.96	93.47
VII	0.35	4.42	97.89
VIII	0.17	2.11	100.00

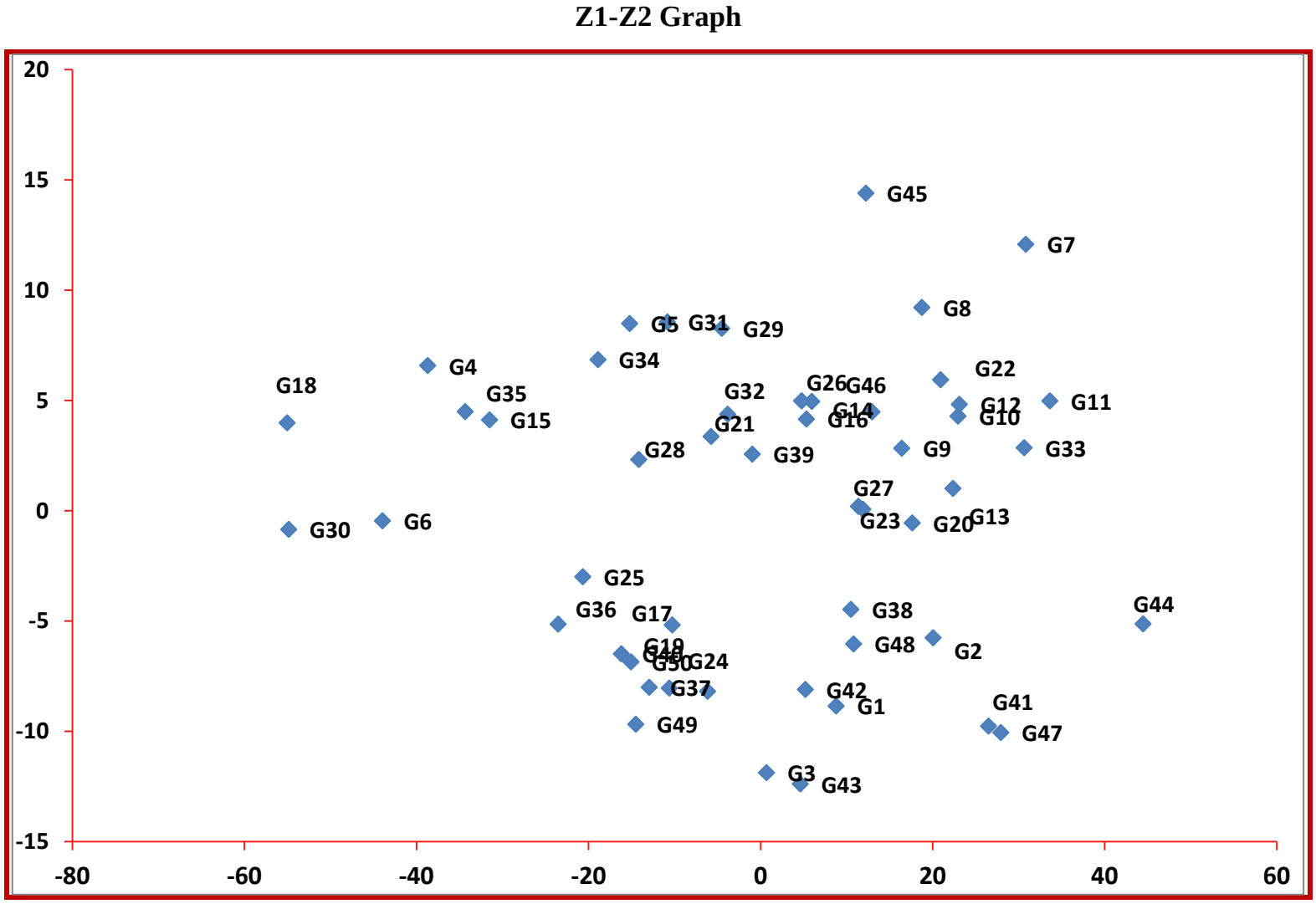


Figure 4. Scatter diagram of *Brassica napus* genotypes of based on their principal component scores.

The higher inter-cluster distances between these clusters indicate to obtain wide spectrum variability of population. However, the highest inter cluster distance was observed between clusters I and IV indicated the genotypes in these clusters were diversed than those clusters. Cluster IV was the most diverse as many other clusters showed maximum inter cluster distance with it. The minimum distance observed between clusters II and III (3.348) indicated close relationship among the genotypes included (Figure 5 and Figure 6).

4.5.4 Intra cluster distance

The intra cluster D^2 values were given in Table 9. The intra cluster distance was observed in the clusters I, II, III and IV. The intra cluster distance was higher in cluster IV (0.054) followed by cluster I (0.015) and lowest in cluster III (0.010). 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 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. Table 9 showed average intra and inter cluster D^2 values of four clusters. The mutual relationships among the four clusters are presented in the diagram (Figure 6). The average inter and intra cluster distance have been used to denote cluster distance.

4.5.5 Cluster diagram

The positions of the genotypes in the scatter diagram were apparently distributed into four groups, which indicated that considerable diversity existed among the genotypes (Figure 6).

Table 9 Intra (Bold) and inter cluster distances (D^2) for 50 genotypes

Cluster	I	II	III	IV
I	**0.015**	3.362	6.377	11.180
II		**0.012**	3.348	8.297
III			**0.010**	5.027
IV				**0.054**

Table 10. The nearest and farthest clusters from each cluster between D^2 values in *Brassica napus*

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	**I**	**II (**3.362)	**IV (**11.180)
2	**II**	**I (**3.362)	**IV (**8.297)
3	**III**	**II (**3.348)	**I (**6.377)
4	**IV**	**III (**5.027)	**I (**11.180)

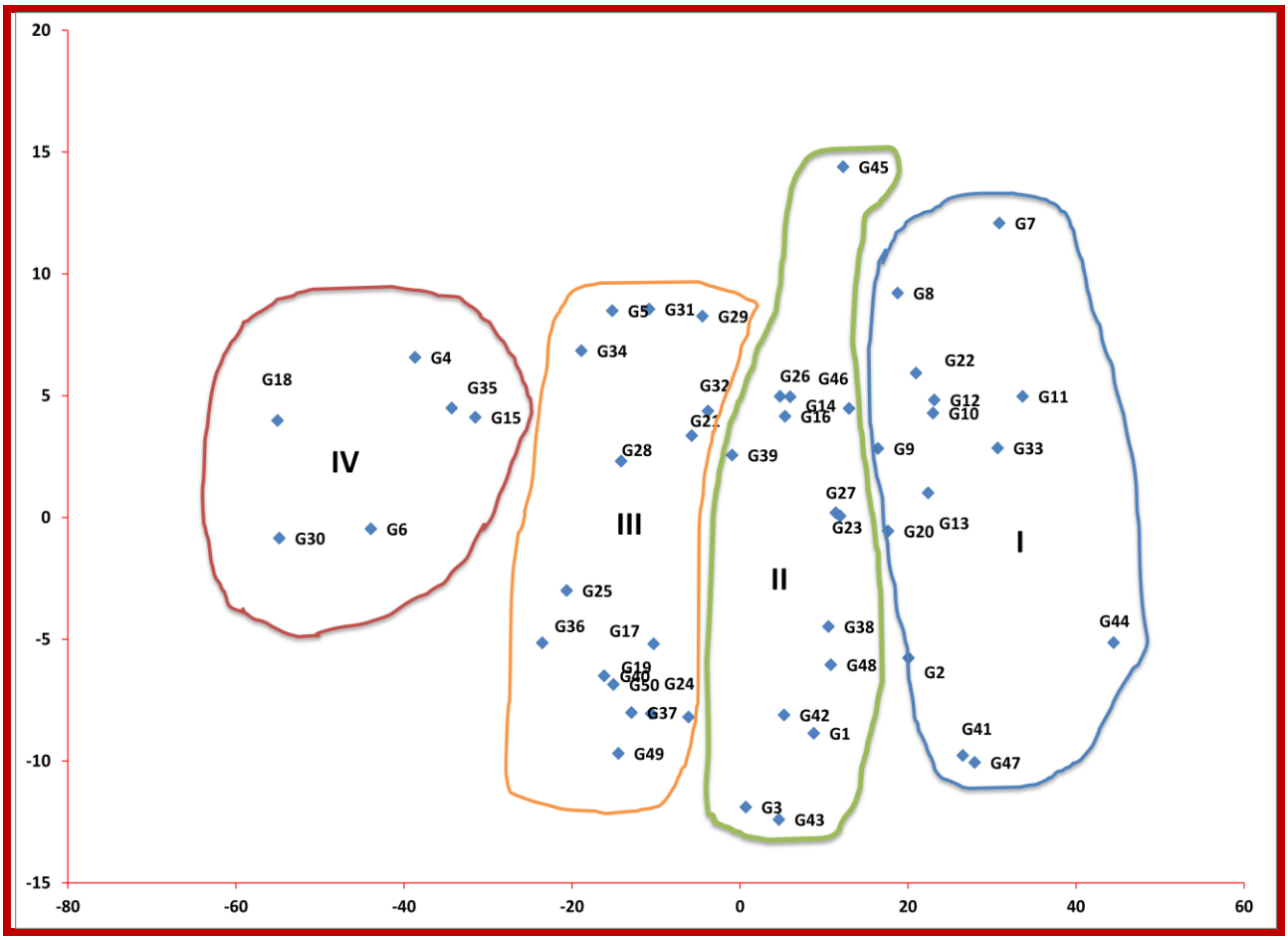


Figure 5. Cluster diagram showing average intra and inter cluster distances of 50 genotypes in *Brassica napus.*

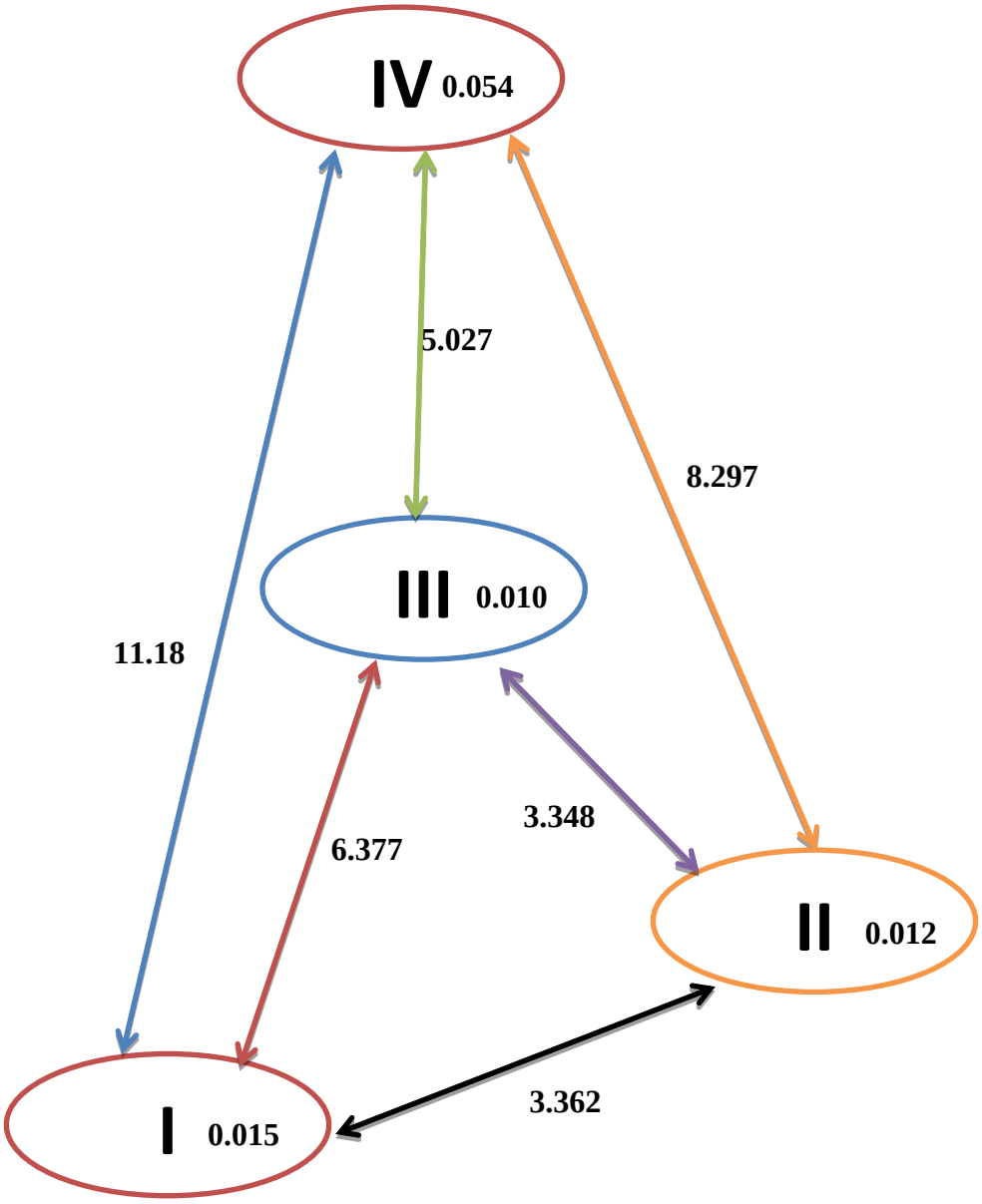


Figure 6. Intra and inter cluster distances of 50 genotypes in *Brassica napus*

Figure 6 Cluster diagram showing the average intra and inter cluster distances of 16 *Brassica napus* genotypes. The values along the lines are inter cluster distances and the values within the circle are intra cluster distances.

4.5.6 Characterization of individual clusters

The mean values of each cluster for eight characters are presented in Table 11. There was wide range of variation in the cluster mean values for all the characters. The mean values of all characters for the respective clusters were categorized into low (L), intermediate (I) and high (H) classes.

Minimum plant height was observed in cluster I (113.43 cm) and Cluster II and III showed intermediate values (112.49 cm and 113.55 cm respectively) and maximum plant height by cluster IV (119.54 cm). Cluster IV had highest number of primary branches (4.27) and cluster I had lowest number of primary branches (3.77). Maximum (4.56) and minimum (3.21) number of secondary branches per plant were observed in cluster IV and II respectively. For siliqua per plant, cluster IV showed maximum value (179.71) and cluster I showed minimum value (111.56). Siliqua length was the highest in cluster IV with a mean value of (7.94cm) and it was least in genotypes belongs to the cluster I (7.39 cm). Highest seeds per plant was recorded by the cluster IV (22.06) while cluster I (21.01) showed the least seeds per plant. The maximum 1000 seed weight was observed in cluster IV (5.63 g), whereas minimum 1000 seed weight was observed in cluster III (4.25g) and cluster I and III showed intermediate values (4.94 & 4.70 g) for this character. A highest seed yield per plant was recorded by the genotype making up cluster IV (8.24 g) while cluster II showed the least seed yield (3.87 g) per plant. Cluster I and III showed intermediate values (4.79 g & 5.30 g) for seed yield per plant.

The six genotypes like G4 (9906 X 205 (P1)), G6 (9908 X 9906 (P4)), G5 (108 X 9901 (P3)), G34 (9908 X 9906 (P3)), G30 (9905 X 9901 (P2)), G18 (9908 X 9906 (P2)) were included in cluster IV possessed high mean value for all the characters studied.

Table 11. Cluster mean for eight yield and yield related characters in 50 mustard genotypes

Characters	I	II	III	IV
Plant height (cm)	113.43 (L)	112.49 (I)	113.55 (I)	119.54 (H)
Primary branches per plant	3.77 (L)	3.87 (I)	3.92 (I)	4.27 (H)
Secondary branches plant	3.29 (I)	3.21 (L)	3.68 (I)	4.56 (H)
Silique per plant	111.56 (L)	129.76 (I)	149.77 (I)	179.71 (H)
Silique length (cm)	7.39 (L)	7.67 (I)	7.92 (I)	7.94 (H)
Seeds per siliqua	21.01 (L)	20.04 (I)	22.02 (I)	22.06 (H)
Thousand seed weight (g)	4.94 (I)	4.25 (L)	4.70 (I)	5.63 (H)
Seed yield per plant (g)	4.79 (I)	3.87 (L)	5.30 (I)	8.24 (H)

H= High value
I=Intermediate value
L= Low value

The plant type and siliqua type of cluster IV, cluster III and cluster I are presented in Plate 6, Plate 7, Plate 8, Plate 9, Plate 10 and Plate 11 respectively.

The present study revealed that the cluster IV with high mean values for all the desirable traits are desired to be crossed with cluster I which possessed low mean values of five characters for getting high heterosis. Same cross between clusters IV and II for three characters. 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.

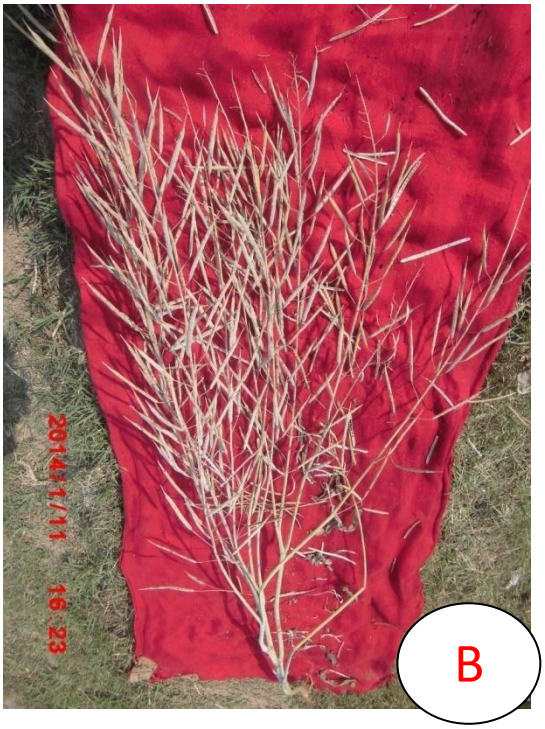
4.5.7 Contribution of characters towards divergence

Contribution of characters towards the divergence obtained from canonical variates analysis is presented in Table 12. The character, which gave high absolute magnitude for vector 1, was considered to be responsible for primary differentiation. Likewise, the characters, which gave higher absolute magnitude for vector 2 was considered to be responsible for secondary differentiation. If the same character given equal magnitude for both the vectors than the character was considered responsible for primary as well as secondary differentiation.

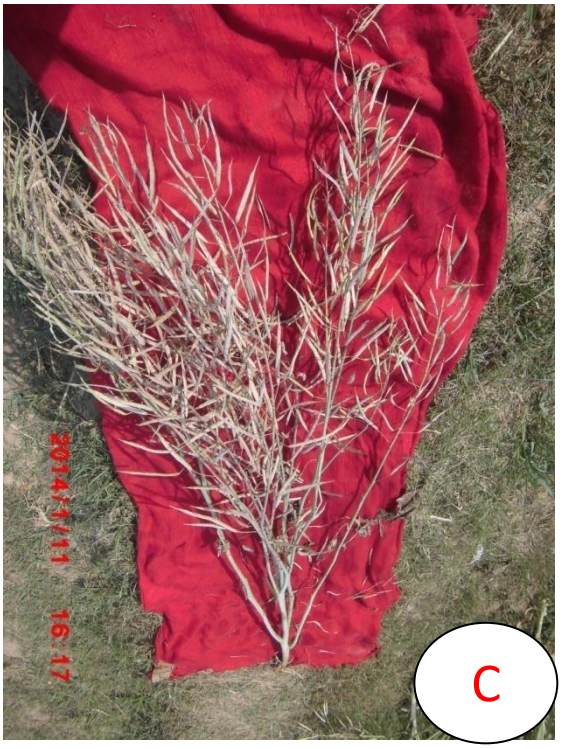
In vector (Z_1) obtained from PCA, the important characters responsible for genetic divergence in the axis of differentiation were plant height (0.040), Secondary branches plant (0.188), Silique per plant (0.153), Silique length (0.362), Seeds per siliqua (0.013) and Yield per plant (0.099). In vector 2 (Z_2), the second axis of differentiation plant height (0.015), Secondary branches plant (0.877), Seeds per siliqua (0.128), Thousand seed weight (0.041) and Yield per plant (0.434) were important because all these characters had positive signs. Plant height, secondary branches plant, seeds per siliqua and yield per plant had positive signs in both the vectors, which indicated they were the

important component characters having higher contribution to the genetic divergence among the materials studied.

A = G4 (9906 X 205 (P1))

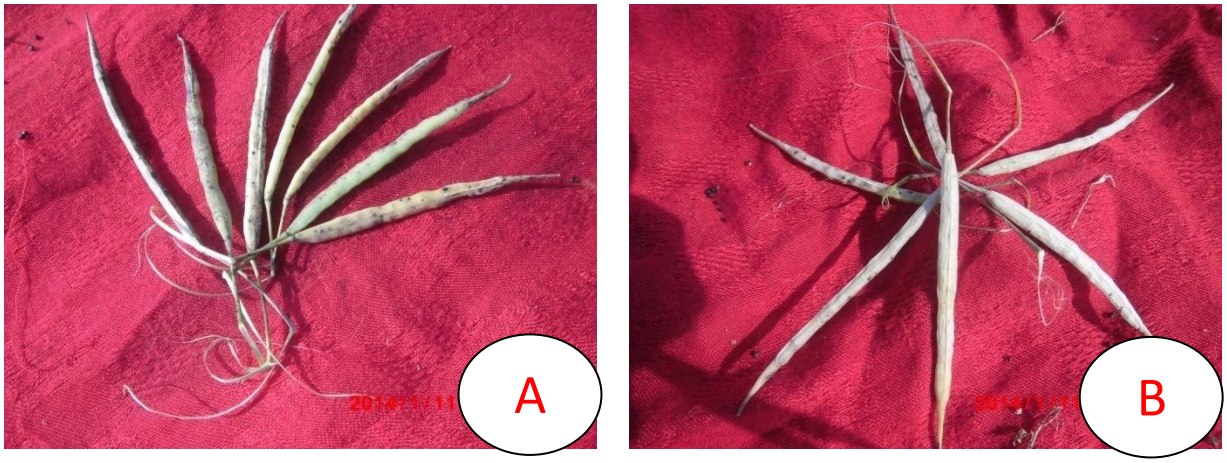


B =G6 (9908 X 9906 (P3))



C = G30 (9905 X 9901 (P2))

Plate 6. Photograph showing plant type of selected *Brassica napus* genotypes of cluster IV



A = G4 (9906 X 205 (P1)) **B = G6 (9908 X 9906 (P3))**

C = G30 (9905 X 9901 (P2))

Plate 7. Photograph showing siliqua type of selected *Brassica napus* genotypes of cluster IV

G 40 (9901 X 2055 (P2))

Plate 8. Photograph showing plant type of selected *Brassica napus* genotypes of cluster III

G 40 (9901 X 2055 (P2))

Plate 9. Photograph showing siliqua type of selected *Brassica napus* genotypes of cluster III

A = G9 (9901 X 2066 (P2)) **B = G7 (9906 X 205 (P2))**

Plate 10. Photograph showing plant type of selected *Brassica napus* genotypes of cluster I

A = G9 (9901 X 2066 (P2)) **B = G7 (9906 X 205 (P2))**

Plate 11. Photograph showing siliqua type of selected *Brassica napus* genotypes of cluster I

4.5.8 Selection of parents

The genotypes under the cluster I exposed intermediate value thousand seeds weight and seed yield per plant (Table 13). The genotypes of cluster II produced intermediate value for siliqua per plant, siliqua length and seeds per siliqua. The genotype of cluster III possessed intermediate value plant height, higher primary and secondary branches per plant. The genotypes of cluster IV produced highest plant height, maximum primary and secondary branches, highest siliqua length, maximum thousand seed weight and highest yield per plant. Considering diversity pattern and other agronomic performance G4 (9906 X 205 (P1)), G34 (9908 X 9906 (P3)), G30 (9905 X 9901 (P2)) from cluster IV (Plate 6 & Plate 7), G40 (9901 X 2055 (P2)) from cluster III (Plate 8 & Plate 9) and G9 (9901 X 2066 (P2)) and G7 (9906 X 205 (P2)) from cluster I (Plate 10 & Plate 11) could be considered 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 are recommended to use as parents in future hybridization program.

Table 12. Relative contributions of the eight characters of 50 varieties to the total divergence

Characters	Principal Component	
	Vector-1	Vector-2
Plant height (cm)	0.040	0.015
Primary branches per plant	-0.085	-0.094
Secondary branches plant	0.188	0.877
Silique per plant	0.153	-0.034
Silique length (cm)	0.362	-0.537
Seeds per plant	0.013	0.128
Thousand seed weight (g)	-0.441	0.041
Yield per plant (g)	0.099	0.434

Table 13. Salient features of genotypes in four different clusters

Cluster	Salient features
I	Intermediate thousand seeds weight Intermediate seed yield per plant
II	Intermediate silique per plant Intermediate Siliqua length Intermediate seeds per plant
III	Intermediate plant height Higher secondary branches per plant Higher primary branches per plant Intermediate Siliqua length Intermediate Siliqua length Intermediate seeds per plant
IV	Highest plant height Most primary branches per plant Highest secondary branches per plant Highest Siliqua length Most thousand seeds weight Highest seed yield per plant

CHAPTER V
SUMMARY AND CONCLUSION

The experiment was conducted with the objective to assess the selection of superior genotypes from 50 *Brassica napus L.* genotypes through study the genetic variation and morphological diversity among the genotypes for improvement of yield. The experiments were carried out at the experimental Farm of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka-1207, Bangaldesh during the period from November 2014 to February 2015. The experiment was laid out in Randomized Complete Block Design (RCBD) with 3 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 plant height was observed the highest in 9905 X 9906 (P1) whereas the minimum plant height was observed in 108 X 130 (P3). The highest primary branches per plant was observed in 9908 X 9901 (P4) whereas the lowest primary branches per plant was observed in 9905 X 9908 (P1). The genotype 9908 X 9906 (P4) was performed the highest secondary branches per plant and lowest by the genotype 2066 X 205 (P1). The highest siliquae per plant was observed by the genotype 9905 X 9901 (P2) whereas the lowest siliquae per plant was observed by 2066 X 130 (P1). Siliqua length was resulted the longest by 9905 X 9906 (P2) whereas the shortest siliqua length was observed by 9908 X 0091 (P3). Maximum seeds per siliqua were observed in 9906 X 2066 (P3) whereas the minimum seeds per siliqua were observed in 108 X 130 (P1). Thousand seed weight was found the maximum in 9905 X 9901 (P2) where as the minimum thousand seed weight was found in 2066 X 130 (P1). 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 9901 X 2055 (P2) whereas the lowest yield per plant observed in 9908 X 9901 (P1).

Thousand seed weight (98.26) exhibited the highest value of heritability while siliqua length (34.84) 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 plant height and siliqua per plant showed higher influence of environment for the expression of these characters. On the other hand, primary ns secondary branches per plant, siliqua length, seeds per siliqua, thousand seed weight and seed yield per plant showed least difference 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 primary branches per plant, siliqua per plant, seeds per siliqua, thousand seed weight and seed yield per plant indicating that these traits were under additive gene control and selection for genetic improvement for these traits would be effective.

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, secondary branches per plant, siliqua per plant, siliqua length and thousand seed weight in both genotypic and phenotypic level suggesting that genotypes with high partitioning efficiency gave increase in seed yield per plant. In addition, there were non-significant positive correlation of seed yield per plant with seeds per siliqua. Only primary branches per plant was negatively correlated with seed yield per plant indicating that seed yield per plant would be increased with the decreased of that character.

The path coefficient analysis was performed using correlation coefficient to determine direct and indirect influence considering eight characters. It was revealed that plant

height, primary branchs per plant, siliqua per plant, siliqua length thousand seed weight had the positive direct effect on yield per plant, whereas, secondary branches per plant and seeds per siliqua had the negative direct effect on yield per plant. The path coefficient studies indicated that plant height, primary branches per plant, siliqua per plant and thousand seed 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 0.292 indicating that the eight characters contributed 70.8 percent of variability in seed yield per plant studied in path analysis. Therefore, the present study suggested that siliqua per plant, and 1000 seeds weight should be included owing to importance in selecting the genotypes for higher seed yield in *Brassica napus*.

Genetic diversity among *Brassica napus* genotypes was performed through Principal Component Analysis (PCA), Cluster Analysis, Canonical Variate Analysis (CVA). The first four characters of the PCA axes with eigen values above unity contribute a total of 78.86% variation towards the divergence. As per PCA, D^2 and Cluster Analysis, the genotypes were grouped into four different clusters. Cluster I, II, III and IV composed of 14, 14, 16 and six lines, respectively. The highest inter-cluster distance was observed between clusters I and IV indicating genotypes from these two clusters are diverse, if involved in hybridization may produce a wide spectrum of segregating population while the lowest inter-cluster distance was observed between cluster II and III.

Based on D^2 value, the genotypes were grouped into four clusters. The cluster III included 16 genotypes, which is the highest followed by cluster I and II which contained 14 genotypes each. Cluster IV contained 4. The cluster III had higher intra cluster distance that indicates the highest amount of genetic divergence within the group. The maximum inter cluster distance was observed between genotypes of cluster I and IV followed by clusters II and IV. Therefore it could be concluded that the genotypes present in combination of those clusters could be utilized for successful breeding programme.

Cluster IV required minimum days for maturity and cluster III required maximum days. Cluster III showed high value and cluster IV showed low value in case of seed yield plant-1. The present study revealed that the clusters I and III possessing high mean values for most of the desirable traits are desired to be crossed with cluster IV which possessed low mean values of days to maturity.

Minimum plant height was observed in cluster I and maximum in cluster IV. Cluster IV had highest primary branches and cluster I had lowest primary branches. Maximum (4.56) and minimum (3.21) secondary branches per plant were observed in cluster IV and II respectively. For siliqua per plant, cluster IV showed maximum value and cluster I showed minimum value.

Siliqua length was the highest in cluster IV and it was least in genotypes belongs to the cluster I (7.39 cm). Highest seeds per plant was recorded by the cluster IV while cluster I showed the least seeds per plant. The maximum 1000 seed weight was observed in cluster IV, whereas minimum 1000 seed weight was observed in cluster III. A highest seed yield per plant was recorded by the genotype making up cluster IV while cluster II showed the least seed yield per plant.

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 G4 (9906 X 205 (P1)), G34 (9908 X 9906 (P3)), G30 (9905 X 9901 (P2)), G40 (9901 X 2055 (P2)), G9 (9901 X 2066 (P2)) and G7 (9906 X 205 (P2)). 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 50 *Brassica napus* F_6 genotypes

Genotype	Plant height (cm)	Primary branches per plant	Secondary branches plant	Silique per plant	Pod length (cm)	Seeds per plant	Thousand seed weight (g)	Yield per plant (g)
G1	104.43	3.87	3.38	128.83	7.90	21.70	4.22	4.89
G2	107.35	5.72	4.12	117.47	8.11	16.43	4.33	4.05
G3	102.72	6.40	4.95	137.22	7.77	14.49	3.55	4.46
G4	123.18	3.85	4.40	175.14	8.49	17.42	6.30	9.41
G5	123.32	3.57	4.04	151.62	8.82	21.68	5.61	6.40
G6	116.09	4.16	5.10	180.85	7.86	24.47	4.34	6.25
G7	123.35	3.37	3.43	105.19	8.45	24.86	5.45	9.55
G8	122.07	3.91	4.09	117.78	7.14	19.94	5.20	4.12
G9	115.57	3.57	3.10	120.30	7.12	18.37	6.39	9.79
G10	116.64	2.68	2.60	113.91	7.26	22.13	5.39	3.35
G11	117.08	4.41	3.91	103.26	7.31	18.19	4.43	3.04
G12	116.84	3.20	2.97	113.60	7.54	25.12	5.43	4.53
G13	113.33	5.43	3.96	114.63	5.78	23.95	4.44	3.50
G14	119.02	3.80	2.96	130.95	6.47	17.75	3.53	2.74
G15	119.65	5.18	5.03	168.03	8.16	25.38	5.58	7.84
G16	117.79	4.16	3.94	131.53	7.52	23.04	3.69	2.44
G17	109.23	4.22	4.04	147.66	7.93	25.46	3.32	2.90
G18	121.35	4.02	4.30	191.62	7.87	21.99	5.45	8.60
G19	106.38	6.52	4.16	148.11	7.38	24.74	5.17	3.60
G20	111.60	3.79	2.95	119.37	7.73	27.25	5.36	5.09
G21	117.67	3.79	3.27	142.58	8.42	21.91	4.44	4.79
G22	118.59	4.16	2.48	115.83	7.40	21.35	4.06	3.86
G23	113.39	4.84	3.17	125.60	7.20	19.44	5.60	7.03
G24	106.23	4.44	4.17	143.69	7.86	20.19	4.39	5.39
G25	111.47	3.70	3.77	157.64	7.62	28.26	6.23	7.21
G26	118.79	3.28	2.20	132.11	7.42	21.18	3.53	2.87
G27	113.10	3.07	2.34	125.23	7.37	23.07	5.17	3.05
G28	116.94	4.00	2.92	151.05	8.72	26.08	3.48	3.45
G29	122.44	3.33	3.37	141.06	7.61	23.56	4.33	3.24
G30	116.37	4.82	4.88	191.68	7.44	22.65	6.68	8.80
G31	123.17	3.91	3.14	147.28	7.23	21.36	4.93	6.42
G32	119.01	4.20	3.54	140.73	7.35	18.45	3.71	3.19
G33	114.75	3.01	4.92	106.25	7.10	20.01	6.45	4.44
G34	122.02	3.68	4.43	155.38	7.08	19.26	5.73	8.25
G35	120.60	3.58	3.67	170.92	7.85	20.44	5.44	8.55

Appendix I. (Contd.)

Genotype	Plant height (cm)	Primary branches per plant	Secondary branches plant	Silique per plant	Pod length (cm)	Seeds per plant	Thousand seed weight (g)	Yield per plant (g)
G36	110.37	3.41	4.06	160.93	8.90	21.81	4.73	3.69
G37	106.96	4.52	3.98	150.52	7.94	20.48	3.54	4.07
G38	108.92	3.51	3.01	126.92	8.32	20.73	3.54	3.36
G39	116.65	3.25	3.67	137.88	7.83	20.38	5.20	4.45
G40	108.47	3.46	2.64	153.46	7.67	16.93	6.41	10.82
G41	103.13	3.21	2.49	111.42	6.39	13.97	3.60	3.21
G42	105.92	4.70	3.43	132.48	7.20	17.56	4.24	3.24
G43	101.55	4.18	2.55	133.36	8.17	19.04	3.51	3.21
G44	105.95	3.52	3.01	93.04	8.18	21.05	3.30	3.23
G45	127.70	2.97	3.09	123.99	8.09	20.43	5.30	3.31
G46	117.66	3.31	3.35	123.83	8.28	20.07	4.68	4.89
G47	101.84	2.82	2.06	109.78	8.02	21.52	5.34	5.31
G48	107.15	2.54	2.85	126.69	7.78	21.65	3.75	4.23
G49	105.21	3.02	3.36	152.15	7.96	20.92	3.74	5.39
G50	107.94	2.99	4.04	152.48	8.16	21.25	5.37	6.02
Mean	113.94	3.90	3.55	137.06	7.70	21.19	4.75	5.11
Min.	101.55	2.54	2.06	93.04	5.78	13.97	3.30	2.44
Max.	127.70	6.52	5.10	191.68	8.90	28.26	6.68	10.82
CV (%)	5.47	14.31	20.94	12.18	8.40	8.67	2.72	6.14

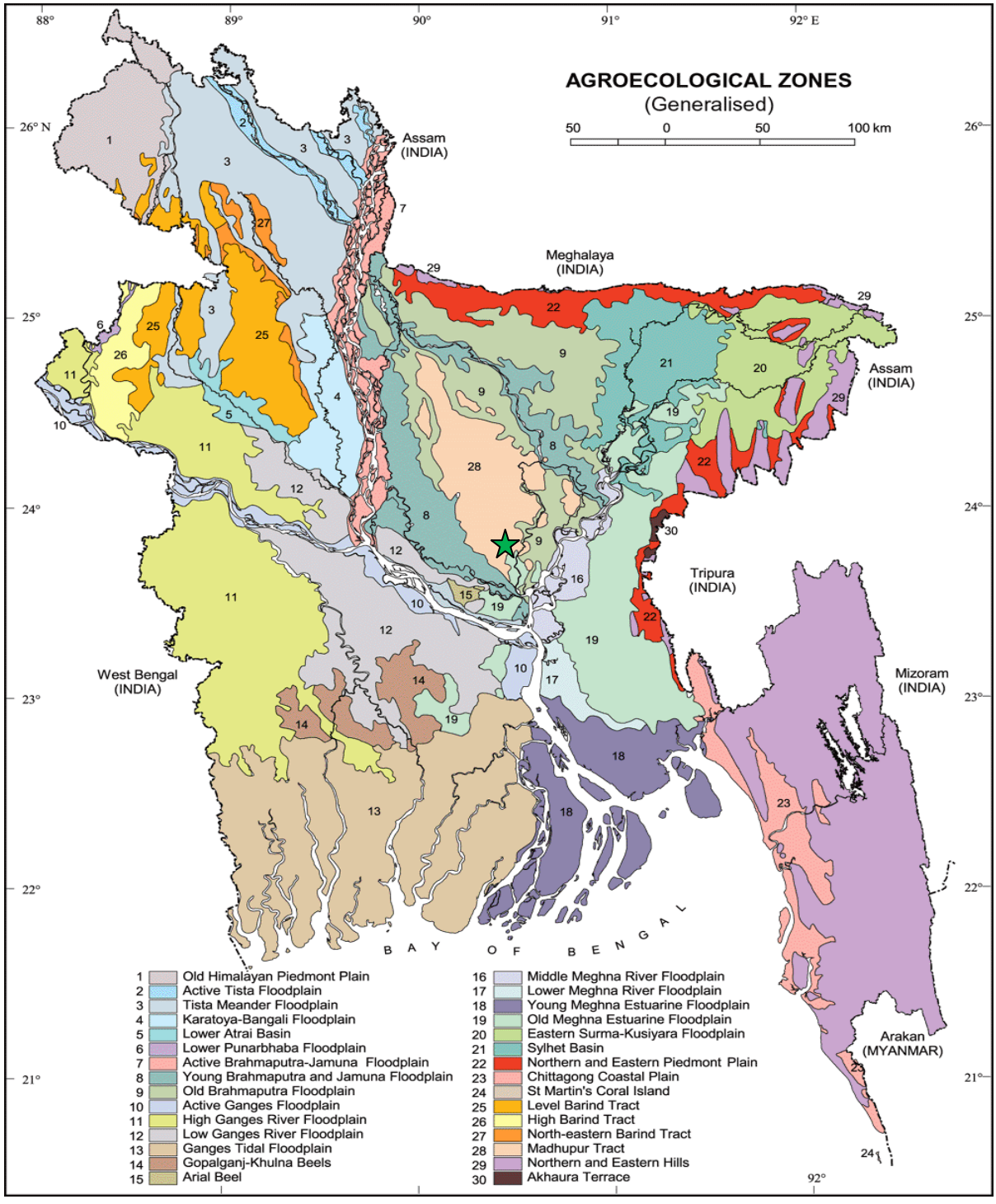
Appendix II. Principal component score 1 & 2

Genotypes	Z_1	Z_2
1	8.80	-8.86
2	20.07	-5.77
3	0.70	-11.89
4	-38.67	6.57
5	-15.19	8.48
6	-43.92	-0.47
7	30.87	12.08
8	18.77	9.21
9	16.44	2.83
10	22.98	4.28
11	33.65	4.97
12	23.14	4.82
13	22.40	1.01
14	5.99	4.95
15	-31.49	4.11
16	5.36	4.15
17	-10.26	-5.19
18	-55.03	3.98
19	-10.58	-8.05
20	17.64	-0.56
21	-5.73	3.36

Appendix II. Principal component score 1 & 2 (contd.)

22	20.95	5.93
23	11.40	0.19
24	-6.13	-8.19
25	-20.63	-3.00
26	4.78	4.97
27	11.92	0.06
28	-14.14	2.31
29	-4.47	8.26
30	-54.83	-0.85
31	-10.82	8.55
32	-3.81	4.37
33	30.68	2.85
34	-18.88	6.84
35	-34.31	4.49
36	-23.52	-5.15
37	-12.91	-8.01
38	10.53	-4.48
39	-0.94	2.56
40	-16.17	-6.50
41	26.52	-9.77
42	5.24	-8.11
43	4.63	-12.40
44	44.48	-5.14
45	12.27	14.39
46	12.99	4.47
47	27.95	-10.06
48	10.82	-6.05
49	-14.48	-9.69
50	-15.05	-6.86

Appendix III. Map showing the experimental site under the study



★ **The experimental site under the study**

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

A. Physical composition of the soil

Soil separates	%	Method employed
Sand	36.90	Hydrometer method (Day, 1915)
Silt	26.90	Do
Clay	36.66	Do
Texture class	Clay loam	DO

B. Chemical composition of the soil

Sl No.	Soil characteristics	Analytical data	Method 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	p^H (1:2.5 soil to water)	5.55	Jackson, 1958
10	CEC	11.23	Chapman, 1965

Source: Central library, Sher-E-Bangal Agricultural Unicersity, Dhaka.

Appendix V. Monthly average temperature, relative humidity and total rainfall and Sunshine of the experimental site during the period from November 2014 to February 2015

Month	Air temperature (^{0}C)		Relative Humidity (%)	Rainfall (mm) total	Sunshine (Hr)
November 2014	35.8	17.0	76	225	5.9
December 2014	33.3	17.3	70	0	7.8
January 2015	28.0	12.0	80	1	3.7
February 2015	27.1	12.1	71	2	5.6

Source: Bangladesh Meteorological Department, Agargaon, Dhaka-1207.