GENETIC VARIATION AND CHARACTER ASSOCIATION IN F_5 ADVANCED POPULATIONS OF *Brassica napus* L.

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DECEMBER, 2018

GENETIC VARIATION AND CHARACTER ASSOCIATION IN F_5 ADVANCED POPULATION OF *Brassica napus*L.

BY

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REGISTRATION NO: 17-08233

A Thesis
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
SEMESTER: July-December, 2018

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CERTIFICATE

This is to certify that the thesis entitled "**GENETIC VARIATION AND CHARACTER ASSOCIATION IN F_5 ADVANCED POPULATIONS OF *Brassica napus* L."** submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING**, embodies the result of a piece of bonafide research work carried out by **KANIZ FATEMA KEYA,** Registration number: 1**7-08233** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

I further certify that any help or source of information received during the course of this investigation has duly been acknowledged.

Date: December, 2018
Place: Dhaka, Bangladesh

Prof. Dr. Firoz Mahmud
Supervisor


DEDICATED TO MY BELOVED PARENTS & MYSELF

ACKNOWLEDGEMENTS

First and foremost, praises and thanks to the Almighty Allah, for His showers of blessings throughout my research work to complete the research successfully.

*I would like to express my deep and sincere gratitude to my research supervisor,**Professor Dr.Firoz Mahmud**, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University,Dhaka,forgivingmetheopportunitytodoresearchandprovidi ng invaluableguidancethroughoutthisresearch. .Hisdynamism,vision,sincerityand motivation have deeply inspired me. He has taught me the methodology to carry out the research and to present the research works as clearly as possible. It was a great privilege and honor to work and study under his guidance. I would also like to thank him for his friendship,empathy,andgreatsenseofhumor.*

*The earnest indebtedness to my Co-supervisorand Chairman**Prof. Dr. Kazi Md. Kamrul Huda**, Department of Genetics and Plant Breeding, SAU for his continuous support, constructive criticism and valuable suggestions.*

*I express my sincere respect to the teachers of **Prof. Dr. Md. Shahidur Rashid Bhuiyan, Prof. Dr. Md. Sarowar Hossain,Prof. Dr. Naheed Zeba,***

Prof. Dr. Jamilur Rahman, Prof. Dr. Mohammad Saiful Islam,Prof. Dr. Ashaduzzaman Siddikee,Prof. Dr. Md. Abdur Rahim,Prof. Dr. Md. Harun-Ur-Rashid,*Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, for their valuable teaching, direct and indirect advice, and encouragement and co-operation during the whole study period.*

I express my sincere respect to the honourable Vice Chancellor ofSher-e-Bangla Agricultural University for his supreme support to the research work.

I am specially thankful to ***Nasrin Jahan****, Scientific Officer, Plant Breeding Division, BARI for her helpful co operation in compiling data and valuablesuggestion to analysis the data and for giving technical support to prepare this thesis paper.*

I am pleased to all staff and workers of Genetics and Plant Breeding Department and all farm labours and stall of Sher-e-Bangla Agricultural University, for their valuable and sincere help in carrying out the research work.

Finally, I would like to express my deepest sense of gratitude and feeling to my beloved parents and friends for their blessings, encouragements, sacrifices, affectionate feelings, dedicated efforts to reach this level.

The Author

December 2018, Dhaka

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ABSTRACT

A research was conducted by using fourty four (44) F_5 advanced populations of*Brassica napus* and grown in the experimental farm of Sher-e-Bangla Agricultural University, Dhaka to study the genetic variability, heritability, correlation and path coefficient analysis during November 2017 to February 2018. Analysis of variance revealed significant variations among the genotypes for all the traits studied. For most of the character the genotypes were found significantly variable. Phenotypic variances were comparatively higher than the genotypic variances for all the studied characters. PCV were higher than the GCV for all the characters studied. Plant height (67.59%), number of primary branches per plant (51.37%), number of secondary branches per plant (57.50%), number of siliqua/plant (91.76%), number of seeds/siliqua (73.20%), thousand seed weight (66.43%) andyield /plant (92.33%)showed high heritability with high genetic advance. Correlation studies revealed significant positive association of number of primary branches per plant (0.330), number of secondary branches per plant (0.353), siliqua length (0.337), number of seeds per siliqua (0.772) and thousand seed weight (0.829) had significant positive correlation with seed yield per plant. Path coefficient indicated positive direct contribution towards seed yield per plant through days to 50% flowering (0.125), number of primary branches per plant (0.238), number of secondary branches per plant (0.029), number of siliquae per plant (0.123), siliqua length (0.116), number of seeds per siliqua (0.299) and

thousand seed weight (0.470). Days of maturity (-0.115) and plant height (-0.002) had the negative direct effect on yield per plant. Genotypes G5, G9, G12, G16, G22, G25 and G32 can be further used for advanced research or varietal improvement program and high yielding variety can be developed.

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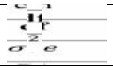
COMMONLY USED SOME ABREVIATIONS

Full word	Abbreviation
At the rate	@
Agro Ecological Zone	AEZ
Analysis of variance	ANOVA
And others	*et al.*
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Bangladesh	BD
Centimeter	cm
Degrees of Freedom	**df**
Environmental variance	
Genetic Advance	GA
Genotypic coefficient of variation	GCV
Heritability in broad sense	
Indian Agricultural Research Institute	IARI
Journal	*J.*
Kilogram	Kg
Phenotypic coefficient of variantion	PCV
Phenotypic variance	
Percentage of Coefficient of Variation	CV%
Thousand seed weight	TSW

Chapter I
Introduction

CHAPTER I
INTRODUCTION

Brassica napus is the most important oilseed crop in Bangladesh. It occupies the first position in respect of area and production among the oil crop grown in Bangladesh (Sharafi *et al.,* 2015;Anonymous,2015). *Brassica napus* is a member of the Brassicaceae family, which consists of approximately 25 tribes, 338 genera and 3709 species (OECD 2012). The genus *Brassica* holds the most economically valuable position in the tribe Brassicaceae.

The Brassicaceae family includes many well-known plants, such as the model plant *Arabidopsis thaliana* (mouse-ear cress), the weedy relative *Sinapisarvensis* (wild mustard) and vegetable crops such as *B. napus* (rutabaga, Siberian kale), *B. rapa* (Chinese cabbage, pai-tsai, mizuna, Chinese mustard, broccoli raab and turnip), *B. oleraceae* (cabbage, broccoli, cauliflower, Brussels sprouts, Kohlrabi, collards, kale) and *Raphanus sativus* (radish). Examples of condiment crops of the Brassicaceae family include *B. nigra* (black mustard), *B. carinata* (Ethiopian mustard), *B. juncea* (brown or Indian mustard), *Armoracearusticana* (horseradish) and a number of other minor pot herbs and salad vegetables (Downey and Rimmer *et al.,* 1993; OECD 2012; Rakow *et al.,* 2004).

Brassica napus is a self-compatible species displaying a high degree of self-pollination, while most *B. rapa* is self-incompatible (except for the Indian subspecies yellow sarson, which is self-compatible) (Downey and Röbbelen, 1989).

Rapeseed (*B. napus*)is an important oleiferous crop.The major producers of rapeseed are Canada, China, India and EU countries. Amphidiploid *B. napus*(AACC,2n=38) resulted from the spontaneous hybridization between its diploid progenitors, *B. oleracea* (CC, 2n=18) and *B. rapa* (AA,2n=20) (Downey and Rimmer 1993; OECD 2012).This cytogenetic relationship was first proposed

in 1935 as the U triangle (Nagaharu, 1935). The triangle depicts the three monogenomic diploids *B. nigra* (B genome, n=8), *B. oleraceae* (C genome, n=9) and *B. rapa* (A genome, n=10) and the three digenomic species *B. carinata* (BC genome, n=17), *B. juncea* (AB genome, n=18) and *B. napus* (AC genome, n=19). This cytogenetic relationship is believed to have evolved naturally, without cultivation (Downey and Rimmer*etal.*,1993). Because tetraploid Brassica species share a genome with their diploid parents, gene flow can continue in both direction.

The seeds of modern varieties typically contain 40% to 45% oil. Despite of oil, it also holds 18 to 22 percent proteins which consist of different protein units like cysteine, methionine and lysine(Khan, 2014). It is not only a high energy food but also a carrier for fat soluble vitamins (A, D, E and K) in the body.

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/ha (BBS, 2015). In our country,*B. rapa* is the main crop producing species of *Brassica*, but its yield is the lowest in the world (FAOSTAT 2013).Annually the country is producing about 832638.72 tons of edible rapeseed oil as which is very low against the requirement (BBS, 2015b). Bangladesh imported 89970.08 tons of edible oil to meet up the annul requirement of the country in the year of 2014-15, which cost 3718457000 Tk. (BBS, 2015c).

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 and it also provides both the essential fatty acids such as linolenic acid and linoleic acid to the human body which is lacking most of the edible oil. But in Bangladesh, there is a limited scope to increase acreage due to pressure of other 3 crops in the rabi season and due to high cost and long growing period, farmers are not interested to mustard seed production. The main reasons

behind these are the use of low yielding local indigenous cultivars, unavailability of locally developed hybrids and low management practices and mostly grown under residual soil moisture in winter season by following poor cultural practices; the average yield is quite low than in the developed countries (Hasanuzzaman and Karim, 2007).

So, development of improved varieties of *Brassica napus* with short durations, better quality, higher yield are the most important issues with high priority. For replacing the long duration low yielding variety of *Brassica napus*, this research was carried out with F_5advanced populations which would be expected to be short durational and high yielding. By comparison among them, it would possible to select for mitigating the demand of edible oil for future.

One of the main objectives of any breeding program is to produce high-yielding and better-quality lines for release as cultivars to farmers. The prerequisite to achieve this goal is to find sufficient amount of variability, in which desired linesare to be selected for further manipulation to achieve the target. Development of high-yielding cultivars requires a thorough knowledge of the existing genetic variation for yield and its components. The observed variability is a combined estimate of genetic and environmental causes, of which only the former one is heritable. However, estimates of heritability alone do not provide an idea about the expected gain in the next generation, but have to be considered in conjunction with estimates of genetic advance, the change in mean value among successive generations (Shukla *et al.*, 2006).

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.

Correlation coefficient is an important statistical procedure to assess breeding programs for high yield, as well as to examine direct and indirect contributions to

yield variables (Ali *et al.,* 2003). It shows 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, 2013).

Path-coefficient technique splits the correlation coefficients into direct and indirect effects via alternative characters or pathways and thus permits a critical examination of components that influence a given correlation and can be helpful in formulating an efficient selection strategy (Sabaghnia *et al.,* 2010). In plant breeding path-coefficient analysis has been used to explain clearly the relations among yield components and assist identification of traits that are useful as selection criteria to improve crop yield (Ali *et al.,* 2013).

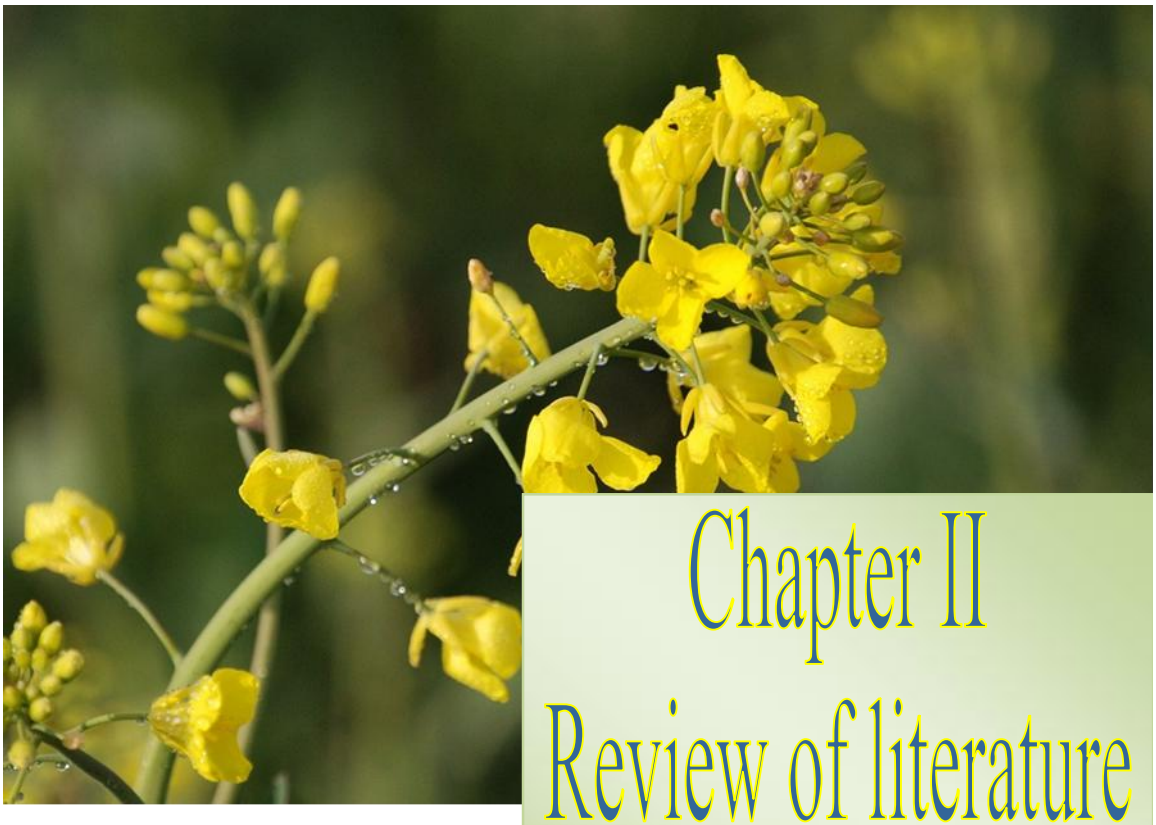
Considering the importance of edible oil in country, an experiment was carried out with following objectives:

1. To study the variability in F_5 advanced populations generated through intergenotypic crosses,

2. To estimate the genetic coefficient of variation, relationship among yield associated traits for improving seed yield of rapeseed advanced lines and cultivars,

3. To assess genetic diversity among the genotypes and also classify the genotypes via factor analysis and

4. To select the best promising genotypes for early maturity and high yielding population.



Chapter II
Review of literature

CHAPTER II

REVIEW OF LITERATURE

Brassica species has obtained much attention by a large number of researchers on various aspects of its production and utilization. It is the most important oil crop of Bangladesh and many countries of the world too. Many studies on the variability, interrelationship, path co-efficient analysis, heritability and genetic advance have been performed in many countries of the world. The review of literature concerning the studies presented under the following heads:

2.1 Variation for yield and yield contributing characters

2.2 Variability, heritability and genetic advance

2.3 Correlation among different characters

2.4 Path co-efficient analysis

2.1 Variation for yield and yield contributing characters

Variation for yield and yield contributing characters yield in *B. napus* is the major object of variety development program. Selection for yield is always associated with selection for yield contributing characters.

Jahan (2008) was conducted to study on inter- genotypic variability and genetic diversity in 10 F_4 lines obtained through intervarietal crosses along with eight released varieties of *Brassica rapa* during November 2007 to March 2008. Significant variation was found among all genotypes for all the characters studied. Considering genetic parameters, high genotypic co-efficient of variation (GCV) was observed for number of secondary branches/plant, siliquae/plant, yield/plant whereas days to maturity showed very low GCV.

While working on 58 genotypes *of Brassica napus* Mahmud (2008) was studied that intergenotypic variability. Significant variation was found 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 wereobtained for days to 50% flowering, number of secondary branches per plant, seeds per siliqua, and siliqua length.

Baradaran *et al.* (2007)undertaken results of the field studies in Iran to determine the variation in 15 rape cultivars. The analysis of variance result showed that significant differences between yield and number of siliqua per plant, harvest index oil percent. They noticed that most important trails for high PCV and GCV for the number siliqua per plant and 1000- grain weight.

A field experiment by Khan *et al*. (2006) was studied that variation for yield and yield contributing characters is rapeseed and reported significant variation for eleven accessions of *Brassica napus* L.. They indicated that a wide range of genetic variation with high PCV and GCV for seed yield, siliquas per plant, seeds per siliqua, siliqua length.

Xu-Suqin *et al.* (2006) reported the presence of considerable amount of variability between yield per plant and 9 yield related characters studied in 24 superior rape cultivars. Results found that phenotypic and genotypic coefficient of variation of siliquas per raceme seeds per siliqua and 1000-seed weight or yield per plant were significant.

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

Kardam and Singh (2005) reported the nature and magnitude of associations for 10 characters in progenies of Indian rapeseed obtained from six crosses during rabi (2002-2003) in Rajasthan, India. PCV were higher in magnitude compared to

GCV for most of the characters. Seed yield per plant was significantly and positively variable with plant height, number of seeds per siliqua and 1000-seed weight.

Rukhsana *et al.* (2005) evaluated the 14 improved cultivars of rapeseed in Bahawalpur, Pakistan. Highly significant variation was observed for plant height, number of siliqua per plant, number of seeds per siliqua and seed yield.

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

A studied by Katiyar *et al.* (2004)on variability for the seed yield in ninety intervarietal crosses of *Brassica campesiris*. Existence of significant variation among parents and crosses indicated the presence of adequate genetic variance between parents which reflected in differential performance of individual cross combinations.

An experiment was carried out by Thakra *et al.* (2004) studied on variation for yield and yield contributing characters in rapeseed and reported significant variation for eight Indian rapeseed parental lines and their 28 F_1 hybrid. They noticed high PCV and GCV for plant height and seed yield characters.

According to Rameah *et al.* (2003) have studied eight genotypes of rape, including six cultivars (Shiralee, Regent, Ceres, PF7045/91, Darmor and Falcon) and two breeding lines (Yaster × Tower (BL1) and Cobra × A.W. (BL2)) to determine the genetic parameter for number of siliquas per main axis, number siliquas per plant, length of siliqua, number of seeds per siliquas, 1000-seed weight, seed yield. Analysis of variance revealed significant general (a) and specific (b) combining

ability. For, 1000-seed weight, only the general combining ability mean square was statistically significant.

Ghosh and Gulati (2001) studied genetic variability and association of yield components in Indian mustard among 12 yield components for 36 genotypes selected from different geographical regions. The genotypic and phenotypic 8 coefficients of variability (GCV and PCV, respectively) were high in magnitude for all the characters except plant height. The differences between the PCV and GCV were narrow for all the characters studied, coupled with high heritability except plant height, indicating the usefulness of phenotypic selection in improving these traits. High heritability, coupled with high genetic advance was observed for oil content, harvest index, number of primary branches, number of siliqua on main shoot, main shoot length and number of seeds per siliqua. The result suggests the importance of additive gene action for their inheritance and improvement could be brought about by phenotypic selection.

Different morphophysiological characters of 29 genotypes of *B. napus* grown under normal and stress condition of production was studied by Sing *et al.,* (2001). They found the existence of significant genetic variability for days to 50% flowering.

2.2 Variability, heritability and genetic advance

Nanda *et al.*(1995) while working with 65 strains of *B. rapa*, he reported that days to first flowering varied both by genotypes and date of sowing.

Lekh *etal.(*1998) reported that secondary branches showed the highest genotypic co- efficient of variation. High genotypic and phenotypic co-efficient of variation was recorded for days to 50% flowering. Thousand seed weight is also an important trait of Brassica oil crops, where the highest consideration is on the seed yield. This trait has been found to vary widely from genotype to genotype and from environment to environment including macro and micro environments. The

coefficient of variation was high for thousand seed weight, pod length and number of seed per pod for both genotypic and phenotypic variability.

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

According to Khulbe*et al*.(2000) was conducted to estimate variability, heritability and genetic advance for yield and its components in Indian mustard revealed maximum variability for seed yield. All the characters except oil content exhibited high heritability with high or moderate genetic advance, suggesting the role of additive gene action in conditioning the traits. Non additive gene action appeared to influence the expression of days to maturity, while environment had a major influence on oil content. The use of pedigree selection or bi-parental mating in advanced generations was advocated to achieve substantial gains.

Tyagi *et al.(*2001) evaluated forty-five hybrids of Indian mustard obtained from crossing 10 cultivars for seed yield and yield components. The highest variation for plant height of parents and their hybrids was reported. The seed yield per plant exhibited the highest coefficient of variation (41.1%).

Genetic variability for nine traits in 25 genotypes study by Pant and Singh (2001); analysis of variance revealed highly significant genotypic differences for all traits studied, except for days to flowering, number of primary branches and oil content. Seed yield per plant had the highest coefficient of genotypic and phenotypic

variability. All traits showed high heritability, with the highest value estimated for seed yield per plant. The estimates of genetic advance were comparatively low for oil content and days to flowering. The genotypic 7 coefficient of variation and heritability estimates for oil content and days to flowering suggest that these traits cannot be improved effectively merely by selection.

Ghosh and Gulati, *et al.* (2001) studied genetic variability and association of yield components in Indian mustard among 12 yield components for 36 genotypes selected from different geographical regions. The genotypic and phenotypic coefficients of variability (GCV and PCV, respectively) were high in magnitude for all the characters except plant height. The differences between the PCV and GCV were narrow for all the characters studied, coupled with high heritability except plant height, indicating the usefulness of phenotypic selection in improving these traits. High heritability coupled with high genetic advance was observed for oil content, harvest index, number of primary branches, number of siliquae on main shoot, main shoot length and number of seeds per siliqua. This result suggests the importance of additive gene action for their inheritance and improvement could be brought about by phenotypic selection.

Shen *et al.* (2002) tested on 66 F_1 hybrids of *Brassica rapa* and significant differences were found between F_{1s} and their parents for yield per plant and seed oil content.

Chowdhary *et al.(*2003) studied variability in Indian mustard for 10 characters during rabi season in India. A wide range of variability was observed for all characters, except for primary branches per plant, siliqua length, number of seeds per siliqua and thousand seed weight. Genotypic and phenotypic coefficient of variability was recorded high for secondary branches per plant, seed yield per plant and number of siliqua per plant. High heritability coupled with high genetic advance as percentage of mean was observed for secondary branches per plant,

seed yield per plant and number of siliquae per plant, indicating preponderance of additive gene action.

Afroz *et al. (*2004) studied genetic variability of 14 genotypes of mustard and rape. The highest genetic advance was observed in percent of pollen sterility.

An experiment was conducted by Mahak *et al.* (2004) on genetic variability, heritability, genetic advance and correlation for eight quantitative characters. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all characters. High heritability coupled with high genetic advance in percentage of mean was observed for days to flowering, followed by thousand seed weight, days to maturity and plant height.

Niraj and Srivastava, (2004) studied on variability and character association in Indian mustard of 21 genotypes of *Brassica juncea*. RH-9704 and IGM-21 recorded the highest seed yield. Phenotypic coefficient of variation was high for oil yield per plant, seed yield per plant and seed weight. Heritability was high for test weight, days to flowering, days to maturity and plant height.

Evaluated by Akbar *et al.(*2007) on eight advanced lines of *Brassica junea* in Pakistan. He studied variability, heritability and genetic advance of different yield components that were under experiment. The highest GCV was found in seed yield per plant followed by plant height, siliqua per plant and thousand grain weights while the lowest GCV was in number of primary branches per plant. The highest heritability was found yield per plant followed by plant height, thousand grain weight, siliqua per plant and number of primary branches per plant. The maximum genetic advance was found in seed yield per plant followed by siliqua per plant, plant height, thousand grain weight and minimum in primary branches per plant.

A studied by Rashid, (2007) on variability of forty *oleiferous Brassica* species. Result revealed that genotypes showed wider variation for morphological

characteristics and thus were categorized under three cultivated species - *B. rapa*, *B. napus* and *B. juncea* considering genetic parameters. High GCV (Genotypic Co-efficient of Variation) value was observed for days to 50% flowering, days to maturity, plant height and number of siliqua per plant.

Parveen *et al.,* (2007) studied variability in F_2 progenies of the inter-varietal crosses of 17 *Brassica rapa* genotypes. The result revealed that there were significant variations among the different genotypes used in the experiment. Number of primary branches/plant and secondary branches/plant showed high heritability 9 coupled with high genetic advance and very high genetic advance in percentage.

A study was conducted by Hosen, (2008) using five parental genotypes of *Brassica rapa* and their ten F_3 progenies including reciprocals. The result revealed that there were large variations present among all the genotypes used in the experiment. Number of primary branches per plant, number of secondary branches per plant, days to 50% flowering, length of siliqua, number of seeds per siliqua, thousand seed weight and yield per plant showed least difference between phenotypic and genotypic variances. The values of GCV and PCV indicated that there was considerable variation among the all characters except days to maturity. The plant height, days to 50% flowering and number of siliqua per plant showed high heritability with high genetic advance and genetic advance in percentage of mean.

A field experiment was conducted by Jahan *et. al. (*2008) to study on inter-genotypic variability and genetic diversity in 10 F_4 lines obtained through inter-varietal crosses along with 8 released varieties of *Brassica rapa L*. Significant variation was observed among all genotypes for all the characters studied. Considering genetic parameters high genotypic coefficient of variation (GCV) was observed for number of secondary branches/plant, siliqua/plant, yield/plant whereas days to maturity showed very low GCV. High heritability with low

genetic advance in percent of mean was observed for days to maturity which indicated that non-additive gene effects were involved for the expression of this character and selection for such trait might not be rewarding. High heritability with moderate genetic advance in percent of mean was observed for plant height and days to 50% flowering indicating that this trait was under additive gene control and selection for genetic improvement for this trait would be effective.

An experiment was conducted out by Mahmud, (2008) with 58 genotypes of *Brassica rapa L.* to study inter-genotypic variability. Significant variation was observed among all the genotypes for all the characters studied except thousand seed weight. High GCV value was observed for number of secondary branches per plant. High heritability values along with high genetic advance in 10 percentage of mean were obtained for days to 50% flowering, number of secondary branches per plant, seeds per siliqua, and siliqua length.

Singh, (2010) studied sixty two F_1 and twenty four parental lines of *Brassica juncea* and observed that higher genotypic variation, high heritability and high genetic advance in seed perplant, secondary branches per plant, primary branches per plant, thousand seed weight and seed per siliqua.

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

Afrin *et al.* (2011) conducted an experiment in *Brassica napus* and studied heritability. The plant height showed the highest value of broad sense heritability while the number of primary branches per plant, number of secondary branches per plant, siliqua length, number of seed per siliqua, number of siliqua per plant,

thousand seed weight and seed yield per plant showed moderate broad sense heritability. Days to 80% maturity showed lowest heritability.

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

Evaluated by Khan *et al.* (2013) thirty F_7 segregating lines and two parents of *Brassica rapa* to study variability, heritability and genetic advance. The result revealed that significant variation was presented among all the genotypes for all the characters except thousand seed weight. The highest genotypic, phenotypic and environmental variances were observed in plant height while the lowest one was in length of siliqua followed by thousand grain weight. Thousand seed 11 weight, number of secondary branches per plant, seeds per siliqua, and siliqua length showed high heritability along with low genetic advance in percent of mean. Considering important performances, the genotypes G-15, G-19, G-1, G3, G-4, G-10, G-18, G21, and G-24 were found suitable for future breeding program.

Abideen *et al.* (2013)studied with eight genotypes of *Brassica napus* and observed that there were highly significant variations among the genotypes for most of the traits studied. Non-significant differences were in primary branches per plant and pods per plant among the genotypes.

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

According to Mekonnen *et al.* (2014) thirty six genotypes of Ethiopian mustard, *Brassica carinata* to study variability. The GCV ranged from 4.3% to 44.14% and PCV from 8.3% to 91.7%. Comparatively high GCV estimates were observed for number of pods per plant, primary and secondary braches per plant, seed yield per plot, and seed yield per hectare. The highest PCV was in primary branches per plant, higher GCV and PCV for seed yield, number of pods per plant, primary and secondary branches which indicated that, it might provide better scope for improvement through selection. Besides these, higher heritability along with higher genetic advance was observed in days to maturity, days to flowering, grain-filling period, number of pods per plant, secondary branches per plant, plant height, seed yield/plot and hectare and the lowest one was in primary branches per plant.

Muhammad *et al.* (2014) studied with four parental genotype along with twelve F_2 generation of *Brassica napus* and reported that days to 50% flowering were significantly different at 5 % level of significance. Plant height and pod 12 length showed high heritability and days to 50% flowering showed moderate heritability.

Ejaz-Ul-Hasan *et al.* (2014) studied on heritability of *Brassica napus* and the result stated that plant height, yield per plant and days to 50% flowering showed high heritability.

2.3 Correlation among different characters

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

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. Correlation between seed yield and yield contributing characters showed significant and positively correlated with number of

siliqua/plant, 1000 seed weight, straw yield, plant height, biological yield and harvest index. Correlation coefficient analysis of yield attributes had the highest and positive association with seed yield.

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 was reported. Significant planting dates and genotypes effect for phonological traits, yield components, seed yield and oil percentage revealed 16 significant differences of planting dates genotypes for these traits. The variation of correlation between duration of flowering and pods per plant was less than the correlation of duration of flowering to other traits in different planting dates by Rameeh, (2012).

An experiment was conducted by Rameeh, (2011) where 36 rapeseed genotypes including four cultivars and 32 advanced lines were evaluated in randomized complete block design with three replications. Siliquae per plant had significant positive correlation (0.80) with seed yield. So any change for this trait will have considerable effect on seed yield.

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

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

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

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

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

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

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

An experiment was conducted and studied correlation for eight quantitative characters by Mahak *et al.* (2004). Seed yield per plant showed positive

correlation with number of primary branches, length of main raceme, 1000-seed weight and oil content. Selection should be applied on these traits to improve seed yield in Indian mustard.

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

An experiment conducted by Niraj and Srivastava, (2004) on character association studies in Indian mustard of 21 genotypes of *Brassica juncea*. Seed and oil yields were positively and significantly correlated with plant height and primary branches but negatively correlated with test weight.

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

Pankaj *et al.* (2002)undertaken an experiment of four parental cultivars and the F_4 progenies of resultant crosses for correlation between yield and yield component traits. The genetic correlation was higher than the phenotypic correlation for the majority of the characters. The number of siliquae per plant, which had the strongest positive and significant correlation with yield per plant at both levels, was positively associated with the number of seeds per siliqua and test weight at both levels. The number of seeds per siliqua was positively associated with siliqua length and yield per plant at both levels.

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

Badsra and Chaudhary, (2001)studied correlation on 14 traits of 16 Indian mustard genotypes. Seed yield was positively correlated with stem diameter, number of siliqua per plant and oil content, while oil content was positively 19 correlated with harvest index only. Among the characters only three characters positively correlated with seed yield.

Ghosh and Gulati,(2001) studied association of yield components in Indian mustard among 12 yield components were found in 36 genotypes selected from different geographical regions. Seed yield exhibited significant positive association with yield contributing traits like days to 50% flowering, days to maturity, plant height, number of secondary branches, number of siliqua on main shoot and oil content.

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

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

A field experiment was carried out a study of correlation by Khulbe and Pant , (1999) using eight Indian mustard (*Brassica juncea*) parents and their 28

F_1hybrids and revealed 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.

The correlation co-efficient on seed yield and yield contributing characters in eight Indian mustard (*Brassica juncea*) parents and their 28 F_1 hybrids grown at Hisar was studied Thakaral *et al.* (1999). The data indicated that higher seed yield could be obtained by selecting for increased plant height.

According to Kumar *et al.* (1999) the 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 (*Brassica nigra*) and reported that dwarf plant gave higher yield.

An experiment was carried out Das *et al.* (1998) with eight genotypes of Indian mustard (*Brassica juncea*) and reported that the length of siliqua, seeds per siliqua had high positive genotypic correlation with seed yield per plant. The number of siliquae per plant, seed weight per plant and thousand seed weight were positively correlated with seed yield per plant were observed by Dileep *et al.*, (1997).

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

Tyagi *et al.* (1996) carried out an experiment with six yield components in three cultivars of mustard and observed that plant height, siliqua per plant, siliqua length, seed weight and seeds per siliqua had positive and significant effects on seed yield per plant.

Arthamwar *et al.* (1995) reported correlation and regression analysis *in Brassica juncea*. Results revealed that weight of siliqua per plant showed the highest

correlation with seed yield followed by number of siliqua per plant, number of seeds per siliqua and thousand seed weight.

2.4 Path co-efficient analysis

The path analysis helps to determine the direct and indirect contribution of traits towards the yield. Direct contribution of each component to the yield and the indirect effects it has through its association with other components cannot be differentiated from mere correlation studies. Path coefficient analysis fulfills this study. It was first developed and described by Wright (1921), as a tool in genetic analysis which partition the association of the components on yield and indirect effects of the characters on yield through other components. The association between the various characters in a rapeseed and mustard and the direct and indirect effects of a variable over the dependent variable has been studied by a number of investigators are reviewed here.

The number of siliqua per plant had the highest positive direct effect on seed yield was observed by Yadava *et al.* (1996) when studied path co-efficient analysis of six yield components of 25 diverse varieties of Indian mustard. The number of siliqua per plant had the highest direct effect on seed yield followed by 1000 seed weight, number of primary branches per plant and plant height. Most of the characters had an indirect effect on seed yield was observed by Shalini *et al.* (2000) while studied path analysis of Indian mustard germplasm.

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

Afroz *et al.(*2004) studied path analysis of 14 genotypes of mustard and observed that maximum direct positive effects on plant height followed by number of

siliqua per plant, seed yield per plant, number of primary branches per plant, 1000-seed weight and number of siliqua shattering per plant.

Zahan, (2006) reported that siliqua/plant had positive direct effect on yield/plant. And days to 50% flowering had negative direct effect on yield/plant.

Khan *et al.(*2006) studied correlation for some quantitative traits relating to yield and quality. The results indicated that a wide range of genetic variation existed among all the characters under study except 1000-grain weight. Correlation analysis revealed that seed yield per plant was positively and significantly correlated with number of primary branches (0.4015), siliqua per plant (0.505), seeds per siliqua (0.79648), siliqua length (0.37037) and seed yield per plot (0.40931). However, it was negatively and non-significantly associated with number of secondary branches (-0.36663) and protein contents (-0.1372) at genotypic level. It was also found that indirect selection for number of seeds per siliqua would be effective in improving the seed yield per plant in present breeding material.

A study was conducted by Tusar*etal.*(2006) to assess the nature and extent of variability of 11 yield related characters of five mustard genotypes. Phenotypic correlation studies indicated that seed yield per hectare was positively and significantly associated with plant height, total dry matter production and husk weight. The number of siliqua per plant, 1000-seed weight, crop growth rate during 60-75 days after sowing and number of branches per plant were also positively associated with seed yield. Path coefficient analysis revealed that the number of siliqua per plant had the greatest direct contribution on seed yield followed by the number of seeds per siliqua and 1000-seed weight while indirect via number of siliqua per plant and 1000-seed weight. Although plant height and husk weight had a total positive correlation with seed yield, their direct effect on yield was negative. The number of seeds per siliqua showed very high positive

direct effect on yield, but its correlation with yield was non-significant and negative.

An experiment was carried out Rashid, (2007) with 40 *oleiferous Brassica* species to estimate path analysis and observed that yield per plant had the highest direct 18 effect on days to maturity, number of seeds per siliqua, number of siliquae per plant and number of primary and secondary branches per plant.

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

The path co-efficient analysis by Hosen, (2008)exhibited that thousand seed weight had the highest positive direct effect followed by days to 50% flowering, length of siliqua, number of primary branches per plant, number of secondary branches per plant, days to maturity and number of seeds per siliqua while working with five parental genotypes of *Brassica rapa* and their ten F_3 progenies including reciprocals.

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

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

Alam, (2010) studied path co-efficient analysis and revealed that plant height, number of primary branches per plant, number of siliqua per plant, seeds per siliquae and siliqua length had the direct positive effect on yield per plant while

days to 50% flowering, number of secondary branches per plant and thousand seed weight had the negative direct effect on yield per plant.

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

An experiment was conducted by Uddin *et al.(*2013) with seven parental and twenty one F_2 progenies of *Brassica rapa* to study path coefficient and reported that days to 50% flowering, number of primary branches per plant, number of 19 secondary branches per plant, number of siliqua per plant, siliquae length, seed per siliqua and thousand seed weight showed direct positive association with seed yield per plant while the plant height and days to maturity had direct negative association.

Mekonnen *et al.* (2014) conducted an experiment to study path co-efficient in *Brassica carinata* and found that days to maturity and secondary braches per plant had positive and direct genotypic correlation with seed yield.

Ejaz-Ul-Hasan *et al.* (2014) conducted an experiment on *Brassica napus* and studied path coefficient. The result revealed that the highest direct positive effect of seeds per plant on yield followed by days to maturity, days to flowering, seeds per siliqua, siliqua length and thousand seed weight while plant height had direct negative effect on the yield per plant.

Chapter III
Materials & Methods

CHAPTER III

MATERIALS AND METHODS

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

3.1 Experimental site

During November 2017 to February 2018, the experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka-1207. The location of the experimental site was situated at 230 74' N latitude and 900 35' E longitude with an elevation of 8.6 meter from the sea level. Photograph showing the experimental site (Appendix I).

3.2 Climate

According to Edris *et al.* 1979the experimental site was located under the subtropical climatic zone, differentiated by three distinct seasons, the dry or cold season from November to February and the pre-monsoon period or hot season from March to April and monsoon period from May to October and also characterized by heavy precipitation during the month of May to August and scanty precipitation from October to March. The mean of air, temperature, humidity and rainfall during the time of experiment were recorded from the Bangladesh Metrological Department, Agargaon, Dhaka (Appendix II, III).

3.3 Soil characteristics

The experimental site soil lies in Agro ecological region of Madhupur Tract (AEZ no. 28) (www.banglapedia.com) of Noda soil series. Soil of the experimental site belongs to the general soil type, Shallow red brown terrace soils under Tejgaon Series. The experimental site soil was loam in texture, medium high land and the pH was 5.6 to 5.8 and organic carbon content was 0.82%. Experimental area was flat which facilitated irrigation and drainage system easily. Physicochemical properties of the soil are presented in Appendix III.

3.4 Experimental materials

The healthy seeds of 44 F_5 advanced populations of *Brassica napus* collected from the Dept. of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka which were used as experimental materials. The materials used in that experiment is shown in (Table 1).

Table 1. Materials used for the experiment

Genotypes	F5 populations	Source
G1	Nap2001XNap206	SAU
G2	Nap94006XNap206	SAU
G3	Nap248XNap159	SAU
G4	Nap9908XBS-13	SAU
G5	Nap94006XBS-7	SAU
G6	Nap2012XNap2013	SAU
G7	Nap94006XNap2013	SAU
G8	Nap284XNap206	SAU
G9	Nap206XNap2012	SAU
G10	Nap2037XNap2022	SAU
G11	Nap9908XNap94006	SAU
G12	Nap2001XNap248	SAU
G13	Nap2057XNap2022	SAU
G14	Nap206XNap2013	SAU

G15	BS-7XNap206	SAU
G16	Nap2001XNap2022	SAU
G17	Nap94006XBS-13	SAU
G18	Nap94006XNap179	SAU
G19	Nap2057XNap2012	SAU
G20	Nap94006XNap2012	SAU
G21	BS-7XNap2013	SAU
G22	Nap179XNap206	SAU
G23	Nap9908XNap206	SAU
G24	Nap94006XNap2022	SAU
G25	Nap2012XNap2022	SAU
G26	Nap248XNap2022	SAU
G27	BS-13XNap2013	SAU
G28	Nap2057XNap248	SAU
G29	Nap2057XBS-13	SAU
G30	BS-13XNap206	SAU
G31	Nap9908XNap2013	SAU
G32	Nap248XNap2013	SAU
G33	Nap179XNap2057	SAU
G34	Nap179XNap2022	SAU
G35	Nap2037XNap2013	SAU
G36	Nap200XNap2022	SAU
G37	Nap94006XNap2057	SAU
G38	BS-7XNap2013	SAU
G39	Nap2057XNap2001	SAU
G40	BS-7XNap2057	SAU
G41	Nap94006XNap2001	SAU
G42	BS-13XNap179	SAU
G43	Nap179XNap2012	SAU
G44	Nap2001XNap179	SAU

3.5 Design and layout

The trial field was laid out in a Randomized Complete Block Design (RCBD) with two replications. The field was divided into two blocks; the blocks were subdivided into 44 plots where genotypes were randomly assigned. The plot size was 12.5 m long with fourty four rows. Row to row distance was 30 cm and plant

to plant distance was 10 cm. The distance between replications was 1 m. The genotypes were randomly distributed in each replication.

3.6 Operational practice

3.6.1 Field preparation

The experimental field was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about good tilt. Weeds and other stubbles were dispelled carefully from the experimental land and leveled duly (Plate 1). The final land preparation was done on 11th November 2017.

3.6.2 Fertilizer andmanure application

For mustard cultivation, many organic and inorganic fertilizer viz. cow dung, Urea, TSP and MP fertilizers are required. The land was fertilized with 10 ton cow dung per ha on 4 November 2017. The land was fertilized as the rate shown in (Table 2). The entire amount of cow dung was used seven days before sowing. Half amount of urea, total TSP, MOP, Gypsum, Zinc oxide and Boron were applied during final land preparation and blend into the soil (Plate 1). The rest amount of urea was applied as top dressing after 25 days of sowing.

3.6.3 Seed sowing

The spacing of row to row was 30 cm and plant to plant in row was 10 cm. Variety to variety distance in each replication was 60 cm. Distance between replication was 1 m. On 11 November 2017, seeds were sown in line in the experimental plot.Before sowing,the seeds are dried on sunlight for few moments. The seeds were placed at about 1.5 cm depth in the soil (Plate 1). After sowing the seeds were covered with soil carefully so that no clods were on the seeds.

Table2.List of fertilizer and manure with quantity and application procedures

Fertilizer	Quantity	Application procedure
Cowdung	10 ton/ha	as basal
Urea	270 Kg/ha	50% basal and 50% at 25 DAS
TSP	170 Kg/ha	as basal
MOP	100 Kg/ha	as basal
Gypsum	150 Kg/ha	as basal
Zinc oxide	5 Kg/ha	as basal
Boron	3 Kg/ha	as basal

Table3. List of Insecticides/fungicides with quantity

Name of Insecticides/Fungicides	Quantity
Malathion-57 EC	2ml/liter
Rovral50WP	2gm/lit
Benicrome-100wec	1ml/ liter

3.6.4 Intercultural operations

Intercultural operations 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 protect uniform germination of the seeds. A good drainage system was maintained for immediate release of rainwater from the experimental land during the growing period. The weeding was committed after 15 days of sowing. 1st thinning was done on 20 November 2017 and another after 7days of 1st thinning for maintaining a distance of 10 cm from plant to plant in rows of 30 cm apart at the same time.

A

B

C

Plate 1.Photograph showing (A. Field preparation, B. Fertilizer and manure application, C. Seed sowing) experimental field

Total experimental land was tagging on 1 December 2017 by bamboo stick by maintaining variety cone and replication number. Second weeding was done after 30 days of sowing. Aphid and disease alternaria spot infection was found in the crop during the siliqua development stage. To control pest Malathion-57 EC @ 2ml/liter with Rovral50WP under Iprodione group @ 2gm/lit of water was applied on 6 December 2017 and second time on 10 December 2017 (Plate 2). The pesticide was applied in the afternoon. The rate of amount of pesticide is shown in (Table 3).

A B

Plate 2.Photograph showing (A= Thining, B= Irrigation)Intercultural operations

3.6.5 Crop harvesting

According to maturity, the crop was harvested in different dates from about 90 days after sowing (DAS). When 80% of the plants showed symptoms of maturity, then harvesting was started from 2nd week of February 2018 and continued to 3rd week of February 2018.Fifteen plants were selected at randomly from each variety in each replication and harvesting was done by my supervision (Plate 3). The plants were harvested by uprooting and then they were tagged duly. Data were recorded on different parameters from these plants.

A B

C D

E F

Plate 3.Photograph showing (A. seedling stage, B. flowering stage, C. siliquae formation stage, D. maturity stage, E. harvesting stage, F. harvesting operation) experimental field

3.7 Data recorded and different trait evaluation

For studying different genetic parameters, association and genetic diversity, data were recorded for 10 traits related to flowering, morphology, yield components on fifteen randomly selected plants for each genotype on the following traits-

3.7.1 Days to 50% flowering

Days to 50% flowering were recorded when the first plant flowered in each plot; 50% and 100% flowering dates were recorded when 50% of plants and 100% of plants in each plot flowered,respectively from the date of sowing to the date of 50% and 100% flowering from each replication.

3.7.2 Days to 100% maturity

Days to maturity were recorded at the 70–80% siliqua ripening stage. 10–15 plants per line in each plot were grown for phenotypic evaluation.

3.7.3 Plant height (cm)

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

3.7.4 Number of primary branches per plant

The total number of braches emerged from the main stem of a plant was calculated as the number of primary branches per plant.

3.7.5 Number of secondary branches per plant

The total number of branches emerged from the primary branch of a plant was counted as the number of secondary branches per plant.

3.7.6 Number of siliquae per plant

The total number of siliquae of each plant was calculated and considered as the number of siliquae per plant.

3.7.7 Siliqua length (cm)

This data was taken in centimeter (cm) from the base to the tip of a siliqua of the five representative siliqua.

3.7.8 Number of seeds per siliqua

Well filled seeds were calculated from five siliqua which was considered as the number of seeds per siliqua.

3.7.9 Thousand seed weight (g)

Weight in grams of randomly calculated thousand seeds of each entry was recorded.

3.7.10 Seed yield per plant (g)

Considering as the seed yield per plant, all the seeds produced by a representative plant was weighed in g .

3.8 Statistical analysis

The mean values of fifteen randomly selected plants were used for recording observations and computed for each of ten traits for each genotype in each replication and were subjected to statistical analysis. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes, Mean, range and co-efficient of variation (CV%) were also estimated using MSTAT-C. Using the formula given by Singh and Chaudhary (1985) and Allard (1960); heritability and genetic advance were measured. Genotypic and phenotypic co-efficient of variation were calculated by the formula of Burton, (1952). Genotypic and phenotypic correlation coefficient was obtained using the formula suggested by Johnson *et al.*, (1955). Path co-efficient analysis was done following the method outlined by Dewey and Lu, (1995).

3.8.1 Analysis of variance

Analysis of Variance (ANOVA) is a statistical method used to test differences between two or more means data in order to assess the genetic variability among genotypes as given by Cochran and Cox (1957). The level of significance was tested at 5% and 1% using F test(SAS, 2008). The model of ANOVA used is presented in Table 4.

Table4. Analysis of variance (ANOVA)

Sources of variation	Degrees of freedom (df)	Mean sum of squares (MSS)	Expected MSS
Replication	(r-1)	Mr	g
Genotype	(g-1)	Mg	
Error	(g-1) (r-1)	Me	
Total	(rg-1)		

Where, r = number of replications

g = number of treatments (genotypes)

$\sigma^2 r$ = variance due to replications

σ^2 g = variance due to treatments (genotypes)

σ^2 e = variance due to error

To test significant of the difference between any two-adjusted genotypic mean, the standard error of mean was computed using the formula.

$$S.E=\sqrt{\frac{2Ee}{r}(1+\frac{rqu}{q+1})}$$

Where, S.E = Standard error of mean

Ee = Mean sum of squares for error (Intra block)

r = Number of replications

q= Number of genotypes in each sub-block

u= Weight age factor computed

3.8.2 Estimation ofgenotypic and phenotypic variances

The variability present in the population was estimated by measure mean, phenotypic and genotypic variance and co-efficient of variation. To estimate the phenotypic and genotypic variance, genotypic and phenotypic co-efficient of variation were estimated based on formula Syukur *et al.*, (2012) as follow:

$\delta^2{}_g$= [(MSG) – (MSE)] $/r$

$\delta^2{}_p$ =($\delta^2{}_g$+$\delta^2{}_e$),

Where,

$\delta^2{}_g$= Genotypic variance;

$\delta^2{}_p$= Phenotypic variance;

$\delta^2{}_e$= environmental variance (error mean square from the analysis of variance);

MSG = mean square of genotypes;

MSE = error mean square;

r = number of replications.

3.8.3 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)= [$(\delta^2{}_g)^{\frac{1}{2}}$ /$\bar{x}$] × 100;

(PCV) = [$(\delta^2{}_p)^{\frac{1}{2}}$ /$\bar{x}$] × 100,

Where,

GCV = Genotypic co-efficient of variation

PCV = Phenotypic co-efficient of variation

δ^2_g= Genotypic variance;

δ^2_p= Phenotypic variance; is grand mean of a character;

$\bar{x}$ = Population mean.

Suggested by Sivasubramanian and Madhamenon (1973);PCV and GCV were classified into three following categories-

Categories Low: Less than 10%

Moderate: 10-20%

High: More than 20%

3.8.4 Estimation of heritabilityin broad sense

Broad sense heritability (h^2) of the all traits were calculated according to the formula as described by Allard (1960) as follow:

$h^2_{bs}=[(\delta^2_g/\delta^2_p)]\times 100$

Where,

h^2_{bs}= heritability in broad sense;

δ^2_g= Genotypic variance;

δ^2_p= Phenotypic variance.

3.8.5 Estimation of genetic advance

Genetic advance (GA) was determined as described by Johnson et al. (1955):

GA = K $(\delta_p)h^2$,

Where,

K = the selection differential (K = 2.06 at 5% selection intensity);

δ_p = the phenotypic standard deviation of the character;

h^2 = broad sense heritability.

The genetic advance as percentage of the mean (GAM) was calculated as described by Johnson *et al.*(1955) as follow:

$$GAM(\%)=\frac{GA}{\bar{x}}\times 100$$

Where,

GAM = genetic advance as percentage of the mean,

GA = genetic advance, and

$\bar{x}$ = grand mean of a character.

Categories:

High (>20%)

Moderate (10-20%)

Low (<10%)

3.8.6 Estimation of genetic advance in percentage of mean

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

Genetic advance (% of mean)= (Genetic advanced/population mean)×100

Suggested by Johnson *et al.* (1955) genetic advance as percent mean was categorized into following groups :

Categories:

Low -<10%

Moderate -10-20%

High ->20%

3.8.7 Genotypic and phenotypic correlation co-efficient

The genotypic co-variance component between two traits and have the phenotypic co-variance component were derived in the same way as for the corresponding variance components. The co-variance components were used to calculate genotypic and phenotypic correlation between the pairs of characters as follows:

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

Where,

$\sigma_{gxy=}$Genotypic co-variance between the traits x and y

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

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

Phenotypic correlation, $r_{pxy}=\frac{PCOV_{xy}}{\sqrt{PVx.PVy}}=\frac{\sigma_{pxy}}{\sqrt{\sigma^2_{px}.\sigma^2_{py}}}$

Where,

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

$\sigma^2_{px.}$ =Phenotypic variance of the trait x

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

3.8.8 Path co-efficient analysis

Suggested by Wright (1921) and illustrated by Dewey and Lu (1959) path coefficient analysis was carried out using phenotypic correlation values of yield components on yield. Standard path coefficients which are the standardized partial regression coefficients were obtained using statistical software packages called

OPSTAT. These values were obtained by solving the following set of 'p' simultaneous equation using above package.

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

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

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

Where, $P_{01}, P_{02}\ldots\ldots\ldots\ldots\ldots\ldots P_{0p}$ are the direct effects of variables 1, 2……P on the dependent variable 0 and $r_{12}, r_{13}\ldots\ldots\ldots\ldots\ldots r_{1p}\ldots\ldots\ldots r_{p(p+1)}$ are the possible correlation coefficient between various independent variables and $r_{01}, r_{02}\ldots\ldots\ldots r_{0p}$ are the correlation between dependent and independent variables. The indirect effects of the i^{th} variable via j^{th} variable was attained as $(P_{0j} * r_{ij})$ The contribution of remaining unknown factor is measured as the residual factor, which is calculated and given below

$$P_{ox}^2 = 1 - (P_{01}^2 + 2P_{01}P_{02}r_{12} + 2P_{01}P_{03}r_{13} + \ldots\ldots P_{02}^2 + 2P_{02}P_{03}r_{13} + \ldots\ldots\ldots + P_{OP}^2)$$

Categories

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

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

$P_{RY}^2 = 1 - (r_{1.y}P_{1.y} + r_{2.y}P_{2.y} + \ldots\ldots\ldots\ldots\ldots + r_{8.y}P_{8.y})$

Where

$P_{RY}^2 = R^2$

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

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

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

Chapter IV
Results & Discussions

CHAPTER IV

RESULTS AND DISCUSSIONS

Study of genetic behavior such as genetic variability, heritability, genetic advance and correlation etc. of the germplasm is a key step for initiation of any breeding program (Mahmud, 2008).

The present study was commenced with a view to determine the genetic variation among 44 genotypes belonging to *Brassica napus L.* related to vegetative, reproductive and yield components parameters emphasizing growth and yield. The data were subjected to biometrical and biochemical analysis and results obtained are presented below under the following headings:

- Performance of genotypes and genetic parameters
- Correlation studies
- Path co-efficient analysis

4.1 Performance of genotypes and genetic parameters

In the study considerable variations were observed for most of the characters among 44 F_5 materials of *Brassica napus.* Under the present study all the genotypes had significant difference for all the characters indicating the existence of genetic variation and provided scope for selection of superior genotypes(Table 5). It seems that there were significant variation among the genotypes for days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, siliqua length (cm), number of seeds per siliqua, 1000 seed weight (g) and yield per plant. Coefficient of variation (% CV) ranged from 3.28 to 24.21 for all characters studied (Table 6).It indicate high variation among the genotypes. The character wise details of these variability are discussed below of the genotypes evaluated for 10 characters are presented in below.

Table 5. Analysis of variance (mean squire values) for various important characters of *Brassica napus* genotypes

Source of variation	Degrees of freedom	Mean sum of square									
		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches/ plant	Number of secondary branches/ plant	Number of siliqua/ plant	Siliqua length (cm)	Number of seeds/ siliqua	1000 seed weight (g)	Yield/ plant
Replication	1	54.10	5.01	2.50	0.057	0.39	70.63	0.16	7.30	0.04	5.01
Genotype	43	23.52**	15.45*	150.06 **	0.73**	1.35**	1010.29**	0.44**	12.61**	0.39**	27.18**
Error	43	6.87	7.73	20.68	0.17	0.26	29.35	0.10	1.37	0.06	0.73

* = Significant at 5% level

** = Significant at 1% level

Table 6. Range, mean, Coefficient of variability (%CV) and SEm (±) for different characters of test genotypes of *Brassica napus* L.

Characters	Range for individual characters		Grand mean	CV (%)	SEm (±)
	Maximum	Minimum			
Days to 50% flowering	43	30	35.78	7.32	6.87
Days of maturity	89	79	84.76	3.28	7.73
Plant height (cm)	124.39	91.50	108.49	4.19	20.68
No. of primary branches/plant	4.85	2.63	3.67	11.42	0.17
No. of secondary branches/plant	4.86	0.63	2.11	24.21	0.26
No. of siliqua/plant	179.60	63.83	116.06	4.67	29.33
Siliqua length (cm)	8.22	6.08	7.14	4.45	0.10
No. of seeds/siliqua	22.39	10.96	16.21	7.23	1.37
1000 seed weight (g)	5.15	3.37	4.25	5.58	0.06
Yield/plant (g)	20.5	6	10.15	8.43	0.73

CV (%) = coefficient of variation SEm=Standard error of mean

4.1.1 Days to 50% flowering

Considerable variations were observed among 44 genotypes of F_5 populations for days to 50% flowering. From the mean values, it was found that among the 43 genotypes, the lowest number of days (30.0) was recorded from G8followed byG27,G19,G17to attain 50% flowering. On the other hand, the highest number of days (43.0) was recorded from G16.Result revealed that days to 50% flowering ranged from 30.0to 43.0 where %CV value was 7.32 among the genotypes with mean values of 35.78(Table 6).

Sing *et al.* (2001) studied that different morpho-physiological characters of 29 genotypes of *B. napus* grown under normal and stress condition of production. While working with 29 genotypes of *B. napus*, they found the existence of significant genetic variability for days to 50% flowering. Jain *et al.* (1988) observed that dominance gene action was important in the expression of days to flowering. Alam (2010) observed that there were significant variations in days to 1st flowering and showed low difference between genotypic and phenotypic coefficient of variation.

The results further showed that small difference between phenotypic coefficients of variation (PCV %) and genotypic coefficients of variation (GCV %) (Table 8) (Figure 1). It indicated that the presence of low influence of environment on this character. High heritability (44.69%) and moderately low genetic advance in percent mean (9.07%) indicated days to 50% flowering was least influenced by environment and the presence of non-additive gene effects and therefore, the character could be improved with heterosis breeding process (Table 8) (Figure 2).

Mahmud (2008) observed high heritability values along with high genetic advance in percentage of mean were obtained for days to 50% flowering.

Basalma*et al.* (2008) was recorded high heritability along with high genetic advance (as percent of mean) for days to flowering.

4.1.2 Days to maturity

The average day to maturity was recorded 84.76with a range of 79.0 to 89.0 day(Table 6). The maximum number of days to maturity was observed in the genotypeG8(Table 6) whereas G36 required the least number of days to maturity.Days to maturity showed low GCV and PCV of 1.89 and 3.79percent, respectively along with moderate heritability of 24.97 percent, low genetic advance 1.65 and low genetic advance as percent of mean 1.95 percent (Table 8).

Naznin (2013) also found low difference between PCV (22.15) and GCV (19.74) in *B. rapa* L.Jahan (2008)exhibited high heritability with low genetic advance in percent of mean was observed for days to maturity and selection for such trait might not be rewarding. The genotypic and phenotypic variances were recorded as 2.57 and 10.31, respectively (Table 7). Considerable influence of environment was present in the expression of genes for this trait when proving that phenotypic variance was larger than genotypic variance.

4.1.3 Plant height (cm)

Variation in plant height was also seen in all the genotypes. The highest plant (124.39 cm)height recorded from G22which was statistically identical with G9where the lowest plant height (91.50 cm)was achieved fromG41 which was statistically identical with G31(Plate 4).Plant height was ranged from 91.50 to124.39 cm with % CV of 4.19 and mean values of 108.49 among the tested genotypes (Table 6).

A B

Plate 4. Photograph showing variation between highest (A) G22 (Nap179 × Nap206) and lowest (B) plant height G41 (Nap94006 × Nap2001) of *Brassica napus*L. genotypes

Khan *et al.* (2013) was reported that the highest genotypic, phenotypic and environmental variances were observed in plant height.

Rukhsana *et al.* (2005) evaluated the 14 improved cultivars of rapeseed and the result showed that highly variation was observed for plant height.

The difference between PCV% and GCV% was observed to be 7.36 & 6.05 for this character (Table 8)(Figure 1). It indicated that the presence of medium influence of environment on this character. Heritability in broad sense was estimated to high (67.59%) with moderate genetic advance (11.12%) (Table 8)(Figure 2). It indicated that individual plant selection might result into better genotypes. Similar results were found from Ara (2010). They found high PCV and GCV for plant height characters. Hosen (2008) was observed that plant height showed high heritability with high genetic advance and genetic advance in percentage of mean.

4.1.4 Number of primary branches per plant

Among all the genotypes, the highest number ofprimary branches per plant (4.85) was found in G22followed by G5.Again, G27produced the lowest number of branches per plant (2.63) which was statistically similar with G3and G39 (Plate 5). Number of primary branches per plants was ranged from 2.63 to 4.85 with mean values of 3.67 and%CV value of 11.42 (Table 6).

Alam (2010) indicated that there were significant variations in number of primary branches per plant. Mekonnen *et al.* (2014) assessed that number of primary branches per plant exhibited comparatively high genotypic and phenotypic coefficient of variation.Whereas, it observed high heritability (51.37%), low genetic advance (0.64) and high genetic gain as percent of mean (17.34%) for this trait (Table 8).

AB

Plate 5. Photograph showing variation between highest (A) G22 (Nap 2012 × Nap 2022) and lowest (B) G3 (Nap 248 × Nap159) primary branch of *Brassica napus* L. genotypes

Table7. Phenotypic, genotypic and environmental variance for different characters of *Brassica napus* L.

Characters	Phenotypic variance	Genotypic variance	Environmental variance
Days to 50% flowering	12.42	5.55	6.87
Days to maturity	10.31	2.57	7.74
Plant height (cm)	63.81	43.13	20.68
No. of primary branches/ plant	0.36	0.17	0.19
No. of secondary branches/ plant	0.61	0.35	0.26
No. of siliqua/plant	356.33	326.98	29.35
Siliqua length (cm)	0.21	0.11	0.1
No. of seeds/siliqua	5.12	3.75	1.37
1000 seed weight (g)	0.17	0.11	0.06
Yield/plant (g)	9.55	8.81	0.74

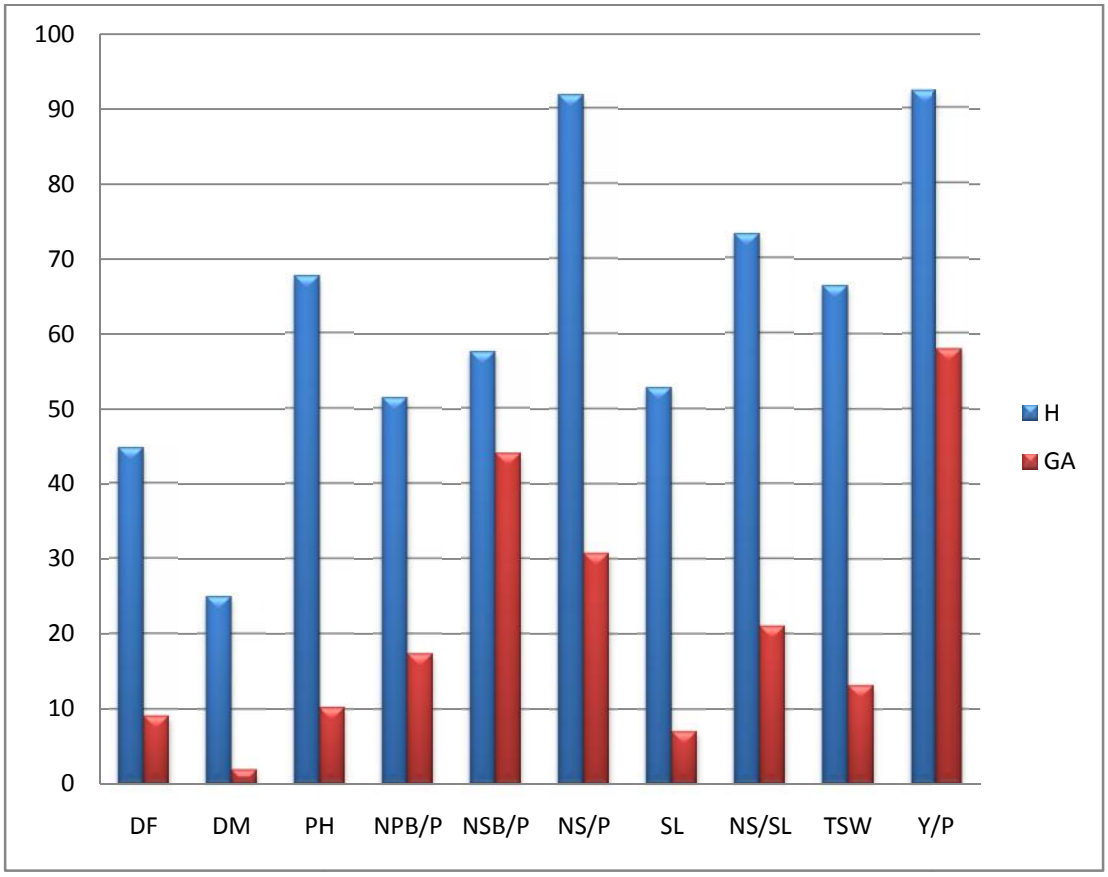


Figure 1. Genotypic and phenotypic coefficient of variation in *Brassica napus* L.

DF = Days to 50% flowering, DM= Days to 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 seeds 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

Table 8. Estimation of genetic parameter of different characters of *Brassica napus* L.

Characters	Heritability	GCV (%)	PCV (%)	GA	GA (%)
Days to 50% flowering	44.69	6.58	9.70	3.24	9.07
Days to maturity	24.97	1.89	3.79	1.65	1.948
Plant height (cm)	67.59	6.05	7.36	11.12	10.25
Number of primary branches/plant	51.37	11.74	16.38	0.64	17.34
Number of secondary branches/plant	57.50	28.16	37.13	0.93	43.99
Number of siliqua/plant	91.76	15.58	16.26	35.68	30.75
Siliqua length (cm)	52.80	4.71	6.48	0.50	7.05
Number of seeds/siliqua	73.20	11.94	13.96	3.41	21.05
1000 seed weight (g)	66.43	7.84	9.62	0.56	13.17
Yield /plant	92.33	29.26	30.45	5.88	57.91

GCV=Genotypic coefficient of variance, PCV=Phenotypic coefficient of variance, GA=Genetic advance , GA(%)= Genetic advance percentage of mean.

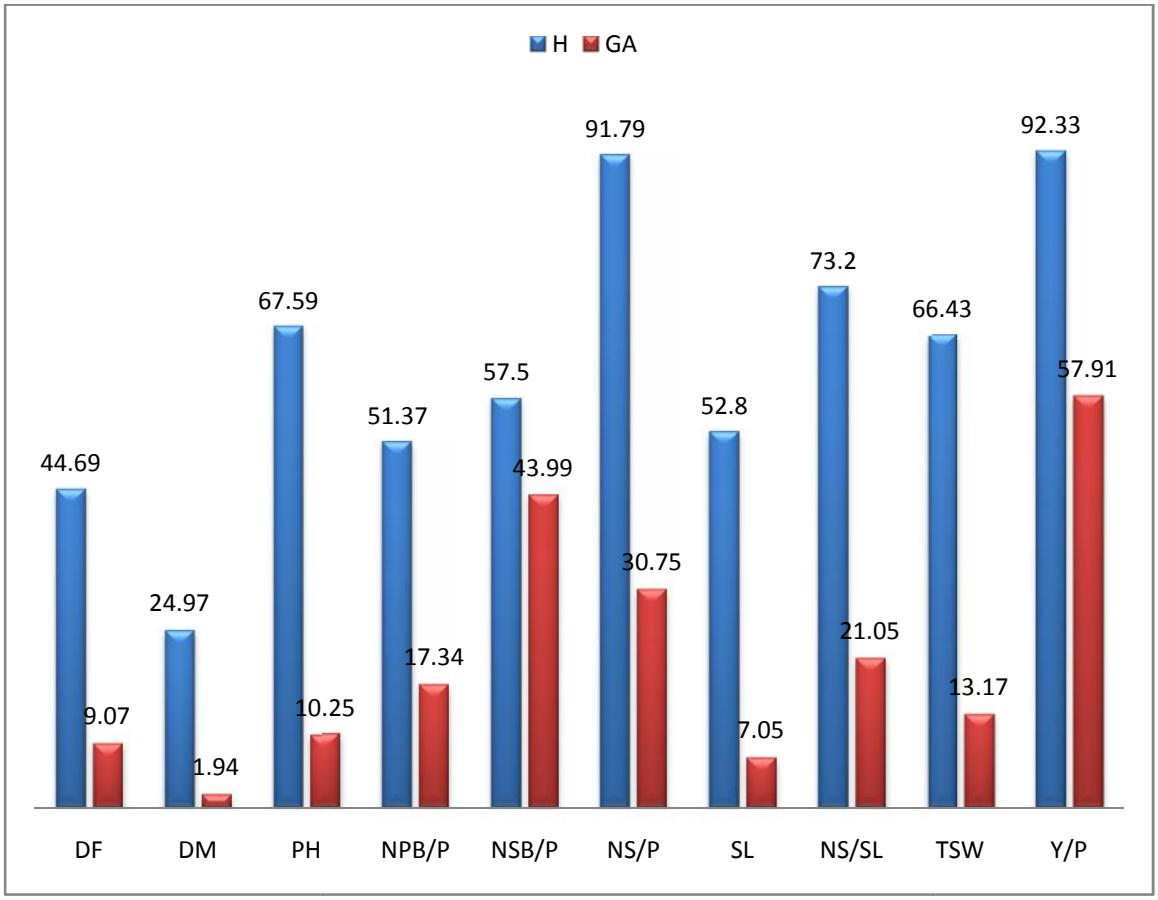


Figure 2. Heritability and genetic advance over mean in *Brassica napus* L.

DF = Days to 50% flowering, DM= Days 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, NSS=Number of seeds per siliqua, SL=Siliqua length, TSW = Thousand Seed Weight (g), SYP=Seed yield per plant, H=Heritability and GA=Genetic Advance

Ghosh and Gulati (2001) found the high heritability coupled with high genetic advance for this trait.

4.1.5 Number of secondary branches per plant

Significant variation for number ofsecondary branches per plant was found among the genotypes. Among all the genotypes, the highest number of secondary branches per plants was found in G26 (4.86) followed by G16 Again, G39 produced the lowest number of secondary branches per plant (0.63) which was statistically similar with G8(Plate 6). Number of secondary branches per plant was ranged from 0.63 to 4.86 with mean value of 2.11 and %CV value of 24.21 (Table 6).

According to Abideen *et al.*(2013) highly significant differences among the genotypes for most of the traits was observed. Non significant differences were observed among the genotypes for secondary branches per plant. Significant differences were found between phenotypic and genotypic variances for the characters. Differences between PCV% and GCV% were also estimated to be high 37.13 and 28.16 (Table 8)(Figure 1). It indicated high influence of environment on this character. Heritability in broad sense was estimated to high (57.50%) with moderate genetic advance (43.99%) indicated that individual plant selection might result into better genotypes (Table 8) (Figure 2).

Ara(2010) and Alam (2010) also found similar results. They found high heritability and genetic advance in percent of mean for number of secondary branches per plant.

A B

Plate 6. Photograph showing variation between highest G16 (Nap2001 × Nap2022) and lowest G39 (Nap 2057 × Nap 2001) secondary branch of *Brassica napus* L. genotypes

4.1.6 Number of siliqua per plant

Significant variation for number siliqua per plant was observed among the genotypes. The highest number of siliquae per plant (179.60) was found in G16 followedG32.The lowest number of siliquae per plant (63.83) was found in G39followed byG7(Plate 7). The average number of siliquae per plant was 116.06 varied from 63.83 to 179.60 (Table 6).

Alam (2010) observed that significant variations in number of siliquae per plant and showed low difference between genotypic and phenotypic coefficient of variation. The results exhibited that the differences between PCV and GCV were very low 16.26 and 15.58 (Table 8) (Figure 1). The phenotypic variance was higher than genotypic variance (Table 7). Thatindicated high influence of environment on this character. The high phenotypic coefficient of variation (16.26%) and genotypic coefficient of variation (15.58%) (Table 8)indicated presence of 43 considerable variability among the genotypes.

Khan *et al.* (2013) was also reported on similar result. Mekonnen *et al.* (2014)found comparatively high GCV for this trait. The heritability (85.67%) estimates for this trait was high, high genetic advance (35.68) and high genetic advance in percent of mean (30.74) were found (Table 8). So, these traits could be utilized for further improvement through selection procedures. Alam (2010) ovserved that pods per plant had moderately high GCV and genetic advance and high heritability.

AB

Plate 7. Photograph showing variation between highest (A) G16 (Nap 2001 × Nap 2022) and lowest (B) G39 (Nap 2057 × NaP2001) siliqua per plant of *Brassica napus L.* genotypes

4.1.7 Length of siliqua (cm)

In respect of siliqua length per plant, significant variation was found. The longest siliqua length (8.22 cm) was obtained inG5 followed byG1 The lowest siliqua length (6.08 cm) was observed inG43 followed byG31(Plate 8). On the other hand, varied siliqua length ranged from 6.08 cm to 8.22 cm with the mean of 7.14 (Table 6).

Alam (2010) estimated that there was a significant variation in length of siliqua and also showed low difference between genotypic and phenotypic coefficient of variation.PCV and GCV values for siliqua length were close to each other (Table 8) (Figure 1). It showed the minimum effect of environment on this character. Medium heritability (52.78%) in broad sense and moderate genetic advance (7.054%)in percentage of mean were also found for this character (Table 8) (Figure 2). It meant slightly genetical, physiological, nutritional or environmental effect upon the expression of the character and additive gene effect could be beneficial for this trait slightly genetical, physiological, environmental effect upon the expression of the character and additive gene effect could be beneficial for this trait.

Ara (2010)length of siliqua showed high heritability with low genetic advance and genetic advance in percentage of mean. Alam (2010) observed length of siliqua was shown low heritability. Similar result was seen by Khan *et al.*, (2013). Low to medium heritability of siliqua length was record by Kachroo and Kumar (1991), Sharma (1984) and Yadava *et al.* (1996). Alam (2010) found length of siliqua showed low heritability.

A

B

Plate 8. Photograph showing variation between highest (A) G5 (Nap 94006 × BS-7) and lowest (B) G43 (Nap 179 × Nap2012) siliqua length of *Brassica napus L.* genotypes

4.1.8 No. of seed per siliqua

Number of seeds per siliqua ranged from 10.21 to 22.39 in different genotypes (Table 6). The highest number of seeds per siliqua (22.39) followedG22. The lowest number of seeds per siliqua (10.21) was found inG13 followed byG1. Average number of seeds per siliqua was 16.21(Table 6). Similar result was found from the findings of Alam, (2010). He estimated that there were significant variations in number of seeds per siliqua.

PCV and GCV values for siliqua length were close to each other 13.95 and 11.94 (Table 8)(Figure 1). It showed the minimum effect of environment on this character. High heritability (73.20%) in broad sense and moderate genetic advance (21.05%)in percentage of mean were also found for this character (Table 8) (Figure 2). It means slightly genetical, physiological, nutritional or environmental effect upon the expression of the character and additive gene effect could be beneficial for this trait slightly genetical, physiological, environmental effect upon the expression of the character and additive gene effect could be beneficial for this trait. Mahmud (2008) observed high heritability values along with high genetic advance in percentage of mean for seed per siliqua. Ara (2010) found seeds per siliqua showed high heritability with low genetic advance and genetic advance in percentage of mean. Low to medium heritability of seeds per siliqua was record by Kachroo and Kumar (1991), Sharma (1984) and Yadava *et al*., (1996).

4.1.9 1000 seed weight (g)

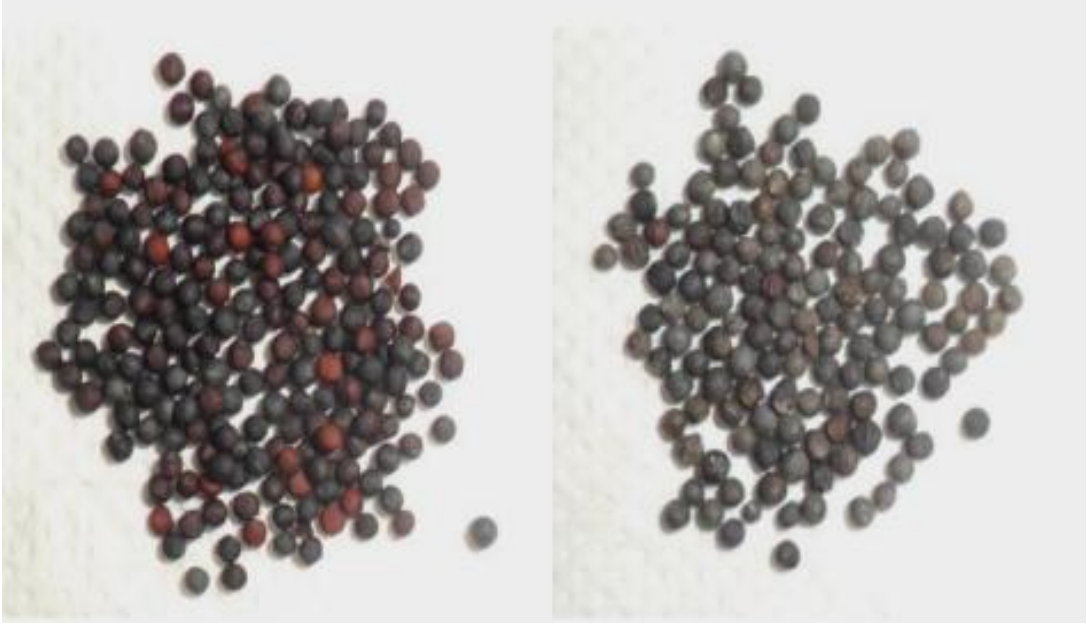
1000 seed weight of different populations ranged from 3.37 g to 5.15 g (Table 6). Significant variation like other characters as described above was found. The highest thousand seed weight (5.15 g) was observed inG16followed byG32 The lowest thousand seed weight (3.37 g) was produced byG30followed byG35(Plate 8). The average 1000 seed weight among the genotypes was 4.25. Alam (2010) found there were significant variations in thousand seed weight and yield per plant.

1000 seed weight was recorded low PCV (9.62%) and GCV (7.84%). There was considerable influence of environment on this trait when PCV was greater than GCV. While it recorded high heritability (66.43%), very low genetic advance (0.56) and moderate genetic gain as percent of means (13.17%) was found for this trait (Table 8). The days to maturity, length of siliqua, seeds per siliqua and thousand seed weight showed high heritability with low genetic advance and genetic advance in percentage of mean. Low to medium heritability of siliqua length was record by Kachroo and Kumar (1991), Sharma (1984) and Yadava *et al.,* (1996). Thousand seed weight showed high heritability with low genetic advance and genetic advance in percentage of mean was observed by Ara, (2010). Low to medium heritability of thousand seed weight was found by Kachroo and Kumar (1991), Sharma (1984) and Yadava *et al.,* (1996).

4.1.10 Seed yield per plant (g)

The maximum yield was recorded (20.5 g) by the population G16 which was statistically identical with G12. The lowest yield was recorded (6.0 g) by the population of G21 followed by G21. The average yield per plant among the genotypes was 10.15 g with the range of 20.5 to 6.0(Table 6).

Abideen *et al.* (2013) record similar findings and concluded highly significant differences among the genotypes for seed yield. Helal *et al.* (2014) revealed that different varieties produced the highest seed yields and 15% variation at genotypic and phenotypic level.



A (5.18g) **B**(3.17g)

Plate 9. Photograph showing variation between highest (A) G16 (Nap 2001 × Nap2022) and lowest (B) G35 (Nap 2037 × Nap2013) genotypes of thousand seed weight of *Brassica napus L.*

Ara, (2010) also observed that there was considerable variation present among all the genotypes used in respect of seed yield. It was also found that yield per plant showed least difference between phenotypic and genotypic variances.

Significant differences were observed between PCV (30.45%) and GCV (29.26%) (Table 8) (Figure1). Heritability (92.33%) and genetic advance (57.92%) in percent of mean were estimated to be high for this character (Table 8)(Figure 2). It showed slightly genetical, physiological, environmental effects upon the 56 expression of the character of vine length at first harvest and a scope for improvement of the character through selection. Aytac *et al.* (2008) observed the highest genotypic and phenotypic variances for seed yield per plant followed by seed yield and high heritability of seed yield per plant, seed yield, pods per main stem coupled with high genetic advance. High genotypic co-efficient of variation (GCV) was observed for yield per plant, Jahan (2008).

4.2 Correlation co-efficient

Correlation co-efficient exposed that most of the characters showed the genotypic correlation co-efficient higher than the corresponding phenotypic correlation co-efficient suggesting a strong inherent association between the characters studied, the phenotypic expression of the correlation being reduced under the influence of the environment. In some cases, phenotypic correlation co-efficient were higher than their corresponding genotypic correlation co-efficient suggesting that both environmental and genotypic correlation acted in the same direction and finally maximized their expression at phenotypic level. Breeders always look for genetic variation among traits to select desirable type. Correlation co-efficient between pairs of trait for F_5 materials of *Brassica napus* are shown in Table 9 and 10.

4.2.1 Genotypic correlation co-efficient

4.2.1.1 Days to 50%flowering

Days to 50% flowering showed significant positive association withnumber of secondary branches/ plant(0.263),siliqua length (cm)(0.376),1000 seed weight (g)(0.370). Similar results were reported by Shivahare *et al.* (1975) and Ali *et al.*(2003). This character also showed highly positive non significant interaction withdays ofmaturity (0.499),number of primary branches per plant (0.096),plant height (0.630), number of siliqua per plant (0.630). Similar result was also found by Rameeh (2012), Parveen (2007) and Zahan (2006).

4.2.1.2 Days to maturity

Days to maturity showed highlysignificant positive correlation with number of secondary branches/ plant (0.292). This trait had significant positive correlation withplant height (0.182),number of primary branches per plant(0.277), number of siliqua per plant(0.565), siliqua length (cm)(0.173),number of seeds per siliqua(0.583),1000-seed weight(0.235) and seed yield per plant (0.396). It also had no negative insignificant correlation with genotypic level. This indicated that if days to maturity increased than number of primary branches per plant so number of secondary branches per plant also increased. Similar agreement with Malek *et al.*,(2000) and Zahan, (2006) but Parveen, (2007) reported insignificant and positive interaction with yield per plant for this trait.

4.2.1.3 Plant height (cm)

This character showed highly positive significant interaction with siliqua length (cm)(0.355),yield per plant(g)(0.293) followed by number of primary branches per plant (0.248),number of secondary branches per plant (0.196), number of siliqua per plant (0.392), number of seeds per siliqua (0.430) and thousand seed weight (0.044) where non-significant negative interaction was not found (Table 9). Similar agreement obtained from the present study was conformity with the

findings of Helal *et al.* (2014), Alam (2010), Basalma (2008), Parveen (2007) and Tusar *et al.*, (2006).

4.2.1.4 Number of primary branches per plant

This character showed highly positive significant interaction with number of secondary branches per plant (0.330), followed by non-significant positive interaction with number of siliqua per plant (0.946), siliqua length (0.181),number of seeds per siliqua (0.619), thousand seed weight (0.510) and yield per plant (0.856) where non-significant negative interaction were not found in (Table 9). Similar agreement was found from the present study was similar with the findings of Alam (2010), Rashid (2007), Mahak *et al.* (2004), Khan and Khan (2003) and Srivastava and Singh (2002).

4.2.1.5 Number of secondary branches per plant

This character showed highly positive significant interaction with yield per plant (0.353) where non-significant positive interaction were found in number of siliqua per plant (0.409), number of seeds per siliqua (0.236),siliqua length (0.162) and thousand seed weight (0.227) (Table 9). Similar agreement was also observed by Rashid (2007), Parveen (2007), Khan and Khan(2003), Srivastava and Singh (2002) and Shalini *et al.* (2000).

4.2.1.6 Number of siliqua per plant

This character showed significant positive non significant interaction with siliqua length(0.240),number of seeds per siliqua (0.531),1000 seed weight (g)(0.477) and yield per plant (0.772) (Table 9).

Table 9. Genotypic correlation coefficient among the different characters of *Brassica napus* L. genotypes

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/ plant	No. of secondary branches/ plant	No. of siliqua/ plant	Siliqua length (cm)	No. of seeds/ siliqua	1000 seed weight (g)
Days to maturity	0.499								
Plant height (cm)	0.097	0.183							
Number of primary branches /plant	0.630	0.277	0.248						
Number of secondary branches/ plant	0.263*	0.292*	0.196	0.330**					
Number of siliqua /plant	0.539	0.566	0.393	0.947	0.409				
Siliqua length (cm)	0.377**	0.173	0.356**	0.182	0.162	0.240			
Number of seeds /siliqua	0.589	0.583	0.430	0.619	0.236	0.532	0.226		
1000 seed weight (g)	0.370**	0.236	0.045	0.510	0.228	0.477	0.105	0.469	
Yield per plant(g)	0.686	0.396	0.293*	0.857	0.353**	0.773	0.337**	0.772	0.829

*** = Significant at 5% level**

**** = Significant at 1% level**

Supported results were found from the findings of Helal *et al.* (2014), Rameeh (2011), Ara (2010), Rashid (2007), Parveen (2007) and Siddikee (2006).

4.2.1.7 Siliqua length (cm)

This character showed significant highly positive significant interaction withyield per plant (0.337) followed by positive significant interaction with number of seeds per siliqua (0.226),thousand seed weight (0.104) (Table 9). The present research results was supported by the findings of Alam (2010), Khan *et al.* (2005), Pankaj *et al.* (2002) and Khulbe &Pant (1999).

4.2.1.8 Number of seeds per siliqua

This character showed non significant positive interaction with thousand seed weight (0.469) andyield per plant (0.771) (Table 9). Similar agreement were found from the findings of Alam (2010), Ara (2010), Rashid (2007) and Parveen (2007).

4.2.1.9 1000 seed weight (g)

Thousand seeds weight showed positive non significant interaction with yield per plant (0.828904) (Table 9). Supported results were found from the findings of *Helal et al.* (2014), Ara (2010), Tusar *et al.* (2006), Gupta *et al.* (2002) and Yadava *et al.* (1996).

4.2.2 Phenotypic correlation co-efficient

4.2.2.1 Days to 50% flowering

This character showed positive significant interaction with number of primary branches /plant(0.314), siliqua length (0.256),1000 seed weight (g) (0.314) followed by days of maturity (0.202), number of secondary branches per plant (0.145), number of siliqua per plant (0.457), number of seeds per siliqua (0.556) and yield per plant (0.582). There was a negative interaction was found on plant height (-0.044)(Table 10). Supported results were found from Rameeh (2012), Parveen (2007) and Zahan (2006).

4.2.2.2 Days to maturity

Days to maturityshowed positive significant interaction with number of seeds /siliqua(0.383) and yield/ plant (g) (0.315), followed by non-significant positive interaction of plant height (0.235),number of primary branches per plant (0.245), number of secondary branches per plant (0.152), number of siliqua per plant (0.432), siliqua length (0.145) and thousand seed weight (0.114). There was no negative interaction was found among the parameters regarding phenotypic correlation co-efficient (Table 10). Similar agreement was also observed by Helal *et al.* (2014), Alam (2010), Basalma (2008), Parveen (2007) and Tusar *et al.*, (2006).

4.2.2.3 Plant height

This character showed highly positive significant interaction with number of primary branches /plant (0.361), siliqua length(0.332), number of seeds per siliqua(0.262), yield/plant(0.263), number of secondary branches /plant(0.114), number of siliqua/ plant(0.250),1000 seed weight (g) (0.097) (Table 10). There was no negative interaction was found among the parameters regarding phenotypic correlation co-efficient (Table 10). Supported results were found from the present study were similar with the findings of Alam (2010), Rashid (2007), Mahak *et al.* (2004), Khan and Khan (2003) and Srivastava and Singh (2002).

4.2.2.4 Number of primary branches per plant

This character showed highly positive significant interaction with number of secondary branches /plant (0.310) and 1000 seed weight (g)(0.284) followed by significant positive interaction withnumber of siliqua/ plant(0.663),silique length (0.228), number of seeds /siliqua(0.387), yield/ plant (g)(0.598). There was no negative interaction was found among the parameters regarding phenotypic correlation co-efficient (Table 10). Supported results were found from the present

study were similar with the findings of Alam (2010), Rashid (2007), Mahak *et al.* (2004), Khan and Khan (2003) and Srivastava and Singh (2002).

4.2.2.5 Number of secondary branches per plant

This character show significant interaction on yield/ plant (g) (0.322). Number of secondary branches per plant also showed non significant positive interaction with number of siliqua per plant (0.426), siliqua length (cm) (0.146),number of seeds per siliqua (0.156) and thousand seed weight (0.177) (Table 10). There was no negative interaction was found. The present research results was supported by the findings of Rashid (2007), Parveen (2007), Khan and Khan, 2003, Srivastava and Singh (2002) and Shalini *et al.*, (2000).

4.2.2.6 Number of siliqua per plant

This character showed positive significant interaction with siliqua length (0.255) followed by non-significant positive interaction with number of seeds per siliqua (0.510),thousand seed weight (0.428),yield per plant (0.757) (Table 10). Supported results were found from the findings of Helal *et al.* (2014), Rameeh (2011), Ara (2010), Rashid (2007), Parveen (2007) and Siddikee (2006).

4.2.2.7 Siliqua length

Siliqua length showed highly significant positive interaction with number of seeds per siliqua (0.268) and yield per plant (0.327) followed by non-significant positive interaction withthousand seed weight (0.103) (Table 10).

The present research results was supported by the findings of Alam (2010), Khan *et al.* (2005), Pankaj *et al.* (2002) and Khulbe and Pant (1999).

Table 10. Phenotypic correlation coefficient among the different characters of *Brassica napus* L. genotypes

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches /plant	No. of secondary branches / plant	No. of siliqua/ plant	Siliqua length (cm)	No. of seeds/ siliqua	1000 seed weight (g)
Days to maturity	0.202								
Plant height (cm)	-0.044	0.235							
Number of primary branches /plant	0.315**	0.245	0.362**						
Number of secondary branches /plant	0.146	0.152	0.114	0.311**					
Number of siliqua/ plant	0.457	0.432	0.250	0.664	0.426				
Siliqua length (cm)	0.256*	0.145	0.332**	0.228	0.146	0.255*			
Number of seeds /siliqua	0.556	0.383**	0.262*	0.387	0.156	0.510	0.268*		
1000 seed weight (g)	0.314**	0.114	0.098	0.285*	0.177	0.429	0.104	0.414	
Yield/ plant (g)	0.582	0.315**	0.263*	0.598	0.322**	0.757	0.327**	0.757	0.776

* = Significant at 5% level

** = Significant at 1% leve

4.2.2.8 Number of seeds per siliqua

This character showed non-significant positive interaction with thousand seed weight (0.413) and yield per plant (0.757)(Table 10). Similar result was observed by Alam (2010), Ara (2010), Rashid (2007), Parveen (2007) and Yadava *et al.* (1996).

4.2.2.9 Weight of thousand seeds

Weight of thousand seeds showed highly positive significant interaction with yield per plant (0.775) (Table 10). Supported results were found from the findings of Helal *et al.* (2014), Ara (2010), Tusar *et al.* (2006), Gupta *et al.* (2002) and Yadava *et al.* (1996).

4.3 PATH COEFFICIENT ANALYSIS

Association of charactersdefinite by correlation co-efficient may not provide an exact picture of the relative importance of direct and indirect influence of each yield components on yield. Correlation co-efficient were divided into direct and indirect effect to find out a clear picture of the inter-relationship between yield and other yield attributes by using path analysis.

In order to find out a clear portrayal of the inter-relationship between seed yield per plant and other yield attributes, direct and indirect effects were worked out using path analysis at genotypic level which also measured the relative importance of each component.

Seed yield per plant was calculated as a resultant (dependent) variable and days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, siliqua length, number of seeds per siliqua, 1000 seed weight and yield per plant were causal (independent) variables. Estimation of direct and indirect effect of path coefficient analysis for *Brassica napus* is presented in Table 11.

4.3.1 Days to 50% flowering

Path co-efficient analysis revealed that days to 50% flowering had positive direct effect (0.124) on yield per plant (Table 11). Days to 50% flowering had negative indirect effect on days of maturity(-0.057), plant height (-0.00018). Days to 50% flowering had positive indirect effect on number of primary branches per plant (0.150211), number of secondary branches per plant (0.007667),no. of siliqua per plant(0.066), siliqua length(0.043),number of seeds per siliqua (0.176)and thousand seed weight (0.174).

4.3.2 Days to maturity

Days to maturity found negative direct effect (-0.115) towards yield per plant. Further, it observed positive indirect effect towards yield per plant via days to 50% flowering(0.062),primary branches plant (0.066), no. of Secondary branches per plant (0.008), no. of siliqua / plant (0.069), siliqua length (0.0201), no. of seeds/ siliqua(0.174), 1000 seed weight (0.110).

4.3.3 Plant height

This character had negative direct effect (-0.002) on yield per plant (Table 11) followed by positive indirect effect on days to 50% flowering (0.012), number of primary branches per plant (0.059), number of secondary branches per plant (0.006), number of siliqua per plant (0.048), siliqua length (0.0413), number of seeds per siliqua (0.128), thousand seed weight (g) (0.021) where plant height had negative indirect effect on days of maturity(-0.021).

Table 11.Direct effect (bold and underlined) and indirect effect of different yield contributing characters yield per plant of *Brassica napus* L.

Characters	Days to 50% flowering	Days of maturity	Plant height (cm)	No. of primary branches / plant	No. of Secondary branches / plant	No. of siliqua / plant	Siliqua length (cm)	No. of seeds/ siliqua	1000 seed weight (g)	Yield/ plant (g)
Days to 50% flowering	**0.125**	-0.056	-0.0002	0.150	0.008	0.066	0.044	0.177	0.174	0.686
Days of maturity	0.062	**-0.115**	-0.0003	0.066	0.008	0.069	0.020	0.174	0.111	0.396
Plant height (cm)	0.012	-0.021	**-0.002**	0.059	0.006	0.048	0.041	0.129	0.021	0.293
Number of primary branches/plant	0.079	-0.032	-0.0004	**0.238**	0.009	0.116	0.021	0.185	0.240	0.857
Number of secondary branches/plant	0.033	-0.034	-0.0004	0.079	**0.029**	0.050	0.019	0.070	0.107	0.353
Number of siliqua/plant	0.067	-0.065	-0.0007	0.225	0.012	**0.123**	0.028	0.159	0.224	0.773
Siliqua length (cm)	0.047	-0.021	-0.0006	0.043	0.005	0.029	**0.116**	0.068	0.049	0.337
Numberof seeds/siliqua	0.074	-0.067	-0.0008	0.147	0.007	0.065	0.026	**0.299**	0.221	0.772
1000 seed weight (g)	0.046	-0.027	-8.14E-05	0.122	0.007	0.058	0.012	0.141	**0.470**	0.829

Bold values are direct effect **Residual effect (R) =0.029**

4.3.4 Number of primary branches

This character had positive direct effect (0.238) on yield per plant (Table 11) followed by positive indirect effect on days to 50% flowering (0.078), no. of Secondary branches / plant(0.0096), no. of siliqua / plant(0.1160),length (0.0211), number of seeds per siliqua (0.185) and thousand seed weight (g) (0.240) where had negative indirect influence on days of maturity(-0.032) and plant height (-0.00045).

4.3.5 Number of secondary branches

This character had positive direct effect (0.029) on yield per plant (Table 11) followed by positive indirect effect on days to 50% flowering (0.032926),number of primary branches per plant (0.0786), number of siliqua per plant (0.050), siliqua length (0.018),number of seeds per siliqua (0.070) and thousand seed weight (0.1071) where had negative indirect effect on days of maturity(-0.033), plant height (-0.00036).

4.3.6 Number of siliqua per plant

Path co-efficient analysis also revealed that, this character had the positive direct effect (0.122) on seed yield per plant followed by positive indirect effect on days to 50% flowering (0.067), number of primary branches per plant (0.225), number of secondary branches per plant (0.011), siliqua length (0.027), number of seeds per siliqua (0.159) and thousand seed weight (g) (0.224) (Table 11). Number of siliqua per plant had negative indirect effect on days to maturity (-0.065) and plant height (-0.00072).

4.3.7 Siliqua length

Siliqua length had positive direct effect (0.116) on yield per plant (Table 11) followed by positive indirect effect on days to 50% flowering (0.0470), number of primary branches per plant (0.043), number of secondary branches per plant (0.0047), number of siliqua per plant (0.0294), number of seeds per siliqua (0.067)andthousand seed weight (0.049) where siliqua length had negative indirect effect on days to maturity(-0.02002) and plant height (-0.00078).

4.3.8 Number of seeds per siliqua

Number of seeds per siliqua had positive direct effect (0.299) on yield per plant (Table 11). Number of seeds per siliqua had positive indirect effect on days to 50% flowering (0.073), number of primary branches per plant (0.147), number of secondary branches per plant (0.0068),number of siliqua per plant (0.065), siliqua length(0.026) andthousand seed weight (g) (0.220). Number of seeds per siliqua had also negative indirect effect on days to maturity (-0.06735) and plant height (-0.00078).

4.3.9 1000 seed weight

Path co-efficient analysis also revealed that thousand seed weight had positive direct effect (0.470) on yield per plant (Table 11). Thousand seed weight had positive indirect effect on days to 50% flowering (0.046), number of primary branches per plant (0.121618), number of secondary branches per plant (0.0066), number of siliqua per plant (0.058), siliqua length (0.0121) and number of seeds per siliqua (0.140). Thousand seed weight had also negative indirect effect on days to maturity (-0.0272) andplant height(-8.14E-05).

The residual effect (R) was0.029, which indicated the characters under study contributed 71% variations on the seed yield per plant (Table 11). It thus meant that there were some other traits those contributed 29% to the seed yield per plant which are not included in the present study might be exert significant effect on seed yield.

Similar agreement was obtained from the findings of Alam (2010) and Afrin (2009).According to Alam (2010), 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 thousand seed weight had the negative effect on yield per plant. Again, Afrin (2009) observed from path co-efficient analysis 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 thousand seed weight had the negative effect on yield per plant.

Both the correlation and path analysis means that number of seeds per siliqua appeared to be the first order yield component and ought to be given top priority in selection due to its high heritability, strong association and direct effect of high magnitude on seed yield.

Chapter V
Summary & conclusion

CHAPTER V

SUMMARY AND CONCLUSION

The present research was carried out during November 2017 to February 2018 at the experimental farm of the Department of Genetics and Plant Breeding, Sher-eBangla Agricultural University using 44 F_5 advanced progenies of *Brassica napus.* The experiment was conducted to study the genetic variation and character association in F_5 advanced generation of *Brassica napus L.* All 44 F_5 progenies varied significantly with each other for all the characters studied. The present study are summarized as follows:

The analysis of variance showed significant differences among the genotypes for all the traits viz. days to 50% flowering, days to maturity, plant height (cm), no. of primary branches per plant, no. of secondary branches per plant, no. of siliqua per plant, length of siliqua (cm), no. of seeds per siliqua, 1000 seed weight (g) and seed yield per plant (g).

Results revealed that the highest days required for 50% flowering (43.0days) was recorded from G16 where the lowest (30 days) fromG8 thehighest days to maturity was found (89 days) in G8 and the lowest found 79 days inG36,the highest plant height (124.39 cm) was observed from G22where the lowest (91.50 cm) was achieved fromG41 , thehighest number of primary branches per plants (4.85cm) was found in G22where the lowest (2.63cm) was from theG3, thehighest number of secondary branches per plants (4.86)was found in G26 and the lowest (0.63) was from G8the highest number of siliqua perplant (179.60) was found in G16where the lowest(63.83) was found inG7,the longest siliqua (8.22 cm) was obtained in G5 and the lowest siliqua length (6.08cm) was observed in G43, the highest number of seeds per siliqua (22.39) was found from G22 and the lowest (10.21) was from G13, the highest 1000-seed weight (5.15 g) was observed in G16and the lowest (3.37g) was produced by G30 and the highest number of seed yield per plant (20.5 g) was obtained from G12where the lowest seed yield plant(6.0 g) was obtained from G38.

In the 44 F_5 progenies for most of the characters wide range of variation observed. The phenotypic variance was higher than the corresponding genotypic variance for all the characters indicating greater influence on environment for the expression of these characters.

Days to 50% flowering, number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua, thousand seed weight exhibited low genotypic and phenotypic co-efficient of variation. Plant height and siliqua length (cm) showed moderate genotypic and phenotypic coefficient of variation. Plant height (cm), number of primary branches per plant, siliqua length (cm), number of seeds per siliqua, 1000 seed weight (g) and yield per plant showed high heritability with high genetic advance and genetic advance in percentage of mean.

These results exposed the possibility of predominance of additive gene action in the inheritance of these traits. Therefore the traits could be improved through selection process.

Days to 50%flowering, number of primary branches per plant, number of secondary branches per plant, length of siliqua, number of seeds per siliqua, 1000 seed weight and yield per plant showed high heritability with moderate genetic advance and genetic advance in percentage of mean indicated medium possibility' of selecting genotypes .

Selection was done among the 44 F_5 advanced progenies of *Brassica napus* for most promising plants with high yield and a short duration. The performance of the replications also compared with four check varieties. Based on the variability and as per the objectives seven most promising genotypes with short duration and higher yield were selected from the F_5 materials.

Considering 10 yield contributing character correlation revealed that number of primary branches per plant, secondary branches per plant, siliqua per plant, siliqua length, number of seeds per siliqua and 1000 seed weight (g) had significant positive correlation with number of secondary branches per plant, number of siliquae per plant, 1000 seed weight at genotypic level where number of primary branches per plant, secondary branches per plant, siliqua per plant, number of seeds per siliqua and 1000 seed weight (g) had significant association with number of secondary branches per plant, number of siliquae per plant and 1000 seed weight at phenotypic level. A significant genotypic positive correlation also showed for days to 50% flowering and length of siliqua.

Path co-efficient analysis exposed that plant height, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, siliqua length, seeds per siliqua and thousand seed weight had the positive direct effect on yield per plant and days to 50% flowering had the negative direct effect on yield per plant.

Conclusion

Results of present studies indicated significant variation among the genotypes for all the characters studied. From the above discussion, it may be concluded that

- The phenotypic variance and phenotype coefficient of variation were higher than the corresponding genotypic variance and genotypic coefficient of variation for all the characters studied.

- High heritability with high genetic advance showed all the traits like plant height, number of primary branches per plant, siliqua length and thousand seed weight.
- Number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, siliqua length, number of seeds per siliqua and 1000 seed weight had significant positive correlation with seed yield per plant.
- Path co-efficient analysis exposed that plant height, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, siliqua length, seeds per siliqua and thousand seed weight had the positive direct effect on yield per plant and days to 50% flowering had the negative direct effect on yield per plant.

Recommendation

Considering the traits like days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant,siliqua length (cm),number of siliqua per plant and 1000 seed weight (g) showed high heritability coupled with high genetic advance in percent of mean, selection would be effective for those traits. Genotypes G5, G9, G12, G16, G22, G25 and G32 can be further used for advanced research or varietal improvement program and high yielding variety can be developed.

REFERANCE

Abbas, S. (2013). Genetic variability, interrelationship, path coefficient in *Brassica napus*L. M.S. Thesis, BAU, Dhaka.

Abideen, S.N.U., Nadeem, F. and Abideen, S.A. (2013). Genetic variability and correlation studies in *Brassica napus*. Genotypes. *Intl. J. Innov. Appl.Stud.***2**(4): 574-581.

Afrin, K.S. (2009). Genetic variability, interrelationship, path coefficient and genetic diversity analysis in*Brassica napus* L. M.S. Thesis, SAU, Dhaka.

Afroz, R., Sharif, M.S.H. and Rahman, L. (2004). Genetic variability, correlation and path analysis in mustard and rape *(Brassica spp.). Bangladesh J. Plant Breed. Genet.***17**(1): 59-63.

Akbar, M., Saleem, U., Tahira, Yaqub, M. and Iqbal, N. (2007). Utilization of genetic variability, correlation and path analysis for seed yield improvement in mustard *Brassica juncea. J. Agric. Res.***45**(1): 25-31.

Alam, M.F. (2010). Variability studies in F_4 progenies of *Brassica rapa* obtained through intervarietal crosses. M.S. thesis, SAU, Dhaka.

Alam, M.S., Rahman, A.R M.S. and Khair, A.B.M.A. (1986). Genetic variability and character association in groundnut (*Arachis hypogaea L.). Bangladesh J. Agron.***10**(4): 9-16.

Ali, N., Javidfar, F., Elmira, J.Y. and Mirza, M.Y. (2003). Relationship among yield components and selection criteria for yield improvement in winter Rapeseed *(Brassica napus* L.*). Pakistan J. Bot.***35**(2): 167-174.

Ali, Y., Farhatullah, H. Rahman, A. Nasim, S.M. Azam and A, Khan. (2013). Heritability and correlation analysis for morphological and biochemical traits in *Brassica carinata.SarhadJ. Agric.***29**(3): 35-37

Andrahennadi, C.P., Weerasena, L.A. and Aberyrantne, M.D.R.S. (1991).Evaluation of brown mustard germplasm in Srilanka. *Cruciferae Newsl*.**14**(15): 62-63.

Anonymous. (2005). FAO Production Year Book, Food and Agricultural Organization of United Nations, Rome 00108, *Italy*. **57**: 115-133.

Ara, S. (2010). Variability, Correlation and Path Coefficient in Segregation population of *Brassica rapa* obtained through intervarietal crosses. M.S.thesis. SAU, Dhaka.

Arthamwar, D.N., Shelke, V.B. and Ekshinge, B.S. (1995). Correlation and regression analysis in mustard. Marathwada Agricultural University. *Indian J. Maharastra. Agril. Univ.***20**(2): 237-239.

Aytac, Z., Kinaci, G. and Kinaci, E. (2008). Genetic variation, heritability and path analysis of summer rape seed cultivars. *J. Appl. Biol. Sci.***2**(3): 35-39.

Badsra, S.R. and Chaudhary, L. (2001). Association of yield and its components in Indian mustard [*Brassica juncea (*L.*)Czern and Coss].Agril. Sci. Digest.***21**(2): 83-86.

Baradaran, R., Majidi, E., Darvish, F., Azizi, M. (2007). Study of correlation relationships and path coefficient analysis between yield and yield components in rapeseed (*Brassica napus* L.*)*. Ph.D. thesis, Birjand unit, I.A. University, Birjand, Iran.

Basalma, D. (2008). The correlation and path analysis of yield and yield components of different winter rapeseed *(Brassica napus ssp. oleifera* L.*)* cultivars. *Res. J. Agric. Biol. Sci.***4**(2): 120-125.

BBS (Bangladesh Bureau of Statistics). (2015a). Statistical Yearbook of Bangladesh. Bangladesh Bureau of Statistics, Stat. Div., Ministry Planning, Govt. Peoples Rep. Bangladesh, Dhaka, p.477.

BBS (Bangladesh Bureau of Statistics). (2015b). Yearbook of Agricultural Statistics of Bangladesh. Bureau of Statistics, Stat. Div., Ministry Planning, Govt. Peoples Rep. Bangladesh, Dhaka. p.101.

BBS (Bangladesh Bureau of Statistics). (2015c). Yearbook of Agricultural Statistics of Bangladesh. Bangladesh Bureau of Statistics, Stat. Div.,Ministry Planning, Govt. Peoples Rep. Bangladesh, Dhaka, p.322.

Behl, R.K., Chowdhury, B.D., Shing, R.P. and Shing, D.P. (1992). Morphological determinatesof oil yield in *Brassica juncea* L. under dryland conditions. *Indian J. Genet. Plant Breed*. **52**(3): 280-284.

Bhardwaj, R.P. and Singh, R.R. (1969). Morphological and genetic variability in brown sarson (*Brassica campestris* var. brown sarson). *Madras Agric. J.***56**(1): 28-31.

Bhuiyan, M.S.R. (2012). Research and development of oilseeds: Past, present and future. Proc. nat. work, on research achievement of past ten years of pulses and oilseeds and future research strategies for sustainable crop production,Mar. 20-21, BARC, Dhaka, Bangladesh, pp.23-41.

Bilal, D., and Bassin, P. (2015). Rapeseed and crambe: Alternative crops with potential industrial uses. Bulletin 656. Manhattan, Kansas: Kansas State University, Agricultural Experiment Station.

Biswas, K.P. (1989). Performance evaluation of 4th genotypes of *oleiferous Brassica*. Proceeding of the 14th Annual Bangladesh*Sci. Conf.*

Butruille, D.V., Guries R.P. and Osborn T.C. (1999). Increasing yield of spring oilseed rape hybrids through introgression of winter germplasm. *Crop Sci*.**39**: 1491-1496.

Chandola, R.F., Dixit, P.K., Sharina, K.N. and Saxena, D.K. (1977). Variability in *B. juncea* under three environments. *IndianJ. Agric. Sci.***47**(9): 680-683.

Chowdhury, P.K. and Kumar, A. (2003). Association and Interdependence of morphophysiological characters under moisture stress in Brassica. *Beitrage Zar Tropichen Landuitshaft.***18**(1): 43-47.

Chen, C., Hwu, K.K., Liu, C.P. and Lin, M.S. (1983). Selection criteria for yield improvement in rape. *J. Agril. Asso. China*. **124**: 63-73.

Chowdhury, B.D., Thakural, S.K., Singh, D.P. and Singh, P. (1987). Genetics of yield and its components in Indian mustard. *Narenda DevaJ. Agril. Res*. **3**(1): 37-43.

Clarke, G.M. (1973). Statistics and Experimental Design. Edward Arnold. London.

Comstock, K. and Robinson, P.R. (1952). Estimation of genetic advance. *Indian J. Hill.***6**(2): 171-174.

Dabholkar, A.R. (1992). Elements of Biometrical Genetics. Concept publishing,New Delhi, India.

Das, K., Barua, P.K. and Hazarika, G.N. (1998). Genetic variability and correlation in Indian mustard. *J. Agril. Sci. Soc*. *North East India*. **11**(2):262-264.

Dewey, D.R. and Lu, K.H. (1995). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron.J*. **51**: 515-518.

Dileep, K., Arvind, S.V.K., Bali, D. and Kumar, K. (1997). Correlation and regression studies between different yield attribute and seed yield in mustard *(Brassica juncea* L.*). Part Univ. Agric. Tech.***14(**2):202-206.

Diwakar and Singh. (1993). Correlation and path analysis of yield and yield attributes of toria (*Brassica rapa var napus). IndianJ. Agril. Sci.***63(**4): 263-266.

Downey RK, Rimmer SR (1993) Agronomic improvement in oilseed *Brassicas. Advances in Agronomy* **50:** 1–66.

Downey, R.K. and Robbelen, G. (1989). Brassica species: Oil crop of the world, their breeding and utilization. Mc Graw Hill Publishing Co., New York. Pp.339-374.

Ejaz-Ul-Hasan, Mustafa, H.S.B., Bibi, T. and Mahmood, T. (2014). Genetic variability, correlation and path analysis in advanced lines of rapeseed (*Brassica napus*) for yield components. Cerce. *Agro.in Moldova.XL*.**1**: (157).

Esmaeeli-Azadgoleh, M.A., Zamani, M. and Esmaeil, Y. (2009). Agronomical important traits correlation in Rapeseed (*Brassica napus* L.*)* genotypes. *Res. J. Agric. Biol. Sc*. **5**(5): 798-802.

FAO. (2013). Food and Agriculture Organization of the United Nations,FAOSTAT. FAO Statistics Division.

FAO. (2014). Food and Agriculture Organization of the United Nations, Trad and Market Division. Food outlook. 33-102.

Friedt, W., Snowdon, R., Ordon, F. and Ahlemeyer, J. (2007). Plant Breeding: assessment of genetic diversity in crop plants and its exploitation in breeding. *Prog. Bot.* **168**: 152- 177 or 178.

Ghosh, S.K. and Gulati, S.C. (2001). Genetic variability and association of yield components in Indian mustard (*Brassica juncea* L.). *CropRes.Hisar***.21**(3): 345-349.

Goswami, P.K. and Behl. R.K. (2006). Exploitation of heterosis and selection of superior combiners in indian mustard. Department of Plant Breeding,CCS Haryana Agricultural University, Hissar. *IndianAnn. Agril. Res***.26**(1): 56-58.

Goswami, P.K., Ghosh, D.V. and Behl, R.K. (2005). Genetic divergence in Indian mustard. *Ann.Agril. Res.***27**(2): 187-190.

Hasanuzzaman, M. and Karim, M.F. (2007). Performance of rapeseed (*Brassica campestris* L.) cv. SAU sarisha 1 under different row spacing and irrigation levels. *Res. J. Biol. Sci*.**3**: 960-965.

Helal, M.M.U., Islam, M.N., Kadir, M. and Miah, M.N.FI. (2014). Genetic variability, correlation and path analysis for selection of mustard (*Brassica Spp*.). *Eco-friendlyAgril. J*. **7**(12): 176-181.

Hosen, M. (2008). Variability, correlation and path analysis in F_2 material of *Brassica rapa*. MS Thesis, SAU, Dhaka.

Hossain, A., Salini, R.P., Malik, B.P.S. and Singh, D.P. (2008). Variation for morphophysiological characters in genotypes of Indian rapeseed. *IndianJ. Agril.Sci.***57**(4): 225-230.

Jagadev, P.N., Samal, K.M. and Lenka, D. (1999). Genetic divergence in rape mustard. *IndianJ. Genet.***51**(4): 465-467.

Jahan, N. (2008). Inter-genotypic variability and genetic diversity analysis in F_4 lines of *Brassica rapa*. MS thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

Jain, A.K., Tiwarii, A.S. and Kushwah, V.S. (1988). Genetics of quantitative traits of Indian mustard. *Indian J. Genet. Pl. Breed.***48**(2): 117-119.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimation of genetic and environmental variability in soybean. *Agron. J.***47**: 314-318.

Kardam, D.K. and Singh, V.V. (2005). Correlation and path analysis in Indian mustard (*Brassica juncea* L. *Czern&Coss*) grown under rainfed condition. Department of Plant Breeding and Genetics, SKN College of Agriculture, Jobner - 303 329, Rajasthan. *Indian J. Spices Aromatic Crop.***14**(i): 56-60.

Katiyar. R.K., Chamola, R., Singh. H.B. and Tickoo, S. (2004). Heterosis and combining ability analysis for seed yield in yellow sarson (*Brassica campestris*) Brassica. **6**(1-2): 23-28.

Khan, F.A., Sajid-Ali., Amir-Shakeel., Asif-Saeed. and Ghulam-Abbas (2006). Correlation analysis of some quantitative characters in *Brassica napus* L. Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, *Pakistan.J. Agril. Res. Lahore*. **44**(1): 7-14.

Khan, M. H., Bhuiyan, S. R., Rashid, M.H., Ghosh, S. and Paul, S.K. (2014). Variability and heritability analysis in short duration and high yielding *Brassica rapa L*. *Bangladesh J. Agril. Res.***38**(4): 647-657.

Khan. R.S.A. and Khan, F.A. (2003). Evaluation of genetic potential of some Brassica germplasm collections. *Int. J. Agric. Biol.***6(**4): 30-31.

Khulbe, R.K. and Pant, D.P. (2000). Correlation and path co-efficient analysis of yield and its components in Indian mustard. *Crop Res. Hisar.***17**(3): 371- 375.

Kudla, M. (1993). Comparative analysis of winter swede rape genotypes. Biuletyn *Instytutu Hodowli Roslin.***90**: 99-107.

Kumar, C.H.M.V., Arunachalam, V. and Rao, P.S.K. (1996). Ideotype and relationship between morpho-physiological characters and yield in Indian mustard (*Brassica juncea*). *Indian J.Agric. Sci.***66**(11): 14-17.

Kumar, N., Bisht, J.K. Joshi, M.C. (1988). Correlation and discriminant function of path analysis in Indian mustard. *Indian J. Agric. Sci.***58**(1): 51-52.

Lebowitz, R.J. (1989). Image analysis measurements of repeatability estimates of siliqua morphological traits in *Brassica campestris* L. *Euphytica.* **43**(1-2):13-116.

Lekh, R., Hari, S., Singh, V.P., Raj, L. and Singh, H. (1998). Variability studies in rapeseed and mustard. *Ann. Agril. Res.* **19**(1): 87-88.

Mahak, S., Singh, H.L., Satyendra and Dixit, R.K. (2004). Studies on genetic variability, heritability, genetic advance and correlation in Indian mustard *[Brassica juncea(L.)Czern and Coss.].Plant Archives*. **4**(2):291-294.

Mahmud, M.A.A. (2014). Inter Genotypic variability study in advanced lines of *Brassica rapa.* MS thesis, Dept. of Genetics and Plant Breeding,SAU, Dhaka.

Maurya, N., Singh, A.K. and Singh, S.K. (2012). Inter-relationship analysis of yield and yield components in indian mustard, *Brassica junceaL.Indian J. Plant Sci.***1** (23): 90-92.

Mekonnen, T.W., Wakjira, A. and Genet, T. (2014). Correlation and path coefficient analysis among yield component traits of Ethiopian mustard (*Brassica carinata* L. Brun) at Adet. Northwestern, *Ethiopia. J. Plant Sci*.**2**(2): 89-96.

Nanda, R., Bhargava, S.C. and Tomar, D.P.S. (1995). Rate and duration of siliqua and seed filling and their rotation to seed yield in Brassica species. *Indian J. Agric. Sci*. **64**(4): 227-232.

Nasim, M., Rahman, L., Quddus, M.A. and Shah-E-Alam, M. (1994). Correlation and path analysis in *Brassica campestris* L. *Bangladesh* J. *Agril. Sci.***21**(10): 15-23.

Naznin, S. (2013). Variability, character association and divergence in rapeseed advanced lines. MS Thesis, Dept. of Genetics and Plant Breeding, SAU,Dhaka.

Niraj, K and Srivastava. S. (2004). Variability and character association studies in Indian mustard. *J. Appl. Bio.***14**(1): 9-12.

Olsson, G. (1990). Rape yield production components. *Sversk Fortdning.***59**(9):194-197. *Cited from Plant Breed. Abs.***61**(5): 588.

Pandey, R., Kumar, B. and Kumar, M. (2013). Genetic divergence for quantitative traits in indian mustard (*Brassica junceaL.* Czern&Coss*). American-EurasianJ. Agric. Environ. Sci.* **13** (3): 348-351.

Pankaj, S., Gyanendra, T., Gontia, A.S., Patil, V.D. and Shah, P. (2002). Correlation studies in indian mustard. Dept. of Genetics and Plant Breeding, Marathwada Agricultural University, *India.Agric. Sci.Digest*.**22**(2): 79-82.

Pant, S.C. and Singh. P. (2001). Genetic variability in Indian mustard. *Agric. Sci. Digest*. **21**(1): 28-30.

Parveen, S. (2007). Variability study in F_2 progenies of Inter-varietal crosses of *Brassica rapa*. MS Thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

Peter, K.V. and Rai, B. (1995). Genetic divergence in rapeseed. *IndianJ.***36**(3): 379-383.

Prakash, S.and Hinata, K. (1980). Polyphyletic origins of *Brassica napus*: new evidence based on organelle and nuclear RFLP analysis. *Genome.***35**: 992- 1001.

Rakow, H.H. and Hari, G.S. (2004). Crop Breeding and Genetics. Kalyani Publishers, New Delhi-110002, p.381.

Rameah, V., Rezai, A. and Saeidi, G. (2003). Estimation of genetic parameters for yield, yield components and glucosinolate in rapeseed (*Brassica napus L.).J. Oilseed Brassica*. **5**(3-4): 143-151.

Rameeh, V. (2011). Correlation and path analysis in advanced lines of rapeseed (*Brassica napus*) for yield components. *J. Oilseed Brassica*. **2**(2): 56-60.

Rameeh, V. (2012). Correlation analysis in different planting days of rapeseed varieties. Agricultual and Natural Resources Research Centre of Mazandran, Sari, *Iran. J. Agril. Sci*. **7**(2): 123-126.

Rameeh,V. (2013). Multivariate analysis of some important quantitative traits in rapeseed (*Brassica napus* L.*)* advanced lines. *J. Oilseed Brassica*. **4**(2): 75-82.

Rashid, M. H. (2007). Characterization and diversity analysis of the *oleiferous Brassica* species. MS thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka

Reddy, N.N. (1991). Correlation studies in Indian mustard (*Brassica juncea* L. *Czern and Coss*). *J. Oilseeds Res.***8**(2): 248-250.

Rukhsana, A., Muhammad, Y., Muhammad, J,, Mumtaz, H,, Nazakat, N. and Amir, A. (2005). Adaptation and yield potential of different genotypes of rapeseed and mustard under agroclimatic conditions of Bahawalpur (Pakistan). *Agriculture.***7**(4): 609-611.

Sabaghnia, N., Dehghani, H., Alizadeh, B. and Mohghaddam, M. (2010) Interrelationships between seed yield and 20 related traits of 49 canola genotypes in non-stressed and water stressed environments. *Spanish J. Agril. Res.***8**: 356-370.

Shalini, T.S., Sheriff, R.A., Kulkarmi, R.S. and Venkataramana, P. (2000). Correlation and path analysis in Indian mustard germplasm. Research on crops Dept. of Genetics and Plant Breeding, University of Agricultural Science, India. **1**(2): 226-229.

Sharafi, S.P. (2015).Variability and correlation studies for oil and seed yield in gobhi sarson. *IndianJ. Agric. Sci.***18(**2): 99-102.

Sheikh, F.A., Rathen, A.G. and Wani, S.A. (1999). Path analysis in toria (.*Brassica campestris* L.) *var. toria*. *Adv. Plant Sci.***12***(*2): 385-388.

Sheikh, F.A., Shashibanga, S.S., Najeeb, G.A. and Rather, A.G. (2009).Hybridization of ethiopian mustard and *Brassica napus* assisted through cytogenetic studies. Ph.D. thesis, Agricultural University. Ludhiana,141004, India.

Shen. J.X., Fu,1W., Yang, 0.5.. Shcn, J.X., Pu. T.D. and Y.9. G.S. (2002). 1 – leterosis of double low , self-incompatibility in oilseed rape (*Brassica rapa* L.*).ChineseAgril. Sci.***7**(i): 732-737.

Shukla. S., Bhargava, A., Chatterjee, A., Srivastava. A. and Singh, S.P. (2006). Genotypic variability in vegetable amaranth (.Amaranthus tricolor L.) for foliage yield and its contributing traits over successive cuttings and years.Euphytica. **151**: 103-110.

Siddikee, M.A. (2006). Heterosis, intergenotypic variability, correlation and path analysis of quantitative characters of *oleiferous Brassica campestri* L. MS thesis. Department of Genetics and Plant Breeding, Sher-e Bangla Agricultural University, Dhaka.

Sing, P., Khera, M. K. and Gupta, V.P. (2001). Variability and correlation studies for oil and seed yield in gobhi sarson. *IndianJ. Agric. Sci.***18**(2): 99-102.

Singh, D., Arya, R. K., Chandra, N., Niwas, R. and Salisbury, P. 2010. Genetic diversity studies in relation to seed yield and its component traits in Indian mustard(*Brassica junceaL.Czern&Coss). J. Oilseed Brassica*.**1**: 19-22

Singh, R.P., Khera, M.K. and Gupta, V.P. (1991). Variability and correlation studies for oil and seed yield in gobhi sarson. *Crop Improv.***18**(2): 99-102.

Singh, R.P., Malik, B.P. and Singh, D.P. (1985). Variation for morpho physiological characters in genotypes of Indian mustard. *Indian J. Agric.Sci.***57:** 227-230.

Singh, R.P., Malik, B.P.S. and Singh, D.P. (1987). Variation for morphological characters in genotypes of Indian mustard. *Indian J. Agric. Sci.***57**(4): 225- 230.

Srivastava, M.K. and Singh, R.P (2002). Correlation and path analysis in Indian mustard. *Crop Res. Hisar.***23**(3): 517-521.

Teresa, W. (1987). Selection criteria of winter rape single plant and its seed yield.In: 7th International Rapeseed Congress, Poland. 11-14, May.

Thakra, N.K., Yadav, T.P., Kumar, P. Singh, A. and Chandra. N. (2004). Association analysis for quantitative traits in Indian rapeseed. *Cruciferae Newsl.***21**: 105-106.

Thakral, N.K., Yadava, T.P., Kumar. P., Singh, A. and Chandra, N. (1999).Association analysis for some quantitative traits in Indian mustard.*Cruciferae Newsl.***21**: 105-106.

Tusar, P., Maiti, S. and Mitra, B. (2006). Variability, correlation and path analysis of the yield attributing characters of mustard {*Brassica spp.). Res. Crops.***7**(1): 191-193.

Tyagi, M.K., Chauhan. J.S., Kumar, P.R. and Singh, K.H. (2001). Estimation of heterosis in Indian mustard [*Brassica juncea* (L.*)* Czern and Coss.]. *Annals Agric. Bio. Res*. **69**(2): 193-200.

Tyagi, P.K., Singh, K., Rao, V. and Kumar, A. (1996). Correlation and path coefficient analysis in Indian mustard (*Brassica juncea* L.). *CropRes. Hisar*.**11**(3): 319-322.

Uddin, M.J., Choudhury, M.A.Z. and Miah, M.F.U. (2005). Genetic variability, character association and path analysis in Indian mustard (Brassica juncea L.). *Ann.Bangladesh Agric*. **5**(1): 51-52.

Uddin, M.S., Bhuiyan, M.S.R., Mahmud, F. and Kabir, K. (2013).Study on correlation and path coefficient in F_2 progenies of rapeseed.*Acad. J. Plant Sci.* **6**(1): 13-18.

Varshney, S.K., Rai, B. and Singh, B. (1986). Component analysis of harvest index in Brassica oilseeds. *IndianJ. Agric. Rev*.**20**(3): 129-134.

Vivek, S., Ram, B. and Kamlesh, K. (2007). Genetic diversity in Indian mustard (*Brassica juncea*L. *Czem and Coss.*). *Prog. Agril.***7**(1/2): 105- 109.

Walle, T., Wakjira, A. and Mulualem, T. (2014). Analysis of genetic parameters on Ethiopian mustard (*Brassica carinata* A. Braun) genotypes in northwestern Ethiopia. *Agric. Sci. Res. J*. **4**(4): 83-88.

Wan, Y.L. and Hu, G.C. (1983). Studies on heritability, genetic correlations and genetic advances of the major characters in rape. *Chinese Oil Crops.***1**: 1-7.

Wright, S. (1921). Correlation and causation. *J. Agric. Res*. **20**: 557-585.

Xu-Suqin. and Yao, XiangTan. 2006. Study on the correlation between yield characters and yield of superior rape (*Brassica napus* L.) in north Zhejiang Province. Jiaxing Academy of Agricultural Sciences, Jiaxing 314016, China. **22**(2): 65-67.

Yadava, O.P., Yadav, T.P. and Kumar, P. (1996). Combining ability studies for seed yield, its components characters and oil content in Indian mustard (*Brassica juncea* L. Czern and Coss.). *J. Oil Seed Res.***9**(1): 14-20.

Yadava, T.P. (1973). Variability and correlation studies *Brassica juncea* L. Czern and Coss. *Madras. Agric. J.***60:** 1508-1511.

Yadava, T.P., Zada, A.K. and Hari, S. (2004). Selection indices for Seed yield in Indian Mustard (*Brassica JunceaL*. Czern&Coss), I. based on physiological attributes. *Indian J. Genet. Plant Breed.***48**(1): 23-29.

Yadava, Y.P., Singh, H. and Singh, D. (1993). Gene action for seed yield and its attributes under research. *Indian J. Genet. Pl. Breed*. **6**(1): 168-172.

Yin, J.C. (1989). Analysis on ecological, physiological and production characteristics of high quality rapeseed cultivars.*Acta Agriculture,Shanghae*. **5**(4): 25-32.

Zahan, M.I. (2006). Morphological characterization and genetic diversity in oleiferous Brassica species. M.S. thesis, SAU, Dhaka.

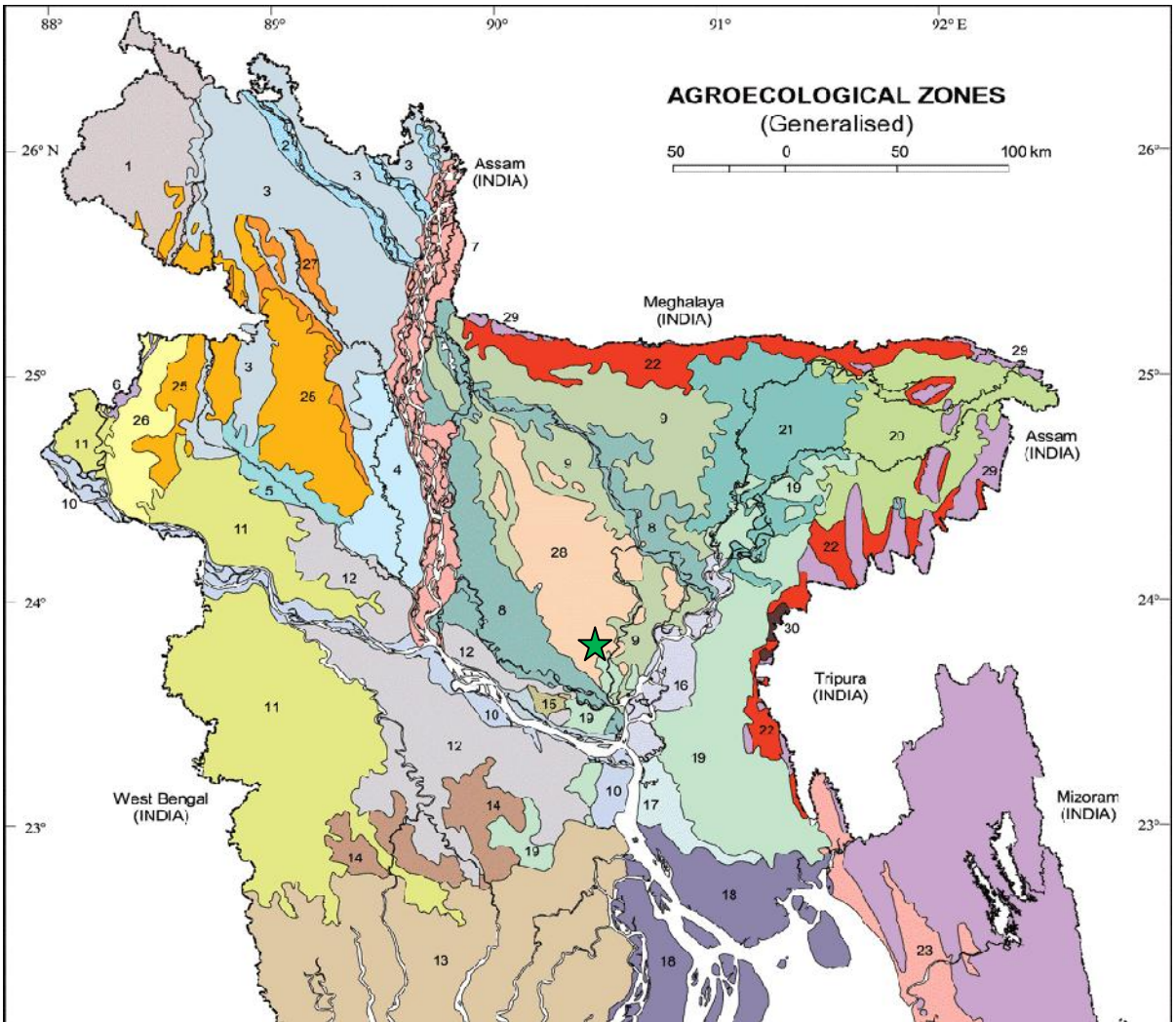
Zaman, M.A., Tuhina-Khatun, M., Ullah, M.Z., Moniruzzamn, M. and Rahman,M. Z. (2010). Multivariate analysis of divergence in advanced lines of mustard (Brassica sp.). *Bangladesh J. Plant Breed. Genet*. **23**(2): 29-34.

Zaman, M.W., Talukdar, M.Z.L., Biswas, K.P. and Ali, M.M. (1992). Development allometry and its implication to seed yield in *Brassica napus* L.Sveriges Utsades Foreign Tidskrift. **102**(2): 68-71

Zebarjadi, A., Kakaei. M. and Mostafaie, A. (2011). Genetic variability of some traits in rapeseed (*Brassica napus* L.) under draught stress and non-stress condition. *Biharean Biologist, Oradea, Romania*.**5**(2): 127-131.

APPENDICES

Appendix I. Map showing the experimental site under the study



★ **The experimental site under the study**

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

A. Physical composition of the soil

Soil separates	%	Methods employed
Sand	36.90	Hydrometer method (Day, 1965)
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, 1947
2	Total N (kg/ha)	1790.00	Bremner and Mulvaney, 1982
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, 2017 to February, 2018.

Month	Air temperature (ºc)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
November, 2017	34.4	18.3	78	225	**5.9**
December,2017	32.1	16.7	69	0	**7.9**
January, 2018	29.1	13.1	79	0	**3.7**
February, 2018	28.2	11	74	1	**5.7**

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

APPENDIX IV. Mean performance of *Brassica napus* genotypes in respect of growth and yield performance

Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/ plant	No. of secondary branches/ plant	No. of siliqua/ plant	Siliqua length (cm)	No. of seeds/ siliqua	1000 seed weight (g)	Yield/ plant (g)
Nap2001 X Nap 206	39	83.5	105.74	3.73	1.4	110.92	8.1	12.74	4.27	11.5
Nap94006 X Nap 206	38	83	117.16	3.7	1.53	112.89	7.61	14.56	4.33	9.5
Nap248 X Nap159	34	86.5	118.2	2.66	2.7	112.26	7.48	15.10	4.52	11
Nap9908 X BS-13	38	83	118.46	3.53	1.565	112.43	7.42	15.84	4.37	10
Nap94006 X BS-7	38.5	88	118.61	4.66	2.6	137.05	8.22	19.35	4.83	16.5
Nap2012 X Nap2013	34.5	86.5	118.26	3.68	2.165	101.96	7.07	16.32	4.12	8.5
Nap94006 X Nap2013	31	87.5	104.23	3.03	1.2	82.56	6.97	16.27	3.62	7
Nap248 X Nap206	30	89	112.33	2.96	1.03	99.33	6.35	16.08	4.32	7.5
Nap206 X Nap2012	40	88.5	122.63	4.49	1.56	133.8	7.38	20.26	4.77	15.5
Nap2037 X Nap2022	32.5	83.5	110.99	3.93	1.43	105.06	6.33	17.22	4.37	9.5
Nap9908 X Nap94006	36	81.5	104.53	3.66	1.795	113.33	7.13	16.57	4.47	11.5
Nap2001 X Nap248	40	86	105.09	4.4	1.83	154.56	7.66	19	4.94	18.5
Nap2057 X Nap2022	32	86.5	106.86	4.36	2.03	111.95	6.73	10.96	4.22	8.5
Nap206 X Nap2013	37.5	87	106.16	3.59	1.665	130.46	7.38	16.06	3.42	7.5
BS-7 X Nap206	36	87	117.86	4.51	1.965	124.37	6.69	13.32	4.32	9
Nap2001 X Nap2022	43	87.5	108	4.43	4.4	179.6	7.15	20.76	5.15	20.5
Nap94006 X BS-13	30	82.5	114.68	3.76	1.83	127.35	7.42	14.24	4.54	10.5
Nap94006 X Nap179	37	83.5	102.08	3	2.215	130.28	6.97	13.93	4.08	9
Nap2057 X Nap2012	30	82.5	120.51	3.53	1.3	122.84	6.98	16.77	4.32	9
Nap94006 X Nap2012	34	88	109.4	4.06	2.115	109.	7.56	16.1	3.62	7.5

			8			15		5		
BS-7 X Nap2013	33.5	81	110.1	3.71	2.33	88.415	7.20	13.9	3.83	6.5
Nap179 X Nap206	39.5	87.5	124.39	4.85	3	135.58	7.55	22.39	4.42	17
Nap9908 X Nap206	35	86	98.11	4	2.3	130.41	6.59	14.18	4.62	10
Nap94006X Nap 2022	32.5	85.5	114.81	3.23	2.15	110.7	7.01	13.8	4.36	8.5
Nap2012 X Nap 2022	41	87.5	106.03	4.59	2.76	161.73	7.25	21.92	4.68	18.5
Nap248 X Nap 2022	36	81	116.53	3.96	4.865	103.96	6.71	15.87	4.17	9

Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/ plant	No. of secondary branches/ plant	No. of siliqua/ plant	Siliqua length (cm)	No. of seeds/ siliqua (g)	1000 seed weight (g)	Yield/ plant (g
BS-13 X Nap 2013	30	81.5	106.16	2.63	2.29	86.73	7.64	14.21	4.37	8.5
Nap2057 X Nap 248	32.5	88	103.12	3.26	3.09	104.4	7.405	16.26	3.87	7
Nap2057 X BS-13	34	85	110.13	3.59	2.86	101.09	7.475	15.60	4.48	9.5
BS-13 X Nap 206	33.5	82.5	111.28	4.43	2.4	131.26	7.15	15.30	3.37	7
Nap9908 X Nap 2013	32	81.5	92.56	3.59	2.16	113.79	6.315	13.96	4.53	9.5
Nap248 X Nap 2013	39.5	88	119.06	4.33	2.5	169.33	7.385	22.06	4.99	18.5
Nap179 X Nap 2057	39	82	100.23	4.39	1.03	115.23	7.415	15.16	4.17	9.5
Nap179 X Nap 2022	37	88	98.33	3.16	2.1	119.96	6.55	17.8	4.57	10
Nap2037 X Nap 2013	35	80.5	120.33	3.39	1.39	105.99	7.47	16.66	3.42	7
Nap200 X Nap 2022	32.5	79	93.03	3.73	2.7	106.73	7.435	14.87	4.63	10
Nap94006 X Nap 2057	38.5	83	98.16	3.26	1.16	89.13	6.755	18.26	4.52	9.5
BS-7 X Nap 2013	36.5	86	97.66	2.96	1.28	84.71	7.285	17.52	3.63	6
Nap2057 X Nap 2001	39	79.5	102.76	2.69	0.63	63.83	6.455	15.795	4.51	9.5
BS-7 X Nap 2057	39	83.5	95.13	3.29	2.16	108.99	6.725	13.76	3.57	7
Nap94006 X Nap 2001	40.5	83.5	91.5	2.7	1.83	101.46	7.065	16.4	4.32	8.5
BS-13 X Nap 179	37	88	107.96	3.63	2.99	127.13	7.31	13.92	3.82	7
Nap179 X Nap 2012	32.5	84	106.09	3.43	2.35	118.13	6.08	16.1	3.58	7
Nap2001 X Nap 179	38	86.5	108.23	2.9	2.03	115.66	7.525	15.88	4.12	8
LSD0.05	5.28	5.61	9.17	0.84	1.03	10.92	0.64	2.36	0.48	1.72
CV (%)	7.32	3.28	4.19	11.42	24.20	4.67	4.45	7.23	5.58	8.43

APPENDIX IV. Continued..