GENETIC DIVERSITY AND INTERRELATIONSHIP BETWEEN YIELD CONTRIBUTING CHARACTERS IN F_6 POPULATIONS OF *Brassica napus* L.

MST. AKLIMA KHANAM

DEPARTMENT OF GENETICS AND PLANT BREEDING

SHER-E-BANGLA AGRICULTURAL UNIVERSITY

DHAKA-1207

June, 2020

GENETIC DIVERSITY AND INTERRELATIONSHIP BETWEEN YIELD CONTRIBUTING CHARACTERS IN F_6 POPULATIONS OF *Brassica napus* L.

BY

MST. AKLIMA KHANAM

REGISTRATION NO. 13-05316

A Thesis
submitted to the Faculty of Agriculture,
Sher-e-Bangla Agricultural University, Dhaka
in partial fulfilment of the requirements
for the degree of

MASTERS OF SCIENCE
IN

GENETICS AND PLANT BREEDING

Semester: January-June, 2020

Approved by

Dr. Firoz Mahmud **Professor** **Supervisor**	**Dr. Md. Ashaduzzaman Siddikee** **Professor** **Co-supervisor**

Prof. Dr. Kazi Md. Kamrul Huda
Chairman
Examination Committee

Dr. Firoz Mahmud
Professor
Department of Genetics and Plant Breeding
Sher-e-Bangla-Agricultural University
Dhaka-1207
Mob: +8801552432589
E-mail: fmahmud08@gmil.com

CERTIFICATE

This is to certify that thesis entitled, " " submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfilment of the requirements for ***GENETIC DIVERSITY AND INTERRELATIONSHIP BETWEEN YIELD CONTRIBUTING CHARACTERS IN F_6 POPULATIONS OF Brassica napus L.*** *the degree of* ***MASTER OF SCIENCE in GENETICS AND PLANT BREEDING****, embodies the result of a piece of bona fide research work carried out by* ***MST. AKLIMA KHANAM****, Registration No****. 13-05316*** *under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

Dated: June, 2020 **Dr. Firoz Mahmud**

Place: Dhaka, Bangladesh **Supervisor**

DEDICATED TO

MY

BELOVED PARENTS

Acknowledgements

Alhamdulillah, first of all I am very thankful to Almighty Allah for giving me such power, knowledge and strength, peace of mind, good health and ability to complete this research work successfully. Completion of any type of research work requires helps from a number of persons. Now, there is little effort to show my deep gratitude to that helpful persons.

I convey my sincere gratitude and also thankful to my supervisor Professor Dr. Firoz Mahmud, Department of Genetics & Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for his valuable suggestions, constant encouragement, scholastic guidance and fatherly behavior throughout the research work and preparation this thesis.

I would like to express my sincere respect to my co-supervisor, Dr. Md. Ashadurzzaan Siddikee, Professor, Department of Genetics & Plant Breeding, Sher-e-Bangla Agricultural University, for his helpful advices, constructive criticism during the period of research work.

I wish to express my gratitude to Prof. Dr. Kazi Md.Kamrul Huda, Chairman, Department of Genetics & Plant Breeding, Sher-e-Bangla Agricultural University, for sharing his knowledge, valuable advice and other academic supports.

I am grateful to Honourable Vice Chancellor, Shere-Bangla Agricultural University, for providing me all possible helps during my studies.

I would like to extend my thanks to those who offered collegial guidance and support over the years: Prof. Dr. Md. Sarowar Hossain, Prof. Dr. Naheed Zeba, and Prof. Mohammad Saiful Islam for their kind help and co-operation throughout my research work. My thankfulness is also to all the staffs of Genetics and Plant Breeding Department for their sincere helps to this thesis preparation.

I also acknowledged the Ministry of Science and Technology for awarding a prestigious 'NST' fellowship for conduction of the research work.

Finally I acknowledge with a deep sense of reverence, gratitude towards my parents for their blessings, endless encouragement and affection, who has always supported me to reach this level.

June, 2020

SAU, Dhaka ***The Author***

GENETIC DIVERSITY AND INTERRELATIONSHIP BETWEEN YIELD CONTRIBUTING CHARACTERS IN F_6 POPULATIONS OF *Brassica napus* L.

BY

MST. AKLIMA KHANAM

ABSTRACT

This research was carried out at experimental field of Sher-e-Bangla Agricultural University, Dhaka, to study the variability, correlation, path analysis and genetic diversity during November 2018 to February 2019 growing seasons with 38 populations. The genotypes were found significantly variable for most of the characters. The maximum plant height was observed by the population G11. Maximum primary branches per plant G9. Comparatively phenotypic variances were higher than the genotypic variances for most of the characters studied. The high GCV value was observed for number of secondary branches per plant (27.20). Days to maturity (70.73) exhibited the highest value of heritability followed by seed yield per plant (67.69) while 1000 seed weight (12.49) exhibited the lowest value of heritability. High heritability with high genetic advance as percent of mean was noticed for secondary branch per plant (43.83), total siliqua per plant (33.52), seed yield per plant (30.96). The significant positive correlation with seed yield per plant was found in number of primary branches, total number of siliqua, days to maturity. Path co-efficient analysis revealed that days to 50% flowering (0.286), days to maturity (0.212), plant height (0.069), root length (0.164), primary branches (0.375), total siliqua per plant (0.383), siliqua length (0.067) and 1000 seed weight (0.082) had the positive direct effect on yield per plant. On the basis of cluster analysis, all the genotypes were classified in six clusters. The highest inter cluster distance was observed between cluster I and IV (34.61). The lowest inter-cluster distance was observed between clusters IV and V (3.20). Considering group distance and other agronomic performance populations G9 (Nap205 x Nap2013), G16 (Nap248 x Nap9901), G23 (Nap9908 x Nap0130), G29 (Nap9905 x Nap2037), G30 (Nap248 x Nap2012) and G31 (Nap9906 x Nap2001) might be suggested for future breeding programme.

TABLE OF CONTENT

TABLE OF CONTENT (CONT'D)

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

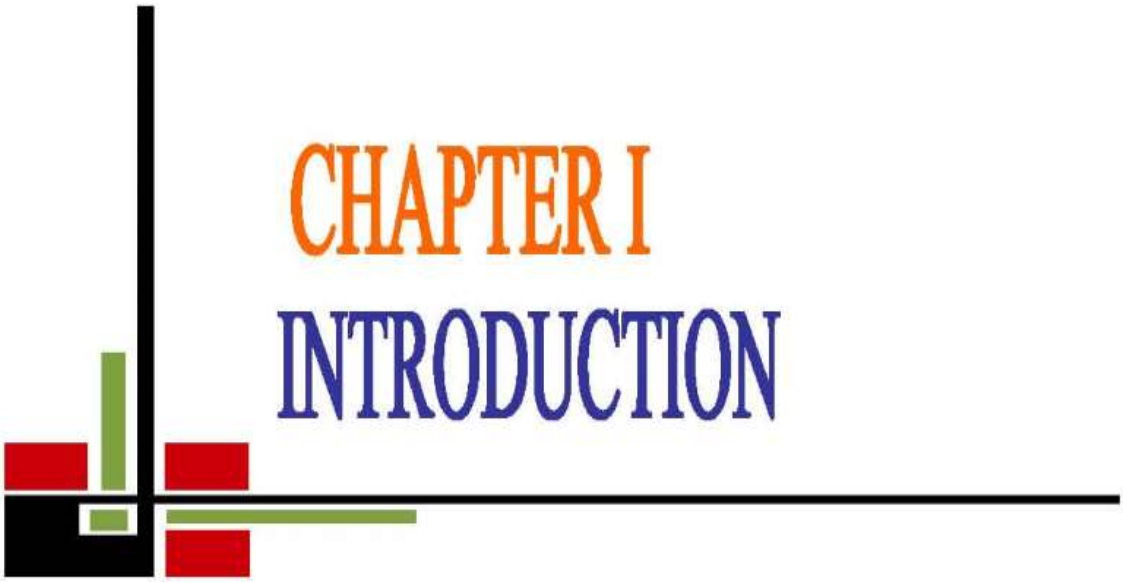
LIST OF APPENDICES

SOME COMMONLY USED ABBREVIATIONS

FULL WORD	ABBREVIATION
Agro-Ecological Zone	AEZ
Agricultural	Agril.
And others	*et al.*
Accessions	ACC
Agronomy	Agron.
Analysis of variance	ANOVA
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Biological	Biol.
Centimeter	cm
Co-efficient of Variation	CV
Ecology	Ecol.
Etcetera	etc.
Environmental variance	$\delta^2 e$
Figure	Fig.
Food and Agricultural Organization	FAO
Genotype	G
Genetic Advance	GA
Genotypic Co-efficient of Variation	GCV
Genotypic Variance	δ^2
Gram	g
Heritability in broad sense	$h^2 b$
Journal	J.
Kilogram	kg

SOME COMMONLY USED ABBREVIATIONS (CONT'D)

FULL WORD	ABBREVIATION
Meter	m
Mean Sum of Square	MSS
Muriate of Potash	MP
Number	No.
Percent	%
Phenotypic Co-efficient of Variation	PCV
Phenotypic variance	$\delta^2 p$
Randomized Complete Block Design	RCBD
Replication	R
Research Science	Res. Sci.
Sher-e-Bangla Agricultural University	SAU



CHAPTER I
INTRODUCTION

CHAPTER I

INTRODUCTION

Brassica napus L is an important oil seed crop belonging to family Brassicaceae, commonly known as the mustard family. This family contains 375 genera and 3200 species including crops, ornamental plants, and many weeds, cabbages, or mustards etc. Common types of brassica used for foods covering cabbage, cauliflower, broccoli, brussel sprouts, and some types of seeds. The genus is tremendous for containing more important agricultural and horticultural crops than any other genus. Most are annual or biennial, but some are small shrubs. Due to their agricultural worth, Brassica plants have been the subject to much scientific interests. Three important species (*Brassica carinata, Brassica juncea, Brassica napus*) are derived by uniting the chromosomes from three diploid species (*Brassica oleracea, Brassica nigra and Brassica rapa*), as described by the Triangle of U theory.

Rapeseed (*Brassica napus* L.) is an amphidiploid (AACC genome, 2n=38) and is believed to have emerged by inter-specific hybridization between diploid *Brassica rapa* L. (AA genome, 2n=20) and *Brassica oleracea* L. (CC genome, 2n=18) (Prakash and Hinata, 1980).

It provides not only significant amount of energy but also porter of fat soluble vitamin A, D, E and K. Oilseed provides oil for industrial and also culinary purpose. Vegetable oils and fats lipids are great source of human diet. Oils from plant source are nutritionally superior to that of animal source. A good number of oil seed crop like mustard, sesame, groundnut, linseed, niger, safflower, sunflower, soybean, castor etc. produced in Bangladesh. Brassica oil crops are leading group of species that purvey major esculent oils in Bangladesh (BBS, 2013). Mustard and rapeseed seeds contain 42% oil, 25% protein (Khaleque,

1985). Mustard oilcake contains protein with high biological value and applicable amount of calcium (Ca) and phosphorus (P). It is used as animal feed and organic manure.

In Bangladesh the total production was 311740 metric ton in 667242 acre land in 2018-19 and 351537 metric ton in 759874 acre land in 2017-18 (Yearbook of Agricultural Statistics-2019). It is required 0.30 Million tons of oil equivalent to 0.85 million tons of oil seeds for nourishing people of Bangladesh. At present, the oil seed production in Bangladesh is about 0.26 million tons, which covers only 30% of the domestic need (BBS, 2011). Bangladesh has been facing acute shortage of edible oil for the last several decades. Therefore we need to import oil and oilseeds to meet up the deficit. Our internal production can meet only about 21% of our consumption and the rest 79% is needed to import (Begum *et al*., 2012).

In Bangladesh Comilla, Tangail, Jessore, Faridpur, Pabna, Rajshahi, Dinajpur, Kushtia, Kishoregonj, Rangpur and Dhaka are the major mustard growing districts (BBS, 2011). Though mustard is an important crop its production area is shrinking day by day due to long termed T. Aman and more holding boro rice. As a result 104,000 hectare of lands and 68,000 ton of mustard production has lost during last decades. Average yield per hectare in our country is very low is about 740 kg compared to other developed countries (2400 kg ha^{-1}) (FAO, 2014). If we can develop new lines it could be successfully cultivated between Aman and Boro rice rotation without affecting present cropping pattern. Within 70-80 days, after Aman rice harvesting and before the transplantation of Boro rice lands are available for cultivating gap filling crop. So, it is need to develop short duration variety and its response for the selection of good mustard genotypes for increasing our cropping intensity.

The yield is complex character and is dependent on many other morphological traits which are mostly inherited quantitatively. It is important to examine the contribution of each of the trait in order to give more attention to those having the greatest influence on seed yield (Tuncturk and Ciftci, 2007). Importance of genotypic and phenotypic variability, heritability and character association have proved by many scientists (Ali *et al*., 2002; Lekh *et al*., 1998; Saini and Sharma, (1995) for further genetic improvement. Gosh and Gulati (2001) also showed that the traits showing high heritability are under the control of additive genes and can be successfully utilized for plant selection on the basis of phenotypic performance.

The major emphasis of the breeders is to enhance seed yield and oil contents along with short duration of a variety to meet up the needs of end consumers. The tendency of the present study was to assess different genotypes with regards to oil content, glucosinolate content and yield contributing characters which can give returns to the farmers.

Genetic diversity is fundamental for genetic improvement. It is widely accepted that information about germplasm diversity and genetic relatedness among elite breeding material is a prime element in plant breeding ((Mukhtar *et al*., 2002 and Khaleque, 1985. With the development of advanced biometrical method such as multivariate analysis (Rao, 1952) based on Mahalanobis' (1936) D^2 statistics and Ward's no-hierarchical squared Euclidean distance method have become possible to quantify magnitude of diversity among germplasm for their evaluation in respect of breeding program.

There must be a thorough knowledge of the existence of genetic variability, the mode of inheritance of economic characters, heritability, the kind of gene action and the relative magnitude of additive, dominance and total genotypic and phenotypic variances of the population. So in the context of the above mentioned situation, the present piece of work was undertaken for fulfilling the following objectives-

- To assess the presence of variability among genotypes;
- To assess genotypic and phenotypic association among different pairs of yield contributing characters;
- To assess the direct and indirect effects of different yield contributing characters on yield and
- To assess genetic diversity among genotypes


CHAPTER II
REVIEW OF LITERATURE

CHAPTER II

REVIEW OF LITERATURE

Extensive researches on Brassica breeding have been performed in many countries for its improvement in respect of yield and yield contributing characters. A large number of literatures are available on variability, correlation and path analysis of yield and yield contributing characters of Brassica grown under a particular environment. An attempt has been made here to summarize the findings of this study relevant to the present investigation. The whole review has been divided into following sections, namely –

2.1 Origin and geographical distribution

2.2 Genetic variability, heritability and genetic advance

2.3 Inter relationship of characters

2.4 Path co-efficient analysis

2.5 Genetic Diversity analysis

2.1 Origin and geographical distribution:

Due to their agricultural importance and economical values, Brassica spp. have been the matter of huge scientific interest. Six particularly important species (*Brassica carinata*, *B. juncea*, *B. oleracea*, *B. napus*, *B. nigra* and *B. rapa*) are derived by combining the chromosomes from three earlier species, as described by the Triangle of U-theory. But the edible oil is obtained from *B. napus*, *B. juncea and B. campestris.* The triangle of U is described on the tri-angular diagram (Figure 1). It shows how three of the *Brassica* spp. were derived from three lineal genomes, denoted by the letters AA, BB, or CC. Each and every one of these diploid genomes produces a common Brassica species.

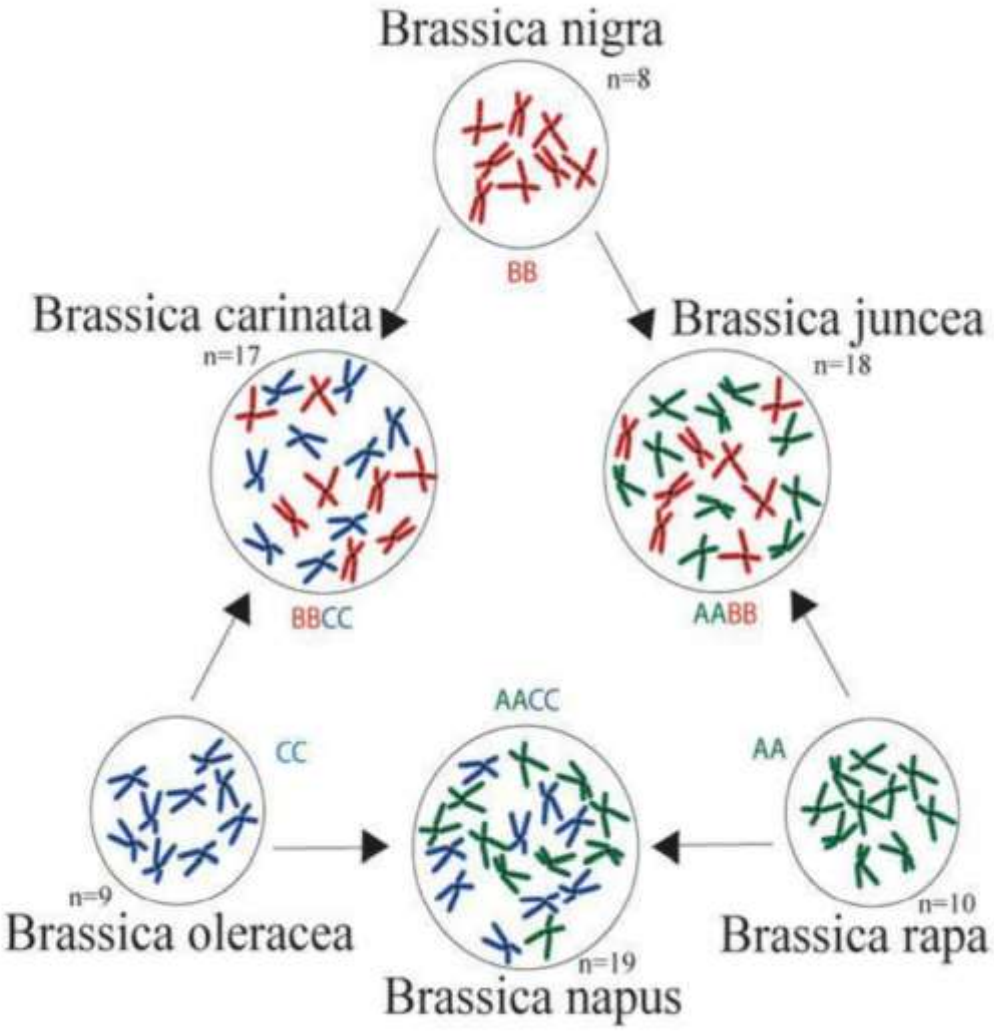


Figure 1:- The "triangle of "U" diagram, showing the genetic relationships between the six species of the genus Brassica. Chromosomes from each of the genomes A, B and C are represented by different colours. The letter "n" denotes the chromosomes number in each genome which is the number found in the pollen or ovule.

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

Mustard is one of the most important oil producing crops in Bangladesh and many countries of the world (FAO, 2012). The crops have received much

attention by a large number of researchers on various aspects of its production and utilization. Identification of suitable parental lines on the basis of their genetic parameters, nature and magnitude of genetic variability and the correlation of different yield attributing characters which are important for successful mustard plant breeding purposes. Yield in mustard is accumulated with many yield contributing characters like plant height, days to maturity, primary and secondary branches, main raceme length etc. which also contribute to rapeseed yield.

Reviewing the information and knowledge on performance of different genotypes, variation for genetic diversity, relationship among yield with other yield contributing characters, genotype-environmental relations, heritability, selection index and molecular marker based analysis in mustard for yield and yield contributing characters is important for future breeding programs for developing short duration high yielding genotypes.

Brassica napus L. is considered second most important protein food resource throughout the globe after cereals. Brassica spp. is grown as a single or in association with other crops like wheat, chickpea, maize etc. in both irrigated and non-irrigated regions of the country. It is necessary for us to take better steps for production and quality improvement of our local cultivars. In that respect, so many strategies and programs are conducted for the betterment of quality and yield of different varieties and cultivars to gain improved quality production. Due to application of different techniques in breeding process, remarkable improvement has been brought in productivity and quality of edible 8 oil for using it in human diet. A huge number of literary materials are available on variability, genetic diversity, correlation and path analysis of yield and yield contributing characters of Brassica grown under a particular environment. An attempt has been made here to summarize the findings of this study relevant to the present investigation.

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

2.2 Genetic variability, heritability and genetic advance

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

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

Aytac and Kinaci (2009) conducted an experiment with 10 winter rapeseed genotypes for variation, genetic and phenotypic correlations and broad sense

heritability for seed yield, yield and quality characters for two years. They observed maximum broad sense heritability get genetic advance seed yield followed.

Aytac *et al*. (2008) reported highest genotypic and phenotypic variances for seed yield per plant followed by seed yield and high heritability of seed yield per plant, seed yield, siliquas per main stem coupled with high genetic advance revealed that additive gene effects are important in determining these characters and could be improved through mass selection.

Belete *et al*. (2012) undertaken a research to estimate various genetic parameters for some agronomic traits of introduced Ethiopian mustard (*Brassica carinata* A. Brun) genotypes. The experiment was laid out in randomized complete block design with three replications at Holetta Research Center, Ethiopia. Plant height and seed yield showed non-significant difference in analysis of variance among the genotypes for traits studied. Phenotypic coefficient of variation and genotypic coefficient of variation ranged from 1.2- 10 10.2% and 1.9-6.8%, respectively. The maximum heritability values was shown by oil content (99.8%) followed by days to flowering (96.5%) and days to maturity (89.1%). Days to flowering and oil content indicated that a very high heritability along with high genetic advance (as percent of mean) were present among that traits. Days to flowering, days to maturity and oil content are vital characters to be considered for further varietal establishment program.

Mekonnen *et al*. (2014); evaluated thirty six genotypes of Ethiopian mustard, *Brassica carinata* to study variability. The GCV ranged from 4.3% to 44.14% and PCV from 8.3% to 91.7%. Comparatively high GCV estimates were 7 observed for number of siliqua 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 siliqua 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 siliqua per plant, secondary branches per plant, plant height, seed yield/plot and hectare and lowest one was in primary branches per plant.

Khan *et al*. (2013); evaluated thirty F_7 segregating lines and two parents of *Brassica rapa* to study variability, heritability and genetic advance. The result revealed that except thousand seed weight, significant variation was presented among all the genotypes for all the characters. Highest genotypic, phenotypic and environmental variances were observed in plant height while lowest one was in length of siliqua followed by thousand grain weight. Thousand seed weight, number of secondary branches per plant, seeds per siliqua, and siliqua length showed high heritability along with low genetic advance in percent of mean. Considering important performances, the genotypes G-15, G19, G-1, G-3, G-4, G-10, G-18, G21, and G-24 were found suitable for future breeding program.

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

and number of primary branches per plant. The maximum genetic advance was found in seed yield per plant followed by siliqua per plant, plant height, thousand grain weight and minimum in primary branches per plant.

An experiment was carried out by Mahmud (2008) with 58 genotypes of *Brassica rapa* 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 percentage of mean were obtained for days to 50% flowering, seed per siliqua and siliqua length.

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. Malik *et al*. (2000); observed very high broad 14 sense heritability (h^2b>90%) for number of primary branches per plant and oil content while working with different strains of *B. napus*. They also observed low heritability (50%) for plant height, number of siliqua per plant, number of seed per siliqua and seed yield. But high heritability for all these characters were found by Lodhi *et al*.(1979) while working with 55 genotypes of *B. napus, B. rapa* and *B. juncea*.

Alam (2010) was conducted a research by using 26 F_4 populations of some inter-varietal crosses of *Brassica rapa* to study the variations present in different characters for their heritability, genetic advance etc. There were significant variations founded in those characters. Plant height, length of siliqua, number of siliqua per plant, days to 50% flowering showed low difference between genotypic and phenotypic coefficient of variation. Plant height, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant showed high heritability coupled with high genetic advance and very high genetic advance in percentage of mean. However, Low heritability was showed in respect of length of siliqua.

Ara (2010) conducted a field experiment by using eight F_2 and eight F_4 populations generated through inter-varietal crosses, along with three check variety of *Brassica rapa* to study the variation. From different values of mean, range and CV (%) of seed yield and yield contributing characters, it indicated that considerable amount of variation present among all the genotypes used in the experiment. The values of phenotypic variances were higher than 11 corresponding genotypic variances. Other characters like days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, length of siliqua, seeds per siliqua, 1000-seed weight and yield per plant showed a very slight difference between phenotypic and genotypic variances. The value of GCV and PCV indicated that there was least variation present among the characters. The days to maturity, length of siliqua, seeds per siliqua and 1000-seed weight showed high heritability with low genetic advance and genetic advance in percentage of mean. Kakroo and Kumar (1991), Sharma (1984) and Yadava *et al*. (1996) observed low to medium heritability of siliqua length.

Aytac and Kinaci (2009) conducted an experiment with 10 winter rapeseed genotypes for variation, genetic and phenotypic correlations and broad sense

heritability for seed yield, yield and quality characters for 2 years. They observed that the maximum broad sense heritability get genetic advance in respect of seed yield performance.

Sheikh *et al*. (2009) implemented a research on the induction of genetic variability in Ethiopian mustard (*Brassica carinata*) for quality traits through inter-specific hybridization. The result revealed that inter-specific hybridization was used to increase the spectrum of genetic variability in mustard for edible oil with meal quality traits from quality lines of *Brassica juncea*.

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

Hosen (2008) conducted a study by using 5 parental genotype of *Brassica rapa* and their ten F_3 progenies including reciprocals. There are large numbers of variations present among all the genotypes used in the experiment. High heritability with high genetic advance and genetic advance in percentage of 12 mean was showed in respect of plant height, days to 50% flowering, and number of siliqua per plant.

Tyagi *et al*. (2001) conducted research and found that variation was the highest in parents and their hybrids for plant height. The seed yield per plant exhibited the highest co-efficient of variation (41.1%). Significant genetic variability was observed for plant height by many researchers like Andarhennadi *et al.* (1991), Kumar and Singh (1994), Yadava *et al*. (1993), Chaturvedi et al. (1988), Gupta *et al*. (1987) and Chauhan and Singh (1995) among different genotypes of *B.napus, B. rapa* and *B. juncea*.

According to Tyagi *et al*. (2001) variation was the highest in parents and their hybrids for plant height. The seed yield per plant exhibited the highest co-efficient of variation (41.1%). Significant genetic variability was observed for this character by many workers like Andarhennadi *et al*. (1991), Gupta and Labana (1989), Malik *et al.* (1995), Kumar and Singh (1994), Yadava *et al*. (1993), Lebowitz (1989), Chaturvedi *et al*. (1988), Gupta *et al*. (1987), Chauhan and Singh (1985) and Sharma (1988) among different genotypes of *B. napus, B. rapa* and *B. juncea*.

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

The highest genotypic co-efficient of variation was calculated for secondary branches. High genotypic and phenotypic co-efficient of variation was recorded for days to 50% flowering among 10 genotypes for each of *Brassica campestris*, *Brassica carinata* and *Brassica napus* and 24 genotypes of *Brassica juncea* by Lekh *et al*. (1998).

Generally high number of seeds per siliqua is desirable. On the variability of this trait a good number of literatures are available. Significant variability in number of seeds/siliqua in oleiferous Brassica materials of diverse genetic base was observed by Kudla (1993) and Kumar and Singh (1994). Similar significant variability in the genotypes of *Brassica napus*, *B. campestris* and *B. juncea* were studied by them.

The maximum genotypic co-efficient of variation was calculated for secondary branches. High genotypic and phenotypic co-efficient of variation was recorded for days to 50% flowering among 10 genotypes for each of *Brassica campestris*, *Brassica carinata* and *Brassica napus* and 24 genotypes of *Brassica juncea* by Lekh *et al*. (1998).

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

Siliqua length is another important character for the development of fruits in oil seed crops like mustard and rape seed. Peduncle, beak as well as siliqua length varies due to difference in genotypes. High genetic variability was found by Olsson (1990) for this character. Lebowitz (1989) found similar results while

working with *B. rapa* for siliqua length. Thurling (1983) reported that selection for increased siliqua length is an effective strategy for yield improvement through raising seed weight per siliqua.

Thousand seed weight is a very important character of rape seed and mustard, where highest consideration is on the seed yield. This character has been found to vary widely from genotypes to genotypes and from environment to environment. A good number of literatures are available on the variability of this trait.

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

Mahak *et al.* (2004); studied heritability and genetic advance for days to flowering, days to maturity, plant height, number of siliqua per raceme, length of main raceme, seed yield per plant, 1000-seed weight and oil content. High 12 heritability coupled with high genetic advance as percentage of mean was observed for days to flowering, followed by 1000-seed weight, days to maturity and weight. Thakral (2004), worked on variation for yield and yield contributing characters in rapeseed and reported significant variation for 8 Indian rapeseed parental lines and their 28 F1 hybrid. They noticed high PCV and GCV for plant height and seed yield characters.

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

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

High degrees of variation for seed yield per plant in *B. rapa* was observed by Yin (1989) and Kudla (1993) in *B. napus* and Kumar *et al*. (1996) in *B. juncea*. Bhardwaj and Singh (1969) found GCV value of 96.99% among different strains of *B. rapa*. Yadava (1973) found 48.76% GCV value among 29 strains of *B. juncea*. While Singh *et al*. (1987) found GCV and PCV values of 44.04% and 46.9% in *Brassica juncea*

High heritability coupled with high genetic advance for seed yield per plant, number of secondary branches per plant, siliqua per plant, 1000 seed weight (g) and number of primary branches per plant was observed by Sheikh *et al*. (1999) while working with 24 genotypes of toria.

Lekh *et al.* (1998) carried out an experiment with 24 genotypes of *B. juncea* and 10 genotypes each of *B. campestris, B. carinata* and *B. napus* and observed highest genetic advance and high genotypic and phenotypic co-efficient of variation for days to 50% flowering and high heritability for other yield contributing characters.

Both additive and dominance genetic components were important for seed yield and yield components in *B. campestris* var. *toria*, and higher heritability for days to maturity and thousand seed weight while studied 8x8 diallel analysis (excluding reciprocals) was reported by Yadava *et al.* (1993).

Plant height and number of seeds per siliqua were highly heritable whereas siliqua length, number of primary branches per plant were less heritable was observed by Labana *et al*. (1980) while working with 104 mutants of Indian mustard *B. juncea* L. Czern and Coss. Chandola (1977) observed high genetic advance for plant height while working with 30 varieties of *B. rapa.*

Yadava *et al.* (1993) reported that additive and dominance genetic components were important for seed yield and yield components in *B. campestris* var. *toria*, and there is a huge heritability found for days to maturity and thousand seed weight while studied 8x8 diallel analysis (excluding reciprocals).

Malik *et al.* (2000) observed very high broad sense heritability (h^2 b>90%) for number of primary branches per plant, days to 50% flowering and oil content 16 while working with different strains of *B. napus*. They also observed low heritability (h^2 1, 50%) for plant height, number of siliqua/plant, number of seeds siliqua and seed yield. But high heritability for all these characters were found by Lodhi *et al*. (1979) while working with 55 genotypes of *B.napus*, *B. rapa* and *B. juncea*.

2.3 Interrelationship of 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:

Correlation coefficient analysis helps to determine the nature and degree of relationship between any two measurable characters. It resolves the complex relations between the events into simple form of association. But measure of 15 correlation does not consider dependence of one variable over the other. Direct contribution of each component to the yield and the indirect effects it has through its association with other components cannot be differentiated from mere correlation studies. Path coefficient analysis fulfils this study. It was first developed and described by Wright (1921), as a tool in genetic analysis which partition the association of the components on yield and indirect effects of the characters on yield through other components.

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

Aytaç and Kinaci (2009) reported that plant height was associated with seed yield, oil yield, protein yield, number of siliquas on main stem and siliqua length.

Esmaeeli Azadgoleh *et al*. (2009) mentioned positively significant correlation of seed yield with number of siliqua per plant, number of siliquas in sub branches and number of seeds per siliqua. 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 siliquas on the main stem and plant height during two years. Plant height indicated negative correlation with seed yield, thousand seed weight and oil ratio.

Basalma (2008) conducted an experiment in the year of 1999-2000 and 2000- 01 using 25 winter rapeseed cultivars. Plant height were increased which affect rise in branching adversely, increased lodging resulting in reduced seed yield. Correlation analysis results showed a high, positive and statistically significant ($P < 0.01$) statistically correlation between branches per plant, the number of siliquas on the main stem and plant height during both years. A negative

correlation showed on plant height with seed yield, 1000-seed weight, and oil ratio during the first year of the trial.

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

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

Maurya *et al*. (2012); carried out an experiment with one hundred genotypes of *Brassica juncea* and observed that a high positive correlation was presented between length of siliqua, seed yield, thousand grain weight and days to 50% flowering. In order to determine the most important traits affecting grain yield in Canola and identify the quantity of direct and indirect effects on grain yield, an experiment was conducted with ten Canola varieties in a RCBD design with three replications by Khayat *et al*. (2012). The evaluation of correlation coefficients illustrated that the total dry matter, harvest index, 1000-grain weight, the number

of grains per siliqua, number of siliquas per plant, plant height; days to maturity and flowering period trait had a positive significant correlation with grain yield. Stepwise regression and path analysis indicated that, the number of siliquas per plant had the highest direct effect on grain yield. In 16 addition, total dry matter, 1000-grain weight, and flowering and days to maturity also had a high direct effect on grain yield.

Aytac *et al.* (2008) conducted an experiment with summer rapeseed and noticed the positive and significant correlation of seed yield with plant height, siliquas per main stem, seeds per siliqua and seed yield per plant.

Highly significant positive correlation and maximum direct contribution for improving seed yield with siliqua per plant were found Akbar *et al*. (2007).

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

Ali *et al*. (2003) conducted research and found out that a positive and significant correlation among seed weight and flower duration. Seed weight and siliqua /plant have shown a direct positive effect on seed production. Direct positive effect of seed weight associated with significant and direct positive correlation with seed yield indicate that these yield components may be a good selection criteria to improve seed quality and yield of winter type rapeseeds.

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

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

Tang *et al*. (1997) discover that in breeding program of yellow-seeded rapeseed, on the basis of variance analysis and path analysis 16 yellow-seeded lines of *Brassica napus* derived from eight genetic sources as evaluated for their genetic variation of the seed coat ratio, cellulose content, oil content of the seed coat and the embryo and correlations between these characters in yellow and brown-seeded plants of the same observable line. The correlation analysis revealed that the seed coat thickness has a highly significant positive correlation with the cellulose content of the seed coat and a highly significant negative correlation with seed coat oil content and the 1000-seed weight. The oil content of the embryo alone has a highly significant negative correlation with 1000-seed weight.

An experiment on oleiferous *Brassica campestris* L. was conducted by Siddikee (2006) to study the correlation analysis. The results revealed that yield per plant had highest significant positive correlation with number of siliqua per plant.

Singh *et al*. (2004) found that seed yield per plant indicated positive connection with number of essential branches, length of fundamental raceme, 1000-seed weight and oil content. Choice ought to be connected on these qualities to enhance seed yield in Indian mustard.

Pankaj *et al.* (2002) studied 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 siliqua per plant, which had the strongest positive and significant correlation with yield per plant at both levels, was positively associated with the number of seeds per 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.

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

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

number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua and number of siliqua per plant.

Shalini *et al*. (2000) evaluated 81 genotypes of Indian mustard for the magnitude of association between their quantitative characters of secondary branches, plant 16 height, number of siliqua and seeds per siliqua were highly associated with seed yield.

Jeromel *et al*. (2008) conducted a field experiment using 30 rapeseed genotypes. They found highest seed yield per plant for cultivars Sremica, B009, Jet Neuf and Falcon. There was an integrated correlation between plant height and height of the first lateral branch and plant height and seed oil content, as well as between plant height and seed yield per plant. The strongest direct effect on seed yield per plant was estimated for plant height, followed by the effect of number of siliquas per plant. This kind of experiment helps rapeseed breeders to optimize their breeding programs.

Khulbe and Pant (1999) carried out a study of correlation in 8 Indian mustard (*Brassica juncea*) parents and their 28 F1 hybrids 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 number of siliqua per plant, number of seeds per siliqua and plant height was significantly positively correlated with seed yield was observed by Masood *et al*. (1999) while studied seven genotypes of *B. campestris* and standard cultivar of *B. napus* to calculate correlation co-efficient.

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

Malek *et al.* (2000) estimated that days to maturity had no further significant correlation with seed yield for both phenotypic and genotypic levels of estimation. Number of branches/plant and number of siliqua/plant showed negative correlation significantly with number of seeds/siliqua and 1000 seed weight. This indicated that genotypes having high number of branches with high number of siliqua reduced the number of seeds/siliqua and seed size.

Thakaral *et al.* (1999) studied correlation co-efficient on seed yield and yield contributing characters in 8 Indian mustard (*Brassica juncea*) parents and their 28 F_1 hybrids grown at Hisar. The data indicated that higher seed yield could be obtained by selecting for increased plant height.

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

An experiment on oleiferous *Brassica campestris* L. was conducted by Siddikee (2006), to study the correlation analysis. The results revealed that 18 yield per plant had highest significant positive correlation with number of siliqua per plant. A study was conducted by Tusar *et al.* (2006); to assess the nature and

extent of variability of eleven yield related characters of five mustard genotypes. Phenotypic correlation studies indicated that seed yield per ha was positively and significantly associated with plant height, total dry matter production and husk weight. The number of 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 examination was completed by Tuncturk and Ciftci (2007) in Van, Turkey amid 2000, 2001 and 2002 to research the connections amongst yield and some yield segments of 16 oilseed rape cultivars (*Brassica napus* ssp. *oleifera* L.) by utilizing relationship and path coefficient examination. The outcomes uncovered that there were factually positive connection between seed yield with the quantity of branch (r=0.219), with number of siliquas per plant (r=0.424), with the quantity of seeds per case (r= 0.247), and with 1000-seed weight (r= 0.161). Number of siliquas per plant, 1000-seed weight and number of seeds per siliqua have demonstrated an impressive direct constructive outcome on seed yield. Positive direct effect of number of siliqua per plant, number of seeds per 19 siliqua and number of branches per plant was associated with significant and positive correlation with seed yield. These yield segments proposed great selection criteria to enhance seed yield for rapeseed breeding.

An experiment was conducted by Poonam and Singh (2004). In forty Indian mustard germplasms to determine the correlation and path coefficient values

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

Uddin *et al*. (1995) while studied correlation analysis in 13 Indian mustard (*B. juncea*) and reported that seed yield per plant had high positive arid significant correlations with plant height and thousand seed weight, but high negative and significant correlations with seeds per siliqua at both genotypic and phenotypic levels.

Arthamwar *et al.* (1995) studied correlation and regression in *B. 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.

The objective of the investigation was to estimate interrelationship between different rapeseed quantitative traits using simple regression coefficients, as well as to assess direct and indirect effects of specific traits to oil yield/ha via path analysis. Three year investigation was carried out including thirty rapeseed genotypes. Number of siliquas per plant, oil content, 1000 seed weight, pre-anthesis duration, post-anthesis duration, seed yield/ha and oil yield/ha were brought under investigation. Almost complete correlation was determined

between seed yield/ha and oil yield/ha and strong correlation between oil content and oil yield/ha. The direct effects to oil yield/ha which effect strongly was estimated for seed yield/ha, where other investigated traits showed low or no effect to oil yield/ha (Jeromel *et al*., 2008).

Nanda *et al*. (1995) studied correlation analysis with 65 strains of *B. juncea, B. rapa* and *B. napus* and observed that positive association between yield and siliqua filling period. Similar results also found by Olsson (1990) in *B. napus*. He also observed positive correlation between siliqua density and yield.

Malik *et al.* (2000) reported highly positive correlation for the characters like primary branches and seed yield both at genotypic and phenotypic level. Seed yield showed positive correlation with siliqua/plant, number of secondary branches and siliqua length. They also reported that a negative and highly significant relation present in days to flower completion and plant height, where seed yield was negatively and non-significantly correlated with seed per siliqua and 1000-seed weight.

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

Nasim *et al*. (1994) studied correlation analysis in *B. rapa* and found 1000 seed weight was significantly and positively correlated with seed yield per plant and number of siliqua per plant but significantly and negatively correlated with siliqua length and number of seeds per siliqua.

Khan *et al*. (2006) conducted research on correlation for some quantitative traits relating to yield and quality in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during 2002-2003. Eleven accessions of *Brassica napus* L. along with DGL as a standard variety were studied. A wide range of genetic variation existed among all the characters under study except 1000-grain weight were found out by them. 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). It was negatively and non-significantly associated with number of secondary branches (-0.36663) and protein contents (-0.1372) at genotypic level. They 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.

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

A study was conducted by Ghosh and Gulati (2001) which estimated that seed yield displayed significant positive combination with yield contributing traits as days to 50% flowering, days to maturity, plant height, number of secondary

branches, number of siliqua on main shoot and oil content. In turn these components presented a significant positive correlation with each other. The findings indicate that selection for one of these characters might automatically accumulate the other variables and these appeared to be the most significant selection parameter for improving seed yield in Indian mustard.

Khan and Khan (2003) conducted a field research to estimate the genetic potentiality of Brassica cultivars. Eight cultivars were sown in Randomized complete block design in four replications. The analysis of variance revealed highly significant differences among all the cultivars for various characters. Plant height, number of primary branches, number of secondary 21 branches, and number of siliqua per plant and seed index were found positively correlated with seed production. Plant height, number of primary branches, number of secondary branches, number of siliquas per plant and seed index were the characters which should gave emphasis during experimentation for improvement in yield of seed in Brassica spp.

Zajac *et al*. (1998), studied phenotypic correlation between yield and its component and reported that strong positive correlation occurred between seeds per siliqua and actual yield. Positive but a weaker correlation was observed between seed yield and siliqua per plant. The number of seeds per siliqua had the greatest influence and number of siliqua per plant had the 22 smallest effect on yield. Kumar *et al.* (1996), studied 12 genotypes of *B. juncea* for correlation analysis and found flowering time and plant height negatively correlated with number of primary branches per plant.

Chay and Thurling (1989), studied the inheritance of siliqua length among several lines of *B.napus* and reported that the siliqua length when increased there was an increase in the number of seeds per siliqua and thousand seed weight.

The siliqua length was positively correlated with both number of seeds per siliqua and thousand seed weight was observed by Singh *et al*.(1987) in *B. rapa*, Lebowitz (1989) and Lodhi *et al*.(1979) in *B.juncea*.

Swain (1990), studied correlations of yield components in 15 genotypes of brown sarson (*B.campestris* var. *dichotoma*) and found that number of siliqua per plant was the most important characters to yield.

2.4 Path co-efficient analysis:

It became more difficult to ascertain the traits which really contribute towards the yield when more characters were involved in correlation study. The path analysis under such condition helps to estimate the direct and indirect contribution of these characters towards the yield.

Han, 1990, reported that negative direct effect of number of siliqua per plant, siliqua length and positive direct effect of seeds per siliqua and plant height on seed yield.

A research was conducted by Alam (2010) using 26 F_4 populations of some inter-varietal crosses of *Brassica rapa* to study the direct and indirect effect of different characters on seed yield. Path co-efficient analysis revealed that plant height, number of primary branches per plant, number of siliqua per plant, seeds per siliqua and siliqua length had the positive and direct effect on yield per plant, days to 50% flowering, number of secondary branches per plant and 1000-seed weight had the direct negative effect on yield per plant.

Afrin (2009) conducted a field experiment with advanced 22 *Brassica napus* L. lines to study path coefficient. Plant height had maximum positive direct effect on seed yield followed by number of siliqua per plant and siliqua length and negative direct effect on number of secondary branches per plant and number of

seeds per siliqua as path coefficient analysis showed. Plant height, number of primary branches per plant and number of siliqua per plant were the most 22 important contributors to seed yield per plant which should take under consideration for future breeding program.

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

The path co-efficient analysis by Hosen (2008) exhibited that 1000 seed weight had the highest positive and direct effect with other characters like 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.

Khulbe and Pant (1999) studied path co-efficient analysis in eight Indian mustard (*B. juncea*) parents and their 28 F1 hybrids. The results revealed that harvest index, 22 siliqua length, seeds per siliqua, siliqua per plant, thousand seed and days to initial flowering were the major traits influencing seed yield.

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

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

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

Sheikh *et al*. (1999) worked with 24 diverse genotypes of toria for assess the direct and indirect effect of seven quantitative and developmental traits on seed yield. Results revealed that thousand seed weight and siliqua per plant had highly positive direct effect on seed yield.

Chauhan and Singh (1995), found high positive direct effect of days to 50% flowering, plant height, primary branches per plant, siliqua per plant and seeds per siliqua on seed yield while working with several strains of *B. juncea*. Uddin *et al*. (1995); studied path analysis in 13 Indian mustard (*B. juncea*) and observed that seeds per siliqua and thousand seed weight had high positive direct effect on seed yield per plant.

Kachroo and Kumar (1991), studied several strains of *B. juncea* and found that thousand seed weight had positive direct effect, but days to 50% flowering and primary branches had negative indirect effect via seeds per siliqua on seed yield. Kumar *et al*. (1988) found the indirect positive effect of days to 50% flowering on seed yield.

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

Uddin *et al*. (1995) studied path analysis in 13 Indian mustard (*B. juncea*) and observed that seeds per siliqua and thousand seed weight had high positive direct effect on seed yield per plant. Chauhan and Singh (1995) observed that plant height, siliqua per plant and seeds per siliqua had high positive direct effect on seed yield. Kachroo and Kumar (1991) studied path co-efficient analysis in *B. juncea* and found that thousand seed weight had positive direct effect but days to flowering and number of primary branches had negative indirect effect via seeds per siliqua on seed yield.

Han (1990) studied *B. napus* and observed negative direct effect of number of siliqua per plant, siliqua length and positive direct effect of seeds per siliqua and plant height on seed yield. Dhillor *et al*. (1990) observed the highest positive direct effect on seed yield per plant. Kudla (1993) reported that 1000 seed weight had positive direct effect on seed yield.

Chowdhury *et al.* (1987); worked with 42 strains of mustard and observed that siliqua length had highest positive direct effect and number of primary branches per plant had the highest negative direct effect on seed yield. On the other hand, Gupta and Badwal (1987), observed that primary branching and thousand seed weight had the direct effect on seed yield.

Kachroo and Kumar (1991) studied several strains of *B. juncea* and found that thousand seed weight had positive direct effect, but days to 50% flowering and

primary branches had negative indirect effect via seeds per siliqua on seed yield. Kumar *et al.* (1988) found the indirect positive effect of days to 50% flowering on seed yield.

Dhillon *et al*. (1999); reported that the plant height had the highest positive direct effect on seed yield per plant in *B. juncea*.

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.

Sharafi *et al*. (2015); were evaluated 28 winter rape seed cultivars and results showed that number of siliquas per plant, number of seeds per siliqua, and 1000 seed weight had positive direct effect on seed yield.

2.5 Genetic Diversity analysis:

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

hybridization programme using these D^2 values cluster are formed. A summary of literature reviewed on mustard and other allied species are in presented below.

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

Peter and Rai (1995), reported on genetic divergence analysis among twenty five genotypes of *Brassica napus*. They revealed that genetic and geographical divergence was highly related with the genotypes. The genotypes were grouped into six clusters of which cluster I was the largest accommodating among these genotypes. The cluster VI had large genetic distance from the remaining clusters.

Iqbal *et al*. (2014) studied to determine the genetic variability and diversity among different mustard genotypes. All the characters demonstrated high heritability (>80%) irrespective of any genotypes. Plant height, number of seeds siliqua-1 , number of siliqua plant-1 and length of siliqua were significantly correlated with seed yield per plant which suggest that genotypes with high partitioning capability gave increase in seed yield plant-1 . Among all other

characters, number of siliqua plant^{-1} , number of seeds siliqua^{-1}and thousand seeds weight had high positive direct effects on grain yield plant^{-1} ,so those characters should be included to obtain higher yield and selecting the genotypes for breeding in mustard. Using Euclidean distance following Ward's method, the genotypes were grouped into four clusters. The cluster III had higher intra cluster distance and the maximum inter cluster distance was observed between genotypes of clusters I and IV followed by clusters III and IV.

Goswami *et al*. (2006) reported the moderate genetic diversity between parents had the good general combining ability (GCA) effect and high specific combining ability (SCA) and high mean values in F_2, had the highest frequency of transgressive segregates in F_2 and the magnitude of transgression were high in Indian Mustard.

Rameeh (2013) evaluated 24 rapeseed genotypes including 2 cultivars and 22 advanced lines, were based on randomized complete block design with three replications. The results of factor analysis exhibited 4 factors including sink factor (siliqua per plant, siliquas length and seed yield), fixed capital factor (phenotypic characters), secondary fixed capital factor (duration of flowering), and metric factor (plant height). The genotypes were classified in four groups, 24 and the group with high seed yield had high mean value of siliquas per plant based on cluster analysis.

Pandey *et al.* (2013); conducted an experiment with 45 Indian mustard genotypes of different origin from India for evaluated for the extent of diversity for utilization in breeding program. D2 analysis was conducted to measure the 30 genetic diversity among the genotypes. The 45 genotypes were grouped in 8 clusters using Tocher's method. Intra cluster distance was maximum for cluster VI followed by cluster III. The maximum inter-cluster distance was found

between cluster II and III indicating high genetic divergence among genotypes of these groups. Maximum contribution towards the divergence was accountable to 1000-grain weight (46.87%) followed by seed yield per plant (20.91%) and number of siliqua on main raceme (8.38%).

Mahmud *et al*. (2011) reported that fifty five advanced line of *Brassica rapa* along with three commercially cultivated varieties as check were evaluated to study the genetic discrepancy through Mahalanobis D^2 statistics in respect of 10 different phenotypic characters. As per principal component analysis (PCA), D^2 and cluster analysis, the genotypes were grouped into 6 different clusters. Relationship was not found between genetic diversity and geographic distribution of the genotypes. Cluster II and cluster III had the maximum (13) and cluster IV had the minimum (6) number of genotypes. The intra cluster distance was lower than the inter cluster distance in most of the cases. The maximum inter cluster distance was observed between cluster III and VI (19.52) and that of the minimum between cluster II and IV (3.02). Highest intra-cluster distance was observed in cluster VI (0.67). Plant height, number of secondary branches per plant and seeds per siliqua contributed maximum towards the total diversity. Considering diversity pattern, genetic status and other agronomic performances, line 39 and line 44 from cluster I; line 42 from cluster II; line 2, line 43 and line 45 from cluster V; line 50, line 52, line 54 and line 58 from cluster VI- might be selected as suitable parents in future breeding purpose.

Choudhary and Joshi (2001) determined genetic diversity among the 88 entries including eighty F_4 derivatives i.e. 20 each selected from Brassica crosses viz. B. 25 *juncea B. napus, B. juncea B. rapa* var. toria, *B. juncea B. rapa* var. yellow sarson and *B. tournefortii B. juncea*, and eight parent genotypes through multivariate analysis (D^2 statistic). The genetic distances calculated among different Brassica species revealed that B. tournefortii had maximum diversity with *B. juncea* followed by *B. napus, B. rapa* var. toria and *B. rapa* var. yellow

sarson. The clustering pattern showed that many derivatives of the cross fell into the same cluster but in many cases in spite of common ancestry many descendants of the cross spread over different clusters. The characters, namely, plant height, secondary branches per plant, days to flowering and 1000-seed weight was contributed maximum towards genetic divergence.

Zaman *et al*. (2010) was conducted a field experiment comprising 18 advanced lines of mustard in a randomized block design with 3 replication for estimation of divergence among advanced lines of mustard. The genotypes were grouped into 4 clusters. Cluster I contained the maximum number of genotypes (6) and the cluster III had the minimum (3). The inter-cluster distances in all cases were larger than the intra-cluster distance which indicated that wider diversity was present among the genotypes of distant grouped. Cluster II showed the highest intra cluster distance where lowest was in cluster I. The highest inter cluster distance was observed between the cluster III and II followed by III and 25 I and the lowest between cluster IV and III. Days to 50% flowering (81.94%), days to maturity (8.24%), plant height (5.82%), branches per plant (1.91%) and siliqua per plant (1.17%) contributed highest towards the total diversity which suggested that these characters were highly responsible for genetic diversity in the experimented materials. But the highest cluster means for primary branches per plant and maximum seeds per siliqua with minimum seed yield per plant were found from the cluster II. The genotypes from cluster I had dwarf plant along with earliness in days to 50% flowering, days to maturity and maximum number of primary branches per plant. Therefore, the genotypes from cluster I and III could be utilized in future breeding program for getting desirable transgressive segregants and high heterotic response due to getting highest yield along with short duration.

Nath *et al.* (2003) conducted and experiment with varieties, inter-variety and interspecies hybrids of Brassica oil crop to determine genetic divergence. The

divergence study indicated that parent, inter-variety and inter-species hybrids almost clearly form five groups indicating that they are divergent and might be of value for future breeding program. Based on the study on genetic divergence of the *Brassica*, the varieties having the performance and located in the distant clusters could be utilized for hybridization program to develop desired high yielding varieties.

Afrin (2009) used different multivariate analysis techniques to classify 22 *Brassica napus* genotypes. The genotypes were grouped into four clusters. The highest inter-cluster distance was observed between clusters II and IV whereas the maximum intra-cluster distance was found in cluster II. Therefore, the genotypes belonging to cluster I and cluster II, cluster II and cluster III and cluster III and cluster IV have been selected for future hybridization program. The PCA gives Eigen values of principal component axes of coordination of genotypes with the first three axes accounted for 68.927% of total variation whereas the first principal components accounted for 28.695%. The role of number of secondary branches per plant and number of siliqua per plant in both the vectors were important components for genetic divergence in these materials. Considering group distance and other agronomic performance the inter-genotypic crosses between G1 and G2, G2 and G6; G6 and G7; G6 and G8 and G7 and G8 might be suggested for future hybridization program.

Vivek *et al*. (2007); studied the genetic diversity in 81 true breeding advanced generation cultivars of Indian mustard based on yield and yield components. They are followed by cluster analysis and showed that out cluster XII, which was most diverse, had very high seed yield and number of siliqua per plant. 31 Cluster VII also represented entries with high seed yield, number of siliqua per plant and highest number of seed per siliqua. Cluster XI with the lowest number of days to maturity could be considered as a good source for earliness. Goswami and Behl (2006), studied 43 genotypes of Indian mustard using D^2 statistics. They

recorded data for plant height, primary branches, secondary branches, main shoot length, number of siliqua on main shoot, siliqua length, seeds per siliqua, 1000-seed weight, seed yield per plant and oil content. The genotypes were grouped into six clusters. The intra cluster distances were almost equal and relatively lower than the inter-cluster distances.

Mahmud *et al.* (2008) studied the genetic diversity of 22 rapeseed (*Brassica napus*) advanced genotypes by using principal component analysis nonhierarchical clustering and canonical vector analysis. The genotypes were 26 grouped into 4 clusters. Cluster II contained the highest number of genotypes (9) and cluster III contained the lowest (2). The highest inter cluster distance was observed between cluster I and cluster III and the lowest between cluster I and cluster II. The highest intra-cluster distance was noticed for cluster III and the lowest for cluster II. Cluster I had the highest mean values for siliqua length and thousand seed weight. Cluster III had the lowest cluster mean values for the number of days to 50% flowering and the number of days to maturity with moderate seed yield. Crosses between genotypes belonging to cluster II with those of cluster I and cluster IV might therefore produce high heterosis in yield as well as earliness.

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

Nath *et al.* (2003) conducted an experiment with different varieties, intervariety and inter-species hybrids of Brassica spp. to determine genetic divergence. The divergence study illustrated that parent, inter-variety and interspecies hybrids had almost clearly form five groups which indicate that they are divergent and

might have value for future breeding program. Based on the study on genetic divergence of the *Brassica*, the varieties could be utilized for hybridization program to develop desired high yielding varieties.

Kardam and Singh (2005), noted that the nature and magnitude of variability for 10 characters in 200 progenies of Indian mustard (*B. juncea*) obtained from six crosses were studied during Rabi 2002-03 in Jobner, Rajasthan, India. Phenotypic coefficients of variation were higher in magnitude compared to genotypic coefficients of variation for most of the characters. Seed yield per plant was significantly associated with plant height, primary branches per plant, and number of siliqua per plant, number of seeds per siliqua and 1000-seed weight. The number of siliqua per plant had the highest direct contribution to seed yield, followed by primary branches per plant, 1000-seed weight, number of siliqua on main shoot and number of seeds per siliqua. Aunwinithul *et al*. (2004); studied 33 genetically diverse genotypes of Indian mustard for diversity. The genotypes were grouped into eight different clusters. The cluster III was the biggest with 11 genotypes followed by cluster-I with 9 genotypes, cluster V and VI consisted of 4 and 3 genotypes respectively. The cluster II and VII both had two genotypes each and similarly, cluster IV and VIII included one genotype each.

The D^2 analysis allowed the 36 genotyped/variety of linseed to be identified into five distinct clusters by Begum *et al.* (2007). The cluster I included 11 genotypes that had medium mean values for 1000-seed weight (g) and seed yield/plant. The cluster II contained six genotypes, which had the highest mean values for number of seeds/capsule, number of branches/plant and seed yield/plant. They also showed the highest mean value for plant height. It is also related with medium mean values for rest of the characters. The cluster IV included three genotypes having the highest mean values for number of capsules/plant and days to maturity. The cluster V included single genotype, which had the lowest mean values for days to maturity and plant height. The highest inter cluster distance

was observed among clusters V, IV and II, while the lowest between III and I. The highest intra cluster distance was observed in cluster III that revealed maximum variability within the clusters. In this study, two traits such as number of branches/plant and number of seeds/capsule contributed the maximum towards divergence in the existing germplasm.

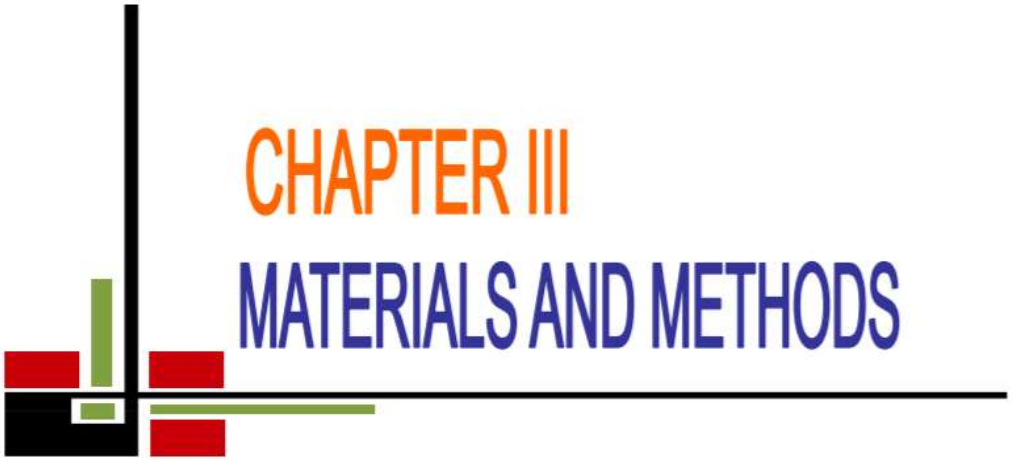
Islam and Islam (2000) reported the genetic diversity in rapeseed and mustard using D^2 analysis of 42 genotypes. The genotypes were grouped into four clusters. The inter-cluster distances were larger than the intra-cluster distances. The characters contributed maximum in divergence analysis is days to 50% flowering, plant height, primary branches/plant and number of siliqua/plant.

Yadava *et al*. (2004); studied 50 lines of *B. napus* and reported that the lines were grouped into twelve clusters with maximum inter cluster distances between the clusters XII and IX (35.51), II and III (33.03) and XI and IX (31.21). The characters contributing to the maximum divergence were in descending order, oil content days to flowering, plant height, siliqua length and siliqua number on the main raceme. Khulbe and Pan (1999), reported that siliqua per plant, siliqua length, seeds per siliqua, 1000 seed weight were positively associated with grain yield. Analysis of variance revealed that siliqua per plant, siliqua length, 1000 seed weight and seeds per siliqua were the major characters influencing grain yield. Jagadev *et al.* (1999); studied on some 19 genotypes of rapeseed (*B. napus*). They studied yield and yield contributing characters grouped the genotypes into 5 clusters with clusters I comprising these genotypes, clusters II and 1112 each and clusters IV and V one each. Singh *et al*. (1997); studied genetic divergence through D^2 statistic with 50 genotypes of *B. napus* growing in 12 environments based on 13 characters. They searched the clustering pattern and their inter and intra cluster distances. On the basis of stability, high yield and divergence among the genotypes, nine crosses were recommended as suitable for use in breeding programme.

Dhillon *et al.* (1999) studied genetic divergence for seed yield and six important yield components in Indian mustard (*Brassica juncea* Czern & Coss) and found 8 clusters. Cluster I comprising of 24 genotypes, whereas clusters VI, VII and VIII comprised of one genotype of each. Seed yield per plant showed maximum divergence followed by number of siliqua on main shoot and minimum by number of primary branches per plant. The inter cluster distance was maximum between clusters V and VIII (713.86) followed by clusters V and III (454.63).

Uddin (1994) conducted an experiment on genetic divergence among 34 genotypes of mustard were estimated using D^2 and principal component analysis. The inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups. Thirty one *toria* genotypes were grown in 12 artificially created environments in order to study genetic divergence by Singh and Gupta (1984). D^2 estimates based on 12 characters were used in obtaining the clustering pattern and inter- and intra-cluster distances. Out of 31 genotypes, on the basis of stability, high yield and divergence six genotypes were found to be suitable for use in a breeding program.

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


CHAPTER III
MATERIALS AND METHODS

CHAPTER III

MATERIALS AND METHODS

The experiment was conducted for character association and diversity analysis of different genotypes of mustard. The details of the materials and methods i.e. location of experimental site, soil and climate condition of the experimental plot, materials used, design of the experiment, data collection procedure and procedure of data analysis that used or followed in this experiment has been presented below under the following headings:

3.1 Experimental Site:

The experiment was carried out in the experimental field of the SAU, during Nov. 2018 to Feb. 2019. The location of the experimental site was situated at 230 74" N latitude and 900 35" E longitudes with an elevation of 8.6 meter from the sea level. Photograph showing experimental sites (Appendix I).

3.2 Soil and Climate:

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

3.3 Experimental materials:

The healthy seeds of thirty eight F_6 *Brassica napus* L. was collected from the Dept. of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, which were used as experimental materials (Table 1).

Table 1. Materials used for the experiment.

Genotype	F_6 Population	Source
G1	Nap9908 × Nap206	SAU
G2	Nap205 × Nap2037	SAU
G3	Nap248 × Nap9904	SAU
G4	Nap9908 × Nap2012	SAU
G5	Nap9905 × Nap206	SAU
G6	BS-13 × Nap2066	SAU
G7	Nap205 × Nap2013	SAU
G8	Nap248 × Nap0130	SAU
G9	Nap108 × Nap206	SAU
G10	Nap 9908 × Nap2037	SAU
G11	Nap248 × Nap2037	SAU
G12	Nap205 × Nap2022	SAU
G13	Nap248 × Nap206	SAU
G14	B-13 × Nap179	SAU
G15	B-13 × Nap0130	SAU
G16	Nap248 × Nap9901	SAU
G17	Nap205 × Nap0130	SAU
G18	Nap108 × Nap2057	SAU
G19	BS-13 × Nap2013	SAU
G20	Nap9908 × Nap2057	SAU
G21	B-13×Nap2022	SAU
G22	B-13×Nap2012	SAU
G23	Nap9908 × Nap0130	SAU
G24	Nap9908 × Nap9901	SAU
G25	Nap205 × Nap2037	SAU
G26	BS-13 × Nap9901	SAU
G27	B-13 × Nap0130	SAU
G28	BS-13 × Nap2001	SAU
G29	Nap 9905 × Nap2037	SAU
G30	Nap248 × Nap2012	SAU
G31	Nap9905 × Nap2001	SAU
G32	Nap205 × Nap179	SAU
G33	Nap9906 × Nap206	SAU
G34	Nap205 × Nap206	SAU
G35	Nap205 × Nap940061	SAU
G36	Nap9906 × Nap0136	SAU
G37	B-13 × Nap2937	SAU
G38	B-13 × Nap2057	SAU

3.4. Methods

3.4.1 Land Preparation:

The experimental plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about good tilth. Weeds and other stubbles were removed carefully from the experimental plot and levelled properly (Plate 1).

3.4.2 Application of Manure and Fertilizer:

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

3.4.3 Experimental Design and Layout:

Field lay out was done after final land preparation. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications (Plate 2). The total area of the experiment was 56m X 14m = 784 m^2. Each replication size was 56m X 3.5m, and the distance between replication to replication was 1m. The spacing between lines to line was 30 cm. Seeds were sown in lines in the experimental plots on 12 November 2018. The seeds were placed at about 1.5 cm depth in the soil. After sowing the seeds were covered with soil carefully so that no clods were on the seeds.

3.4.4 Intercultural Operations:

Intercultural operations, such as weeding, thinning, irrigation, pest management, etc. were done uniformly in all the plots. Irrigation was given with cane after

Plate 1. Photograph showing land preparation of experimental field

Plate 2. Photograph showing layout of experimental field

sowing of seeds to bring proper moisture condition of the soil to ensure uniform germination of the seeds. A good drainage system was maintained for immediate release of rainwater from the experimental plot during the growing period. The first weeding was done after 15 days of sowing. At the same time, 1st thinning was done and another after 7days of 1st thinning was done for maintaining a distance of 10 cm from plant to plant in rows of 30 cm apart (plate 3). Second weeding was done after 35 days of sowing. Sap sucking insect aphid infestation was found in the crop during the siliqua development stage. Insecticide Malataf 57 EC under Malathion group @ 2 ml/litter of water was applied for controlling aphid. The insecticide was applied in the afternoon. Tagging was done timely. Field inspection was done time to time.

3.4.5 Crop Harvesting

Harvesting was done from about 90 days after sowing (DAS) depending upon the maturity. When 80% of the plants showed symptoms of maturity i.e. straw colour of siliqua, leaves, stems desirable seed colour in the mature siliqua, the crop was assessed to attain maturity. Fifteen plants were selected at random F_6 progenies in each replication. The plants were harvested by uprooting and then they were tagged properly. Data were recorded on different parameters from these plants. A pictorial view of experimental field harvesting stage is presented in Plate 7& 8.

3.4.6 Data Collection

For studying different genetic parameters and inter-relationships, eleven characters were taken into consideration. The data were recorded on five plants from each line from each replication which means nearly 570 plants on the following traits-

Plate 3. Pictorial view of thinning of mustard field

Plate 4. Pictorial view of experimental plot showing different population with tags

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

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

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

iv. Root Length (cm): It was taken in centimetre (cm) from the base of the plant to root tip.

v. Shoot Length (cm): It was measuresd in centimetre (cm) from the root tip to shoot tip.

vi. Number of Primary Branches per Plant: The total number of branches arisen from the main stem of a plant was counted as the number of primary branches per plant.

vii. Number of Secondary Branches per Plant: The total number of branches arisen from the primary branch of a plant was counted as the number of secondary branches per plant.

viii. Number of Siliqua per Plant: Total number of siliqua of each plant was counted and considered as the number of siliqua per plant.

ix. Siliqua Length (cm): This measurement was taken in centimeter (cm) from the base to the tip of a siliqua of the five representative siliqua .

xi. 1000-Seed Weight (g): Weight in grams of randomly counted thousand seeds of each entry was recorded.

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

Plate 5. Pictorial view of flowering stage of experimental plot

Plate 6. Photograph showing field observation by supervisor

Plate 7. Photograph showing harvesting at maturity stage

Plate 8. Photograph showing harvested plant properly tagging according to accession number

3.5 Statistical analysis

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

i) Estimation of genotypic and phenotypic variances:

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

a. Genotypic varianc, $\sigma_g^2 = \frac{\text{MSG}-\text{MSE}}{\text{r}}$

Where,

MSG = Mean sum of square due to genotypes

MSE = Mean sum of square due to error, and

r = Number of replication

b. Phenotypic variance, Where, $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$

Where, δ^2g = Genotypic variance,

δ^2e=Environmental variance = Mean square due to error

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

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

$$\text{GCV} = \frac{\sigma_g \times 100}{\bar{x}}$$

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

Where, GCV = Genotypic co-efficient of variation

PCV = Phenotypic co-efficient of variation

δ_g = Genotypic standard deviation

δ_p = Phenotypic standard deviation

x= Population mean

Sivasubramanian and Madhavamenon (1973) categorized phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) as

Low (0-10%),

Moderate (10-20%) and

High (>20%)

iii) Estimation of heritability:

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

$$h_b^2(\%) = \frac{\delta_g^2}{\delta_p^2} \times 100$$

Where,

h_b^2=Heritability in broad sense

σ_g^2= Genotypic variance

σ_p^2= Phenotypic variance

Robinson *et al.* (1966) suggested the following categories for heritability estimates in cultivated plants:

Categories: Low: 0-30%

Moderate: 30-60%

High: >60%

iv) Estimation of genetic advance:

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

$$GA = \frac{\sigma_g^2}{\sigma_p^2} . K . \sigma_p$$

Where,

GA = Genetic advance

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

σ_p = Phenotypic standard deviation

K= Standard selection differential which is 2.06 at 5% selection intensity.

Categories: Low (<10%)

Moderate (10-20%)

High (>20%)

v) Estimation of genetic advance in percentage of mean

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

$$\text{GA in percent of mean} = \frac{\text{GA}}{\text{Grand mean}} \times 100$$

Johnson *et al*. (1955) suggested that genetic advance in percent of mean was categorized into following groups:

Categories:

Less than 10% - Low

10-20% -Moderate

More than 20% High

vi) Estimation of simple correlation co-efficient:

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

$$r_g(xy) = \frac{Cov_g\ xy}{\sqrt{\sigma_x^2}.\sqrt{\sigma_y^2}}$$

$$r_p(xy) = \frac{Cov_p\ xy}{\sqrt{\sigma_x^2}.\sqrt{\sigma_y^2}}$$

Where,

$r_g(xy), r_p(xy)$ The genotypic and phenotypic correlation coefficients, respectively.

Cov_g, Cov_p are the genotypic and phenotypic covariance of xy respectively.

σ_g^2 and $\sigma_p^2$and are the genotypic and phenotypic variance of x and y, respectively.

The calculated value of 'r' was compared with table 'r' value with n-2 degrees of freedom at 5% and 1% level of significance, where, n refers to number of pairs of observation. Thus, the data obtained from various experimental objectives were subjected to pertinent statistical analysis to draw meaningful inference towards the genetic divergence of mustard populations.

vii) Path co-efficient analysis:

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985) and Dabholkar (1992), using simple correlation values. In path analysis, correlation co-efficient is partitioned into direct and indirect independent variables on the dependent variable. In order to estimate direct & indirect effect of the correlated characters, say x_1, x_2 and x_3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

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

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

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

In order to estimate direct & indirect effect of the correlated characters, say x_1, x_2 and x_3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

Where, r's denote simple correlation coefficient and P's denote path coefficient (unknown).

P's in the above equations may be conveniently solved by arranging them in matrix from. Total correlation, say between x1 and y is thus partitioned as follows:

P_{yx1} = the direct effect of x_1 on y.

$P_{yx2}r_{x1x2}$ = the indirect effect of x_1 via x_2 on y.

$P_{yx3}r_{x1x3}$ = the indirect effect of x_1 via x_3 on y.

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

$$P_{RY}^2 = 1 - \sum P_{iy} \cdot r_{iy}$$

Where,
$P_{RY}^2 = (R^2)$

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

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

r_{iy}=Correlation of the character with yield

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)

viii) Estimation of Genetic Diversity

Principal component analysis, one of the multivariate techniques, is used to examine the interrelationship among several characters and can be done from 41 the sum of squares and product matrix for the characters. Therefore, principal component were computed from the correlation matrix and genotype scores obtained from the first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than the unity (Jageret *et al*., 1983). Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components**.**

b. Principal Coordinate Analysis (PCO)

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

c. Canonical Vector Analysis (CVA)

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

d. Average Intra-cluster Distances

The average intra-cluster distances for each cluster was calculated by taking possible D^2 values within the member of a cluster obtained from the Principal

Coordinate Analysis (PCO). The formula used was D^2/n, where D^2 is the sum of distances between all possible combinations (n) of the genotype included in the cluster. The square root of the average D^2 values represents the distances (D) within cluster.

e. Clustering

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

CHAPTER IV
RESULTS AND DISCUSSION

CHAPTER IV

RESULTS AND DISCUSSION

In the present investigation the data was collected from thirty eight diverse *Brassica napus* genotypes on twelve traits related to vegetative, reproductive and yield components parameters emphasizing growth and yield. All these accessions were grown in November, 2018-February, 2019 in the field of Sher-e-Bangla Agricultural University. The data ware recorded on the basis of different characters such as plant height (cm), number of primary branches per plant, number of secondary branches per plant, days of 50% flowering, days to maturity, number of siliqua per plant, no. of seeds per siliqua, siliqua length (cm), 1000 seeds weight(g) and seeds in per plant (g). The data were statistically analysed and thus obtained results are described below under the following heads:

4.1 Varietal performance and genetic parameters

4.2 Correlation studies

4.3 Path co-efficient analysis

4.4 Genetic diversity

4.1 Varietal performance and genetic parameters

4.1.1 Variability among the thirty eight materials of *Brassica napus* L.

Results of analysis of variance of different yield contributing characters of thirty eight advanced lines of *Brassica napus* L. summarized in Table 2. The success of crop improvement program depends on the amount of genetic variability presented in the population. The extent of genetic variability can determine the speed and quantum of genetic improvement through selection or hybridization followed by selection. Phenotypic variance measures the magnitude of variability arising out of differences in phenotypic values while the genotypic variance measures the magnitude of variation due to difference within the genotypic values. The mean sum of squares of all the twelve characters are

presented in Table 2. Significant differences among the genotypes was observed by many researcher like Shalini *et al*. (2000), Pant and Singh (2001), Thakra *et al*. (2004), Rukhsana *et al*. (2005), Uddin *et al*. (2005), Khan *et al*. (2006), Parveen (2007), Zebarjadi *et al*. (2011) and Walle *et al*. (2014).

4.1.1.1 Days to 50% flowering

The data for 50% flowering exhibited significant differences among all genotypes (13.69) (Table 2). The collected values ranged from 30.33 to 38.67 days for 50% flowering. The minimum days to 50% flowering were observed the (30.33 days) in G22 and the maximum (38.67 days) was observed in G4 (Table 3). Phenotypic and genotypic variance for days to 50% flowering was observed as 7.38 and 5.85 respectively with moderate differences between them, suggested moderate influence of environment on the expression of the genes controlling this trait.

The value of PCV is higher than GCV which indicated that variability for the character was influenced by genotypes and environment both. The highest co-efficient of variation for both genotypic and phenotypic measures was observed by Lekh *et al.* (1998).

Significant genetic variability in days to 50% flowering in *B. napus* was also observed by Singh *et al*. (1991).

4.1.1.2 Days to Maturity

Data mentioning days to maturity showed significant differences amongst the breeding materials (52.45**) (Table 2). The data ranged from 90.00-107.67 days for days to maturity. Days to maturity varied significantly among the breeding materials. The maximum days to maturity was observed in G5 (107.67 days) and the minimum days to maturity was observed in G11 (90.00 days) (Appendix IV). In days to maturity, Genotypic and phenotypic variance of was found 3.96 and 4.91 respectively (Table 4).

Table 2. Analysis of variance for different characters in mustard genotypes

Characters	Mean sum of square		
	Replication (r-1) = 2	**Genotype (g-1) = 37**	**Error (r-1)(g-1) = 74**
Days to 50% flowering	2.00	13.69**	2.24
Days of maturity	8.06	52.45**	6.35
Plant height (cm)	209.94	197.24**	31.74
Root length (cm)	0.38	4.24**	1.78
Shoot length (cm)	78.43	710.69**	428.05
Primary branch per plant	0.48	0.44**	0.22
Secondary branch per plant	0.84	1.73**	0.30
Total siliquas per plant	6,145.49	1,932.10**	326.42
Siliqua length (cm)	0.97	0.83**	0.38
Seeds per siliqua	0.57	12.56**	2.16
1000 seeds weight (g)	0.18	0.32	0.22
Seed yield per plant(g)	4.99	5.44**	0.74

* Denote Significant at 5% level of probability ** Denote Significant at 1% level of Probability

Table 3. Range, mean and CV (%) of 38 genotypes in *Brassica napus* L

Parameters	Range		Mean	CV (%)
	Min	Max		
Days to 50% flowering	30.33	38.67	33.38	4.49
Days of maturity	90.00	107.67	98.89	2.55
Plant height (cm)	87.81	120.80	105.43	5.34
Root length (cm)	8.17	13.39	10.36	12.90
Shoot length (cm)	97.09	194.95	117.69	17.58
Primary branch per plant	2.27	4.27	2.87	16.41
Secondary branch per plant	1.07	4.50	2.54	21.66
Total siliqua per plant	69.13	159.60	112.06	16.12
Siliqua length (cm)	7.08	9.27	8.20	7.60
Seeds per siliqua	21.50	29.63	25.17	5.84
1000 seeds weight (g)	3.67	5.00	4.29	11.16
Seed yield per plant(g)	3.81	9.51	6.85	12.62

Higher genotypic variances indicated the better transmissibility of a character from parent to the offspring. Similar result for this trait was also observed by Katiyar *et al*. (1974).

4.1.1.3 Plant Height (cm)

The genotypes revealed that the significant variation in plant height (197.24**) (cm) of *Brassica napus*. From the mean values, it was found that among the total genotypes of the present study, the highest plant Variation in plant height was also observed. Data regarding plant height ranged from 87.81 cm - 120.80 cm with the mean value of 105.45 cm (Table 3). Minimum plant height (87.81 cm) were observed in genotype G33 whereas, maximum plant height was found in G11 (120.80cm) (Appendix IV). Ali *et al*. (2002) and Khan *et al*. (2008) also reported significant difference among rape seed genotypes for plant height. Genotypic and phenotypic variances for plant height were 7.04 and 8.84 (table.4) respectively. The phenotypic variance appeared to be higher than the genotypic variance which suggested that variation was not only due to genotypic effect but also due to the influence of environment on the expression of the genes controlling this trait. The highest variation in plant height among parents and their hybrid was observed by Tyagi *et al*. (2001).

4.1.1.4 Root Length (cm)

Root length of plant was significantly influenced by different genotypes (4.24**) (Table 2). The collected values ranged from 8.17 to 13.39 cm of root length with mean value of 10.36 cm (Table 3). Minimum root length (8.17 cm) were observed in genotype G9 whereas, maximum plant height was found in G37 (13.39cm) (Appendix IV). Genotypic and phenotypic variances for plant height were 0.82 and 2.60 (table 4.) respectively.

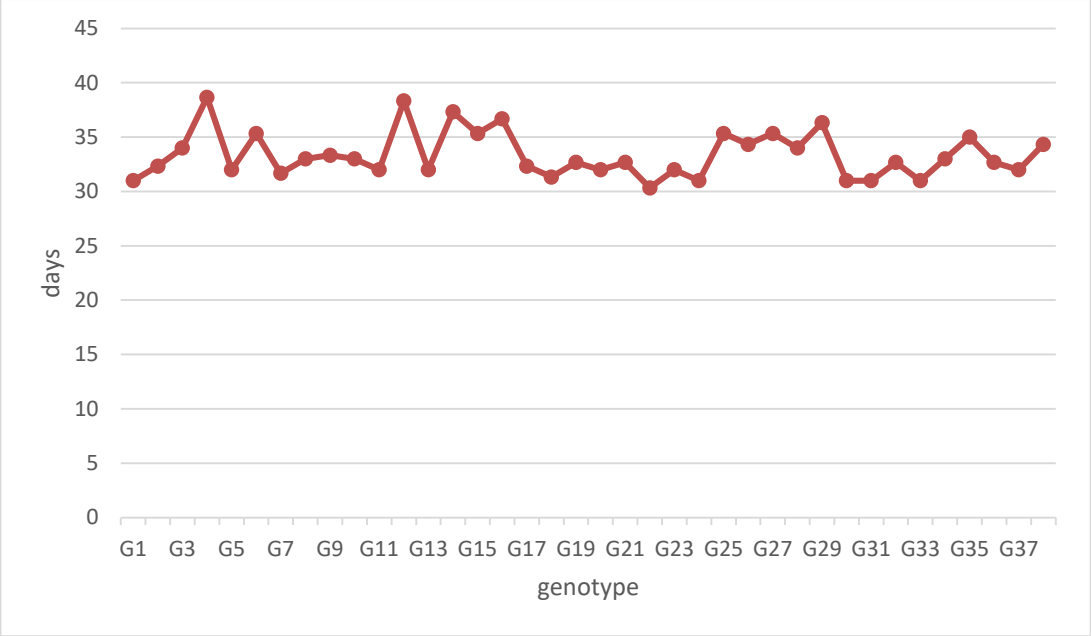


Figure 2: Days to 50% flowering of 38 genotypes in *Brassica napus* L.

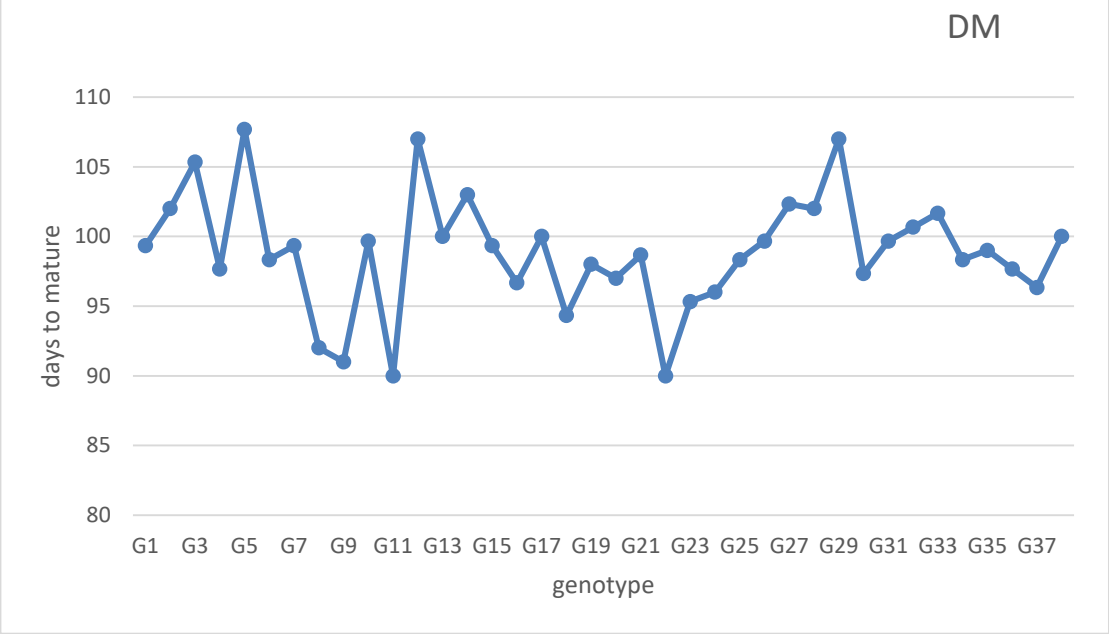


Figure 3: Days to maturity of 38 genotypes in *Brassica napus* L.

4.1.1.5 Shoot Length (cm)

Root length of plant was significantly influenced by different genotypes (710.69**) (Table 2). The collected values ranged from 97.09 to 194.95 cm of shoot length with mean value of 117.69 cm (Table 3.). Minimum shoot length (97.09 cm) were observed in genotype G33 whereas, maximum plant height was found in G31 (194.95 cm) (Appendix IV). Genotypic and phenotypic variances for plant height were 94.21 and 522.27 (Table 4) respectively. The phenotypic variance was higher than genotypic variance which indicates that there was an influence of environment on the expression of the genes.

4.1.1.6 Number of Primary Branches per Plant

Number of branches per plant was significantly influenced by different genotypes (0.44**) (Table 2). Among all the genotypes, the highest number of primary branches per plant was found in G9 (4.27). However, G37 produced the lowest number of branches per plant (2.27) (Table 3) (Appendix IV). Abideen *et al*. (2013) revealed that highly significant differences among the genotypes for most of the traits. Non-significant differences were observed among the genotypes for primary branch.

Phenotypic variance (PCV) and genotypic variance (GCV) were found as 18.99 and 9.54, respectively (Table 4). The phenotypic variance was moderately higher than genotypic variance which indicates that there was a moderate influence of environment on the expression of the genes. Chowdhury *et al*. (1990) also found significant differences for number of primary branches per plant in their study.

4.1.1.7 Number of Secondary Branches per Plant

The no. of secondary branches per plant varied significantly among the genotypes 1.73** (table.2). The data collected from the population ranged from 1.07 to 4.50 for number of secondary branches per plant with the mean value of

2.54 (Table 3). Maximum number of secondary branches per plant was observed in G4 whereas the minimum was observed in G22 (Appendix IV)

Higher estimate of PCV (34.77) and GCV (27.20) values that there is slight environmental influence for the expression of characters for these genotypes (Table 4). Lekh *et al.* (1998) found highest genotypic coefficient of variation for number of secondary branches while working on 24 genotypes of *Brassica napus*. Chowdhury *et al*. (1987) found significant differences for number of secondary branches per plant. Genotypic and phenotypic variability in mustard are shown in Figure 4.

4.1.1.8 Number of Siliqua per Plant

The no. of siliqua per plant varied significantly among the genotypes 1,932.10** (Table 2). In respect of number of siliqua per plant, the highest siliqua was produced by G10 (159.60) followed by the lowest number of siliqua per plant was found in G7 (69.13) with mean 112.06 (Table 3). Alam (2010) found that significant variations number of siliqua per plant and showed low difference between genotypic and phenotypic coefficient of variation. Number of siliqua per plant showed the highest phenotypic variance (861.65) and genotypic variance (535.22) with large environmental influence and the difference between the PCV (26.20) and GCV (20.65) indicated existence of adequate variation among the genotype (Table 4). High genetic variation was also found by Kudla (1993). High genetic variation was also found by Zare and Sharafzadeh, (2012). The data collected for siliqua length indicate significant differences amongst the genotypes (0.83**) (Table 2). The mean values was 8.20 and its values ranges from 7.08 to 9.27 cm for siliqua length. Maximum siliqua length (9.27 cm) was exhibited by G18 and the minimum was observed in G18 (7.08 cm) (Table 3) (Plate 9).

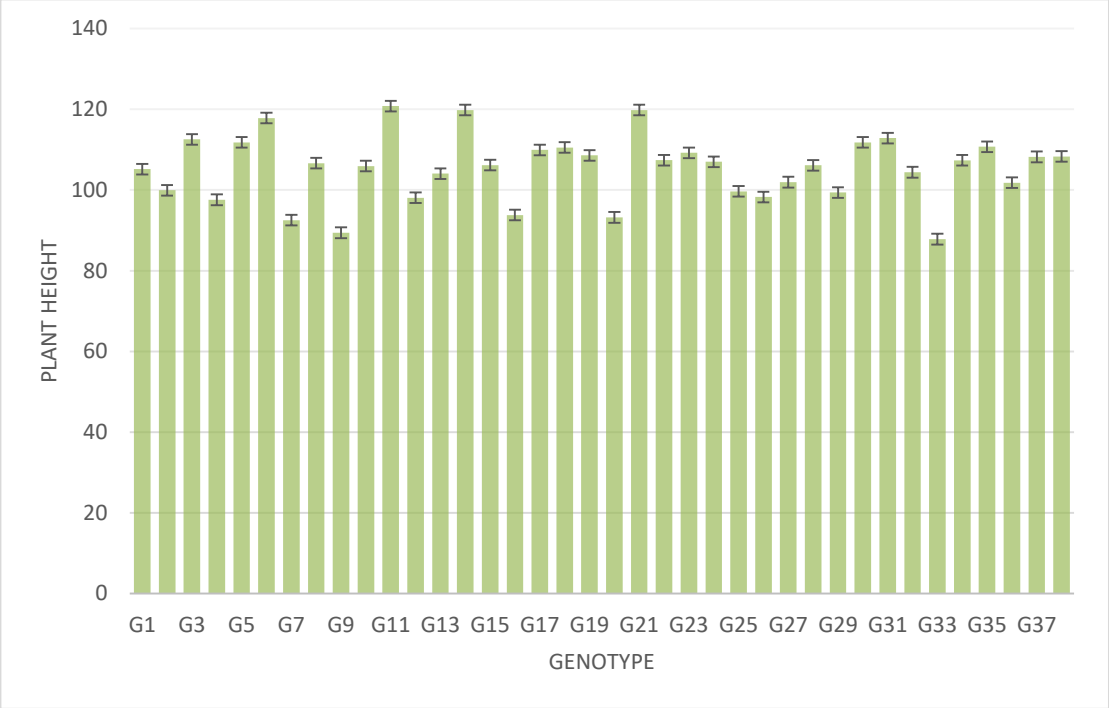


Figure 4: Plant height of 38 genotypes in *Brassica napus* L.

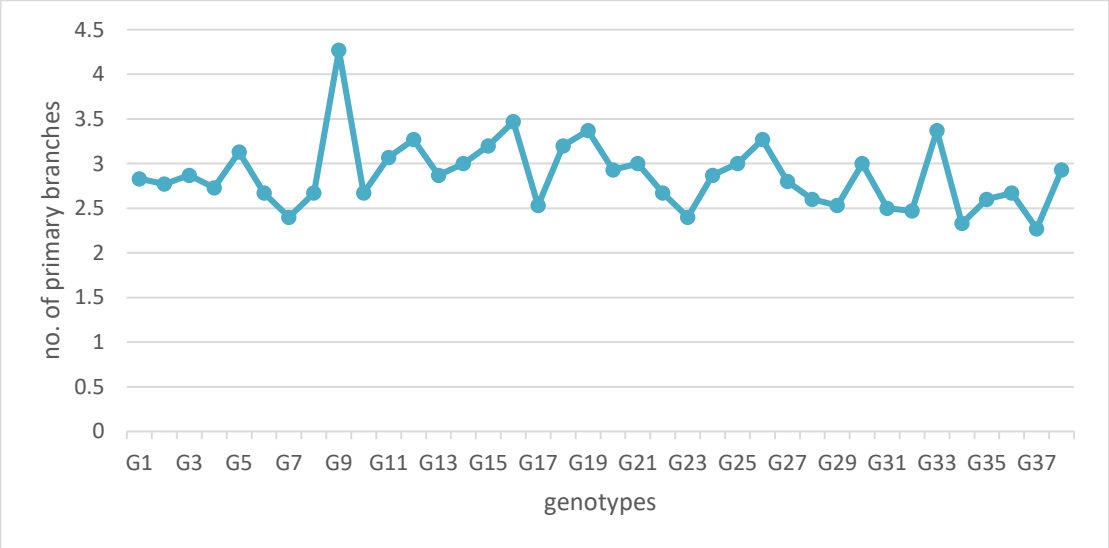


Figure 5: Number of primary branches of 38 genotypes in *Brassica napus* L.

4.1.1.9 Length of Siliqua (cm)

Length of siliqua showed phenotypic variance (0.54) and genotypic variance (0.15) with little difference between them indicating that they were less responsive to environmental factors. Medium PCV (8.94%) and GCV (4.70%) indicating that there was moderate variation from each other (Table 4). High co-efficient of variation for this trait for both genotypic and phenotypic variability was recorded by Masood *et al*. (1999). High genetic variability for this trait was also found by Olson (1990).

4.1.1.10 Number of Seeds per Siliqua

The data collected for no. of seeds per siliqua indicating significant differences amongst the genotypes (12.56**) (Table 2). In case of number of seeds per siliqua, G22 produced significantly highest number of seeds (29.63).The lowest number of seeds per siliqua was found in G5 (21.50) with mean 25.17 (Table 3). Similar result was found from the findings of Alam (2010). He observed that there were significant variations in number of seeds per siliqua.

Number of siliqua per plant showed the highest phenotypic variance (5.63) and genotypic variance (3.47) which indicating the large environmental influence over genotypes (Table 4).

The value of PCV and GCV were 9.42% and 7.40% respectively (Table 4) for number of seeds per siliqua which indicating that medium variation exists among different genotypes. Similar variability was also recorded by Kumar and Singh (1994).

4.1.1.11 Thousand Seed Weight (g)

Insignificant differences were observed among the genotypes for 1000-seed weight (0.32) (Table 2.). Maximum 1000-seed weight (5.00) was observed in G8, G9, and G34 whereas the minimum was found in G4 (3.67g) (Table 3) (Appendix IV) (Plate10).

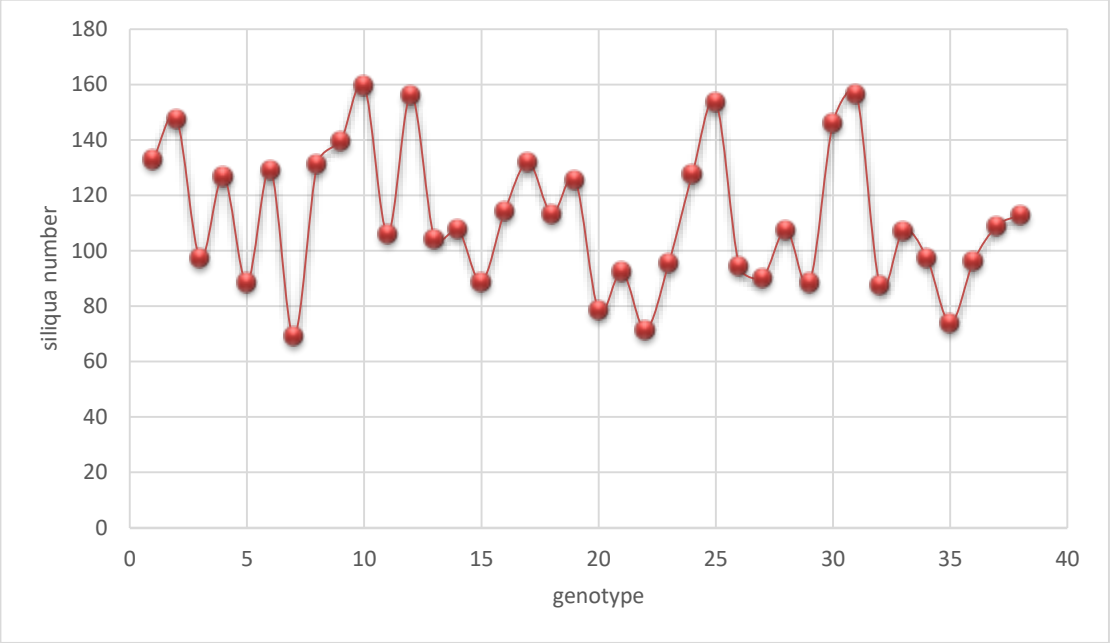


Figure 6: Number of siliqua per plant in *Brassica napus* L.

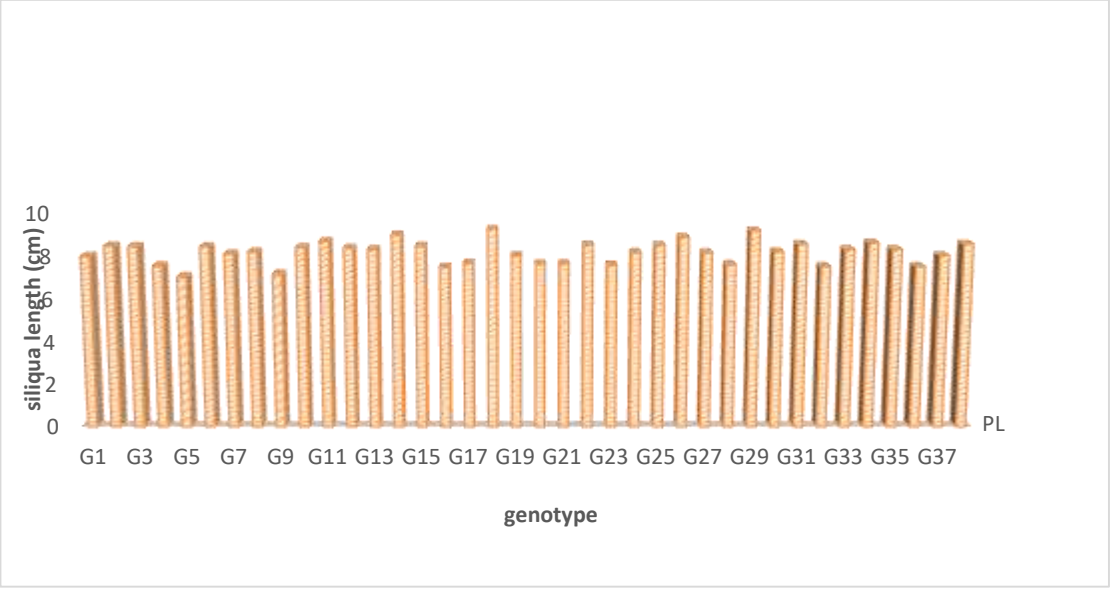


Figure 7. Siliqua length of 38 genotypes in *Brassica napus* L.

Thousand seed weight showed the phenotypic variance and genotypic variance of 0.26 and 0.03 respectively (Table 4).

The phenotypic coefficient of variation (11.93%) and genotypic coefficient of variation (4.22 %) were not close to each other (Table 4). The difference between phenotypic and genotypic co-efficient of variation indicating major environmental influence on this character. Significant variability for this trait was also found by Kumar and Singh (1994). Masood *et al.* (1999) found high coefficient of variation for thousand seed weight while working with seven genotypes of *Brassica napus* to study genetic variability.

4.1.1.12 Yield per Plant (g):

Significant differences were observed among the genotypes for yield per plant (5.44**) (Table 2). In respect of number of seed yield per plant, the genotype which produced higher seed yield per plant (9.51g) was recorded from G15 The lowest seed yield per plant (3.81g) was recorded in G23 (Table 3) (Appendix IV). Abideen *et al*. (2013) observed similar findings and results revealed that highly significant differences among the genotypes for seed yield.

The phenotypic variances and genotypic variances for this population were 2.31 and 1.57, respectively (Table 4). The values indicated a slight environmental influences for this character.

In significant differences were observed between PCV (22.20%) and GCV (18.27%) (Table 4) (Figure 9). Aytac *et al*. (2008) reported highest genotypic and phenotypic variances for seed yield per plant followed by seed yield and high heritability of seed yield per plant, seed yield, siliqua per main stem coupled with high genetic advance. Considering genetic parameters, high genotypic co-efficient of variation (GCV) was observed for yield per plant (Jahan, 2006).

Plate 9. Photograph showing variation between highest and lowest siliqua length of *Brassica napus* L.

Plate 10. Photograph showing variation between highest 1000 seed weight of *Brassica napus* L.

4.1.2 Heritability and genetic advance

The heritability estimates separate environmental influence from the total variability and indicates the accuracy with which a genotype can be identified by its phenotypic performance more effectively. Its aim was to determine the relative amount of heritable portion of variation. As such the heritability in broad sense is the proportion of genotypic variability to the total variability, its importance has been emphasized by Lush (1949) in animals and Johnson *et al*. (1995) in plants. The values of genetic advance and heritability for different yield contributing characters are showed in Table 4. The results clearly revealed that presence of high variability for yield and yield contributing characters among the genotypes studied. Therefore there is a lot of scope for selection for the traits in the genotypes.

4.1.2.1 Days to 50% Flowering

The days to 50% flowering exhibited moderate heritability (62.99%) with low genetic advance (3.19%) and genetic advance in percentage of mean (9.57%) (Table 4) indicated that this trait was controlled by non-additive gene. This results supported the reports of Malik *et al*. (1995). Belete *et al.* (2012), who also found high heritability with high genetic advance (as percent of mean) for days to flowering.

4.1.2.2 Days to Maturity:

Days to maturity showed high heritability (70.73%) with low genetic advance (6.79) and genetic advance in percentage of mean (6.87%) (Table 4) indicated that selection based on phenotype for this character would not be effective. High heritability with low genetic advance for this character was also observed by Afrin *et al*. (2011). In some of the crosses the frequency of the segregating plants showing reduced maturity was comparatively higher than the 63 other crosses. Low heritability coupled with low genetic advance for this trait was also observed by Sharma (1988).

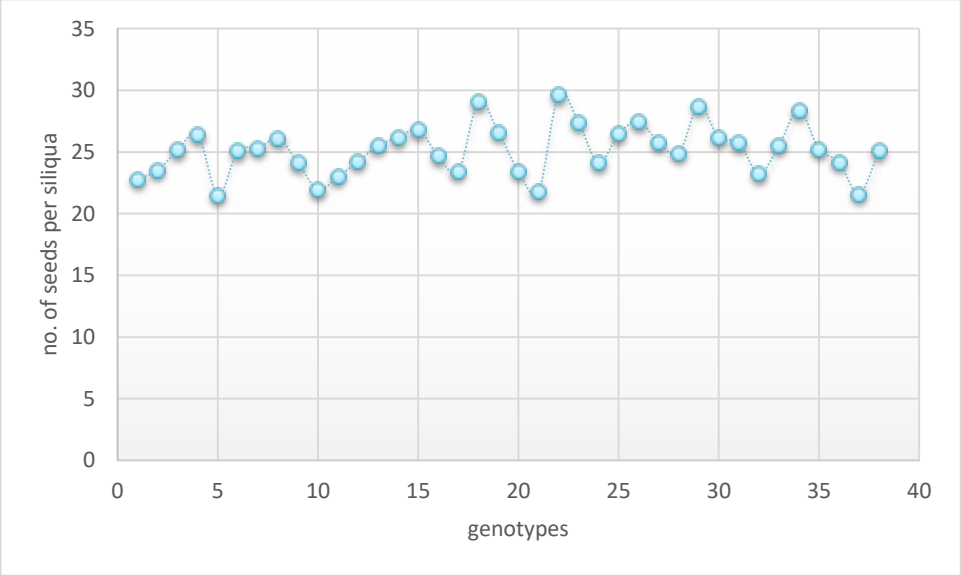


Figure 8. Number of seeds per siliqua in *Brassica napus* L.

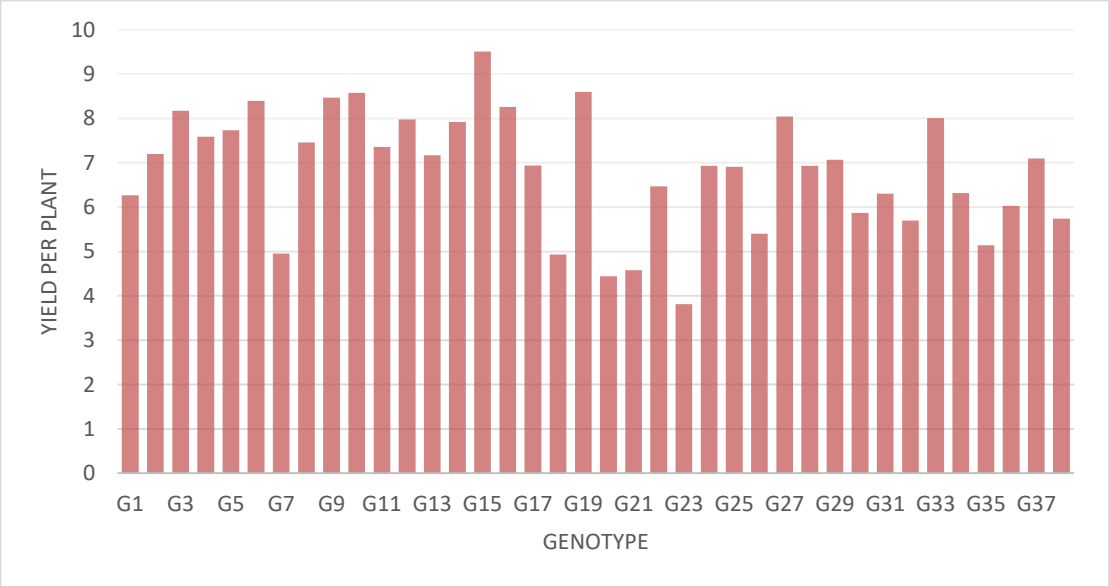


Figure 9. Yield per plant of 38 genotypes in *Brassica napus* L.

Table 4. Estimation of genetic parameters for different characters in mustard

Parameters	σ^2p	σ^2g	σ^2e	PCV	GCV	ECV	Heritability	GA (5%)	GAM
Days to 50% flowering	6.06	3.82	2.24	7.38	5.85	1.53	62.99	3.19	9.57
Days of maturity	21.72	15.37	6.35	4.71	3.96	0.75	70.73	6.79	6.87
Plant height (cm)	86.91	55.17	31.74	8.84	7.05	1.79	63.47	12.19	11.56
Root length (cm)	2.60	0.82	1.78	15.58	8.74	6.84	31.48	1.05	10.10
Shoot length (cm)	522.27	94.21	428.06	19.42	8.25	11.17	18.04	8.49	7.22
Primary branch per plant	0.30	0.08	0.22	18.99	9.54	9.45	25.26	0.28	9.88
Secondary branch per plant	0.78	0.48	0.30	34.77	27.20	7.57	61.19	1.11	43.83
Total pods per plant	861.65	535.22	326.43	26.20	20.65	5.55	62.12	37.56	33.52
Pod length (cm)	0.54	0.15	0.39	8.94	4.70	4.24	27.66	0.42	5.09
Seeds per pod	5.63	3.47	2.16	9.42	7.40	2.02	61.61	3.01	11.96
1000 seeds weight (g)	0.26	0.03	0.23	11.93	4.22	7.71	12.49	0.13	3.07
Seed yield per plant(g)	2.31	1.57	0.74	22.20	18.27	3,93	67.69	2.12	30.96

σ^2p: Phenotypic variance
σ^2g: Genotypic variance
σ^2e: Environment variance
PCV: Phenotypic coefficient of variation
GCV: Genotypic coefficient of variation
ECV: Environmental coefficient of variation
GA (5%): Genetic advance
GAM: Genetic advance (% of mean)

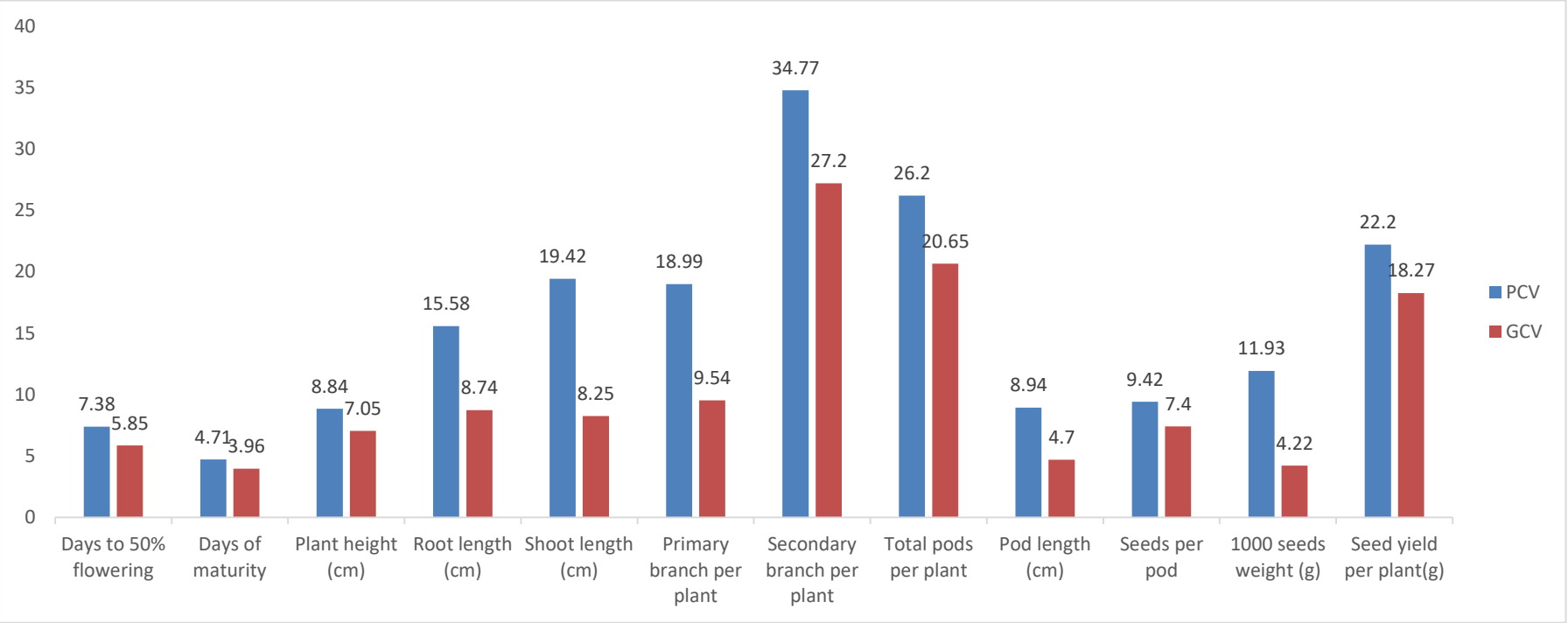


Figure 10. Genotypic and phenotypic coefficient of variation in *Brassica napus* L.

4.1.2.3 Plant Height (cm):

Plant height of these 38 genotypes showed high heritability 63.47% with moderate genetic advance of 12.19% and genetic advance in percentage of mean of 11.56% (Table 4) which revealed that the character was influenced by the environmental effects and the possibility of predominance of additive gene action in the inheritance of this trait and indicating that this trait's performance could be enhanced through selection process. High variability in plant height for *B. juncea*, *B. rapa* and *B. napus* was also observed by Varshney *et al*. (1986). Chandola (1977) observed high genetic advance for plant height while working with 30 varieties of *Brassica rapa*. Heritability and genetic advance in percentage of mean are shown in Figure 10.

4.1.2.4 Root length (cm)

Root length of these 38 genotypes mentioned moderate heritability 31.48% with low genetic advanced 1.05% and genetic advance in percentage of mean of 10.10 % (Table 4.) which revealed the moderate possibility of selecting genotypes for this trait.

4.1.2.5 Shoot Length (cm)

Shoot length of these 38 genotypes mentioned low heritability 18.04% with low genetic advanced 8.49 % and genetic advance in percentage of mean of 7.22 % (Table 4). As a whole, the low heritability and the consequent low genetic advance indicated the lower possibility of selecting genotypes for this trait.

4.1.2.6 Number of Primary Branches per Plant

Number of primary branches per plant expressed low heritability 25.26 % with low genetic advance 0.28% and low genetic advance in percentage of mean of 9.88% (Table 4) , which revealed that the lower possibility of predominance of additive gene action in the inheritance of this trait. As a whole, the low heritability and the consequent low genetic advance indicated the lower possibility of selecting genotypes for this trait. However, some of the individual

plants showed quite a reasonable lower primary branches which were selected for further study in the next generation. Low heritability coupled with low genetic advance was also found by Singh *et al.* (1987). Yadava *et al.* (1985) found high heritability and genetic advance for number of primary branches per plant.

4.1.2.7 Number of Secondary Branches per Plant

Number of secondary branches per plant exhibited high heritability (61.19%) with low genetic advance 1.11% and genetic advance in percentage of mean (43.83%) (Table 4). As a whole, the high heritability and the low genetic advance indicated the lower possibility of selecting genotypes but high genetic advance in percentage of mean which indicated that possibility of predominance of additive gene, which have a huge scope to improve. Khan *et al.* (2013) found high heritability coupled with high genetic advance for number of secondary branches per plant.

4.1.2.8 Number of Siliqua per Plant

Number of siliqua per plant exhibited high heritability 62.12% with moderately high genetic advance 37.56% and genetic advance in percentage of mean 33.52 % (Table 4). These results revealed that heritability was due to additive gene effects. It provides a wider scope to the breeders for direct selection during crop improvement. Sadat *et al.* (2010) reported high heritability with the later reporting it coupled with high genetic advance.

High heritability coupled with high genetic advance for this trait was also observed by Sheikh *et al*. (1999). Mahmood *et al*. (2003) reported that the number of siliqua per plant were highly heritable coupled with high genetic advance. Akbar *et al*. (2007) also found higher GCV, higher heritability and genetic advance for this trait.

4.1.2.9 Siliqua Length (cm)

Siliqua length showed low heritability (27.66%) with low genetic advance (0.42) and low genetic advance in percentage of mean 5.09% in Table 4 indicated that this trait was controlled by non-additive gene.

Selection based on this character will not be rewarding for future breeding program. High heritability for this trait was observed by Aytac and Kinaci (2009) and Zare and Sharafzadeh (2012) found low broad sense heritability for siliqua length in rapeseed (*Brassica napus* L).

4.1.2.10 Number of Seeds per Siliqua

Number of seeds per siliqua showed high heritability 61.61% coupled with low genetic advance 3.01% and high genetic advance in percentage of mean 11.96% in Table 4 indicated that this trait was controlled by additive gene and selection for this character would be effective.

Sadat *et al.* (2010) reported high heritability with the later reporting it coupled with high genetic advance.

4.1.2.11 Thousand Seed Weight:

Thousand seed weight exhibited low heritability 12.49% (Table 4) with low genetic advance 0.13% and genetic advance in percentage of mean 3.07%, revealed that this trait was controlled by non-additive gene but provided opportunity for selecting high valued genotypes for this trait.

Walker (2001) reported that moderate values of heritability and the genetic advance may be due to non-additive gene action which includes dominance and epistasis. Johnson *et al*. (1955) reported that heritability estimates along with genetic group were more useful in prediction selection of the best individual. High heritability for this trait was also observed by Yadava *et al*. (1993).Singh *et al*. (2002) reported the high heritability and genetic advance for thousand seed weight.

4.1.2.12 Seed yield per Plant:

High heritability 67.69 % with low genetic advance (2.12) and high genetic advance in percentage of mean 30.96% (Table 4) for seed yield per plant indicated this trait was controlled by additive gene and this character should consider for future breeding program.

Aytac and Kinaci (2009) mentioned the high heritability and genetic advance for seed yield selection for this character would be effective. Rameeh (2014) also found high heritability with high genetic advance for seed yield in *B. napus*. L.

High heritability coupled with high genetic advance for this trait was also observed by Sheikh *et al*. (1999). High heritability and genetic advance for seed yield per plant was reported by Singh (1986) while working with 22 genotypes of *Brassica napus*.

4.2 Correlation Coefficient

Seed yield is a complex product being influenced by several quantitative traits. Some of these traits are highly associated with seed yield. The analysis of the relationship among those traits and their association with seed yield is very much essential to establish selection criteria.

Yield is controlled by polygene and very often influenced by environment. For this reason, selection based on only yield itself is ineffective. Correlation coefficient helps the way to select plant for breeding purpose by the plant breeders. Genotypic and phenotypic correlation coefficients among 12 characters are presented in Table 5. In most instances, there was a close agreement between genetic correlations and phenotypic correlations.

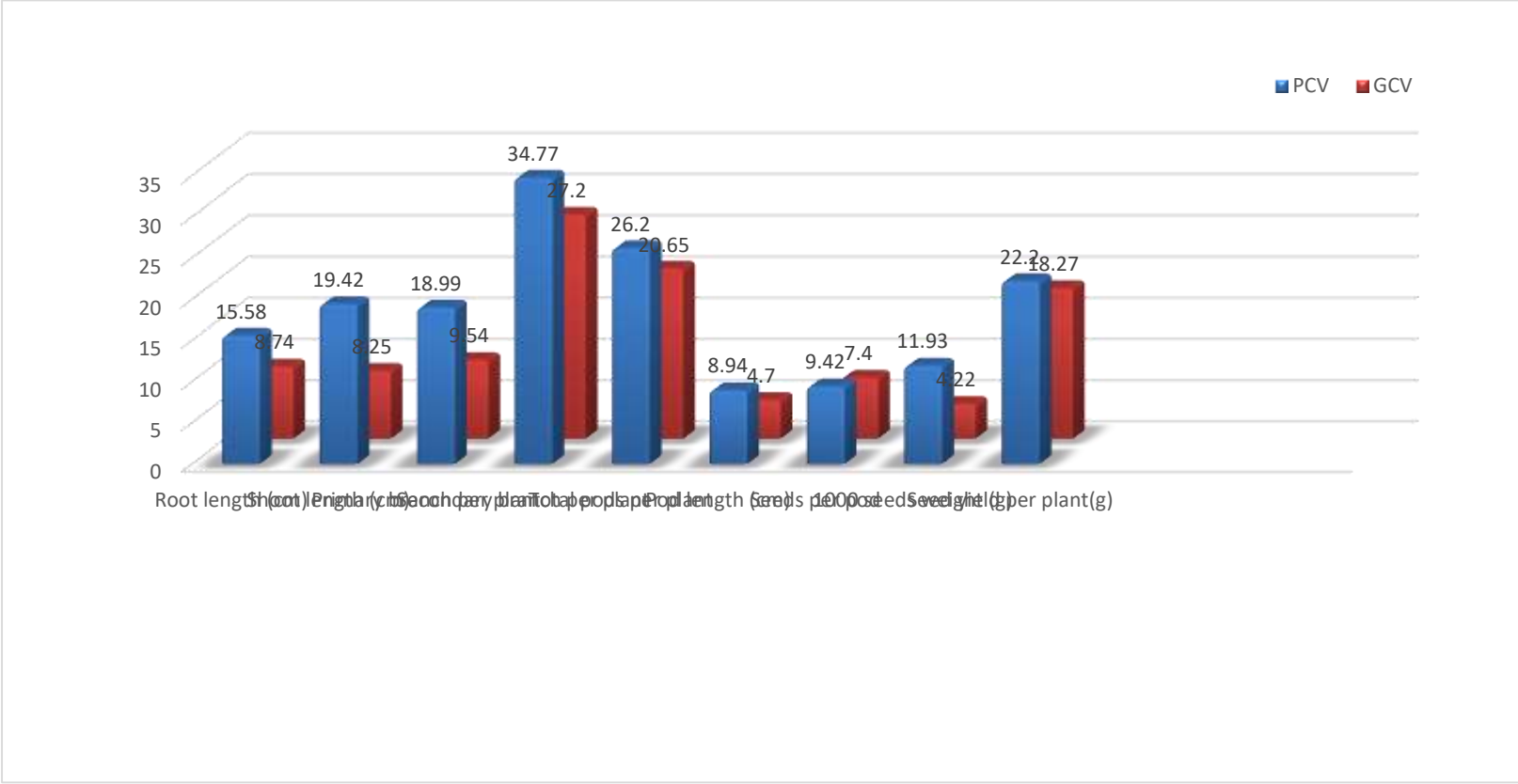


Figure 11. Heritability and genetic advance over mean in *Brassica napus*

Table 5. Genotypic (G) and phenotypic (P) correlations among different pairs of traits for different genotype of mustard

		D50%F	DM	PH	RL	SL	PB	SB	TP	PL	SPP	TSW
DM	G	0.423**										
	P	0.319**										
PH	G	-0.126	-0.079									
	P	-0.115	-0.017									
RL	G	-0.340**	-0.181	0.532**								
	P	-0.093	-0.019	0.397**								
SL	G	-0.466**	-0.103	0.110**	0.449**							
	P	-0.140	0.041	0.421**	0.229*							
PB	G	0.234*	-0.137	-0.497**	-0.464**	-0.532**						
	P	0.095	-0.113	-0.159	-0.013	-0.173						
SB	G	0.171	-0.025	-0.410**	-0.126	-0.403**	0.395**					
	P	0.158	-0.022	-0.244**	0.112	-0.141	0.160					
TP	G	0.129	0.003	-0.031	-0.571**	0.324**	0.207*	0.205*				
	P	0.025	-0.054	0.046	-0.202*	0.083	0.230*	0.217*				
PL	G	0.155	0.094	0.272**	0.110	0.288**	-0.356**	-0.091	0.053			
	P	0.056	0.057	0.215*	0.328**	0.164	0.007	-0.009	0.070			
SPP	G	0.183	-0.160	-0.124	-0.049	-0.032	-0.103	-0.143	-0.244**	0.677**		
	P	0.100	-0.141	-0.033	0.113	-0.065	0.026	-0.081	-0.128	0.444**		
TSW	G	0.033	-0.394**	-0.312**	-0.069	-0.538**	0.395**	0.200*	-0.061	-0.315**	-0.304**	
	P	-0.050	-0.124	0.004	-0.069	-0.054	0.050	0.167	0.044	-0.141	0.009	
SYPP	G	0.469**	0.241**	-0.128	-0.345**	-0.141	0.388**	0.142	0.358**	-0.014	-0.135	0.112
	P	0.278**	0.114	0.014	-0.106	-0.085	0.383**	0.131	0.369**	0.076	-0.050	0.113

D50%F: days to 50% flowering, DM: days to maturity, PH: plant height (cm), RL: root length (cm), SL: shoot length (cm), PB: primary branches of plant, SB: secondary branches per plant, TP: total pods per plant, PL: pod length (cm), SPP: seeds per pod, TSW: 1000 seed weight (g) and SYPP: seed yield per plant (g).

4.2.1 Days to 50% Flowering

Days to 50% flowering was positively and highly significantly correlated with days to maturity (r_g= 0.423** r_p=0.319$^{**)}$ indicated that if days to 50% flowering increased then days to maturity also increased whereas negative and significantly correlated with plant height in genotypic correlation (r_g= -0.126) and phenotypic correlation (r_p= -0.115) and also with total seed weight (r_g=-0.033, r_p=-0.050). Here correlation was significant and negative so the association between two characters was low, indicated that it will not be beneficial for breeders. It also revealed that insignificant and positive correlation with secondary branch (r_g=0.171, r_p=0.158), total seed per plant (r_g=0.183, r_p=0.100) that revealed clearly the independent nature of those characters. However, it had significant and positive interaction with primary branch (r_g= 0.234*and r_p=0.095), siliqua length (r_g=0.155, r_p=0.056), total siliqua (r_g=0.129, r_p=0.025). Again it disclosed that there is significant and negative correlation with root length (r_g=-0.340**, r_p=-0.093$^{)}$, and shoot length (r_g=-0.466**, r_p=-0.140) (Table 5). Insignificant association of these traits indicated that the association between these traits was largely influenced by environmental factors. Nasim *et al*. (2013) observed negative correlation with thousand seed weight.

4.2.2 Days to Maturity

Days to maturity expressed that there was positive and significant correlation with seed yield per plant (r_g=0.241**, r_p=0.114) while negative and significant correlation with thousand seed weight (r_g=-0.394**, r_p=-0.124). Significant positive correlation between plant height and seed yield was found by Khan and Khan (2003). It also revealed that there was negative and insignificant correlation with plant height (r_g=-0.079, r_p=-0.017), root length (r_g=-0.181, r_p=-0.019), shoot length (r_g=-0.103, r_p=0.041), primary branches (r_g=-0.137, r_p=-0.113), secondary branches (r_g=-0.137, r_p=-0.113), seeds per siliqua (r_g=-0.160, r_p=-0.141) (Table 5). Insignificant association of these traits indicated that the association between these traits were largely influenced by environmental factors. Parveen (2007) also revealed that days to maturity had insignificant and positive interaction with yield per plant.

4.2.3 Plant Height (cm)

Plant height showed significant and positive correlation with root length (r_g=0.532**, r_p =0.397**), shoot length (r_g=1.010**, r_p=0.421**) and siliqua length (r_g=0.272**, r_p=0.215*). It had negative interrelation with primary branches (r_g=-0.497**, r_p=-0.159), secondary branches (r_g=,-0.410**, r_p=-0.244**) total seeds per plant (r_g=-0.124, r_p=-0.033). Again total siliqua (r_g=-0.031, r_p=0.046), thousand seed weight (r_g=-0.312**, r_p=0.004) seed yield per plant (r_g=-0.128, r_p=0.014) (Table 5) exhibited negative genotypic correlation but positive correlation. Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Shalini *et al.* (2000) also observed that plant height was highly associated with seed yield. Basalma (2008) reported opposite result for this trait.

4.2.4 Root Length (cm)

Root length showed positive significant correlation with shoot length (r_g= 0.449**, r_p= 0.229*), plant height (r_g= 0.532**, r_p= 0.397**), siliqua length (r_g= 0.110, r_p= 0.328**). These suggesting if root length increases then plant shoot length and plant height also increases. It had negative interrelation with days to 50% flowering (r_g= -0.340**, r_p= -0.093), total siliqua (r_g= -0.571**, r_p= -0.202*), seed yield per plant (r_g= -0.345**, r_p= -0.106) (Table 5).

4.2.5 Shoot Length (cm)

Shoot length showed positive significant correlation with root length (r_g= 0.449**, r_p= 0.229*), plant height (r_g=0.110**, r_p=0.421**), total siliqua (r_g=0.324**, r_p=0.083), siliqua length (r_g=0.288**, r_p=0.164) whereas, it had negative correlation with days to 50% flowering (r_g=-0.466**, r_p=-0.140), primary branches (r_g=-0.532**, r_p=-0.173), secondary branches (r_g=-0.403**, r_p=-0.141) (Table 5).

4.2.6 Number of Primary Branches per Plant

Number of primary branches revealed that there was positive and significant interrelation with secondary branches (r_g=0.234*, r_p=0.095), days to 50% flowering (r_g=0.395**, r_p=0.160), total siliqua (r_g=0.207*, r_p=0.230*), thousand seed weight (r_g=0.395**, r_p= 0.050), seed yield per plant (r_g=0.388**, r_p=0.383**). These suggesting if number of primary branches increases then yield per plant also increases. Malik *et al*. (2000) reported similar result for number of primary branches and seed yield both at genotypic and phenotypic level. It had negative correlation with days of maturity (r_g=-0.137, r_p=-0.113), plant height (r_g=-0.497**, r_p=-0.159), root length (r_g=-0.464**, r_p=-0.013), shoot length (r_g=-0.532**, r_p=-0.173) (Table 5). Insignificant association of these traits indicated that the association between these traits was largely influenced by environmental factors and mostly independent in nature.

4.2.7 Number of secondary Branches per Plant

Number of secondary branches per plant disclosed that there was positive and significant correlation with days to days to 50% flowering (r_g=0.171, r_p=0.158), primary branches (r_g=0.395**, r_p=0.160), total siliqua (r_g=0.205*, r_p=0.217*), thousand seed weight (r_g=0.200*, r_p=0.167), seed yield per plant (r_g=0.142, r_p=0.131) indicated in Table 5 that the traits were governed by same gene and simultaneous improvement would be effective and branching was an important contributor to yield, independent of its association with plant size. However, it had insignificant and negative interaction with days to maturity (r_g=-0.025, r_p=-0.022), plant height (r_g=-0.410**, r_p=-0.244**), root length (r_g=-0.126, r_p=0.112), shoot length (r_g=-0.403**, r_p=-0.141). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. These findings are showing similar to the reports of Chowdhary (1987).

4.2.8 Number of Siliqua per Plant

Siliqua length showed highly significant and positive interaction with plant height (r_g=0.272**, r_p=0.215*), root length (r_g=0.110, r_p=0.328**), shoot length (r_g=0.288**, r_p=0.164), seed per plant (r_g=0.358**, r_p=0.369**) indicated that if siliqua length increased then number of seeds per plant ,seed yield per plant and thousand seed weight would also increase. Supported results were found from the findings of Alam (2010). Whereas the insignificant and negative interaction was found in primary branches (r_g=-0.356**, r_p=0.007), thousand seed weight (r_g=-0.315**, r_p=-0.141) (Table 5). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Tyagi *et al.* (1996) reported that no. of seed per siliqua had positive and insignificant effect on seed yield per plant.

4.2.9 Siliqua Length (cm)

Siliqua length showed significant and positive correlation with seed per plant (r_g=0.677**, r_p=0.444**), plant height (r_g=0.272**, r_p=0.215*), root length (r_g=0.110, r_p=0.328**), shoot length (r_g=0.288**, r_p=0.164) indicated that the traits were governed by same gene and simultaneous improvement would be effective. Primary branches (r_g=-0.356**, r_p=0.007), thousand seed weight (r_g=-0.315**, r_p=-0.141) (Table 5) showed significant and negative correlation. Nasim *et al.* (1994) reported that seed yield per plant was significantly and negatively with siliqua length.

4.2.10 Number of Seeds per Siliqua

Number of seeds per siliqua showed highly significant and positive interaction with siliqua length (r_g=0.677**, r_p=0.444**) (table 5).That means the number of seeds per siliqua will increase if the siliqua length increases. Highly significant positive associations between number of seeds per siliqua and seed length indicated that the traits were governed by same gene and simultaneous improvement would be effective. It had significant and negative interaction with total siliqua (r_g=-0.244**, r_p=-0.128), thousand seed weight (r_g=-0.315**, r_p=-0.141). Insignificant association of these traits indicated that the association

between these traits largely influenced by environmental factors. Nasim *et al.* (1994) reported that no. of seeds per siliqua had negative and significant effects on seed yield per plant. Ahmed (1993) also found similar results for this trait.

4.2.11 Thousand Seed Weight

Thousand seed weight showed significant and positive interaction with primary branches (r_g=0.395**=, r_p=0.050), secondary branches (r_g=0.200*, r_p=0.167). It also revealed that insignificant and negative interaction with yield per plant (r_g=-0.135, r_p=-0.050) (Table 5). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Saini and Kumar (1995), Kakroo and Kumar (1991) and Olsson (1990) found positive associations which support the results. Tuncturk and Ciftci (2007) reported positive correlation between seed yield with 1000-seed weight which does not support the present findings.

4.2.12 Seed Yield per Plant (g)

Seed yield per plant had highest significant negative correlation with days to 50% flowering (r_g=0.469**, r_p=0.278**), days to maturity (r_g=0.241**, r_p=0.114), primary branches (r_g=0.388**, r_p=0.383**), total siliqua (r_g=0.358**, r_p=0.369**) (Table 5) at both phenotypic and genotypic level suggesting, if the number of primary branches per plant, number of secondary branches per plant and number of siliqua per plant increases then seed yield per plant will also increase. This trait had also negative significant correlation with root length (r_g=-0.345**, r_p=-0.106). Kumar *et al*. (1999) reported that seed yield had positive correlation with plant height, number of siliqua per plant and thousand seed weight. Jeromel *et al*. (2007) found complete positive correlation between plant height and yield. Siddikee (2006) revealed that yield per plant had highest significant positive correlation with number of siliqua per plant. Srivastava and Singh (2002) revealed that number of primary branches per plant and number of secondary branches per plant were positively associated with seed yield.

4.3 Path Co-efficient Analysis

Seed yield is the ultimate product of several yield contributing characters. The direct and indirect effects of yield contributing characters on seed yield were done by using path analysis. Seed yield being the complex outcome of different characters was considered as the resultant variable and other characters as causal variable. Here seed yield per plant was considered as effect (dependent variable) and days to 50% flowering, days to Maturity, plant height, siliqua length, number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua, number of siliqua per plant and 1000-seed weight were treated as causes or independent variables. Estimation of direct and indirect effect of path co-efficient analysis for *Brassica napus* is presented in Table 6.

4.3.1. Days to 50% Flowering

Path co-efficient analysis described that, days to 50% flowering had a positive direct effect (0.286) on yield per plant. This trait showed indirect positive effect on days to maturity (0.090), shoot length (0.039), primary branches (0.088), total siliqua (0.049) and siliqua length (0.010). On the other hand it had a negative indirect effect on number of secondary branches (-0.022) plant height (-0.009), finally it made positive correlation with seed yield (0.469) (Table 6). Chauhan and Singh (1995) revealed that days to 50% flowering had positive direct effect on yield per plant. Afrin *et al.* (2011) observed that days to 50% flowering had negative direct effect on seed yield per plant.

4.3.2. Days to Maturity

The relationship between days to maturity and seed yield per plant as genotypic coefficient of correlation was (0.248). However, its direct effect was low and positive (0.102) (Table 6). It had indirect and positive effect in root length (0.087), siliqua length (0.018), secondary branches (0.053) and seeds per siliqua (0.01). Alam (2010), Ali *et al.* (2003) and Han (1990) also reported direct positive result for this character

4.3.3. Plant Height (cm)

The relationship between number of plant height and seed yield per plant as genotypic coefficient of correlation was (-0.128). However, its direct effect was low and positive (0.069). It was indirect and positive effect in most of the characters with secondary branches (0.053), siliqua length (0.018), seed per siliqua (0.01), and root length (0.087) (Table 6). Alam (2010), Ali *et al*. (2003) and Han (1990) also reported direct positive result for this character.

4.3.4 Root Length (cm)

The relationship between number of plant height and seed yield per plant as genotypic coefficient of correlation was negative (-0.345). However, its direct effect was low and positive **(**0.164). It had indirect and positive effect in plant height (0.037), secondary branches (0.016) and siliqua length (0.007) (Table 6).

4.3.5 Shoot Length (cm)

The relationship between number of plant height and seed yield per plant as genotypic coefficient of correlation (-0.141). However, its direct effect was low and negative (-0.083). It was indirect and positive effect in plant height (0.070), root length (0.074), secondary branches (0.052), total siliqua (0.124) and siliqua length (0.019) (Table 6).

4.3.6 Number of Primary Branches per Plant

Number of primary branches per plant had the positive direct effect on yield per plant (0.375). This trait had positive indirect effect on days to 50% flowering (0.013), total siliqua (0.079), thousand seed weight (0.03). Number of primary branches per plant finally made positive and significant genotypic correlation with seed yield (0.388) (Table 6). It indicated that indirect selection through another such trait will be a good decision for yield improvement. Basalma (2008) and Rashid (2007) observed that primary branching had the direct negative effect on seed yield

4.3.7 Number of Secondary Branches per Plant

Number of secondary branches per plant showed negative direct effect (-0.130) on seed yield per plant. It had positive indirect effect on days to 50% flowering (0.049), primary branches (0.148), total siliqua (0.079), and thousand seed weight (0.02). On the other hand, it had negative effect on days to maturity (-0.005), siliqua length (-0.006). Number of primary branches per plant finally made positive and significant correlation with seed yield (0.142) (Table 6). Yadava *et al.* (1996) found the number of secondary branch had the highest positive direct effect on seed yield.

4.3.8 Siliqua Length (cm)

Estimated correlation coefficient at genotypic level between siliqua length and seed yield per plant was significantly negative (-0.014). Its direct effect to seed yield per plant was positive (0.067). It had indirect and positive effect on days to 50% flowering (0.044), days to maturity (0.020), plant height (0.019), number of secondary branches (0.012), and total siliqua (0.020). On the other hand, primary branches (-0.134), seeds per siliqua (-0.03), thousand seed weight (-0.03) showed indirect negative effect on length of siliqua (Table 6). Hence, selection should be practiced for this trait which had longer siliqua in order to improve seed yield. Han (1990) reported that siliqua length had negative direct effect on yield per plant.

4.3.9 Number of Siliqua per Plant

Path co-efficient analysis revealed that number of siliqua per plant had the positive direct effect (0.383) on seed yield. Positive indirect effect found on days to 50% flowering (0.037), days to maturity (0.001), number of primary branches (0.078), siliqua length (0.004), seeds per siliqua (0.01) (Table 6). Finally this trait had significant positive genotypic correlation (0.358) with yield per plant. These results indicated that correlation was mainly due to the direct effect of a character and it was realized via indirect positive and negative effects.

Table 6. Partitioning of genotypic correlation into direct (bold) and indirect effects of eleven traits by path analysis of mustard

	D50%F	DM	PH	RL	SL	PB	SB	TP	PL	SPP	TSW	Genotypic Correlation with FYP
D50%F	**0.286**	0.090	-0.009	-0.056	0.039	0.088	-0.022	0.049	0.010	-0.01	0.00	0.469
DM	0.121	**0.212**	-0.005	-0.030	0.009	-0.051	0.003	0.001	0.006	0.01	-0.03	0.241
PH	-0.036	-0.017	**0.069**	0.087	-0.084	-0.186	0.053	-0.012	0.018	0.01	-0.03	-0.128
RL	-0.097	-0.038	0.037	**0.164**	-0.037	-0.174	0.016	-0.219	0.007	0.00	-0.01	-0.345
SL	-0.133	-0.022	0.070	0.074	**-0.083**	-0.200	0.052	0.124	0.019	0.00	-0.04	-0.141
PB	0.067	-0.029	-0.034	-0.076	0.044	**0.375**	-0.051	0.079	-0.024	0.00	0.03	0.388
SB	0.049	-0.005	-0.028	-0.021	0.033	0.148	**-0.130**	0.079	-0.006	0.01	0.02	0.142
TP	0.037	0.001	-0.002	-0.094	-0.027	0.078	-0.027	**0.383**	0.004	0.01	-0.01	0.358
PL	0.044	0.020	0.019	0.018	-0.024	-0.134	0.012	0.020	**0.067**	-0.03	-0.03	-0.014
SPP	0.05	-0.03	-0.01	-0.01	0.00	-0.04	0.02	-0.09	0.05	**-0.046**	-0.02	-0.135
TSW	0.01	-0.08	-0.02	-0.01	0.04	0.15	-0.03	-0.02	-0.02	0.01	**0.082**	0.112

Residual effect: 0.325 ** = Significant at 1%. * = Significant at 5%.

D50%F: days to 50% flowering, DM: days to maturity, PH: plant height (cm), RL: root length (cm), SL: shoot length (cm), PB: primary branches of plant, SB: secondary branches per plant, TP: total pods per plant, PL: pod length (cm), SPP: seeds per pod, TSW: 1000 seed weight (g) and SYPP: seed yield per plant (g).

It revealed that true relationship between them and direct selection for this trait will be rewarding for yield improvement. Sharafi *et al*. (2015) found the number of siliqua per plant had the highest direct effect on seed yield.

4.3.10 Number of Seeds per Siliqua

Path analysis revealed that number of seeds per siliqua had direct negative effect (-0.046) on yield per plant (Table 6). This trait had also indirect positive effect on days to 50% flowering (0.05), secondary branches (0.02), and siliqua length (0.05). Lastly, this trait had highly significant negative genotypic correlation (-0.135) with yield per plant (Table 6). Sharafi *et al*. (2015) and Rashid (2007) reported that number of seeds per siliqua had direct positive effect on yield per plant. But Basalma (2008) reported that seeds per siliqua had negative direct effect on seed yield per plant.

4.3.11 Thousand Seed Weight

Correlation coefficient at genotypic level between thousand seed weight and seed yield per plant was positive (0.112). Its direct effect to seed yield per plant was positive (0.082). It had also positive indirect effect on days to 50% flowering (0.01), number of primary branches (0.15), and number of seed per siliqua (0.01). Sharafi *et al*. (2015) and Siddikee (2006) reported that thousand seed weight had the highest positive direct effect on seed yield per plant. But Alam (2010) reported that thousand seed weight had direct negative effect on yield per plant.

The value of residual effect was 0.325 (Table 6)**.** It indicated that beside the characters studied, there were some other attributes (approx. 21.1%) which contributed for yield.

4.4 Genetic Diversity Analysis

4.4.1 Principal Component Analysis (PCA)

The analysis of variance showed significant differences among the genotypes for all the 12 characters under study revealing the presence of notable genetic variability among the genotypes. Principal component analysis was carried out with 38 genotypes of *Brassica napus*. The computed Eigen values for the 12

variables subjected to principal component analysis (PCA) together with the corresponding proportion and cumulative explained variance are given in Table 8. Following the proportion of variance criterion, two principal components were retained and these are the principal components whose cumulative explained variances were equal to or more than 99%. The PCA gives Eigen values of principal component axes of coordination of genotypes with the first axes totally accounted for the variation among the genotypes (22.74). These three principal components account for 50.44% of the total variation (Table 8). Zaman *et al*. (2010) reported that first three axes accounted for 94.00% of the total variation whereas the first principal components accounted for 81.94%. Khan (2014) reported that the contribution of first three PCs in overall PCs was 26.96%.

4.4.2 Non-Hierarchical Clustering

Thirty eight genotypes were grouped into six clusters through non-hierarchical clustering (Table 9). Most of the genotypes (11) were grouped into cluster VI. They were G3, G5, G11, G13, G14, G18, G21, G28, G34, G37, G38 followed by cluster III (7) G1, G4, G6, G8, G17, G19, G24 and cluster V (7) G16, G23, G26, G27, G29,G33, G36. Five genotypes were grouped into cluster II (G2, G9, G10, G12, G25 and G30) and cluster IV (G7, G15, G20, G22, G32 and G35). G38 alone was in cluster I. Rameeh (2015) reported three clusters, Iqbal *et al.* (2014) reported four clusters and Begum *et al*. (2007) reported five clusters in linseed.

Table 7. Eigen Values and Yield Percent Contribution of 12 Characters in 38 Genotypes

Principal component axes	Eigen values	Percent variation	Cumulative % of Percent variation
I	2.729	22.74	22.74
II	1.739	14.49	37.23
III	1.586	13.21	50.44
IV	1.339	11.16	61.6
V	1.070	8.91	70.51
VI	0.907	7.56	78.07
VII	0.791	6.59	84.66
VIII	0.537	4.47	89.13
IX	0.453	3.77	92.9
X	0.382	3.18	96.08
XI	0.257	2.14	98.22
XII	0.212	1.78	100

Table 8. Distribution of 38 genotypes in different clusters

Cluster No.	Genotypes	No. of populations	Percent
I	G31	1	2.63
II	G2, G9, G10, G12, G25, G30	6	15.79
III	G1, G4, G6, G8, G17, G19, G24	7	18.42
IV	G7, G15, G20, G22, G32, G35	6	15.79
V	G16, G23, G26, G27, G29,G33, G36	7	18.42
VI	G3, G5, G11, G13, G14, G18, G21, G28, G34, G37, G38	11	28.95

4.4.3 Cluster Mean

The genotypes from cluster I earned the lowest cluster mean value for days to 50% flowering (31.00*) and highest cluster mean value for plant height (112.86**), total siliqua per plant (156.47**), siliqua length (8.58**) (Table 9). Thus indicates that genotype of this cluster could be used for parent in future hybridization program for early flowering and higher siliqua number. On the other hand cluster II produced highest primary branches (3.16**), secondary branches (2.76**), thousand seed weight (4.33**), seed yield per plant (7.50**) and lowest number of seeds per siliqua (24.42*). Thus indicates that genotype of this cluster could be used for parent in future hybridization program for primary branches, secondary branches and seed yield. Cluster III earned the lowest value of days to maturity (97.33*) that indicate the genotype of this cluster could be used for future hybridization program for early maturity plant. Cluster IV produced the lowest number of siliqua per plant (78.28*) can be selected for lower number of siliqua. Cluster V gave the highest days to 50% flowering (34.05**), days to maturity (100.05**) and seeds per siliqua (26.26**) indicating the genotype of this cluster could be used for future hybridization program for seeds per siliqua. Zaman *et al.* (2010) reported that the highest cluster means for primary branches per plant and maximum seeds per siliqua with minimum seed yield per plant were obtained from the cluster.

4.4.3.1 Cluster Distance

The highest inter-cluster distance was found between clusters I and IV (34.61) followed by between cluster IV and I (34.61), V and I (34.39), VI and I (31.62) and II and I (31.60).

Table 9. Cluster mean for 12 yield and yield related characters in 38 mustard genotypes

Characters	I	II	III	IV	V	VI
Days to 50% flowering	31.00*	33.89	33.43	32.83	34.05**	33.15
Days of maturity	99.67	99.22	97.33*	97.56	100.05**	99.61
Plant height (cm)	112.86**	100.80	107.53	102.40	98.88*	111.76
Root length (cm)	10.49	9.01*	10.03	10.45	10.55	11.11**
Shoot length (cm)	194.95**	108.90	118.16	113.80	107.67*	123.67
Primary branch per plant	2.50*	3.16**	2.81	2.71	2.93	2.84
Secondary branch per plant	2.00*	2.76**	2.68	2.16	2.41	2.66
Total pods per plant	156.47**	150.48	129.34	78.28*	98.11	103.38
Pod length (cm)	8.58**	8.22	8.04*	8.12	8.19	8.32
Seeds per pod	25.77	24.42*	24.94	25.61	26.26**	24.75
1000 seeds weight (g)	4.00*	4.33**	4.33**	4.28	4.28	4.27
Seed yield per plant(g)	6.30	7.50**	7.46	6.03*	6.66	6.72

* Lower value

** Higher value

The higher inter-cluster distances between these clusters indicate to obtain wide spectrum variability of population. However, the highest inter cluster distance was observed between clusters I and IV indicated the genotypes in these clusters were diverse than those clusters. The greater the distance between two clusters the greater the divergence (Table 11). The minimum distance observed between clusters III and I (30.65) indicated close relationship among the genotypes included and genotypes in these clusters were less diverse than others.

4.4.3.2 Intra Cluster Distance

The intra cluster D^2 values were given in Table 10. The intra cluster distance was observed in the clusters. The intra cluster distance was higher in cluster II (1.22) and lowest in cluster I (0.00) (Table 10). The intra cluster distances in all the six clusters were lower than the inter cluster distances and which indicated that genotypes within the same cluster were closely related. The inter cluster distances were larger than the intra cluster distances which indicated wider genetic diversity among the genotypes of different groups. It is assumed that the maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. Furthermore, for a practical plant breeder, the objective is to achieve high-level 81 production in addition to high heterosis. In the present study the maximum distance existence between cluster I and IV (34.61) (Table 10). Pandey *et al*. (2013) found maximum inter-cluster distance was found between cluster II and III indicating high genetic divergence among genotypes of these groups. Zaman *et al.* (2010) reported that the genotypes from cluster I and III could be utilized in the hybridization program for getting desirable transgressive segregants and high heterotic response due to getting maximum yield along with short duration. Keeping this

Table 10. Intra (Bold) and inter cluster distances (D^2) for 38 genotypes

Cluster	I	II	III	IV	V	VI
I	**0.00**	31.60	30.65	34.61	34.39	31.62
II		**1.22**	3.81	11.01	8.44	7.37
III			**0.32**	8.27	6.20	4.17
IV				**0.95**	3.20	4.95
V					**2.33**	3.96
VI						**0.65**

Table 11. The nearest and farthest clusters from each cluster between D^2 values in mustard

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	I	III (30.65)	IV (34.61)
2	II	III (3.81)	I (31.60)
3	III	II (3.81)	I (30.65)
4	IV	V (3.20)	I (34.61)
5	V	IV (3.20)	I (34.39)
6	VI	V (3.96)	I (31.62)

4.4.4 Contribution of Traits towards Divergence of the Genotype

The latent vectors (Z1 and Z2) obtained from principal component analysis (PCA). The important characters responsible for genetic divergence in the axis of differentiation in vector I (Z1) were days to 50% flowering (0.0438), plant height (0.2199), siliqua length (0.8070), seed yield per plant (0.0308) and lastly in vector II Days of maturity (0.0485), primary branches (0.4871), secondary branches (0.0961), total siliqua per plant (0.1185), seeds per plant (0.0258) and 1000 seed weight (0.2179) (Table 12.). The characters contributing the most to the divergence are given greater importance when deciding on the cluster for the purpose of further selection and choice of parents for hybridization. The role of plant height and number of primary branches in both the vectors were important components for genetic divergence in these materials. Islam and Islam (2000) reported days to 50% flowering, plant height, primary branches per plant and number of siliqua per plant contribute maximum in divergence in rapeseed and mustard. Begum *et al.* (2007) reported that branches per plant and number of number of seeds siliqua contributed the maximum towards divergence in the existing linseed germplasm.

Table 12. Relative contributions of the twelve characters of 38 genotypes to the total divergence

Characters	Principal Component	
	Vector-1	Vector-2
Days to 50% flowering	0.0438	-0.1427
Days to maturity	-0.0647	0.0485
Plant height (cm)	0.2199	0.1745
Root length (cm)	0.3850	-0.3124
Shoot length (cm)	-0.3700	-0.1672
Primary branch per plant	0.1528	0.4871
Secondary branch per plant	-0.3375	0.0961
Total pods per plant	-0.0895	0.1185
Pod length (cm)	0.8070	-0.2021
Seeds per pod	-0.2799	0.0258
1000 seeds weight (g)	-0.2141	0.2179
Seed yield per plant(g)	0.0308	-0.0622

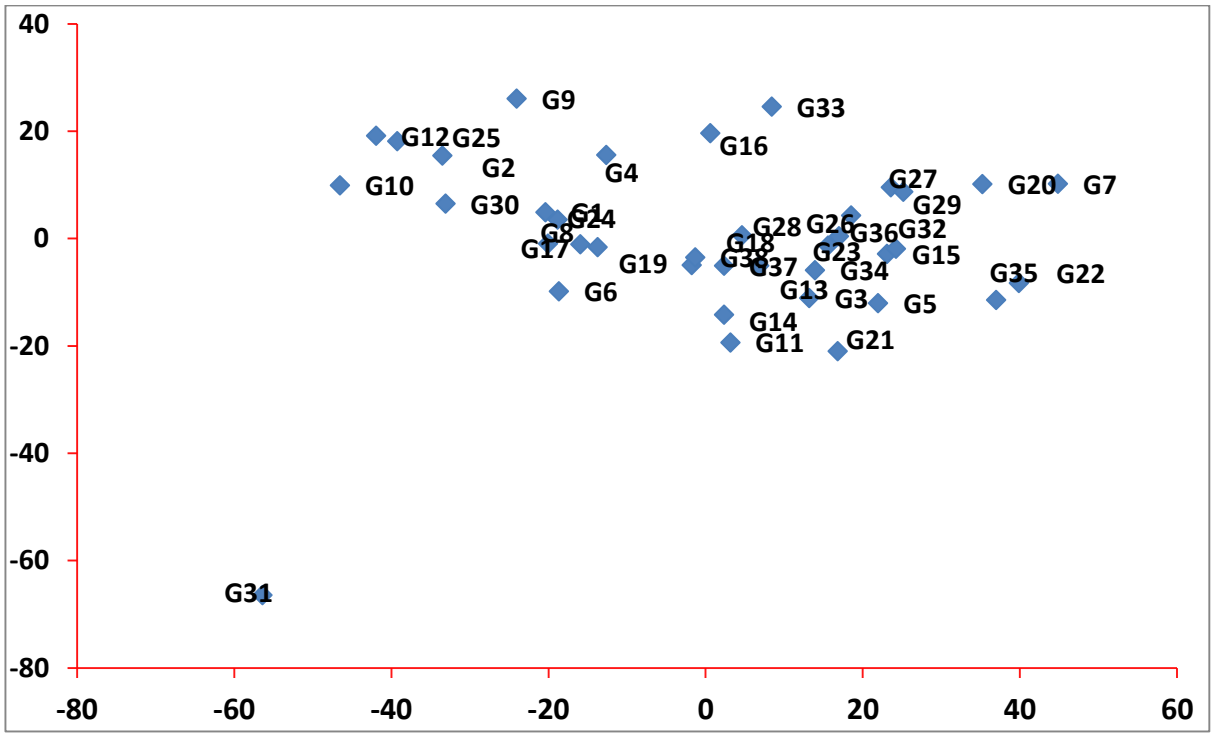


Figure 12. Scatter pattern of *Brassica napus* populations based on their principal component scores

4.4.5 Cluster Diagram

The position or the genotypes in the scatter diagram were apparently distributed into six groups, which indicated that considerable diversity existed among the genotypes (Figure 13).

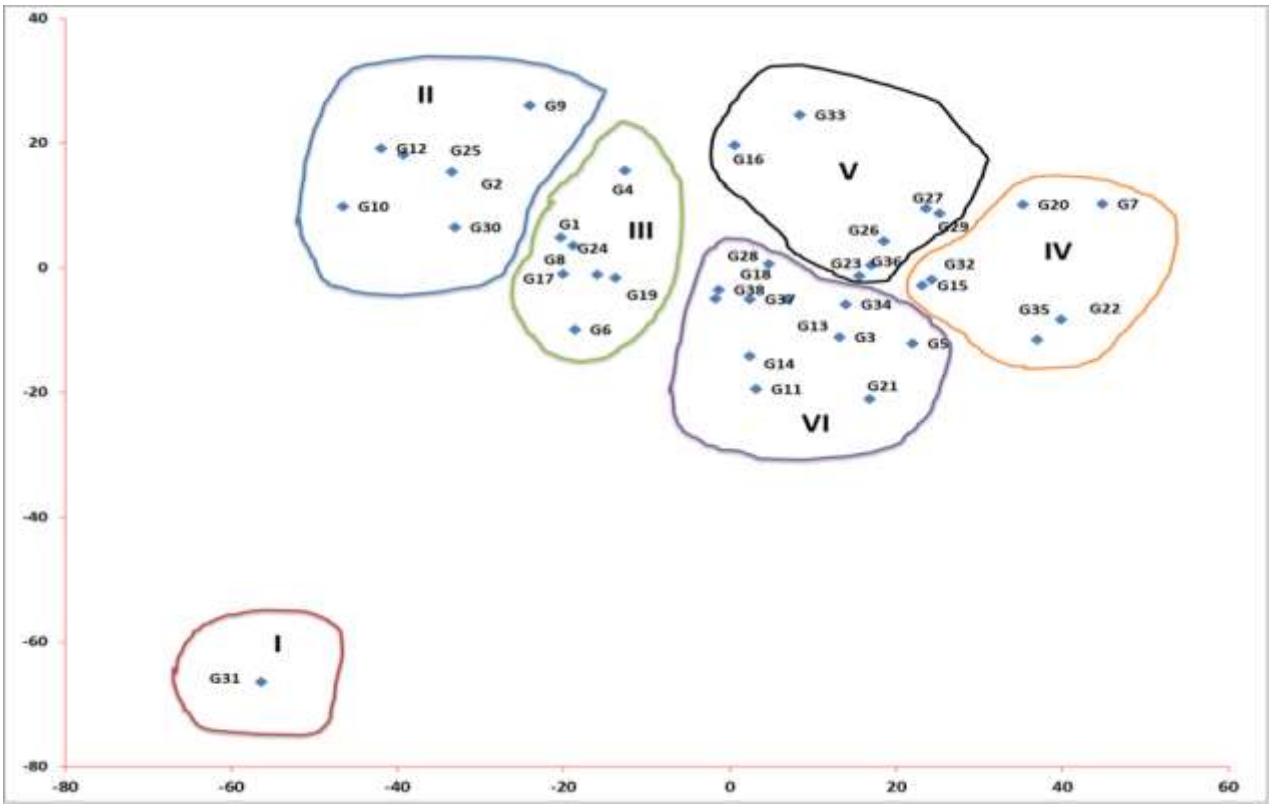


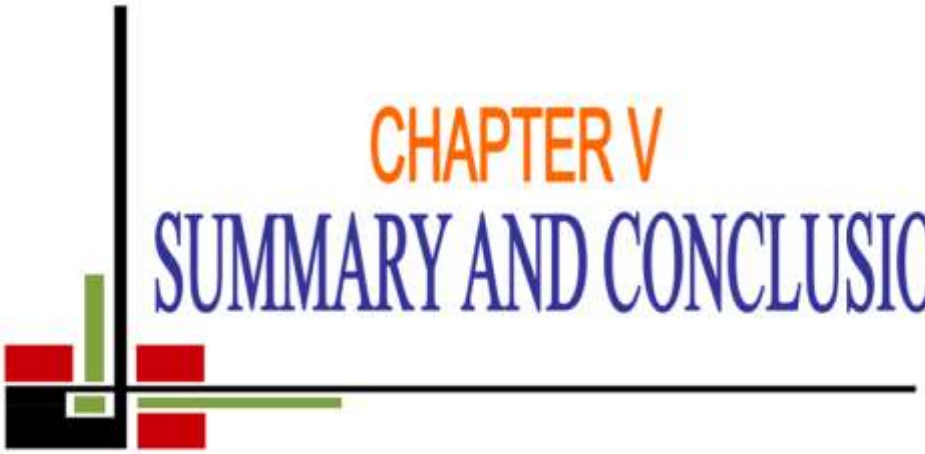
Figure 13. Scatter diagram of *Brassica napus* populations based on their principal component scoress

4.4.6 Selection of Genotypes

Considering the cluster analysis (Table 12) Cluster I genotypes exposed higher plant height, shoot length, total siliqua per plant and siliqua length. Cluster II possess primary branches per plant, secondary branches per plant, 1000 seeds weight and seed yield per plant. Under cluster III genotypes possessed early maturity, lower siliqua length. Less number of siliqua per plant and ultimate lower yield were observed under genotypes of cluster IV. Early flowering, late maturity, highest Plant height, more seeds per siliqua were expressed in cluster V. Highest root length was observed in cluster VI. On the basis of diversity pattern and agronomic performance genotypes G31 were selected from cluster I. The genotype G9 and G30 were selected from cluster II. The genotype selected from cluster III was G8. G32 was selected from cluster IV.G16, G23, G29 were selected from cluster V. G37 was selected from cluster VI. It will produce more diverse line for future early variety release. Among these cultivars, the superior genotypes may be used in future breeding program to develop short duration cultivar of mustard. This variability may be used for the selection of superior and short duration populations for commercial cultivation at farmer's level.

Table 13. Salient features of genotypes in six different clusters

Cluster	Salient feature
I	Higher plant height Higher shoot length More siliqua per plant and Higher siliqua length
II	High Primary branch per plant, Higher Secondary branch per plant, High 1000 seeds weight and More Seed yield per plant
III	Early maturity, Lower siliqua length.
IV	Less number of siliqua per plant and Lower yield
V	Early flowering, Late maturity, Highest Plant height, More seeds per siliqua
VI	Highest root length



CHAPTER V
SUMMARY AND CONCLUSION

CHAPTER V

SUMMARY AND CONCLUSION

The present investigation was carried out to study genetic variability, character association, and path analysis and to assess the selection of superior genotypes from 38 *Brassica napus* L. genotypes through study the genetic variation and morphological diversity among the genotypes for improvement of yield. The experiments were carried out at the experimental Farm of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh during the period from November 2018 to February 2019. The experiment was laid out in Randomized Complete Block Design (RCBD) with 3 replications. The data was recorded on seed yield per plant and various other morphological traits viz. days to 50% flowering, days to maturity, plant height, root length, shoot length, primary branches per plant, secondary branches per plant, siliqua per plant, siliqua length, seeds per siliqua, 1000 seed weight and seed yield per plant. Analysis of variance showed significant differences for the genotypes. On different morphological characters were recorded time to time and analysed statistically. The results of the studies have been summarized as follows:

The analysis of variance showed significant differences for the genotypes. From variability analysis of different progenies, it was observed that significant variation exist for characters like days of flowering, days to maturity, plant height, siliqua length, number of seed per siliqua and seed yield per plant. The genotype G11 and G33 exhibited highest and lowest plant height, respectively. The highest number of primary branches per plant was recorded in G9 and lowest number was recorded in G37. The maximum number of secondary branches per plant was observed in in G4 and minimum in G22. The minimum days to 50%

flowering was found in G22 whereas highest in G4. The lowest days to maturity was also observed in G11 and the highest in G5. The number of siliqua per plant showed the highest in G10 and lowest in G7. The highest siliqua length was recorded in G18 and the lowest in G5. The number of seeds per siliqua was found highest in G22 and the lowest in G5. The highest amount of thousand seed weight was found in G8, G9, and G34 and the lowest in G4. The seed yield per plant was the highest in G15 and the lowest observed in G23.

However, the genotypic variance and genotype coefficient of variation were lower than the corresponding phenotypic variance and phenotypic coefficient of variation for all the characters under study. Phenotypic coefficients of variation were close to genotypic coefficients of variation for most of the characters except primary branches, secondary branches, siliqua length and 1000 seed weight. On the other hand, days to 50% flowering, days of maturity, plant height, seeds per siliqua showed least difference between phenotypic and genotypic variance suggesting that environmental effect had a huge role for the expression of the characters. PCV ranged from 4.71 % for Days to maturity to 34.77% for secondary branches per plant and GCV from 3.96 % (days to maturity) to 27.20% (secondary branches). . The Maximum PCV and GCV were recorded for number of secondary branches per plant (34.77% and 27.20%). Higher PCV and GCV were recorded for seed yield per plant (22.20% and 18.27%), total siliqua per plant (26.20% and 20.65).

Days to maturity (70.73) exhibited the maximum value of heritability while1000 seed weight (12.49) exhibited the minimum value of heritability. High heritability was observed in days to 50% flowering (62.99), days of maturity (70.73), plant height (63.47), secondary branches per plant (61.19), total siliqua per plant (62.12), and seeds per siliqua (61.61) and seed yield per plant (67.69). The genetic advance in root length, shoot length, primary branches per plant, siliqua length, 1000 seeds weight were 31.48, 18.04, 25.26, 27.66, 12.49. High

heritability with high genetic advance as percent of mean was noticed for secondary branches per plant (43.83), total siliqua per plant (33.52), seed yield per plant (30.96) indicating that these traits were under additive gene control and selection for genetic improvement for these traits would be effective and beneficial.

Correlation coefficients among the characters were studied to determine the association between yield and yield contributing characters. In general, most of the characters showed the genotypic correlation co-efficient were lower than the corresponding phenotypic correlation co-efficient which suggested suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values. In most cases, phenotypic correlation co-efficient were higher than their corresponding genotypic correlation co-efficient suggesting that both environmental and genotypic correlation in these cases act in the same direction and finally maximize their expression at phenotypic level. The significant positive correlation with seed yield per plant were found in days of 50% flowering (0.469^{**} and 0.278^{**}), days to maturity (0.241^{**} and 0.114), number of primary branches (0.388^{**} and 0.383^{**}) and total siliqua (0.358^{**} and 0.369^{**}). Significant and negative correlation with seed yield per plant were root length (-0.345^{**} and -0.106). Insignificant but positive interaction was found for secondary branches (0.142 and 0.131), 1000 seed weight (0.112 and 0.113).

Path co-efficient analysis revealed that days to 50% flowering, days to maturity, plant height, root length, total siliqua per plant, siliqua length had the positive direct effect on yield per plant whereas shoot length, secondary branches per plant, seeds per siliqua had the negative direct effect on yield per plant. The genotypic correlation with seed yield per plant was positive and considerably higher in magnitude in days to 50% flowering, days to maturity, primary branches per plant, secondary branches per plant, total siliqua per plant and 1000

seed weight and negative for plant height, root length, shoot length, siliqua length, seeds per siliqua. It is mainly due to high positive direct effect and positive indirect effects via the other characters and selection would be effective for these characters. The path coefficient studies indicated that days to 50% flowering, days to maturity, primary branches of plant, secondary branches per plant, total siliqua per plant and 1000 seed weight were the most important contributors to seed yield per plant which could be taken in consideration for future hybridization program.

Genetic diversity among *Brassica napus* genotypes was performed through Principal Component Analysis (PCA), Cluster Analysis and Canonical Variate Analysis (CVA). The 38 genotypes fell into six distant clusters. The cluster VI comprised the maximum number (11) of genotypes followed by same in cluster III and V (7). The cluster II and IV comprised 6 genotypes. The lowest number of genotypes was present in cluster I (1). The highest inter-cluster distance was observed between the clusters I and III (34.61), if involved in hybridization may produce a wide spectrum of segregating population. The lowest inter-cluster distance was observed between clusters IV and V (3.20).

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

CONCLUSION

Considering the cluster analysis (Table 14) Cluster I genotypes exposed higher plant height, shoot length, total siliqua per plant and siliqua length. Cluster II possess primary branches per plant, Secondary branches per plant, 1000 seeds weight and Seed yield per plant. Under cluster III genotypes possessed early maturity, lower siliqua length. Less number of siliqua per plant and ultimate lower yield were observed under genotypes of cluster IV. Early flowering, late maturity, highest Plant height, more seeds per siliqua were expressed in cluster V. Highest root length was observed in cluster VI. On the basis of diversity pattern and agronomic performance genotypes G31 (Nap9905 x Nap2001) are selected from cluster I. The genotype G9 (Nap108 x Nap206) and G30 (Nap248 x Nap2012) are selected from cluster II. The genotypes selected from cluster III are G8 (Nap248 x Nap0130). G32 (Nap205 x Nap179) is selected from cluster IV.G16 (Nap248 x Nap9901), G23 (Nap9908 x Nap0130), G29 (Nap9905 x Nap2037) are selected from cluster V.G37 (B-13 x Nap2037) is selected from cluster VI. It will produce more diverse line for future early variety release. Among these cultivars, the superior populations may be used in future breeding program to develop short duration populations for commercial cultivation at farmer's level.


REFERENCES

REFERENCES

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

Afrin, K. S., Mahmud, F., Bhuiyan, M. S. R. and Rahim, M. A. (2011). Assessment of genetic variation among advanced lines of *Brassica napus* L. *Agronomski Glasnik.* **73**(4-5): 201-226.

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

Ahmed, M.R. (1993). Study of agronomic value of resynthesized rapeseed lines and early generations of crosses "rsyn-lines x improved varieties". *Iranian J. Agril. Sci*. **24**(3/4):1-13.

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, Dept. of Genetics and Plant Breeding, SAU, Dhaka

Ali N., Javidfar, F. and Attary, A. A. (2002). Genetic variability, correlation and path analysis of yield and its components in winter rape seed (*Brassica napus* L.). *Pakistan. J. Bot*. **34**: 145-150.

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.

Allard, R.W. (1960). Principles of Plant Breeding. John Willey and Sons. Inc. New York. pp. s36.

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.

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 studies in mustard. Marathwada Agricultural University. *Indian J. Maharashtra. Agril. Univ.* **20**(2): 237-239

Aunwinithul, Patil, S., Charjan, S. U., Thakare, P. G. and Wankhade, M. (2004). Genetic divergence studies in Indian mustard. *Soil Crops*. **14**(2): 297-304.

Aytac, Z. and Kinaci, G. (2009). Genetic variability and association studies of some quantitative characters in winter rape seed (*Brassica napus* L.). *African J. Biotech*. **8**(15): 3547-3554.

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.

Baradaran, R., Majidi, E., Dervish, F. and Azizi, M. (2007). Study of correlation relationships and path coefficient analysis between yield and yield components in rapeseed (*Brassie napus* L.). Birjand unit, IAA. University, Birjand, *Fram. J. Agril. Sci. Islamic Azad Univ*. **12**(4): 811-819.

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. (2013). Hand book of Agricultural Statistics, December (2010). Bangladesh Bureau of Statistics (BBS), Ministry of Planning Govt. People's Republic Bangladesh.p. 14.

BBS. (2017). Hand book of Agricultural Statistics, December (2010). Bangladesh Bureau of Statistics (BBS), Ministry of Planning Govt. People's Republic Bangladesh.p. 14.

Begum, H., Alam, A. K. M. M., Chowdhury, M. J. A. and Hossain, M. I. (2007).Genetic Divergence in Linseed (*Linun usitatissimum* L.). *Int. J. Sustain. Crop Prod*. **2**(1): 04-06.

Belete, Y.S., Yohannes, M.T.W. and Wami, T.D. (2012). Analysis of genetic parameters for some agronomic traits of introduced Ethiopian Mustard (*Brassica carinata* A. Brun) Genotypes. *Int. J. Agric. Res*.**7**: 160-165.

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.

Burton, G. W. (1952). Quantitative inheritance in grasses. pp. 277-283. Proceeding 6th International Grassland Congress, Pennsylvania.17-23 August. Pennsylvania State College, State College, Pennsylvania, USA.

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

Chaturvedi, G.S., Singh, B.B. and Chauhan. Y.S. (1988). Physiological analysis of yield in Indian mustard under irrigated condition. *Indian J. Plant Physiology*. **31**(1): 38-44.

Chauhan, J. and Singh, P. (1995). Association of some morpho-physiological determinants with seed yield in toria (*Brassica campestris* L var. toria). *Thesis Abst.* **XI-1**: 42-43.

Chay, P. and Thurling, N. (1989). Identification of Genus controlling siliqua length in spring rapeseed and their utilization for yield improvement. *Pl. Breed.* **103**(1): 54-62.

Choudhary, B. D., Singh, P., Singh, D. P. and Pannu, R. K. (2003). Path analysis in Indian mustard. *Haryana J. Agron*. **9**(2): 161-166.

Choudhary, B.R. and Joshi, P. (2001). Genetic diversity in advanced derivatives of Brassica interspecific hybrids. *Euphytica*. **121**(1): 1-7.

Chowdhury, B.D., Thakural. S.K. Singh, D.P. and Singh, P. (1987). Genetics of yield and its components in Indian mustard. *Narenda Deva J. Agril. Res*. **3**(1): 3743

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

Dabholkar, A.R. (1992). Elements of biometrical genetics. Concept Publishing, New Delhi, India.

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.

Dhillon, S.S., Singh, K. and Brar, K.S. (1999), Diversity analysis of highly selected genotypes in Indian mustard. 10th International Rapeseed Congress, Canbera, Australia, 1999.

Digby, P. Galway, M. and Lane, P. (1989). GENSTAT^5. A second course. Oxford Science Publications, Oxford. pp. 103-108.

Ejaz-Ul-Hasan., Mustafa, H. S. B., Bibi. T. and Mahmood, T. (2014). Genetic variability, correlation and path analysis in advanced lines of rape

seed (*Brassica napus*) for yield components. *Cercetari Agronomice in Moldova*. *XL*. **1** (157).

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

FAO (Food and Agriculture Organization). (2012). Production Year Book. Food and Agriculture Organization of the United Nations, Rome. Italy.

Ghosh, S. K. and Gulati, S. C. (2001). Genetic variability and association of yield components in Indian mustard (*Brassica juncea* L.). *Crop Res. 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. Indian Ann. 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.

Gupta, M.L. Labana, K.S. and Badwal, S.S. (1987). Correlation and path coefficient of metric traits contributing towards oil yield in Indian mustard. International rape seed congress, Poznan, Poland, pp. 107.

Han, J.X. (1990). Genetic analysis of oil content in rape *Brassica napus*. *Oil Crops China.* **2**: 1-6.

Hasan, M., Seyis, F., Badani, A.G., Pons-Kühnemann, J., Friedt, W., Lühs, W., and Snowdon, R.J. (2006). Analysis of genetic diversity in the *Brassica napus* L. gene pool using SSR markers. *Genet. Resour. Crop.Evol*. **53**: 793-802.

Hosen, M. (2008). Variability, correlation and path analysis in F_3 materials of *Brassica rapa*. MS Thesis, Department of Genetic and Plant Breeding, SAU, Dhaka.

Iqbal S., Haque S., Nath U. K., and Hamim I. (2014). Genetic diversity analysis of mustard germplasm based on phenotypic traits for selection of short duration genotypes, *Int. J. Agric. Sci. Res*, **3**(8): 141-156.

Islam, M.S. and Islam, M.O. (2000). Genetic diversity in rapeseed and mustard (*Brassica* sp.). *Bangladesh J. Pl. Breed .Genet*. **13** (2): 25-30.

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

Jahan. N. (2008). Inter-genotypic variability and genetic diversity analysis in F4 lines of *Brassica rapa*. MS Thesis, Dept, of Genetics and Plant Breeding. SAU, Dhaka.

Jeromel, A.M., Marinkovi, R. Miji, A., Zduni, Z., Ivanovska, S. and Jankulovsk, M. (2008). Correlation and path analysis of quantitative traits in winter rapeseed (*Brassica napus* L.). *Agriculturae Conspectus Scientificus*. **73**(1): 13-18

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

Joshi, A. B., and Dhawan, N. L. (1966). Genetic improvement of yield with special reference to self-fertilizing crop. *Indian J. Genet. Pl. Breed*. **26**: 101-113.

Kachroo, P. and Kumar, S. (1991). Genetic determination of seed yield through its components in mustard (*Brassica juncea* L.). *Indian J. Genet. Plant Breed*. **17**(1): 82.

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.

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

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.s

Khan, M. H., Bhuiyan, S. R., Rashid, M.H., Ghosh, S. and Paul, S.K. (2013). Variability and heritability analysis in short duration and high *yielding Brassica rapa* L. *Bangladesh J. Agril. Res*. **38**(4): 647-657.

Khayat, M., Lack, S. H. and Karami, H. (2012). Correlation and path analysis of traits affecting grain yield of canola (*Brassica napus* L.) Varieties. *J. Basic. Appl. Sci. Res*. **2**(6): 5555-5562.

Khulbe, R.K. and Pant, D.P. (1999). 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 (*B. juncea*). *Indian J. Agric. Sci*. **66**(11): 14-17

Kumar, S., Snagwan, R. S. and Yadav, I. S. (2009). Correlations studies in *Brassica* species under dry land conditions. *Cruciferae Newsl*. **21**:151-152.

Kumar, V. and Singh, D. (1994). Genetics of yield and its components in Indian mustard (*Brassica juncea* L. Czern and Coss). *Crop Res*. **7**(2): 243-246.

Labana, K.S., Chaurasia, B.D. and Singh. B. (1980). Genetic variability and inter-character associations in the mutants of Indian mustard. *Indian J. Agric. Sci.* **50**(1): 803-806.

Lebowitz, R.J. (1989). Image analysis measurements of repeatability estimates of siliqua morphological traits in *Brassica campestris* L. *Euphytica*. **43**(1-2): 13116.

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

Lodhi, G.P., Singh. R.K. and Sharma, S.C. (1979). Correlated response in brown sarson. *Indian J. Genet*. **39**: 373-377.

Lush, J.L. 1949. Inter size correlation, regression of offspring on dams as a method of estimating heritability of characters. Proc. Amer. Soc. Anim. Prod., 33: 293-301.

Mahak, S., Singh, H. L. and Dixit, R. K. (2004). Studies on genetic variability, heritability, genetic advance and correlation in Indian mustard *(Brassica juncea* L. Czem and Coss). *Indian Pl. Arc*. **4**(2): 291-294.

Mahalanobis, P. C. (1936). On the generalized distance in statistics *Indian. Proc. Natl. Acad. Sa*. **12**: 49-55.

Mahmud, F., Rasul, M.G and Rahim, M.A. (2008). Genetic diversity analysis in some advanced lines of *Brasssica napus*. *Sci. Asia,* 3**4**:432-434.

Mahmud, M.A.A. (2008). Intergenotypic variability study in advanced lines of *Brassica rapa*. MS Thesis, Department of Genetics and Plant Breeding, SAU, Dhaka.

Malek, M.A., Das, M.L. and Rahman, A. (2000). Genetic variability, character association and path analysis in rapeseed. *Bangladesh J. Agric. Sci*. **27**(1): 25-59

Malik, M.A., Das. M.L. and Rahman, A. (2000). Genetic variability, character association and path analysis in rapeseed. *Bangladesh J. Agric. Sci*. **27**(1): 2559.

Malik, M.A., Khan, A.S., Shafiullah, Khan, M.A., Khan, B.R. and Mohamand, A.S. (2000). Study of correlation among morphological parameters in different varieties/accessions of Brassica species. *Pakistan J. Biol. Sci*. **3**(7): 1180-1182.

Masood, T., Gilani, M.M. and Khan, F.A. (1999). Path analysis of the major yield and quality characters in *Brassica campestris. J. Ani. P1. Sci*. **9**(4): 69-72.

Maurya, N., Singh, A. K. and Singh, S. K. (2012). Inter-relationship analysis of yield and yield components in Indian mustard, *Brassica juncea* L. *Indian J. Pl. 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* a. Brun) at Adet, Northwestern, Ethiopia. *J. Plant Sci*. **2**(2): 89-96.

Mukhtar M. S., Rahman, M. and Zafar, Y. (2002). Assessment of genetic diversity among wheat (*Triticum aestivum* L.) cultivars from a range of localities across Pakistan using random amplified polymorphic DNA (RAPD) analysis. *Euphytica*.**128**: 417-425.

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): 1523

Nath, U.K., Naz, S. and Rahman, M.M (2003). Genetic divergence of *Brassica campestris, Brassiac juncea* parents and their hybrids. Pakistan *J. Biol. Sci.* **6**(10): 936-938.

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

Pandey, R., Kumar, B. and Kumar, M. (2013). Genetic Divergence for Quantitative Traits in Indian mustard (*Brassica juncea* L. Czern & Coss). American Eurasian *J. 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.

Parveen, S. (2007). Variability study in F2 progenies of the inter-varietal crosses of *Brassica rapa*. MS thesis, Department of Genetics and Plant Breeding, Shere-e-Bangla Agricultural University, Dhaka

Peter, K. V. and Rai, B. (1995). Genetic divergence in rape seed. *Indian J.* **36**(3): 379- 383.

Poonam, S. and Singh, D. N. (2004). Path coefficient analysis in Indian mustard (*Brassica juncea* L.). *J. Res. Bisra Agric. Univ. Ranchi,* **16**(2): 293-295.

Rameeh, V. (2011). Correlation and path analysis in advanced lines of rape seed (*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).

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

Rao, C. R. (1952). Advance statistical method in biometrical research. Ednl John Willey and Sons, New York.

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

Rashid, M.H. (2007). Characterization and diversity analysis of the oleiferous *Brassica* species. MS thesis, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka.

Saini H. P., Sharma, (1995). Model plant architecture through association and path coefficient analysis in Indian colza. *Indian J. Agri. Res*. **29**: 109–115.

Shalini, T. S. Sheriff, R. A., Kulkarni, R. S. and Venkataramana, P. (2000). Variability studies in Indian mustard [*Brassica juncea* L. Czern and Coss*]*. *Res. Crops*. **12**(3): 230-234.

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, Y., Majidi, M. M., Jafarzadeh, M., & Mirlohi, A. (2015). Multivariate analysis of genetic variation in winter rapeseed (*Brassica napus* L.) cultivars. *Journal of Agricultural Science and Technology*. **17**(5): 1319-1331.

Sharma, S.K. (1984). Variation and correlation studies in Indian mustard *(B. juncea). Indian J. Agril. Sci*. **54**(2): 146-147.

Sheikh, F.A., Rathen, A.G. and Wani, S.A. (1999). Path analysis in toria (*Brassica campestris* L.) *var.* toria. *Adv. P1. 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. Agricultural University. Ludhiana, 141004, India.

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

Singh, B. (2004). Character association and path analysis under dryland condition in Indian mustard (*Brassica juncea* L.). *Cruciferae Newsl*. **25**: 99–100.

Singh, R. P., Malik, B.P. and Singh, D.P. (1997). Variation for morpho-physiological characters in genotypes of Indian mustard. *Indian J. Agric. Sci.* **57**: 227-230.

Singh, R.K. and Chaudhary, B.D. (1985). Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi, India.

Singh, R.S., Singh, P. and Dixit, R.K. (1987). Combining ability analysis of yield and developmental traits in Indian canola (*Brassica campestris* L. var. yellow sarson prain). *Farm Sci*. **12**(2): 170-174.

Srivastava, M. K. and Singh, R. P. (2002). Correlation and path analysis in Indian mustard. Crop Res. Hisar, Dept. of Genetics and Plant Breeding. *Indian Univ. Agril. Tech.* **23**(3): 517-521.

Swain, S.K. (1990). Correlation and path analysis in brown sarson (*Brassica campestris* var. *dichotoma* watt.). *Orissa J. Agril. Res*. **3**(3-4): 197-200.

Thakral, N. K. (2004). To study the association of some morpho physiological attributes with yield in toria. Thesis Abst. **8**(11): 66-67.

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.

Thurling, N. (1983). Variation in siliqua length in spring rape (*B. napus*) and its relationship to yield. In Proceedings, Australian Plant Breeding conference. Adelaide, South Australia. pp. 14-18.

Tuncturk, M. and Ciftci, V. (2007). Relationships between yield and some yield components in rapeseed (*Brassica napus* ssp. *Oleifera* L.) cultivars by using correlation and path analysis. *Pakistani. J. Bot*. **39**(1):81-84

Tusar, P., Maiti, S. and Mitra, B. (2006). Variability, correlation and path analysis of the yield attributing characters of mustard (*Brassica* sp.). *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.). *Crop Res. Hisar*. **11**(3): 319-322.

Uddin, M. J., Chowdhury, M. A. Z. and Miah, M.F.U. (1995). Genetic variability, character association and path analysis in Indian mustard (*Brassica juncea* L.). *Bangladesh Ann. Agric*. **5**(1): 51-52.

Uddin, M.J. (1994). Genetic divergence in mustard. *Bangladesh J. Pl Breed. Genet*. **7** (2): 23-27

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.

Wright, S. (1921). Correlation and causation. J. Agric. Res. 20: 557-585. Yadava V. P., Deb S. and Singh H. (1996). Morpho-physiological determinates of yield under water stress conditions in Indian mustard. Acta Hort. 407: 155-160

Yadava, A.K., Verma, A.K., Singh, D.N. and Singh, S.K. (1996). Path coefficient analysis in Indian mustard (*Brassica Juncea* L. Czern and Coss). *J. Res. Birsa. Agril. Univ.* **8**(2): 135-137.

Yadava, T. P., Zada, A. K. and Hari, S. (2004). Selection Indices for Seed Yield in Indian mustard (*Brassica Juncea* L. Czern & Coss), I. Based on Physiological Attributes. *Indian J. Genet. Pl. Breed*. **48**(1): 23-29.

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

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

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

Zajac, T., Bieniek, J., Witkowiez, R. and Gierdziewicz, M. (1998). Individual share of field components in winter oilseed rape yield formation. Academia Rolniezaw Kraikowie. Poland. **19**(2): 413-422.

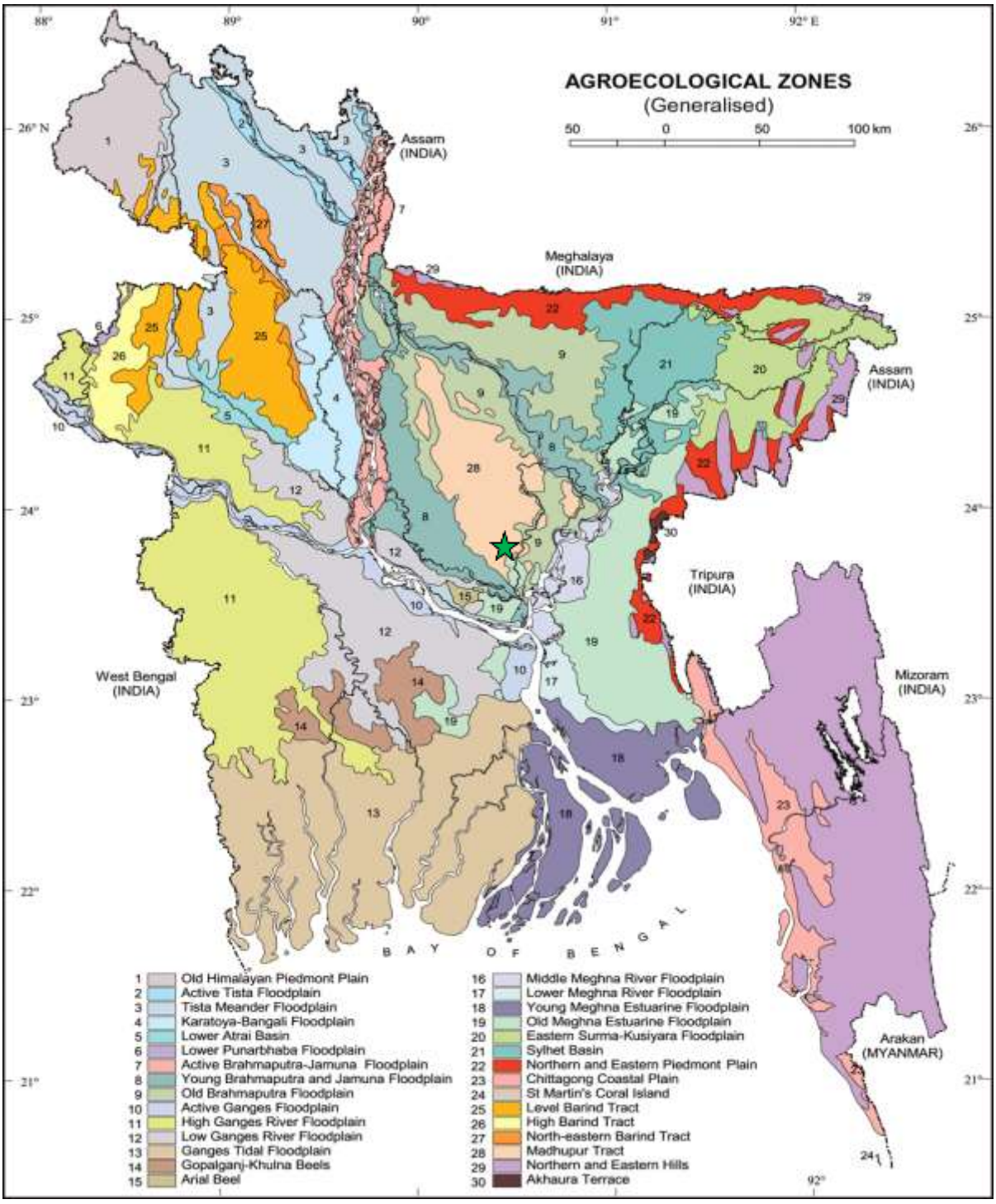
Zaman M.A., M Tuhina-Khatun, M.Z,Ullah, M.Moniruzzamn and M.Z. Rahman(2010). Multivariate analysis of divergence in Advanced Lines of mustard (*Brassica* spp). *Bangladesh J. Pl. Breed. Genet*. **23**(2): 29-34.

Zare, M. and Sharafzadeh, S. (2012). Genetic variability of some rapeseed (*Brassica napus* L.) cultivars in Southern Iran. *African J. Agric. Res*. **7**(2): 224- 229.

APPENDICES

APPENDICES

Appendix I. Map showing 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, 1915)
Silt	26.40	Do
Clay	36.66	Do
Texture class	Clay loam	Do

B. Chemical composition of the soil

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

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

Appendix III. Monthly average temperature, relative humidity, total Rainfall and sunshine of the experimental site during the period from November, 2018 to February, 2019.

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
November, 2018	34.7	18.0	77	227	**5.8**
December, 2018	32.4	16.3	69	0	**7.9**
January, 2019	29.1	13.0	79	0	**3.9**
February, 2019	**28.1**	**11.1**	**72**	**1**	**5.7**

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

Appendix IV. Mean performance of 38 mustard genotypes

Code	D50%F	DM	PH	RL	SL	PB	SB	TP	PL	SPP	TSW	SYPP
G1	31.00	99.33	105.17	10.07	115.94	2.83	3.60	133.00	8.03	22.80	4.33	6.27
G2	32.33	102.00	99.93	8.91	109.13	2.77	3.10	147.53	8.51	23.53	4.00	7.20
G3	34.00	105.33	112.55	10.43	124.45	2.87	2.17	97.40	8.49	25.17	4.00	8.17
G4	38.67	97.67	97.57	8.44	106.67	2.73	4.50	126.80	7.58	26.41	3.67	7.59
G5	32.00	107.67	111.78	9.99	124.29	3.13	2.20	88.53	7.08	21.50	4.67	7.73
G6	35.33	98.33	117.83	10.54	126.43	2.67	1.87	129.27	8.47	25.13	4.33	8.40
G7	31.67	99.33	92.53	9.19	104.30	2.40	2.73	69.13	8.14	25.30	4.33	4.95
G8	33.00	92.00	106.65	9.18	116.61	2.67	2.70	131.27	8.23	26.10	5.00	7.46
G9	33.33	91.00	89.40	8.17	100.51	4.27	3.40	139.53	7.21	24.13	5.00	8.47
G10	33.00	99.67	105.93	9.27	114.88	2.67	2.07	159.60	8.44	21.97	4.00	8.58
G11	32.00	90.00	120.80	11.40	131.47	3.07	2.86	106.20	8.72	23.03	4.67	7.36
G12	38.33	107.00	98.07	8.17	107.70	3.27	3.10	156.33	8.40	24.23	4.33	7.98
G13	32.00	100.00	104.05	10.38	122.40	2.87	2.07	104.40	8.35	25.53	4.00	7.17
G14	37.33	103.00	119.81	11.31	126.79	3.00	2.47	107.87	9.02	26.17	4.00	7.92
G15	35.33	99.33	106.17	12.10	116.55	3.20	2.43	88.80	8.50	26.80	4.00	9.51

Appendix IV. Mean performance of 38 mustard genotypes (continued)

G16	**36.67**	**96.67**	**93.79**	**10.05**	**101.48**	**3.47**	**2.60**	**114.33**	**7.52**	**24.67**	**4.67**	**8.26**
G17	**32.33**	**100.00**	**109.93**	**10.95**	**120.21**	**2.53**	**1.87**	**131.87**	**7.70**	**23.43**	**4.33**	**6.94**
G18	**31.33**	**94.33**	**110.53**	**10.86**	**121.07**	**3.20**	**2.70**	**113.27**	**9.27**	**29.07**	**4.00**	**4.93**
G19	**32.67**	**98.00**	**108.59**	**11.31**	**120.44**	**3.37**	**2.47**	**125.47**	**8.05**	**26.60**	**4.33**	**8.60**
G20	**32.00**	**97.00**	**93.21**	**10.76**	**105.68**	**2.93**	**2.13**	**78.60**	**7.67**	**23.47**	**4.00**	**4.44**
G21	**32.67**	**98.67**	**119.82**	**11.42**	**131.30**	**3.00**	**2.57**	**92.47**	**7.68**	**21.80**	**4.00**	**4.58**
G22	**30.33**	**90.00**	**107.40**	**9.65**	**118.79**	**2.67**	**1.07**	**71.47**	**8.54**	**29.63**	**4.00**	**6.47**
G23	**32.00**	**95.33**	**109.20**	**10.94**	**112.71**	**2.40**	**1.27**	**95.67**	**7.62**	**27.40**	**4.33**	**3.81**
G24	**31.00**	**96.00**	**106.98**	**9.75**	**120.79**	**2.87**	**1.73**	**127.67**	**8.20**	**24.13**	**4.33**	**6.93**
G25	**35.33**	**98.33**	**99.65**	**8.83**	**107.47**	**3.00**	**2.47**	**153.67**	**8.53**	**26.47**	**4.67**	**6.91**
G26	**34.33**	**99.67**	**98.27**	**12.02**	**112.80**	**3.27**	**2.40**	**94.33**	**8.90**	**27.47**	**4.00**	**5.40**
G27	**35.33**	**102.33**	**101.93**	**9.81**	**105.07**	**2.80**	**1.87**	**90.30**	**8.19**	**25.80**	**4.33**	**8.04**
G28	**34.00**	**102.00**	**106.13**	**9.17**	**116.04**	**2.60**	**1.87**	**107.60**	**7.64**	**24.90**	**4.00**	**6.93**
G29	**36.33**	**107.00**	**99.38**	**9.70**	**106.71**	**2.53**	**1.66**	**88.53**	**9.21**	**28.73**	**4.33**	**7.07**
G30	**31.00**	**97.33**	**111.80**	**10.68**	**113.69**	**3.00**	**2.40**	**146.20**	**8.23**	**26.17**	**4.00**	**5.87**

Appendix IV. Mean performance of 38 mustard genotypes (continued)

G31	**31.00**	**99.67**	**112.86**	**10.49**	**194.95**	**2.50**	**2.00**	**156.47**	**8.58**	**25.77**	**4.00**	**6.30**
G32	**32.67**	**100.67**	**104.39**	**9.57**	**115.97**	**2.47**	**2.13**	**87.80**	**7.55**	**23.23**	**4.67**	**5.70**
G33	**31.00**	**101.67**	**87.81**	**10.64**	**97.09**	**3.37**	**4.30**	**107.29**	**8.34**	**25.53**	**4.33**	**8.01**
G34	**33.00**	**98.33**	**107.36**	**12.15**	**120.76**	**2.33**	**4.13**	**97.47**	**8.65**	**28.40**	**5.00**	**6.32**
G35	**35.00**	**99.00**	**110.73**	**11.43**	**121.49**	**2.60**	**2.47**	**73.87**	**8.34**	**25.23**	**4.67**	**5.14**
G36	**32.67**	**97.67**	**101.79**	**10.68**	**117.83**	**2.67**	**2.80**	**96.33**	**7.55**	**24.20**	**4.00**	**6.03**
G37	**32.00**	**96.33**	**108.20**	**13.39**	**121.37**	**2.27**	**3.03**	**109.00**	**8.06**	**21.60**	**4.33**	**7.10**
G38	**34.33**	**100.00**	**108.29**	**11.73**	**120.47**	**2.93**	**3.20**	**112.93**	**8.59**	**25.10**	**4.33**	**5.74**

Appendix V. Principal component score I and II

GENOTYPES	PCA 1	PCA 2
1	-20.38	4.91
2	-33.51	15.48
3	13.20	-11.06
4	-12.64	15.60
5	21.96	-12.06
6	-18.70	-9.83
7	44.82	10.24
8	-18.84	3.55
9	-24.07	26.06
10	-46.53	9.89
11	3.15	-19.36
12	-41.94	19.15
13	6.84	-5.03
14	2.35	-14.18
15	23.10	-2.83
16	0.58	19.65
17	-20.05	-0.93
18	-1.76	-4.95
19	-13.74	-1.61
20	35.24	10.15

Appendix V. Principal component score I and II (continued)

GENOTYPES	PCA1	PCA2
21	16.80	-20.97
22	39.86	-8.29
23	16.98	0.41
24	-15.95	-1.05
25	-39.27	18.14
26	18.52	4.31
27	23.57	9.53
28	4.64	0.62
29	25.18	8.75
30	-33.12	6.51
31	-56.42	-66.41
32	24.22	-1.87
33	8.43	24.60
34	13.93	-5.87
35	36.97	-11.45
36	15.57	-1.29
37	2.34	-5.04
38	-1.34	-3.48