GENETIC VARIATION AND CORRELATION ANALYSIS IN AGROMORPHOLOGICAL TRAITS OF F_4 GENERATION IN *Brassica napus* L.

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CERTIFICATE

*This is to certify that thesis entitled, "**GENETIC VARIATION AND CORRELATION ANALYSIS IN AGROMORPHOLOGICAL TRAITS OF F_4 GENERATION IN 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 (M.S.)** in **GENETICS AND PLANT BREEDING** , embodies the result of a piece of bona fide research work carried out by **JOYOTI PAUL**, Registration No: **11-04447** 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 :
Place:: Dhaka, Bangladesh

…… ….
(Dr. Firoz Mahmud)
Professor
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DEDICATED
TO
MY BELOVED PARENTS

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GENETIC VARIATION AND CORRELATION ANALYSIS IN AGROMORPHOLOGICAL TRAITS OF F_4 GENERATION IN *Brassicanapus* L.

By

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ABSTRACT

Seventy genotypes of *Brassicanapus* were evaluated to study the variability, correlation, path analysis and genetic diversity based on agro-morphological traits at Sher-e-Bangla Agricultural University, Dhaka during November 2016 to February 2017. Significant variations were observed among the genotypes for all the traits studied. Considering genetic parameters, high GCV values were observed for number of primary branches per plant, number of secondary braches per plant and seed yield per plant. High heritability values with high genetic advances in percent mean were obtained for number of secondary branches per plant, number of siliquae per plant, number of seeds per siliqua, 1000 seed weight and seed yield per plant. Correlation studies revealed significant positive association of seed yield per plant with days to 50% flowering and siliquae per plant at both genotypic and phenotypic levels. Path coefficient indicated positive direct contribution towards days to flowering, siliquae per plant, seeds per siliqua and 1000 seed weight. The genotypes were grouped into five clusters. Cluster III contained the maximum number of genotypes (20) and the cluster I contained the minimum number of genotypes (11). The highest inter-cluster distance was observed between clusters I and III 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 IV. Considering cluster group distance, seed yield per plant and other agronomic performance the genotype of G4, G43, G54, G31, G41, G14 and G59 might be used as open pollinated verities by further purification and need to further performance studies and stability test; and could be used as parents in future hybridization program.

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SOME COMMONLY USED ABREVIATIONS

Full word	Abbreviation
Percent	%
Degree Celsius	^{0}C
At the rate	@
Phenotypic variance	σ^2_p
Genotypic variance	σ^2_g
Environmental variance	σ^2_e
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 fourth generation of a cross between two dissimilar homozygous parents	F_4
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
Centimeter	cm

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 variation	PCV
Randomized Complete Block Design	RCBD
Sher-e-Bangla Agricultural University	SAU
Triple Super Phosphate	TSP

CHAPTER I

INTRODUCTION

Mustard is one of the most important edible oil crops of Brassicace family. It is commonly known as oilseed, rapeseed or canola. Oilseed *Brassica* is commonly known as rapeseed and mustard and occupy an important position in the rain fed agriculture of Bangladesh. Rapeseed is one of the most important source of protein rich annual crops in the world. They provide the most concentrated source of energy and also help to absorb vitamins A, D, E and K.

Rapeseed is the second highest source of edible oils supply in the world after soybean (FAO, 2014). This edible oil seed is very nutritionally rich as it contains 40-45% oil and 20-25% protein and minerals and lowest amount of saturated fatty acids (Mondal and Wahhab, 2001). Significantly, it provides both the essential fatty acids such as linolenic acid and linoleic acid to the human body which is lack in most of the edible oil.However,the mustard oil is used not only for edible purposes but also in hairdressing, body massaging and in different types of pickles preparation.During last decades,mustard oil cultivation has increased dramatically in most of the regions of the world.

Approximately 70% of the total cultivated mustard in Bangladesh is the varieties of either *Brassicanapus* or *Brassicarapa*. *Brassica spp* occupies first position in respect of area and production among the oilseed crops grown in this country (BBS, 2011). In the year of 2010-11, it covered 6, 23,294acres land and the production was 2,46,494 metric ton (MT) which contributed to 52% of the total production and 61.2% of the oilseed production of Bangladesh (BBS, 2011). *Brassica* oil crops are the most important group of species that supply major edible oils in Bangladesh (BBS, 2013). However,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).In

Bangladesh, thetotal cultivated area under soybean cultivation was 41440 hectares which produces 65883 tons of oil per year (FAO, 2011).Despite of higher production of mustard on Bangladesh, due to unavailability of improved method of oil extraction soybean isconsumed more than of mustard.

The yield of *Brassica napus*was0.9 – 1.1 metric ton(MT) per hectarewith short durational and oil percentage 38-41 %. On the other hand, the yield of *Brassica rapa*was1.0-1.1 metric ton(MT)but it was long durational and oil percentage less than 40% (Krishi Diary, 2015). So, development ofhigh yielding, short durable and higher quality of *Brassica napus* is an essential task for itsbest fit of our cropping system. For replacing the long durational low yielding variety of *Brassicanapus*, my objective of this study to work on F_4materials which are generated by crossing among 25 parents of mustard varieties. Analyzing the performance of their yield and yield contributing characters, it would be possible to select for aiming short durable and high yielding F_4genotypes of *Brassica napus* in future.

In Bangladesh, there is a limited scope to increase acreage of mustard production due to pressure of other crops in the Rabi season. Due to high cost of production and long growing period, farmers are not interested to mustard seed production. Improvement of existing oilseed crops and introduction of a new oilseedvarietiesneed to urgent attention which can fits well between Aman-mustard-boro cropping pattern for increasing the domestic production.To fulfill the purpose, it is urgent to analyze the genetic diversity and its response for the selection of thegenotypes for increasing our cropping intensity.

Seed yield, a complex character is usually controlled by non-additivegene actions. It is not only influenced by a number of morphological characters, governing by a large number of genes andenvironment. Thereby, the heritable variation creates difficulty in a selection programme. Therefore, it is necessaryto partition the overall variability into heritable and non-heritable

components.It enables the breeders to adopt suitable breeding procedure for further improvement of genetic stocks.

A plant breeding program can be divided into three steps; 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 are 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 of genetic variability and character association are 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 thus it 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 breedingmaterial is a fundamental element in plant breeding ((Mukhtar *et al.*,2002). 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, analyzing the morphological traits or using molecular markers. Multivariate analysis (Rao**,**

1952)based on Mahalanobis' (1936) D^2 statistics and Ward's non-hierarchical squared Euclidean distance method are used to quantity magnitude of diversity among germplasm in respect of breeding program.

Objectives:

- To analyze the variability of the seventyF_4progenies of *Brassicanapus*genotypes in respect of different morphological characters;
- To assess the contribution of different traits towards divergence; and
- To select promising genotypes considering high yield with early maturity for next generation.

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

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. However, 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 character's plant height, primary and secondary branches, siliquae 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. 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

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, siliquae 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.

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.

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.

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 siliquae per plant showed a high heritability estimate with low expected genetic advance indicating non-additive gene effects.

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 siliquae 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.

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 siliquae 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.

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

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, siliquae per plant, seeds per siliqua and siliqua length.

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 siliquae per plant, harvest index, oil percent. They noticed most important trails for high PCV and GCV for the number siliquae per plant and 1000-grain weight. Akbar *et al.* (2007) evaluated eight advanced lines and two check variety of *Brassica juncea* in Pakistan and studied variability, heritability and genetic advance of different yield components. The highest GCV was found in seed yield per plant followed by plant height, siliquae 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, siliquae per plant and number of primary branches per plant. The maximum genetic advance was found in seed yield per plant followed by siliquae 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 siliquae 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.

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 siliqua, 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.

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 eight 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.

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.

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 siliqua, number of siliquae per plant, thousand seed weight and seed yield per plant showed moderate broad sense heritability. Days to 80% maturity showed lowest heritability.

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 and Khan (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 siliqua followed by thousand grain weight. Thousand seed weight, number of secondary branches per plant, seeds per siliqua, and siliqua 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.

Walle *et al.* (2014) carried out a study with thirty-six genotypes of Ethiopian mustard (*Brassica carinata*) and result revealed that there was 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.

2.3 Correlation coefficient

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

Reddy (1991) studied correlation analysis in Indian mustard (*B. juncea*) and reported that positive and significant correlation between seed yield and number of primary branches per plant, number of secondary branches per plant, siliquae per plant and seeds per siliqua.

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

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

Ghosh 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, siliquae per plant, seeds per siliqua and thousand seed weight was significant and positively correlated with seed yield.

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

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

Zajac *et al.* (1998) studied phenotypic correlation between yield and its component and reported that strong positive correlation occurred betweenseeds

per siliqua and actual yield. Positive but a weaker correlation was observed between seed yield and siliquae per plant. The number of seeds per siliqua had the greatest influence and number of siliquae per plant had the smallest effect on yield.

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

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.

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.

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 siliquae per plant, which had the strongest positive and significant correlation with yield per plant at both levels, was positively associated with the number of seeds per 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 siliquae per raceme and seed number per siliqua, while plant height was significantly correlated with number of siliquae per raceme. In, general genotypic correlations were greater than phenotypic or environmental correlations. Seed yield was positively correlated with number of siliquae per raceme and 1000-seed 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 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 first flowering.

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, siliquae 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. juncea* 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.

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 siliquae 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 siliqua but insignificant negative association with days to 50% flowering, days to maturity.

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

Akbar *et al.* (2007) evaluated eight advanced lines and two check variety of *Brassica juncea* in Pakistan and reported that siliquae 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 siliquae per plant and primary branches per plant.

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 siliquae per plant.

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

A study was conducted by Hosen (2008) using five parental genotypes of *Brassica rapa*and their ten F_3 progenies including reciprocals. He found yield

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

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 was higher in magnitude them than this correspond phenotypic correlation coefficients. Seed yield was positively correlated with plant height and 1000 seed weight.

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 siliquae per plant. Highest significant positive correlation was found between days to 50% flowering and plant height.

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.

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 siliquae per plant at both phenotypically and genotypically and significant positive correlation at genotypically in days to flowering and days to maturity.

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.

2.4 Path co-efficient analysis

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.

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

Kudla (1993) reported that 1000 seed weight had positive direct effect on seed yield. Yadava *et al.* (1993) when studied path co-efficient analysis of six yield components of 25 diverse varieties of Indian mustard and observed that number of siliquae per plant had the highest positive direct effect on seed yield.

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.

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 siliquae per plant had highly positive direct effect on seed yield.

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

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

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.

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 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 1st flowering.

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

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

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

By path analysis, Zahan (2006) reported that siliquae per plant had positive direct effect on yield/plant. And days to 50% flowering had negative direct effect on yield per 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), siliquae 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 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.

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

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

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

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 siliquae per plant,

seeds per siliquae had highest and positive direct effect on yield per plant for all cultivars except cv. Star.

Alam (2010) studied path co-efficient analysis that revealed that plant height, number of primary branches per plant, number of siliquae 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.

Afrin *et al.* (2011) studied with *Brassica napus* to identify the path co-efficient among the characters. The plant height was found the highest positive and direct effect on seed yield per plant followed by number of siliquae per plant and siliqua length.

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.

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 siliquae per plant, siliquae length,

seed per siliqua 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.

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 siliqua, 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.

2.5 Genetic diversity 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.

Peter and Rai (1995) studied genetic divergence using the D^2 statistics and canonical analysis among 25 genotypes of *Brassica napus*.They reported that genetic and geographical divergence was highly related with the genotypes. The genotypes were grouped into six clusters of which cluster I was the largest accommodating among these genotypes. The cluster VI had large genetic distance from the remaining clusters.

Singh *et al.* (1997) studied genetic divergence through D^2 statistic with 50 genotypes of *B. napus* growing in 12 environments based on 13 characters. They searched the clustering pattern and 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.

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

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 siliquae number on the main raceme.

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.

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.

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.

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 siliquae 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.

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 siliquae on main raceme (8.38%).

CHAPTER III

MATERIALS AND METHODS

This chapter helps to know 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, seed sowing, intercultural practices, harvesting, data recording procedure and statistical analysis etc. which are presented as follows:

3.1 Experimental site

The experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka-1207 during November 2016 to February 2017. 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 seventy F_4 of *Brassica napus* collected from the Dept. of Genetics and Plant Breeding, Sher-e-Bangla 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 tilt. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly. The final land preparation was done on 15th November 2016.

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), 90 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. The fertilizer dose is shown below:

3.4.3 Experimental design and layout

Field lay out was done after final land preparation. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The unit plot size was 4 m long with two rows.

Table 1. Materials used for the experiment

No. of genotype	F_4 population (Crosses)	Source	No. of genotype	F_4 population (Crosses)
G1	Nap 248 X Nap 2037	SAU	G22	Nap 9908 X Nap 9901
G2	Nap 9908 X Nap 2057	SAU	G23	Nap 205 X Nap 940061
G3	Nap 248 X Nap 2012	SAU	G24	Nap 248 X Nap 2001
G4	Nap 248 X Nap 0130	SAU	G25	Nap 9905 X Nap 2022
G5	BS-13 X Nap 2001	SAU	G26	Nap 9906 X Nap 94006
G6	Nap 9906 X Nap 179	SAU	G27	Nap 108 X Nap 2022
G7	Nap 248 X Nap 206	SAU	G28	Nap 9905 X Nap 94006
G8	Nap 9908 X Nap 2037	SAU	G29	Nap 9908 X Nap 2008
G9	Nap 298 X Nap 2057	SAU	G30	Nap 205 X Nap 179
G10	Nap 9908 X Nap 206	SAU	G31	Nap 248 X Nap 9904
G11	BS-13 X Nap 2013	SAU	G32	Nap 108 X Nap 2057
G12	Nap 9908 X Nap 0130	SAU	G33	BS - 13 X Nap 9901
G13	Nap 9905 X Nap 206	SAU	G34	Nap 248 X Nap 179
G14	Nap 205 X NAP 0136	SAU	G35	Nap 9905 X Nap 9904
G15	Nap 9905 X Nap 9904	SAU	G36	BS - 13 X Nap 2022
G16	Nap 9908 X Nap 179	SAU	G37	Nap 205 X Nap 2037
G17	Nap 9908 X Nap 9904	SAU	G38	Nap 9908 X Nap 2066
G18	Nap 205 X Nap 2013	SAU	G39	Nap 108 X Nap 2037
G19	Nap 9905 X Nap 0130	SAU	G40	Nap 205 X Nap 2013
G20	Nap 9908 X Nap 2013	SAU	G41	Nap 9908 X Nap 2022
G21	Nap 108 X Nap 206	SAU	G42	Nap 9905 X Nap 2066

BS : Bari Sarisha

Table 1.Materials used for the experiment (Continued)

No. of genotype	F_4 population (Crosses)	Source	No. of genotype	F_4 population (Crosses)
G43	BS-13 X Nap 2012	SAU	G57	Nap 9905 X Nap 179
G44	Nap 205 X Nap 2022	SAU	G58	BS-13 X Nap 2066
G45	Nap 248 X Nap 2022	SAU	G59	BS-13 X Nap 0130
G46	BS - 13 X Nap 179	SAU	G60	Nap 108 X Nap 179
G47	Nap 205 X Nap 2266	SAU	G61	BS -13 X Nap 2037
G48	Nap 9906 X Nap 206	SAU	G62	Nap 298 X Nap 2066
G49	Nap 9908 X Nap 2012	SAU	G63	Nap 205 X Nap 206
G50	Nap 9905 X Nap 2037	SAU	G64	Nap 205 X Nap 9901
G51	Nap 9906 X Nap 0136	SAU	G65	BS -13 X Nap 2057
G52	Nap 9908 X Nap 9901	SAU	G66	Nap 9906 X Nap 2022
G53	Nap 248 X Nap 94006	SAU	G67	Nap 9905 X Nap 9901
G54	Nap 9905 X Nap 2054	SAU	G68	Nap 9906 X Nap 2012
G55	Nap 9908 X Nap 94006	SAU	G69	Nap 9905 X Nap 2001
G56	Nap 248 X Nap 9901	SAU	G70	Nap 9906 X Nap 9904

3.4.4 Seed sowing

The spacing of row to row was 30 cm and plant to plant in row was 10 cm. Variety to variety distance in each replication was 60 cm. Distance between replication was 1 m. Seeds were sown in line in the experimental plot on 20 November 2015. The seeds were placed at about 1.5 cm depth in the soil. After sowing the seeds were covered with soil carefully so that no clods were on the seeds.

3.4.5 Intercultural operations

Intercultural operations, such as weeding, thinning, irrigation, pest management, etc. were done uniformly in all the plots. Irrigation was given with cane after sowing of seeds to bring proper moisture condition of the soil to ensure uniform germination of the seeds. A good drainage system was maintained for immediate release of rainwater from the experimental plot during the growing period. The first weeding was done after 15 days of sowing. At the same time, thinning was done for maintaining a distance of 10 cm from plant to plant in rows of 30 cm apart. First thinning was done 14 days after sowing and second thinning was done seven days after first thinning. Second weeding was done after 35 days of sowing. Sap sucking insect aphid infestation was found in the crop during the siliquae 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.

3.4.6 Crop harvesting

The crop was harvested in different dates according to maturity. Harvesting was started on 6th February 2017 and continued on 13th February 2017 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. 15 plants were selected at randomly from F_4 progenies in each replication. The plants

wereharvested by uprooting and then they were tagged properly. Data were recorded on different parameters from these plants.

3.4.7 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.

Days to 50% flowering

Days to 50% flowering were recorded fromsowing date to the date of 50% flowering of every entry.

Days to maturity

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

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

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

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

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

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

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

3.4.8 Statistical analysis

Mean data of the characters were used to statistical analyze like analysis of variance (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 was calculated by the formula of Burton (1952). Genotypic and phenotypic correlation coefficient was obtained using the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956); path coefficient analysis was done following the method outlined by Dewey and Lu (1959). Multivariate analysis viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA) were done by using GENSTAT 5.13 and Microsoft Excel 2007 software.

3.4.8.1 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

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

Where,

σ^2_g = Genotypic variance
EMS = Error mean sum of square
σ^2_e = Error variance

3.4.8.2 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)

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

Where,

σ^2_g = Genotypic variance
$\bar{x}$= Population mean

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

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

Where,

σ^2_p = Phenotypic variance
$\bar{x}$= Population mean

3.4.8.3 Estimation of heritability

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

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

Where,

h^2_b = Heritability in broad sense
σ^2_g = Genotypic variance
σ^2_p = Phenotypic variance

3.4.8.4 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, $GA = K. \frac{\pm^2 g}{\pm^2 p} . \pm_p$

Where,

K = Selection intensity, the value which is 2.06 at 5% selection intensity
σ_p = Phenotypic standard deviation
h^2_b= Heritability in broad sense
σ^2_g = Genotypic variance
σ^2_p = Phenotypic variance

3.4.8.5 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):

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

3.4.8.6 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

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

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

3.4.8.7 Estimation of path co-efficient

Path coefficient analysis was carried out using phenotypic correlation values of yield components on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1959). Standard path coefficients which are the standardized partial regression coefficients were obtained using statistical software packages called OPSTAT. These values were obtained by solving the following set of 'p' simultaneous equation using above package.

$P_{01} + P_{02}\ r_{12} + \ldots\ldots\ldots\ldots\ldots + P_{0p}\ r_{1p} = r_{01}$
$P_{01} + P_{12}\ r_{02} + \ldots\ldots\ldots\ldots\ldots + P_{0p}\ r_{2p} = r_{02}$
$P_{01} + r_{1p} + P_{02}\ r_{2p} + \ldots\ldots\ldots\ldots + P_{0p} = r_{0p}$

Where, P_{01}, P_{02}, ……. P_{0p} are the direct effects of variables 1, 2……P on the dependent variable 0 and r_{12}, r_{13},.....r_{1p}……$r_{p(p+1)}$ are the possible correlation coefficient between various independent variables and r_{01}, r_{02},

r_{03}..... r_{0p} are the correlation between dependent and independent variables. The indirect effects of the i^{th} variable via j^{th} variable was attained as (P_{0j} * r_{ij}). The contribution of remaining unknown factor is measured as the residual factor, which is calculated and given below.

P^2_{ox} = 1- (P^2_{01} + $2P_{01}P_{02}r_{12}$ + $2P_{01}$ $P_{03}r_{13}$ +…...+ P^2_{02} + $2P_{02}$ $P_{03}r_{13}$ +…….. +P^2_{0P})

Categories

Negligible - 0.00 to 0.09; Low- 0.10 to 0.19; Moderate 0.20 to 0.29; High – 0.30 to 1.0; Very High- >1.00

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

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

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.

3.4.8.8 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance (D^2) statistic and its auxiliary analyses. The parent's 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:

3.4.8.8.1 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.

3.4.8.8.2 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).

3.4.8.8.3 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.

3.4.8.8.4 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 is 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.

3.4.8.8.5 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.

3.4.8.8.6 Computation of average intra-cluster distances

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

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

3.4.8.8.7 Computation of average inter-cluster distances

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

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

3.4.8.8.8 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.

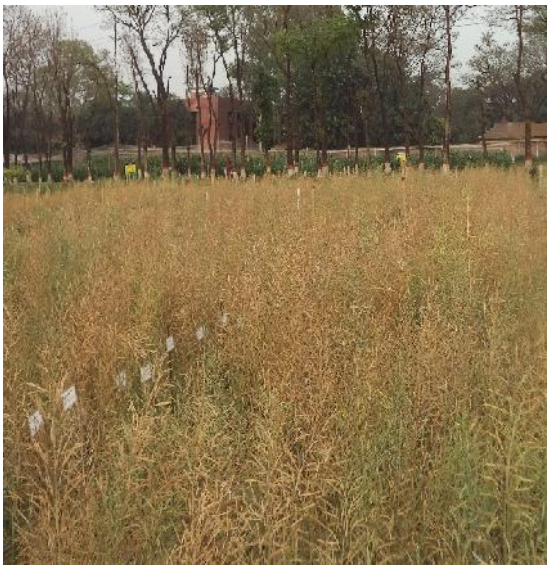
(A) **(B)**

Plate 1: Photograph (A) and (B) showing the seedling stage of *Brassica napus*L.

Plate 2: Photograph showing flowering stage of *Brassica napus*L.

A. 80% flowering stage **B. 50% maturity stage**

C. Tag of F_4 generation of *Brassica napus* L.



D. 80% maturity stage **E. Harvesting stage**

Plate 3: Photograph (A), (B), (C), (D), (E) showing the experimental field of *Brassica napus*L.

CHAPTER IV

RESULTS AND DISCUSSIONS

The results of the present exploration of genetic variability, character association, path analysis and diversity studies in F_4 segregating generations of *Brassica napus* carried out during Rabi season 2015-16 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*., days to 50% flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, siliquae 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 ten characters is presented in (Table 2). Significant differences among the genotypes was observed by many researchers like 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.

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.* (1995) in plants.

The presence of narrow gap between PCV and GCV for all the characters suggested that these traits studied had low environmental influence expect number of primary branches per plant, secondary branches per plant and seed yield per plant under study. The estimates of heritability alone fail to indicate the response to selection (Johnson *et al.,* 1955). Therefore, the heritability estimates appear to be more meaningful when accompanied by estimates of genetic advance. The genetic advance as percent 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 & 4) and depicted in (Figure 1 and 2). The mean performance of *Brassica napus* F_4 segregating genotypes for various growth characters and yield components are presented in (Appendix 1).

4.2.1 Days to 50% flowering

Highly significant mean sum of square was observed in days to 50% flowering with the value of 9.32. The maximum duration to days to 50% flowering was found in G11 with 40.33 DAS which was followed by both G8 and G17 (40.00). The minimum days to 50% flowering was observed in both G47 and G59 with 33.00 DAS which was followed by both the genotypes G7 and G41

Table 2. Analysis of variance of ten characters of 70 genotypes in *Brassica napus*

Characters	Mean sum of square		
	Replication (r-1) = 2	Genotype (g-1) = 69	Error (r-1)(g-1) = 138
Days to 50% flowering	41.7762	9.3226**	1.5346
Days to 80% maturity	39.3762	22.9594**	3.8351
Plant height (cm)	85.1651	107.6865**	17.0168
No. of primary branches per plants	0.0200	1.2122**	0.2417
No.of Secondary branches per plants	0.1401	1.8421**	0.2985
No. of siliquae per plant	56.5375	682.3422**	96.2305
Length of siliqua (cm)	0.0109	1.1920**	0.1647
No. of seed per siliqua	1.2723	19.1892**	1.6974
1000 seed weight (g)	0.0574	1.1845**	0.1832
Seed yield per plant (g)	3.1411	25.5770**	3.2830

** Denote significant at 1% level of probability

With 33.67 days (Table 3 and Appendix 1). The mean value of days to 50% flowering was 36.60(Table 3).

The genotypic variance (2.60) is lower than phenotypic variance (4.13). Thus, genes controlling this trait possessed considerable influence of environment on the expression of the character. The Genotypic co-efficient of variation and Phenotypic co-efficient of variation were low with value of 4.40 and 5.55 percent respectively, along with high heritability of 62.85% with low genetic advance as percent of mean 7.19% and low genetic advance 2.63% (Table 4). Partially support this finding by Niraj and Srivastava (2004) and Hosen (2008), who reported that days to 50% flowering showed high heritability with genetic advance in percentage of mean. The flowering trait of the plant is moderate sensitive and influenced by the environmental temperature fluctuation which is reflected in the present study. High heritability couple with low genetic advance indicating this character was predominantly controlled by environment with complex gene interaction and this also indicated the importance of both additive and non-additive genetic effects for the control of this character.These findings supported with Jahan (2008) results for this trait. Thus, it is indicating that this trait was under additive gene control and selection for genetic improvement for this trait would be effective. In the present study was shown that high heritability along with high genetic advance as percent of mean for this trait. Thus, selection for this trait might be rewarding.

4.2.2 Days to maturity

The average days to maturity were recorded 83.20 with a range of 77.00 to 89.00 day (Table 3). Genotypes G19 required the least number of days to maturity (77.00 days) which was similar with G12 (77.67). Whereasthe maximum number of days to maturity was observed in the genotype G50 (89.00 days) which was similar with G10 (88.67) (Appendix 1). Days to maturity exhibited low PCV and GCV of 3.84 and 3.03 percent respectively along with high heritability of62.44 percent, low genetic advance 4.11 and low

genetic advance as percent of mean 4.94 percent (Table 4).Naznin (2013)also found low difference between PCV (22.15) and GCV (19.74) in *B. rapa*L. Heritability was high for days to maturity reported by Niraj and Srivastava (2004). This high heritability with low genetic advance indicates of non-additive gene action. High heritability is being exhibited due to additive gene effect. Jahan (2008) found high heritability with low genetic advance in percent of mean was observed for days to maturity and selection for such trait might not be rewarding. The genotypic and phenotypic variances were recorded as 6.37 and 10.21, respectively**(**Table 4**).** As phenotypic variance is larger than genotypic variance proving that considerable influence of environment is present in the expression of genes for this trait.

4.2.3 Plant height (cm)

The grand mean plant height recorded was 105.10cm. It ranged from 92.00cm to 122.93 cm (Table 3). The analysis of variance revealed highly significant differences among the genotypes with respect to plant height. The maximum plant height (122.93 cm) was recorded by the G14 and the lowest plant height (92.00 cm) was recorded by G35. The PCV and GCV were 6.54 and 5.23 percent respectively (Appendix 1). The estimate of heritability was moderate at 63.98 per cent with low genetic advance in percent of mean (9.06%) (Table 4).

4.2.4 Primary branches per plant

It ranged from 2.13to 4.90with a mean value of 3.43 (Table 3). Maximum number of primary branches were recorded in G39 (4.90) and G36 (2.13) genotype showed the minimum number of primary branches. The PCV and GCV observed were 21.95 and 16.60 percent, respectively (Appendix 1). Moderate 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

Plate 4. Photograph showing variation between highest G_{14}(Nap205×Nap 0136) and lowest plant height(cm) G_{35}(Nap 9905× Nap 9904)of *Brassica napus* L.

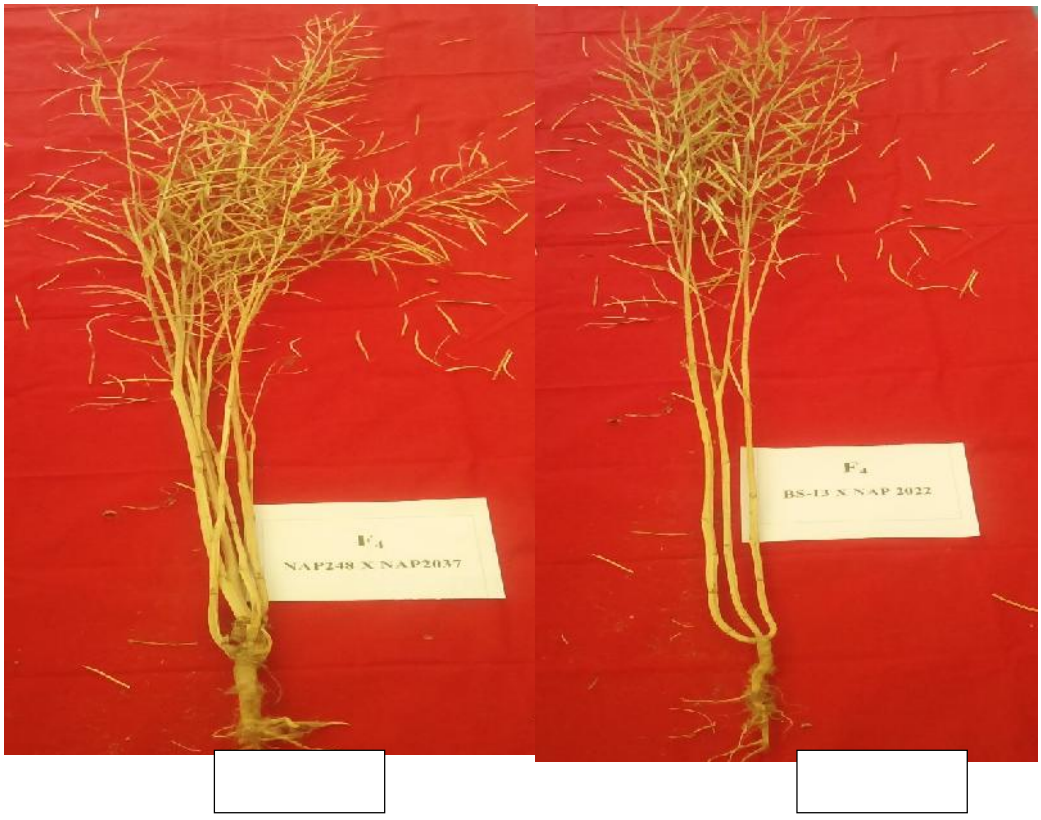


Plate 5. Photograph showing variation between highest G_{39} (Nap 248 × Nap 2037) and lowest primarybranch G_{36} (BS 13× Nap 2022) of *Brassica napus* L.

Table 3. Range, mean, CV (%) and standard deviation in ten characters of 70 genotypes of*Brassicanapus*L.

Parameters	Range		Mean	CV (%)
	Min	Max		
Days to 50% flowering	33.00	40.33	36.60	3.39
Days to 80% maturity	77.00	89.00	83.20	2.35
Plant height (cm)	92.00	122.93	105.10	3.92
No. of primary branches per plants	2.13	4.90	3.43	14.35
No.of Secondary branches per plants	1.68	5.58	2.91	18.77
No. of siliquae per plant	81.83	144.75	108.18	9.07
Length of siliqua (cm)	6.80	10.52	8.54	4.75
No.of seed per siliqua	15.02	24.90	19.36	6.73
1000 seed wt.(g)	2.88	5.56	4.06	10.55
Seed yield per plant (g)	4.16	17.86	8.74	20.74

Table 4. Estimation of genetic parameters in ten characters of 70 genotypes in *Brassicanapus*L.

Parameters	$\pm^2$p	$\pm^2$g	$\pm^2$ e	PCV	GCV	ECV	Heritability	GA (5%)	GAM
Days to 50% flowering	4.13	2.60	1.53	5.55	4.40	3.39	62.85	2.63	7.19
Days to 80% maturity	10.21	6.37	3.84	3.84	3.03	2.35	62.44	4.11	4.94
Plant height (cm)	47.24	30.22	17.02	6.54	5.23	3.92	63.98	9.06	8.62
No. of primary branches per plants	0.57	0.32	0.24	21.95	16.60	14.35	57.24	0.89	25.88
No.of Secondary branches per plants	0.81	0.51	0.30	30.98	24.65	18.77	63.29	1.18	40.39
No. of siliquae per plant	291.60	195.37	96.23	15.79	12.92	9.07	67.00	23.57	21.79
Length of siliqua (cm)	0.51	0.34	0.16	8.34	6.85	4.75	67.52	0.99	11.60
No.of seed per siliqua	7.53	5.83	1.70	14.17	12.47	6.73	77.45	4.38	22.61
1000 seed weight (g)	0.52	0.33	0.18	17.73	14.24	10.55	64.56	0.96	23.58
Seed yield per plant (g)	10.71	7.43	3.28	37.46	31.20	20.73	69.37	4.68	53.53

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,GA% :genetic advance percentage.

was supported by Walle *et al.* (2014) findingsand environment has a significant role on the expression of this trait. Medium heritability (bs) of 57.24 percent coupled with high genetic advance over percentage of mean 25.88percent were noticed. The similar findings were found by Alam (2010).

4.2.5 Secondary branches per plant

The number of secondary branches per plant ranged from 1.68to 5.58with a mean of 2.91**(**Table 3**).** The genotypic, phenotypic and environmental variances observed were 0.51, 0.81 and 0.30, respectively. The PCV and GCV were 30.98 and 24.65, respectively. The high heritability estimates of 63.29 percent with a high expected genetic advance over mean of 40.39percent were recorded for this trait(Table 4).The maximum number of secondary branches per plant was recorded in the G1 (5.58) and the minimum number in the G62 (1.68) (Appendix 1).

4.2.6 Siliquaeper plant

The number of siliquae per plant ranged from 81.83to 144.75with mean of 108.18(Table 3).The minimum number of siliquae per plant was observed in G50 (81.83) while maximum number of siliquae per plant was found in the G54 (144.75)(Appendix 1). The coefficient of variance at phenotypic and genotypic level was15.79 and 12.92 percent respectively(Table 4). The values for high heritability and high genetic gain over mean percentage were 67.00 and 21.79percent, respectively(Table 4). High heritability with high genetic advance was found by Alam (2010) for this trait that supported the results.

4.2.7 Siliqua length (cm)

It ranged from 6.80to 10.52 cm with a mean of 8.54 cm(Table 3). The minimum siliqua length was recorded by the G10 (6.80) and G26 (10.52) showed the maximum siliqua length (Appendix 1)and GCV obtained were 8.34 and 6.85 percent, respectively.The values of high heritability (67.52%) along with medium genetic advance as percent of mean (11.60%) were observed for this trait (Table 4).

Plate 6. Photograph showing variation between highest G_{54} (Nap9905× Nap2054) and lowest siliquae per plantG_{50} (Nap 9905 × Nap2037) of *Brassicanapus*L.

Plate 7. Photograph showing variation between highest G_{26} (Nap108 × Nap206) and lowest siliqua length G_{10} (Nap9906 × Nap206) of *Brassicanapus* genotypes

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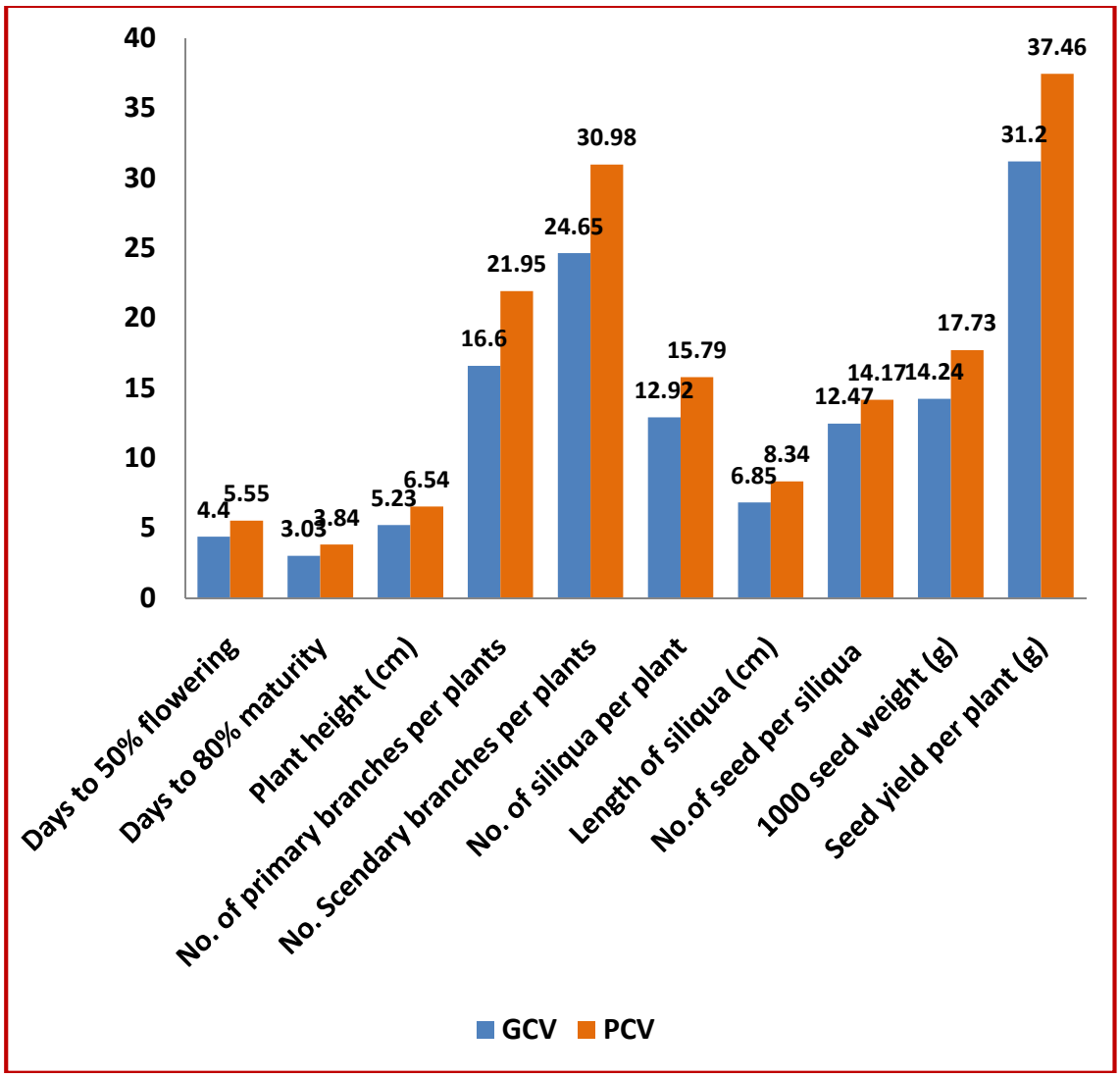

Figure1. Genotypic and phenotypic coefficient of variability in *Brassica napus*

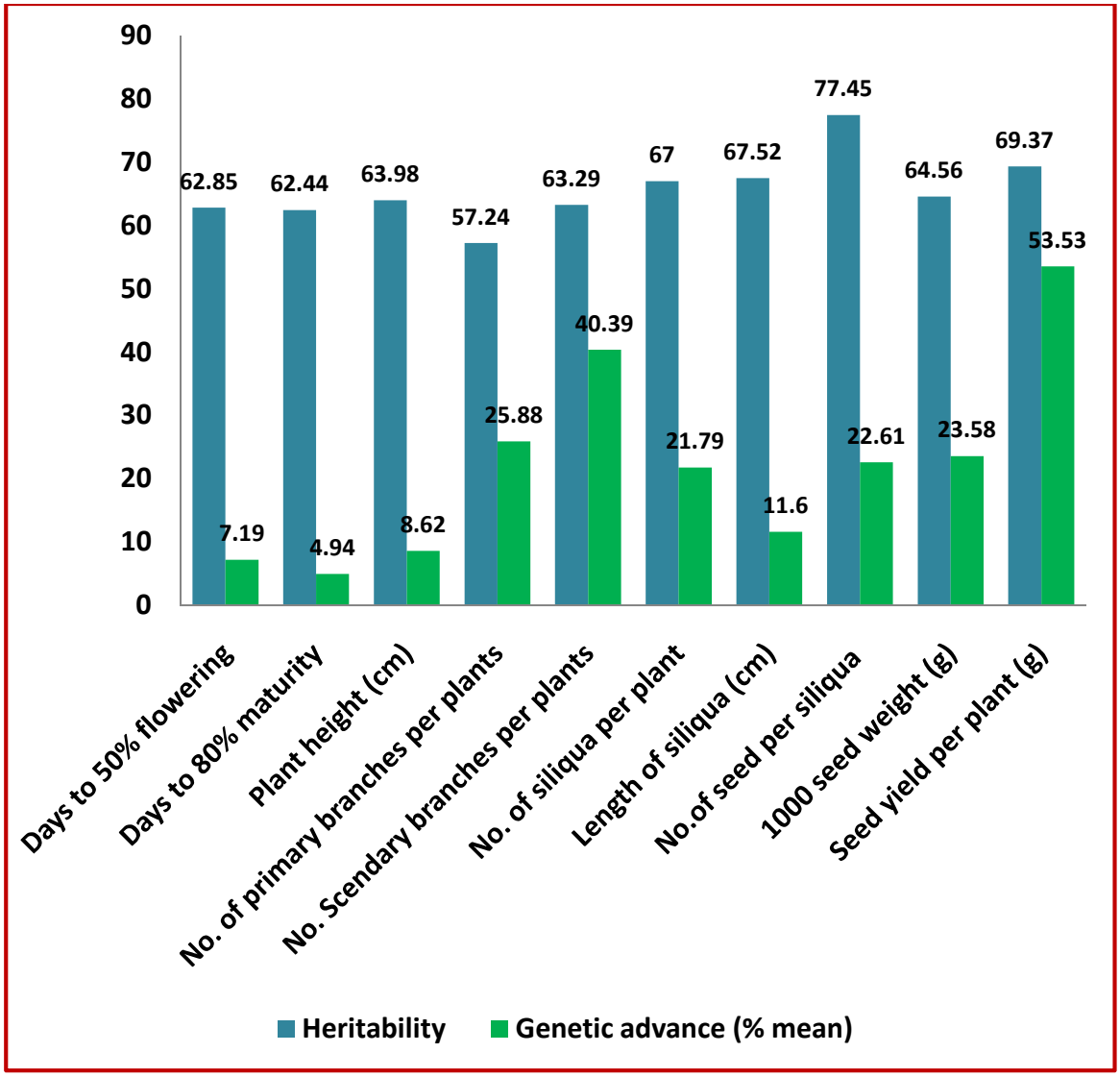

Figure 2. Heritability and genetic advance over mean in *Brassica napus*

4.2.8Seeds per siliqua

Significant difference among genotypes for seeds per siliqua was noticed. It ranged from 15.02to 24.90 with a mean of 19.36(Table 3). The highest seeds per siliqua were recorded by the G20 (24.90) while G63 (15.02) showed the lowest seeds per siliqua (Appendix 1). The PCV and GCV for this character were 14.17 and 12.47 percent, respectively. It showed high heritability of 77.45 percent along with high genetic advance over mean 22.61percentsuggested that this character was controlled by additive gene action which is very useful in section(Table 4).

4.4.2.6 Siliqua per plant

Siliquae per plant showed positive indirect effect via days to 50% flowering (0.0014), length of siliqua (0.0004), seeds per siliqua (0.0175) and 1000 seeds weight (0.0896) on seeds yield. Siliquae per plant had negative indirect effect via plant height (-0.0017), primary branches per plant (-0.0036) and secondary branches per plant (-0.0123) on seed yield (Table 7).

4.2.10 Seed yield per plant (g)

The mean seed yield per plant was noticed 8.74 g with a range from 4.16 g to 17.86g in the G51and G54, respectively (Table 3 & Appendix 1). The highest phenotypic coefficient of variability (37.46%) and genotype coefficient of variability (31.20%) was observed the highest GCV and PCV for seed yield per plant which indicated that, it might provide better scope for improvementthrough selection which was also reported by Mekonnen (2014). High heritability (69.37%) and genetic advance over mean (53.53%) were recorded(Table 4).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.

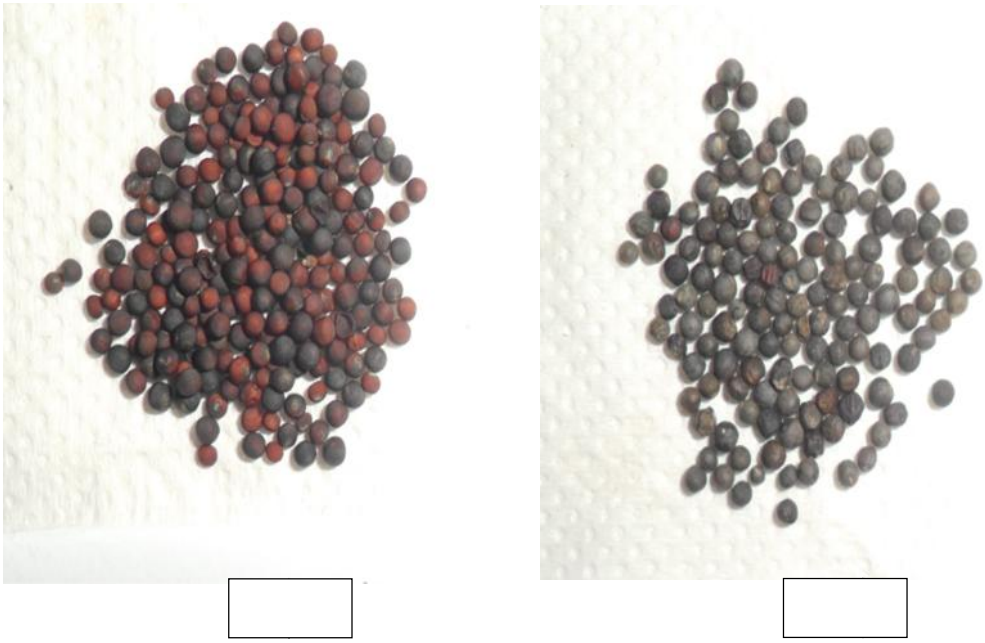

Plate 8. Photograph showing variation between the highest G_{27} (Nap 108 X Nap 2022) and the lowest G_{20} (Nap 9908 X Nap 2013) genotypes of thousand seed weight (g) of *Brassica napus* L.

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 ten characters were presented in Table 5for Pearson and Table 6 for genotypic and phenotypic correlation coefficient, respectively.

4.3.1 Pearson correlation

In Pearson correlation coefficient seed yield per plant was significantly and positively correlated with siliquae per plant (0.543), length of siliqua (0.372), seeds per siliqua (0.818) and 1000 seeds weight (0.894) indicating these are the main contributing traits when selection a genotype.

4.3.2 Genotypic and phenotypic correlation

In genotypic and phenotypic correlations out of 45 associations 13 associations were significant in genotypic level and 8 associations were significant in phenotypic level. Among the genotypic 11significant associations, nine associations were positively significant and the rest two were negatively significant. From the phenotypic eight significant associations, six were positively significant. The significant and positive association between the characters suggested additive genetic model thereby less affected by the environmental fluctuation. Besides, 23 relationships were positive and non-significant and nine relationships were negative and non-significant in genotypic level and 22 relationships were positive and non-significant and sixrelationships 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.

4.3.2.1 Correlation of seed yield per plant with yield component

Seed yield per plant was significant positive correlation with siliquae per plant (0.746 and 0.643) at both genotypic and phenotypic levels and with days to 50% flowering (0.366) at genotypic level (Table 6) suggesting that genotypes

with high partitioning efficiency gave increase in seed yield per plant. Positive insignificant correlation of seed yield per plant with plant height (0.160 and 0.111), secondary branches per plant (0.097 and 0.045), length of siliqua (cm)(0.078 and 0.037), seeds per siliqua (0.211 and 0.117) and 1000 seeds weight (g) (0.063 and 0.039) at both levels. Only days to maturity 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 siliquae 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 siliquae per plant supported this results. Siliquae per plant had significant positive correlation with seed yield reported by Rameeh(2011).

4.3.2.2 Days to 50% flowering

Days to 50% flowering had positive significant correlation with secondary branches per plant (0.722 and 0.611) at both genotypic and phenotypic level and with plant height (0.402) and siliquae per plant (0.265) at genotypic level.It was negative significant correlation with days to maturity (-0.772 and -0.470) at genotypic and phenotypic level (Table 6).

4.3.2.3 Days to maturity

Days to maturity had positive correlation with primary branches per plant (0.043 and 0.012), secondary branches per plant (0.286 and 0.052), length of siliqua (0.213 and .034) and seeds per siliqua (0.104 and 0.032) at both genotypic and phenotypic level. It was negative significant correlation with plant height (-0.964 and -0.588) and siliquae per plant (-0.544 and -0.401) at genotypic and phenotypic level (Table 6).

4.3.2.4 Plant height

Study of correlation at yield components levels exhibited that plant height showed positive and significant correlation with secondary branches per plant (0.508 and 0.456) and siliquae per plant (0.853 and 0.672) at genotypic and phenotypic level and significant positive correlation with days to 50% flowering (0.402) at genotypic level. Plant height also showed positive and insignificant correlation with primary branches per plant (0.039 and 0.057) and it was negatively and significantly correlated with days to maturity (-0.964 and -0.588) at genotypic and phenotypic level (Table 6).

4.3.2.5 Primary branches per plant

Primary branches showed positive and significant correlation with siliquae per plant (0.612 and 0.535) at both level and positive correlation with days to 50% flowering (0.044 and 0.014), days to maturity (0.043 and 0.012), plant height (0.039 and 0.057) and secondary branches per plant (0.061 and 0.029) at genotypic and phenotypic level. Negative correlation was observed of primary branches per plant with seeds per siliqua (-0.005) and 1000 seed weight (-0.001) at genotypic level (Table 6).

4.3.2.6 Secondary branches per plant

Secondary branches per plant showed positive and significant correlation with days to 50% flowering (0.722 and 0.611), plant height (0.508 and 0.456), siliquae per plant (0.646 and 0.553) at both genotypic and phenotypic level. Basalma (2008) reported significant positive correlation of branches per plant with siliquae per plant supported this finding.

It was positive correlation with days to maturity (0.286 and 0.052) and primary branches per plant (0.061 and 0.029) at genotypic and phenotypic level**.** Negative correlation of secondary branches per plant was observed with length of siliquae (-0.075 and -0.014) and seeds per siliqua (-0.067 and -0.008) at genotypic and phenotypic level (Table 6).

4.3.2.7 Siliquae per plant

Siliquae per plant showed significant positive correlation with plant height (0.853 and 0.672), primary branches per plant (0.612 and 0.535) and secondary branches per plant (0.646 and 0.553) at genotypic and phenotypic level and significant correlation with days to 50% flowering (0.265) at genotypic level. Significant negative correlation of siliquae per plant was exhibited with days to maturity (-0.544 and -0.401) and negative insignificant correlation with length of siliqua (-0.073 and -0.042) at genotypic and phenotypic level (Table 6).

4.3.2.8 Siliqua length

Siliqua length showed positive correlation with days to 50% flowering (0.211 and 0.066), days to maturity (0.213 and 0.034), seeds per siliqua (0.077 and 0.045) and 1000 seeds weight (0.019 and 0.012) and negative association with plant height, primary branches per plant and siliquae per plant at both level (Table 6).

4.3.2.9 Seeds per siliqua

Seeds per siliqua showed positive correlation with days to 50% flowering (0.131 and 0.024), days to maturity (0.104 and 0.032), siliquae per plant (0.238 and 0.256), length of silique (0.077 and 0.045) and 1000 seeds weight (0.046 and 0.035) at both genotypic and phenotypic level. It was negative correlation with plant height (-0.062 and -0.027), secondary branches per plant (-0.067 and -0.008) at genotypic and phenotypic level (Table 6).

4.3.2.10 1000 seed weight

1000 seed weight had positive correlation with days to 50% flowering (0.055 and 0.012), siliquae per plant (0.189 and 0.162), length of siliqua (0.019 and 0.012) and seeds per siliqua (0.046 and 0.035) at both genotypic and phenotypic level (Table 6).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, siliquae per plant and thousand

Table 5. Pearson correlation-coefficient among yield and yield components of ten characters of 70 genotypes of *Brassica napus*L.

	D50%F	DM	PH	PBP	SBP	SPP	LS	SPS	TSW	SYP
D50%F	1									
DM	-0.079	1								
PH	0.035	-0.144	1							
PBP	0.077	0.040	0.183	1						
SBP	0.129	0.030	0.197	0.512**	1					
SPP	0.101	-0.233	0.333**	0.403**	0.561**	1				
LS	0.126	0.053	-0.082	0.029	-0.154	-0.021	1			
SPS	0.055	0.026	-0.046	-0.056	-0.101	0.052	0.489**	1		
TSW	0.084	0.001	-0.022	-0.012	-0.031	0.170	0.433**	0.878**	1	
SYP	0.117	-0.099	0.115	0.136	0.180	0.543**	0.372**	0.818**	0.894**	1

* $p < 0.05$, ** $p < 0.01$

D50%F: days to 50% flowering, DM: days to 80% maturity, PH: plant height (cm), PBP: no. of primary branches per plant, SBP: no. of secondary branches per plant, SPP: no. of siliquae per plant, LS: length of siliqua (cm), SPS: no. of seed per siliqua, TSW: 1000 seed weight (g) and SYP: seed yield per plant (g).

Table 6. Genotypic (G) and phenotypic (P) correlation-coefficients of yield and yield component traits of 70 genotypes in *Brassica napus*L.

		DM	PH	PBP	SBP	SPP	LS	SPS	TSW	SYP
D50%F	G	-0.772**	0.402**	0.044	0.722**	0.265*	0.211	0.131	0.055	0.366**
	P	-0.470**	0.174	0.014	0.611**	0.166	0.066	0.024	0.012	0.069
DM	G		-0.964**	0.043	0.286	-0.544**	0.213	0.104	-0.002	-0.727**
	P		-0.588**	0.012	0.052	-0.401**	0.034	0.032	0.001	-0.081
PH	G			0.039	0.508**	0.853**	-0.093	-0.062	-0.012	0.160
	P			0.057	0.456**	0.672**	-0.034	-0.027	0.000	0.111
PBP	G				0.061	0.612**	0.001	-0.005	-0.001	0.005
	P				0.029	0.535**	0.001	0.000	0.001	0.009
SBP	G					0.646**	-0.075	-0.067	-0.008	0.097
	P					0.553**	-0.014	-0.008	0.001	0.045
SPP	G						-0.073	0.238	0.189	0.746**
	P						-0.042	0.256	0.162	0.643**
LS	G							0.077	0.019	0.078
	P							0.045	0.012	0.037
SPS	G								0.046	0.211
	P								0.035	0.117
TSW	G									0.063
	P									0.039

D50%F: days to 50% flowering, DM: days to 80% maturity, PH: plant height (cm), PBP: no. of primary branches per plant, SBP: no. of secondary branches per plant, SPP: no. of siliquae per plant, LS: length of siliqua (cm), SPS: no. of seed per siliqua, TSW: 1000 seed weight (g) and SYP: seed yield per plant (g).

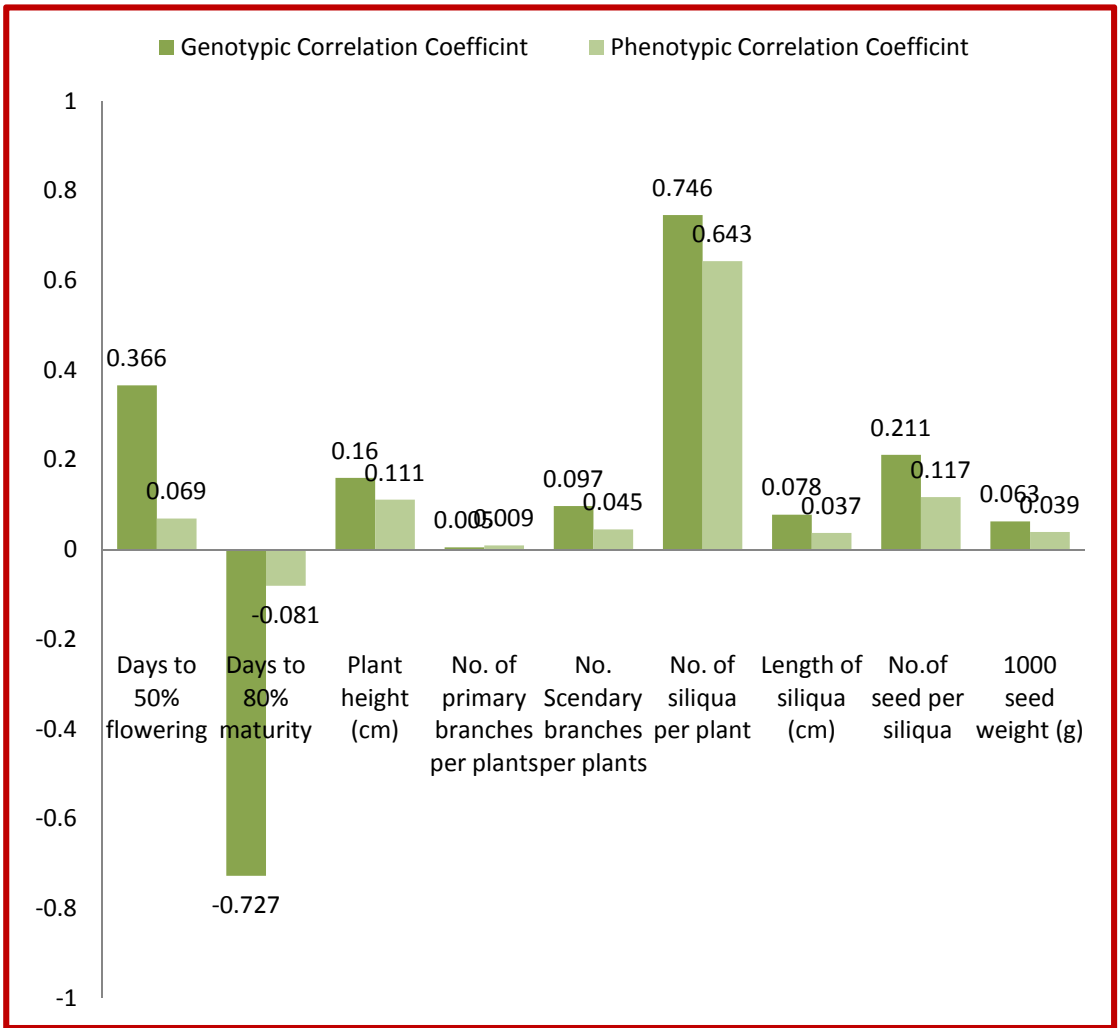

Figure 3. Genotypic and Phenotypic Correlation Coefficient for nine characters with seed yield per plant of *Brassica napus*.

seeds weight asthey 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 ten characters viz. days to 50% flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, siliquae per plant, siliqua length, seeds per siliqua and 1000 seeds weight to seed yield per plant. Seed yield being the complexoutcome of different characters, was considered as the resultant variable and other characters as causal variable. Estimates of direct and indirect effects of ten yield contributing characters are shown in (Table 7).

4.4.1 Direct effect

Among the characters that have positive direct effect on seed yield per plant were days to 50% flowering (0.014), siliquae per plant (0.452), seeds per siliqua (0.337) and 1000 seed weight (0.527). The genotypic and phenotypic correlation of days to 50% flowering, siliquae per plant, seeds per siliqua and

1000 seed weight 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 finding. Uddin *et al.* (2013) and Alam (2010) reported primary branches per plant, siliquae per plant, siliqua length and thousand seed weight showed direct positive association with seed yield per plant that supported these findings.

4.4.2 Indirect effects

4.4.2.1 Days to 50% flowering

Days to 50% flowering was observed positive indirect effect via siliquae per plant (0.0457), seeds per siliqua (0.0185) and 1000 seed weight (0.0443) toseed yield per plant. It had negative indirect effect via plant height (-0.0002), secondary branches per plant (-0.0028) length of siliqua (-0.0021) to seed yield per plant(Table 7).

4.4.2.2 days to maturity

Days to maturity had positive indirect effect on seed yield via seed per siliqua (0.0088), 1000 seed weight (0.0005) and plant height (0.0007). It was negative indirect effect via primary branches per plant (-0.0004), secondary branches per plant (-0.0007) and siliquae per plant (-0.1053) on seed yield (Table 7).

4.4.2.3 Plant height

Plant height showed indirect positive effect through siliquae per plant (0.1505), length of siliqua (0.0014), days to maturity (0.0001) and days to 50% flowering (0.0005) on seed yield. Its negative indirect effect observed via primary branches per plant (-0.0016), secondary branches per plant (-0.0043), seeds per siliqua (-0.0155) and 1000 seed weight (-0.0116) (Table 7).

4.4.2.4 Primary branches per plant

Primary branches per plant showed positive indirect effect through days to 50% flowering (0.0011) and siliquae per plant (0.1822) on seed yield. It had negative indirect effect via plant height (-0.0009), secondary branches plant (-0.0113), length of siliqua (-0.0005), seeds per siliqua (-0.0189) and 1000 seeds weight (-0.0063) on seed yield (Table 7).

4.4.2.5 Secondary branches per plant

Secondary branches per plant exhibited positive indirect effect via days to 50% flowering (0.0018), siliquae per plant (0.2536) and length of siliqua (0.0026). It was negative indirect effect via plant height (-0.001), primary branches per plant (-0.0046), seeds per siliqua (-0.034) and 1000 seed weight (-0.0163) on seed yield (Table 7).

4.4.2.6 Siliqua per plant

Siliquae per plant showed positive indirect effect via days to 50% flowering (0.0014), length of siliqua (0.0004), seeds per siliqua (0.0175) and 1000 seeds weight (0.0896) on seeds yield. Siliquae per plant had negative indirect effect via plant height (-0.0017), primary branches per plant (-0.0036) and secondary branches per plant (-0.0123) on seed yield (Table 7).

4.4.2.7 Length of siliqua

Length of siliqua showed positive indirect effect on seed yield via days to 50% flowering (0.0018), secondary branches per plant (0.0034), seeds per siliqua (0.1648) and 1000 seed weight (0.2282). Length of siliqua exhibited negative indirect effect on seed yield via primary branches per plant (-0.0003) and siliquae per plant (-0.0095) (Table 7).

4.4.2.8 Seeds per siliqua

Seeds per silqua showed positive indirect effect through days to 50% flowering (0.0008), plant height (0.0002), primary branches per plant (0.0005), secondary branches per plant (0.0022), siliquae per plant (0.0235)

Table 7. Partitioning the correlations into direct (bold) and indirect effects of ten characters of 70 genotypes by path analysis of *Brassicanapus*

	D50%F	DM	PH	PBP	SBP	SPP	LS	SPS	TSW	Correlation with SYP
D50%F	**0.0140**	0.0001	-0.0002	-0.0007	-0.0028	0.0457	-0.0021	0.0185	0.0443	0.117
DM	-0.0011	**-0.0010**	0.0007	-0.0004	-0.0007	-0.1053	-0.0009	0.0088	0.0005	-0.099
PH	0.0005	0.0001	**-0.0050**	-0.0016	-0.0043	0.1505	0.0014	-0.0155	-0.0116	0.115
PBP	0.0011	0.0000	-0.0009	**-0.0090**	-0.0113	0.1822	-0.0005	-0.0189	-0.0063	0.136
SBP	0.0018	0.0000	-0.0010	-0.0046	**-0.0220**	0.2536	0.0026	-0.0340	-0.0163	0.180
SPP	0.0014	0.0002	-0.0017	-0.0036	-0.0123	**0.4520**	0.0004	0.0175	0.0896	0.543***
LS	0.0018	-0.0001	0.0004	-0.0003	0.0034	-0.0095	**-0.0170**	0.1648	0.2282	0.372**
SPS	0.0008	0.0000	0.0002	0.0005	0.0022	0.0235	-0.0083	**0.3370**	0.4627	0.818**
TSW	0.0012	0.0000	0.0001	0.0001	0.0007	0.0768	-0.0074	0.2959	**0.5270**	0.894***

Residual effect (R): 0.135** = 1% level ofSignificant. *** = 0.1% level of Significant.

D50%F : days to 50% flowering, DM : days to 80% maturity, PH : plant height (cm), PBP : no. of primary branches per plant, SBP : no. of secondary branches per plant, SPP : no. of siliquae per plant, LS : length of siliqua (cm), SPS : no. of seed per siliqua, TSW : 1000 seed weight (g) and SYP : seed yield per plant (g)

and 1000 seeds weight (0.4627) on seed yield. It negative inditrect effect via length of siliqua (-0.0083) only on seed yield (Table 7).

4.4.2.9 1000 seed weight

1000 seed weight showed positive indirect effect via days to 50% flowering (0.0012), secondary branches per plant (0.0007), siliquae per plant (0.0768) and seeds per siliqua (0.2959) on seed yield (Table 7).

The residual effect (R) was 0.135, indicating that the nine characters contributed 86.5 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, seeds per siliqua, thousand seeds weight and days to 50% flowering 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 siliquae per plant, seeds per silqua and 1000 seeds weight should be included owing to importance in selecting the genotypes for higher seed 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, 70 populations of *Brassica napus* were considered for the assessments of genetic diversity by multivariate analysis as per Mahalanobis' (1936) concept of generalize distance (D^2) considering ten important quantitative characters. Based on D^2-value, the genotypes were grouped into five clusters (Table 7).

4.5.1 Nonhierarchical clustering

With the application of covariance matrix for nonhierarchical clustering, 70 *Brassica napus* populations were grouped into five different clusters. It is stated that 28.57% populations were included in cluster III and it was followed by 20% in clusters II, 18.57% in cluster V, 17.14% incluster IV and the remaining were in cluster I. The composition of clusters with different populations is presented in (Table 8). The cluster III included 20populations, which is the highest, followed by cluster IIcontained 14 populations, cluster V with 13 populations, cluster IV composed 12 population and rest 11 populations in cluster I. 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 *etal.*(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 9). The results showed that the first principal axis, days to 50% flowering largely accounted for the variation among the populations which alone contributed 31.359% of the total variation among the genotypes. The first four characters of the principal component axes with eigen values above unity accounted for 75.248% of the total variation among the ten characters. The rest six characters contributed remaining 24.752% 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& 5).

4.5.3 Inter cluster distance

The average intra and inter cluster D^2 values are given in (Table 10)and the nearest and farthest cluster from each cluster based on D^2 value is given in (Table 11**).** It was observed that inter cluster distance were always higher than those of intra cluster distance. The maximum inter cluster distance was observed between populations of cluster I and III**(**10.897) followed by clusters I and V (8.124) and III and IV (7.885). Thus, hybridization among populations 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.

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 III indicated the genotypes in these clusters were diversed than those clusters. Cluster III was the most diverse as many other clusters showed the maximum inter cluster distance with it. The minimum distance observed between clusters II and IV (3.058) indicated close relationship among the populations included (Table 11 and Figure 6).

4.5.4 Intra cluster distance

The intra cluster D^2 values were given in (Table 10). The intra cluster distance was observed in the clusters I, II, III, IV and V. The intra cluster distance was higher in cluster I (2.45) followed by cluster III (1.81) and lowest in cluster V (0.64). 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 five

clusters were lower than the inter cluster distances and which indicated that populations 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 populations of different groups. Hence, there is a lot of scope for exchange of genes among populations within these clusters. The mutual relationships among the five clusters are presented in the diagram (Figure 5). The averages 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 five groups, which indicated that considerable diversity existed among the genotypes (Figure 5). Cluster diagram showing the average intra and inter cluster distances of 70 *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 ten 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) and high (H) classes.

Minimum days to 50% flowering was found in the V (25.90 days) while the maximum in cluster I (37.03 days). Cluster III exhibited the maximum days to maturity (84.43 days) and cluster I showed the minimum (81.82 days) days to maturity. Minimum plant height was observed in cluster V (101.99cm) and Cluster IV showed maximum plant height (109.39cm).Cluster I had highest number of primary branches (3.72) and cluster III had lowest number of primary branches (3.11). The Maximum (3.57) and the minimum (2.31) number of secondary branches per plant were observed in cluster IV and III respectively.

Table 8. Distribution of seventy genotypes in different clusters

Cluster no.	Genotypes	No. of population	Name of Genotypes
I	G1, G2, G4, G12, G42, G43, G47, G48, G52, G54, G68,	11 (15.71)	Nap 248 X Nap 2037, Nap 9908 X Nap 2057, Nap 9905 X Nap 2037, Nap 9908 X Nap 0130, Nap 9905 X Nap 2066, BS-13 X Nap 2012, Nap 205 X Nap 2266, Nap 9906 X Nap 206, Nap 9908 X Nap 9901, Nap 248 X Nap 9904, Nap 9906 X Nap 2012,
II	G8, G16, G17, G22, G23, G27, G28, G29, G39, G46, G53, G63, G67, G70,	14 (20)	Nap 9908 X Nap 2037, Nap 9908 X Nap 179, Nap 9908 X Nap 9904, Nap 9908 XNap 9901, Nap 205 X Nap 940061, Nap 108 X Nap 2022, Nap 9905 X Nap 94006, Nap 9908 X Nap 2008, Nap 108 X Nap 2037, BS - 13 X Nap 179, Nap 248 X Nap 94006, Nap 205 X Nap 206, Nap 9905 X Nap 9901, Nap 9906 X Nap 9904
III	G5, G15, G19, G25, G26, G30, G31, G34, G35, G36, G41, G49, G50, G51, G56, G57, G60, G62, G65, G69,	20 (28.57)	BS-13 X Nap 2001, Nap 9905 X Nap 9904, Nap 9905 X Nap 0130, Nap 9905 X Nap 2022, Nap 9906 X Nap 94006, Nap 205 X Nap 179, Nap 9905 X Nap 2054, Nap 248 X Nap 179, Nap 9905 X Nap 9904, BS - 13 X Nap 2022, Nap 9908 X Nap 2022, Nap9908 X Nap 2012, Nap 248 X Nap 0130, Nap 9906 X Nap 0136, Nap 248 X Nap 9901, Nap 9905 X Nap 179, Nap 108 X Nap 179, Nap 298 X Nap 2066, BS -13 X Nap 2057, Nap 9905 X Nap 2001,
IV	G6, G7, G9, G10, G11, G14, G18, G21, G38, G40, G45, G64,	12 (17.14)	Nap 9906 X Nap 179, Nap 248 X Nap 206, Nap 298 X Nap 2057, Nap 9908 X Nap 206, BS-13 X Nap 2013, BS-13 X Nap 2066, Nap 205 X Nap 2013, Nap 108 X Nap 206, Nap 9908 X Nap 2066, Nap 205 X Nap 2013, Nap 248 X Nap 2022, Nap 205 X Nap 9901,
V	G3, G13, G20, G24,G32, G33, G37, G44, G55, G58, G59, G61, G66,	13 (18.57)	Nap 248 X Nap 2012, Nap 9905 X Nap 206, Nap 9908 X Nap 2013, Nap 248 X Nap 2001, Nap 108 X Nap 2057, BS - 13 X Nap 9901, Nap 205 X Nap 2037, Nap 205 X Nap 2022, Nap 9908 X Nap 94006, Nap 205 X Nap 0136, BS-13 X Nap 0130, BS -13 X Nap 2037, Nap 9906 X Nap 2022,
Total		70	

* Percent in parenthesis

Table 9. Latent root (Eigen values) and yield percent contribution of ten characters of 70 genotypes of *Brassica napus*L.

Principal component axes	Eigen values	Percent variation	Cumulative % of variation
I	3.136	31.359	31.359
II	2.233	22.325	53.684
III	1.151	11.507	65.191
IV	1.006	10.057	75.248
V	.795	7.953	83.201
VI	.718	7.182	90.384
VII	.482	4.822	95.206
VIII	.356	3.563	98.769
IX	.112	1.116	99.884
X	.012	.116	100.000

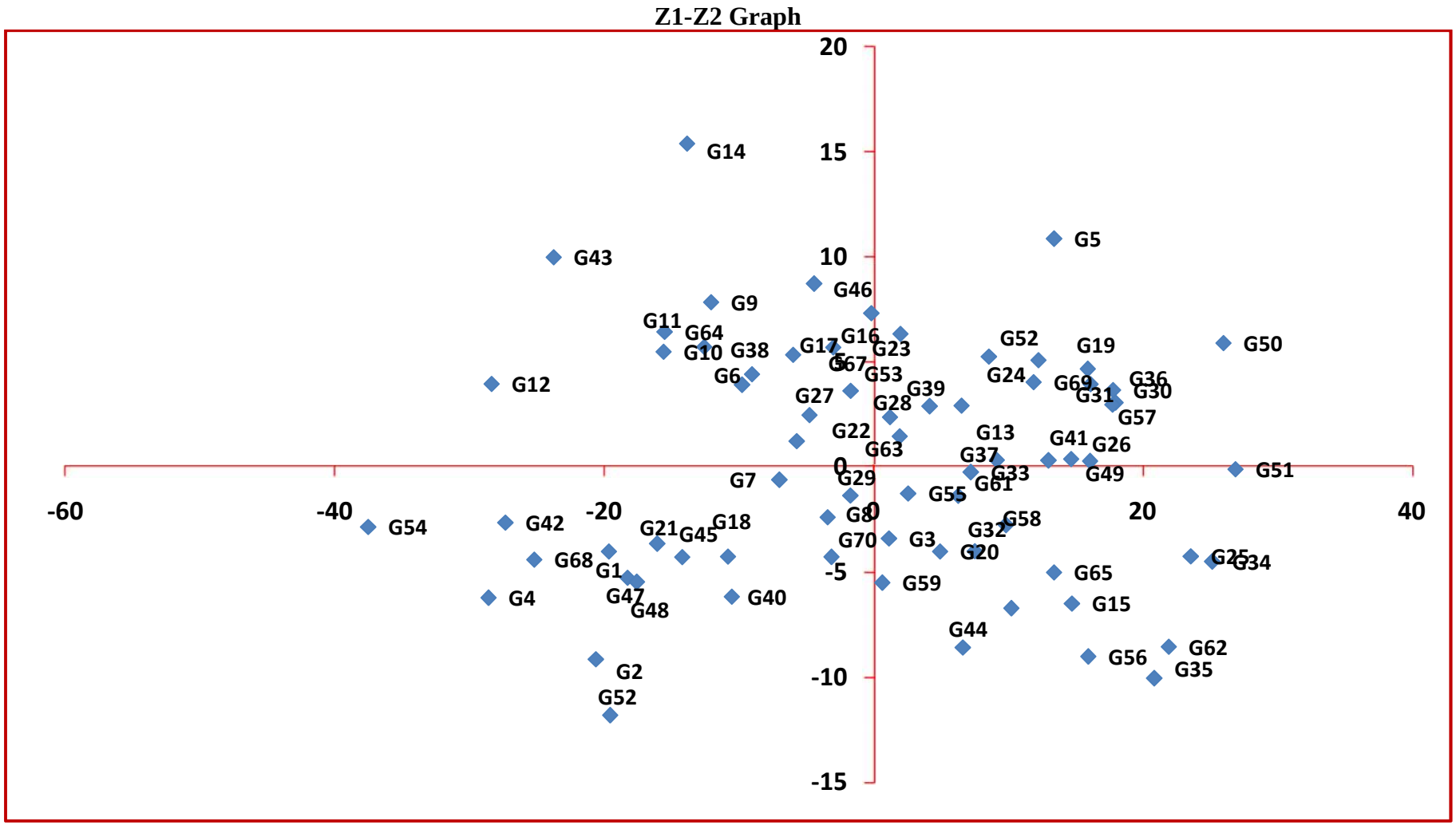

Figure 4. Scatter distribution of 70*Brassicanapus* genotypes based on their principal component scores

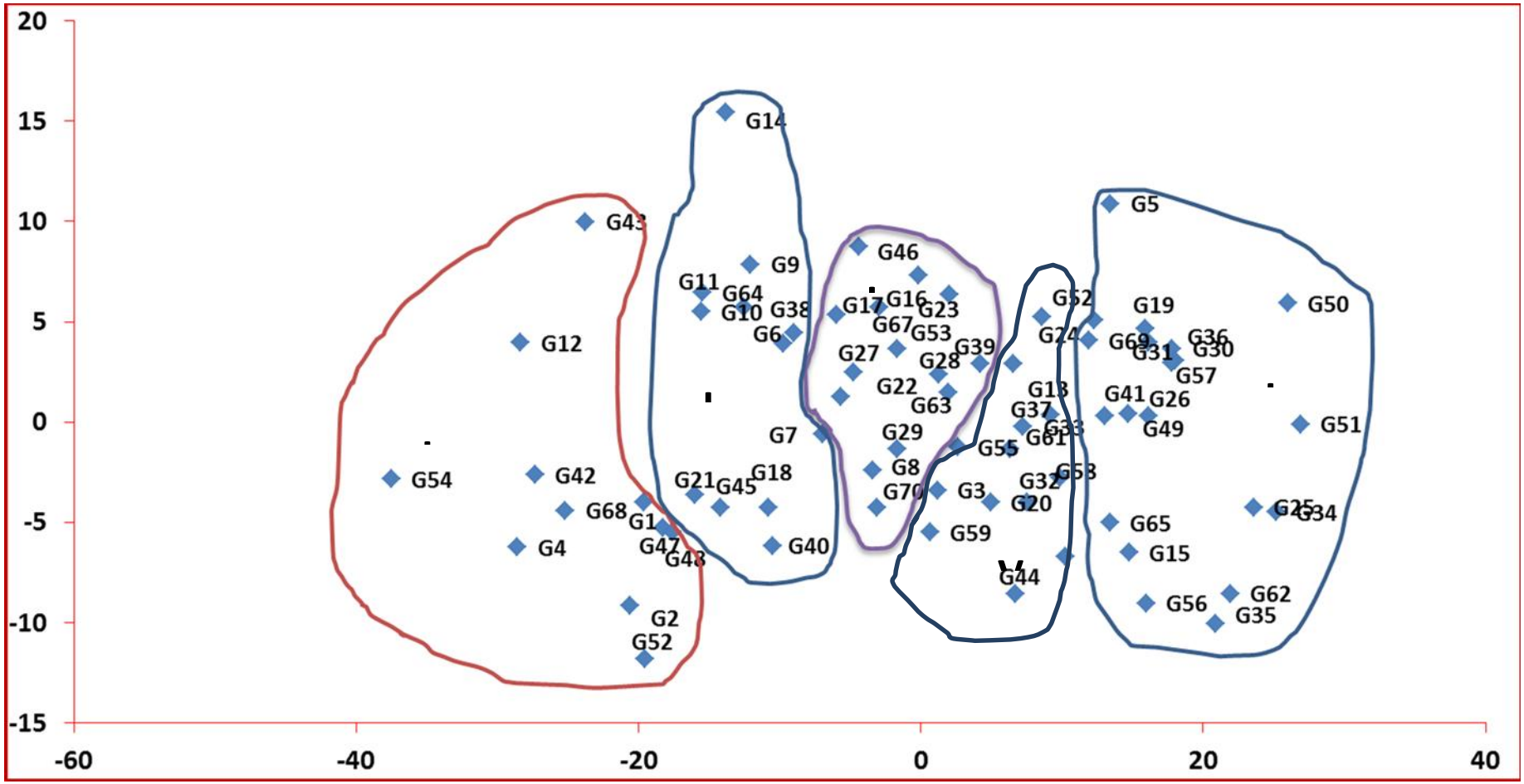

Figure 5. Cluster distribution of 70 *Brassicanapus* genotypes based on their principal component scores

Table 10. Intra (Bold) and inter cluster distances (D^2) for 70 genotypes of *Brassica napus* L.

Cluster	I	II	III	IV	V
I	**2.45**	6.251	10.897	3.929	8.124
II		**0.76**	5.215	3.058	3.310
III			**1.81**	7.885	3.303
IV				**1.54**	5.338
V					**0.64**

Table 11. The nearest and farthest clusters from each cluster between D^2 values of 70 genotypes in *Brassicanapus* L.

Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
I	IV (3.929)	III (10.897)
II	IV (3.058)	I (6.251)
III	V (3.303)	I (10.897)
IV	II (3.058)	III (7.885)
V	III (3.303)	I (8.124)

For siliquae per plant, cluster I showed the maximum value (132.24) and cluster III showed the minimum value (90.71). Siliqua length was the highest in cluster I with a mean value of (8.76 cm) and it was least in genotypes belongs to the cluster IV (8.29 cm). Highest seeds per plant was recorded by the cluster I (20.98) while cluster II (17.44) showed the least seeds per plant. The maximum 1000 seed weight was observed in cluster I (4.52 g), whereas minimum 1000 seed weight was observed in cluster II (3.59 g). A highest seed yield per plant was recorded by the genotype making up cluster I (12.75 g) while cluster II showed the least seed yield (7.00 g) per plant. The three genotypes like G4, G43 and G54 were included in cluster I possessedhigh mean value for number of siliquae per plant, length of siliqua, number of seeds per siliqua, 1000 seed weight and seed yield per plant and early maturing.

4.5.8 Selection of F_4 progeny

The genotypes under the cluster I exposed high value for primary branches per plant, number of siliquae per plant, length of siliqua, number of seeds per siliqua, 1000 seed weight and seed yield per plant and minimum days to maturity (Table 13). The genotypes of cluster III possessed intermediate days to 50% flowering, plant height, 1000 seed weight and seed yield per plant. The genotypes of cluster IV produced high value for plant height. The genotype of cluster V possessed minimum value of days to 50% flowering. Considering diversity pattern and other agronomic performance G4. G43 and G54 from cluster I, genotype G31 and G41 from cluster III, genotype G14 from cluster IV and G59 from cluster V could be considered suitable genotypes for developing open pollinated varieties after purification 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.

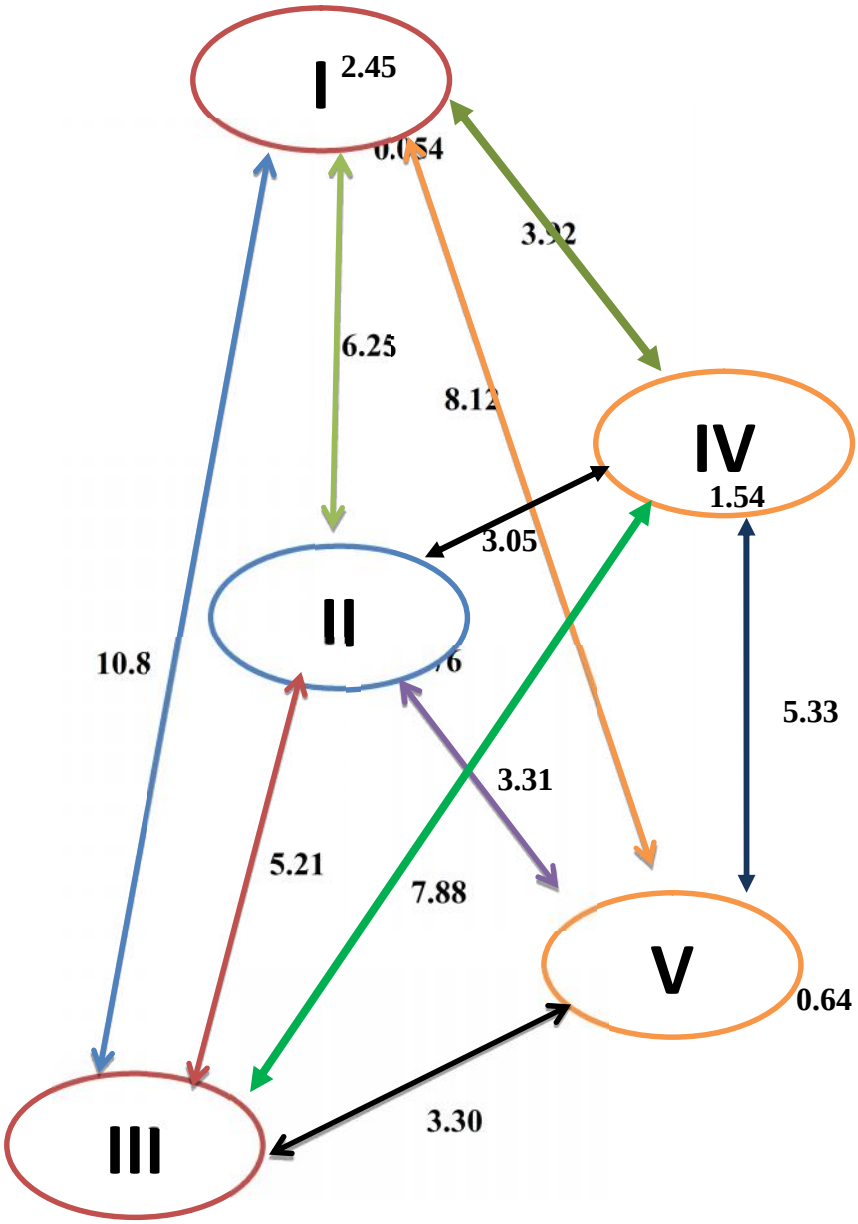

Figure 6. Intra and inter cluster distances of 70 genotypes in *Brassica napus*

Table 12. Cluster mean for ten yield and yield related characters in 70 mustard genotypes

Characters	I	II	III	IV	V
Days to 50% flowering	37.03**	37.05	36.57	36.47	35.90*
Days to 80% maturity	81.82*	83.14	84.43**	83.78	82.02
Plant height (cm)	105.47	107.93	102.37	109.39**	101.99*
No. of primary branches per plants	3.72**	3.61	3.11*	3.61	3.29
No.of Secondary branches per plants	3.37	3.02	2.31*	3.57**	2.73
No. of siliquae per plant	132.24**	109.71	90.71*	119.97	102.15
Length of siliqua (cm)	8.76**	8.50	8.57	8.29*	8.56
No.of seed/siliqua	20.98**	17.44*	19.58	18.78	20.25
1000 seed wt.(g)	4.52**	3.59*	3.98	3.95	4.38
Seed yield per plant (g)	12.75**	7.00*	7.26	9.01	9.25

* Lower value
** Higher value

Table 13. Salient features of selected genotypes in different clusters

Cluster	Genotypes	Salient feature
Cluster I	G4, G43, G54	Highest primary branches per pant Highest siliquae per plant Highest length of siliqua Highest number of seeds per siliqua Highest 1000 seed weight Hugest seed yield per plant Lowest days to maturity
III	G31, G41	Intermediate days to 50% flowering Intermediate plant height Intermediate 1000 seed weight and Intermediate seed yield per plan
IV	G14	high plant height
V	G59	minimum days to 50% flowering

CHAPTER V
SUMMARY AND CONCLUSION

The experiment was conducted with the objective to assess the selection of superior genotypes from 70 genotypes of*Brassica napus L.* through study the genetic variation and morphological diversity 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, Bangladesh.The experimental season was November 2015 to February 2016. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Data of different agro-morphological characters were recorded time to time and analyzed statistically. The results of the studies have been summarized as follows:

It was revealed from the analysis of variance that there were highly significant differences among the genotypes for all the characters. From the mean performance,it was observed that the minimum value for days to 50% flowering was observed in both G33 and G59 while the highest value of days to50% flowering was observed in G11. G19 showed early maturity and late maturing was G50. HighestPlant height was exhibitedon G14 but lowest in G35. The primary branches per plant was observed in highest G39 whereas the lowest primary branches per plant was observed in G36. The genotype G1 was performed the highest secondary branches per plant and the lowest by the genotype G62. The highest siliquae per plant was observed by the genotype G54 whereas the lowest siliquae per plant was observed by G50. Siliqua length was resulted the longest by G26 whereas the shortest siliqua length was observed by G10.Themaximum seeds per siliqua were observed in G20 whereas the minimum seeds per siliqua were observed in G63. Thousand seed weight was found the maximum in G20whereas the minimum thousand seed weight was found in G27. Yield is the most outstanding character and all the

research work and objectives are depend on yield. The highest yield per plant was observed in G54 whereas the lowest yield per plant observed inG51.

Number of seeds per siliqua (77.45) exhibited the highest value of heritability while number of primary branches per plant (57.24) 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 number of primary branches per plant, secondary branches per plant and seed yield per plant showed higher influence of environment for the expression of these characters. On the other hand, days to 50% flowering, days to maturity, plant height and length of siliqua 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 number of secondary branches per plant, number of siliqua per plant, number of seeds per siliqua, 1000 seed weight and seed yield per plant indicating that these traits were under additive gene control and selection for genetic improvement for these traits would be effective.

Relationship between yield and yield contributing characters was studied through analysis of correlation between them. The significant positive correlations of seed yield per plant were found with days to 50% flowering and siliquae per plant in both genotypic and phenotypic level suggesting that genotypes with high partitioning efficiency gave increase in seed yield per plant. In addition, there was non-significant positive correlation of seed yield per plant with plant height, secondary branches per plant and seeds per siliqua. Only days to maturity 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 ten characters. It was

revealed that days to flowering, siliquae per plant, seeds per siliqua and 1000 seed weight had the positive direct effect on seed yield per plant, whereas, secondary branches per plant and length of siliqua had the negative direct effect on seed yield per plant. The path coefficient studies indicated that siliqua per plant, seeds per siliqua and 1000 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 0.135 indicating that the ten characters contributed 99.865 percent of variability in seed yield per plant studied in path analysis. Therefore, the present study suggested that siliquae per plant, seeds per siliqua 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 75.248% variation towards the divergence. As per PCA, D^2 and Cluster Analysis, the genotypes were grouped into five different clusters. Cluster I, II, IIIIV and V composed of 11, 14, 20, 12 and 13genotypes, respectively. The highest inter-cluster distance was observed between clusters I and III 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 IV.

Based on D^2 value, the genotypes were grouped into five clusters. The cluster III included 20 genotypes, which is the highest followed by cluster II and V which contained 14 and 13 genotypes respectively. The cluster I 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 III followed by clusters I and V. Therefore, it could be concluded that the genotypes present in combination of those clusters could be utilized for successful breeding programme.

Cluster IV required medium days for 50% flowering and the highest plant height; and cluster III required the maximum days to maturity. Cluster I showed high value in case of seed yield per plant. The present study revealed that the clusters I possessing high mean values for the maximum desirable traits are desired to be crossed with cluster III, IV and V which possessed low to medium mean value of traits.

The minimum plant height was observed in cluster V and the maximum in cluster IV. Cluster I had the highest primary branches and cluster III had the lowest primary branches. Themaximum and the minimum secondary branches per plant were observed in cluster III and IV respectively. For siliquae per plant, cluster I showed the maximum value and cluster III showed the minimum value.

Siliqua lengthwas the highest in cluster IVand it was least in genotypes belongs to the cluster IV. The highest seeds per plant were recorded by the cluster I while cluster II showed the least seeds per plant. The maximum 1000 seed weight was observed in cluster I, whereas the minimum 1000 seed weightwas observed in cluster II. the highest seed yield per plant was recorded by the genotype making up cluster I while cluster II showed the least seed yield per plant.

Conclusion

The results of the present investigation revealed that the variability existed among the selected *Brassica napus* genotypes for all the characters studied.Among the genotypes the superior genotypes were G4, G43, G54, G31, G41, G14 and G59. They might be used as open pollinated verities by further purification and parents in future hybridization program.

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APPENDICES

Appendix I. Mean performance of ten characters of 70 genotypes of *Brassica napus*(F_4generation)

G	D50%F	DM	PH	PBP	SBP	SPP	LS	SPS	TSW	SYP
1	37.67	86.33	104.59	3.53	5.58	127.74	8.70	22.59	4.74	13.65
2	39.67	79.33	99.05	3.93	3.43	129.50	8.95	19.72	4.67	11.92
3	36.00	82.33	101.56	3.63	2.80	107.40	8.82	18.97	4.58	9.57
4	38.00	80.67	103.47	4.03	4.36	136.67	8.84	21.77	4.91	14.88
5	35.33	82.67	114.11	3.33	2.40	93.07	8.49	21.84	4.39	8.91
6	34.67	82.00	110.26	2.63	2.73	117.35	8.28	17.99	4.00	8.43
7	33.67	83.00	105.62	2.70	3.47	115.10	8.78	20.24	4.20	9.75
8	40.00	87.00	103.06	3.17	3.84	112.32	8.32	16.19	3.57	6.55
9	35.67	82.67	114.36	3.73	2.73	119.23	8.09	16.53	3.63	7.17
10	37.67	88.67	112.81	4.03	4.58	123.20	6.80	16.93	3.50	7.51
11	40.33	79.67	112.63	3.73	4.03	119.40	8.50	20.71	4.19	10.30
12	38.67	77.67	112.90	3.73	2.67	135.53	8.19	18.79	3.70	9.45
13	36.00	78.67	106.84	2.93	2.64	101.13	8.30	19.60	4.14	8.05
14	37.00	83.00	122.93	3.33	2.50	118.93	8.34	22.05	5.30	14.15
15	37.33	87.33	96.31	3.67	2.37	95.04	7.34	16.61	3.49	5.55
16	37.67	80.00	114.20	4.03	3.42	111.12	8.49	18.32	4.04	8.43
17	40.00	78.00	110.79	4.10	3.40	113.31	8.75	17.04	3.50	6.79
18	38.67	84.33	102.37	3.43	3.61	119.67	9.06	18.10	3.75	8.14
19	37.33	77.00	106.69	2.80	2.67	91.94	9.11	15.66	3.04	4.47
20	37.33	80.33	100.96	2.80	2.40	102.98	8.87	24.90	5.56	14.25
21	36.00	82.67	102.62	3.67	4.79	123.13	7.31	17.24	3.38	7.19
22	38.00	84.33	107.24	4.07	2.50	113.67	10.03	19.68	3.92	8.72
23	35.00	81.33	110.73	2.63	1.97	105.54	8.43	16.85	3.51	6.22
24	35.00	81.00	109.03	2.50	2.00	98.83	7.63	20.62	3.97	8.16
25	39.67	87.33	97.99	3.03	2.27	85.27	10.36	23.72	4.69	9.51

Appendix 1. Mean performance of ten characters of 70 genotypes of *Brassica napus*(F_4generation)Continued…

G	D50%F	DM	PH	PBP	SBP	SPP	LS	SPS	TSW	SYP
26	38.33	88.33	103.71	3.07	2.03	91.93	10.52	23.57	4.91	11.02
27	36.33	83.00	107.80	3.47	2.40	113.03	7.35	16.02	2.88	5.20
28	38.00	81.67	107.23	2.33	2.83	106.57	8.39	20.07	3.85	8.19
29	35.00	85.00	104.48	2.76	2.37	109.78	9.54	22.76	4.61	11.52
30	36.67	83.00	106.09	2.97	2.70	90.06	8.32	19.88	3.88	7.01
31	34.00	82.00	105.59	3.63	1.80	89.80	8.77	21.38	4.23	8.20
32	34.00	81.67	99.85	2.87	1.97	101.51	8.73	19.70	3.35	6.68
33	36.00	84.33	104.20	4.01	3.00	100.73	9.01	22.91	4.59	10.62
34	38.67	84.00	96.79	2.50	2.30	84.16	7.65	18.60	3.65	5.80
35	38.00	80.67	92.00	3.73	1.77	88.91	8.50	21.01	4.06	7.60
36	36.00	80.67	105.00	2.13	1.68	90.43	7.54	16.65	3.50	5.28
37	35.00	79.33	104.19	3.87	3.17	98.61	9.21	21.86	4.71	10.21
38	37.33	81.67	110.82	3.87	4.27	116.27	8.38	20.09	4.08	9.54
39	36.00	83.67	106.96	4.90	3.60	104.00	8.25	15.67	3.37	5.48
40	34.00	87.00	100.70	3.17	3.27	119.70	8.74	19.56	3.91	9.23
41	33.67	87.00	103.41	2.63	2.73	95.68	7.54	17.04	3.85	6.32
42	34.33	79.00	105.94	3.30	2.90	135.93	8.77	15.89	3.33	7.19
43	38.00	79.67	118.96	3.41	2.88	129.31	8.92	22.93	5.21	15.39
44	36.00	82.00	95.79	4.10	3.37	102.53	8.49	21.62	4.73	10.45
45	36.00	84.33	103.71	4.23	2.94	124.85	8.88	17.54	3.78	8.25
46	38.00	86.00	112.39	2.93	2.53	107.50	8.35	18.46	3.64	7.28
47	33.00	83.67	102.69	3.73	4.09	126.94	8.61	20.09	4.14	10.79
48	35.00	85.67	102.67	3.27	2.33	126.19	9.20	21.56	4.47	12.18
49	36.00	82.33	103.27	3.03	2.83	93.63	8.23	20.28	3.70	7.11
50	34.67	89.00	107.40	4.13	2.57	81.83	8.78	20.56	3.85	6.59

Appendix1. Mean performance of ten characters of 70 genotypes of *Brassica napus*(F_4generation)Continued…

G	D50%F	DM	PH	PBP	SBP	SPP	LS	SPS	TSW	SYP
51	36.00	86.00	100.76	2.37	1.90	82.14	8.99	16.04	3.17	4.16
52	37.33	82.33	96.66	4.03	2.57	128.73	8.60	22.51	4.81	13.98
53	37.67	84.33	108.63	3.57	3.30	109.70	8.21	16.06	3.40	5.99
54	38.67	81.67	108.46	3.80	2.72	144.75	8.59	23.53	5.22	17.86
55	35.00	80.33	103.04	3.37	3.73	106.03	8.35	16.99	3.35	6.10
56	35.00	84.33	93.52	3.33	2.53	94.10	8.33	16.53	3.55	5.84
57	37.00	86.00	106.72	3.20	2.27	91.80	8.83	19.15	4.02	7.21
58	37.33	84.33	100.54	3.00	2.33	99.27	8.11	15.04	3.76	5.65
59	33.00	83.33	100.11	2.88	2.34	107.72	8.47	23.34	5.50	13.87
60	36.00	86.67	108.50	4.13	2.37	95.46	8.44	20.22	3.82	7.39
61	37.00	84.00	102.84	4.13	2.97	102.13	8.93	18.87	4.44	8.56
62	39.00	82.33	93.32	2.30	1.68	87.77	8.14	19.77	4.09	7.18
63	37.00	82.67	105.75	3.43	2.77	106.53	8.83	15.02	2.99	4.85
64	36.67	86.33	113.79	4.77	3.87	122.77	8.38	18.32	3.74	8.41
65	36.33	85.33	98.41	3.40	2.78	95.56	8.41	21.29	4.45	9.12
66	39.00	84.67	96.94	2.73	2.77	99.10	8.38	18.88	4.28	8.06
67	35.67	85.00	110.89	4.90	4.17	110.68	8.11	15.93	3.35	6.06
68	37.00	84.00	104.79	4.17	3.50	133.40	9.01	21.44	4.48	12.93
69	36.33	86.67	107.87	2.77	2.57	95.53	9.20	21.84	5.24	10.93
70	34.33	82.00	100.91	4.27	3.13	112.20	7.97	16.11	3.63	6.67

D50%F : days to 50% flowering, DM : days to 80% maturity, PH : plant height (cm), PBP : no. of primary branches per plant, SBP : no. of secondary branches per plant, SPP : no. of siliqua per plant, LS : length of siliqua (cm), SPS : no. of seed per siliqua, TSW : 1000 seed weight (g) and SYP : seed yield per plant (g).

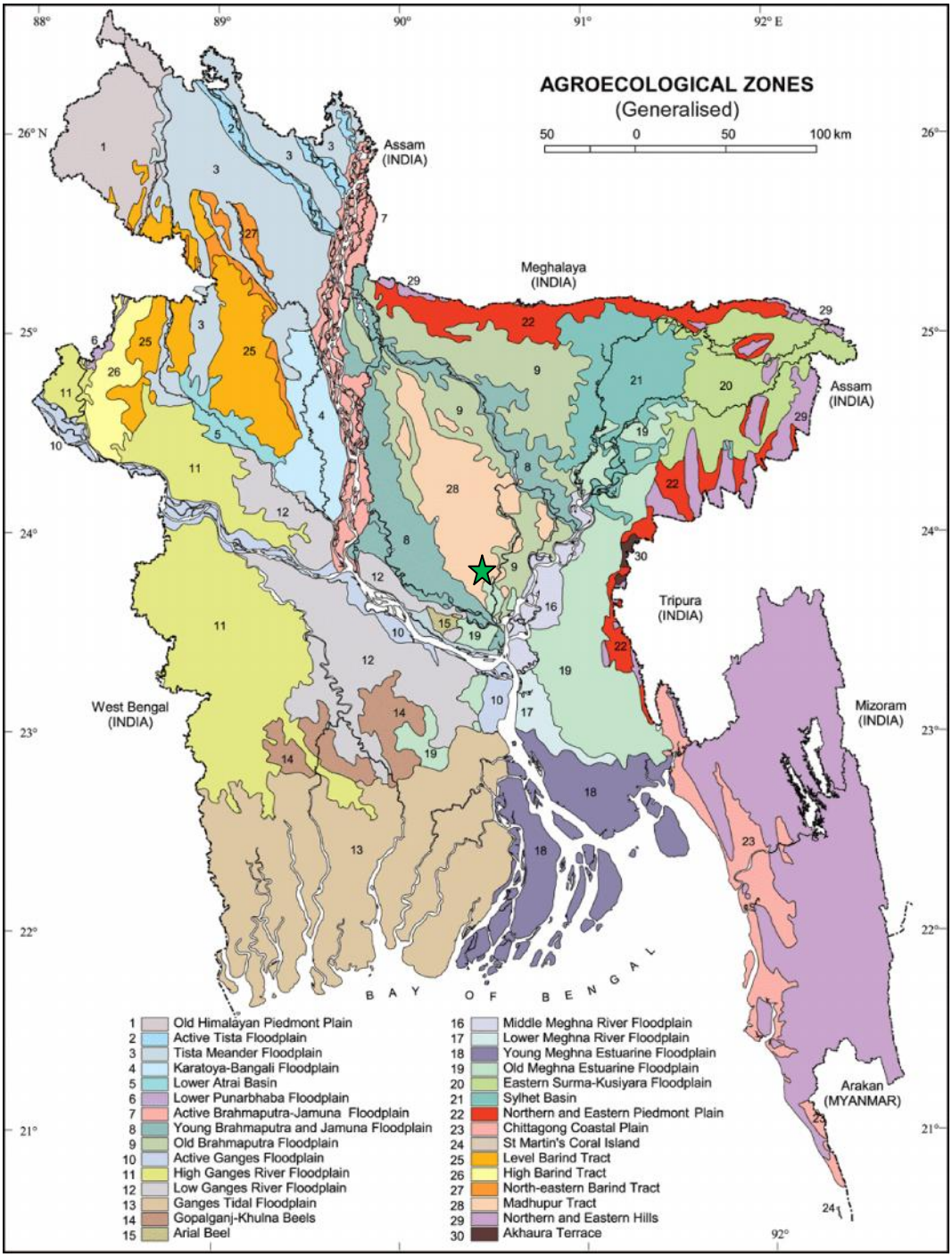
Appendix II. Principal component score 1 & 2

No. of genotype	PCA 1	PCA 2
1	-19.634	-4.013
2	-20.593	-9.146
3	1.174	-3.394
4	-28.577	-6.224
5	13.435	10.878
6	-9.740	3.922
7	-6.967	-0.605
8	-3.389	-2.387
9	-12.050	7.857
10	-15.572	5.498
11	-12.560	5.724
12	-28.345	3.961
13	6.548	2.929
14	-13.835	15.410
15	14.762	-6.496
16	-4.387	8.737
17	-5.950	5.350
18	-10.787	-4.259
19	15.930	4.675
20	4.959	-4.017
21	-14.187	-4.285
22	-5.678	1.242
23	2.017	6.343
24	8.595	5.268
25	23.583	-4.244
26	16.097	0.284
27	-4.743	2.479
28	1.245	2.379
29	-1.690	-1.348
30	17.812	3.674
31	18.001	3.075
32	7.548	-4.001
33	7.247	-0.237
34	25.178	-4.495
35	20.873	-10.053

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

No.of genotype	PCA 1	PCA 2
36	17.781	2.980
37	9.173	0.337
38	-9.015	4.421
39	4.191	2.900
40	-10.511	-6.167
41	13.017	0.321
42	-27.312	-2.638
43	-23.736	9.991
44	6.657	-8.587
45	-16.039	-3.643
46	-0.138	7.332
47	-18.253	-5.269
48	-17.557	-5.470
49	14.692	0.390
50	26.001	5.907
51	26.903	-0.098
52	-19.545	-11.818
53	-1.672	3.633
54	-37.504	-2.846
55	2.594	-1.251
56	15.970	-9.020
57	16.132	3.951
58	9.862	-2.756
59	0.675	-5.505
60	12.267	5.091
61	6.311	-1.361
62	21.938	-8.553
63	1.959	1.467
64	-15.490	6.443
65	13.421	-5.013
66	10.257	-6.720
67	-2.972	5.704
68	-25.173	-4.403
69	11.906	4.049
70	-3.111	-4.277

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-Bangla Agricultural University, Dhaka.

Appendix V. Monthly average temperature, relative humidity and total rainfall and Sunshine of the experimental site during the period from November 2016 to February 2017

Month	Air temperature (^{0}C)		Relative Humidity (%)	Rainfall (mm) total	Sunshine (Hr)
November 2016	35.8	17.0	76	225	5.9
December 2016	33.3	17.3	70	0	7.8
January 2017	28.0	12.0	80	1	3.7
February 2017	27.1	12.1	71	2	5.6

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