GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS IN F_4 GENERATION OF *Brassica napus* L.

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GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS IN F_4 GENERATION OF *Brassica napus* L.

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CERTIFICATE

This is to certify that thesis entitled, ***"Genetic variability, correlation and path analysis in F_4 generation of Brassica napus L."*** *submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of* ***MASTER OF SCIENCE in GENETICS AND PLANT BREEDING,*** *embodies the result of a piece of bona fide research work carried out by* ***SHARMIN SULTANA****, Registration No.* ***10-04013*** *under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

Dated: December, 2015
Place: Dhaka, Bangladesh

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DEDICATED

TO

MY BELOVED PARENTS

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ABSTRACT

A huge part of Bangladeshi economy is spent on importing edible oil every year to meet its own requirements. The need is to enhance and improve the production of the local cultivars and for that purpose the genetic diversity of the local cultivars must be fully explored. Sixty two F_4 genotypes of *Brassica napus* L. were evaluated based on randomized complete block design with three replications at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, to study the variability, correlation, path analysis and genetic diversity during November 2015 to February 2016 growing seasons. The genotypes were found significantly variable for most of the characters. Comparatively phenotypic variances were higher than the genotypic variances for most of the character studied. The high GCV value was observed for number of secondary branches per plant (42.31). Number of secondary branches (98.70) exhibited the highest value of heritability followed by seed yield per plant (98.03) while days to maturity (88.02) exhibited the lowest value of heritability. The significant positive correlation with seed yield per plant were found with all most all the characters except days to 50% flowering (0.033) and days to maturity (-0.096). Path co-efficient analysis revealed that days to 50% flowering, number of secondary branch, number of siliqua per plant, number of seed per siliqua, and thousand seed weight had the positive direct effect on yield per plant whereas days to 80% maturity, plant height, number of primary branch and siliqua length had the negative direct effect on yield per plant. On the basis of cluster analysis, all the genotypes were classified in five clusters. The highest inter cluster distance was observed between cluster I and IV (10.309). The lowest inter-cluster distance (3.513) was observed between the cluster III and IV. Considering group distance and other agronomic performance genotypes G3, G4, G24, G35, G51 and G55 might be suggested for future breeding program.

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SOME COMMONLY USED ABBREVIATIONS

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

CHAPTER I

INTRODUCTION

The genus *Brassica* L. holds the most economically valuable position in the tribe Brassiceae, which is a part of family Brassicaceae. This genus consists of a versatile batch of species that includes major oilseed crops and vegetables. There are different species in *Brassica* family i.e., turnip, cauliflower, broccoli, brusssels sprouts, cabbage, weeds and various mustards which are so much important due to their presence in different food, feed and edible oil etc.

Brassicaceae family comprises of 338 genera and 3709 species. The genus is remarkable for containing more important agricultural and horticultural crops than any other genus. Most are annual or biennial, but some are small shrubs. Due to their agricultural importance, Brassica plants have been the subject of much scientific interest (Bilal *et al*., 2015). Six economically valuable species are comprises in this genus with huge genetic and morphological variation and is cultivated in all over the world. Among these, three species are diploid (*Brassica oleracea*, 2n = 18; *Brassica rapa*, 2n = 20; *Brassica nigra*, 2n = 16), and three are amphidiploid (*Brassica napus*, 2n = 38; *Brassica juncea*, 2n = 36; *Brassica carinata*, 2n = 34). Rapeseed-mustard (*Brassica napus, Brassica campestris and Brassica juncea*) are grown all over the world as an important source of edible oil as described by the Triangle of U theory (Abideen *et al*., 2013).

Brassica napus L. also known as rapeseed, oilseed rape and canola, is the best one with respect of oil production. Rape seed originated in either the Mediterranean area or Northern Europe. Oilseed rape (*Brassica napus L.)* is the second most important oilseed crop in the international oilseed market following soybean (Sharafi *et al*., 2015). The seeds of modern varieties typically contain 40% to 45% oil. Despite of oil, it also hold 18 to 22 percent proteins which consist of different protein units like cystine, methionine and lysine. In cereal the amount of these amino acids is too much low so *Brassica napus* L. is the alternate source to get these proteins (Khan, 2014).

Rapeseed (mustards) is the second largest oilseed crop in the world providing 13% of the world's edible oil after soybean. During 2014, rapeseed/ mustard were globally grown on area of 36.5 million hectare with the total production of 72.7 million metric tons having average yield of 1991.0 kg ha-1 (FAO Statistics, 2014).

It is used as a condiment, salad, green, organic manure and fodder crop and as a leaf and stem vegetable in various mustard growing countries of the world. Rapeseed is grown for the production of animal feed, vegetable oil for human consumption, and biodiesel. Brassica vegetables are full of indole-3-carbinol, a compound which enhances DNA repair in cells and tissues and appears to block the growth regarding cancer tissues.

It is the most important oilseed crop in Bangladesh and it occupies the 1st position in respect of area and production among the oil crops grown in Bangladesh. In Bangladesh, 252238.13 ha of land was under rapeseed cultivation during 2014-15 which produced about 246494 tons of seed and average yield was 0.977 ton per ha (BBS, 2015a). Bangladesh has been facing acute shortage of edible oil for the last several decades. Our internal production can meet only about 21% of our consumption. The rest 79 % is met from the import (BBS, 2015a). The major reasons for such poor yield in Bangladesh may be attributed due to pressure of other crops, lack of improved varieties and poor management practices.

In spite of the large benefits and as a good source of vegetable oil it is used in minute amounts because it contains very high amount of erucic acid and glucosinolates which cause harm to the cardiac muscle and make the animal feed weaker and innutritious. For improving seeds yield and adaptability of rapeseed and other *Brassica* species, important breeding strategies are; understand and utilization of genetic, physiological and morphological basis of yield linked traits in different environmental conditions.

Due to its wide acclimatization to the many regions of the world, the breeders mostly are trying to improve its cultivars and production as compared to other oily crops. Seed yield is a complex character that can be determined by several components reflective positive or negative effects upon this trait, whereas it is important to examine the contribution of each of the various components in order to give more attention to those having the greatest influence on seed.

Success of any crop improvement depends upon the presence of substantial amount of genetic variability, heritability, as well as genetic gain in selection. The potential of a crop to favorably respond to breeding/selection and bioengineering programs depends upon nature and magnitude of genetic variability (Shaukat *et al*., 2015).

Generally, correlation coefficients show relationships among independent characteristics and the degree of linear relation between these characteristics. For plant breeders it is thus essential to learn the relationships among pairs of characters in order to make a decision on the proper selection criteria for a breeding program. Information about genetic variability gives a dependable tool to the breeder for improvement in crops. Higher genetic variability and correlation of yield with yield components are important requirements of breeders who wish to improve production and quality of *Brassica* (Abbas *et al.*, 2013).

Therefore, the path coefficient analysis has been used by many researchers for a more and complete determination of impact of independent variable on dependent one. The path coefficient analysis helps the breeder(s) to explain direct and indirect effects and hence has extensively been used in breeding work in different crop species by various researchers (Ali *et al*., 2003).

Rapeseed is an important oil seed crop. Hence, a thorough study of the genetic mechanism of the plant characteristics is required. Considering the importance of edible oil in country, an experiment was carried out with following objectives:

Objectives:

1. To study the variability in F_4 segregating generations generated through intergenotypic crosses to select the best promising lines,
2. To find out the relationship among the different traits and their contribution to the yield,
3. To assess genetic diversity among the genotypes and
4. To select promising genotypes considering early maturity, high yielding plants.

CHAPTER II

REVIEW OF LITERATURE

Brassica napus L. is considered second most important protein food resource throughout the globe after cereals. *Brassica* is grown throughout the country as a single or in combination with other crops like wheat, chickpea, etc in both irrigated and unirrigated regions of the country. It is the order of the day to take better steps for production and quality improvement of our local cultivars. In that respect so many strategies are applied for the enhancement of quality and yield of different canola varieties and cultivars to gain improved production. Due to application of different techniques in breeding process remarkable improvement has been brought in both productivity and quality of canola oil for using it in human diet. A large number of literatures are available on variability, genetic diversity, correlation and path analysis of yield and yield contributing characters of *Brassica* grown under a particular environment. An attempt has been made here to summarize the findings of this study relevant to the present investigation. The whole review has been divided into following sections, namely –

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

2.1 Genetic variability, heritability and genetic advance

Information about genetic variability gives a dependable tool to the breeder for improvement in crops. Higher genetic variability and correlation of yield with yield components are serious requirements of breeders who wish to improve production and quality of *Brassica*. Genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another. Variability is different from genetic diversity, which is the amount of variation seen in a particular population.

Large numbers of literatures concerning the variability in the *Brassica spp*. are available. These literatures are outlined here.

Bilal *et al*. (2015); evaluated 23 genotypes of *Brassica napus*. The study was undertaken to evaluate some indigenous rapeseed genotypes for adaptability and yield traits in the agro-climatic condition of Mansehra. These genotypes were evaluated in randomized complete block design with three replications. Heritabilities (broad sense) were moderate to high in magnitude for all traits. 1000-seed weight exhibited significant ($p \leq 0.01$) differences validating the presence of genetic variation among the tested accessions. Greater variability among the accessions for 1000-seed weight was observed.

21 rapeseed (*Brassica napus* L.) genotypes which were selected based on diversity of agronomic characters. The genotypes were evaluated based on randomized complete block design with three replications. Rameeh (2015) reported that Broad sense heritability estimates varied from 0.18 to 0.98 for pods length and days to end of flowering after. High broad sense heritability was determined for phenological traits, plant height and seed yield demonstrating selection gain for improving these traits will be high. Pods on main axis and pods per plant had high value of genetic coefficient of variation.

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

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

An experiment was conducted by Helal *et al*. (2014) to study genetic variability, correlation of yield and yield contributing characters and coefficient of variance in rapeseed or mustard. The results revealed that varieties produced the highest seed yields and 15% variation at genotypic and phenotypic level.

The material under study consisted of 28 rapeseed (*B. napus* L.) genotypes which were selected based on different agronomic characters. Broad sense heritability estimates ranged from 0.12 to 0.98 for plant height and days to flowering, respectively. Genetic coefficient of variation, an indicator of the genetic diversity of the genotypes, varied from 18.7 to 26.8 for days to maturity and seed yield, respectively. (Rameeh, 2014).

Muhammad *et al*. (2014); evaluated F_2 populations of *Brassica napus* L. to determine combining ability and heritability for important traits. Both GCA and SCA effects were highly significant ($P \leq 0.01$). Analysis of variance revealed significant ($P \leq 0.01$) differences for plant height, main raceme length, pod length, while significant ($P \leq 0.05$) differences were observed for days to 50% flowering, main raceme length. Broad sense heritability recorded was 0.26, 0.52, 0.65 and 0.73 for days to 50% flowering, main raceme length, plant height and pod length respectively.

Abideen *et al*. (2013); evaluated eight *Brassica napus* L. genotypes to find out the variability and association in these different genotypes. For plant height of these genotypes the differences found were highly significant ($P<0.01$). The differences found among the genotypes for primary branches per plant and pod per plant were non-significant ($P> 0.05$), while for pod per siliqua, pod length, seed yield per plant, 1000-seed weight and seeds per pod highly significant differences were found.

Khan *et al*. (2013); evaluated 20 *Brassica napus* L. accessions with one check cultivar to find out the heritability and heritable potential of these germplasm for yield and its related components. For all the parameter highly significant differences ($P<0.01$) were recorded. For all the parameters they found higher level of broad sense heritability. They inferred from their study that all these parameters were more under control of genetic differences found in these genotypes than environmental differences.

Nasim *et al*. (2013); evaluated 10 *Brassica napus* L. cultivars through agro-morphological parameters to study the genetic differences, inter relationships and the

rate of heritability in these genotypes. For morphological parameters of 1000-seed weight, days to half flowering, days to full flowering, siliqua width, siliqua length, seed per siliqua and plant height they found highly significant differences while for main raceme length, siliquae on main raceme and primary branches per plant, they found non-significant differences. Similarly for flower initiation, fifty percent flowering, complete flowering, plant height, seeds per siliqua and 1000-seed weight they found high heritability and high heritable advances. High heritability (92.48%) with moderate genetic advance (18.87%) was also found by Saifullah (2010).

Rameeh (2013), characterized two genotypes and twenty two advanced line of *Brassica napus* L. in RCBD (randomized complete block design) with 3 replications. He observed that the range of heritability in broad sense for the parameters of siliquae per plant and days to flowering were in the range of 21 percent to 94 percent, correspondingly.

Belete *et al*. (2012); evaluated 5 *Brassica carinata* L. They found for all the parameters apart from two i.e., plant height and seed yield significant differences amongst these genotypes, for the traits of days to maturity and plant height they found the lowest phenotypic coefficient of variation and genotypic coefficient of variation which were 2.0 and 1.9 percent for days to maturity and 1.2 and 0.7 percent for plant height, respectively. The heritability values of 99.8 percent were recorded for oil content which was the top most of all and the second highest heritability value of 96.5 percent was found for days to flowering. While the lowest value found for plant height which was 36.0 percent due to greater ecological effect on this trait.

Zare and Sharafzadeh (2012), evaluated 8 *Brassica napus* L. genotypes through agro-morphological traits to investigate the differences, heritability and correlation among these genotypes for the traits of seed yield and related. Apart from siliqua length and seeds per siliqua, they found significant genetic differences for the traits of seed yield and related traits. Very high heritability in broad sense was found for days to flowering which was 93.3 percent and the lowest of 14.3 percent for siliqua length, while for the rest of parameters they found high heritability. Saifullah (2010) reported high heritability and moderate genetic advance for plant height.

Rameeh (2011), evaluated 36 *Brassica napus* L. cultivars to determine the associations for yield components in these genotypes. The broad sense heritability

was in the range of 0.42 and 0.81 percent which were the heritability values respectively for 1000-seed weight and pods per plant. Similarly morphological parameters of pods main per raceme, seed per pod and pods per plant were highly heritable with heritability values of seventy percent, seventy seven percent and eighty one percent, correspondingly.

Afrin *et al*. (2011); reported that the number of primary branches per plant, number of secondary branches per plant, siliqua length, number of seeds per siliqua, number of siliqua per plant, 1000-seed weight and seed yield per plant showed moderate broad base heritability while plant height exhibited the highest heritability.

Three rapeseed varieties (Foseto, Option500 and Goliath) including the offspring of their F_2 and F_3 generations were planted for two years at complete randomized block design with three replications at experimental field of Rice and Citrus Research Institute, University of Agricultural Science and Natural Resources of Sari, Iran. The results indicated that all traits except date of maturity and number of seed per pod were significant at 1% probability. Also the estimation of coefficient of genotypic variation (GCV) showed less than the estimate of coefficient phenotypic variation (PCV). GCV values for number of pod per plant (16.93 and 23.57 in F_2 and F_3 generations, respectively) and seed yield (21.69 and 26.60 in F_2 and F_3 generations, respectively) was high, but for some traits were negligible. (Sadat *et al*., 2010).

An experiment was conducted by Aytac and Kinaci (2009) with 10 winter rapeseed genotypes for variation, genetic and phenotypic correlations and broad sense heritability for seed yield, yield and quality characters for 2 years. They observed maximum broad sense heritability, get genetic advance for seed yield.

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

Aytac *et al.* (2008); investigated rapeseed genotypes and reported that highest genotypic and phenotypic variances for seed yield per plant followed by seed yield and high heritability of seed yield per plant, pods per main stem coupled with high

genetic advance revealed that additive gene effects are important in determining these characters and could be enhanced through mass selection.

Basalma (2008), evaluated 25 winter rapeseed genotypes for correlation and path analysis. Positively high correlation were found ($P<0.01$) among the parameters of branches per plant, siliquae per main raceme and for plant height in both years. The correlation of plant height was negative with seed yield, 1000-seed weight and for the trait of oil ratio in the first year of his study. He found from the judgment of seed and oil yield on other various yield constituent that oil contents are affected directly by seed yield.

Hosen (2008), studied five parental genotype of *Brassica rapa* and their ten F_2 progenies including reciprocals. They reported that large numbers of variations present among all the genotypes used in the experiment. The plant height, days to 50% flowering, and number of siliquae per plant showed high heritability with high genetic advance and genetic advance in percentage of mean.

Mahmud (2008), evaluated 58 genotypes of *Brassica rapa* to study inter-genotypic variability. Significant variation was noticed 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 procured for days to 50% flowering, seed per siliqua and siliqua length.

An experiment was conducted by Ali *et al*. (2003) with 25 *Brassica napus* genotypes to study and find out the connection in yield components and how to increase yield in these genotypes. They found significant differences ($P<0.01$) for different parameters under study in these cultivars. The highest phenotypic and genotypic differences among the studied parameters were observed for siliquae per plant and on the second position was plant height. While seed yield per plant and siliquae per plant, correspondingly were the highest in phenotypic and genotypic coefficients of variability. They found highest (0.903) heritability value in broad sense for the parameter of days to maturity and 0.662 for flower duration, 0.548 for seed weight and 0.477 for seed yield.

Ali *et al*. (2002) observed high genotypic and phenotypic variances for plant height in Indian mustard with high estimates of coefficient of variability for seed yield and seeds per pod. They also reported high genotypic and phenotypic variances for pods plant height, but highest genotypic and phenotypic coefficient of variability were obtained for seed weight and pods per plant. He also reported high heritability coupled with high genetic advance for seed weight and pods per plant.

Choudhary and Joshi (2001), evaluated genetic variation of some genotypes derivatives of *Brassica* inter-specific hybrids and found high genetic diversity for days to flowering, plant height, number of branch per plant, and 1000-seed weight. In a study, days to flowering and oil percent had the highest heritability while pods number per plant and defoliation had the least heritability.

Tyagi *et al.* (2001); studied different genotypes of *Brassica* species and reported that variation was the highest in parents and their hybrids for plant height. The seed yield per plant exhibited the highest co-efficient of variation (41.1%). Significant genetic variability was observed for this character by many workers like Malik *et al.* (1995), Kumar and Singh (1994) and Yadava *et al.* (1993) among different genotypes of *Brassica napus*, *Brassica rapa* and *Brassica juncea*.

Malik *et al.* (2000); conducted an experiment with different strains of *Brassica napus* and observed very high broad sense heritability (>90%) for number of primary branches per plant, days to 50% flowering and oil content. They also reported low heritability (50%) for plant height, number of siliqua per plant, number of seeds per siliqua and seed yield per plant. But high heritability for all these characters were found by Lodhi *et al.*, (1979) while working with 55 genotypes of *Brassica napus*, *Brassica rapa* and *Brassica juncea*.

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

According to Lekh *et al.* (1998) genotypic co-efficient of variation was the highest for secondary branches. High genotypic and phenotypic co-efficient of variation was recorded for days to 50% flowering among 10 genotypes for each of *Brassica*

campestris, *Brassica carinata* and *Brassica napus* and 24 genotypes of *Brassica juncea*.

Kumar and Singh (1994), reported that thousand seed weight is a very important character of rape seed 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.

Yadava *et al.* (1993); studied *Brassica campestris var. toria* using 8x8 diallel analysis (excluding reciprocals). They reported that both additive and dominance genetic components were important for seed yield and yield components and higher heritability for days to maturity and thousand seed weight.

Olsson (1990), reported that siliqua length is important character for the development of fruits in oil seed crops like mustard and rape seed. Peduncle, beak as well as siliqua length varies due to difference in genotypes. High genetic variability was found for this character.

179 genotypes of Indian mustard were studied by Singh *et al.* (1987) and found high heritability for seed yield per plant and oil content and the lowest heritability for number of primary branches per plant.

Varshney *et al.* (1986); observed high heritability and genetic advance for number of siliqua per plant in *Brassica rapa* and *Brassica juncea*, but they found high heritability and genetic advance for plant height in all the three species. Diwakar and Singh (1993) studied with segregating populations of yellow seeded Indian mustard (*Brassica juncea* L. Czern and Coss) and reported that high narrow sense heritability and genetic advance for days to flowering and plant height.

Katiyar *et al.* (1974); observed high genetic co-efficient of variation for days to first flowering, plant height (cm) and seed yield per plant (g) where as low values were observed for other characters like days to maturity and number of primary branches per plant, while observing on genetic variability and genetic advance of seed yield and its components in Indian mustard.

Yadava (1973), found 48.76% GCV value among 29 strains of *Brassica juncea*. While Singh *et al.* (1987) found GCV and PCV values of 44.04% and 46.9% in *Brassica juncea*.

2.2 Correlation among different characters

Correlation coefficient analysis helps to determine the nature and degree of relationship between any two measurable characters. It resolves the complex relations between the events into simple form of association. But measure of correlation does not consider dependence of one variable over the other. Analysis of correlation among different traits is important in breeding program. A good number of literatures are available on correlation among characters of *Brassica sp.* Some of these literatures are reviewed here:

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

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

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

Abideen *et al*. (2013); studied 8 genotypes like (G-1, G-2, G-3, G-4, G-5, G-6, G-7 and G-8) of *Brassica napus* and positive significant phenotypic correlation of plant

height with pods per main raceme (r = o.77) and pod length (r = 0.71) was recorded. Similarly significant positive phenotypic correlation of seed yield with pods per plant (r = 0.71) was also recorded.

Nasim *et al*. (2013); studied ten *Brassica napus* L. genotypes to determine correlation between various traits and observed that pod length was positive highly significantly ($p \leq 0.01$) and significantly ($p \leq 0.05$) correlated with 100-seed weight (0.59**) and pod width (0.37*) respectively. Pod width was revealed to have negative significant correlation with days to flowering inititaion (-0.40*) whereas positive significant correlations with100-seed weight (0.37*).

Khayat *et al.* (2012); assessed ten canola and reported that the association coefficients expounded that the parameters of total dry matter, harvest index, 1000-grain weight, number of seeds per siliqua, number of siliqua per plant, plant height, days required to maturity and blooming period have a positive and significant relationship with grain yield.

Rameeh (2012), studied 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 for these traits. The correlation between duration of flowering and pods per plant was less than the correlation of duration of flowering to other traits in different planting dates.

Rameeh (2011), evaluated 36 *Brassica napus* L. cultivars to determine the associations for yield components in these genotypes in RCBD experimental design which consisted of three replications. Siliquae per plant was significantly and highly correlated with seed yield with correlation value of 0.80.

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

Esmaeeli Azadgoleh *et al.* (2009); observed positively significant correlation of seed yield with number of pod per plant, number of pods in sub branches and number of seeds per pod.

10 rapeseed cultivars were evaluated by Aytaç and Kı nacı (2009) and they observed that plant height had positive genotypic and phenotypic correlations with pods per main stem, pod length, oil yield and protein yield. Number of pods per plant has positive genotypic and phenotypic correlation with oil yield, protein yield, pod length, plant height and branches per plant.

Basalma (2008), conducted an experiment with 25 winter oil seed rape cultivars to study the correlation. They observed high positive and statistically significant correlation between branches per plant, the number of pods on the main stem and plant height during two years. Plant height indicated negative correlation with seed yield, thousand seed weight and oil ratio.

An experiment was conducted with 40 oleiferous *Brassica* species by Rashid (2007) 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.

Jeromela *et al.* (2007); studied 30 rapeseed varieties and demonstrated that pods per plant have the highest correlation with seed yield.

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 were observed by Parveen (2007) while working with F_2 population of *Brassica rapa*.

Siddikee (2006), reported that yield per plant had the highest significant positive correlation with number of siliquae per plant while working with oleiferous *Brassica campestris L*.

Eight quantitative characters of *Brassica* species were evaluated by Mahak *et al.* (2004) to study the correlation among them. Seed yield per plant showed positive correlation with number of primary branches, length of main raceme, 1000-seed weight and oil content. Selection should be applied on these traits to improve seed

yield in Indian mustard. Afroz *et al.* (2004) also studied correlation and found seed yield per plant had significant and positive correlation with number of primary branches per plant and number of siliquae per plant.

Ali *et al*. (2003); carried out an experiment with 25 winter rapeseed and observed that positive flowering duration was significantly correlated (0.238) with seed yield. Seed yield per plant was negatively and non-significantly correlated with days to maturity and branches per plant. The seed weight of these genotypes was positively and significantly correlated with harvest index, flower duration and seed yield

Srivastava and Singh (2002), conducted an experiment with 24 strains of Indian mustard along with 2 varieties and evaluated correlation in Indian mustard [*Brassica juncea* L. Czern and Coss] for 10 characters. They found that number of primary branches per plant, number of secondary branches per plant, 1000 seed weight (g) and oil percent were positively associated with seed yield.

Correlation analysis of yield related traits of *Brassica napus* was studied by Malik *et al*. (2000) and reported that days to maturity showed insignificant correlation with seed yield at both genotypic and phenotypic levels. They also reported that number of branches per plant and number of siliquae per plant showed significant negative correlation with number of seeds per siliqua and 1000 seed weight.

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

Khulbe and Pant (1999), evaluated eight Indian mustard (*Brassica juncea*) parents and their 28 F_1 hybrids and reported that the number of siliqua per plant, length of siliqua, number of seeds per siliqua, thousand seed weight and harvest index were positively associated with seed yield.

Seven genotypes of *B. campestris* and standard cultivar of *B. napus* were evaluated by Masood *et al.* (1999) to study the correlation co-efficient and they observed that the number of siliquae per plant, number of seeds per siliqua and plant height was significantly positively correlated with seed yield.

An experiment was conducted with 8 Indian mustard (*Brassica juncea*) parents and their 28 F_1 hybrids to study correlation between seed yield and yield contributing characters by Thakaral *et al.* (1999). The data indicated that higher seed yield could be obtained by selecting for increased plant height.

Kumar *et al.* (1999); reported that 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. Gurdial and Hardip (1998) carried out an experiment with gobhi sarson (*B. nigra*) and reported that dwarf plant gave higher yield.

According to Tyagi *et al.* (1996) plant height, siliqua per plant, siliqua length, seed weight, and seeds per siliqua had positive and significant effects on seed yield per plant while working with six yield components in three cultivars of mustard.

Thirteen Indian mustard (*B. juncea*) were studied by Uddin *et al.* (1995) for correlation and reported that seed yield per plant had high positive and significant correlations with plant height and thousand seed weight, but high negative and significant correlations with seeds per siliqua at both genotypic and phenotypic levels.

Nasim *et al.* (1994); reported that 1000 seed weight was significantly and positively correlated with seed yield per plant and number of siliqua per plant but significantly and negatively correlated with siliqua length and number of seeds per siliqua while working with *B. rapa* to study correlation.

Ahmed (1993), conducted an experiment with 8 cv. of *Brassica campestris* and *Brassica juncea* for study of nature and degree of interrelationship among yield components and observed that siliqua length, number of siliqua per plant, number of seeds per siliqua and seed weight per siliqua were 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.

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

Chay and Thurling (1989), studied the inheritance of siliqua length among several lines of *Brassica napus* and reported that increased of siliqua length resulted an increased in the number of seeds per siliqua and thousand seed weight. The siliqua length was positively correlated with number of seeds per siliqua and thousand seed weight which was observed by Singh *et al.* (1987) in *B. rapa*, Chowdhury *et al.* (1987) and Lodhi *et al.* (1979) in *B. juncea*.

Singh *et al.* (1987); mentioned that number of primary branches per plant negatively correlated with siliqua length and 1000 seed weight, but positively correlated with number of siliqua per plant while working with *Brassica* species.

Srivastava *et al.* (1983); conducted an experiment with *Brassica juncea* to study the correlation. The number of primary branches per plant and secondary branches per plant, plant height and days to maturity showed significant positive association with the seed yield per plant. The number of primary branches showed positive and significant association with the number of secondary branches per plant, plant height and days to maturity. They also reported that plant height showed positive and significant correlation with the number of secondary branches and days to maturity. Shivahare *et al.*, (1975) also observed days to flowering were positively correlated with primary branches per plant and plant height.

Katiyar and Singh (1974), reported that increasing the number of branches is a means of increasing yield, since the number of primary and secondary branches have a significant positive correlation with seed yield.

2.3 Path co-efficient analysis.

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

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

Two canola cultivars were evaluated and found that negative indirect effect of plant height via number of seeds per fruits and 1000 seed weight could mask the positive direct effect of plant height on seed yield per plant and positive correlation between number of fruits per plant and seed yield despite the indirect effects of number of fruits per plant via number of seeds per fruit and 1000 seed weight. (Emrani *et al*., 2012).

Khayat *et al*. (2012); reported that the number of pods per plant had the highest direct effect on grain yield. In addition, total dry matter, 1000- grain weight, and flowering and days to maturity also had a high direct effect on grain yield.

Afrin *et al*. (2011); studied 22 advanced lines of *Brassica napus* and observed that days to 50% flowering had negative direct effect on seed yield per plant. The highest indirect positive effect was found via plant height followed by number of siliqua per plant. Plant height had direct positive effect on seed yield per plant. It had positive indirect effect on seed yield via days to maturity, number of seeds per siliqua, number of siliquae per plant and 1000-seed weight per plant.

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

Basalma (2008), reported that the direct effects of plant height, branches per plant, and number of seeds per pod and oil ratio were all negative and the effects of others characters were positive on seed yield.

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

Parveen (2007), reported that number of seeds per siliqua showed the highest direct effect on yield per plant while working with F_2 population of *Brassica rapa* to study the path analysis.

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

Ali *et al*. (2003); carried out an experiment with 25 winter rapeseed and observed that the direct effect of seeds per pod on plant yield was less but positive. Negative direct effects on plant yield were exhibited by days to maturity and branches per plant with values of -0.015 and -0.164, harvest index and seed weight were the only characteristics that exhibited the highest direct effect on yield per plant.

Srivastava and Singh (2002), conducted an experiment with Indian mustard (*B. juncea* L.) and 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. Results suggested that number of primary branches and 1000 seed weight were vital selection criteria for improvement in productivity of Indian mustard.

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

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

An experiment was conducted by Masood *et al.* (1999) with seven genotypes of *Brassica campestris* and standard cultivar of *Brassica napus* and observed that number of seeds per siliqua exerted the highest effect on seed yield.

Yadava *et al.* (1996); observed that the number of siliqua per plant had the highest positive direct effect on seed yield when they studied path co-efficient analysis of six yield components of 25 diverse varieties of Indian mustard.

Uddin *et al.* (1995); conducted an experiment with 13 Indian mustard (*B. juncea*) to study the path analysis and observed that seeds per siliqua and thousand seed weight had high positive direct effect on seed yield per plant. Chauhan and Singh (1995) observed that plant height, siliqua per plant and seeds per siliqua had high positive direct effect on seed yield.

The plant height had the highest positive direct effect on seed yield per plant in *B. juncea* was observed by Dhillon *et al.* (1990), but Singh *et al.* (1978) found negative direct effect of the trait on seed yield.

Han (1990), studied *B. napus* and observed negative direct effect of number of siliquae per plant, siliqua length and positive direct effect of seeds per siliqua and plant height on seed yield. But many scientists like Chen *et al.* (1983) in *B. napus* and Srivastava *et al.* (1983) in *B. juncea* observed that plant height, days to maturity, siliqua per plant, seeds per siliqua and thousand seed weight had positive direct and indirect effect on seed yield.

Siliqua length had the highest positive direct effect and number of primary branches per plant had the highest negative direct effect on seed yield were observed by Chowdhury *et al.* (1987) while working with 42 strains of mustard.

Varshney (1986), conducted an experiment with several strains of *B. rapa* and observed that plant height, siliqua per plant and thousand seed weight had the negative direct effect on yield.

Kumar *et al.* (1984); worked with *B. juncea* and observed that days to flowering via plant height and siliqua length had negative indirect effect, but negative direct effect of these traits was observed by Singh *et al.* (1978).

2.4 Genetic Diversity analysis

Diversity is the base of improvement, if there were no diversity in nature no improvement would possible. But during continuous selection process for better quality and productivity, the gene pool of the selected final varieties has been made narrow down due to eliminating of genes for undesirable traits for example, declining amount of erucic acid in oil and glucosinolates in seeds. Due to which the differences

at genetic level in *Brassica napus* L. has been made very limited which were so much important for many other promising characters

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

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

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

An experiment was conducted with 45 Indian mustard genotypes of different origin from India for evaluated for the extent of diversity for utilization in breeding program. To measure the genetic diversity among the genotypes D^2 analysis was used. The genotypes were grouped in eight clusters using Tocher's method. Intra-cluster distance was maximum for cluster VI followed by cluster III. The maximum inter-cluster distance was found between cluster II and III indicating high genetic divergence among genotypes of these groups. The maximum contribution towards the divergence was accountable to 1000-grain weight (46.87%) followed by seed yield

per plant (20.91%) and number of siliqua on main raceme (8.38%) (Pandey *et al*., 2013).

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

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

Mahmud *et al.* (2011); evaluated fifty five advanced line of *Brassica rapa* along with three commercially cultivated varieties as check to study the genetic divergence through Mahalanobis D^2 statistics in respect of 10 different morphological characters. As per principal component analysis (PCA), D^2 and cluster analysis, the genotypes were grouped into six different clusters. Cluster II and cluster III had the maximum (13) and cluster IV had the minimum (6) number of genotypes. The inter cluster distance in most of the cases was larger than the intra cluster distance. The highest inter cluster distance was observed between cluster III and VI (19.52) and that of the lowest between cluster II and IV (3.02). Highest intra-cluster distance was observed in cluster VI (0.67). Plant height, number of secondary branches per plant and seeds per siliqua contributed maximum towards the total divergence.

Yousuf *et al*. (2011); evaluated 114 genotypes of *Brassica campestris* L. through cluster and principal component analysis. From the result obtained from the study carried in 2005 and 2006 through cluster analysis they inferred that a lot of differences were found among the genotypes due to variations found in the morphological and seed quality traits of the mentioned genotypes. They found that

from the study carried out in 2005 it was found through principal component analysis that only 7 out of twenty one principal components with eigen value higher than 1 contributed 74.09 percent of the whole variation among these genotypes and in 2006 it was found that 5 out of twenty one principal components with eigenvalue higher than 1 contribute 66.08 percent.

A field experiment was conducted comprising eighteen advanced lines of mustard in a randomized block design with three replications for estimation of divergence among advanced lines of mustard. The genotypes were grouped into four clusters. Cluster I contained the highest number of genotypes (6) and the cluster III contained the lowest (3). The highest inter cluster distance was observed between the cluster III and II followed by III and I and the lowest between cluster IV and III. Days to 50% flowering (81.94%), days to maturity (8.24%), plant height (5.82%), branches per plant (1.91%) and siliquae per plant (1.17%) contributed maximum towards the total divergence which suggested that these characters were highly responsible for genetic divergence in the present materials. The genotypes from cluster I had dwarf plant along with earliness in days to 50% flowering, days to maturity and maximum number of primary branches per plant (Zaman *et al*., 2010).

Different multivariate analysis techniques were used by Afrin (2009) to classify 22 *Brassica napus* genotypes. The genotypes were grouped into four clusters. The highest inter-cluster distance was observed between clusters II and IV whereas the maximum intra-cluster distance was found in cluster II. Therefore, the genotypes belonging to cluster I and cluster II, cluster II and cluster III and cluster III and cluster IV have been selected for future hybridization program. The PCA gives eigen values of principal component axes of coordination of genotypes with the first three axes accounted for 68.927% of total variation whereas the first principal components accounted for 28.695%.

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

divergence and cluster IV and these genotypes were suggested for use in heterosis breeding.

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

Begum *et al.* (2007); evaluated 36 genotypes of linseed through D^2 analysis and genotypes were grouped into five distinct clusters. The cluster I included 11 genotypes that had medium mean values for 1000-seed weight (g) and seed yield/plant. The cluster II contained 6 genotypes, which had the highest mean values for number of seeds/capsule, number of branches/plant and seed yield/plant. They also showed the highest mean value for plant height. It is also related with medium mean values for rest of the characters. The cluster IV included 3 genotypes having the highest mean values for number of capsules/plant and days to maturity. The cluster V included single genotype, which had the lowest mean values for days to maturity and plant height. The highest inter cluster distance was observed among clusters V, IV and II, while the lowest between III and I.

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

An experiment was conducted by Nath *et al.* (2003) with varieties, inter-variety and interspecies hybrids of *Brassica* oil crop to determine genetic divergence. The diversity study indicated that parent, inter-variety and inter-species hybrids almost clearly form five groups indicating that they are divergent. Based on the study on genetic divergence of the *Brassica*, the varieties having the achievement and located in the distant clusters could be utilized for hybridization program to develop desired high yielding varieties.

Choudhary and Joshi (2001), studied different *Brassica* species to determine the genetic distances among them revealed that *B. tournefortii* had maximum diversity with *B. juncea* followed by *B. napus*, *B. rapa* var. toria and *B. rapa* var. yellow sarson. The clustering pattern showed that many derivatives of the cross fell into the similar cluster but in many cases in spite of common ancestry many descendants of the cross spread over different clusters. The characters, namely, plant height, secondary branches per plant, days to flowering and 1000-seed weight was contributed maximum towards genetic divergence.

Islam and Islam (2000), evaluated 42 genotypes of rapeseed and mustard using D^2 analysis to study the genetic divergence among them. They found four clusters. The inter-cluster distances were larger than the intra-cluster distances. The characters contributed maximum in divergence analysis is days to 50% flowering, plant height, primary branches/plant and number of siliquae per plant.

Singh and Gupta (1984), used D^2 analysis to study genetic diversity based on 12 characters. Out of 31 genotypes, on the basis of stability, high yield and divergence six genotypes were found to be suitable for use in a breeding program.

Rawhat and Anad (1981), studied genetic divergence using Mahalanobis D^2 statistic with 27 strains of Indian brown mustard (*Brassica juncea* L. Czern and Coss) for seven characters related to yield and fitness using . The various strains were grouped in seven clusters on three diverse lines. Parallel variation was observed between clusters III, IV and VII on one line, and I, II and V on the other, with cluster VI diverging from the rest. The geographical diversity of strains was found not to be related with the genetic diversity. The maximum divergence characters were days to flowering, plant height and 1000-seed weight in that order.

CHAPTER III

MATERIALS AND METHODS

3.1 Experimental site

This part of the present research study was carried out in the experimental fields of Sher-e-Bangla Agricultural University, Dhaka–1207 during November 2015 to February 2016. The location of the experimental site was situated at 23^0 74' N latitude and 90^0 35' E longitudes with an elevation of 8.6 meter from the sea level. Photograph showing experimental sites (Appendix I).

3.2 Soil and Climate

The experimental site was situated in the subtropical zone. The soil of the experimental site belongs to Agro ecological region of "Madhupur Tract" (AEZ No. 28). The soil was clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH was 5.47 to 5.63 and organic carbon content was 0.82% (Appendix II). The records of air temperature, humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix III).

3.3 Experimental materials

The healthy seeds of sixty two F_4 of *Brassica napus* L. collected from the Dept. of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, which were used as experimental materials. The materials used in that experiment is shown in Table 1.

3.4 Methods

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

3.4.1 Land preparation

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

Table 1. Materials used for the experiment

Genotype	F_4 Population	Source
G1	Nap- 9908 × Bs- 13	SAU
G2	Nap- 179 × Nap- 2001	SAU
G3	Nap- 248 × Nap- 159	SAU
G4	Nap- 2037 × Nap- 2057	SAU
G5	Nap- 94006 × Bs- 7	SAU
G6	Nap- 2012 × Nap- 2013	SAU
G7	Nap- 94006 × Nap- 2013	SAU
G8	Nap- 248 × Nap- 206	SAU
G9	Nap- 206 × Nap- 2012	SAU
G10	Nap- 2037 × Nap- 2022	SAU
G11	Nap- 9908 × Nap- 94006	SAU
G12	Nap- 9908 × Nap- 2037	SAU
G13	Nap- 2037 × Nap- 248	SAU
G14	Nap- 206 × Nap- 2013	SAU
G15	Bs- 7 × Nap- 206	SAU
G16	Nap- 2001 × Nap- 2022	SAU
G17	Nap- 94006 × Bs- 13	SAU
G18	Nap- 2037 × Nap- 2012	SAU
G19	Nap- 2037 × Nap- 206	SAU
G20	Nap- 9908 × Nap- 2022	SAU
G21	Bs- 13 × Nap- 2022	SAU
G22	Nap- 179 × Nap- 206	SAU
G23	Nap- 9908 × Nap- 206	SAU
G24	Nap- 9908 × Nap- 248	SAU
G25	Nap- 2012 × Nap- 2022	SAU
G26	Nap- 248 × Nap- 2022	SAU
G27	Bs- 13 × Nap- 2013	SAU
G28	Nap- 9908 × Nap- 2001	SAU
G29	Nap- 2037 × Bs- 13	SAU
G30	Bs- 13× Nap- 206	SAU
G31	Nap- 9908 × Nap- 2013	SAU

Table 1. Continued

G32	Nap- 248 ✕ Nap- 2013	SAU
G33	Nap- 179 ✕ Nap- 2057	SAU
G34	Nap- 179 ✕ Nap- 2022	SAU
G35	Nap- 2037 ✕ Nap- 2013	SAU
G36	Nap- 248 ✕ Nap- 2057	SAU
G37	Nap- 94006 ✕ Nap- 2057	SAU
G38	Bs- 7 ✕ Nap- 2013	SAU
G39	Nap- 2057 ✕ Nap- 2001	SAU
G40	Bs- 13 ✕ Nap- 2001	SAU
G41	Nap- 94006 ✕ Nap- 2001	SAU
G42	Bs- 13 ✕ Nap- 2057	SAU
G43	Nap- 179 ✕ Nap- 2012	SAU
G44	Nap- 2001 ✕ Nap- 179	SAU
G45	BS- 13 ✕ Nap- 179	SAU
G46	BS- 7 ✕ Nap- 2057	SAU
G47	Nap- 206 ✕ Nap- 2022	SAU
G48	Nap- 206 ✕ Nap- 2057	SAU
G49	Nap- 9908 ✕ Nap- 2012	SAU
G50	Nap- 179 ✕ Nap- 2013	SAU
G51	Nap- 248 ✕ Nap- 2012	SAU
G52	Nap- 2057 ✕ Nap- 248	SAU
G53	BS- 7 ✕ Nap- 2013	SAU
G54	Nap- 94006 ✕ Nap- 179	SAU
G55	Nap- 2001 ✕ Nap- 2013	SAU
G56	Nap- 94006 ✕ Nap- 2022	SAU
G57	Nap- 2057 ✕ Nap- 2012	SAU
G58	Nap- 2001 ✕ Nap- 248	SAU
G59	Nap- 2057 ✕ Nap- 2022	SAU
G60	Nap- 94006 ✕ Nap- 2012	SAU
G61	Nap- 94006✕ Nap- 206	SAU
G62	Nap- 2001 ✕ Nap- 206	SAU

3.4.2 Application of manure and fertilizer

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

3.4.3 Experimental design and layout

Field lay out was done after final land preparation. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The total area of the experiment was $56m \times 14m = 784m^2$. Each replication size was $56m \times 3.5m$, and the distance between replication to replication was 1m. The spacing between lines to line was 30cm. Seeds were sown in lines in the experimental plots on 14 November, 2015. The seeds were placed at about 1.5 cm depth in the soil. After sowing the seeds were covered with soil carefully so that no clods were on the seeds.

3.4.4 Intercultural operations

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

3.4.5 Crop harvesting

Harvesting was done from about 90 days after sowing (DAS) depending upon the maturity. When 80% of the plants showed symptoms of maturity i.e. straw color of

siliqua, leaves, stems desirable seed color in the mature siliqua, the crop was assessed to attain maturity. Fifteen plants were selected at random F_4 progenies in each replication. The plants were harvested by uprooting and then they were tagged properly. Data were recorded on different parameters from these plants. A pictorial view of experimental field at flowering and harvesting stage is presented in Plate 1 & 2.

3.4.6 Data collection

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

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

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

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

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

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

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

vii. **Siliquae length (cm):** This measurement was taken in centimeter (cm) from the base to the tip of a siliqua of the five representative siliquae.

Plate 1: Photograph showing the experimental field at SAU at flowering stage

Plate 2: Photograph showing the experimental field at SAU at harvesting stage

Plate 3: Photograph showing observation and data collection

viii. **Number of seeds per siliqua:** Well filled seeds were counted from five siliquae which was considered as the number of seeds per siliqua.

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

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

3.5 Statistical analysis

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

i) Estimation of genotypic and phenotypic variances:

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

a. **Genotypic variance,** $\delta^2 g = \frac{MSG - MSE}{r}$

Where, MSG = Mean sum of square for genotypes

MSE = Mean sum of square for error, and

r = Number of replication

b. **Phenotypic variance**, Where, $\delta^2 p = \delta^2 g + \delta^2 e$

Where, $\delta^2 g$ = Genotypic variance,

$\delta^2 e$ = Environmental variance = Mean square of error

ii) Estimation of genotypic and phenotypic co-efficient of variation:

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

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

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

Where, GCV = Genotypic co-efficient of variation

PCV = Phenotypic co-efficient of variation

δ_g = Genotypic standard deviation

δ_p = Phenotypic standard deviation

$\bar{x}$ = Population mean

iii) Estimation of heritability:

Broad sense heritability was estimated by the formula suggested by Singh and Chaudhary (1985).

$$h^2_b(\%) = \frac{\delta^2_g}{\delta^2_p} \times 100$$

Where, h^2_b = Heritability in broad sense

δ^2_g = Genotypic variance

δ^2_p = Penotypic variance

iv) Estimation of genetic advance:

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

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

Where, GA = Genetic advance

δ^2_g = Genotypic variance

δ^2_p = Phenotypic variance

δ_p = Phenotypic standard deviation

K = Selection differential which is equal to 2.06 at 5% selection intensity.

v) Estimation of genetic advance in percentage of mean

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

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

vi) Estimation of simple correlation co-efficient:

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

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

Where, $\sum$ = Summation

x and y are the two variables correlated

N = Number of observation

vii) Path co-efficient analysis:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

riy = Correlation of the character with yield.

viii) Estimation of Genetic Diversity

a. Principal Component Analysis (PCA)

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

b. Principal Coordinate Analysis (PCO)

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

c. Canonical Vector Analysis (CVA)

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

d. Average Intra-cluster Distances

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

e. Clustering

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

CHAPTER IV

RESULTS AND DISCUSSION

During the present study sixty two F_4 materials of *Brassica napus* L. genotypes were evaluated to determine the variability among these genotypes and also to study the correlation, path co-efficient for seed yield and different yield contributing characters and genetic diversity among them. All these accessions were grown in 2015-2016 in the field of Sher-e-Bangla Agricultural University. The data were recorded on different characters such as plant height (cm), no. of primary branches per plant, no. of secondary branches per plant, days to 50% flowering, no. of siliqua per plant, days to maturity, no. of seeds per siliqua, siliqua length (cm) thousand seed weight (g) and seed yield per plant (g). The data were statistically analyzed and thus obtained results are described below under the following heads:

- Variability study in *Brassica napus* L.
- Correlation coefficient of characters
- Path coefficient analysis
- Genetic diversity analysis

4.1 Variability study in *Brassica napus*

4.1.1 Variability among the sixty two F_4 materials for *Brassica napus*

Results of analysis of variance of the studied data on different yield components of sixty two F_4 materials of *Brassica napus* genotypes, values of mean, range, CV%, phenotypic variances, genotypic variances summarized in Table 2a and Table 2b showed the values of genetic advance, heritability for different yield related characters. Among the genotypes, almost all characters showed highly significant variation indicating wide scope of selection for these characters. This considerable variability provides a good opportunity for improving traits of interest in breeding programs.

Table 2a. Estimation of genetic parameters in ten characters of 62 genotypes in *Brassica napus* L.

Parameters	Min	Max	Mean	MS	CV(%)	$\sigma^2 g$	$\sigma^2 e$	$\sigma^2 P$
50F	27.00	44.00	36.25	53.25**	3.88	17.75	1.98	19.73
DM	75.00	91	81.70	59.22**	1.96	18.88	2.57	21.45
PH	88.83	120.53	103.12	198.93**	1.8	65.14	3.50	68.67
NPB	1.42	4.40	2.67	1.15**	3.7	0.38	0.01	0.39
NSB	0.90	5.77	2.06	2.28**	4.71	0.76	0.01	0.77
NSP	47.85	137.67	87.93	1436.44**	6.13	475.83	29.08	505.33
SL	6.37	8.70	7.61	1.05**	2.27	0.34	0.03	0.37
NSS	14.20	27.93	20.93	17.075**	2.87	5.57	0.36	5.93
TSW	2.91	4.12	3.41	0.216**	1.31	0.071	0..002	0.073
SYP	3.11	10.47	5.95	9.039**	4.1	2.99	0.06	3.05

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

50F = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), NPB=Number of Primary Branches per plant, NSB=Number of secondary branches per plant, NSP=Number of Siliqua per plant, NSS=Number of seed per silique, SL=Siliqua length, TSW = Thousand Seed Weight (g), SYP=Seed yield per plant, MS = mean sum of square, CV (%) = Coefficient of Variation, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance and σ^2 e = Environmental variance.

Table 2b. Estimation of genetic parameters in ten characters of 62 genotypes in *Brassica napus* L.

Parameters	GCV	ECV	PCV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
50F	11.62	3.88	12.25	89.96	8.19	22.59
DM	5.30	1.96	5.65	88.02	8.35	10.20
PH	7.82	1.8	8.04	94.85	16.11	15.62
NPB	23.09	3.7	23.39	97.43	1.25	46.82
NSB	42.31	4.71	42.59	98.70	1.78	86.41
NSP	24.80	6.13	25.04	94.16	43.39	51.08
SL	7.66	2.27	7.99	91.89	1.14	14.98
NSS	11.27	2.87	11.63	93.92	4.69	22.41
TSW	7.81	1.31	7.92	97.26	0.53	15.54
SYP	29.10	4.1	29.35	98.03	3.51	58.99

50F = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), NPB=Number of Primary Branches per plant, NSB=Number of secondery branches per plant, NSP=Number of Siliqua per plant, NSS=Number of seed per silique, SL=Siliqua length, TSW = Thousand Seed Weight (g), SYP=Seed yield per plant, GCV = Genotypic Coefficient of Variation, PCV = Phenotypic Coefficient of Variation and ECV = Environmental Coefficient of Variation.

4.1.1.1 Plant height (cm)

The final plant height reflects the growth behavior of a crop. Both genetic and environmental factors play a vital role in determining the plant height of a plant. Analysis of variance showed highly significant differences ($P \leq 0.01$) among all the genotypes for plant height (198.93) (Table 2a) which indicated genotypic differences present among the genotypes under the study. Data regarding plant height ranged from 88.83 to 120.53 cm with the mean value of 103.12 cm. Minimum plant height (88.83 cm) were recorded for genotype G19 (Nap-2037 × Nap-206) (Plate 4) whereas, maximum plant height was observed in G4 (Nap-2037 × Nap-2057) (120.53) (Plate 3) (Table 2a). Ali *et al.* (2002) and Khan *et al.* (2008) also reported significant difference among rape seed genotypes for plant height. Genotypic and phenotypic variances for plant height were 65.14 and 68.67, respectively. The phenotypic variance appeared to higher than the genotypic variance suggested that the apparent variation was not only due to genotypes but also due to the influence of environment on the expression of the genes controlling this trait. The estimates of PCV (7.82%) and GCV (8.04%) also indicated presence of variability among the genotypes for this trait (Table 2b). The highest variation in plant height among parents and their hybrid was observed by Tyagi *et al*. (2001).

4.1.1.2 Number of primary branches per plant

Primary branches per plant varied significantly among among the genotypes (1.5) at the level of 1% probability. The data ranged from 1.42 to 4.40 for number of primary branches per plant with the mean value of 2.67 (Table 2a). Minimum number of primary branches per plant was observed in G53 (Bs-7× Nap 2013) (1.42) followed by G36 (Nap 248× Nap 2057) (Plate 4) whereas the maximum number of primary branches/plant was observed in G3 (Nap 248× Nap 159) (4.40) (Plate 5). Phenotypic variance and genotypic variance were observed as 0.39 and 0.39, respectively (Table 2a). The phenotypic variance was slightly higher than genotypic variance suggested that there was little influence of environment on the expression of the genes controlling this trait. The PCV and GCV was 23.39 and 23.09 respectively which stated that the existence of inherent variability among the population (Table 2b).

G4 **G19**

Plate 4. Photograph showing variation between highest G4 (Nap 2037 × Nap 2057) and lowest plant height G19 (Nap 2037 × Nap 206) of *Brassica napus* L. genotypes

G3 **G53**

Plate 5. Photograph showing variation between highest G3 (Nap 248× Nap 159) and lowest G53 (Bs 7× Nap 2013) primary branches of *Brassica napus* L. genotypes

The value of PCV and GCV value indicated the apparent variation mostly by genotypes but there was little influence of environment (Table 2b). Chowdhury *et al*. (1987) also found significant differences for number of primary branches per plant.

4.1.1.3 Number of secondary branches per plant

Secondary branches per plant varied significantly among the genotypes (2.28) at the level of 1% probability. The data ranged from 0.90 to 5.77 for number of primary branches per plant with the mean value of 2.06. Maximum number of secondary branches per plant was observed in G3 (Nap 248 × Nap 159) (Plate 5) whereas the minimum was observed in G36 (Nap 248 × Nap 2057) (Plate 6 and Table 2a). Phenotypic variance and genotypic variance were observed as 0.77 and 0.76, respectively which indicated low environmental influence to the genotypes for expression of this character. The PCV and GCV was 42.59 and 42.31, respectively which stated presence of considerable variability among the genotypes for this trait (Table 2b). Lekh *et al.* (1998) found highest genotypic coefficient of variation for number of secondary branches while working on 24 genotypes of *Brassica napus*. Hosen *et al*. (2008) found significant differences for number of secondary branches per plant. Genotypic, phenotypic and environmental coefficient of variation in *Brassica napus* L. are shown in Figure 1.

4.1.1.4 Days to 50% flowering

The data recorded for pod length exhibited significant ($p \leq 0.01$) differences among all the genotypes (53.25). The mean values ranged from 27 to 44 days for 50% flowering. Minimum days to 50% maturity was found in G35 (Nap 2037 × Nap 2013) (27 days) and highest (44 days) was observed in G28 (Nap-9908 × Nap-2001); G44 (Nap 2001 x Nap 159) (Table 2a). Phenotypic and genotypic variance for days to 50% flowering was observed as 12.25% and 11.65% respectively (Table 2b). The value of PCV is higher than GCV which indicated that variability for the character was influenced by genotypes and environment both. High genotypic and phenotypic co-efficient of variation was recorded by Lekh *et al.* (1998). Significant genetic variability in days to 50% flowering in *B. napus* was also observed by Hosen (2008).

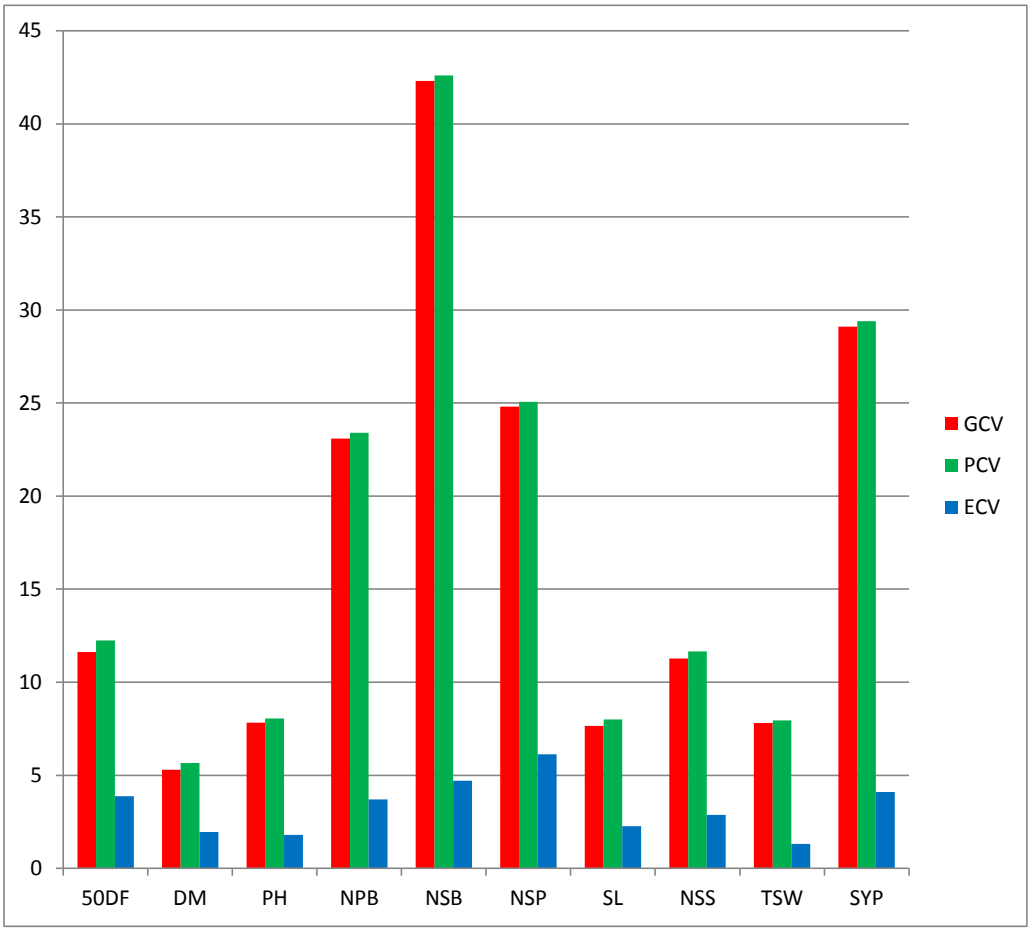


Figure 1. Genotypic, phenotypic and environmental coefficient of variation in *Brassica napus* L. genotypes

G3 **G36**

Plate 6. Photograph showing variation between highest G3 (Nap 248×Nap 159) and lowest G36 (Nap 248 × Nap 2057) secondary branches of *Brassica napus* L. genotypes

4.1.1.5 Days to maturity

Data concerning days to maturity showed significant ($p \leq 0.01$) differences amongst the accessions (59.22). The data ranged from 75 to 91 days for days to maturity. Days to maturity varied significantly among the studied accessions. The highest days to maturity was observed in G14 (Nap 206 × Nap 2013) (91 days) and the minimum days to maturity was observed in G24 (Nap 9908 × Nap 248); G35 (Nap 2037 × Nap 2013) (75 days) (Table 2a). Genotypic and phenotypic variance of days to 50% maturity was found 18.88 and 21.45, respectively. Phenotypic variance was higher than genotypic variance indicating environmental influence on their phenotypic expression for the trait of the genotypes. The phenotypic coefficient of variation (5.65%) was moderately higher than the genotypic coefficient of variation (5.30%) (Table 2b), which suggested that environment has a role on the expression of this trait. Higher genotypic variances indicated the better transmissibility of a character from parent to the offspring. Similar result for this trait was also observed by Rameeh (2014) and Katiyar *et al*. (1974).

4.1.1.6 Number of siliqua per plant

Data concerning number of pods per plant showed significant ($p \leq 0.01$) differences amongst the genotypes (1436.44). The data ranged from 47.85 to 137.67 for siliqua per plant with the mean value of 87.93 (Table 2a). Maximum siliqua per plant was recorded for G4 (Nap 2037 × Nap 2057) (137.87), whereas, minimum was recorded for G53 (Bs-7× Nap 2013) (47.85) (Plate 6). Number of siliqua per plant showed the highest phenotypic variance (505.33) and genotypic variance (475.83) which indicating the large environmental influence over genotypes. The PCV (25.04) was higher than GCV (24.79) also referring existence of adequate variation among the genotype (Table 2b and Plate 7). High genetic variation was also found by Zare and Sharafzadeh, (2012).

4.1.1.7 Length of siliqua (cm)

The data recorded for siliqua length exhibited significant *($P \leq 0.01$)* differences amongst the genotypes (1.05). The mean values ranged from 6.37 to 8.70 cm for pod length. Maximum siliqua length (8.70 cm) was exhibited by G3 (Nap 248 × Nap 159), G26 (Nap 248 × Nap 2022) and the minimum was observed in G15 (Bs -7 × Nap 206)

G4 **G53**

Plate 7. Photograph showing variation between highest G4 (Nap 2037 × Nap 2057) and lowest G53 (Bs 7 × Nap 2013) siliqua per plant of *Brassica napus* L. genotypes

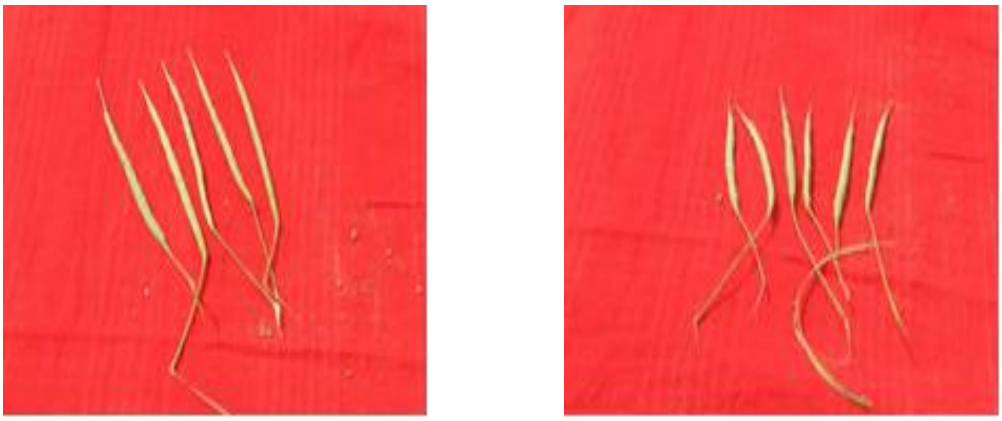
(6.37 cm) (Table 2a & Plate 8). The genotypic (0.34) and phenotypic variances (0.37) showed little differences, which indicating the lowest environmental influence on genotypes little difference between them indicating that minimum environmental influence on phenotypic expression and genotypic (GCV) and phenotypic coefficients of variation (PCV) values for siliqua length were 7.66% and 7.99%, respectively (Table 2b). High co-efficient of variation for this trait for both genotypic and phenotypic variability was recorded by Masood *et al.* (1999). and Zare and Sharafzadeh, (2012) also reported similar result.

4.1.1.8 Number of seeds per siliqua

Number of seeds per siliqua showed highly significant variations (17.075) among the genotypes from at 1% level of probability (Table 2a). The number of seeds per siliqua was observed highest in G51 (Nap 248 × Nap 2012) (27.93) and minimum was observed in G61 (Nap 94006 × Nap 206) (14.20) (Table 2a). The phenotypic and genotypic variances for this trait were 5.93 and 5.57, respectively. The phenotypic variance appeared to be slightly higher than the genotypic variance suggested little influence of environment on the expression of the genes controlling this trait. The value of GCV and PCV were 11.27% and 11.63%, respectively for number of seeds per siliqua which indicating that little variation exists among different genotypes (Table 2b). Similar variability was also recorded by Sheikh *et al*. (2009), Kumar and Singh (1994).

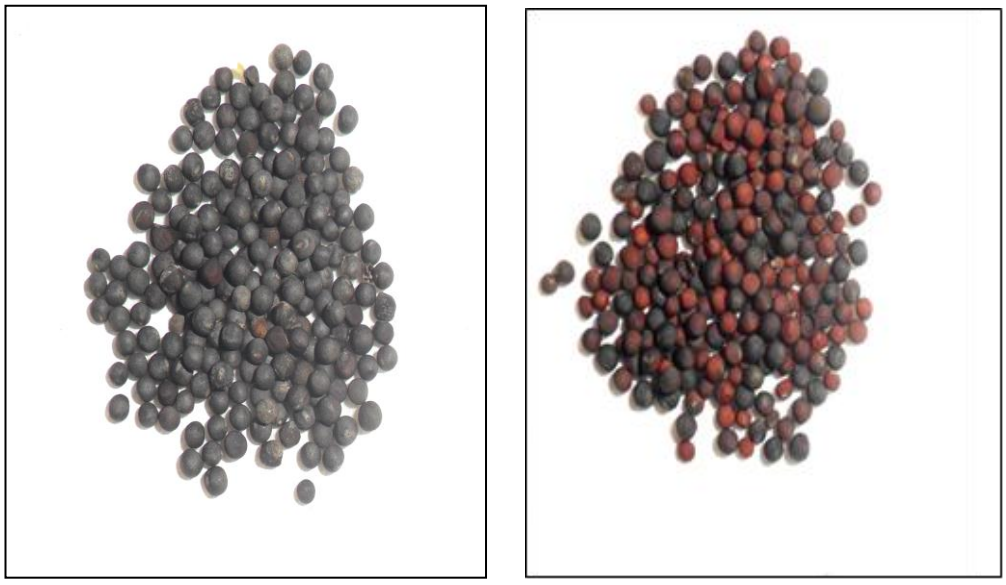
4.1.1.9 Thousand seed weight (g)

The perusal of the data pertaining to 1000-seed weight exhibited significant ($p \leq 0.01$) differences validating the presence of genetic variation among the tested accessions (0.216). Maximum 1000-seed weight (4.12 g) was observed in G4 (Nap 2037 × Nap 2057), G51 (Nap 248× Nap 2012), whereas the minimum was found in G32 (Nap 248 × Nap 2013) (2.91 g) (Table 2a and Plate 9). Thousand seed weight showed low genotypic (0.071) and phenotypic (0.073) variance with little differences indicating that they were low responsive to environmental factors. The PCV and GCV were 7.92% and 7.81% respectively (Table 2b). There was a very little difference between phenotypic and genotypic co-efficient of variation, indicating little environmental



G3 **G15**

Plate 8. Photograph showing variation between highest G3 (Nap248×Nap 159) and lowest G15 (Bs 7 × Nap 206) siliqua length of *Brassica napus* L. genotypes



2.91 g **4.12 g**

Plate 8. Photograph showing variation between lowest G32 (Nap 248×Nap 2013) and lowest G4 (Nap 2037 × Nap 2057) genotypes of thousand seed weight of *Brassica napus* L. genotypes

influence on this character. Significant variability for this trait was also found by Aytac & Kinaci, 2009).

4.1.1.10 Seed Yield per plant (g)

Seed yield per plant showed highly significant variations (9.039) among the genotypes at 1% level of probability. Yield per plant was found maximum in G4 (Nap 2037 × Nap 2057) (10.47 g) and minimum for G61 (Nap 9906 × Nap 206) (3.11g) (Table 2a). The phenotypic variances and genotypic variances for this trait were 3.05 and 2.29, respectively. The values indicated environmental influences on this trait. The values of GCV and PCV were 29.10% and 29.35%. PCV was slightly higher than GCV indicated that the genotype had moderate variation for this trait (Table 2b). Similar variability was also found by Ali *et al.* (2003) and Rameeh (2014). Abideen *et al*. (2013) observed similar findings and results revealed that highly significant differences among the genotypes for seed yield.

4.1.2 Heritability, genetic advance and selection

Heritability is the measure of value of selection of a particular character and an index of transmissibility of genes controlling the character. In estimating the selection effects, heritability accompanied with genetic advance is rather useful than heritability alone. These are also indicative of the mode of gene action operated in trait expression.

4.1.2.1 Plant height (cm)

Plant height of F_4 showed high heritability 94.85% with moderately high genetic advance of 16.11 and genetic advance in percentage of mean of 15.62% (Table 2b), revealed that the character was least influenced by the environmental effects and the possibility of predominance of additive gene action in the inheritance of this trait and indicating that this trait could be improved through selection process. High variability in plant height for *B. juncea*, *B. rapa* and *B. napus* was also observed by Varshney *et al*. (1986). Hosen (2008) also observed that plant height showed high heritability with high genetic advance and genetic advance in percentage of mean. High heritability (92.48%) with moderate genetic advance (18.87%) was found by Saifullah (2010).

4.1.2.2 Number of primary branches per plant

Number of primary branches per plant exhibited high heritability 97.43 with low genetic advance 1.25 and high genetic advance in percentage of mean of 46.82%, which revealed that this character was governed by non-additive gene but high genetic advance in percentage of mean which indicated that possibility of predominance of additive gene, so much scope to improve. As a whole, the high heritability was being exhibited due to favourable influence of environment rather than genotypes and the consequent low genetic advance indicated the lower possibility of selecting genotypes for this trait. However, some of the individual plants showed quite a reasonable lower primary branches which were selected for further study in the next generation. Low heritability coupled with low genetic advance was also found by Singh *et al*. (1987). Afrin *et al*. (2011) found low heritability with high genetic advance in percentage of mean.

4.1.2.3 Number of secondary branches per plant

High heritability (98.70) along with low genetic advance (1.78) and high genetic advance in percentage of mean (86.41) indicated moderate effect of environment and presence of non-additive gene in the expression of character As a whole, the moderately high heritability and the consequent low genetic advance indicated the lower possibility of selecting genotypes but high genetic advance in percentage of mean which indicated that possibility of predominance of additive gene, so much scope to improve. Moderately high heritability coupled with low genetic advance was also found by Singh *et al*. (1987). Khan *et al*. (2013) found high heritability coupled with high genetic advance for number of secondary branches per plant.

4.1.2.4 Days to 50% flowering

Days to 50% flowering exhibited high heritability (89.96%) with low genetic advance (8.19) and moderately high genetic advance in percentage of mean (22.59%) indicated that this trait was controlled by non-additive gene. This results support the reports of Malik *et al*. (1995). Belete *et al*. (2012) found that high heritability along with high genetic advance (as percent of mean) was recorded for days to flowering.

4.1.2.5 Days to maturity

Days to maturity showed high heritability (88.02%) with low genetic advance (8.35) and genetic advance in percentage of mean (10.20%) indicated that refers that the character was mostly governed by non-additive genes and more influence of environment in the phenotypic expression of the characters. Selection of genotypes for minimum days to maturity may not be effective. High heritability coupled with low genetic advance for this trait was also observed by Afrin *et al*. (2011). Heritability and genetic advance in percentage of mean are shown in Figure 2.

4.1.2.6 Number of siliqua per plant

Number of siliqua per plant exhibited high heritability 94.16% with high genetic advance 43.39 and genetic advance in percentage of mean 51.08%. These results revealed that most likely heritability was due to additive gene effects. It provides a wider scope to the breeders for direct selection during crop improvement. Sadat *et al.* (2010) reported high heritability with the later reporting it coupled with high genetic advance.

4.1.2.7 Siliqua length

Siliqua length showed high heritability (91.89%) with low genetic advance (1.14) and moderate genetic advance in percentage of mean 14.98% indicated that this trait was controlled by non-additive gene. Selection based on this character will not be rewarding for future breeding program. High heritability for this trait was observed by Aytac and Kinaci (2009) and Zare and Sharafzadeh (2012) found low broad sense heritability for pod length in rapeseed (*Brassica napus* L).

4.1.2.8 Number of seeds per siliqua

Number of seeds per siliqua showed high heritability 93.92% coupled with low genetic advance 4.69 indicated that this trait was controlled by non-additive gene. Selection based on this character will not be rewarding for future breeding program but with moderate high genetic advance in percentage of mean 22.41%, a better opportunity for selecting high valued genotype for breeding program. Mahmud (2008)

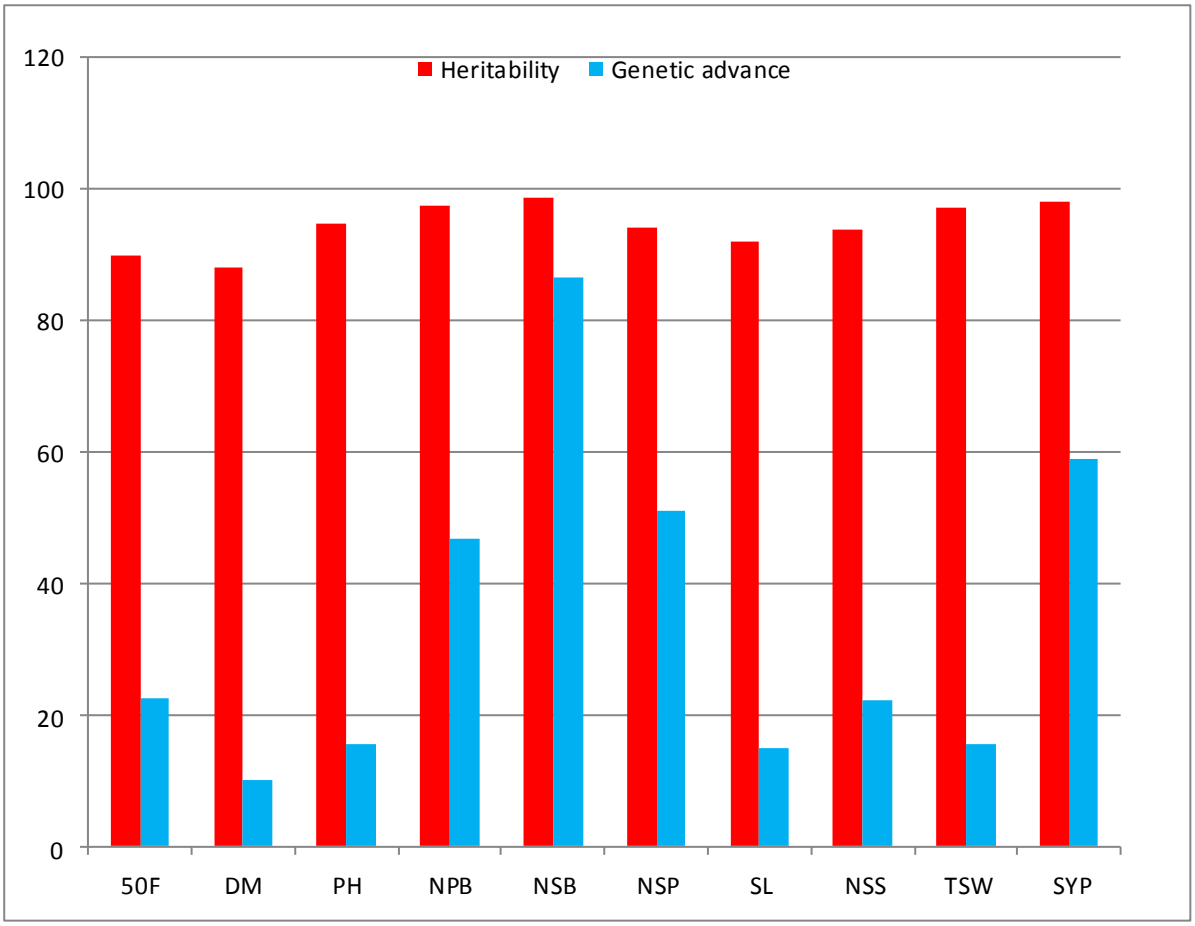


Figure 2. Heritability and genetic advance over mean in *Brassica napus* L. genotypes

observed seeds per siliqua showed high heritability with low genetic advance and genetic advance in percentage of mean.

4.1.2.9 Thousand seed weight

Thousand seed weight exhibited high heritability 97.26% with low genetic advance 0.53 and moderate genetic advance in percentage of mean 15.54%, revealed that this trait was controlled by non-additive gene but possibility of predominance of additive genes action. The environmental variance was low indicated that more influence of genetic components to express the character. In accordance with our result, low genetic advance was reported by Saifullah (2010) for the traits in *Brassica rapa.*. High heritability for this trait was also observed by Yadava *et al*. (1993). Singh *et al.* (2002) reported the high heritability and genetic advance for thousand seed weight. includes dominance and epistasis. The high heritability along with considerable genetic advance in percentage of mean was reported by Afrin *et al.* (2011).

4.1.2.10 Seed yield per plant

Seed yield per plant showed high heritability 98.03% with low genetic advance (3.51) and high genetic advance in percentage of mean 58.99% indicated this trait was controlled by additive gene and selection based on this character will be rewarding for future breeding program. Aytac and Kinaci (2009) mentioned the high heritability and genetic advance for seed yield selection for this character would be effective. Rameeh (2014) also found high heritability with high genetic advance for seed yield in *B. napus*.

4.2 Correlation coefficient

Yield is controlled by polygene and highly influenced by environment. For this reason, selection based on only yield itself is ineffective. Correlation co-efficient helps the plant breeders to select the yield contributing traits to be given importance by its nature and magnitude. Simultaneous improvement of various characters along with the yield is also possible through correlation co-efficient.

Genotypic and phenotypic correlation coefficients among 10 characters are presented in Table 3. In most instances, there was a close agreement between genetic correlations and phenotypic correlations.

4.2.1 Days to 50% flowering

Days to 50% flowering was positively and highly significantly ($p \leq 0.01$) correlated with days to maturity (r_g= 0.732**, r_p= 0.721**), whereas positive and significantly ($p \leq 0.05$) correlated with plant height (r_g= 0.121*, r_g= 0.113*). Here correlation was significant and positive so the association between two characters was high, indicated that it will be beneficial for breeders because it will help in simultaneous improvement of both characters. It also exhibited insignificant and positive correlation with number of primary branches (r_g= 0.016, r_p= 0.013), number of siliqua per plant (r_g= 0.101, r_p= 0.091), number of seed per siliqua (r_g= 0.018, r_p= 0.012) and yield per plant (r_g= 0.033, r_p= 0.031) that revealed clearly the independent nature of two characters. However, it had insignificant and negative interaction with siliqua length (r_g= - 0.146, r_p= - 0.133), number of secondary branches (r_g= - 0.011, r_p= - 0.013) and thousand seed weight (r_g = -0.076, r_g= - 0.068) (Table 3). Insignificant association of these traits indicated that the association between these traits was largely influenced by environmental factors. Similar result was also observed by Rameeh (2012) and Ali *et al.* (2003). Nasim *et al.* (2013) observed negative correlation with thousand seed weight.

4.2.2 Days to maturity

Days to maturity showed non-significant positive correlation with number of primary branches (r_g= 0.068, r_p= 0.067), number of secondary branches (r_g= 0.077, r_p= 0.076), number of siliqua per plant (r_g= 0.118, r_p= 0.114). However, it had insignificant and negative interaction with siliqua length (r_g= -0.141, r_p= - 0.138), number of seed per siliqua (r_g= -0.098, r_p= -0.087), thousand seed weight (r_g= -0.043, r_p= - 0.037) and seed yield per plant (r_g= - 0.096, r_p= - 0.093) (table 3). Insignificant association of these traits indicated that the association between these traits was largely influenced by environmental factors. However it showed significant relation with plant

Table 3. Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of *Brassica napus* L.

		DM	PH	NPB	NSB	NSP	SL	NSS	TSW	SYP
50F	r_g	0.732**	0.121*	0.016	-0.011	0.101	-0.146	0.018	-0.076	0.033
	r_p	0.721**	0.113*	0.013	-0.013	0.091	-0.133	0.012	-0.068	0.031
DM	r_g		0.147*	0.068	0.077	0.118	-0.141	-0.098	-0.043	-0.096
	r_p		0.139*	0.067	0.076	0.114	-0.138	-0.087	-0.037	-0.093
PH	r_g			0.306**	0.425**	0.427**	0.298*	0.138*	0.109	0.368**
	r_p			0.304**	0.413**	0.422**	0.291*	0.134*	0.098	0.356**
NPB	r_g				0.806**	0.418**	-0.322**	-0.096	0.192*	0.472**
	r_p				0.802**	0.412**	-0.316**	-0.086	0.189*	0.464**
NSB	r_g					0.238	-0.248*	-0.123	0.105	0.366**
	r_p					0.233	-0.241*	-0.116	0.099	0.361**
NSP	r_g						0.158	0.118	0.038	0.696**
	r_p						0.154	0.111	0.032	0.688**
SL	r_g							0.551**	0.039	0.318**
	r_p							0.541**	0.033	0.312**
NSS	r_g								-0.142	0.421**
	r_p								-0.139	0.417**
TSW	r_g									0.228**
	r_p									0.222**

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

50F= Days to 50% flowering, DM= Days to 80% maturity, PH= Plant height (cm), NPB= Number of primary branches per plant, NSB= Number of secondary branches per plant, NSP= Number of siliqua per plant, NSS= Number of seed per siliqua, SL= Siliqua length, TGW= Thousand seed weight (g), SYP= Seed yield per plant, r_g= Genotypic correlation coefficient, r_p= Phenotypic correlation coefficient

height (r_g= 0.147, r_p= 0.139) ($p \leq 0.05$) (Table 3). This indicated that if days to maturity increased then plant height also increased. Khayat *et al*. (2012) and Bilal *et al*. (2015) observed that days to maturity had positive interaction with yield per plant.

4.2.3 Plant height (cm)

Plant height showed highly significant and positive interaction with number of number of primary branches (r_g= 0.306**, r_p= 0.304**) and number of secondary branches (r_g= 0.425**, r_p= 0.413**), number of siliqua per plant (r_g= 0.427**, r_p= 0.422**) seed yield per plant (r_g= 0.368**, r_p= 0.356**). It had positive and significant interaction with siliqua length (r_g= 0.298*, r_p= 0.291*) and number of seed per siliqua (r_g= 0.138*, r_p= 0.134*) (Table 3). It indicated if plant height increased then number of primary branches, secondary branches, siliqua length, number of seed per siliqua and yield also increased. It also implied that highly significant positive associations between plant height and other characters indicate that the traits were governed by same gene and simultaneous improvement would be effective and It had positive and insignificant interaction with thousand seed weight (r_g= 0.109, r_p= 0.098) (Table 3). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. These findings are showed resemblance to the reports of Alam (2010), Parveen (2007) and Abideen *et al*. (2013). Shalini *et al*. (2000) also observed that plant height was highly associated with seed yield. Basalma (2008) reported opposite result for this trait.

4.2.4 Number of primary branches per plant

Number of primary branches per plant showed highly significant positive correlation with number of secondary branches per plant (r_g= 0.806**, r_p= 0.802**), number of siliqua per plant (.r_g= 0.418**, r_p= 0.412**) and seed yield per plant (r_g= 0.472**, r_p= 0.464**). It had also significant and positive relation with thousand seed weight (r_g= 0.192*, r_p= 0.189*). These suggesting if number of primary branches increases then yield per plant also increases. Malik *et al.* (2000) reported similar result for number of primary branches and seed yield both at genotypic and phenotypic level. It had highly significant but negative correlation with siliqua length (r_g= - 0.322**, r_p= - 0.319**). It indicated that if primary branches per plant increased then siliqua length will be

decreased. However, it had insignificant and positive interaction was found in number of seed per siliqua (r_g= - 0.096, r_p= - 0.086) (Table 3). Insignificant association of these traits indicated that the association between these traits was largely influenced by environmental factors and mostly independent in nature. Similar results were obtained by Basalma (2008) and Alam (2010).

4.2.5 Number of secondary branches per plant

Number of secondary branch showed significant and positive interaction with seed yield (r_g= 0.366**, r_p= 0.3614**) ($p \leq 0.01$). These suggesting if number of secondary branches increased then yield per plant also increased. But it had significant and neagtive correlation with siliqua length. But it had significant and neagtive correlation with siliqua length (r_g= - 0.248*, r_p= - 0.241*) ($p \leq 0.05$). These indicated if number of secondary branches increased then siliqua length decreased. Insignificant positive association was found for thousand seed weight (r_g= 0.105, r_p= 0.099) and insignificant negative relation was found for number of seed per siliqua (r_g= - 0.123, r_p= - 0.116) (Table 3). Insignificant association of these traits indicated that secondary branching was an important contributor to yield, independent of its association with thousand seed weight. These findings are showing similar to the reports of Afrin *et al*. (2011) and Chowdhary *et al*. (1987).

4.2.6 Number of siliqua per plant

Highly significant positive correlation was found among pod per plant and seed yield per plant (r_g= 0.696**, r_p= 0.688**). Malik *et al.* (2000) and Jeromela *et al*. (2007) reported positive correlation between siliqua per plant and seed yield. These indicated if number of primary branches increased then yield per plant also increased that helps in simultaneous improvement of both the characters. Whereas the insignificant and positive interaction was found in siliqua length (r_g= 0.158, r_p= 0.154), number of siliqua per seed (r_g= 0.118. r_p= 0.111) and thousand seed weight (r_g= 0.038, r_p= 0.032) (Table 3). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Bilal *et al*. (2015) and Rameeh *et al*. 2011) also found positive significant correlation between pods per plant and seed yield. But Hosen (2008) reported negative correlation of the trait with length of siliquaa, yield and thousand seed weight.

4.2.7 Siliqua length (cm)

Siliqua length showed highly significant and positive interaction with number of seed per silique (r_g= 0.551**, r_p= 0.541**) and seed yield per plant (r_g= 0.318**, r_p= 0.312**) indicated that if siliqua length increased then number of seed per siliqua and yield per plant also increased. Supported results were found from the findings of Alam (2010). It also showed insignificant and positive correlation with thousand seed weight (r_g= 0.039, r_p= 0.033) (Table 3). Nasim *et al.* (2013) reported positive correlation between pod length and 1000- seed weight. Nasim *et al*. (1994) reported that seed yield per plant was significantly and negatively with siliqua length.

4.2.8 Number of seeds per siliqua

Number of seeds per siliqua showed highly significant positive correlation with yield per plant (r_g= 0.421**, r_p= 0.417**). Highly significant positive associations between number of seeds per siliqua and yield per plant indicated that the traits were governed by same gene and if number of seeds per siliqua increased then yield per plant also increased and simultaneous improvement would be effective. It had insignificant and negative interaction with thousand seed weight (r_g= - 0.142, r_p= - 0.139) (Table 3). Alam (2010) and Rameeh (2015) reported that number of seeds per siliqua had positively correlated with seed yield per plant. Nasim *et al*. (1994) reported that no. of seeds per siliqua had negative and significant effects on seed yield per plant.

4.2.9 Thousand seed weight

The perusal of the data pertaining to 1000-seed weight exhibited highly significant positive correlation with seed yield per plant (r_g= 0.228**, r_p= 0.222**) (Table 3). Jeromela *et al*. (2007) found positive associations which support the results. Zare and Sharafzadeh (2012) found positive significant relation between these traits.

The results of correlation analysis showed that all characters were positively correlated with seed yield except days to maturity. Comparing correlation coefficient values of ten variables on seed yield, significant differences were observed. As genetic correlation coefficient was higher than phenotypic correlation coefficient, it implied that the apparent association of two characters was due to mainly genes, but the phenotypic value was lessened by the significant interaction of environment.

4.3 Path Co-efficient analysis

Seed yield is the ultimate product of several yield contributing characters. The direct and indirect effects of yield contributing characters on seed yield were worked out by using path analysis. Here seed yield per plant was considered as effect (dependent variable) and days to 50% flowering, days to 80% maturity, plant height, siliqua length, number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua, number of siliqua per plant and 1000-seed weight were treated as causes or independent variables. Estimation of direct and indirect effect of path co-efficient analysis for *Brassica napus* is presented in Table 4.

4.3.1. Days to 50% flowering

Path co-efficient analysis revealed that, days to 50% flowering had positive direct effect (0.174) on yield per plant. This trait showed indirect positive effect on yield per plant through number of primary branches (0.004), number of siliqua per plant (0.067), siliqua length (0.043). On the other hand, it showed indirect negative effect via days to maturity (-0.057) followed by plant height (-0.018), number of secondary branches (-0.002), number of seed per siliqua (-0.092), thousand seed weight (-0.086) finally it made positive correlation with seed yield (0.033) (Table 4). Chauhan and Singh (1995) revealed that days to 50% flowering had positive direct effect on yield per plant. But Afrin *et al*. 2011) observed that days to 50% flowering had negative direct effect on seed yield per plant.

4.3.2. Days to maturity

The relationship between days to maturity and seed yield per plant was insignificant and negative as was pointed out by genotypic coefficient of correlation (-0.096). However, its direct effect was low and negative indeed (-0.078). This trait showed indirect negative effect on yield through plant height (-0.009), number of primary branches per plant (-0.013), number of secondary branches per plant (-0.003), number of seed per siliqua (-0.092) and thousand seed weight (-0.083). On the other hand, it showed positive indirect effect via days to flowering (0.084), number of siliqua per plant (0.072) and siliqua length (0.026) (Table 4). It indicated that correlation was

Table 4. Path coefficient analysis showing direct and indirect effects of different characters on yield of *Brassica napus* L.

Characters	Direct effect	Indirect effect									Genotypic correlation with yield
		50F	DM	PH	NPB	NSB	NSP	SL	NSS	TSW	
50F	0.174	-	-0.057	-0.018	0.004	-0.002	0.067	0.043	-0.092	-0.086	0.033
DM	-0.078	0.084	-	-0.009	-0.013	-0.003	0.072	0.026	-0.092	-0.083	-0.096
PH	-0.117	0.078	-0.003	-	0.032	0.016	0.28	-0.003	0.078	0.007	0.368**
NPB	-0.06	-0.007	-0.008	0.113	-	0.14	0.381	-0.051	-0.056	0.02	0.472**
NSB	0.18	0.015	-0.018	-0.016	-0.008	-	0.28	-0.031	-0.016	-0.02	0.366**
NSP	0.685	0.012	-0.009	-0.014	-0.018	0.003	-	-0.041	0.061	0.017	0.696**
SL	-0.157	-0.028	0.010	-0.086	0.038	0.003	0.121	-	0.398	0.019	0.318**
NSS	0.548	-0.019	0.014	-0.018	0.029	0.016	0.072	-0.142	-	-0.079	0.421**
TSW	0.16	-0.014	0.02	0.006	-0.01	0.001	0.12	-0.007	-0.048	-	0.228**

Residual effect: **0.216**

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

50F = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), NPB=Number of Primary branches per plant, NSB=Number of secondary branches per plant, NSP=Number of Siliqua per plant, NSS=Number of seed per silique, SL=Siliqua length, TGW = Thousand Grain Weight (g), SYP=Seed yeild per plant.

mainly due to indirect effects of the character through another component trait, indirect selection through such trait should be practiced to reduce the undesirable effect. Rashid (2007) revealed that days to maturity had positive direct effect on yield.

4.3.3. Plant height

The relationship between number of plant height and seed yield per plant was highly significant, as was pointed out by genotypic coefficient of correlation (0.368). However, its direct effect was low and negative indeed (-0.117). It was indirectly realized via 50% flowering (0.078), number of primary branches (0.032), number of secondary branches (0.016), number of siliqua per plant (0.28), number of seed per siliqua (0.078) and thousand seed weight (0.007) positively, but the indirect effect of days to maturity (-0.003) and siliqua length (-0.003) were negative (Table 4). Varshney (1986) worked with several strains of *Brassica rapa* and observed that plant height had the negative direct effect on yield. These results indicated that if plant height increases than seed yield also increases mostly through the positive indirect effect of plant height with other characters. Alam (2010), Ali *et al*. (2003) and Han (1990) also reported direct positive result for this character.

4.3.4. Number of primary branches per plant

Number of primary branches per plant had the negative direct effect on yield per plant (-0.06). This trait had positive indirect effect on plant height (0.113), number of secondary branch (0.14), number of siliqua per plant (0.381) and thousand seed weight (0.02). On the other hand, negative indirect effect was found on days to 50% flowering (-0.007), days to maturity (-0.008) and siliqua length (-0.051 (Table 4). Number of primary branches per plant finally made positive correlation with seed yield (0.472) which was highly significant. It indicated that correlation was mainly due to indirect effects of the character through another component trait, so indirect selection through another such trait will be live in yield improvement. Basalma (2008) and Rashid (2007) observed that primary branching had the direct negative effect on seed yield. Alam (2010) and Srivastava and Singh (2002) reported that number of primary branches per plant had direct positive effect on seed yield.

4.3.5. Number of secondary branches per plant

Number of secondary branch per plant showed positive direct effect (0.18) on seed yield per plant and the relationship between number of plant height and seed yield per plant was highly significant, as was pointed out by genotypic coefficient of correlation (0.366). It had positive indirect effect via 50% flowering (0.015) and number of siliqua per plant (0.28) on seed yield per plant. On the other hand, days to maturity (-0.018), plant height (-0.016), number of primary branches (-0.008), siliqua length (-0.031), number of seed per siliqua (-0.16) and thousand seed weight (-0.02) had negative indirect effect on yield per plant (Table 4). These results indicated that correlation between yield and this character was due to both direct and indirect effects via other component traits. Yadava *et al*. (1996) found the number of secondary branch had the highest positive direct effect on seed yield. Rashid (2007) observed that number of secondary branches per plant had the highest direct effect on seed yield per plant.

4.3.6. Number of siliqua per plant

Path co-efficient analysis revealed that number of siliqua per plant had the positive direct effect (0.685) on seed yield followed by positive indirect effect on days to 50% flowering (0.012), number of secondary branches (0.003), number of seed per siliqua (0.061) and thousand seed weight (0.017). This trait had negative indirect effect on yield via days to maturity (-0.009), plant height (-0.014), number of primary branches (-0.018) and siliqua length (-0.041) (Table 4). Finally this trait had highly significant positive genotypic correlation (0.696) with yield per plant. These results indicated that correlation was mainly due to the direct effect of a character and it was realized via indirect positive and negative effects. It revealed that true relationship between them and direct selection for this trait will be rewarding for yield improvement. Sharafi *et al*. (2015) found the number of siliqua per plant had the highest direct effect on seed yield.

4.3.7. Siliqua length

Estimated correlation coefficient at genotypic level between siliqua length and seed yield per plant was highly significantly positive (0.318). Its direct effect to seed yield per plant was negative (-0.157). It was indirectly realized via positive effect on days

to maturity (0.010), number of primary branches (0.038), number of secondary branches (0.003), number of siliqua per plant (0.121) number of seed per siliqua (0.398) and thousand seed weight (0.019). On the other hand, length of siliqua showed indirect negative effect on 50% flowering (-0.028) and plant height (-0.086) (Table 4). Hence, selection should be practiced for this trait which had longer siliquae in order to improve seed yield. Han (1990) and Singh *et al.* (1978) reported that siliqua length had negative direct effect on yield per plant. But Alam (2010) reported that siliqua length had positive direct effect on yield per plant.

4.3.8. Number of seeds per siliqua

Path analysis revealed that number of seeds per siliqua had direct positive effect (0.548) on yield per plant. This trait had also indirect positive effect on days to maturity (0.014), number of primary branches (0.029), number of secondary branches (0.016) and number of siliqua per plant (0.072). On the other hand, this trait showed indirect negative effect on 50% flowering (-0.019), plant height (-0.018), siliqua length (-0.142) and thousand seed weight (-0.079). Its direct effect was higher and positive than genetic correlation coefficient, it was indirectly realized via its effects. Finally this trait had significant positive genotypic correlation (0.421) with yield per plant (Table 4). In such situation direct selection for this trait shoud be practiced for yield improvement. Sharafi *et al*. (2015) and Rashid (2007) reported that number of seeds per siliqua had direct positive effect on yield per plant. But Basalma (2008) reported that seeds per siliqua had negative direct effect on seed yield per plant.

4.3.9 Thousand seed weight

Estimated correlation coefficient at genotypic level between thousand seed weight and seed yield per plant was highly significantly positive (0.228). Its direct effect to seed yield per plant was positive (0.16). It had also positive indirect effect on days to maturity (0.02), plant height (0.006), number of secondary branches (0.001) and number of siliqua per plant (0.12) (Table 4). On the other hand, this trait showed negative indirect effect on 50% flowering (-0.014), number of primary branches (-0.01), siliqua length (-0.007), and number of seed per siliqua (-0.048) (Table 4). Sharafi *et al*. (2015) and Siddikee (2006) reported that thousand seed weight had the

highest positive direct effect on seed yield per plant. But Alam (2010) reported that thousand seed weight had direct negative effect on yield per plant.

The value of residual effect was 0.216. It indicated that beside the characters studied, there were some other attributes (approx. 21.6%) which contributed for yield.

4.4 Genetic Diversity Analysis

Genetic diversity is the total number of genetic characteristics in the genetic makeup of a species. It is distinguished from genetic variability, which describes the tendency of genetic characteristics to vary. Genetic diversity serves as a way for populations to adapt to changing environments. The genetic diversity of 62 F_4 materials of *Brassica napus* genotypes are presented in Table 5 to 10 and Figure 3 and 4.

4.4.1 Principal Component Analysis (PCA)

The analysis of variance showed significant differences among the genotypes for all the 10 characters under study revealing the presence of notable genetic variability among the genotypes. Principal component analysis was carried out with 62 genotypes of *Brassica napus*. The computed Eigen values for the 10 variables subjected to principal component analysis together with the corresponding proportion and cumulative explained variance are given in Table 5. Following the proportion of variance criterion, two principal components were retained and these are the principal components whose cumulative explained variances were equal to or more than 99%. The PCA gives Eigen values of principal component axes of coordination of genotypes with the first axes totally accounted for the variation among the genotypes (40.44). These three principal components account for 77.3% of the total variation (Table 5). Zaman *et al.* (2010) reported that first three axes accounted for 94.00% of the total variation whereas the first principal components accounted for 81.94%. Khan (2014) reported that the contribution of first three PCs in overall PCs was 26.96%. According to the principal axes I and II, a two dimensional chart (Z1 – Z2) of the genotypes using component score 1 as X axis and component score 2 as Y axis. The scatter diagram revealed that there were five apparent clusters. The genotypes were distantly located from each other (Figure 3). The genotypes of cluster I were more diverse than those of cluster III (Fig. 4).

Table 5. Eigen values and yield percent contribution of 10 characters of 62 genotypes of *Brassica napus* L.

Principal component axes	Eigen values	Percent variation	Cumulative % of Percent variation
I	4.044	40.44	40.44
II	1.994	19.94	60.38
III	1.692	16.92	77.3
IV	0.836	8.36	85.66
V	0.622	6.22	91.88
VI	0.385	3.85	95.73
VII	0.192	1.92	97.65
VIII	0.135	1.35	99
IX	0.057	0.57	99.57
X	0.043	0.43	100

Z1-Z2 Graph

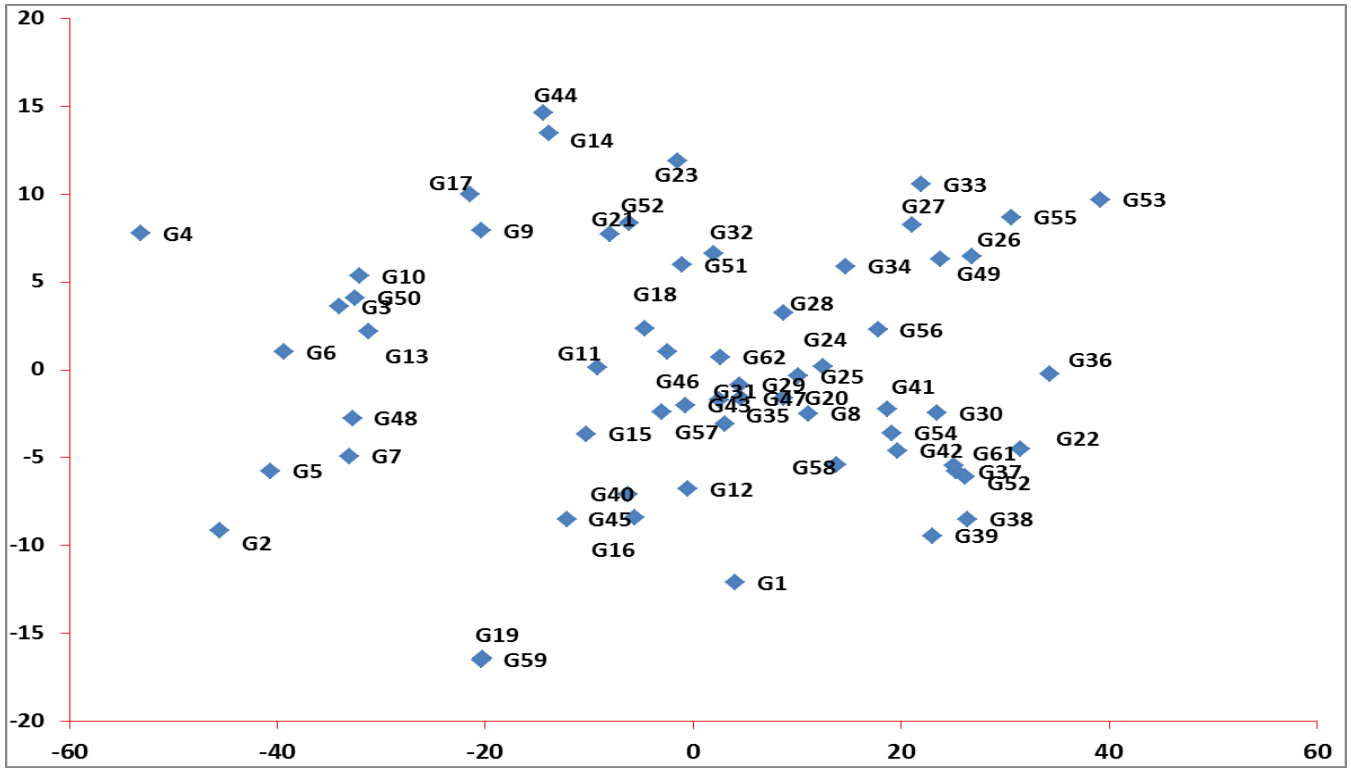


Figure 3. Scatter pattern of *Brassica napus* genotypes of based on their principal component scores

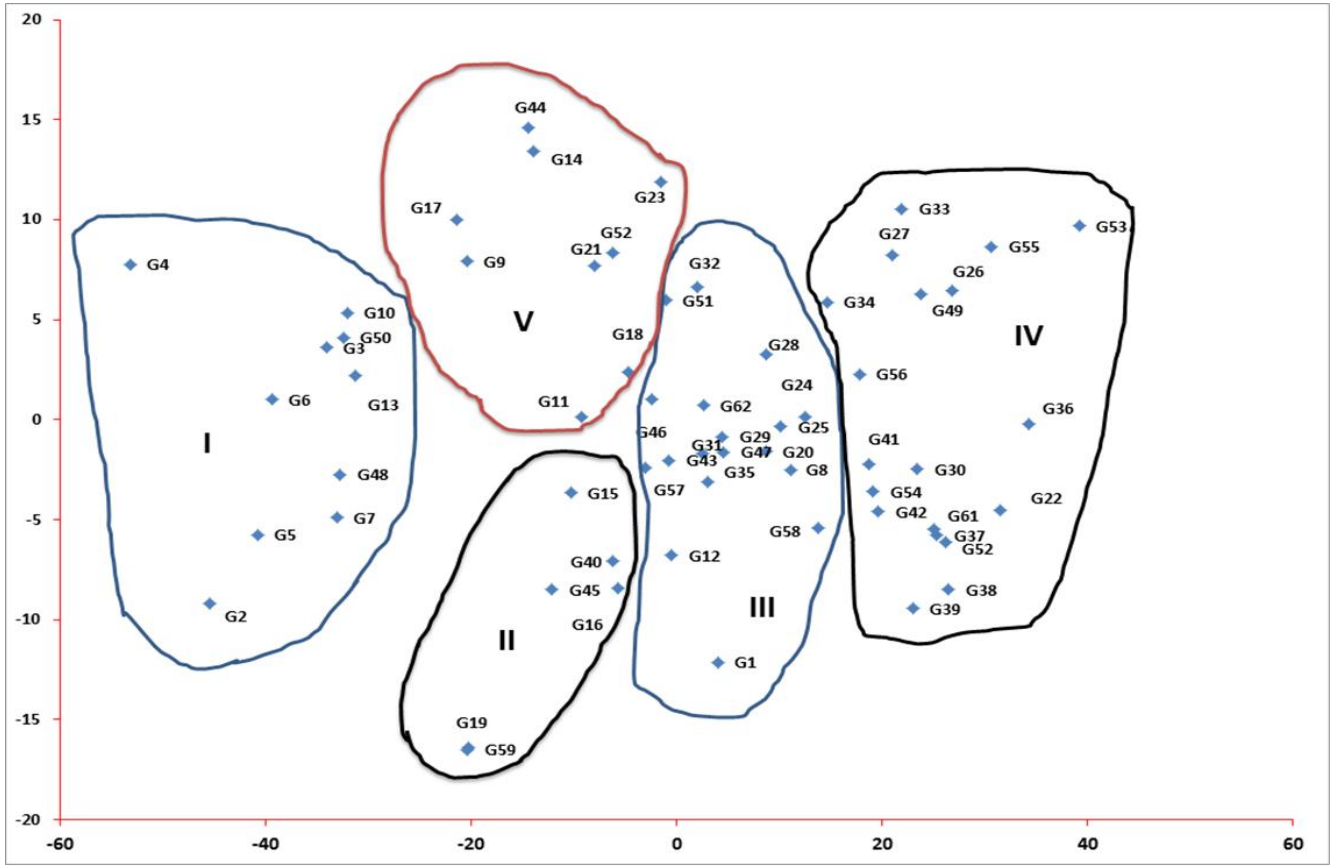


Figure 4. Scatter diagram of *Brassica napus* genotypes of based on their principal component scores.

4.4.2 Non-Hierarchical Clustering

The 62 genotypes were grouped into five clusters through non-hierarchical clustering (Table 6). Most of the genotypes (19) were grouped into cluster IV, followed by 18 III, respectively. 10 and 9 genotypes were grouped into cluster I and V (Table 6). Rameeh (2015) reported three clusters, Iqbal *et al.* (2014) reported four clusters and Begum *et al.* (2007) reported five clusters in linseed. Cluster I have G2, G3, G4, G5, G6, G7, G10, G13, G48, G50 (Table 6). The genotypes from cluster I earned the highest cluster mean value for number of primary branch (3.30), number of secondary branch (3.29), number of siliqua per plant (123.65), thousand seed weight (3.52 g) and seed yield per plant (8.75) (Table 7). Thus indicates that genotype of this cluster could be used for parent in future hybridization program for early maturity.

On the other hand Cluster II produced the highest mean for seeds per siliqua (21.81) and 1000-seed weight (3.52 g) and lowest plant height (94.71). It indicated the genotype of this cluster could be used for future hybridization program for higher seeds per siliqua. The genotypes included in cluster III were highest mean value for siliqua length (7.78 cm) and lowest mean value for days to 50% flowering (35.41), days to maturity (80.93) and 1000 seed weight (3.27). It indicated the genotype of this cluster could be used for future hybridization program for early maturity plant Moreover, Cluster IV had lower cluster mean for number of primary branch (2.10), number of secondary branch (1.38), siliqua per plant (63.39), siliqua length (7.42), seeds per siliqua (19.61) and seed yield per plant (4.20). On the other hand, cluster V showed the late 50% flowering (39.89), late maturity plant (84.85) and highest plant height (112.55) (Table 7). It indicated the genotype of this cluster could be used for future hybridization program for late maturity plant. Zaman *et al*. (2010) reported that

Table 6. Distribution of genotypes in different clusters

Cluster no.	No. of Genotypes	No. of populations	Name of genotypes
I	G2, G3, G4, G5, G6, G7, G10, G13, G48, G50	10	Nap 179 × Nap 2001, Nap 248 × Nap 159, Nap 2037 × Nap 2057, Nap 94006 × Bs 7, Nap 2012 × Nap 2013, Nap 94006 × Nap 2013, Nap 2037 × Nap 2022, Nap 2037 × Nap 248, Nap 206 × Nap 2057, Nap 179 × Nap 2013
II	G15, G16, G19, G40, G45, G59	6	Bs 7× Nap 206, Nap 2001 × Nap 2022, Nap 2037 × Nap 206, Bs 13 × Nap 2001, Bs 13 × Nap 179 , Nap 2057 × Nap 2022
III	G1, G8, G12, G20, G24, G25, G28, G29, G31, G32, G35, G43, G46, G47, G51, G57, G58, G62	18	Nap- 9908 × BS- 13, Nap- 248 × Nap- 206, Nap- 9908 × Nap- 2037, Nap- 9908 × Nap- 2022, Nap- 9908 × Nap- 248, Nap- 2012 × Nap- 2022, Nap- 9908 × Nap- 2001, Nap- 2037 × BS- 13, Nap- 9908 × Nap- 2013, Nap- 248 × Nap- 2013, Nap- 2037 × Nap- 2013, Nap- 179 × Nap- 2012, BS- 7× Nap- 2057, Nap- 206 × Nap- 2022, Nap- 248 × Nap- 2012, Nap- 2057 × Nap- 2012, Nap- 2001 × Nap- 248, Nap- 2001 × Nap- 206
IV	G22, G26, G27, G30, G33, G34, G36, G37, G38, G39, G41, G42, G49, G53, G54, G55, G56, G60, G61	19	Nap 179 × Nap 206, Nap 248× Nap 2022, Bs 13× Nap 206, Bs 13 × Nap 206, Nap 179 × Nap 2057, Nap 179× Nap 2022, Nap 248 × Nap 2057, Nap 94006 × Nap 2057, Bs 7× Nap 2013, Nap 2057× Nap 2001, Nap 94006 × Nap 2001, Bs 13 × Nap 2057, Nap 9908× Nap 2012, Bs7 × Nap 2013, Nap 94006 × Nap 179, Nap 2001× Nap 2013, Nap 94006× Nap 2022, Nap 94006 × Nap 2012, Nap 94006 × Nap 206
V	G9, G11, G14, G17, G18, G21. G23, G44, G52	9	Nap 206 × Nap 2012, Nap 9908 × Nap 94006, Nap 206 × Nap 2013, Nap 94006 × Bs 13, Nap 2037 × Nap 2012, Bs 13 × Nap 2022, Nap 9908 × Nap 206, Nap 2001 × Nap 179, Nap 2057 × Nap 248
	Total	62	

Table 7. Cluster mean values of 10 different characters of 62 genotypes of *Brassica napus* L.

Characters	I	II	III	IV	V
Days to 50% flowering	35.90	36.17	35.41	35.54	39.89
Days to maturity	82.07	81.56	80.93	81.40	84.85
Plant height (cm)	112.00	94.71	101.37	98.16	112.55
Primary branches per plant	3.30	2.95	2.70	2.10	2.89
Secondary branches per plant	3.29	2.05	1.88	1.38	2.50
Siliqua per plant	123.65	101.99	83.23	63.39	96.52
Siliquae length (cm)	7.75	7.64	7.78	7.42	7.54
Seeds per siliqua	21.75	21.81	21.64	19.61	20.75
1000-seed weight (g)	3.52	3.52	3.27	3.40	3.50
Seed yield per plant (g)	8.75	6.96	5.74	4.20	6.26

the highest cluster means for primary branches per plant and maximum seeds per siliquae with minimum seed yield per plant were obtained from the cluster II.

4.4.3 Canonical Variate Analysis (CVA)

Canonical Variate Analysis (CVA) was done to compute the inter-cluster distances. The intra and inter-cluster distance (D^2) values were shown in Table 8 and the nearest and farthest cluster from each cluster based on D^2 value is given in Table 9. In this experiment, the inter-cluster distances were higher than the intra-cluster distances thus indicating broader genetic diversity among the genotypes of different groups. Islam and Islam (2000) reported that the inter-cluster distances were larger than the intra-cluster distances.

Inter cluster distance

The highest inter-cluster distance was observed between clusters I and IV (10.309), followed by between cluster III and I (7.112), V and IV (6.390), II and IV (6.373). The higher inter-cluster distances between these clusters indicate to obtain wide spectrum variability of population. However, the highest inter cluster distance was observed between clusters I and IV indicated the genotypes in these clusters were diversed than those clusters. The greater the distance between two clusters the greater the divergence (Table 8). The minimum distance observed between clusters III and IV (3.513) (Table 9) indicated close relationship among the genotypes included and genotypes in these clusters were less diversed than others.

Intra cluster distance

The intra cluster D^2 values were given in Table 8. The intra cluster distance was observed in the clusters. The intra cluster distance was higher in cluster IV (0.086) and lowest in cluster II (0.032) (Table 8). The intra cluster distances in all the five clusters were lower than the inter cluster distances and which indicated that genotypes within the same cluster were closely related. The inter cluster distances were larger than the intra cluster distances which indicated wider genetic diversity among the genotypes of different groups.

Table 8. Intra (Bold) and inter cluster distances (D^2) for 62 genotypes of *Brassica napus* L.

Cluster	I	II	III	IV	V
I	**0.062**	5.440	7.112	10.309	4.642
II		**0.032**	3.605	6.373	4.243
III			**0.073**	3.513	3.675
IV				**0.086**	6.390
V					**0.047**

Table 9. The nearest and farthest clusters from each cluster between D^2 values in *Brassica napus* L. genotypes

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	**I**	**V (**4.642)	**IV (**10.309)
2	**II**	**III (**3.605)	**IV (**6.373)
3	**III**	**IV (**3.513)	**I (**7.112)
4	**IV**	**III (**3.513)	**I (**10.309)
5	**V**	**III (**3.675)	**IV (**6.390)

It is assumed that the maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. Furthermore, for a practical plant breeder, the objective is to achieve high-level production in addition to high heterosis. In the present study the maximum distance existence between cluster I and IV (Table 9). Pandey *et al*. (2013) found maximum inter-cluster distance was found between cluster II and III indicating high genetic divergence among genotypes of these groups. Zaman *et al*. (2010) reported that the genotypes from cluster I and III could be utilized in the hybridization program for getting desirable transgressive segregants and high heterotic response due to getting maximum yield along with short duration. Keeping this in view, it appears that the crosses between genotypes from cluster I with cluster IV might produce high level of segregating population. The crosses between the genotypes belonging cluster V with cluster IV, cluster III with cluster I, might produce high heterosis in respect of earliness and yield. So the genotypes belonging to these genotypes have been selected for future hybridization program.

4.4.4 Contribution of traits towards divergence of the genotypes

The latent vectors (Z_1 and Z_2) obtained from principal component analysis (PCA). The important characters responsible for genetic divergence in the axis of differentiation in vector I (Z_1) were siliqua per plant (0.1487), siliqua length (0.1598) and seed yield per plant (0.1108). In vector II (Z_2), 50% flowering (0.1901), plant height (0.1659), number of secondary branch per plant (1.1125) (Table 10). The characters contributing the most to the divergence are given greater importance when deciding on the cluster for the purpose of further selection and choice of parents for hybridization. The role of days to 50% flowering, plant height and number of secondary branch in both the vectors were important components for genetic divergence in these materials. Islam and Islam (2000) reported days to 50% flowering, plant height, primary branches per plant and number of siliqua per plant contribute maximum in divergence in rapeseed and mustard. Begum *et al.* (2007) reported that branches per plant and number of number of seeds siliquae contributed the maximum towards divergence in the existing linseed germplasm.

Table 10. Relative contributions of the ten characters of 62 genotypes of *Brassica napus* L. to the total divergence

Characters	Principal Component	
	Vector-1	**Vector-2**
Days to 50% flowering	0.1256	0.1901
Days to maturity	-0.1310	-0.1407
Plant height (cm)	0.0643	0.1659
Primary branches per plant	-0.1931	-0.6343
Secondary branches per plant	0.1770	1.1125
Siliqua per plant	0.1487	-0.0443
Siliquae length (cm)	0.1598	-0.1166
Seeds per siliqua	-0.0725	-0.0539
1000-seed weight (g)	-0.1634	-0.6464
Seed yield per plant (g)	0.1108	-0.1884

CHAPTER V

SUMMARY AND CONCLUSION

From the present research work "Genetic variability, correlation and path analysis in F_4 generation of *Brassica napus* L." the following conclusions have been derived;

The present experiment was undertaken to study the variability, character association and diversity in 62 genotypes of *Brassica napus* L. based on ten characters. The salient findings of the present study have been summarized on the basis of the characters studied. Analysis of variance showed significant differences for the genotypes.

From variability analysis of F_4 progenies, it was observed that significant variation exist among all the genotypes used for most of the characters studied. Plant height exhibited highest in G4 and lowest in G19. The highest number of primary branches per plant was recorded in G3 and lowest number was recorded in G53 and G36. The highest number of secondary branches per plant was observed in in G3 and lowest in G36. The minimum days to 50% flowering was found in G35 and highest in G28. The lowest days to maturity was also observed in G24 and G35 and the highest in G14.

The number of siliqua per plant showed the highest in G4 and lowest in G53. The highest siliqua length was recorded in G3, G26 and the lowest in G15. The number of seeds per siliqua was found highest in G51 and the lowest in G61. The thousand seed weight was found highest in G4 and the lowest in G61. The seed yield per plant was the highest in G4 and the lowest observed in G53.

However, the phenotypic variance and phenotype coefficient of variation were higher than the corresponding genotypic variance and genotypic coefficient of variation for all the characters under study. Phenotypic coefficients of variation were also close to genotypic coefficients of variation for most of the characters except Plant height, days to 50% flowering, days to maturity and number of siliqua per plant. On the other hand, number of primary branch, number of secondary branch, number of seeds per siliqua, siliqua length , 1000 seed weight and seed yield per plant showed

least difference between phenotypic and genotypic variance suggesting least environmental influence and additive gene action for the expression of the characters.

Number of secondary branches per plant (98.70) exhibited the highest value of heritability while days to maturity (88.02) exhibited the lowest value of heritability. High heritability with high genetic advance in percent of mean was observed for number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, number of seed per siliqua 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.

High heritability with moderate genetic advance was observed for days to 50% flowering, plant height, siliqua length, number of seed per siliqua and thousand seed weight indicating medium possibility of selecting genotypes. High heritability with low genetic advance in percent of mean was observed for days to maturity indicating that non-additive gene effects were involved for the expression of these characters.

Correlation coefficients among the characters were studied to determine the association between yield and yield components. In general, most of the characters showed the genotypic correlation co-efficient were higher than the corresponding phenotypic correlation co-efficient suggesting a strong inherent association between the characters under study and suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values. In few cases, phenotypic correlation co-efficient were higher than their corresponding genotypic correlation co-efficient suggesting that both environmental and genotypic correlation in these cases act in the same direction and finally maximize their expression at phenotypic level. The significant positive correlation with seed yield per plant were found with all most all the characters except days to 50% flowering which was positive but non-significant and days to maturity (non-significant negative) with seed yield per plant.

Path co-efficient analysis revealed that days to 50% flowering, number of secondary branch, number of siliqua per plant, number of seed per siliqua, and thousand seed weight had the positive direct effect on yield per plant whereas days to 80% maturity,

plant height, number of primary branch and siliqua length had the negative direct effect on yield per plant.

The genotypic correlation with seed yield per plant was positive and considerably higher in magnitude except days to 50% flowering which was non-significant but positive and days to maturity non-significant negative. It is mainly due to high positive direct effect and positive indirect effects via the other characters and selection would be effective for this trait. The path coefficient studies indicated that number of primary branch, number of secondary branch, siliqua per plant, number of seeds per siliquae and thousand seed weight were the most important contributors to seed yield per plant which could be taken in consideration for future hybridization program

Genetic diversity among *Brassica napus* genotypes was performed through Principal Component Analysis (PCA), Cluster Analysis, Canonical Variate Analysis (CVA) using GENSTAT computer program. The 62 genotypes fell into five distant clusters. The cluster IV comprised the maximum number (19) of genotypes followed by same in cluster cluster III (18). The cluster I and V comprised 10 and 9 genotypes respectively. The lowest number of genotypes was present in cluster II. The highest inter-cluster distance (10.309) was observed between the cluster I and IV, if involved in hybridization may produce a wide spectrum of segregating population. The lowest inter-cluster distance (3.513) was observed between the cluster III and IV.

The inter-cluster distances were larger than the intra-cluster distances. The intra-cluster distance in the entire five clusters was more or less low indicating that the genotypes within the same cluster were closely related.

Based on the results of the study, the following conclusions and recommendations may be drawn:

1. The high heritability coupled with high genetic advance in percent of mean observed in number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, number of seed per siliqua 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.

2. The significant positive correlation with seed yield per plant were found with all most all the characters except days to 50% flowering which was positive but non-significant and days to maturity (non-significant negative) with seed yield per plant. This results suggested that yield per plant can be increased by improving these characters.

3. The days to 50% flowering, number of secondary branch, number of siliqua per plant, number of seed per siliqua, and thousand seed weight had the positive direct effect on yield per plant. So yield improvement was associated with these characters.

4. Wide genetic diversity was observed in 62 genotypes of *Brassica napus* L., which were grouped into five clusters. The highest inter-cluster distance (10.309) was observed between the cluster I and IV. The genotypes of clusters I and V were more diversed from the genotypes of other cluster.

5. The role of days to 50% flowering, plant height and number of secondary branch in both the vectors were important components for genetic divergence in these materials.

Recommendations:

1. Considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotypes G4 for higher seed yield per plant, plant height, number of siliqua per plant. G3 for higher number of primary branches and secondary branches per plant, highest siliqua length and G51 for seed per siliqua. G24 and G35 for short duration and early maturity.

2. The genotypes of cluster I and IV could be used as parents for future breeding programme to developed *Brassica napus L*. variety.

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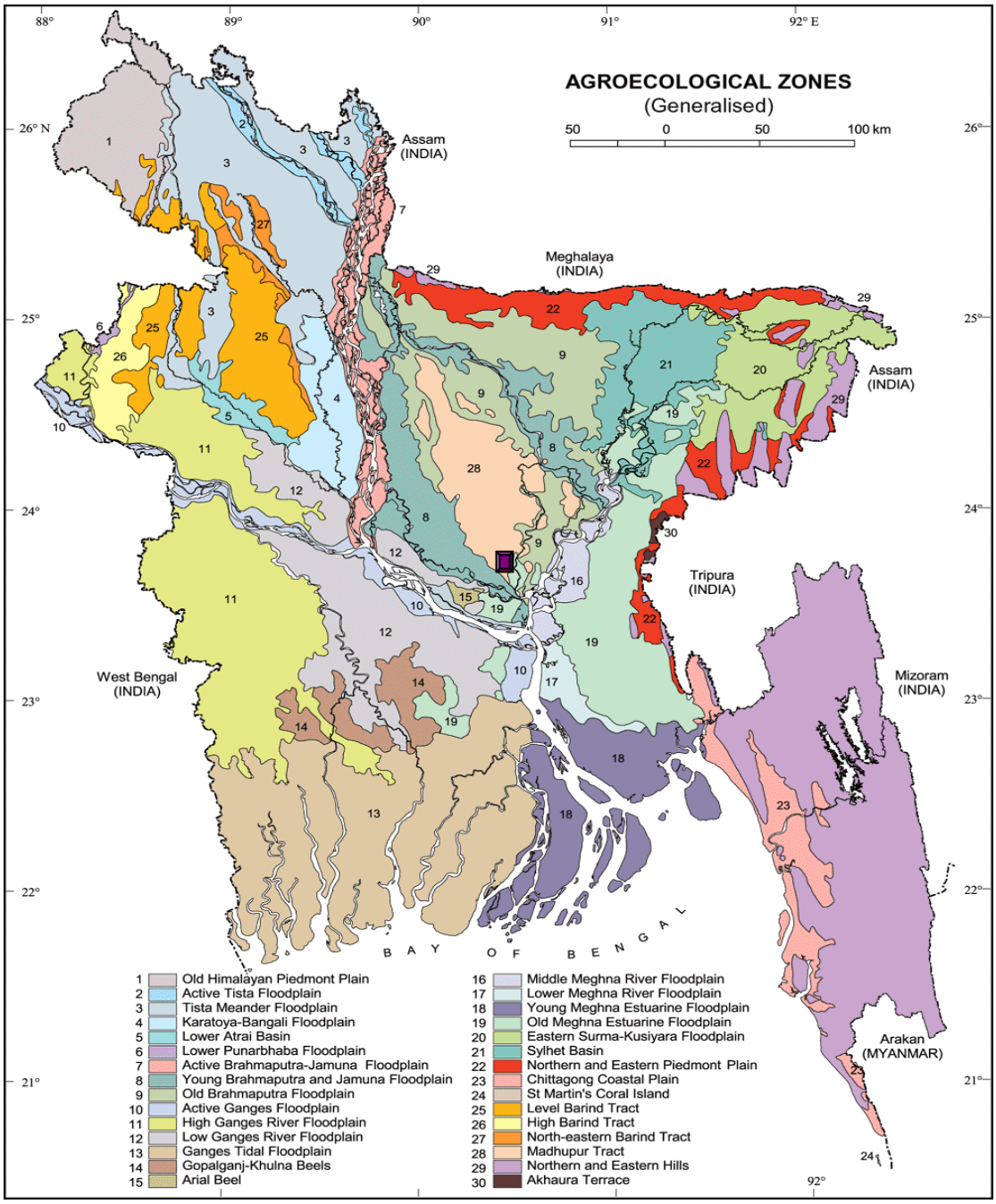
APPENDICES

Appendix I. Map showing the experimental site under the study



The experimental site under study

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

A. Physical composition of the soil

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

B. Chemical composition of the soil

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

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

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

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

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

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

Genotype	50F	DM	PH	NPB	NSB	NSP	SL	NSS	TSW	SYP
G1	31.00	78.00	92.20	3.22	3.06	85.67	8.44	22.57	3.50	7.17
G2	33.00	79.00	105.77	3.99	3.80	133.30	7.94	22.64	3.62	9.83
G3	38.00	85.00	113.03	4.40	5.77	119.78	8.70	19.64	3.70	8.60
G4	41.00	86.00	120.53	3.11	3.27	137.67	7.10	19.45	4.12	10.47
G5	31.00	78.00	109.78	2.91	2.49	127.83	7.70	20.59	3.33	8.28
G6	30.33	77.00	117.83	3.51	3.33	124.57	7.17	22.39	3.45	8.86
G7	29.00	76.00	110.60	2.62	3.23	119.89	6.91	19.59	3.54	8.38
G8	31.00	77.67	101.63	2.68	2.26	76.47	8.38	23.33	3.73	6.24
G9	41.00	86.00	113.11	3.26	2.98	105.82	8.19	21.19	3.57	6.40
G10	37.00	84.00	115.40	3.35	2.55	117.53	7.91	20.65	3.43	6.70
G11	33.00	77.00	108.73	3.13	3.08	95.84	8.20	21.88	3.45	5.44
G12	32.00	79.00	98.46	3.08	3.19	88.93	8.00	21.99	3.25	7.31
G13	36.67	82.00	112.60	3.06	3.29	117.03	8.01	23.31	3.61	9.11
G14	43.00	91.00	115.02	2.74	2.60	98.57	7.65	21.73	3.48	7.01
G15	41.00	87.00	97.22	3.58	2.71	99.17	6.37	15.87	3.96	6.10
G16	34.00	78.00	97.37	2.46	2.12	94.66	7.72	21.00	3.50	5.45
G17	42.00	86.67	115.03	2.71	3.10	106.53	7.58	20.43	3.74	6.45
G18	39.00	82.00	105.63	3.66	2.73	91.53	7.38	19.33	3.94	6.68
G19	37.00	82.00	88.83	2.63	1.89	111.09	7.98	23.17	3.40	8.80
G20	32.00	77.00	103.03	2.47	1.31	78.92	7.22	19.27	3.49	4.80
G21	36.00	82.00	113.72	2.56	2.32	93.46	7.09	16.73	3.54	5.47
G22	37.00	81.00	90.71	1.63	1.06	57.90	8.20	22.29	3.56	4.35
G23	41.00	84.00	114.06	3.19	1.98	86.53	6.92	18.98	3.19	4.89
G24	32.00	75.00	104.97	2.65	1.58	74.37	8.19	23.67	2.94	5.07
G25	42.00	85.00	96.65	2.44	1.37	78.27	7.40	20.41	3.27	5.32
G26	37.00	84.00	103.03	1.93	1.41	59.93	8.70	21.43	3.41	4.49
G27	36.00	82.00	107.60	2.09	1.24	64.99	7.29	19.87	3.34	4.37
G28	44.00	89.00	98.60	2.60	1.33	79.09	8.35	21.43	3.14	5.17
G29	35.00	81.00	101.96	3.02	1.74	83.24	7.09	19.59	3.06	5.11
G30	32.00	76.00	99.02	2.92	1.89	64.59	7.25	19.34	3.67	4.87
G31	34.67	80.00	102.03	2.38	1.89	85.00	8.01	24.66	3.13	6.18
G32	33.00	79.00	112.72	2.49	1.72	83.27	7.23	25.63	2.91	6.25
G33	35.00	81.00	110.87	2.60	1.68	63.22	8.52	23.11	3.67	5.27
G34	38.67	82.00	105.30	1.89	1.31	71.93	8.05	22.29	2.94	4.22
G35	27.00	75.00	105.57	2.20	1.61	84.18	7.97	20.83	3.50	6.11
G36	30.00	76.00	99.87	1.43	0.90	53.47	7.18	18.54	3.55	3.80
G37	31.00	77.00	94.84	2.09	1.46	63.63	6.94	20.67	2.97	3.83
G38	28.00	75.00	93.59	1.75	1.06	62.91	6.92	20.10	3.59	3.97
G39	28.00	77.00	92.47	2.13	1.36	66.67	7.39	18.68	3.19	3.86
G40	32.00	81.00	98.70	2.87	1.58	94.73	8.55	24.53	3.11	7.08

Appendix IV. Continued

G41	**33.00**	**81.00**	**97.95**	**2.71**	**2.22**	**69.51**	**7.22**	**21.29**	**3.10**	**4.64**
G42	35.00	81.00	94.18	2.66	1.85	69.49	6.83	16.77	3.53	4.57
G43	43.00	88.00	95.63	2.64	1.59	89.53	7.45	22.06	3.07	4.99
G44	44.00	89.00	116.86	2.48	2.14	98.67	7.46	23.11	3.24	7.16
G45	40.00	85.00	93.44	2.95	2.04	101.62	7.70	23.50	3.26	7.55
G46	31.00	79.00	108.17	3.05	2.32	89.19	7.18	17.24	3.20	4.82
G47	31.33	78.00	103.83	2.72	2.18	82.85	8.19	18.53	3.29	5.65
G48	41.00	87.00	103.50	4.04	3.22	120.44	8.70	23.76	3.36	8.04
G49	43.00	89.00	99.00	2.12	1.13	63.70	7.36	21.21	3.35	4.35
G50	42.00	86.67	110.93	2.05	1.93	118.43	7.37	25.50	3.05	9.23
G51	41.00	87.00	106.07	2.13	1.52	87.40	8.19	27.93	3.24	5.99
G52	40.00	86.00	110.77	2.26	1.56	91.76	7.37	23.34	3.38	6.81
G53	41.00	87.00	100.90	1.42	1.06	47.85	6.38	15.77	3.81	3.14
G54	32.00	81.00	96.70	2.29	1.75	69.46	8.43	19.27	3.34	4.36
G55	42.00	87.00	101.31	1.87	1.16	56.46	7.49	16.65	3.62	3.24
G56	41.00	87.00	97.47	2.35	1.11	70.33	6.61	19.20	3.34	4.49
G57	38.00	81.00	100.69	3.14	1.42	91.04	7.33	21.02	3.38	6.41
G58	36.00	80.00	94.63	2.50	1.52	75.33	7.05	18.43	3.38	4.47
G59	33.00	76.33	92.71	3.21	1.94	110.67	7.53	22.79	3.91	6.79
G60	36.67	79.33	90.96	2.37	1.44	63.30	7.29	21.97	3.20	4.78
G61	39.00	83.33	89.27	1.71	1.09	65.05	6.85	14.20	3.46	3.11
G62	43.33	88.00	97.83	3.27	2.20	85.48	8.30	21.02	3.32	6.29
Mean	36.25	81.89	103.08	2.67	2.06	87.41	7.61	20.93	3.41	5.95
Min.	27.00	75.00	88.83	1.42	0.90	47.85	6.37	14.20	2.91	3.11
Max.	44.00	91.00	120.53	4.40	5.77	137.67	8.70	27.93	4.12	10.47

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

Appendix V. Principal component score 1 & 2.

Genotype	Z_1	Z_2
G1	4.03	-12.11
G2	-45.48	-9.16
G3	-34.01	3.6
G4	-53.11	7.77
G5	-40.69	-5.74
G6	-39.33	1.01
G7	-33.03	-4.9
G8	11.06	-2.49
G9	-20.33	7.92
G10	-32.05	5.35
G11	-9.24	0.14
G12	-0.5	-6.79
G13	-31.2	2.2
G14	-13.89	13.45
G15	-10.3	-3.64
G16	-5.65	-8.4
G17	-21.43	10.01
G18	-4.65	2.36
G19	-20.3	-16.4
G20	8.66	-1.59
G21	-7.96	7.72
G22	31.45	-4.52
G23	-1.49	11.9
G24	12.54	0.17
G25	10.14	-0.35
G26	26.79	6.45
G27	21.04	8.23
G28	8.75	3.25
G29	4.46	-0.85
G30	23.44	-2.47
G31	2.52	-1.69

Appendix V. Continued

G32	1.96	6.63
G33	21.91	10.54
G34	14.65	5.88
G35	3.01	-3.09
G36	34.29	-0.24
G37	25.32	-5.78
G38	26.43	-8.48
G39	23	-9.44
G40	-6.27	-7.06
G41	18.68	-2.22
G42	19.63	-4.59
G43	-0.74	-2.02
G44	-14.39	14.61
G45	-12.15	-8.48
G46	-2.42	1.03
G47	4.59	-1.61
G48	-32.77	-2.74
G49	23.75	6.3
G50	-32.46	4.11
G51	-1.08	5.98
G52	-6.17	8.36
G53	39.15	9.69
G54	19.12	-3.6
G55	30.61	8.67
G56	17.78	2.29
G57	-3.06	-2.41
G58	13.82	-5.38
G59	-20.34	-16.49
G60	26.16	-6.1
G61	25.07	-5.47
G62	2.63	0.72