GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS IN F_5 GENERATION OF *Brassica napus* L.

SHAKIRA ISLAM

DEPARTMENT OF GENETICS AND PLANT BREEDING
SHER-E-BANGLA AGRICULTURAL UNIVERSITY
DHAKA-1207

DECEMBER, 2016

GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS IN F_5 GENERATION OF *Brassica napus* L.

BY

SHAKIRA ISLAM

REGISTRATION NO. 15-06929

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

MASTER OF SCIENCE

IN

GENETICS AND PLANT BREEDING

SEMESTER: July-December, 2016

Approved by:

(Dr. Firoz Mahmud)	**(Dr. Md. Shahidur Rashid Bhuiyan)**
Professor	**Professor**
Supervisor	**Co-supervisor**

(Professor. Dr. Jamilur Rahman)
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, " ***Genetic variability, correlation and path analysis in F_5 generation of Brassica napus L."*** *submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of* ***MASTER OF SCIENCE in GENETICS AND PLANT BREEDING****, embodies the result of a piece of bona fide research work carried out by* ***SHAKIRA ISLAM****, Registration No.* ***15-06929*** *under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

Dated: December, 2016
Place: Dhaka, Bangladesh

(Dr. Firoz Mahmud)
Professor
Supervisor

DEDICATED

TO

My Mother

A strong and gentle soul who taught me to trust in Allah, believe in hard work and that so much could be done with little

My Father

For earning an honest living for us and for supporting me

My Grandfather & Grandmother

For being my first teacher

My sister

For encouraging me

My Husband

For his patience, motivation, love and friendship

Acknowledgements

Al hamdulillah, 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, Professor Dr. Shahidur Rashid Bhuiyan, 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 Professor Dr. Jamilur Rahman, 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 Professor Dr. Kamal Uddin Ahmed, Honourable Vice Chancellor, Sher-e-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, Prof. Mohammad saiful Islam, Associate Prof. Dr. Md. Ashadurzzaan Siddikee of the Genetics and Plant Breeding Department 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.

I am extremely grateful to my husband for his personal support, great patience and motivation in my study and in difficult times in my life.

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

December, 2016 *The Author*

SAU, Dhaka.

GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS IN F_5 GENERATION OF *Brassica napus* L.

BY

SHAKIRA ISLAM

ABSTRACT

For meet our own requirements every year we are importing edible oil and spent huge economy. This requirement will be fulfill by developing the high yielding varieties from the local germplasm. The need is to enhance and improve the production of the local cultivars and for that purpose the genetic variability and diversity of the local cultivars must be fully explored. Sixty two F_5 population of *Brassica napus* L. were evaluated through randomized complete block design with two replications at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, to study the variability, correlation, path analysis and genetic diversity during November 2015 to February 2016 growing seasons. The population were found significantly difference for all the traits studied. The maximum plant height and secondary branches per plant was observed by the population G62. Maximum primary branches per plant and siliqua per plant was found in G45. Higher estimates of PCV than GCV were observed for all the traits. Maximum GCV and PCV were recorded for number of secondary branches per plant (37.15 and 29.48). Broad sense heritability values were higher (more than 61%) for all the traits and it ranged from 51.62% (1000 seed weight) to 98.80 % (days to maturity). Genetic advance as percent of mean was highest (48.19%) for secondary branches per plant and lowest (8.44%) for days to maturity. The significant positive correlation with seed yield per plant was found with all most of the traits except days to 50% flowering. Path analysis revealed that days to 50% flowering (0.188), days to maturity (0.293), plant height (0.038), primary branches per plant (0.627), number of siliqua per plant (0.614), number of seeds per siliqua (0.362) and 1000 seeds weight (0.397) had positive direct effects on seed yield per plant. By genetic divergence analysis 62 population were grouped into five clusters and maximum population (25) were included into cluster II. The maximum inter cluster distance was observed between population of cluster I and III **(**14.763) followed by clusters II and III (10.475) and I and V (8.689). On the basis of diversity pattern and agronomic performance population G45 and G62 were found for high yielder, early flowering and bold seeded. Population G2 and G6 were found for early maturity and dwarf plant type. These superior population may be used in future breeding program to develop short duration cultivar of mustard.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF PLATES (*Continued...*)

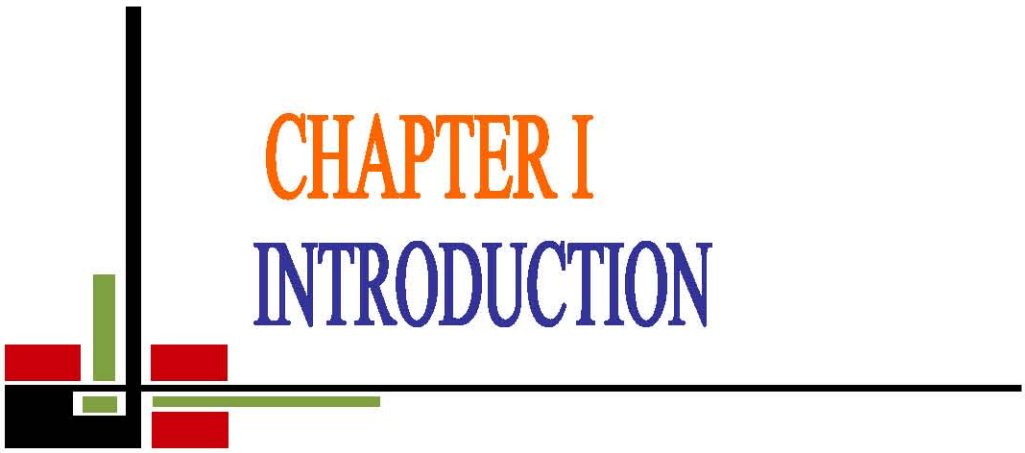
LIST OF APPENDICES

SOME COMMONLY USED ABREVIATIONS

FULL WORD	ABBREVIATION
Agricultural	Agril.
Agriculture	Agric.
Agro Ecological Zone	AEZ
Agronomy	Agron.
Analysis of variance	Anova
And others	*et al.*
At the rate	@
Bangladesh	BD
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Centimeter	cm
Cultivars	cv.
days after sowing	DAS
Degree Celsius	^{0}C
Degrees of Freedom	Df
Environmental variance	σ^2_e
Etcetera	etc.
Food and Agricultural Organization	FAO
Genetic Advance	GA
Genotype	G
Genotypic coefficient of variation	GCV
Genotypic variance	σ^2_g
Gram	g
Harvest Index	HI
Heritability in broad sense	h^2_b
Indian Agricultural Research Institute	IARI
International Center for Agricultural Research in Dry Areas	ICARDA
Journal	J.
Kilogram	Kg
Meter	M
Mean sum of square	MS
Ministry of Agriculture	MoA
Murate of Potash	MoP
Percent	%

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

FULL WORD	ABBREVIATION
Percentage of Coefficient of Variation	CV%
Phenotypic variance	σ^2_p
Phenotypic coefficient of variantion	PCV
Randomized Complete Block Design	RCBD
Sher-e-Bnagla Agicultural University	SAU
Square meter	m^2
The fifth generation of a cross between two dissimilar homozygous parents	F_5
Triple Super Phosphate	TSP



CHAPTER I
INTRODUCTION

CHAPTER I

INTRODUCTION

Rape seed (*Brassica napus* L.) is an amphidiploid (AACC genome, 2n=38) and is believed to have arisen 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). *Brassica napus* is second most important oilseed crop in the international oilseed market after soybean and important source of vegetable oil (Hasan *et al.*, 2006).

Oilseed *Brassica* is commonly known as rape seed and mustard is an important member of the cruciferae family consisting of over 3200 species with high diverse morphology. Among the oilseed crops *Brassica rapa*, *Brassica napus* and *Brassica juncea* is known as rape seed, oilseed rape or canola (Khan *et al*., 2008). *Brassica rapa* and *Brassica napus* is referred as rape seed where the rest one is known as mustard. It is the second highest source of edible oils supply in the world.

They provide the most concentrated source of energy and also help to absorb vitamins A, D, E and K. It is the second highest source of edible oils supply in the world after soybean (FAO, 2014). Rape seed is one of the most important oil and protein rich annual crops in the world. Oilseed provides oil both for industrial and culinary purpose. Vegetable oils and fats lipids constitute an important component of human diet. Oils from plant origin are nutritionally superior to that of animal origin. Therefore, vegetable oil has been always considered as a major component for food preparation.

Bangladesh produces good number of oil seed crop like mustard, sesame, groundnut, linseed, niger, safflower, sunflower, sunflower, soybean and castor etc. *Brassica* oil crops are the most important group of species that supply major edible oils in Bangladesh (BBS, 2013). Mustard and rape seed seeds contain 42% oil, 25% protein (Khaleque, 1985). The oil cake contains proteins of high biological value and

applicable quantities of calcium and phosphorus. It is used as a very good animal feed as well as organic manure for various crops.

Bangladesh required 0.30 million tons of oil equivalent to 0.85 million tons of oil seed for nourishing her people. At present, the oil seed production is about 0.26 million tons, which covers only 30% of the domestic need (BBS, 2011). About 70% of requirement of oil has been imported every year by spending huge amount of foreign currency involving Tk.2951 core (BBS, 2011). Per capita consumption of edible oil is the lowest in Bangladesh from the world (11g/head/day) which is one fifth of the recommended requirement for a balanced diet (FAO, 2014).

In Bangladesh the seed yield of mustard/rape seed is about 740 kg/ha, which is very low in comparison to other developed countries (2400 kg/ha) (FAO, 2011). On the other hand, Bangladesh produces soybean but no method for oil extraction from soybean available whereas Bangladesh has extraction mechanism available for mustard so giving emphasis on mustard can help us to save foreign currency. Improvement of existing oilseed crops and introduction of a new oilseed need urgent attention to increase the domestic production that may reduce the huge shortage of oils. The most of the released mustard cultivars are generally long in duration and thus, did not fit well for cultivation in cropping pattern. If we can develop new lines which would be successfully cultivated between Aman and Boro rice rotation without affecting present cropping pattern, since after Aman rice harvest and before the transplantation of Boro rice 70-80 days are available for cultivating gap filling crop. So, it is urgent to analyze the genetic diversity and its response for the selection of good mustard population for increasing our cropping intensity.

Crop improvement program through plant breeding, as a result, occurs through selection operating on genetic variability. Selection by plant breeders or by farmers can be intense and has resulted in major improvements. 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.

However, continued success in plant breeding can only be realized in so far as new variability is available for selection (Copper *et al.*, 2001). Such variability provides adaptability, which is the capacity for genetic change in response to selection (Sigmmonds, 1962). Genetic variability is therefore essential for crop improvement. The simple correlation analysis could not fully explain the relationship among the characters. Therefore, path coefficient analysis is suggested to exploit for more and complete determination of impact of independent variable on dependent one (Korkut *et al.*, 1993). It helps the breeders to explain direct and indirect effects and had extensively been used in breeding work in different crop species by various researchers.

Genetic diversity is the basic for genetic improvement. It is widely accepted that information about germplasm diversity and genetic relatedness among elite breeding material is a fundamental element in plant breeding ((Mukhtar *et al.*, 2002). It is very important factor for any hybridization program aiming at genetic improvement of yield especially in self-pollinated crops (Joshi and Dhawan, 1966). Different methods have been used to assess genetic diversity. This can be obtained from pedigree analysis, morphological traits or using molecular markers. With the development of advanced biometrical method such as multivariate analysis (Rao, 1952) based on Mahalanobis' (1936) D^2 statistics and Ward's no-hierarchical squared Euclidean distance method have become possible to quantity magnitude of diversity among germplasm for their evaluation in respect of breeding program.

Main objectives of any breeding program is to produce high yielding and better quality lines for release as cultivars to farmers. We had selected F_5 generation because the plant height, days of maturity, primary branches, secondary branches per plant, seed weight, seed yield per plant were positive and considerably higher in magnitude. Also some population were found for high yielder, early flowering and bold seeded.

Therefore the present study was, executed with the objectives of estimating the genetic variability, correlation, path analysis and diversity seed yield and its related traits of sixty two *Brassica napus* L. population.

Objectives:

1. To study the variability of important characters in F_5 generations generated through intergenotypic crosses to select the best promising lines,

2. To find out the interrelationship among the different traits and their contribution towards divergence of the population,

3. To assess genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters and

4. To select promising population considering early maturity, high yielding plants to release as a new variety.

CHAPTER II
REVIEW OF LITERATURE

CHAPTER II

REVIEW OF LITERATURE

Many studies on the genetic analysis of *Brassica* that means genetic estimation, character relations, cause and effect analysis and genetic divergence analysis have been carried out in many countries of the world. The review of literature concerning the studies presented under the following heads:

2.1 Genetic variability

2.2 Correlation studies

2.3 Path co-efficient analysis

2.4 Genetic divergence

2.1 Genetic variability

Thousand-seed weight is an important trait of rape seed and mustard for seed yield. It has been found vary widely variation for genotypes and environments. High heritability coupled with high genetic advance was observed for the traits seed yield per plant, number of secondary branches per plant, siliqua per plant, 1000 seed weight (gm) and number of primary branches per plant while working with 24 genotypes (Sheikh *et al.*,1999).

Khulbe and Pan (1999); were estimated variability, heritability and genetic advance for yield and its components in Indian mustard and revealed maximum variability for seed yield. All the traits except oil content shown high heritability coupled with high or moderate genetic advance. It was suggested that the presence 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.

An experiment was conducted by Shalini *et al.* (2000) on 81 diverse Indian mustard (*Brassica juncea* L). The analysis of variance indicated the prevalence of sufficient genetic variation among the genotypes for all 10 traits 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 sense heritability (h^2b>90%) for number of primary branches per plant and oil content while working with different strains of *Brassica napus*. They also found low heritability (50%) for plant height, number of siliqua per plant, number of seed per siliqua and seed yield.

Tyagi *et al*. (2001); evaluated 45 hybrids of Indian mustard for seed yield and yield components. Variation was highest for plant height. The seed yield per plant exhibited the highest coefficient of variation (41.1%).

An experiment was conducted for studies of genetic variability in 25 genotypes by Pant and Singh (2001). Highly significant genotypic differences were observed for all traits studied, except days to flowering, number of primary branches and oil content. Seed yield per plant had the highest coefficient of genotypic and phenotypic variability. All traits showed high heritability, with the highest value for seed yield per plant. Genetic advance were comparatively low for oil content and days to flowering, suggested that these traits cannot be improved effectively merely by selection.

Ghosh and Gulati (2001), studied on 36 genotypes and found that the GCV and PCV were high in magnitude for all the traits except plant height. The differences between the PCV and GCV were narrow for all the traits studied, coupled with high heritability except plant height, indicating the usefulness of phenotypic selection in improving these traits. Number of primary branches, number of siliqua on main shoot, main shoot length and number of seeds per siliqua represented high heritability coupled with high genetic advance. 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); revealed that the existence of significant genetic variability for days to 50% flowering.

Gupta *et al.* (2002); studied in 18 strains of *Brassica napus* for morphological and phenological yield traits and reported that the high expected genetic advance and high heritability for plant height, 1000-seed weight and yield per plant, indicating additive gene effects for these traits. Number of siliqua per plant showed a high heritability estimate with low expected genetic advance indicating non-additive gene effects.

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

Yadava *et al.* (2004), studied heritability and genetic advance and found 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 days to first flowering.

Niraj and Srivastava (2004), studied on variability and character association in 21 mustard genotypes of *Brassica juncea*. Genotypes RH-9704 and IGM-21 performed 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), found high heritability coupled with high genetic advance as percentage of mean was for days to flowering, followed by 1000-seed weight and days to maturity and weight.

Thakral (2004), worked on 8 Indian rape seed parental lines and their 28 F_1 hybrid for yield and yield contributing characters and reported high PCV and GCV was found for plant height and seed yield characters. Results showed that the coefficient of variation of siliqua per plant were significant. So, there was considerable variability for the above character studied (Goswami *et al.*, 2005).

Kardam and Singh (2005), studied the nature and magnitude of associations for 10 traits in progenies of Indian rape seed. PCV were higher in magnitude compared to GCV for most of the characters. Seed yield per plant was significantly and positively variable with plant height, number of seeds per siliqua and 1000-seed weight.

Uddin *et al.* (2005); evaluated variation for yield and yield contributing traits in rapeseed and reported significant variation was observed for yield and yield components indicating considerable high genotypic and phenotypic coefficients of variation occurred for 1000 seed weight, seed yield per plant and siliqua per plant.

Khan *et al.* (2006), studied variation for yield and yield contributing traits in rape seed and reported significant variation for eleven accessions of *Brassica napus* L. They indicated that a wide range of genetic variation with high PCV and GCV for seed yield, siliqua per plant, seeds per siliqua, siliqua length.

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 among the genotypes for number of siliqua per plant, harvest index, oil percent. They noticed most important trails for high PCV and GCV were number siliqua per plant and 1000-grain weight.

Akbar *et al.* (2007); studied on eight advanced lines and two check variety of *Brassica junea* and reported the highest GCV 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. The highest heritability was found yield per plant followed by plant height, thousand grain weight, siliqua per plant and number of primary branches per plant. The maximum genetic advance was found in seed yield

per plant followed by siliqua per plant, plant height, thousand grain weight and minimum in primary branches per plant.

Rashid (2007), studied variability on forty oleiferous *Brassica* species and reported high GCV value was observed for plant height and number of siliqua per plant.

Yadava *et al.* (2007); studied twelve genotypes of *Brassica 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 traits showed relatively constant values over a range of environments. Yield showed a wide variation and estimated genetic advance showed wide variation for all traits except number of days to first flowering, plant height and 1000 seed weight.

A field experiment was conducted by Jahan (2008) to study on inter-genotypic variability in 10 F_4 lines along with 8 varieties of *Brassica rapa*. Considerable variation was experiential among all genotypes for all the traits studied. High GCV was obtained for secondary branches per plant, siliqua per plant and yield per plant. High heritability with low genetic advance in percent of mean was performed for days to maturity which indicated that non-additive gene effects were involved for the expression of this trait and selection for such trait might not be worthwhile. High heritability with moderate genetic advance in percent of mean was observed for plant height indicating that this trait was under additive gene control and selection for genetic improvement for this trait would be effective.

A study was carried out by Hosen (2008) using five parent and ten F_3 progenies of *Brassica rapa and* revealed that there was large variations denoted among all the genotypes. Traits number of primary branches per plant, number of secondary branches per plant, length of siliqua, number of seeds per siliqua, thousand seed weight and yield per plant showed least difference between phenotypic and genotypic variances. The values of GCV and PCV indicated that there was significant variation among all the traits except days to maturity. The plant height and number of siliqua per plant showed high heritability with high genetic advance and genetic advance in percentage of mean.

An experiment was conducted by Mahmud *et al.* (2008) with 58 genotypes of *Brassica rapa* and revealed significant variation was observed among all the genotypes for all the traits studied except thousand seed weight. High GCV value was observed for number of secondary branches per plant. High heritability values along with high genetic advance in percentage of mean were obtained for seed per siliqua and siliqua length.

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

Aytac and Kinaci (2009), conducted an experiment with 10 winter rape seed genotypes for variation, genotypic and phenotypic correlations and heritability for seed yield, yield and quality traits for two years. They observed the maximum heritability and genetic advance for seed yield.

Alam (2010), conducted an experiment 26 F_4 populations of *Brassica rapa* L. revealed higher phenotypic variation was present than the genotypic variation. High heritability with high genetic advance was found for plant height, number of primary branches per plant, number of secondary branches per plant and number of siliqua per plant.

Zebarjadi *et al.* (2011); carried out an experiment to estimate genetic parameters with 16 rapeseed genotypes and showed significant differences among the genotypes for 13 different traits including plant height, oil percent, oil yield etc. In stress condition heritability was maximum in oil percentage, whereas low genetic advance was observed for thousand kernel weight.

Rameeh (2011), studied with 36 rape seed genotypes and found that the most variations among the genotypes were in seeds per siliqua and siliqua on main raceme with 18.0 and 25.3 per cent coefficient of variation, respectively. Heritability

estimates were high for siliqua on main raceme, seeds per siliqua and siliqua per plant (0.70, 0.77 and 0.81, respectively).

Afrin *et al.* (2011), reported in *Brassica napus* that the plant height showed highest value of heritability while the number of primary branches per plant, number of secondary branches per plant, siliqua length, numbr of seed per siliqua, number of siliqua per plant, thousand seed weight and seed yield per plant showed moderate heritability. Days to 80% maturity showed lowest heritability.

Abideen *et al.* (2013); conducted an experiment in *Brassica napus* and *r*esults revealed that highly significant differences among the genotypes for most of the traits. Non-significant differences were observed among the genotypes for primary branches and pods.

Khan *et al.* (2013), studied 30 F_7 segregating lines and two parents of *Brassica rapa* and result revealed that significant variation was found among all the genotypes for all the characters except 1000-seed weight. Highest genotypic, phenotypic and environmental variances were observed in plant height while lowest one was in length of siliqua followed by thousand grain weight. 1000-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 G15, G19, G1, G3, G4, G10, G18, G21, and G-24 were found suitable for future breeding program.

Ali *et al.* (2013), reported on 30 lines of *Brassica carinata* that PCV and GCV ranged from 4.92-48.24% and 3.2-38.1%, respectively. The highest heritability values were recorded for pod length (0.83) followed by pods on main raceme and the genetic advance as percent of mean was the highest for seed yield per plant and pods on main raceme.

Walle *et al.* (2014), studied on 36 Ethiopian mustard (*Brassica carinata*) and result revealed that significant difference in days to 50% flowering, plant height and primary branches per plant. GCV was lower than the PCV for all yield related

characters studied. High heritability with high genetic advance was observed in plant height, number of secondary branches per plant and days to 80% maturity.

Mekonnen *et al.* (2014), evaluated 36 genotypes of *Brassica carinata* and found the GCV ranged from 4.3% to 44.14% and PCV from 8.3% to 91.7%. Higher GCV and PCV for seed yield, number of pods per plant, primary and secondary branches which indicated it provide the better scope for improvement through selection. Besides these, higher heritability along with higher genetic advance was observed in days to maturity, days to flowering, grain-filling period, number of pods per plant, secondary branches per plant, plant height, seed yield/plot and hectare and the lowest one was in primary branches per plant.

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

Bilal *et al*. (2015), studied 23 *Brassica napus* genotypes and found heritability was moderate to high in magnitude for all traits. 1000 seed weight exhibited significant ($p \leq 0.01$) differences validating the presence of genetic variation among the tested accessions.

Rameeh (2015), reported that heritability estimates varied from 0.18 to 0.98 for pods length and days to end of flowering. High heritability was determined for plant height and seed yield demonstrating selection gain for improving these traits will be high. Pods on main axis and pods per plant had high value of genetic coefficient of variation.

Sharafi *et al*. (2015), studied twenty eight rape seeds and reported that yield, number of branches per plant and plant height had the highest variation. Heritability ranged from 6% to 87% for seed yield and pod length, respectively. Results showed that cultivars with higher number of pod per plant had higher seed production.

2.2 Correlation studies

Correlation studies helps to determine the nature and degree of relationship between any two measurable traits.

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

Reddy (1991), conducted research on Indian mustard (*Brassica juncea*) and reported that positive and significant correlation between seed yield and number of primary branches per plant, number of secondary branches per plant, siliqua per plant and seeds per siliqua.

Zaman *et al.* (1992), experimented in several Swedish advanced rape lines and reported that number of seeds per siliqua negatively correlated with siliqua per plant.

Ahmed (1993), worked with eight cv. of *Brassica campestris* and *Brassica juncea* and observed that siliqua length, number of siliqua per plant, number of seeds per siliqua and seed weight per siliqua was linearly and positively correlated with seed yield per plant.

Research deliberatedin Tori-7 (*Brassica campestris var. toria*) and found that plant height, siliqua per plant, seeds per siliqua and 1000 seed weight was positively and significantly associated with seed yield (Gosh and Mukhopadhyay, 1994).

Nanda *et al.* (1995), worked with 65 *Brassica juncea*, *Brassica rapa* and *Brassica napus* genotypes and found that positive correlation between yield and siliqua filling period.

Uddin *et al.* (1995); conducted experiment in 13 Indian mustard (*Brassica juncea*) and found that seed yield per plant had high significant and positive association with plant height and thousand seed weight, but high significant and negative association with seeds per siliqua at both genotypic and phenotypic levels.

Kumar *et al.* (1996), reported in 12 genotypes of *Brassica juncea* and found flowering time and plant height negatively correlated with number of primary branches per plant.

Zajac *et al.* (1998), calculated 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 smallest effect on yield.

Kumar *et al.* (1999); reported that genotypic correlation co-efficient was higher than corresponding phenotypic correlation co-efficient for most traits. The plant height, siliqua on main shoot, siliqua per plant and thousand seed weight were positively correlated 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 in seven genotypes of *Brassica campestris* and standard cultivar of *Brassica napus.*

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).

Badsra and Chaudhary (2001), examined in 16 Indian mustard genotypes and observed that seed yield was positively correlated with stem diameter, number of siliqua per plant and oil content. Among the characters only three were positively correlated with seed yield.

Association of yield components in 36 mustards was studied 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.

Pankaj *et al.* (2002), studied four parental cultivars and 174 progenies and revealed that 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 seeds per siliqua were positively associated with siliqua length and yield per plant at both levels.

Srivastava and Singh (2002), reported in Indian mustard (*Brassica juncea* L.) and results revealed that number of primary branches per plant, number of secondary branches per plant, 1000-seed weight (gm) and oil percent were positively associated with seed yield.

Gupta *et al.* (2002); studied 18 lines rapeseed reported significant correlation between plant height, number of siliqua per raceme and seed number per siliqua, while plant height was significantly correlated with number of siliqua per raceme. In general, genotypic correlations were greater than phenotypic or environmental correlations. Seed yield was positively correlated with number of siliqua per raceme and 1000-seed weight.

Choudhary *et al.* (2003), reported in 28 genotypes of Indian mustard and recorded days to first flowering, days to maturity, length of main axis, primary branches per plant, secondary branches per plant, number of siliqua per plant, siliqua length, number of seeds per siliqua, 1000-seed weight had highly significant and positive correlation with seed yield per plant.

An experiment was observed by Poonam and Singh (2004) in 40 Indian mustard and reported that 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 that seed yield per plant showed positive correlation with number of primary branches, length of main raceme, 1000-seed weight and oil content. Selection should be applied on these traits to improve seed yield in Indian mustard.

Sudan *et al.* (2004) studied in *Brassica juncea* and reported that seed yield showed significant and positive correlation with number of primary branches per plant, number of secondary branches per plant and 1000 seed weight. Path analysis indicated that number of primary branches was the most important character with the highest direct effect on seed yield. Other characters, viz., days to maturity, 1000 seed weight and number of seeds per siliqua had high positive effect on yield via other characters suggesting the scope of their simultaneous improvement through selection.

Niraj and Srivastava (2004), studied in 21 Indian *Brassica juncea* genotypes and revealed that seed yields were positively and significantly correlated with plant height and primary branches but negatively correlated with test weight.

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

Afroz *et al.* (2004); studied seed yield per plant had significant and positive correlation with number of primary branches per plant and number of siliqua per plant.

An experiment in *Brassica campestris* L. was conducted by Siddikee (2006) and results revealed that yield per plant had the highest significant positive correlation with number of siliqua per plant.

A study was conducted by Tusar *et al.* (2006); and 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.

Yadav *et al.* (2006); observed that 1000 seed weight, days to flowering, seeds per siliqua and plant height were the most important yield related characters and positively correlated with yield.

Zahan (2006), studied correlation and reported that yield per plant had highly significant positive association with plant height, length of siliqua, siliqua per plant and seed per siliqua but insignificant negative association with days to 50% flowering, days to maturity.

Parveen (2007), studied an experiment of *Brassica rapa* 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.

Akbar *et al.* (2007); conducted research in *Brassica junea* in Pakistan and reported that siliqua per plant had strong positive correlation with the seed yield followed by plant height while non-significantly negative correlation with thousand grain weight. But significantly negative correlation was present in siliqua per plant and primary branches per plant.

Rashid (2007), carried out an experiment with 40 *Brassica* species 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.

Basalma (2008), studied with 25 winter oil seed rape cultivars and showed a high positive and statistically significant correlation between branches per plant, the number of pods on the main stem and plant height during two years. Plant height indicated negative correlation with seed yield, 1000 seed weight and oil ratio.

A study was conducted by Hosen (2008) in *Brassica rapa* and 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.

In an experiment Mahmud *et al.* (2008); reported that 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.

Kumar *et al.* (2009), studied in 15 *Brassica napus* and *Brassica campestris* genotypes and found that genotypic correlation coefficient were higher than this correspond phenotypic correlation coefficients. Seed yield was positively correlated with plant height and 1000 seed weight.

Rameeh (2011), studied with 36 rapeseed genotypes and revealed 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. The highest significant positive correlation was found between days to 50% flowering and plant height.

Maurya *et al.* (2012), studied an experiment with 100 *Brassica juncea* genotypes and observed that a high positive correlation was presented between length of siliqua, seed yield, thousand grain weight and days to 50% flowering.

An experiment was conducted with ten Canola varieties by Khayat *et al.* (2012) and illustrated that the total dry matter, harvest index, 1000-grain weight, the number of grains per pod, number of pods per plant, plant height; days to maturity and flowering period trait had a positive significant correlation with grain yield.

Uddin *et al*. (2013); reported with *Brassica rapa* genotypes 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 phenotypic and genotypic levels and significant positive correlation at genotypic level in days to flowering and days to maturity.

Ejaz- Ul- Hasan *et al*. (2014); studied in *Brassica napus* and found high and positively significant phenotypic correlation between plant height and seeds per plant.

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

Rameeh (2015), studied in 36 rape seed (*Brassica napus* L.) genotypes and found that pods per plant, seeds per plant and 1000 seed weight traits were positively correlated with seed yield.

2.3 Path Co-efficient analysis

Direct contribution of each component to the yield and the indirect effects it has through its association with other components cannot be differentiated from mere correlation studies. Path coefficient analysis fulfills this study. It was first developed and described by Wright (1921), as a tool in genetic analysis which partition the association of the components on yield and indirect effects of the characters on yield through other components.

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.

Research reported was published that the plant height had the highest positive direct effect on seed yield per plant in *Brassica juncea* (Dhillor *et al.,* 1990). Kudla (1993), studied that 1000-seed weight had positive direct effect on seed yield.

Path analysis was studied by Uddin *et al*. (1995) in 13 Indian mustard (*Brassica juncea*) and found that seeds per siliqua and 1000 seed weight had high positive direct effect on seed yield per plant.

Yadava *et al.* (1996); studied on path coefficient analysis and found that the siliqua number per plant had the highest positive direct effect on seed yield. Singh *et al.* (1997); reported that negative direct effect of plant height on seed yield.

Sheikh *et al.* (1999), worked with many diverse mustard genotypes and revealed that 1000 seed weight and number of siliqua per plant had highly positive direct effect on seed yield.

Studied on path analysis of mustard genotypes and found that siliqua per plant had the highest direct effect on seed yield which was followed by 1000 seed weight, primary branches per plant and plant height, that was reported by Shalini *et al.* (2000). Most of the characters were studied had an indirect effect on seed yield.

Research found that primary branches per plant, secondary branches per plant and 1000 seed weight had highest direct effect on seed yield while working with Indian mustard (*Brassica juncea* L.) (Srivastava and Singh, 2002).

Afroz *et al.* (2004); studied path coefficient analysis and revealed that maximum direct positive effects was observed by plant height followed by number of siliqua per plant, number of primary branches per plant, 1000-seed weight and number of siliqua shattering per plant on seed yield per plant.

An experiment was conducted by Poonam and Singh (2004) in 40 Indian mustard genotypes and revealed that plant height had the highest positive direct effect (0.836) on seed yield followed by number of seeds per siliqua (0.791). The number of primary branches per plant, siliqua per plant and days to maturity had low but negative direct effects on seed yield.

Sudan *et al*. (2004); studied path analysis in Indian mustard and revealed that number of primary branches was the most important character with the highest direct effect on

seed yield. Other characters i.e. days to flowering, 1000 seed weight and number of seeds per siliqua had high positive effect on yield via other character suggesting the scope of their simultaneous improvement through selection.

Yadava *et al.* (2004); studied path analysis and revealed that only seeds per siliqua and 1000-seed weight had a direct effect on yield. Seed yield was positively associated with days to flowering and plant height.

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

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

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

Rashid (2007), studied with 40 *Brassica* genotypes 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.

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

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

The path co-efficient analysis by Hosen (2008), studied on *Brassica rapa* and found that 1000-seed weight had the highest positive direct effect followed by days to 50% flowering, length of siliqua, number of primary branches per plant, number of secondary branches per plant, days to maturity and number of seeds per siliqua.

Alam (2010), studied path co-efficient analysis and revealed that plant height, number of primary branches per plant, number of siliqua per plant, seeds per siliqua and siliqua length had the direct positive effect on yield per plant while days to 50% flowering, number of secondary branches per plant and thousand seed weight had the negative direct effect on yield per plant.

Afrin *et al.* (2011), estimated path analysis with *Brassica napus* and revealed that plant height was the highest positive and direct effect on seed yield per plant followed by number of siliqua per plant and siliqua length.

An experiment was conducted with 10 Canola varieties by Khayat *et al*. (2012), stepwise regression and path analysis indicated that, the number of pods per plant had the highest direct effect on grain yield. In addition, total dry matter, 1000-grain weight, and flowering and days to maturity also had a high direct effect on grain yield.

Uddin *et al.* (2013); conducted an experiment with *Brassica rapa* genotypes to study path coefficient and reported that days to 50% flowering, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, siliqua length, seed per siliqua and thousand seed weight showed direct positive association with seed yield per plant while the plant height and days to maturity had direct negative association.

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

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 pods per plant, number of seeds per pod, and 1000 seed weight had positive direct effect on seed yield.

2.4 Genetic divergence

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

Peter and Rai (1995), 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.

Singh *et al.* (1997); studied genetic divergence with 50 genotypes of *Brassica napus* growing in 12 environments. They observed 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 program.

Jagadev *et al*. (1999); studied on 19 genotypes of rape seed (*Brassica napus*) and found that the yield and yield contributing traits grouped the genotypes into five clusters with clusters I comprising these genotypes, clusters II and 12 each and clusters IV and V one each.

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

Yadava *et al.* (2004); studied on 50 *Brassica napus* genotypes and reported that the genotypes 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 traits 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.

Goswami and Behl (2006), studied 43 genotypes of Indian mustard using D^2 statistics. They collected 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.

Vivek *et al.* (2007); studied the genetic diversity in 81 advanced generation cultivars of Indian mustard. 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. 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.

Hossain *et al.* (2008); studied the genetic divergence using D^2 statistic in 40 genotypes of rape seed. The genotypes differed significantly for 10 yield and yield contributing traits, and they grouped them into nine clusters. They observed that there was no close correspondence between geographical distribution and genetic divergence. Number of siliqua on the main raceme, seeds per siliqua and harvest index had major contribution to genetic divergence. The genotypes under cluster IV were suggested for use in heterosis breeding.

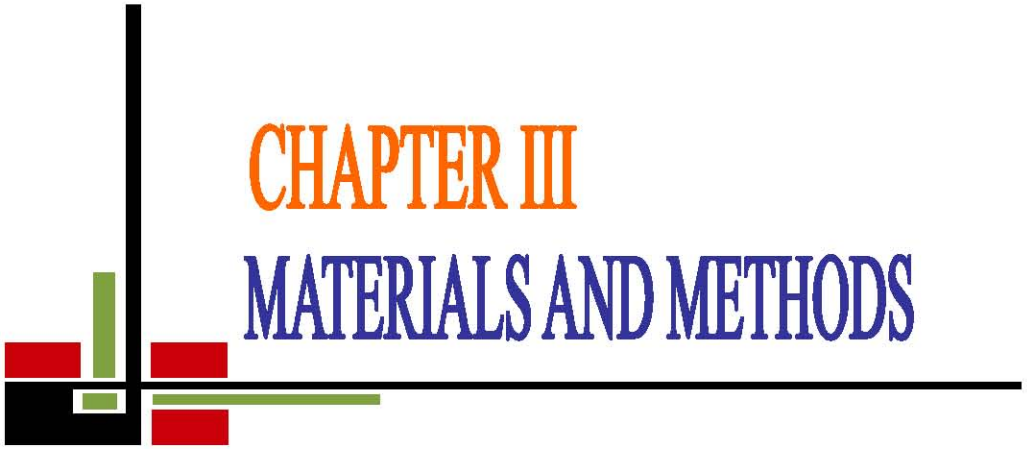
Zaman *et al.* (2010); examined a field experiment for estimation of divergence among 45 advanced lines of mustard. The genotypes were grouped into four clusters. Cluster I contained the highest number of genotypes (6) and cluster III contained the lowest (3). The highest intra cluster distance was observed in cluster II and the lowest in I. The highest inter cluster distance was observed between the cluster III and II followed by III and I; and the lowest between cluster IV and III. Days to 50% flowering (81.94%), days to maturity (8.24%), plant height (5.82 %), branches per plant (1.91%) and siliqua per plant (1.17%) contributed maximum towards the total divergence which suggested that these characters were highly responsible for genetic divergence in the present materials.

Pandey *et al.* (2013); studied with 45 Indian mustard genotypes of different origin from India for evaluated of diversity. D^2 analysis was conducted to measure the genetic diversity among the genotypes. The 45 genotypes were grouped into eight clusters using Tocher's method. Intra cluster distance was maximum for cluster VI followed by cluster III. The maximum inter-cluster distance was found between cluster II and III indicating high genetic divergence among genotypes of these groups. 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%).

Iqbal *et al.* (2014); reported on different genotypes to determine the genetic diversity among different mustard genotypes. The genotypes were grouped into four clusters by using Euclidean distance following Ward's method. The cluster III had higher intra cluster distance and the maximum inter cluster distance was observed between genotypes of clusters I and IV followed by clusters III and IV.

Khan (2014), studied in 211 *Brassica napus* genotypes to evaluate the genetic diversity. Through cluster analysis all the genotypes were divided into five main groups. It was found that seven out of 21 principal components with an eigenvalue of ≥ 1.0 accounted for 69.99% of the overall differences found among 211 genotypes of *Brassica napus* L. The contribution of first three PCs in overall PCs was 26.96%, 10.00% and 8.9%, respectively.

Rameeh (2015), studied on twenty one rape seed genotypes. On the basis of cluster analysis, the genotypes were the high seed yield genotypes with high mean value of pods on main axis and pods per plant were classified in group 1 (C1). Group 1 (C1) and group 2 (C2) had 1545.56 and 2160.55 kg per ha of seed yield.



CHAPTER III

MATERIALS AND METHODS

CHAPTER III

MATERIALS AND METHODS

3.1 Experimental site

The research work was conducted at the experimental farm of the Department of the Genetics and Plant Breeding, Sher-e-Bangla Agricultural University (SAU), Dhaka-1207, Bangladesh. The duration of the experiment was November 2015 to February 2016. The soil of the experimental plot was clay loam with medium high with medium fertility level. The general climatic feature of the experimental site was subtropical climatic weather having wet summer and dry winter. The location of the experimental site was situated at 23^0 74' N latitude and 90^0 35' E longitudes with an elevation of 8.6 meter from the sea level. Photograph showing experimental sites (Appendix I).

3.2 Soil and climate

The experimental site was situated in the subtropical zone. The soil of the experimental site belongs to Agroecological 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 is 0.82% (Appendix II). The records of air temperature, humidity and rainfall during the period of experiment were noted from the weather station, Sher-e-Bangla Agricultural University, Dhaka 1207 (Appendix III).

3.3 Experimental materials:

The healthy seeds of 62 advanced lines of F_5 of *Brassica napus* L. collected from the Dept. of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, which were used as experimental materials. These materials were developed through intergenotypic crosses. The materials used in that experiment is shown in (Table 1).

Table 1. Materials used for the experiment

Population	F_5 Population	Source
G1	Nap- 9908 ×BS- 13	SAU
G2	Nap- 179 × Nap- 2001	SAU
G3	Nap- 248 × Nap- 159	SAU
G4	Nap- 2037 × Nap- 2057	SAU
G5	Nap- 94006 ×BS- 7	SAU
G6	Nap- 2012 × Nap- 2013	SAU
G7	Nap- 94006 × Nap- 2013	SAU
G8	Nap- 248 × Nap- 206	SAU
G9	Nap- 206 × Nap- 2012	SAU
G10	Nap- 2037 × Nap- 2022	SAU
G11	Nap- 9908 × Nap- 94006	SAU
G12	Nap- 9908 × Nap- 2037	SAU
G13	Nap- 2037 × Nap- 248	SAU
G14	Nap- 206 × Nap- 2013	SAU
G15	BS- 7 × Nap- 206	SAU
G16	Nap- 2001 × Nap- 2022	SAU
G17	Nap- 94006 ×BS- 13	SAU
G18	Nap- 2037 × Nap- 2012	SAU
G19	Nap- 2037 × Nap- 206	SAU
G20	Nap- 9908 × Nap- 2022	SAU
G21	BS- 13 × Nap- 2022	SAU
G22	Nap- 179 × Nap- 206	SAU
G23	Nap- 9908 × Nap- 206	SAU
G24	Nap- 9908 × Nap- 248	SAU
G25	Nap- 2012 × Nap- 2022	SAU
G26	Nap- 248 × Nap- 2022	SAU
G27	BS- 13 × Nap- 2013	SAU
G28	Nap- 9908 × Nap- 2001	SAU
G29	Nap- 2037 ×BS- 13	SAU
G30	BS- 13× Nap- 206	SAU
G31	Nap- 9908 × Nap- 2013	SAU

Table 1. Continued

Population	F_5 Population	Source
G32	Nap- 248 × Nap- 2013	SAU
G33	Nap- 179 × Nap- 2057	SAU
G34	Nap- 179 × Nap- 2022	SAU
G35	Nap- 2037 × Nap- 2013	SAU
G36	Nap- 248 × Nap- 2057	SAU
G37	Nap- 94006 × Nap- 2057	SAU
G38	BS- 7 × Nap- 2013	SAU
G39	Nap- 2057 × Nap- 2001	SAU
G40	BS- 13 × Nap- 2001	SAU
G41	Nap- 94006 × Nap- 2001	SAU
G42	BS- 13 × Nap- 2057	SAU
G43	Nap- 179 × Nap- 2012	SAU
G44	Nap- 2001 × Nap- 179	SAU
G45	BS- 13 × Nap- 179	SAU
G46	BS- 7 × Nap- 2057	SAU
G47	Nap- 206 × Nap- 2022	SAU
G48	Nap- 206 × Nap- 2057	SAU
G49	Nap- 9908 × Nap- 2012	SAU
G50	Nap- 179 × Nap- 2013	SAU
G51	Nap- 248 × Nap- 2012	SAU
G52	Nap- 2057 × Nap- 248	SAU
G53	BS- 7 × Nap- 2013	SAU
G54	Nap- 94006 × Nap- 179	SAU
G55	Nap- 2001 × Nap- 2013	SAU
G56	Nap- 94006 × Nap- 2022	SAU
G57	Nap- 2057 × Nap- 2012	SAU
G58	Nap- 2001 × Nap- 248	SAU
G59	Nap- 2057 × Nap- 2022	SAU
G60	Nap- 94006 × Nap- 2012	SAU
G61	Nap- 94006× Nap- 206	SAU
G62	Nap- 2001 × Nap- 206	SAU

3.4 Methods

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

3.4.1 Land preparation

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

3.4.2 Application of manure and fertilizer

The crop was fertilized at the rate of 10 tons of cowdung, The fertilizers like urea, triple super phosphate, muriate of potash, gypsum and zinc sulphate were applied in quantities of 270,170,100,150 and 5kg/ha, respectively. The half amount of urea, total amount of cowdung, TSP, MoP, 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 two replications. The total area of the experiment was 56m × 14m = 784 m^2. Each replication size was 56m × 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 14 November 2015. The seeds were placed at about 1.5 cm depth in the soil. After sowing the seeds were covered with soil carefully so that no clods were on the seeds. A pictorial view of experimental plot was shown in (Plate 1).

3.4.4 Intercultural operations

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

Plate 1. Pictorial view of experimental plot showing different population with tags at flowering stages

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. Second thinning was performed after seven days of 1st thinning for maintaining a distance of 10 cm from plant to plant in rows of 30 cm apart. The critical weed free period for *Brassica* is 15 to 30 days after sowing. Second weeding was done after 30 days of sowing. Plants were flowering on 12 December 2015. Aphid infection was found in the crop during the siliqua development stage. Siliqua formation starting date was 1 January 2016. To control aphids Malathion-57 EC @ 2ml/liter of water was applied. The insecticide was applied in the afternoon.

3.4.5 Crop harvesting

Harvesting was done after 90 days after sowing (DAS) depending upon the maturity. Harvesting was done on 29 February 2016. When 80% of the plants showed symptoms of maturity i.e. straw color of siliqua, leaves, stems desirable seed color in the mature siliqua, the crop was assessed to attain maturity (Plate 2). A photograph of plant harvesting was shown in (Plate 3). Ten plants were selected at random F_5 progenies in each replication. The plants were harvested by uprooting and then they were tagged properly (Plate 4). Data were recorded on different parameters from these plants.

3.4.6 Data collection

For studying different genetic studies, ten characters were taken into consideration. Data were collected from all replications start from 10 March 2016. A pictorial view of observation and data collection is presented in (Plate 5). The data were recorded on ten selected plants on the following traits:

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

ii. **Days to 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 centimeter (cm) from the base of the plant to the tip of the longest inflorescence. Data were taken after harvesting.

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

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

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

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

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

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

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

Plate 2. Straw color of siliqua, leaves and stems are the symptoms of 80% plant maturity

Plate 3. Photograph showing the harvesting of *Brassica napus* L.

Plate 4. Photograph showing harvested plant properly tagging according to accession number.

Plate 5. Photograph showing field observation (above) and data collection (below).

3.5 Statistical analysis

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

i) Estimation of genotypic and phenotypic variances:

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

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

Where, MSG = Mean sum of square for population

MSE = Mean sum of square for error, and

r = Number of replication

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

$\bar{x}$ = Population mean

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

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

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

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

Where, GCV = Genotypic co-efficient of variation

PCV = Phenotypic co-efficient of variation

δ_g = Genotypic standard deviation

δ_p = Phenotypic standard deviation

$\bar{x}$ = Population mean

iii) Estimation of heritability:

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

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

Where, h^2_b = Heritability in broad sense

δ^2_g = Genotypic variance

δ^2_p = Penotypic variance

iv) Estimation of genetic advance:

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

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

Where, GA = Genetic advance

δ^2_g = Genotypic variance

δ^2_p = Phenotypic variance

δ_p = Phenotypic standard deviation

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

v) Estimation of genetic advance in percentage of mean

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

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

vi) Estimation of genotypic and phenotypic correlation co-efficient

The calculation of genotypic and phenotypic correlation co-efficient for all possible combinations through the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956) were adopted. The genotypic co-variance component between two traits and have the phenotypic co-variance component were derived in the same way as for the corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows:

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

Where,

σ_{gxy} = Genotypic co-variance between the traits x and y

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

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

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

Where,

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

σ^2_{px} = Phenotypic variance of the trait x

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

vii) Path co-efficient analysis:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

riy = Correlation of the character with yield.

viii) Estimation of Genetic Diversity

a. Principal Component Analysis (PCA)

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

b. Principal Coordinate Analysis (PCO)

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

c. Canonical Vector Analysis (CVA)

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

d. Average Intra-cluster Distances

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

e. Clustering

To divide the population of the study into some number of mutually exclusive groups clustering were done using non-hierarchical classification. Starting from some initial classification of the population into required groups, the algorithm repeatedly transfers population 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 population of different classes and so on.

CHAPTER IV

RESULTS AND DISCUSSION

CHAPTER IV

RESULTS AND DISCUSSIONS

The results of the present investigation of genetic analysis that means genetic variability, associations of characters, path coefficient analysis and diversity studies of *Brassica napus* are described in this chapter. The data ware recorded on 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 weigh t(g) and seeds in per plant (g). The data ware presented and discussed under the following sections.

- Variability study in *Brassica napus* L.
- Estimates of genetic parameters (PCV, GCV, h^2 and GAM).
- Relationship among yield and yield contributing traits (Correlationan and path co-efficient).
- Genetics diversity

4.1 Variability study in *Brassica napus* L.

4.1.1 Analysis of variance

The analysis of variance of different *Brassica napus* population for yield and yield contributing traits are shown in (Table 2). Analysis of variance indicated that the highly significant difference among population for all the traits ($p<0.01$) under the study viz., days to 50% flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, siliqua per plant, siliqua length (cm), seeds per siliqua, 1000 seed weight (g) and seed yield per plant (g), indicating the presence of sufficient genetic variability in the population. This suggested that adequate scope was available for selection of superior population aimed at enhancing genetic yield potential of *Brassica napus*. High magnitude of variability has been earlier reported in mustard germplasm and varieties for these traits by Walle *et al.* (2014); Khan *et al.* (2013); Mahmud *et al* (2008); Choudhary *et al.* (2003).

Table 2. Analysis of variance for different characters of *Brassica napus* L.

Characters	Mean sum of square		
	Replication (r-1) = 1	Population (g-1) = 61	Error (r-1)(g-1) = 61
Days to 50% flowering	52.911	9.7593**	0.173
Days to maturity	75.879	23.453**	0.141
Plant height (cm)	72.268	148.960**	29.238
Primary branches per plant	1.011	1.058**	0.186
Secondary branches per plant	0.002	1.353**	0.307
Siliqua per plant	34.282	1,023.550**	231.603
Siliqua length (cm)	0.490	0.726**	0.156
Seeds per siliqua	8.840	22.608**	4.848
1000-seed weight (g)	0.152	1.145**	0.365
Seed yield per plant (g)	1.306	3.681**	0.882

** Denote Significant at 1% level of probability

The reason for high magnitude of variability in the present study may be due the fact that the population selected were developed in different breeding programs representing different agro-climatic conditions of the country.

4.1.2 Performance of the population for yield and yield contributing traits

The mean performances of the 62 *Brassica napus* population for their traits are described as follows.

4.1.2.1 Days to 50% flowering

Days to 50% flowering differed significantly in all the population ranging from 31.50 to 40.50 with the mean value of 36.54 (Table 3). The CV value of days to 50% flowering was observed 1.14%. The maximum days to 50% flowering was observed in population G17 (40.50) and the lowest found in the population G12 (31.50) (Appendix IV).

4.1.2.2 Days to maturity

Days to maturity was observed from the result of the experiment that days to maturity varied significantly among the 62 population. The average value of days to maturity varied from 76.50 to 89.50 with grand mean value of 82.78 (Table 3). According to the study maximum days to maturity (89.50) was found in G10 whereas minimum (76.50) from G12 (Appendix IV). High days to maturity determined late maturing population and in opposite lowest days to maturity represented early maturing population and it was essential for release early maturing variety.

4.1.2.3 Plant height (cm)

Plant height represent varied from 89.51 cm to 135.30 cm with average of 110.63 cm (Table 2). The coefficient of variation of this trait was 4.89%. The maximum plant height was observed by the population G62 (135.30 cm) and minimum in G2 (89.51 cm) (Appendix IV) (Plate 6).

G62 **G02**

Plate 6. Photograph showing variation between highest G62 (Nap 2001*Nap 206) and lowest plant height G02 (Nap 179*Nap 2001) of *Brassica napus* L.

4.1.2.4 Primary branches per plant

From the result of the experiment it was observed that primary branches per plant were varied significantly among the 62 *Brassica napus* population. The ranges of primary branches per plant were from 2.20 to 5.70 with the grand mean value of 3.14 (Table 3). A maximum primary branch per plant (5.70) was found in G45 whereas minimum (2.20) from G48 (Appendix IV) (Plate 7). According to the study G45 *Brassica napus* population has the highest primary branches per plant.

4.1.2.5 Secondary branches per plant

The population G62 recorded maximum secondary branches per plant (5.50) while the minimum was observed by the population G36 (1.30) (Table 3) (Plate 8).

4.1.2.6 Siliqua per plant

Siliqua per plant was observed from 56.88 to 186.35 with the grand mean of 117.92. The maximum siliqua per plant was found in the population G45 (186.35) while the minimum was observed in G4 (56.88). (Table 3) (Plate 9).

4.1.2.7 Siliqua length (cm)

Siliqua length was ranged from 7.44 cm to 9.87 cm with the grand mean value of 8.63 cm. (Table 3). Maximum siliqua length was observed in the population G33 (9.87 cm) while the minimum was observed in the population G54 (7.44 cm) (Plate 10).

4.1.2.8 Seeds per siliqua

Seeds per siliqua ranged were observed from 17.33 to 31.14 with the average of 24.78. The coefficient of variation was 8.88%. Maximum seeds per siliqua was found by the population G52 (31.14) and the minimum was observed from the population G61 (17.33) (Appendix IV).

4 .1.2.9 1000 seed weight (g)

1000 seed weight was observed from 1.56 g to 5.59 g with the grand mean value of 4.00 g. The maximum 1000 seed weight was observed in the population G27 (5.59 g) and the minimum was observed in the population G6 (1.56 g). (Plate 11).

Table 3. Range, mean, CV (%) and standard deviation of 62 population of *Brassica napus* L.

Parameters	Range				Grand Mean	MS	CV (%)	SD	SE
	Min		Max						
	Population	Value	Population	Value					
Days to 50% flowering	G12	31.50	G17	40.50	36.54	9.76	1.14	0.42	0.16
Days to maturity	G12	76.50	G10	89.50	82.78	23.45	0.45	0.38	0.14
Plant height (cm)	G2	89.51	G62	135.30	110.63	148.96	4.89	5.41	2.04
Primary branches per plant	G48	2.20	G45	5.70	3.14	1.06	13.87	0.44	0.16
Secondary branches per plant	G36	1.30	G62	5.50	2.45	1.35	22.61	0.55	0.21
Siliqua per plant	G4	56.88	G45	186.35	117.92	1023.55	12.91	15.22	5.75
Siliqua length (cm)	G54	7.44	G33	9.87	8.63	0.73	4.58	0.39	0.15
Seeds per siliqua	G61	17.33	G52	31.14	24.78	22.61	8.88	2.20	0.83
1000-seed weight (g)	G6	1.56	G27	5.59	4.00	1.15	15.12	0.60	0.23
Seed yield per plant (g)	G24	3.78	G32	9.49	6.40	3.68	14.68	0.94	0.36

CV (%) = coefficient of variation, SD = standard deviation and SE = standard error

G45 **G48**

Plate 7. Photograph showing variation between highest G45 (BS-13*Nap 179) and lowest G48 (Nap 206* Nap 2057) primary branches of *Brassica napus* L.

G62 **G36**

Plate 8. Photograph showing variation between highest G62 (Nap 2001*Nap 206) and lowest G36 (Nap 248*Nap 2057) secondary branches of *Brassica napus* L.

G45 **G04**

Plate 9. Photograph showing variation between highest G45 (BS-13*Nap 179) and lowest G04 (Nap 2037*Nap 2057) siliqua per plant of *Brassica napus* L.

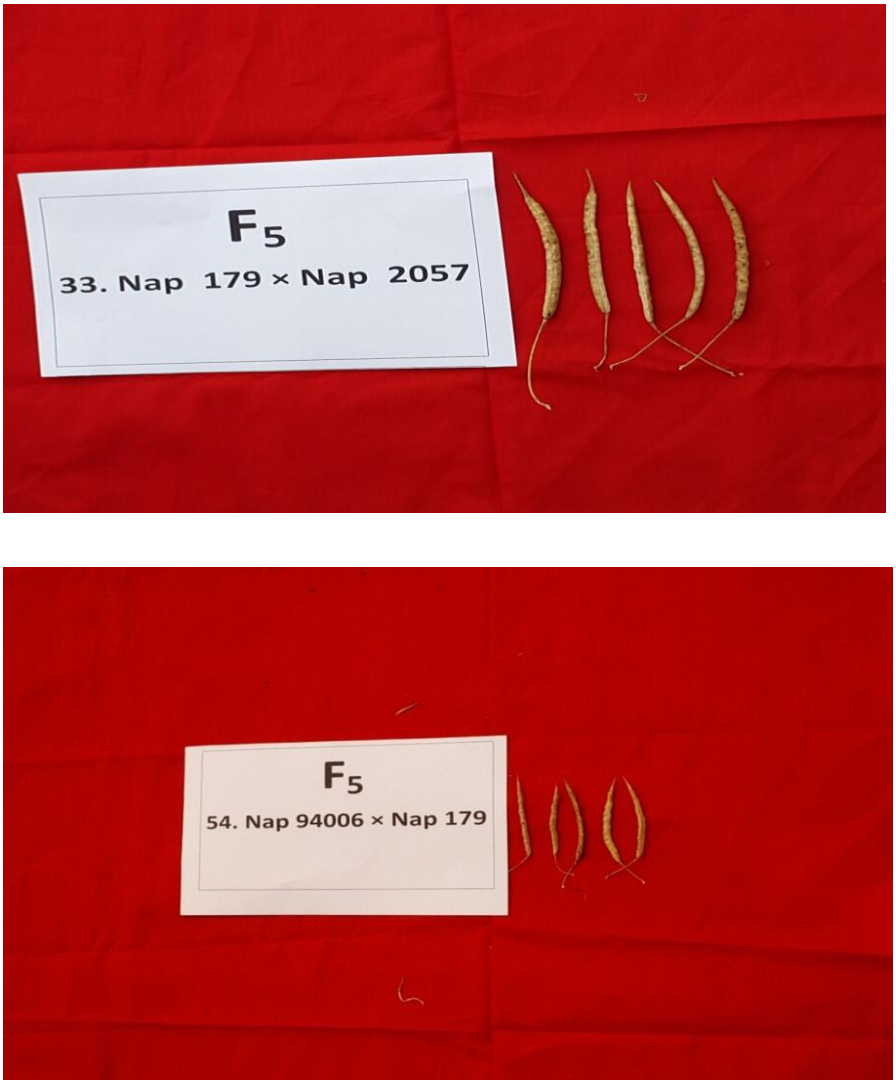


Plate 10. Photograph showing variation between highest G33 (Nap 179*Nap 2057) and lowest G54 (Nap 94006*Nap 179) siliqua length of *Brassica napus* L.

2 G06

Plate 11. Photograph showing variation between highest G22 (BS-13*Nap 2013) and lowest G06 (Nap 2012*Nap 2013) of 1000 seed weight of *Brassica napus* L.

4.1.2.10 Seed yield per plant (g)

Seed yield per plant was observed from 3.78 g to 9.49 g with an average of 6.40 g. The maximum seed yield per plant was observed in G32 (9.49 g) while minimum was observed in G24 (3.78 g). (Appendix IV).

4.2. Estimates of Genetic Parameters

Genetic parameters (Table 4) were studied to examine genetic worth of yield and yield contributing traits, based on genetic variability estimates viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2), and genetic advance as percent of mean (GAM).

4.2.1. Estimates of Variance Components

The variance components include genotypic variance, environmental variance and phenotypic variance which are presented in (Table 4) and discussed here. Estimated genetic variance ranged from 0.29% for siliqua length to 395.97% for siliqua per plant (Table 4). Likewise phenotypic variance ranged from 0.62% for primary branches per plant to 627.58% for siliqua per plant.

The highest environmental variance observed 231.60% was siliqua per plant which indicated that environmental component in total variation is high. Maximum genotypic and phenotypic variances were exhibited by siliqua per plant (627.58% and 395.97%) followed by plant height (89.10% and 59.86%).The highest genotypic and phenotypic variance was 627.58% and 395.97% respectively in the same trait; indicate the presence of high variation for this trait. The lowest environmental, genotypic and phenotypic variances were 0.16, 0.29 and 0.44, respectively for siliqua length, this indicated the presence of low variation for this trait. All of the above results showed the potential of variation that exist in different traits. According to Engida (2007) traits that showed the different genotypic, phenotypic and environmental values indicates the presence of variation among the traits used.

Table 4. Estimation of phenotypic, genotytpic and environmental variance for different characters of *Brassica napus* L.

Parameters	**$\sigma^2 p$**	**$\sigma^2 g$**	**$\sigma^2 e$**
Days to 50% flowering	4.97	4.79	0.17
Days to maturity	11.80	11.66	0.14
Plant height (cm)	89.10	59.86	29.24
Primary branches per plant	0.62	0.43	0.19
Secondary branches per plant	0.83	0.52	0.31
Siliqua per plant	627.58	395.97	231.60
Siliqua length (cm)	0.44	0.29	0.16
Seeds per siliqua	13.73	8.88	4.85
1000-seed weight (g)	0.76	0.39	0.37
Seed yield per plant (g)	2.28	1.40	0.88

$\sigma^2 p$ = Phenotypic variance, $\sigma^2 g$ = Genotypic variance and σ^2 e = Environmental variance

4.2.2. Estimates of Genotypic and Phenotypic Coefficient of Variation

The results of Coefficient of variation indicated that the estimates of phenotypic coefficient of variation (PCV) were higher than the corresponding genotypic coefficient of variation (GCV) for all the traits studied (Table 5). Similar findings pertaining to presence of high genetic variability were reported for different traits including seed yield/plant (Singh 2004).Higher estimates of phenotypic coefficient of variation (PCV) than genotypic coefficient of variation (GCV) for all the traits reflected the influence of environmental factor on these traits. Phenotypic coefficients of variation ranged from 4.15% for days to maturity to 37.15% for secondary branches per plant. Genotypic coefficients of variation ranged from 4.12% for days to maturity to 29.48% for secondary branches per plant**.** Maximum genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was recorded for number of secondary branches per plant (37.15 and 29.48) followed by primary branches per plant (25.17 and 21.00) and seed yield per plant (23.61 and 18.49).These results were well supported by similar findings by Kumar *et al.* (2007). Singh *et al.* (2011) and Kumar *et al.* (2013) reported high values for PCV and GCV for the number of secondary branches per plant and for seed yield per plant. PCV and GCV were classified as suggested by Shiva Subramanian and Menon (1973) as follows, 0–10% -low, 10-20 – moderate, 20% and above – high. The high values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for these traits suggested the possibility of yield improvement through selection of these traits. High values for PCV and GCV indicates that the population could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for these characters. High to moderate PCV and GCV values were shown by all the characters except days to 50% flowering, days to maturity, plant height and siliqua length that showed low PCV and GCV values. The present result revealed that, higher PCV and GCV were recorded for primary branches per plant (25.17% and 21.00%), secondary branches per plant (37.15% and 29.48%), siliqua per plant (21.24% and 16.88%), 1000 seed weight (21.73% and 15.62%) and seed yield per plant (23.61% and 18.49%) (Table 5) (Figure 1). The difference between PCV and GCV values was low indicating the low effects of environment in these characters. The difference in genotypic coefficient of variation and phenotypic coefficient of variation values were closer in the days to 50% flowering, days to maturity, plant height, siliqua length

Table 5. Estimation of phenotypic, genotypic and environmental coefficient of variation for different characters of *Brassica napus* L.

Parameters	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
Days to 50% flowering	6.10	5.99	1.14	96.50	4.43	12.12
Days to maturity	4.15	4.12	0.45	98.80	6.99	8.44
Plant height (cm)	8.53	6.99	4.89	67.18	13.06	11.81
Primary branches per plant	25.17	21.00	13.87	69.61	1.13	36.09
Secondary branches per plant	37.15	29.48	22.61	62.97	1.18	48.19
Siliqua per plant	21.24	16.88	12.91	63.10	32.56	27.61
Siliqua length (cm)	7.70	6.19	4.58	64.64	0.88	10.25
Seeds per siliqua	14.95	12.02	8.88	64.68	4.94	19.92
1000-seed weight (g)	21.73	15.62	15.12	51.62	0.92	23.11
Seed yield per plant (g)	23.61	18.49	14.68	61.34	1.91	29.84

PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation.

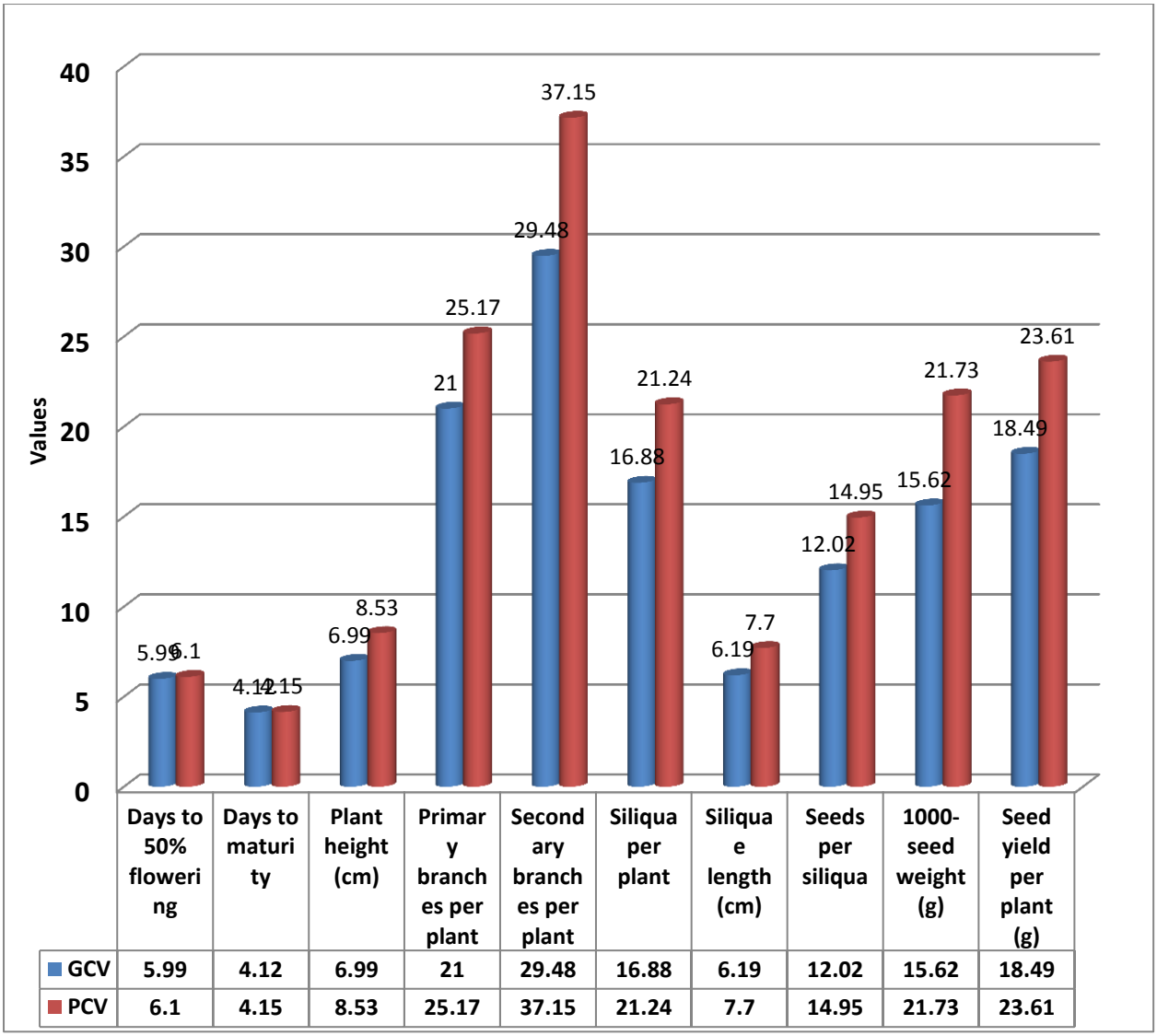


Figure 1. Genotypic and phenotypic co-efficient of variation of *Brassica napus* L.

indicates that there was a minimum influence of environment on these characters. Phenotypic coefficient of variation values was higher than their corresponding genotypic coefficient variation values in the characters primary branches per plant, secondary branches per plant, siliqua per plant 1000 seed weight and seed yield per plant indicating environmental influences have some extend on the expression of these traits.

4.2.3. Estimates of Heritability and Genetic Advance

Broad sense heritability values were higher (more than 61%) for all the characters except 1000 seed weight (51.62%). Broad sense heritability ranged from 51.62% (1000 seed weight) to 98.80 % (days to maturity). These broad sense heritability values were likely to be overestimated as in this calculation it was not possible to exclude variation due to different genetic components and their interactions.

The present estimation of high heritability was observed in days to 50% flowering (96.50), days to maturity (98.80), plant height (67.18), primary branches per plant (69.61), secondary branches per plant (62.97), siliqua per plant (63.10), siliqua length (64.64), seeds per siliqua (64.68) and seed yield per plant (61.34). The heritability of the highest magnitude was noticed for days to maturity (98.80). Thus, it indicated that larger proportion of phenotypic variance has been attributed to genotypic variance and reliable selection could be made on the basis of phenotypic expression. High estimates of heritability in broad sense indicate that substantial improvement can be made using standard selection procedures. In general, characters which exhibited high heritability suggest that the selection would be more effective whereas characters showing low heritability indicate that the selection would be affected by environmental factors. Based on the observation, in the present study, it can be surly concluded that selection of population based on days to 50% flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, siliqua per plant, siliqua length, seeds per siliqua and seed yield per plant would be more satisfactory.

The heritability estimates were, therefore, to be considered with these limitations in view. However, genetic advance (GA) expressed as percentage of mean was high

(>20%) for the characters like primary branches per plant, secondary branches per plant, siliqua per plant, 1000 seed weight and seed yield per plant. Moderate genetic advance as percent of mean was shown by days to 50% flowering, plant height, siliqua length and seeds per siliqua. The estimate of genetic advance as percent of mean was highest (48.19%) for secondary branches per plant and lowest (8.44%) for days to maturity. Momena (2015) revealed that seed yield per plant exhibits the highest value of heritability while days to 50% flowering exhibit the lowest value of heritability. According to Johnson *et al*. (1955) high heritability estimates along with the high genetic advance is usually more helpful in predicting gain under selection than heritability estimates alone. The estimates of heritability accompanied by estimates of genetic advance as percent of means are more meaningful from the point of expected genetic gain. Genetic advance is the measure of improvement that can be achieved by practicing selection in a population.

The present study revealed high heritability coupled with high expected genetic advance as percent of means were observed in case of primary branches per plant (69.61 and 36.09), secondary branches per plant (62.97 and 48.19), siliqua per plant (63.10 and 27.61), seeds per siliqua (64.68 and 19.92) and seed yield per plant (61.34 and 29.84) (Table 6) (Figure 2) respectively indicating good response to selection for these characters. High heritability and high genetic advance for the above mentioned characters revealed that such characters are controlled additive gene action and selection based on these characters will be effective. Mahla *et al.* (2003) also observed high estimates of heritability coupled with high genetic advance for seed yield per plant, number of siliqua on main branch and number of branches per plant. The above results were also well supported by similar findings by Kumar *et al.* (2007) who reported high heritability along with high genetic advance for days to 50% flowering and number of secondary branches per plant. Mahamood *et al.* (2003) also reported high heritability and corresponding genetic advance values for number of siliqua per plant, seed yield per plant and plant height. Lodhi *et al.* (2014) reported high heritability in conjunction with high genetic advance were observed for seed yield/ plant, number of secondary branches/ plant, 1000 seed weight, number of seeds/ siliqua, primary branch angle, number of primary branches/ plant, siliqua angle, siliqua on main shoot, and siliqua length suggesting predominant role of additive gene action for expression of these traits.

Table 6. Estimation of heritability in broad sense and genetic advance for different characters of *Brassica napus* L.

Parameters	Heritability	Genetic advance (5%)	Genetic advance (% mean)
Days to 50% flowering	96.50	4.43	12.12
Days to maturity	98.80	6.99	8.44
Plant height (cm)	67.18	13.06	11.81
Primary branches per plant	69.61	1.13	36.09
Secondary branches per plant	62.97	1.18	48.19
Siliqua per plant	63.10	32.56	27.61
Siliqua length (cm)	64.64	0.88	10.25
Seeds per siliqua	64.68	4.94	19.92
1000-seed weight (g)	51.62	0.92	23.11
Seed yield per plant (g)	61.34	1.91	29.84

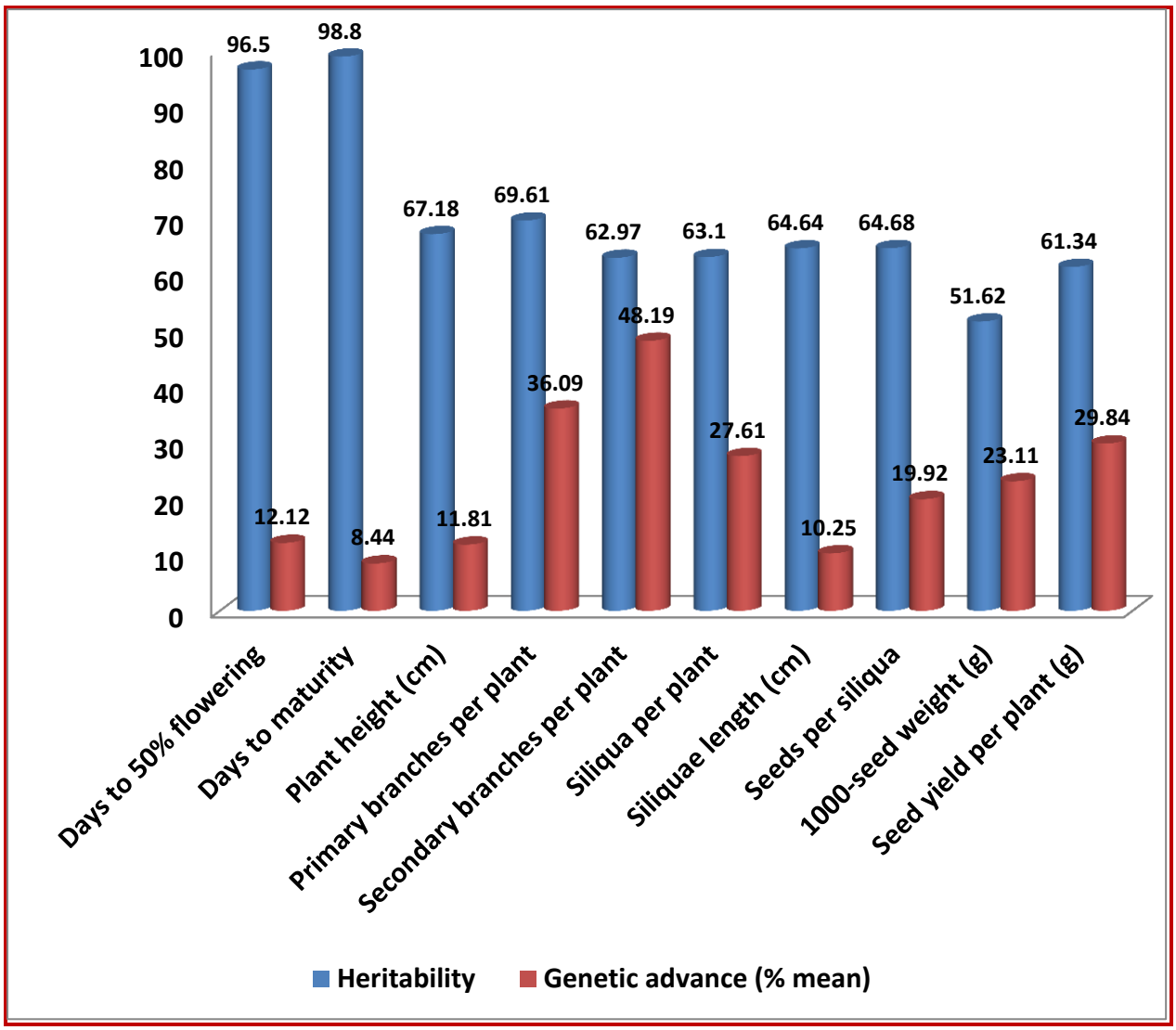


Figure 2. Heritability and genetic advance over mean of *Brassica napus* L.

The medium heritability is being exhibited due to medium environmental effects. Medium heritability accompanied with high genetic advance for the character 1000 seed weight. High heritability along with low and moderate genetic advance was observed for days to 50% flowering (96.50 and 12.12), days to maturity (98.80 and 8.44), plant height (67.18 and 11.81), siliqua length (64.64 and 10.25) indicating that these traits are less amenable for selection, which may be attributed to both non-additive and additive gene effects and these traits can be improved through hybridization and use of hybrid vigour.

4.3 Relationship among yield and yield contributing traits

4.3.1 Estimation of correlation co-efficient

Relationship between seed yield and yield contributing characters was studied through analysis of correlation between them. The correlation coefficients between all the ten characters were presented in genotypic and phenotypic level in (Table 6 and Table 7). The genotypic and phenotypic correlation of seed yield per plant with different characters was presented in (Figure 3).

Seed yield per plant was significant and positive correlation with days to maturity (0.262 and 0.201), plant height (0.385 and 0.420) primary branches per plant (0.534 and 0.524), secondary branches per plant (0.419 and 0.453), siliqua per plant (0.597 and 0.610) at both genotypic and phenotypic level, seed yield per plant was positive significant co relation with siliqua length (0.216), seeds per siliqua (0.249) at phenotypic level and with 1000 seed weight (0.228) at genotypic level. These results were supported by the findings of Sultana (2016), Momena (2015), Siddika (2015) and Rameeh (2015) in mustard. Similar results were obtained by Sirohi*et al.* (2004). Chowdhary *et al.* (1987), Nagaraja (1990), Srivastava and Singh (2002) observed positive significant correlation of seed yield with number of secondary branches. According to Kumar and Kakroo (2009), 1000 seed weight showed positive correlation with seed yield.

Study of correlation at yield component levels exhibited that days to 50% flowering was positively and significantly correlated with siliqua length (0.472 and branches per plant (0.627), number of siliqua per plant (0.614), number of seeds per siliqua (0.362) and 1000 seeds weight 0.362), seeds per siliqua (0.267 and 0.214) at both genotypic

Table 7. Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different population of *Brassica napus* L.

		50F	DM	PH	NPB	NSB	NSP	SL	NSS	TSW
DM	G	0.161								
	P	0.166								
PH	G	0.124	0.157							
	P	0.100	0.115							
NPB	G	0.122	-0.030	0.129						
	P	0.084	-0.040	0.180*						
NSB	G	0.113	0.085	0.114	0.849**					
	P	0.072	0.061	0.157	0.754**					
NSP	G	-0.019	0.040	0.449**	0.632**	0.700**				
	P	-0.014	0.024	0.392**	0.619**	0.665**				
SL	G	0.472**	0.328**	0.166	0.040	-0.099	0.148			
	P	0.362**	0.252**	0.245**	0.040	-0.016	0.123			
NSS	G	0.267**	0.088	0.321**	0.319**	0.058	0.104	0.614**		
	P	0.214*	0.059	0.348**	0.272**	0.125	0.152	0.647**		
TSW	G	0.047	0.189*	-0.153	-0.203*	-0.107	0.023	-0.175	-0.686**	
	P	0.004	0.141	-0.092	-0.057	0.047	0.018	-0.253**	-0.537**	
SYP	G	0.166	0.262**	0.385**	0.534**	0.419**	0.597**	0.129	0.166	0.228*
	P	0.140	0.201*	0.420**	0.524**	0.453**	0.610**	0.216*	0.249**	0.109

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

P: phenotypic correlation coefficient, G: genotypic correlation coefficient.

D50F = days to 50% flowering, DM = days to 80% maturity, PH = plant height (cm), NPB = number of primary branches, NSB = number of secondary branches, NSP = number of siliqua per plant, SL = siliqua length (cm), NSS = number of seeds per siliqua, TSW = 1000 seed weight (g) and SYP = seed yield per plant (g).

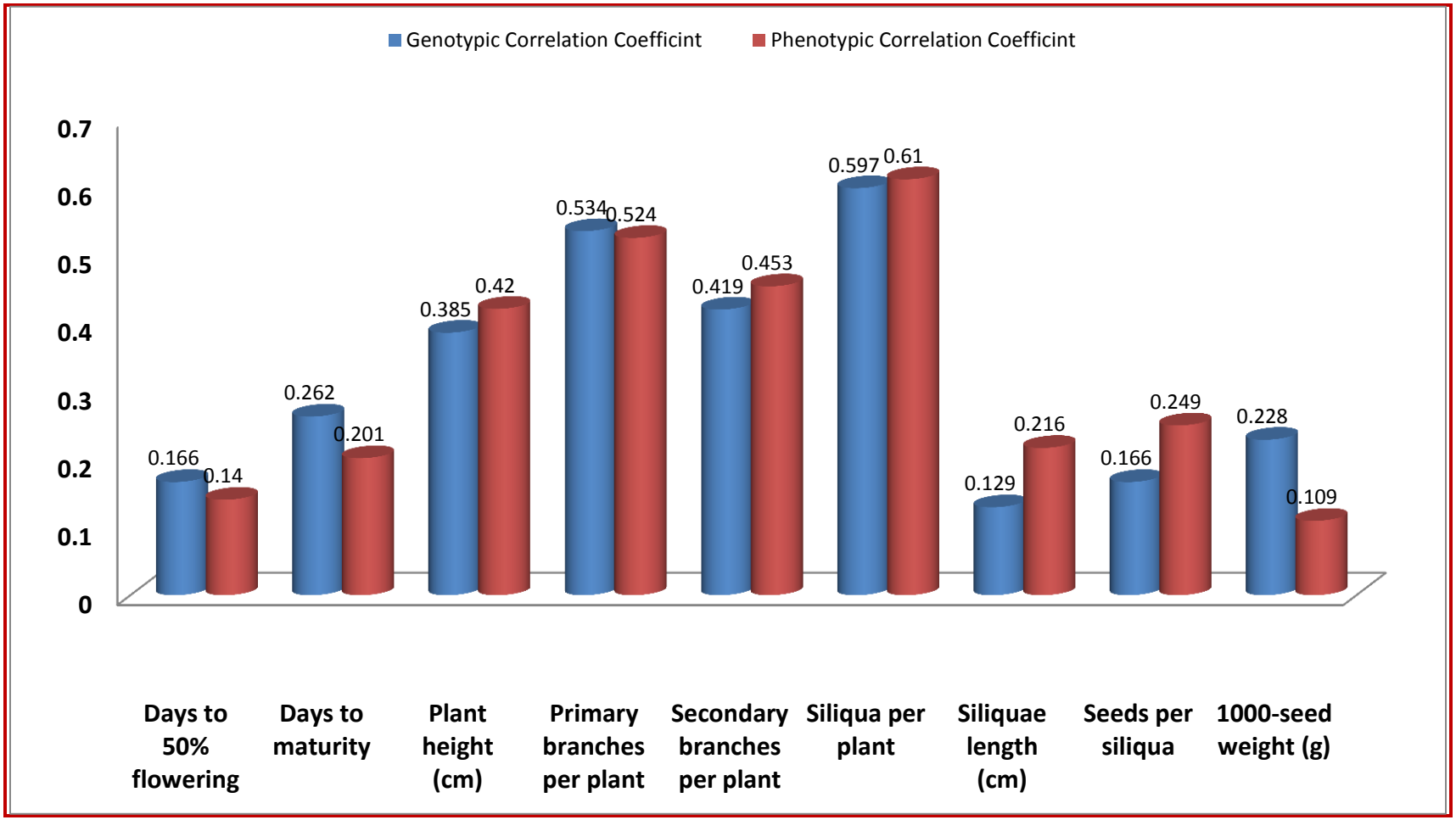


Figure 3. Genotypic and phenotypic correlation co-efficient of nine characters with seed yield of *Brassica napus* L.

and phenotypic level. Association studies of days to maturity was observed positive and significant correlation with siliqua length (0.328and 0.252) at both level.

Plant height was significantly correlated with number of siliqua per plant (0.449 and 0.392) and seeds per siliqua (0.321 and 0.348) at both genotypic and phenotypic levels. Similar associations for plant height seeds per siliqua (Azadgoleh *et al*., 2009) were reported earlier.

Number of primary branches per plant was positively significant correlation with number of secondary branches per plant (0.849 and 0.754), number of siliqua per plant (0.632 and 0.619) and number of seeds per siliqua (0.319 and 0.272) at both genotypic and phenotypic levels. Similar observation was also made by Chowdhary *et al.* (1987), Kumar *et al.* (1987), Srivastava and Singh (2002) and Rai *et al*. (2005).Number of secondary branches per plant was positively significantly correlated with number of siliqua per plant (0.700 and 0.665) at both levels. Siliqua length was positively significant correlated with number of seeds per siliqua (0.614 and 0.647) at both levels. Number of seeds per siliqua was negatively significant correlated with 1000 seed weight (-0.686 and -0.537) at both levels indicating that 1000 seeds weight would be increased with the decrease of number of seeds per siliqua.

4.3.2 Estimation of path co-efficient

As such from existing agro climatic situation based performed using correlation coefficient to determine direct and indirect influence considering ten characters. Seed yield being the complex outcome of different characters was considered as the resultant variable and other characters as causal variable. Estimates of direct and indirect effects of ten yield contributing characters are shown in (Table 8). Among the characters that have positive direct effect on seed yield per plant, days to 50% flowering (0.188), days to maturity (0.293), plant height (0.038), primary (0.397) had positive direct effects on seed yield per plant (Figure 4). These results were agreed with findings of Sultana (2016), Siddika (2015), Momena (2015) and Parvin (2015). The genotypic correlation of days to maturity, plant height, primary branches per plant, number of siliqua per plant, number of seeds per siliqua and 1000 seed weight with seed yield per plant was high. Such high correlation with seed yield per plant

Table 8. Partitioning of genotypic correlations into direct and indirect effects of eight important characters by path analysis of *Brassica napus* L.

Characters	Direct effect	Indirect effect via								Total Indirect Effect	Genotypic correlation with seed yield
		50F	DM	PH	NPB	NSB	NSP	PL	NSS	TSW		
D50F	0.188	-	0.047	0.005	0.076	-0.069	-0.012	-0.185	0.097	0.019	-0.022	0.166
DM	0.293	0.030	-	0.006	-0.019	-0.052	0.025	-0.129	0.032	0.075	-0.032	0.262**
PH	0.038	0.023	0.046	-	0.081	-0.070	0.276	-0.065	0.116	-0.061	0.346	0.385**
PBP	0.627	0.023	-0.009	0.005	-	-0.519	0.388	-0.016	0.115	-0.081	-0.094	0.534**
SBP	-0.611	0.021	0.025	0.004	0.532	-	0.430	0.039	0.021	-0.042	1.03	0.419**
SPP	0.614	-0.004	0.012	0.017	0.396	-0.428	-	-0.058	0.038	0.009	-0.018	0.597**
PL	-0.392	0.089	0.096	0.006	0.025	0.060	0.091	-	0.222	-0.069	0.52	0.129
SPS	0.362	0.050	0.026	0.012	0.200	-0.035	0.064	-0.241	-	-0.272	-0.196	0.166
TSW	0.397	0.009	0.055	-0.006	-0.127	0.065	0.014	0.069	-0.248	-	-0.169	0.228*

Residual effect: **0.576**** = Significant at 1%. * = Significant at 5%.

D50F = days to 50% flowering, DM = days to 80% maturity, PH = plant height (cm), NPB = number of primary branches, NSB = number of secondary branches, NSP = number of siliqua per plant, SL = siliqua length (cm), NSS = number of seeds per siliqua, TSW = 1000 seed weight (g) and SYP = seed yield per plant (g).

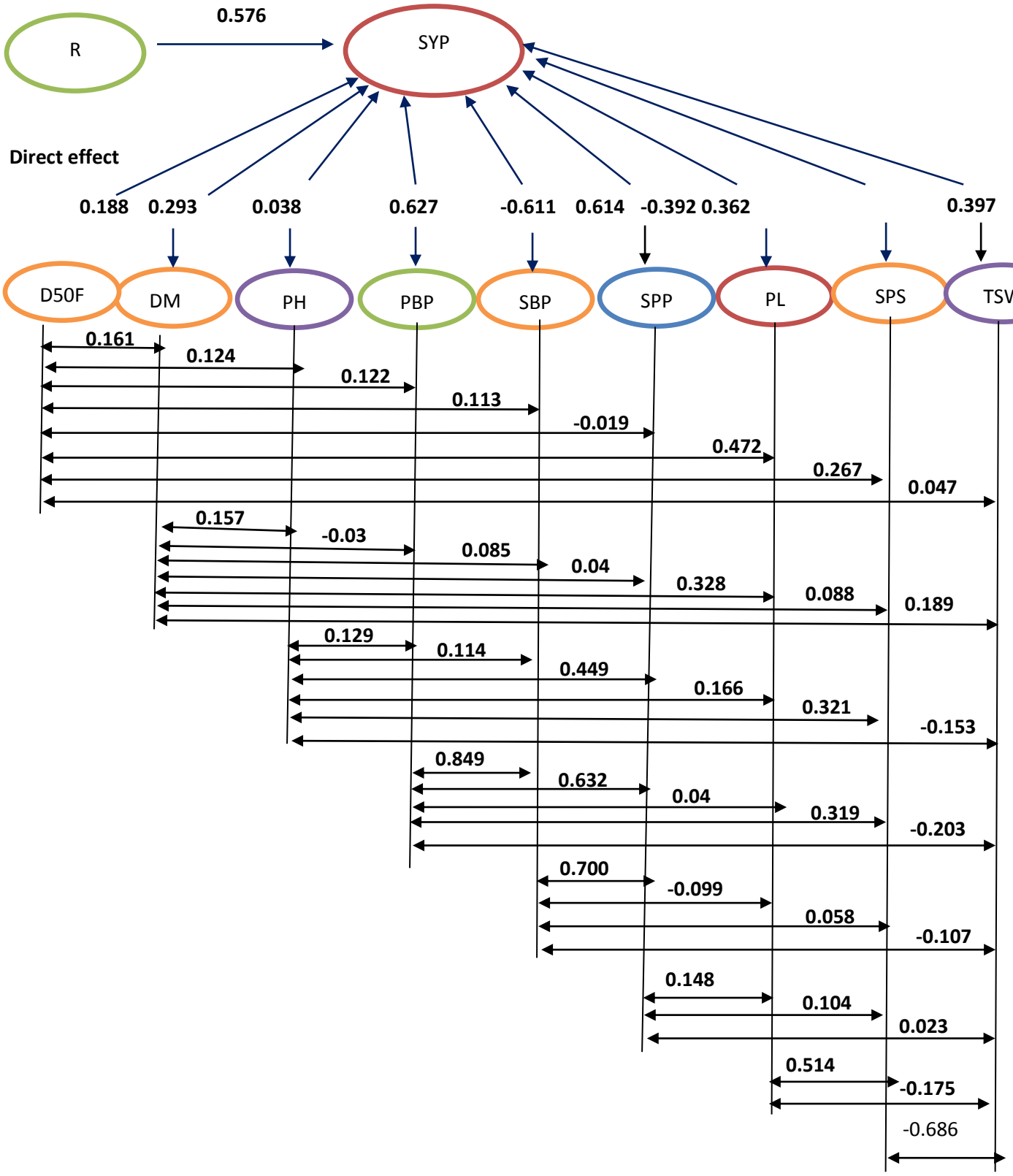


Figure 4. Path diagram of yield contributing traits on yield

was mainly due to the high positive direct effect of these characters. Similar results were in accordance with studies of Dastidar and Patra (2004). Both correlation and path co-efficient studies revealed for days to maturity, primary branches per plant, number of siliqua per plant and 1000 seeds weight were the most important components for getting higher yield. Recent breeding research also emphasized on giving importance of these characters. Therefore, the present study suggested that days to maturity, primary branches per plant, number of siliqua per plant and 1000 seed weight should be included owing to importance in selecting the population for higher seed yield in *Brassica napus*.

4.4 Genetic diversity

Genetic diversity is the total number of genetic characteristics in the genetic makeup of a species. It is distinguished from genetic variability, which describes the tendency of genetic characteristics to vary. Genetic diversity serves as a way for population to adapt to changing environments. The genetic diversity of 62 F_5 materials of *Brassica napus* population are presented in (Table 8 to 14) and (Figure 5 and 6).

4.4.1 Principal Component Analysis (PCA)

The computed Eigen values for the 10 variables subjected to principal component analysis together with the corresponding proportion and cumulative explained variance are given in (Table 9). 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 population with the first axes totally accounted for the variation among the population (32.44).These three principal components account for 66.95% 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%. According to the principal axes I and II, a two dimensional chart (Z1 – Z2) of the population using component score 1 as X axis and component score 2 as Y axis. The scatter diagram revealed that there were five apparent clusters. The population were distantly located

Table 9. Eigen values and yield percent contribution of 10 characters of 62 population of *Brassica napus* L.

Principle component axis	Eigen values	Percent variation	Cumulative % of Percent variation
I	3.244	32.44	32.44
II	2.027	20.27	52.71
III	1.424	14.24	66.95
IV	0.974	9.74	76.69
V	0.768	7.68	84.37
VI	0.546	5.46	89.83
VII	0.428	4.28	94.11
VIII	0.299	2.99	97.10
IX	0.150	1.50	98.60
X	0.139	1.40	100.00

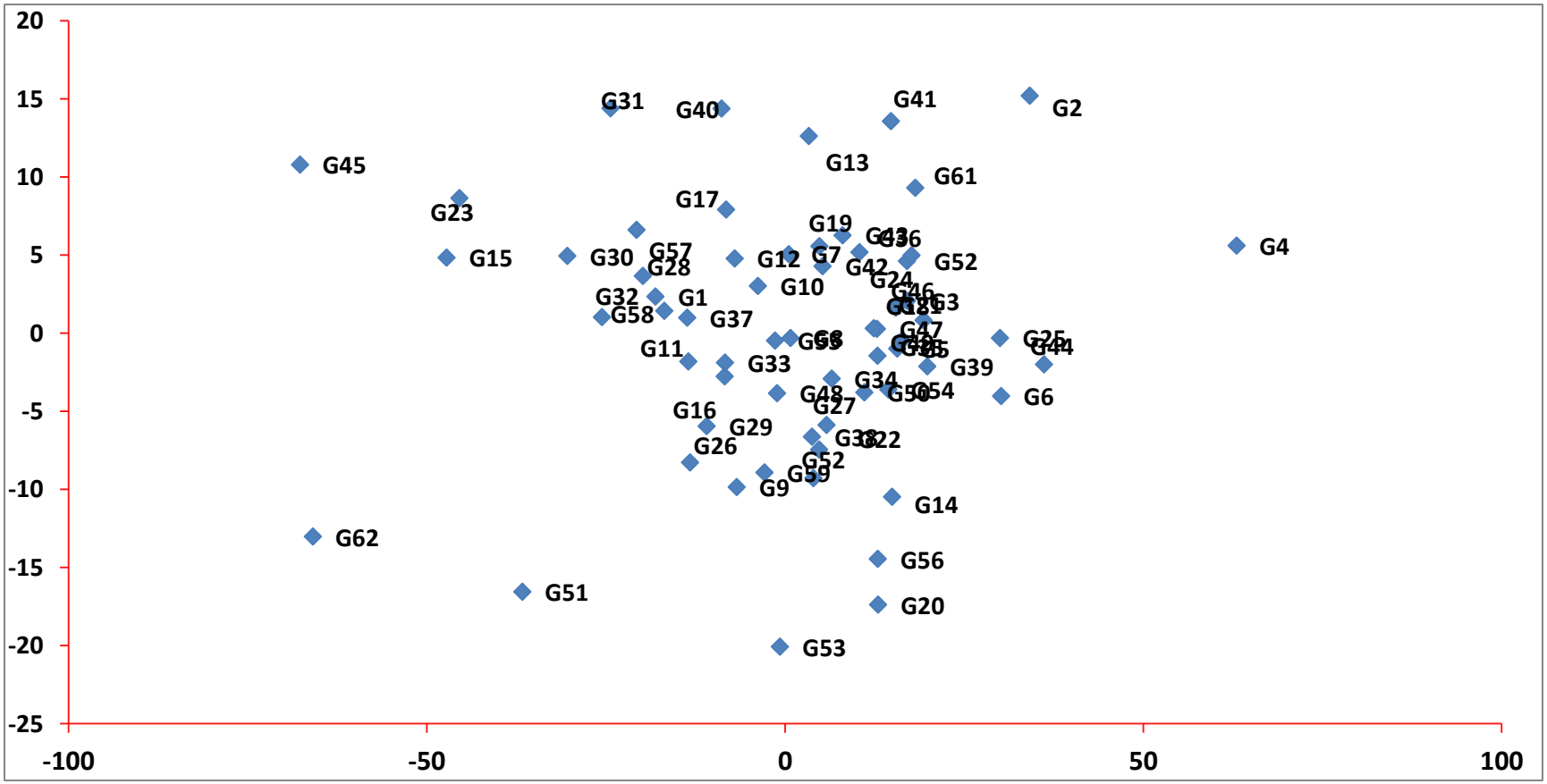


Figure 5. Scatter pattern of *Brassica napus* population of based on their principal component scores

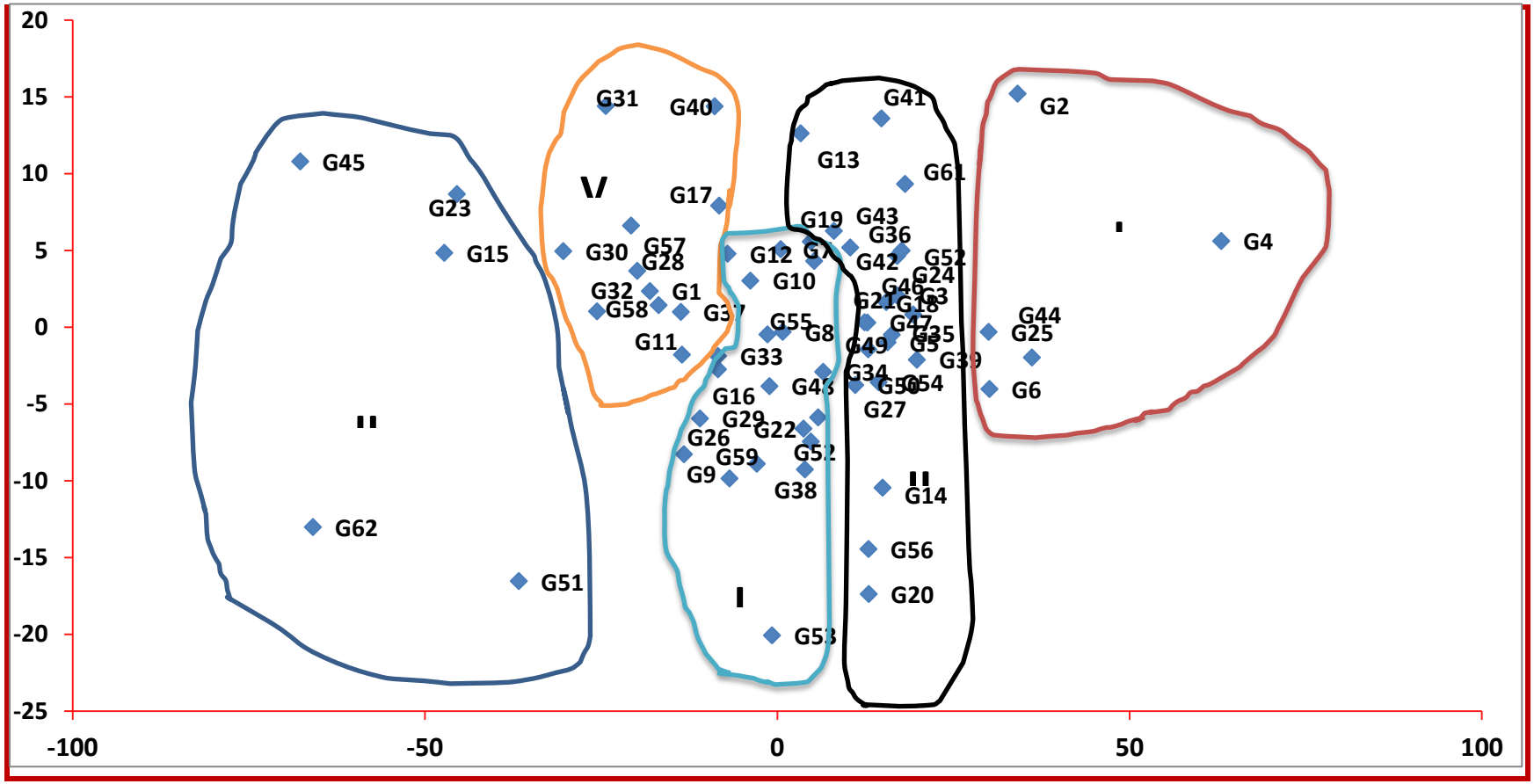


Figure 6. Scatter diagram of *Brassica napus* population of based on their principal component scoress.

from each other (Figure 5).The population of cluster I were more diverse than those of cluster III(Figure 6).

4.4.2 Non-Hierarchical Clustering

Sixty two population were grouped into five clusters through non-hierarchical clustering (Table 9). Most of the population (25) were grouped into cluster II, followed by IV (16) and cluster V (11). Five population were grouped into cluster I and III (Table 10). It is stated that 40.32% population were included in cluster II and it was followed by 25.81% in clusters IV and 17.74% in cluster V and the remaining were in cluster both cluster I and III and 8.06% in each. Rameeh (2015) reported three clusters, Iqbal *et al.* (2014) reported four clusters and Begum *et al.* (2007) reported five clusters in linseed.

4.4.3 Cluster mean

The population from cluster III earned the lowesy cluster mean value for days to 50% flowering (35.3) and highest cluster mean value for plant height (121.21 g), number of primary branch (4.19), number of secondary branch (3.93), number of siliqua per plant (169.41), thousand seed weight (4.33 g) and seed yield per plant (7.8 g) (Table 11). Thus indicates that population of this cluster could be used for parent in future hybridization program for early flowering, more branches, more siliqua, bold seeded and high seed yield.

On the other hand cluster IV produced the highest mean for days to maturity (83.56), siliqua length (9.05 cm), seeds per siliqua (27.24) and lowest 1000-seed weight (3.75). It indicated the population of this cluster could be used for future hybridization program for higher seeds per siliqua and long siliqua. The population included in cluster I were lowest mean value for days to maturity (81.8) and plant height (100.84 cm). It indicated the population of this cluster could be used for future hybridization program for early maturity plant type. Moreover, Cluster II had lower cluster mean for siliqua length (8.41 cm) and seeds per siliqua (23.41). On the other hand, cluster V showed the late 50% flowering (37.23) (Table 11). It indicated the population of this cluster could be used for future hybridization program for late maturity plant type. Zaman *et al*. (2010) reported that the highest cluster means for primary branches per

Table 10. Distribution of sixty two population of *Brassica napus* in different clusters

Cluster no.	No. of Population	No. of population	Name of population	Per cent
I	G2, G4, G6, G25, G44	5	Nap179*Nap2001, Nap2037*Nap2057, Nap2012*Nap2013, Nap2012*Nap2022, Nap2001*Nap179,	8.06
II	G3, G5, G13, G14, G18, G19, G20, G21, G24,G27, G34, G35, G36, G39, G41, G42, G43, G46, G47, G49, G50, G54, G56, G60, G61	25	Nap-248*Nap159, Nap94006*BS-7, Nap2037*Nap248, Nap206*Nap2013, Nap2037*Nap2012, Nap2037*Nap206, Nap9908*Nap2022, BS-13*Nap2022, Nap9908*Nap248, 135-13*Nap2013, Nap179*Nap2022, Nap2037*Nap2013, Nap248*Nap2057, Nap2057*Nap2001, Nap94006*Nap2001, BS-13*Nap2037, Nap179*Nap2012, BS-7*Nap2057, Nap206*Nap2022, Nap9908*Nap2012, Nap179*Nap2013, Nap94006*Nap179, Nap94006*Nap2022, Nap94006*Nap2012, Nap94006*Nap206	40.32
III	G15, G23, G45, G51, G62	5	BS-7*Nap206, Nap9908*Nap206, BS-13*Nap179, Nap248*Nap2012, Nap2001*Nap206,	8.06
IV	G7, G8, G9, G10, G12, G16,G22, G26, G29, G33, G38,G48, G52, G53, G55, G59,	16	Nap94006*Nap2013, Nap248*Nap206, Nap206*Nap2012, Nap2037*Nap2022, Nap9908*Nap2037, Nap2001*Nap2022, Nap179*Nap206, Nap248*Nap2022, Nap2057*BS-13, Nap179*Nap2057, BS-7*Nap2013, Nap206*Nap2057, Nap2057*Nap248, BS-7*Nap2013, Nap2001*Nap2013, Nap2057*Nap2022,	25.81
V	G1, G11, G17, G28, G30, G31, G32, G37, G40, G57, G58	11	Nap9908*BS-13, Nap9908*Nap94006, Nap94006*BS-13, Nap9908*Nap2001, BS-13*Nap206, Nap9908*Nap2013, Nap248*Nap2013, Nap94006*Nap2057, BS-13*Nap2001, Nap2057*Nap2012, Nap2001*Nap248	17.74
Total		62		

Table 11. Cluster mean values of 10 different characters of 62 population of *Brassica napus* L.

Characters	I	II	III	IV	V
Days to 50% flowering	36.8	36.36	35.3 (L)	36.66	37.23 (H)
Days to maturity	81.8 (L)	82.62	83.3	83.56 (H)	82.23
Plant height (cm)	100.84 (L)	108.26	121.21 (H)	115.3	108.91
Primary branches per plant	2.61 (L)	2.88	4.19 (H)	3.2	3.4
Secondary branches per plant	1.65 (L)	2.24	3.93 (H)	2.39	2.72
Siliqua per plant	80.38 (L)	105.38	169.41 (H)	120.24	136.69
Siliqua length (cm)	8.45	8.41 (L)	8.45	9.05 (H)	8.7
Seeds per plant	24.6	23.41 (L)	25.02	27.24 (H)	24.29
1000-seed weight (g)	3.99	4.11	4.33 (H)	3.75 (L)	3.97
Seed yield per plant (g)	5.35 (L)	5.81	7.8 (H)	6.62	7.27

H = high
L = low

plant and maximum seeds per siliqua with minimum seed yield per plant were obtained from the cluster II.

4.4.4 Cluster distance

The average intra and inter cluster D^2 values are given in (Table 11) and the nearest and farthest cluster from each cluster based on D^2 value is given in (Table 12)**.** It was observed that inter cluster distance were always higher than those of intra cluster distance. The maximum inter cluster distance was observed between population of cluster I and III**(**14.763) followed by clusters II and III (10.475) and I and V (8.689) (Table 13). Thus, hybridization among population drawn from these widely divergent clusters with high yield potential would likely to produce heterotic combinations and wide variability in segregating generations. Therefore it could be concluded that the population present in combination of those clusters could be utilized for successful breeding program. The minimum distance observed between clusters II and IV (2.816) (Table 12) indicated close relationship among the population included and population in these clusters were less diverged than others. Pandey *et al*. (2013) found maximum inter-cluster distance was found between cluster II and III indicating high genetic divergence among population of these groups. Zaman *et al*. (2010) reported that the population from cluster I and III could be utilized in the hybridization program for getting desirable transgressives segregates and high heterotic response due to getting maximum yield along with short duration. It appears that the crosses between population from cluster I with cluster III might produce high level of segregating population.

The intra cluster D^2 values were given in Table 12.The intra cluster distance was higher in cluster III (0.83) and lowest in cluster IV (0.36) (Table 12). The intra cluster distances in all the five clusters were lower than the inter cluster distances and which indicated that population 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 population of different groups.

Table 12. Intra (Bold) and inter cluster distances (D^2) for 62 population of *Brassica napus* L.

Cluster	I	II	III	IV	V
I	**0.52**	4.366	14.763	6.858	8.689
II		**0.43**	10.475	2.816	4.613
III			**0.83**	8.141	6.564
IV				**0.36**	2.855
V					**0.77**

Table 13.The nearest and farthest clusters from each cluster between D^2 values of *Brassica napus* L.

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	I	II (4.366)	III (14.763)
2	II	IV (2.816)	III (10.475)
3	III	V (6.564)	I (14.763)
4	IV	II (2.816)	III (8.141)
5	V	IV (2.855)	I (8.689)

4.4.5 Contribution of traits towards divergence of the population

The latent vectors (Z_1 and Z_2) obtained from principal component analysis (PCA). The important characters responsible for genetic divergence in the axis of differentiation in vector I (Z_1) were days to 50% flowering (0.0852), primary branches per plant (0.1332), secondary branches per pant (0.0884), siliqua length (0.3563) and seed yield per plant (0.4116). In vector II (Z_2), days to maturity (0.0542), plant height (0.1145), primary branches per plant (0.3262), secondary branches per plant (0.6459), siliqua length (0.4126), seeds per siliqua (0.1906) and 1000-seed weight (0.7866) (Table 14). 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 primary branches per plant, secondary branches per plant and siliqua length 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.

4.4.6 Selection of population

The population under the cluster I exposed early maturity and short plant type (Table 15). The population of cluster II produced intermediate value for plant maturity. The population of cluster III possessed early flowering, highest plant height, more primary and secondary branches per plant, more siliqua per plant, bold seeded because of highest 1000-seed weight and highest seed yield per plant. The population of cluster IV produced late maturity, highest siliqua length and most seeds per siliqua. The population of cluster V exposed late flowering. Considering diversity pattern and other agronomic performance population G2 (Nap- 179 X Nap- 2001) (Plate 6), G6 (Nap- 2012 X Nap- 2013)(Plate 7)from cluster I; population G19 (Nap- 2037 X Nap- 206) (Plate 8), G42 (BS- 13 X Nap- 2057) (Plate 9)and G43 (Nap- 179 X Nap- 2012) (Plate 10) from cluster II; population G45 (BS- 13 X Nap- 179) (Plate 11) and G62

(Nap- 2001 X Nap- 206) (Plate 12)from cluster III; population G30 (BS- 13X Nap-206) (Plate 13), G31 (Nap- 9908 X Nap- 2013) (Plate 14), G32 (Nap- 248 X Nap-2013) (Plate 15)and G58 (Nap- 2001 X Nap- 248) (Plate 16) from cluster V could be considered suitable population for developing open pollinated varieties and further use for efficient hybridization in future. Involving of such diverse lines in inter cluster population crossing program could produce desirable segregates. So, more divergent population are recommended to use as parents in future hybridization program.

Table 14. Relative contributions of the ten characters of 62 population of *Brassica napus* L. to the total divergence

Characters	Principal Component	
	Vector-1	Vector-2
Days to 50% flowering	0.0852	-0.2959
Days to maturity	-0.0720	0.0542
Plant height (cm)	-0.0501	0.1145
Primary branches per plant	0.1332	0.3262
Secondary branches per plant	0.0884	0.6459
Siliqua per plant	-0.1651	-0.0355
Siliqua length (cm)	0.3563	0.4126
Seeds per siliqua	-0.0963	0.1906
1000-seed weight (g)	-0.3935	0.7866
Seed yield per plant (g)	0.4116	-0.5082

Table 15. Salient features of population in five different clusters

Cluster	Salient features
I	Early maturity Short plant type
II	Intermediate maturity
III	Early flowering Highest plant height Higher secondary branches per plant Higher primary branches per plant Highest siliqua per plant Highest 1000-seed weight Highest seed yield per plant
IV	Late maturity Highest siliqua length Most seeds per siliqua
V	Late flowering

At flowering **After harvest** **siliqua**

Plate 12. Photograph showing population G2 at flowering, after harvest stage and siliqua under cluster I

At flowering **After harvest** **siliqua**

Plate 13. Photograph showing population G6 at flowering, after harvest stage and siliqua under cluster I

At flowering **After harvest** **siliqua**

Plate 14. Photograph showing population G19 at flowering, after harvest stage and siliqua under cluster II

At flowering **After harvest** **siliqua**

Plate 15. Photograph showing population G42 at flowering, after harvest stage and siliqua under cluster II

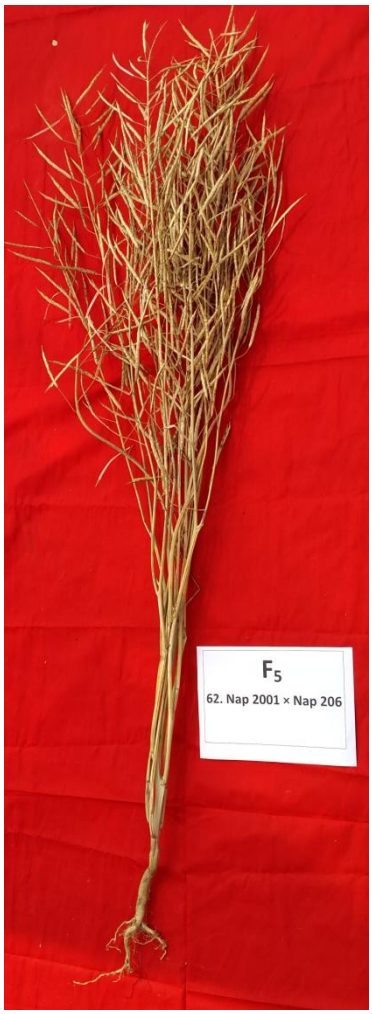
At flowering **After harvest** **siliqua**

Plate 16. Photograph showing population G43 at flowering, after harvest stage and siliqua under cluster II

At flowering **After harvest** **siliqua**

Plate 17. Photograph showing population G45 at flowering, after harvest stage and siliqua under cluster III

At flowering



After harvest

siliqua

Plate 18. Photograph showing population G62 at flowering, after harvest stage and siliqua under cluster III

At flowering **After harvest** **siliqua**

Plate 19. Photograph showing population G30 at flowering, after harvest stage and siliqua under cluster V

At flowering **After harvest** **siliqua**

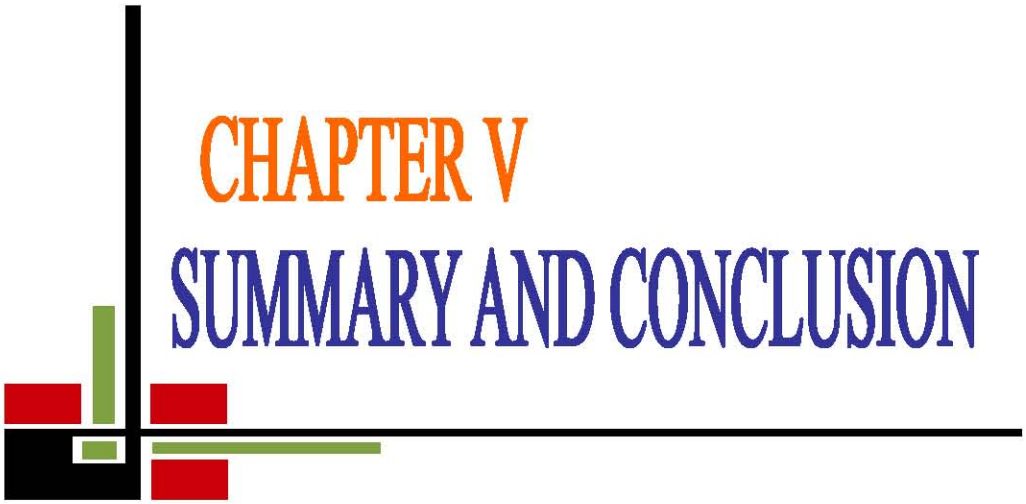
Plate 20. Photograph showing population G31 at flowering, after harvest stage and siliqua under cluster V

At flowering **After harvest** **siliqua**

Plate 21. Photograph showing population G32 at flowering, after harvest stage and siliqua under cluster V

At flowering **After harvest** **siliqua**

Plate 22. Photograph showing population G58 at flowering, after harvest stage and siliqua under cluster V



CHAPTER V

SUMMARY AND CONCLUSION

CHAPTER V

SUMMARY AND CONCLUSION

The present investigation was carried out to study genetic variability, character association, path analysis on seed yield and related traits in *Brassica napus* to identify the superior population on yield and other desirable attributes. The experimental material consisting of 62 population of *Brassica napus* were raised in RCBD with two replications at Experimental Farm, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka during Rabi season November 2015 to February 2016. The data was recorded on seed yield per plant and various other morphological traits viz., days to 50% flowering, days to maturity, plant height, 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 population.

From variability analysis of F_5 progenies, it was observed that significant variation exist among all the population used for all the traits studied. The maximum days to 50% flowering was observed in population G17 (40.50) and the lowest found in the population G12 (31.50). Maximum days to maturity was found in G10 (89.50) whereas minimum from G12 (76.50). The maximum plant height was observed by the population G62 (135.30 cm) and minimum in G2 (89.51 cm). Maximum primary branches per plant was found in G45 (5.70) whereas minimum from G45 (2.20). The population G62 (5.50) recorded maximum secondary branches per plant while the minimum was observed by the population G36 (1.30). The maximum siliqua per plant was found in the population G45 (186.35) while the minimum was observed in G4 (56.88). Maximum siliqua length was observed in the population G33 (9.87 cm) while the minimum was observed in the population G54 (7.44 cm). Maximum seeds per siliqua was found by the population G52 (31.14) and the minimum was observed from the population G61 (17.33). The maximum 1000 seed weight was observed in the population G27 (5.59 g) and the minimum was observed in the population G6 (1.56 g). The maximum seed yield per plant was observed in G32 (9.49 g) while minimum was observed in G24 (3.78 g).

Estimated genetic variance ranged from 0.29% for siliqua length to 395.97% for siliqua per plant and phenotypic variance ranged from 0.62% for primary branches per plant to 627.58% for siliqua per plant. The highest environmental variance observed 231.60% was siliqua per plant. Maximum genotypic and phenotypic variances were exhibited by siliqua per plant (627.58% and 395.97%). The lowest environmental, genotypic and phenotypic variances were 0.16, 0.29 and 0.44, respectively for siliqua length.

PCV was higher than the corresponding genotypic coefficient of variation (GCV) for all the traits studied. Higher estimates of PCV than GCV were observed for all the traits. PCV ranged from 4.15% for Days to maturity to 37.15% for Secondary branches per plant and GCV from 4.12% (Days to maturity) to 29.48% (Secondary branches per plant). Maximum GCV and PCV were recorded for number of secondary branches per plant (37.15 and 29.48). Higher PCV and GCV were recorded for primary branches per plant (25.17% and 21.00%), secondary branches per plant (37.15% and 29.48%), siliqua per plant (21.24% and 16.88%), 1000 seed weight (21.73% and 15.62%) and seed yield per plant (23.61% and 18.49%). The difference in genotypic coefficient of variation and phenotypic coefficient of variation values were closer in the traits days to 50% flowering, days to maturity, plant height, siliqua length.

Broad sense heritability values were higher (more than 61%) for all the characters except 1000 seed weight (51.62%). Heritability ranged from 51.62% (1000 seed weight) to 98.80 % (days to maturity). The present estimation of high heritability was observed in days to 50% flowering (96.50), days to maturity (98.80), plant height (67.18), primary branches per plant (69.61), secondary branches per plant (62.97), siliqua per plant (63.10), siliqua length (64.64), seeds per siliqua (64.68) and seed yield per plant (61.34).

Genetic advance (GA) expressed as percentage of mean was high (>20%) for the characters like primary branches per plant, secondary branches per plant, siliqua per plant, 1000 seed weight and seed yield per plant. Moderate genetic advance as percent of mean was shown by days to 50% flowering, plant height, siliqua length and seeds per siliqua. Genetic advance as percent of mean was highest (48.19%) for secondary

branches per plant and lowest (8.44%) for days to maturity. High heritability coupled with high expected genetic advance as percent of means were observed in case of primary branches per plant (69.61 and 36.09), secondary branches per plant (62.97 and 48.19), siliqua per plant (63.10 and 27.61), seeds per siliqua (64.68 and 19.92) and seed yield per plant (61.34 and 29.84) respectively. Medium heritability accompanied with high genetic advance for the character 1000 seed weight.

Seed yield per plant was significant and positive correlation with days to maturity (0.262 and 0.201), plant height (0.385 and 0.420) primary branches per plant (0.534 and 0.524), secondary branches per plant (0.419 and 0.453), siliqua per plant (0.597 and 0.610) at both genotypic and phenotypic level. Plant height was significantly correlated with number of siliqua per plant (0.449 and 0.392) and seeds per siliqua (0.321 and 0.348) at both genotypic and phenotypic levels. Number of primary branches per plant was positively significant correlation with number of secondary branches per plant (0.849 and 0.754), number of siliqua per plant (0.632 and 0.619) and number of seeds per siliqua (0.319 and 0.272) at both genotypic and phenotypic levels. Siliqua length was positively significant correlated with number of seeds per siliqua (0.614 and 0.647) at both levels. Number of seeds per siliqua was negatively significant correlated with 1000 seeds weight (-0.686 and -0.537) at both levels.

Through path analysis it was revealed that days to 50% flowering (0.188), days to maturity (0.293), plant height (0.038), primary branches per plant (0.627), number of siliqua per plant (0.614), number of seeds per siliqua (0.362) and 1000 seeds weight (0.397) had positive direct effects on seed yield per plant.

By genetic divergence analysis Eigen values of principal component axes of coordination of population with the first axes totally accounted for the variation among the population (32.44). and three PCA account for 66.95% of the total variation. 62 population were grouped into five clusters through non-hierarchical clustering and maximum population (25) were included into cluster II. The population included 40.32%, 25.81% and 17.74% in cluster II, IV and V, respectively and 8.06% in both cluster I and III.

Cluster III performed lowest value for days to 50% flowering (35.3) and highest for plant height (121.21 g), number of primary branch (4.19), number of secondary branch (3.93), number of siliqua per plant (169.41), thousand seed weight (4.33 g) and seed yield per plant (7.8 g) . Cluster IV produced the highest value for days to maturity (83.56), siliqua length (9.05 cm), seeds per siliqua (27.24) and lowest 1000-seed weight (3.75). Cluster I was lowest value for days to maturity (81.8) and plant height (100.84 cm). Cluster II had lower cluster mean for siliqua length (8.41 cm) and seeds per siliqua (23.41). cluster V showed the late 50% flowering (37.23).

By cluster distance it was observed that inter cluster distance was always higher than those of intra cluster distance. The maximum inter cluster distance was observed between population of cluster I and III **(**14.763) followed by clusters II and III (10.475) and I and V (8.689). The minimum distance observed between clusters II and IV (2.816). The intra cluster distance was higher in cluster III (0.83) and lowest in cluster IV (0.36). Primary branches per plant, secondary branches per plant and siliqua length in both the vectors were important components for genetic divergence under studied materials.

Cluster I population exposed early maturity and short plant type and cluster II produced intermediate value for plant maturity. Under cluster III population possessed early flowering, highest plant height, more primary and secondary branches per plant, more siliqua per plant, bold seeded and highest seed yield per plant. Late maturity, highest siliqua length and most seeds per siliqua were observed under population of cluster IV. The population of cluster V exposed late flowering.

On the basis of diversity pattern and agronomic performance population G2 (Nap-179 × Nap- 2001), G6 (Nap- 2012 × Nap- 2013) selected from cluster I. Population G19 (Nap- 2037 × Nap- 206), G42 (BS- 13 × Nap- 2057) and G43 (Nap- 179 × Nap- 2012) selected from cluster II. The population G45 (BS- 13 × Nap- 179) and G62 (Nap- 2001 × Nap- 206) selected from cluster III; and population G30 (BS- 13× Nap- 206), G31 (Nap- 9908 × Nap- 2013), G32 (Nap- 248 × Nap- 2013) and G58 (Nap- 2001 × Nap- 248) selected from cluster V.

CONCLUSIONS

Best performing population were G45 and G62 were found for high yielder, early flowering and bold seeded. G2 and G6 were found for early maturity and dwarf plant type. The results of the present experiment revealed that the variability which existed among the selected mustard population were much wide. Crossing program should be taken between cluster I and cluster III; cluster II and cluster III population and cluster I and cluster V. It will produce more diverse line for future early variety release. Among these population, the superior population 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 population 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.

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

Ahmed, M. R. (1993). Study of agronomic value of resynthesized rape seed 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.). *Pak. J. Bot.* **34**: 145-150.

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

Allard, R. W. (1960). Principles of Plant Breeding. John Willey and Sons. Inc. New York. Pp. 36.

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.

Azadgoleh E, Zamani M. A. and Yasari E. M. (2009). Agronomical important traits correlation in rape seed (*Brassica Napus* L.) Genotypes, *Res. J. of Agril. And Biol. Sci.* **5**(5): 798-802.

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

Baradaran, R., Majidi, E., Dervish, F. and Azizi, M. (2007). Study of correlation relationships and path coefficient analysis between yield and yield components in rape seed *(Brassica 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 rape seed (*Brassica napus* ssp. *oleifera* L.) cultivars. *Res. J. Agric. Biol. Sci.* **4**(2): 120-125.

BBS. (2011). Hand book of Agricultural Statistics, December (2010). Bangladesh Bureau of Statistics (BBS), Ministry of Planning Govt. People's Republic Bangladesh. p. 12.

BBS. (2013). 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.

Bilal, M., Khan, S. A., Raza, H., Ali, F., Khan, S. M., Ali, N., Hussain, I. and Khan, J. (2015). Evaluation of some indigenous rape seed genotypes for adaptability and yield traits in the agro-climatic conditions of Mansehra. *Int. J. Biosci.* **7**(5): 127-135.

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.

Chaudhury, P. K., Singh, P. and Kumar, A. (1990). Association and Interdependence of morpho physiological characters under moisture stress in *Brassica. Beitrage Zar Tropichen Landuitshaft*. **18**(1): 43-47

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.

Chowdhary M. A., Miah A. J., Rahman L. and Rahman A. (1987). Correlation and path coefficient analysis of nine important characters of Mustard (*Brassica juncea* L. Czern and Coss). *Bangladesh J. Agric.*, **12**: 149-154.

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

Comstoc, R. E. and Robinson, H. F. (1952). Genetic parameters. Their estimation and significance. P. 284-291.

Copper H. D. C., Spillane H. and Hogkin. (2001). Broadening the Genetic bases of crop production. FAO, IPGRI.

Dastidar K. K. G. and Patra M. M. (2004). Character association for seed yield components in Indian mustard (*Brassic*a *juncea* L. Czem and Coss), **8**(2): 155-160.

Dhillor, S. S., Labana, D. S. and Ahuja, K. L (1990). Association analysis in Indian mustard. *J. Agric. Res.* **27**(3): 385-388.

Digby, P., Galway, N. 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).

Engida T. S. (2007). Genetic variability for yield and other agronomic traits in seed potato. *J. Agron*. **6**: 94-99.

FAO. (2014). Production Yearbook. Food and Agricultural Organization, UN, Rome 00108, Italy.

Ghosh, D. V. and Mukhopadhyay, D. (1994). Path analysis of yield and yield attributes of toria (*Brassica rapa* var. *napus*) as affected by date of sowing and plant density. *Indian J. Agril. Sci.* **64**(1): 56-58.

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., Labana, K. S. and Badwal, S. S. (2002). Correlation and path coefficient of metric traits contributing towards oil yield in Indian mustard. In the International rape seed congress, pozan, Poland, 107(En).

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

Hanson, CH; Robinson, HP; Comstock, RE. (1956). Biometrical studies of yield in segregating populations of Korean Lespedeza. *Agron J*. **48**: 268-272.

Hasan M. F., Seyis, A. G., Badani, J., Pons-Kühnemann, W., Friedt, W., Lühs, R. J. and Snowdon, (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.

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

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

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

Jager, M. I., Garethojones, D. and Griffiths, E. (1983). Components of partial resistance of wheat seedlings of Septoria nodorum. *Euphytica*. **32**: 575-584.

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

Johnson, R. W., Robinson, H.F. and Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. *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.

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.

Khaleque, M. A. (1985). A guide book on production of oil crops in Bangladesh. DAE and FAO#UNDP Project BGD#79#034, Strengthening the Agrecultural Extension Service Khamarbari, Firmgate, Dhaka.

Khan S., Farhatullah, Khalil I. H. (2008). Phenotypic correlation analysis of elite F3:4 *Brassica* populations for quantitative and qualitative traits. *J. Agric. and Bio. Sci.* **3**(1):38-42.

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

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

Khan, S. A. (2014). The Extent of Intra-Specific Genetic Divergence in *Brassica Napus* L. Population Estimated through Various Agro-Morphological Traits. *European academic rese*. II(2).

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 Pan, D. P. (1999). Comparative analysis of yield and correlation for yield and its component in Indian Mustard. *Crop Res. Hisar*. **17**(3): 371-375.

Korkut Z. K., and Başer, S. (1993). The studies path coefficient and correlation of drum wheat's. Symposium of Durum Wheat and Its Products, Ankara, 183-187.

Kumar B, Pandey A, Singh KR (1987). Genetic diversity for agro-morphological and oil quality traits in Indian mustard (*Brassica juncea* L. Czern & Coss). The Bioscan. **8** (3): 771-775.

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**(1): 14-17.

Kumar, M., Singh, T. S. and Kumar, V. (2007). Genetic variability, heritability, genetic advance and character association in Indian mustard (*Brassica juncea* L. czern and Coss) grown in semi- alkali soils. *J. Farming Systems Rese. Deve*. **13** (3): 284-287.

Kumar, S., Sangwan, R. S. and Yadava, I. S. (1999). Path coefficient analysis in *Brassica* species under rainfed conditions. *Cruciferae Newsl*. **24**:59-60.

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

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, B, Thakral, N. K., Avtar, R. and Singh, A. (2014). Genetic variability, association and path analysis in Indian mustard (*Brassica juncea*), *J. oilseed Brassica.* **5**(1): 26-31.

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

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.

Mahamood, T., Muhammad, A., Iqbal, S. and Anwar, M. (2003). Genetic variability and heritability estimates in summer mustard (*Brassica juncea* L.). *Asian J. Plant Sci.* **2**(1): 77-79.

Mahla, H. R., Jambhulkar, S. J., Yadav, D. K. and Sharma, R. (2003). Genetic variability, correlation and path analysis in Indian mustard (*Brassica juncea* (L.) Czern and Coss.). *The Indian J. Genet. Pl. Breed.* **63** (2): 171-172.

Mahmud, F., Rasul, M. G and Rahim, M. A. (2008). Genetic diversity analysis in some advanced lines of *Brasssica napus*. *Sci. Asia*. **34**: 432-434.

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

Masood, T., Gilani, M. M. and Khan, F. A. (1999). Path analysis of the major yield and quality characters in *Brassica campestris. J. Animal Pl. 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.

Miller, P. A., Willams, C., Robiwson, H. F. and Comstock, R. E. (1958). Estimates of genotypic and environmental variance and covariance and their implication in section. *Agron. J.* **50**: 126-131.

Momena B. (2015). Genetic variability, correlation and path analysis in BC_1F_5 segregating generation of *Brassica napus* L. MS Thesis. Department of genetics and plant breeding, Sher-e-Bangla Agricultural University, Dhaka-1207.

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.

Nagaraja T. E. (1990). Genetic variability study in rape seed (*Brassica compestris* L.) and mustard (*Brassica juncea* (L) Czern and Coss). M.Sc. (Agri.) Thesis, Univ. Agric. Sci. Bangalore.

Nair, K. R., and Mukherjee, H. K. (1960). Classification of natural and plantation teak (*Tectona grandis*) grown at different localities of India and Burma with respect to its mechanical and physiological properties. *Sankhya*.**22**: 1-20.

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.

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.

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

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

Parvin, F. (2015). Genetic variability and character association in BC_1F_4 generation of *Brassica napus* L. MS Thesis. Department of genetics and plant breeding, Sher-e-Bangla Agricultural University, Dhaka-1207.

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.

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

Rai, S. K., Verma, A., Pandey, D., (2005), Genetic variability and character association analysis in Indian mustard (*Brassica juncea* (L.) Czern and Coss*). Ann. Agri. Bio. Res.*, **10** : 29-34.

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. (2015). Heritability, genetic variability and correlation analysis of some important agronomic traits in rape seed advanced lines. *Cercetări Agronomice în Moldova.* XLVIII (4): 164.

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.

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

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. *Indian.Univ. Agril. Sci.* **1**(2): 226-229.

Sharafi Y., Majidi M. M. Jafarzadeh, M. and Mirlohi, A. (2015). Multivariate Analysis of Genetic Variation in Winter Rape seed (*Brassica napus* L.) Cultivars. *J. Agril. Sci. Tech.* **17**: 1319-1331.

Shaukat, S., Raziuddin, F. Khan and Khalil, I. A. (2015). Genetic variation and heritability estimates of quality traits in *Brassica napus* L. *J. Bio. Agril. Health care*. **4**(20): 1-5.

Sheikh, F. A., Rathen, A. G. and Wani, S.A. (1999). Path analysis in toria (*Brassica campestris* L.) var. toria. *Adv. P1ant. Sci*. **12**(2): 385-388.

Siddika, K. S. (2105). Genetic variability, correlation and path analysis in F_2 segregating generation of *Brassica napus* L. MS Thesis. Department of genetics and plant breeding, Sher-e-Bangla Agricultural University, Dhaka-1207.

Siddikee, M. A. (2006). Heterosis inter genotypic variability, correlation and path analysis of quantitative characters of oleiferous *Brassica campestris* L. MS Thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka. Rashid, M. H. (2007).

Sigmmonds N. W. (1962). Variability in crop plants, its use and conservation. Biological reviews. **37**: 422465.

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

Singh, M., Singh, S.P. and Dhirendra, S. (2001). Genetic analysis for seed yield and its genotypes in yellow sarson (*Brassica compestris* L.). *Indian J. Agril. Sci.* **70**(9): 624-626.

Singh, R. K., and Chaudary, B.D. (1985). Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi, India.p.56.

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.

Sirohi S. P. S., Sanjai M. and kumar A. (2004). Correlation and path analysis of Indian mustard (*Brassica juncea* L. Czern and Coss). *Ann. Agric. Res.*, **25**(4): 491-494.

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.

Sudan, R. S., Singh, S. P. and Kashyap, S. C. (2004). Path analysis of yield and its components in Indian mustard (*Brassica juncea* L. Czern and Coss). *Ann. Agric. Bio. Res.* **9**(2): 119-122.

Sultana R. (2016). Assessment of genetic variation among advanced lines of *Brassica napus* L. *J. Sci. Techno*. **73**(4-5): 201-226.

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

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). Estimaiton of heterosis in Indian mustard [*Brassica juncea* L.) Czren and Coss]. *Annl. Agril. Bio. Res*. **6**(2): 193-200.

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

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

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**: 155-60.

Yadava, C. K. Yadav, A. K. and Singh, H. (2006). Studies on genetics of yield and its components in Indian mustard (*Brassica juncea* L.) Czern and Coss. Thesis Abst. **9**(2): 186-187.

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

Yadava, T. P., 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., Zada, A. K. and Hari, S. (2007). 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.

Zahan, M. I. (2006). Morphological characterization and genetic diversity in oleiferous *Brassica species.* MS Thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

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

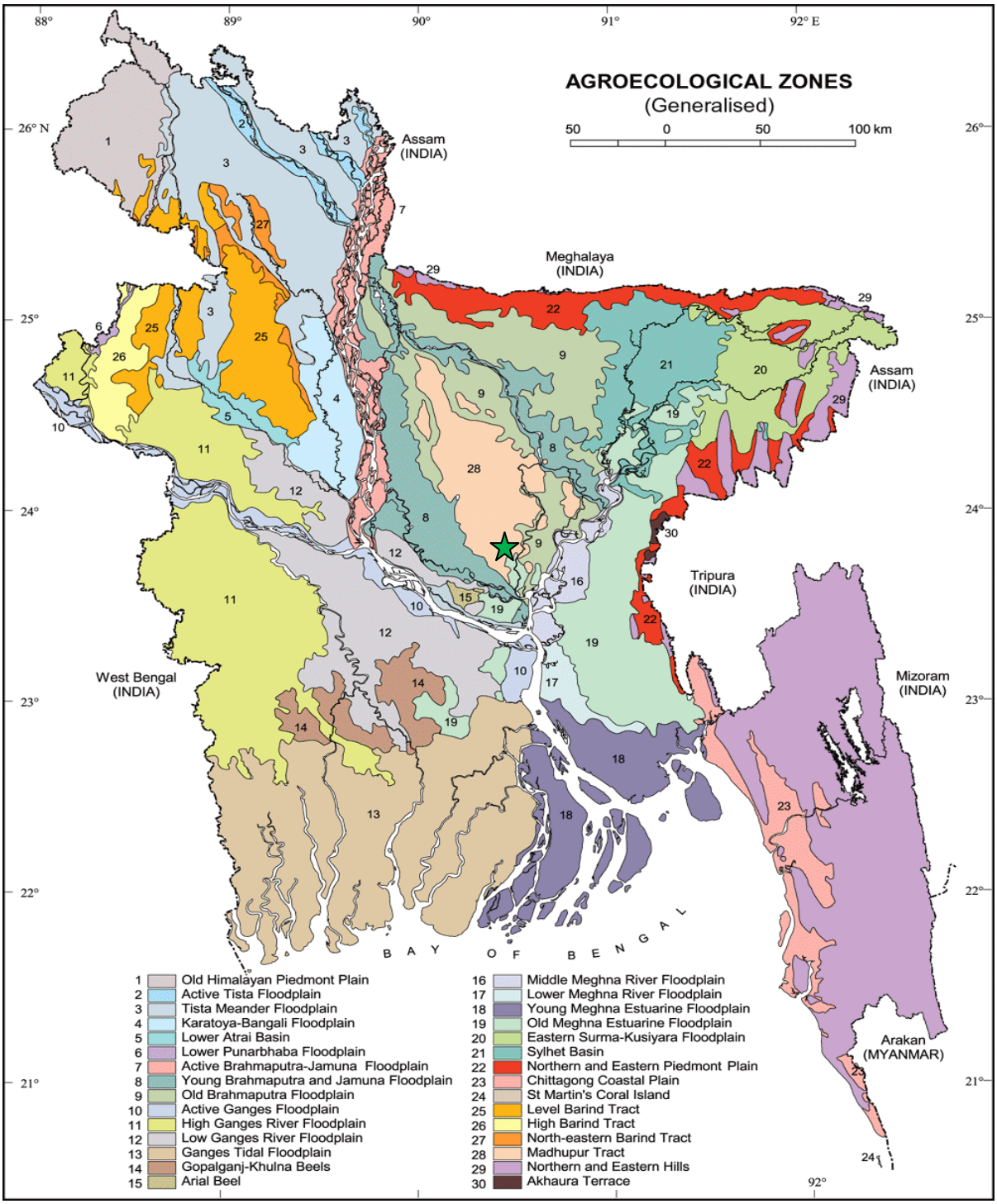
Zaman, M. W., Talukder, M. Z. I., Biswas, K.P. and Au, M. M. (1992). Development allometry and its implication to seed yield in *Brassica napus L. Sveriges Utsades Foreign Tidskrift.* **102**(2): 68-71.

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

APPENDICES

APPENDICES

Appendix I. Map showing the experimental site under the study



The experimental site under the study

Appendix II: Morphological, physical and chemical characteristics of initial soil (015 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, 2015 to February, 2016.

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

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

Appendix IV. Mean performance of different characters of 62 rape seed population of *Brassica napus* L.

Genotype	50F	DM	PH	NPB	NSB	NSP	SL	NSS	TSW	SYP
G1	38.00	86.00	110.85	4.80	3.40	136.06	9.26	27.01	3.30	8.45
G2	40.50	79.00	89.51	2.50	2.05	87.10	8.89	23.96	4.64	4.83
G3	36.00	82.00	106.18	4.25	3.07	101.50	7.94	21.55	5.37	4.85
G4	32.50	80.00	94.60	2.35	1.50	56.88	7.76	21.56	5.24	4.29
G5	34.50	84.00	108.92	2.40	1.40	102.35	8.31	24.03	4.44	5.93
G6	35.00	80.50	109.13	2.80	1.45	87.54	8.63	26.54	1.56	5.85
G7	34.50	81.50	105.74	3.80	3.10	118.26	8.21	24.40	3.71	6.42
G8	39.50	89.00	109.77	3.70	2.75	117.10	9.60	27.37	4.45	7.82
G9	36.50	84.00	120.65	4.90	3.50	122.69	9.06	30.58	3.52	8.78
G10	38.50	89.50	106.90	3.85	3.55	122.23	9.74	29.89	3.72	6.58
G11	40.50	79.00	114.50	3.75	2.10	130.90	9.03	27.66	3.22	6.76
G12	31.50	76.50	107.58	3.55	1.70	125.68	8.85	26.36	2.78	4.88
G13	36.50	77.50	97.64	4.55	2.55	116.86	8.19	26.05	3.63	5.64
G14	37.50	85.00	117.42	2.80	1.55	101.34	9.02	29.26	3.87	7.85
G15	34.50	86.50	115.12	3.30	2.95	165.20	7.56	18.75	5.55	8.75
G16	38.50	79.00	114.82	3.55	3.00	125.68	8.42	26.66	3.51	6.25
G17	40.50	77.50	104.17	3.05	2.55	127.45	9.03	26.22	3.39	6.46
G18	39.50	86.00	107.57	2.55	2.30	101.90	8.86	26.49	4.15	5.47
G19	33.50	77.00	104.29	3.20	2.40	114.13	8.50	27.62	3.37	6.67
G20	38.50	80.00	125.61	2.90	1.90	102.05	8.61	26.12	3.33	5.33
G21	36.50	83.50	106.52	2.65	2.00	99.10	8.25	23.52	4.65	4.84
G22	38.50	85.50	117.27	2.80	1.85	111.95	8.92	22.98	4.62	5.37
G23	33.50	80.00	111.02	3.95	3.80	164.10	7.59	22.18	4.43	6.47
G24	35.50	79.00	107.40	2.45	2.65	103.00	7.58	19.85	3.12	3.78
G25	40.50	88.50	104.92	3.00	1.65	88.40	8.78	24.77	4.66	6.10
G26	39.50	87.50	120.57	2.95	2.75	129.50	9.76	26.35	4.54	6.98
G27	37.50	84.50	116.33	2.65	2.00	111.10	8.08	18.27	5.59	7.64
G28	38.50	80.50	109.81	3.00	2.65	138.15	9.30	29.94	3.14	5.86
G29	35.50	86.50	117.87	3.20	2.40	127.60	8.32	27.50	4.24	8.38
G30	37.50	81.50	111.34	4.00	3.80	148.62	7.75	24.25	4.12	7.50
G31	33.50	79.50	101.54	3.25	2.82	144.35	8.38	21.50	5.11	7.49
G32	34.50	82.50	115.21	3.65	2.55	143.10	7.84	19.06	4.83	9.49
G33	36.50	85.50	113.44	2.75	2.10	125.80	9.87	26.71	4.24	8.63
G34	39.50	84.50	112.47	2.85	2.15	111.00	9.48	22.47	4.34	6.53
G35	37.50	81.50	110.50	2.45	1.45	104.90	8.36	20.19	5.17	7.48
G36	34.50	79.50	104.38	2.25	1.30	108.69	8.42	22.17	4.38	4.22
G37	35.50	78.50	113.14	2.50	2.00	131.50	9.05	20.58	4.24	6.25
G38	38.50	80.50	115.62	2.95	2.14	113.05	9.29	31.06	3.77	7.28
G39	36.50	82.50	109.33	2.45	1.40	98.05	9.05	24.03	4.45	5.27
G40	34.50	88.50	97.90	2.65	2.35	129.25	9.08	22.43	4.14	6.14

Appendix IV. *Continued*.

Genotype	50F	DM	PH	NPB	NSB	NSP	SL	NSS	TSW	SYP
G41	35.50	86.50	94.69	3.00	3.64	105.80	8.24	21.70	3.12	4.94
G42	33.50	77.50	106.66	3.10	3.20	113.40	7.80	20.30	4.64	6.66
G43	38.50	78.50	103.45	2.65	2.05	111.10	8.90	22.73	4.93	6.86
G44	35.50	81.00	106.04	2.40	1.60	82.00	8.20	26.17	3.84	5.67
G45	36.50	83.00	111.12	5.70	4.90	186.35	9.33	30.56	3.50	9.23
G46	37.50	85.00	103.17	3.00	3.00	102.00	7.74	22.30	3.14	5.22
G47	33.50	82.00	107.84	3.20	2.75	105.28	8.53	27.02	3.33	7.20
G48	34.50	86.00	114.18	2.20	1.50	118.42	9.32	27.15	3.68	4.68
G49	36.50	83.00	108.52	2.65	2.45	105.80	8.86	22.29	4.53	4.72
G50	35.50	88.00	111.46	2.45	1.45	106.45	9.38	28.63	3.07	5.38
G51	33.50	85.00	133.47	3.25	2.50	151.05	8.60	27.00	3.82	6.50
G52	36.50	81.00	118.33	2.65	1.90	112.45	9.10	31.14	2.92	5.23
G53	38.00	83.00	130.21	2.70	2.10	115.03	9.07	27.97	3.32	7.71
G54	39.00	80.00	112.12	3.50	2.55	103.05	7.44	22.46	3.60	6.00
G55	36.00	79.00	111.79	2.65	1.55	119.23	8.75	24.16	3.51	4.78
G56	35.00	85.50	122.71	2.40	2.10	102.60	7.97	24.36	4.01	6.11
G57	37.50	87.00	107.97	3.10	2.55	139.50	8.14	21.22	4.09	7.42
G58	39.00	84.00	111.61	3.70	3.10	134.71	8.82	27.33	4.06	8.18
G59	34.00	83.00	120.05	3.00	2.30	119.15	8.50	25.61	3.50	6.09
G60	35.00	88.00	102.17	2.75	2.45	101.45	8.58	24.60	3.78	6.03
G61	36.00	85.00	99.15	2.85	2.35	101.72	8.26	17.33	4.84	4.60
G62	38.50	82.00	135.30	4.75	5.50	180.34	9.18	26.61	4.36	8.05

D50F = days to 50% Flowering, DM = days to 80% Maturity, PH = plant height (cm), PBP = primary branches per plant, SBP = secondary branches per plant, SPP = siliqua per plant, SL = Siliqua length (cm), SPS = Seeds per siliqua, TSW = 1000 seed weight (g) and SYP = seed yield per plant (g).