EVALUATION OF 15 POPULATIONS OF *Brassica rapa* L. BASED ON MORPHOLOGICAL AND BIOCHEMICAL TRAITS

NAHID BENTH SHAMS

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

JUNE, 2017

EVALUATION OF 15 POPULATIONS OF *Brassica rapa* L. BASED ON MORPHOLOGICAL AND BIOCHEMICAL TRAITS

BY

NAHID BENTH SHAMS

REGISTRATION NO. : 11-04272

A Thesis
submitted to the Department of Genetics and Plant Breeding
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: JANUARY- JUNE, 2017

Approved by:

Prof. Dr. Md. Shahidur Rashid Bhuiyan	**Prof. Dr. Jamilur Rahman**
Supervisor	**Co-Supervisor**

Prof. Dr. Jamilur Rahman
Chairman
Examination Committee

Dr. Md. Shahidur Rashid Bhuiyan
Professor
Department of Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Sher-e-Bangla Nagar, Dhaka-1207, Bangladesh
Mobile: +8801552467945
E-mail: msbhuiyan@yahoo.com

CERTIFICATE

*This is to certify that thesis entitled, "**EVALUATION OF 15 POPULATIONS OF Brassica rapa L. BASED ON MORPHOLOGICAL AND BIOCHEMICAL TRAITS**" 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 **Nahid Benth Shams**, Registration No. : 11-04272 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 been duly been acknowledged.

Dated: June, 2017
Place: Dhaka, Bangladesh

(Prof. Dr. Md. Shahidur Rashid Bhuiyan)
Supervisor


Dedicated To
My Beloved Parents

Acknowledgements

All of the gratefulness to Almighty Allah who enabled the author to accomplish this thesis.

The author would like to express her heartiest respect, deepest sense of gratitude, profound appreciation to her supervisor, Prof. Dr. Md. Shahidur Rashid Bhuiyan, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for his continuous guidance, cooperation, constructive criticism and helpful suggestions, valuable opinion in carrying out the research work and preparation of this thesis, without his intense cooperation this work would not have been possible.

The author feels proud to express her deepest respect, sincere appreciation and immense indebtedness to her co-supervisor Prof. Dr. Jamilur Rahman, Professor, Department of Genetics and Plant Breeding SAU, Dhaka for his scholastic and continuous guidance during the entire period of course, research work and preparation of this thesis.

She express her sincere respect to the Chairman, Prof. Dr. Jamilur Rahman and all the teachers of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for providing the facilities to conduct the experiment and for their valuable advice and sympathetic consideration in connection with the study. The author would also thankful to all of the staffs of the Department of Genetics and Plant Breeding.

Mere diction is not enough to express her profound gratitude and deepest appreciation to the author's family and her heartfelt thanks to Md. Maskurur Rahman, Md. Eaftakher Rosul Siddik, Md. Jahidul Islam, Reemana Fatema, Fahmida Sultana, Marzana Rahman and for their ever ending prayer, encouragement, sacrifice and dedicated efforts to educate her to this level.

June, 2017
SAU, Dhaka ***The Author***

EVALUATION OF 15 POPULATIONS OF *Brassica rapa* L. BASED ON MORPHOLOGICAL AND BIOCHEMICAL TRAITS

BY

NAHID BENTH SHAMS

ABSTRACT

The investigation was started with the selection process of potential populations of *Brassica rapa* L. After a continuous process of selection from various lines of these populations the present investigation was carried out under field conditions to evaluate morphological and biochemical traits of the selected populations. The research was based on the evaluation of 15 advanced lines received from the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, considering 10 agro-morphological and 7 biochemical traits, using randomized complete block design with three replications during rabi season from November 2016 to February 2017 in research farm of Sher-e-Bangla Agricultural University. The analysis of variance showed significant variation in all the traits except number of secondary branches per plant, length of siliqua and thousand seed weight. The phenotypic variances were lower than genotypic variances with little differences in all traits except days to 50% flowering, days to 80% maturity, plant height, number of sliliquae per plant, number of seeds per siliqua and yield per plant. High heritability coupled with high genetic advance was found in number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua, thousand seed weight and yield per plant. The correlation studies revealed that yield per plant had highly significant positive relation with number of primary branches per plant, number of siliquae per plant, number of seeds per siliqua. Path analysis showed that siliquae per plant had highly significant and positive direct effect on the yield per plant. Biochemical analysis of various fatty acids of seven populations was done. Among the populations lowest amount of palmitic, stearic and erucic acid was found in P3 (1.98%), P4 (0.80%) and P10 (50.21%) respectively. The highest amount of oleic, linoleic and linolenic acid was found in P15 (17.27%), P14 (15.40%) and P10 (9.48%) respectively. In case of short duration P2 (80.67 days) and P14 (78.67 days) showed the lowest result comparing with the two check varieties BARI 15 (84 days) and Tori-7 (82 days). Higher yield/plant was found in P7 (9.77 g), P8 (9.57 g), P12 (13.48 g) and P14 (14.00 g) comparing with the check varieties BARI 15 (8.45) and Tori-7 (6.82). Among the populations P14 was found as the best lines comparing with the checks on the basis of days to 80% maturity, number of secondary branches/plant, number of siliquae/plant, yield/plant, and linoleic acid. By comparing, it might be concluded that populations P1, P2, P7, P8, P10, P12 and P14 had potential for improvement based on the genetic merit of yield and yield contributing factors.

LIST OF CONTENTS

LIST OF CONTENTS (CONT'D)

LIST OF CONTENTS (CONT'D)

LIST OF CONTENTS (CONT'D)

LIST OF TABLES

LIST OF PLATES

LIST OF FIGURES

LIST OF APPENDICES

SOME COMMONLY USED ABBREVIATIONS

FULL WORD	ABBREVIATION
Agro-Ecological Zone	AEZ
Analysis of variance	ANOVA
And others	*et al.*
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Carbon	C
Centimeter	cm
Co-efficient of variation	CV
Days after sowing	DAS
Degree of Celsius	^{o}C
Degree of freedom	D.F.
Et cetera	etc.
Eighth generation of a cross between two dissimilar homozygous parent	F_8
Food and Agriculture Organization Corporate Statistical Database	FAOSTAT
Fifth generation of a cross between two dissimilar homozygous parent	F_5
Fourteenth generation of a cross between two dissimilar homozygous parent	F_{14}
Genetics and Plant Breeding	GPB
Genotypic correlation	r_g
Gram	g
Genotypic Coefficient of variation	GCV
Genotypic variation	$\delta^2 g$

SOME COMMONLY USED ABBREVIATIONS (CONT'D)

FULL WORD	ABBREVIATION
Genetic Advance	GA
Hectare	ha
Heritability in broad sense	h^2b
Hydrogen ion potentiality	pH
Hour	hr
Hydrochloric acid	HCl
Kilogram	kg
Least significant difference	LSD
Millimeter	mm
Mean Sum of Square	MS
Muriate of Potash	MP
Milliliter	mL
Milli gram	mg
Meter	m
Metric ton	MT
Minute	min
Micro meter	µm
Number	No.
Per cent	%
Phenotypic variance	δ^2p
Phenotypic coefficient of variation	PCV
Phenotypic correlation	r_p

SOME COMMONLY USED ABBREVIATIONS (CONT'D)

FULL WORD	ABBREVIATION
Potassium hydroxide	KOH
Randomized Complete Block Design	RCBD
Sher-e-Bangla Agricultural University	SAU
Sixth generation of a cross between two dissimilar homozygous parent	F_6
Species	*sp.*
Square meter	m^2
Standard error	SE
Standard deviation	SD
Triple Super Phosphate	TSP
Videlicet (Namely)	*viz.*
Variety	Var.
Zinc Oxide	ZnO

CHAPTER I
INTRODUCTION

Brassica rapa belongs to the Brassicaceae family, also known as the mustard family. *Brassica rapa* (2n = 20, AA) is an important member of *Brassica* species grown widely for leafy vegetables in Korea, China, and Japan, for vegetable oil in India, China, and Canada, for edible oil in Bangladesh, and Indian sub-continents, and as a fodder crop in Europe. It is predominating as the first position for its medicinal attributes and on the other hand, the second most important edible oil source in the world (www.pfaf.org).

The rapeseed group includes *Brassica rapa* L. and *Brassica napus* L. The genetic constitution of *Brassica rapa* is AA and of *Brassica napus* is AACC (Islam *et al.*, 2015). The mustard group includes *Brassica juncea* and *Brassica nigra.* The genetic constitutions of these two are AABB and BB, respectively. With the smallest genome size in the *Brassica* genus, the rapid life cycle of some of its genotypes, and the relatively close relationship to the model plant species *Arabidopsis thaliana, Brassica rapa* is considered to be one of the model dicot crops for genetic studies (Wang *et al.*, 2011).

Edible oil plays a key role as a source of high energy component of food in human nutrition. Many edible oils lack one of the two essential fatty acids; on the other hand mustard provides both the essential fatty acids, linoleic and linolenic acid to the human body (Khan *et. al.*, 2009). Mustard seeds contain 40-45% oil and 20-25% protein and minerals (Mondal and Wahhab, 2001).

In 2015-2016, the edible oil production from major oilseed crops in the world is 533 million tons where rapeseed contributes 68 million tons. (FAOSTAT, 2017). Total area of mustard and rapeseed in the world is 35.52 million hectares. Global consumption of oils/fats has reached around 211 million tons in 2015-16, up by less than 3 per cent year-on-year and below the average growth of recent years. Production of oils/fats recorded average annual increases of 4–5 per cent during

the last three seasons, but the latest crop forecasts for 2015-16 would translate into a 1.6 per cent slide. The year-on-year drop would mainly be on account of lower cottonseed, soybean and rapeseed production (FAOSTAT, 2017).

In Bangladesh, it is very important to cultivate oil crops. The cultivated crops are mustard, linseed, sunflower, soybean, sesame, etc. These covers 4.86 lakh ha areas and the production oil is 6.61 lakh MT. This production rate is one-third of our daily requirement (www.bari.gov.bd). Per capita consumption of edible oil is 11.25 kg per year (FAOSTAT, 2017). Total edible oil consumption is forecast to rise 2.7 per cent in 2015-16 owing to increased population, rising income levels, changing consumer behavior, and increasing oil use as an ingredient in various feeds (www.thebangladeshpost.com).

In Bangladesh, *Brassica rapa* is the main oil yielding species of *Brassica* (FAOSTAT, 2017). Among the oil crops grown in Bangladesh *Brassica rapa* L. occupies the first position in respect of area and production (Naznin *et al*., 2015). It dominates with 68% in terms of total oilseed planted area (FAOSTAT, 2017). About 787025 acres of land was under rape and mustard cultivation. The production rate of the seed was about 68 million tones, and national average yield was 361909 MT in this country (BBS, 2017).

In Bangladesh, the cultivation practice of mustard has been implemented in a span of time. From the last few decades, the cultivation of rice is increasing day by day which is replacing the cultivated area of mustard. For accomplishing the demand, we import 70% oil from foreign countries. Bangladesh has to spend a huge amount of foreign exchange on imports of edible oils and oilseeds to meet the increasing demand of its population. The value of imports is increasing year after year which is burden for us. As the population of Bangladesh is increasing and economic prosperity has been growing fast, it is now a challenge for accelerating the production of oils. It is essential to reduce the import dependence of it to insulate the domestic market from the volatility of the world market (Hossain, 2013). Farmers usually cultivate the existing low yielding varieties

with low input and management. There is no improved short duration variety. They need short duration varieties of T. Aman and boro rice so that they can successfully cultivate oilseed crops in between two rice crops. But, due to the unavailability of short-duration rice varieties (i.e., BINAdhan-7, BRRIdhan-33), farmers cannot cultivate mustard at the desired level.

Future edible oil requirement can only be achieved through the improvement of seed quality by breeding *Brassica sp*. and using cropping pattern. Short duration variety like Tori-7 of *Brassica rapa* is still popular in outlying area of Bangladesh because it fits well into the T. Aman - Mustard - Boro cropping pattern. To enhance oilseed production for in Bangladesh, existing improved short-duration rice and oilseed varieties should be disseminated among the farmers. Most of the mustard farmers opine that they want to cultivate boro rice just after harvesting of oilseed crops (Miah *et al.*, 2017).

In present status, there are many varieties of *Brassica sp.* which is released from different institutions in this country. Among them, 17 are released from Bangladesh Agricultural Research Institute (BARI), 3 from Sher-e-Bangla Agricultural University (SAU), 8 from Bangladesh Institute of Nuclear Agriculture (BINA), 1 from Bangladesh Agricultural University (BAU) (www.bari.gov.bd). The rate of adoption of these improved varieties at farm level is encouraging and have created positive impact and saved foreign exchange for the country (Miah *et al*., 2015).

In this context, different populations were developed through selection of the materials from different segregating generations obtained through inter-varietal hybridization of *Brassica rapa* L. The 15 populations obtained were in F_5, F_6, F_8, F_{14} generations and used in this experiment. These populations were compared with leading checks of mustard and the performance was evaluated to find out varieties that may solve the current problems of mustard.

Therefore, to evaluate 15 different populations on the basis of morphological and biochemical traits the following objectives were set:

i. To compare the different populations of *Brassica rapa*.

ii. To study the genetic variability of the populations.

iii. To study on the saturated and unsaturated fatty acids of the populations.

iv. To select early maturing and high yielding populations for variety release.

CHAPTER II
REVIEW OF LITERATURE

Yield is a complex trait, polygenic in inheritance, more prone to environmental fluctuations than ancillary traits such as branches per plant, seeds per siliqua and thousand seed weight. Understanding the association between yield and its components is of paramount importance for making the best use of these relationships in selection. The path coefficient analysis helps breeders to explain direct and indirect effects, and hence been extensively used in breeding experiments in different crop species (Akbar *et al*., 2003). An evaluation is a scientific method, in which the acquired knowledge is tested by observation by setting a standard. It can use quantitative or qualitative data, and often includes both. The analysis of the relationship among the traits and their association with seed yield is very much essential to establish selection criteria. Breeders always look for genetic variation among traits to select desirable type.

A retrospect of pertinent literature on "Evaluation of 15 populations of *Brassica rapa* L. in terms of morphological and biochemical traits" has been reviewed under mentioned broad heads:

2.1 Genotypic and phenotypic coefficient of variation
2.2 Genetic variability, heritability and genetic advance in *Brassica spp.*
2.3 Correlation analysis
2.4 Path co-efficient analysis
2.5 Nutrient component analysis

2.1 Genotypic and phenotypic coefficient of variation

The genetic worth of the genotypes studied is reflected by their significant variability, which could be further utilized in initiating an efficient breeding programme. Further, we can partition the available variability into genetic and non genetic factors and influence of environment on different characters with the

help of GCV and PCV. Quantitative characters are more influenced by environment and variation arises due to joint action of genotype and environment. Phenotypic and genotypic variation are the important component of variation. The amount of variation is measured and expressed in the term of variance. For phenotypic variability it is measured as phenotypic coefficient of variation. Genetic variability can be measured with the aid of genetic parameters such as genotypic coefficient of variation. The success of selection for superior genotypes depends upon available genetic diversity present in the plant population.

Dash *et al.* (2007) conducted an experiment on fifty genotypes of toria. Fourteen characters were included in the investigation, to estimate genetic variability, character association, direct and indirect effect on seed yield and genetic divergence for earliness and other yield attributes in toria (*Brassica rapa* L. Var. toria). Analysis of variance revealed considerable variability among 50 toria genotypes for all the fourteen characters under study. For all the characters, PCV was higher than GCV. Secondary branches per plant and leaf area index reflected high estimates of GCV and PCV. High estimates of broad sense heritability coupled with high genetic advance as per cent of mean were observed for secondary branches per plant, leaf area index, and specific leaf weight, reflecting greater contribution of genetic component.

Jahan *et al*. (2014) conducted a field experiment to study variability in 10 F_4 lines obtained through inter-varietal crosses along with 8 released varieties of *Brassica rapa* L. Significant variation was observed among all the genotypes for all the characters studied. Considering genetic parameters high genotypic co-efficient of variation (GCV) was observed for number of secondary branches per plant, siliquae per plant, yield per plant, whereas days to maturity showed very low GCV. High heritability with low genetic advance in percent of mean was observed for days to maturity which indicated that non-additive gene effects were involved for the expression of this character and selection for such trait

might not be rewarding. High heritability with moderate genetic advance in percent of mean was observed for plant height and days to 50% flowering indicated that this trait was under additive gene control and selection for genetic improvement for this trait would be effective.

Iqbal *et al.* (2015) carried out an investigation to study the genetic variability parameters of procured germplasm for various traits *viz*., days to 50% flowering, days to maturity, plant height (cm), no. of primary branches plant^{-1}, no. of secondary branches plant^{-1}, no. of pods plant^{-1}, thousand seed weight (g) and seed yield ha^{-1}. The set of 49 genotypes of brown sarson (*Brassica rapa* Var. Brown sarson) were grown. PCV was higher than corresponding GCV for all the traits studied. High GCV was observed in seed yield plant^{-1}, whereas moderate GCV was revealed in no. of primary branches plant^{-1} and no. of secondary branches plant^{-1}. High values of heritability have been recorded for 50% flowering, days to maturity, no. of primary branches plant^{-1}, no. of secondary branches plant^{-1} and seed yield ha^{-1} (g).

Salam *et al.* (2017) carried out a research on experimental materials comprised 30 F_1 from a 6 x 6 diallel crosses to estimate the genetic variability, heritability, genetic advance. Analysis of variance revealed presence of sufficient variability present as per different biometrical analysis except for days to maturity and oil content (%). Relative magnitude of phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation. The high GCV and PCV were observed for only two traits *viz.* number of branches per plant and harvest index (%). The traits plant height (cm), siliqua length (cm), number of siliquae per plant and seed yield per plant had moderate GCV and PCV. The highest heritability estimates were observed for the traits erucic acid content followed by plant height, branches per plant, seed yield per plant, siliqua length, days to 50% flowering and harvest index (%). Genetic advance as percentage of mean was observed high for the character number of siliquae per plant, followed by seed yield per plant, days to maturity and plant height.

2.2 Genetic variability, heritability and genetic advance in *Brassica spp.*

Heritability and genetic advance are important selection parameters as they provide an idea about the effectiveness of the selection of a genotype based on phenotypic performance. Genetic advance estimates are normally more helpful in predicting the gain under selection than heritability estimates alone. A trait having high heritability and high genetic advance was considered under the control of additive genes thus highlighting the usefulness of plant selection on the basis of phenotypic performance (Mondal and Khajuria, 2000). According to Falconer and Mackay (1996) heritability is the measure of the correspondence between breeding values and phenotypic values. Heritability estimates provide an indication of the expected response to selection in a segregating population. It is one of the main interest to the plant breeders, mainly as a measure of the value of selection for particular characters and as index of transmissibility. The importance of genotypic and phenotypic variability, heritability and trait association have demonstrated by numerous researchers (Ali *et al*., 2002) for further hereditary change.

Katiyar and Singh (1974) observed on high genetic co-efficient of variation for the traits of days to first flowering, plant height (cm) and seed yield per plant (g), on the contrary, low values and for other traits like days to maturity and number of primary branches per plant, at the time of observation on genetic variability and genetic advance of seed yield and its components in Indian mustard.

Dewan *et al.* (1998) evaluated an experiment on growth and yield of doubled haploid lines of oilseed *Brassica rapa* L. A total of 162 *Brassica rapa* DH lines were evaluated in field tests and 10 DH lines were tested in four-row plot, multilocation, replicated tests. Seed of DH lines was produced by bud selfing in the greenhouse. Approximately one-fifth of all DH lines tested were chlorophyll deficient, presumably due to the expression of recessive alleles. Inbreeding depression was evident in low seed and biological yields, low number of seeds per pod and delayed flowering. Seed yield of DH lines was positively associated

with the number of seeds per pod, early flowering and a long pod-filling period. One DH line was equal in yield to its donor population (DP), suggesting that dominance deviation was the genetic basis for high seed yield in this species.

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

Hosen (2008) carried out a study by including 5 parental genotypes of *Brassica rapa* L. and their ten F_3 progenies including reciprocals. There were large numbers of variations present among all the genotypes employed in the experiment. The plant height, days to 50% flowering and number of siliquae per plant expressed high heritability with high genetic advance and genetic advance in percentage of mean.

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

Saleh (2009) carried out a field experiment by exploiting twenty F_2 populations developed through inter-varietal crosses, along with three check variety of *Brassica rapa* L. to sought the variation in different traits, correlation between pairs of different traits and direct and indirect effects of different traits on seed yield per plant. From the values of mean, range and CV (%) of seed yield and yield contributing traits, the results showed that there were considerable variations present among all the genotypes exploited in the experiment. The

value of GCV and PCV pointed out that there were least variation existing among most of the characters. The days to maturity, length of siliqua, seeds per siliqua and thousand seed weight showed high heritability along with low genetic advance and genetic advance in percentage of mean.

Alam (2010) carried out an experiment using 26 F_4 populations of some inter-varietal crosses of *Brassica rapa* L. to study the magnitude of variations in different traits, heritability and genetic advance. Significant variations were shown in number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, days to 50% flowering, length of siliqua, number of seeds per siliqua, thousand seed weight and yield per plant. Plant height, length of siliqua, number of siliquae per plant, days to 50% flowering displayed low difference between genotypic and phenotypic coefficient of variation. Plant height, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant showed high heritability coupled with high genetic advance and very high genetic advance in percentage of mean. However, length of siliqua showed low heritability.

Khan *et al.* (2013) carried out an experiment on thirty F_7 segregating lines and two parents of *Brassica rapa* L. for studying variability, heritability and genetic advance. The result showed that a significant variation presented among all the genotypes for all the traits except thousand seed weight. Highest genotypic, phenotypic and environmental variances were observed in plant height. On the contrary, the lowest one was in length of siliquae followed by thousand seed weight. High heritability along with low genetic advance in percent of mean was found in thousand seed weight, number of secondary branches per plant, seeds per siliqua, and siliqua length but moderate heritability with high genetic advance was found in number of siliquae per plant.

Rameeh (2013) conducted an experiment using twenty four rapeseed genotypes including two cultivars and 22 advanced lines. Significant genotypic effects were displayed for phenotypic traits, plant height, yield components and seed yield,

indicating significant genetic differences among the genotypes. High broad sense heritability was found for phenotypic traits, pods on main axis and seed yield, signifying selection gain to improve these traits. Duration of flowering and pods on main axis had high value of genetic coefficient of variation.

Fayyaz and Afzal (2014) studied on indigenous lines which was planned with an aim to check locally collected *Brassica rapa* (*B. campestris*, L.) accessions for genetic variability, heritability and genetic advance. Observations was done on eight quantitative parameters *viz*. primary branches, siliqua main raceme-1, main raceme length, siliqua length, siliqua width, plant height, seed silique-1, and thousand seed weight were made. Highly significant differences were observed in all traits except siliqua width, which showed significant variation. The highest heritability coupled with higher genetic advance was noticed in plant height which provided the evidence that this trait was under the control of additive genetic effects, while rest of the traits exhibited variable trends. Hence, it was observed that indigenous accessions have great proportion of genetic variability, which can be manipulated in future breeding programs for utilizing their genetic potential.

Suman (2014) investigated on elite lines of Indian mustard to study the extent of genetic variability by estimation of different parameters such as genotypic and phenotypic coefficients of variation, heritability, and the expected genetic advance for 11 quantitative characters. The analysis of variance (ANOVA) revealed significant differences among the genotypes in respect of seed yield and its component traits. The characters like days to first flowering, days to 50 % flowering, days to maturity, plant height, siliqua length , number of seeds per siliqua and 1000-seed weight were found less influenced by the environmental factors as indicated by lower differences in magnitudes between GCV and PCV. On the contrary, the characters like number of primary branches, number of siliquae per plant, harvest index and seed yield per plant were much influenced by the environmental factors as evident from higher magnitude of difference

between PCV and GCV. High to moderate heritability with low genetic advances for days to maturity and other quantitative characters suggested the predominant role of non - additive gene action.

Ara *et al.* (2015) carried out an experiment by using the F, population of 12 inter-varietal crosses, including reciprocals, of the species *Brassica rapa* L. for estimating the magnitude of variations in characters, heritability and genetic advance. There were significant variations among different F, materials used in the experiment.

Parveen *et al.* (2015) studied on genetic variability and correlation between yield contributing traits using 15 rape seed genotypes. The results indicated that the phenotypic variance for all the characters was considerably higher than the genotypic variance denoting little influence of environmental factors on their expression.

Afrin *et al*. (2016) studied on variability and comparison analysis among the fifteen F_4 population considering different morphological attributes of *Brassica rapa* which obtained through inter-varietal crosses to find out the best genotype as well as trait for improving the yield in future. Highly significant variation was observed among the genotypes for almost all of the characters studied. The cross combination SAU sarisha 1 x SAU sarisha 3 performed the best for highest yield per plant along with most of the traits. The number of secondary branches per plant exhibits the highest value for heritability while the primary branches per plant shows lowest value. Yield per plant, thousand seed weight, siliquae length, days to 50% flowering, days to 50% maturity and plant height showed moderate heritability.

Ali *et al*. (2016) conducted an investigation to study the mean performance, heritability and genetic gain of yield and its components of *Brassica rapa* L. genotypes. Six genotypes of *Brassica rapa* were chosen for one or more several important traits for genetic improvement and were crossed in a half diallel design

and genetic analyses were conducted based on different generations. The inherent genetic differences among the genotypes were found which might be exploited through selection. The life span of the parent SAU 3 was the lowest but its yield was moderate compared to other parents. The highest yield and 1000-seed weight were noticed in TORI 7 and its 80% maturity was achieved in 81 days. In case of hybrids, the lowest life time of 79.33 days was found in SAU 3 X TORI 7. The highest yield per plant and 1000-seed weight was observed in BARI 6 X SAU 2 and BARI 6 X SAU 1, respectively. The highest heritability was recorded by days to maturity (99.99%) in the hybrid P1×P3 followed by plant height (99.93%) in P2×P6 and length of siliqua (99.83%) in P1×P4. In the cross P1×P2, length of siliqua showed high (58.06%) narrow sense heritability with very low genetic gain (0.65). Considering the yield contributing traits in connection with the heritability and genetic gain, it might be concluded that TORI 7 was the ideal parent and the hybrid combination BARI 6 × SAU1 was the ideal hybrid for *Brassica rapa.*

Mumtaz *et al*. (2017) studied on four *B. rapa* accessions (UAF11, Toria, BSA and TP-124-1) and their hybrid progenies obtained from complete diallel mating crossings designed to ascertain the genetic expression of descriptive and seed yield-related traits in Heterosis and heterobeltiosis. Number of siliqua/primary branches of plant, number of siliquae/secondary branches of plant and total number of siliquae/plant directly affect seed yield of plant while effect of plant height is indirect. Variability was observed in heterosis and heterobeltiosis for all traits.

Sikawar *et al.* (2017) carried out an experiment to assess the genetic variability, heritability and genetic advance in 21 diverse genotypes of yellow sarson (*Brassica rapa* Var. yellow sarson) for ten yield and its contributing characters. Analysis of variance for the design of the experiment indicated highly significant differences for all the characters. High Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were observed for number

of secondary branches per plant followed by seed yield per plant, number of primary branches per plant and number of siliqua on main raceme. Hence, direct selection of these traits will prove effective. Days to flowering, plant height and length of siliqua showed low PCV and GCV. Higher estimates of broad sense heritability were observed for all the characters. High heritability coupled with high genetic advance was observed for number of secondary branches per plant, seed yield per plant, length of main raceme, number of siliqua on main raceme, number of seeds per siliqua and number of primary branches per plant. High heritability with moderate genetic advance in case of length of siliqua and thousand seed weight whereas, High heritability and low genetic advance was observed for days to flowering and plant height.

Sohail *et al.* (2017) studied on intra-specific quantitative characters among 253 *Brassica rapa* genotypes. The two years mean morphological data were recorded for all these characters under field condition. Significant variations were recorded among genotypes for days to flower initiation, days to 50% flowering completion, days to flowering completion, days to maturity, leaf length and width, plant height, primary branches plant-1, main raceme length, pod length, pod width, stem thickness, ,thousand seed weight, seed yield plant-1 and pod shattering (stage I-IV). Many elite lines such as Br-505, Br512, Br-536, Br-547, Br-560, Br-760, etc. had excellent morphogenic responses in both years.

Ullah *et al.* (2017) investigated on genetic variability, heritability and correlation among different biochemical traits, six advanced lines (F10:11) of *Brassica rapa* L. Significant differences were observed for glucosinolate, oil content, protein content, oleic acid, linolenic acid and erucic acid. Genotypic variances were greater than the environmental variances for majority of the traits. Majority of the traits exhibited high heritability. Overall the studied parameters indicated significantly varied results among the advanced lines.

Singh *et al.* (2017) conducted an experiment in the heterosis, heritability in broad sense, inbreeding depression and inter-relationships among

the quantitative traits in six intra-specific crosses developed in yellow sarson. The experimental material comprised six parental genotypes, 12 F_1 and F_2 populations. Results revealed significant differences for all yield and quality characters indicated the presence of sufficient genetic variability for effective selection. In all cross combinations, hybrids performed better than their respective parents and significant positive standard and better parent heterosis was observed for the trait seed yield per plant. High heritability coupled with high genetic advance were noticed for length of fruiting zone (Ragni × YST-151) and for seed yield per plant in Jagrati × YST-151, NDYS-427 × YST-151, Pusa Gold × Jagrati and Ragni × NDYS-425 crosses.

2.3 Correlation analysis

The estimation of correlation is one of the most common and useful statistical techniques in research. For improvement in yield and quality, study of association among its components is important. It contributes to ascertain which of the postulated components have positive and significant relationship with grain yield and quality traits. Pearson's correlation determines the extent to which values of the two traits are "proportional" to each other. Correlation coefficient is a statistical measure which is used to find out the degree and direction of relationship between two or more variables.

Pauw *et al.* (1978) conducted an experimant on seed yield, height, days to mature and oil content were measured on 16–25 lines of turnip rape (*Brassica campestris* L.) grown at both Beaverlodge and Saskatoon in the years 1970 through 1975. Dividing the total variation observed in each year into sources relating to genetic differences, genotype–location interaction and plot-to-plot error revealed that the last component accounted for most of the variation, particularly for yield, height and maturity. The phenotypic correlation of line mean performance between locations was significantly less than the heritability in only 5 of 20 cases at Beaverlodge and less than the heritability in none of the cases at Saskatoon.

Gouping *et al.* (1999) studied on the phenotypic and genotypic correlations of 11 agronomic characters with 14 cultivars of mustard. The results showed that the phenotypic correlations were lower than genetic correlations. The genetic correlation coefficients between flower stalk weight and flower stalk width in diameter, leaves number, blade weight, petiole weight and plant height were highly significant.

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

Kashyap and Mishra (2004) studied 11 morphological characters of *Brassica campestris* Var. Toria using 16 genetically diverse genotypes and reported that seed yield had exhibited significant and positive correlation with plant height, branches per plant, siliqua per plant, seeds per siliqua and 1000 seed weight. He found that these characters were also significantly and positively correlated 18 with each other, suggesting the scope of their simultaneous improvement through selection.

Halder *et al.* (2016) studied on eleven advanced lines and three popular check varieties of *Brassica rapa* L. and reported that the correlation co-efficient analysis had direct and indirect effect of eleven characters on yield per hectare. Yield per hectare was positively and highly significantly correlated with days to first flowering, days to 80% flowering and number of primary branches per plant which indicated that the yield would be higher by improving these characters while would be decreased with the increase of days to 50% flowering and length of siliquae as they were negatively correlated with yield.

Jamali *et al.* (2016) studied on correlation among yield and yield contributing traits in *Brassica compestris* L. using six *Brassica* varieties including three commercial varieties and three candidates selected from the available germplasm. The results revealed that among *Brassica* genotypes significant differences were observed for plant height, days to 75% flowering, pods plant-1, seeds pod-1, seed index and seed yield plant-1; while non-significant for branches plant-1 and days to 90% maturity.

Kumari *et al.* (2017) conducted a research on correlation analysis using forty four genotypes of yellow sarson (*Brassica rapa*. Var. yellow sarson) were evaluated for thirteen quantitative and qualitative characters. Seed yield per plant revealed significant and positive correlation with biological yield, while positive but non-significant correlation with siliqua length, harvest-index, seeds per-siliqua, day to maturity, 1000-seed weight, while non-significant negative correlation with plant height and primary branches per plant, significant and negative correlation coefficient of oil content was observed with siliqua on main raceme. Oil content showed negative and non-significant association with plant height length, length of main raceme and primary branches per plant, while seeds per siliqua and days to 50 percent flowering showed significant and positive correlation with oil content. 1000 seed weight exhibited significant positive correlation with siliqua length and seed per siliqua.

Siddique *et al.* (2017) conducted a study using six genotypes. According to results genotype S-9 (check) surpassed all other genotypes for plant height. Correlation results were positively significant among plant stature with pods plant, height with yield of single plant, days to flower with seed index, days to flower with yield of single plant, pods per plant with seed index, pods per plant with single plant yield, seed index with single plant yield. Negative and significant relationship was examined between plant height and seeds per pod, branches per plant and ripeness days and pods per plant and seeds per pod.

2.4 Path co-efficient analysis

Path coefficient analysis calculates the correlations between yield and its contributing components, taking account of the cross correlation, either positive or negative. It is useful to partition the total correlation into direct and indirect effects on different components (Tollenaar *et al*., 2004). In agriculture, plant breeders seek assistance in identifying traits that are useful as selection criteria to improve crop yield with help of path analysis.

Uddin *et al.* (2013) conducted an experiment to study the variability among seven parental genotypes and their twenty one F progenies of *Brassica rapa* L. and results showed that seed yield plant had significant positive association with number of primary branches/ plant, number of secondary branches/ plant, number of siliquae/ plant. Path co-efficient analysis revealed that days to 50% flowering, number of primary branches, secondary branches and siliquae/ plant , siliqua length, seeds /siliqua and thousand seed weight had the positive direct effect on seed yield plant. Days to maturity and plant height had the negative direct effect on yield plant.

Helal *et al.* (2014) conducted an experiment to study Genetic variability, correlation of yield and yield contributing characters and coefficient of variance in rapeseed or mustard and reported that path coefficient analysis of different yield contributing characters showed biological yield contributed maximum to seed yield with the highest correlation.

Nazneen *et al*. (2015) evaluated on thirty three genotypes of *Brassica rapa* L. in order to find out their inter-genotypic variability; character association and path coefficient of seed yield/plant and its component characters. BARI sarisha-6 x TORI-7 showed the best result in terms of early maturity (75 days) and higher seed yield/plant (5.28 g) than check varieties. The character, plant height, was highly influenced by the environment whereas, all other characters influenced the least. Number of secondary branches/plant showed the highest phenotypic

and genotypic coefficient of variation. Moreover, number of siliquae/plant, number of secondary branches/plant and number of primary branches/plant showed high heritability.

Rashid *et al.* (2015) studied on 40 oleiferous *Brassica sp*. and reported that his path analysis revealed number of primary branches/plant, number of secondary branches/plant, days to 50% flowering, days to maturity and number of siliquae/plant demonstrated positive direct effect and plant height, length of siliqua, number of seeds/siliqua and 1000 seed weight showed negative direct effect on yield/plant.

Halder *et al.* (2016) studied on eleven advanced lines and three popular check varieties of *Brassica rapa* L. and showed clearly picture on the inter-relationship through path co-efficient analysis. Plant height showed highest positive and highly significant direct association with the yield per hectare followed by number of primary branches per plant. Highest negative significant direct effect was found in number of siliquae per plant followed by days to maturity. The high direct effect gave the massage that selection of the traits might be effective for yield improvement. Low residual effect indicated that the considered traits of the study explained almost all the variability towards yield.

Islam *et al*. (2016) studied on twenty one (21) F_9 populations which is derived from inter-varietal crosses of *Brassica rapa* L. Path co-efficient analysis revealed that plant height, number of primary branches per plant, number of siliquae per plant, seeds per siliqua, and siliqua length had the positive direct effect on yield per plant and days to 50% flowering, number of secondary branches per plant, and thousand seed weight had the negative direct effect on yield per plant.

Kumari *et al.* (2017) reported that the path coefficient analysis of biological yield showed maximum direct effect, while silique length and oil content exerted negative direct effect on seed yield and days to 50 percent flowering exerted negative indirect effect on seed yield.

2.5 Nutrient component analysis

Biochemical analysis is one of the important features of this study. In oil seed crops, the quality seed production is the major objective beside a high yielding variety. The quality of oil seed *Brassica sp.* depends on high percentage of oil, protein, oleic, linolenic, linoleic acid and low percentage of palmitic, stearic, eicosenoic, erucic acid. One of the major undesirable and problematic components of the oil seed *Brassica sp.* is its higher level of erucic acid content.

Dorrell *et al.* (1964) studied on reciprocal crosses between a plant of *Brassica campestris* L. containing no erucic acid in its seed oil and two plants of the Indian varieties Yellow and Brown Sarson grown from seed containing approximately 59% erucic acid. The erucic acid content in the oil from F_1 embryos was intermediate between the parents indicating embryonic control of the synthesis of this acid. Seed oil analysis of F_2, F_3, and backcross populations supported the hypothesis that erucic acid synthesis is controlled by a single non-dominant gene. Analysis of oil extracted from immature and partially germinated seed showed that erucic acid content was highest in fully matured non-germinated seed.

Velasco *et al.* (1998) evaluated an experiment on a germplasm collection consisting of 1475 entries from 21 species of *Brassica*, including 36 lower taxa to study on the fatty acid composition of the seed oil. A total of 358 entries representing the taxonomic variability in the collection were selected and analyzed by gas-liquid chromatography (GLC). The remaining 1117 entries were analyzed by near-infrared reflectance spectroscopy (NIRS), after developing multi-species calibration equations. The results demonstrated that NIRS is an effective technique to assess variability for oleic, linoleic, linolenic and erucic acid in intact-seed samples of multiple *Brassica sp*., provided that calibration equations be developed from sets containing large taxonomic and chemical variability. Some fatty acid ratios were used to estimate the efficiency of the different biosynthetic pathways. Two well-defined patterns were observed. The first one was characterized by high elongation efficiency and accumulation of

high levels of erucic acid. The highest erucic acid content (>55% of the total fatty acids) was found in the cultivated species *B. napus* L., *B. oleracea* L., and *B. rapa* L. The second pattern was characterized by high desaturation efficiency, resulting in the accumulation of high levels of the polyunsaturated linoleic and linolenic acid (up to more than 55%).

Luhs *et al.* (1999) studied that the traditional rapeseed and mustard oils are characterized by high contents of erucic acid (22:1) and other monounsaturated fatty acids with chain lengths of C20 to C24. Breeding of low erucic acid cultivars of *Brassica napus*, *B. rapa*, *B. juncea* and *B. carinata* has led to an almost complete abolishment of 22:1 synthesis. In general, erucic acid content in the genus *Brassica* varies with the allelic constitution of the genotype, differences in the ploidy level, the genetic background and environmental impact. Series of alleles have been identified in *B. napus* (genome AACC) and *B. rapa* (AA), which make it possible to breed strains containing almost any level of 22:1 from less than 1% to about 60% of total fatty acids. Regarding *B. oleracea* (CC), which normally displays a 22:1 content ranging from 28 to 63%, they were able to identify individual plants being nearly free of erucic acid.

Bhardwaj *et al.* (2000) conducted a research to characterize the winter hardy rapeseed germplasm for oil, erucic acid, and glucosinolate contents for use in breeding programs to develop commercial production of rapeseed. Significant variation existed among the 455 accessions of *Brassica napus* L. and the 44 accessions of *Brassica rapa* L. for oil, erucic acid, and glucosinolate contents. *B. napus* had significantly higher mean oil content in the seeds than the *Brassica rapa*. The glucosinolate content was higher in *napus* than the *rapa* meal. The erucic acid content was higher in *rapa* than the *napus* accessions. Within species, the correlation between oil and glucosinolate contents was significantly negative among the *napus* accessions, but was significantly positive among *rapa* accessions. The results indicated that plant material from either *napus* or *rapa* species could be used in breeding for increasing erucic acid

content. Accessions with high, medium, and low contents of oil, erucic acid, and glucosinolate contents were identified.

Khan *et al.* (2008) evaluated on six F_3:4 derived interspecific *Brassica* populations together with three checks were evaluated for their genetic variability and correlation among quality traits. Highly significant genetic variation existed among *Brassica* populations for oil content, glucosinolate, oleic acid, linolenic acid and erucic acid contents. Non-significant variation was recorded for protein content. The maximum oleic acid and minimum linolenic acid were recorded for the population, while minimum glucosinolates and erucic acid were recorded in population. Genetic variances for most of the traits were generally 3 to 15 times greater than the environmental variance indicating significant genetic control over expression of quality traits. Heritability estimates were high for glucosinolate, linolenic acid, oleic acid and erucic acid contents, while low heritability was observed for protein content.

Islam *et al.* (2009) studied on twenty-two genotypes of *Brassica* (*B. rapa, B. juncea,* and *B. napus*) for correlation co-efficient between major fatty acids and path co-efficient analysis to partition the cause and effect relationship into direct and indirect components. Correlation coefficient of major fatty acids revealed that significant and positive correlation was between palmitic and oleic acids, palmitic and linoleic acids, palmitic and cicosenoic acids, oleic and eicosenoic acids, linoleic and linolenic acids and eicosenoic and erucic acids, while significant and negative correlation was observed between palmitic and erucic acids, stearic and linolenic acids and oleic and erucic acids. Path coefficient revealed that direct effect of all fatty acids except palmitic acid on oil content was positive. Indirect effect of erucic acid through all other fatty acids except palmitic acid on oil content was negative, indirect effect of palmitic acid via all other fatty acids except erucic acid was positive.

Ahmad *et al*. (2016) evaluated on eight rapeseed genotypes and significant differences were observed for all the parameters except oil and protein percentage. For yield contributing characters like 1000 seed weight, Seed pod-1 and pods plant-1, genotype PI-26369 again showed good results that are, 4g, 20 and 343 pods plant-1, respectively. The genotype H-19 showed low glucosinolate, genotype PI-26369 have lowest amount of erucic acid and higher amounts of oleic acid.

Ko *et al.* (2017) studied on total of 447 accessions consisting of seven Brassica *spp*.; *Brassica carinata* (34*), B. juncea* (199), *B. rapa subsp. dichotoma* (18), *B. rapa*. *subsp. oleifera* (14), *B. rapa subsp. rapa* (36), *B. rapa subsp. trilocularis* (56) and *B. alba subsp. alba* (90) were studied for their morphological characters and fatty acid compositions. There was a wide variation for morphological traits, oil content and fatty acid composition among *Brassica* species. Among *Brassica sp., B. rapa subsp*. trilocularis exhibited the highest oil, stearic acid and erucic acid content. *B. carinata* had the highest content of palmitic, oleic and linolenic acid. *B. rapa subsp*. *dichotoma* and *B. rapa subsp*. *oleifera* exhibited the highest content of linoleic and behenic acid, respectively. *B. rapa subsp*. *trilocularis* exhibited the highest erucic acid content and significant positive relationship was observed between oleic acid and linoleic acid. This variation of agronomic and fatty acid compositions in *Brassica* species can be utilized to develop new varieties.

CHAPTER III
MATERIALS AND METHODS

The present investigation entitled **"Evaluation of 15 populations of *Brassica rapa* L. in terms of morphological and biochemical traits''** was carried out at the experimental field of Sher-e-Bangla Agricultural University, Dhaka. The detail information regarding the materials and methodology of this experiment is discussed below:

3.1 Location of experimental site

The research work was conducted at the Sher-e-Bangla Agricultural University, Dhaka-1207 from November 2016 to February 2017. The experimental area was situated at 23°46'16" N latitude and 90°22'46" E longitude at an altitude of 4 meter above the sea level (Digital Globe, Google). The experimental field belongs to the Agro-ecological zone of "The Modhupur Tract", AEZ-28 (www.banglapedia.com). The experimental site was shown in the map of AEZ of Bangladesh in (Appendix I).

3.2 Soil and climate

The soil of the experimental fields was clay loam. The land was medium high and the fertility level was medium. The site was in the subtropical climate zone. Climatic feature of this region was wet summer and dry winter. During the Rabi season, generally the rainfall is very few, the temperature is moderate and the day length is short. 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.

3.3 Planting materials

The research work was carried out by using 15 advanced lines of *Brassica rapa* which was collected from Sher-e-Bangla Agricultural University, Dhaka.

These populations were developed by selecting the materials from different segregating generations obtained through various inter-varietal hybridization of *Brassica rapa* L. The advanced lines which were used in the experiment are shown below in Table 1.

3.4 Experimental layout

The field experiment was designed in Randomized Complete Block Design (RCBD) with three (3) replications. The plot size was 300 m^2. Row length was maintained as 4 m having 75 cm irrigation channels among the rows. The distance between line to line was 30 cm and plant to plant was 10 cm.

3.5 Operational practice

3.5.1 Soil and field preparation

The field was prepared by doing several plough and cross plough followed by laddering and harrowing using power tiller to have fine tilth and optimum level of moisture condition. Weeds and stubbles were removed from the field. During final land preparation, cowdung was applied and leveled the field properly.

3.5.2 Fertilizer and manure application

Urea, triple super phosphate (TSP), muriate of potash (MOP), gypsum, zinc oxide (ZnO) and boric acid was applied to the field at the proper rate and proper time. Urea was applied by two installments. First half of urea and total TSP, MOP, gypsum, boric acid, ZnO and cowdung was applied during final land preparation as a basal dose. The remaining half of urea was applied as a top dressing at the time of flower initiation. The rate of fertilizer and manure is shown below in Table 2.

Table 1: Name of the populations used in the study

Sl. No.	Designation	Populations	Sources
1	P1	SAU sarisha- 1 × BARI sarisha- 15 F_5	GEPB, SAU
2	P2	SAU sarisha- 1 × BARI sarisha- 15 F_6	GEPB, SAU
3	P3	BARI sarisha- 6 × BARI sarisha- 15 F_8	GEPB, SAU
4	P4	F_6 × BARI sarisha- 9 F_{14}	GEPB, SAU
5	P5	BARI sarisha- 6 × Tori-7 F_6	GEPB, SAU
6	P6	BARI sarisha- 6 × Tori-7 F_{14}	GEPB, SAU
7	P7	SAU sarisha- 2 × BARI sarisha 6 F_5	GEPB, SAU
8	P8	SAU sarisha- 2 × BARI sarisha 15 F_5	GEPB, SAU
9	P9	BARI sarisha- 15 × SAU sarisha- 3 F_6	GEPB, SAU
10	P10	BARI sarisha- 15 × SS_{75} F_8	GEPB, SAU
11	P11	Tori-7 × SAU sarisha-1 F_6	GEPB, SAU
12	P12	SAU sarisha- 1 × BARI sarisha 6 F_5	GEPB, SAU
13	P13	Tori-7 × BARI sarisha-6 F_{14}	GEPB, SAU
14	P14	BARI sarisha- 9 × BARI sarisha- 6 F_{14}	GEPB, SAU
15	P15	Yellow Special	GEPB, SAU

Table 2. List of fertilizers and manures with doses and application procedures

Sl. No.	Fertilizers/ manures	Dose		Application procedure
		Applied in the plot	Quantity/ha	
1.	Urea	7 kg	225 kg	50% basal and 50% at the time of flower initiation
2.	TSP	4.75 kg	235 kg	as basal
3.	MOP	2.25 kg	78 kg	as basal
4.	Gypsum	4 kg	135 kg	as basal
5.	Boric acid	320 g	11 kg	as basal
6.	ZnO	80g	3 kg	as basal
7.	Cowdung	100 kg	5 ton	as basal

3.5.3 Seed selection and sowing time

Healthy and pure seeds were taken by avoiding the unfilled seeds. Seeds were sown as lines in the experimental field on 17 November, 2016. The seeds were placed at about 1.5 cm depth in the soil. Clods were removed during sowing. Seeds were started to germinate after 3 days of sowing.

3.5.4 Intercultural operations

Different intercultural operations like weeding, thinning, irrigation, top dressing, pest management and etc. were applied in appropriate time to ensure proper growth and development of the plants. A good drainage system was maintained to release the rain water immediately from the experimental field during the growing period.

3.5.4.1 Tagging and Tying

When the plants are visible after 1 week of germination, then tagging of each population of all replication was done. The field was bound with rope to protect the plants from leaning by using bamboo. Tagging of each population of all replication was done after a week of sowing (Plate 4).

3.5.4.2 Weeding and thinning

Two times weeding and thinning was done according to the requirement of maintaining uninterrupted growth of the crop. The first weeding was done after 13 days of sowing. Thinning was done at the same time for maintaining 30 cm from line to line and 10 cm from plant to plant. Second weeding was done after 20 days of sowing.

3.5.4.3 Irrigation and after care

The experimental plot was lightly irrigated after sowing by using watering canes to bring proper moisture condition of the soil ensuring uniform germination of seeds. Second irrigation was given (22 DAS) before the flower

initiation. Third irrigation was given (40 DAS) when the pod appeared. Fourth irrigation was given (60 DAS) when seeds appeared in the pod. Good drainage system was maintained to drain out the excess water. During irrigation, special care was taken of so that the water pressure might not break the shoots of the plants.

3.5.4.4 Pesticide application

Aphid infection was found during the siliqua development stage of the crop. Malathion-57 EC @ 2mL/liter of water was sprayed to control aphids. Insecticide was applied in the afternoon to protect the beneficial insect.

3.5.5 Harvesting

Harvesting was started from 12 February to 17 February, 2017 depending upon maturity of the plants. Plants are harvested when 80% showed symptoms of maturity such as, straw color of siliqua, leaves, stem and desirable seed color in the mature siliqua. At maturity, 10 plants were selected for morphological and 30 plants were selected for biochemical analysis from the populations. The sample plants were harvested by uprooting and tagging was done specifically for analyzing morphological and biochemical traits. Photograph showing experimental field during land preparation in Plate 1, experimental field during seed sowing in Plate 2, experimental field during growth stage in Plate 3, the entire view of experimental field during fruiting stage in Plate 5 and field view during maturity of *Brassica rapa* L. in Plate 6.

3.5.6 Collection of data

To study different genetic parameters and inter-relationships the following ten characters were taken into consideration: plant height, days to 50% flowering, days to 80% maturity, no. of primary branches/ plant, no. of secondary branches/ plant, no. of siliqua/ plant, length of siliqua, no. of seeds/ siliqua, thousand seed wt., yield/plant.

Plate 1: The view of experimental field during land preparation

Plate 2: The view of experimental field during seed sowing

Plate 3: The view of experimental field during growth stage

Plate 4: Tagging of each population of entire field

Plate 5: The entire view of experimental field during fruiting stage

Plate 6: The entire view of experimental field during maturity stage

3.6 Data collection methods

3.6.1 Days to 50% flowering

Days to 50% flowering was counted from the date of sowing to the date of 50% flowering of each population.

3.6.2 Days to 80% maturity

Days to 80% maturity was counted from the date of sowing to the date of 80% maturity of each population.

3.6.3 Plant height (cm)

Ten plants were randomly selected measuring from the base of the plant to the tip of the longest inflorescence with the help of meter scale in cm after final harvest. Mean height was recorded.

3.6.4 Number of primary branches/ plant

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

3.6.5 Number of secondary branches/ plant

The total number of branches originated from the primary branches of the plant were counted as the number of secondary branches per plant.

3.6.6 Number of siliqua/ plant

Total number of siliquae of each plant was counted from the selected ten plants and considered as the number of siliqua/ plant.

3.6.7 Length of siliqua (cm)

Five representative siliqua were selected randomly and measurement was taken in centimeter from the base to the tip of a siliqua without beak.

3.6.8 Number of seeds/ siliqua

All siliqua from the sample plants was collected and five siliqua was randomly selected. Seeds obtained from them, were counted and average numbers of the seeds per siliqua was recorded.

3.6.9 Thousand-seed weight (g)

Ten plants of each line was selected and thousand seed weight was recorded in grams.

3.6.10 Yield/ plant (g)

All the seeds produced by a representative plant was weighted in g by considering it as the seed yield per plant.

3.6.11 Nutrient component analysis

Biochemical analysis is one of the important features of this study. In oil seed crops, the quality seed production is the major objective beside a high yielding variety. The quality of oil seed *Brassica sp.* depends on high percentage of oil, protein, oleic acid and low percentage of erucic acid. Quantification of fatty acids composition (%) was performed with Gas Liquid Chromatography (GLC) method by Philips PU4500 Chromatograph in Analytical Service Cell, Bangladesh Council of Scientific and Industrial Research (BCSIR). In the GLC column temperature was fixed at 185°C, injector temperature was 220°C and the detector temperature was 240°C. 50g of mustard of all populations were grinded and analysis below was done:

3.6.11.1 Methylation of Fatty Acid

Total lipid (400-600 mg) was taken in a ground joint flask and saponified with 15-30 mL 2M KOH (ethanolic) in water bath at 70°C for 1 hour by joining with a condenser. After cooling, the solution was diluted with equal volume of distilled water and acidified with concentrated HCl to PH <2 as ascertained with a PH meter. The liberated fatty acids (a mixture) were extracted with 30-60 mL

of diethyl ether. Small amount of water was also extracted along with free fatty acids. This undesired water was removed by adding anhydrous sodium sulphate. The ether extract devoid of water was collected in another joint flask. The extract was then evaporated to dryness under N_2. Dry methanolic HCl (25-50 mL) prepared, was added into the flask containing the fatty acid mixture and the content was heated at 85°C under reflux for 2 hours. After cooling, the fatty acids methyl esters (FAME) were extracted three times with equal volume of petroleum spirit (bp 40-600). All extracts were combined and evaporated to a small volume under N_2.

3.6.11.2 Purification of Fatty Acid Methyl Esters (FAME)

3.6.11.2.1 Preparation of TLC Plate

A slurry of silica gel G for thin layer chromatography was made with water (2 mL water per g silica gel G) in a beaker (500 mL capacity) and spread on 2 mm thick glass plates 20×20 cm by a TLC spreader. The silica gel coating was 250 µm. The slurry thus spread was kept on platform about 10 minutes, transfer to the metal racks and dried in an oven at 110°C for about an hour. The plates was then ready for use.

3.6.11.2.2 Thin Layer Chromatographic (TLC)

Standard fatty acids preparation (~3-5 mL) was then spotted on the plates with a glass capillary taking precaution so that not more than 2-3 µL are spotted on the plates at a distance nearly ¾ for an inch from one edge on the plates. The gaps between two spots should be around half an inch and the spots should be as small as possible for better resolution of the fatty acids. The unknown should be spotted on the two locations. After air drying the plate was dipped in the solvents (n- hexane: Diethyl ether: glacial acetic acid 70:30:1) in the TLC jar which was pre-equilibrated with the solvent system for about an hour. The solvent rise up the silica gel (ascending chromatography) and was allowed to rise approximately anywhere between 15-18 cm (nearly one hours) at which point the plate was removed from the jar, air dried, placed in the iodine chamber for 5 minutes. The

FAME band in the plate was visualized in the iodine chamber. The FAME in the sample can be identified by their R_f values when compared to standard. After the yellow color vanished the band was scraped into a centrifuge tube and eluted with methanol. The tube was then centrifuged and the supernatant was transferred into a dry flask. The FAME solution was evaporated to dryness under nitrogen. A small volume of dichloromethane solution was added to re-dissolve the FAME band and a 5-10 mm aliquot was analyzed in Gas-liquid chromatography.

3.6.11.3 Gas-Liquid Chromatographic (GLC) analysis of fatty acid methyl esters

The fatty acid methyl esters, prepared and purified as above, were analyzed by gas-liquid chromatography (GLC). A 2×4 mm inside diameter column (Preferably glass) packed with 12-15% (w/w) ethylene glycol succinate liquid phase coated on 100/200 mesh Gas-chrom P was used. The injector temperature was 190° C and the detector temperature was 260° C. The temperature of the column was programmed initially at 170° C for 8 minutes, then it was allowed to rise to 200° C at a rate of 10° C/min and the isothermal final period was 55 minutes. Thermal conductivity detectors were excellent. Nitrogen was used as a carrier gas at a flow rate of 11.4 mL/min. Hydrogen flow was 10% above nitrogen flow. Standard fatty acid methyl esters were used for the identification of the sample fatty acid peaks. The following Standard fatty acids were used, the methyl esters of C16:0, C18:0, C18:1, C20:1, C22:1, C18:2, C18:3. The peak area of each component was measured automatically by chromatograph machine. The total mm of all peak areas were taken as 100% and the percent population of a given fatty acid peak was calculated accordingly. The fatty acids were expressed as weight percentages of total fatty acids.

Calculation

Fatty acid compositions (%) were calculated from the chromatograph. Unit area for each peak of respective fatty acid was calculated against starting time by GLC. Fatty acid composition was calculated as follows:

$$\text{Factor} = \frac{100}{100 - \text{unit area of solvent}}$$

% fatty acid = Unit area of respective fatty acid x Factor

3.7 Statistical analysis

Data were recorded for seventeen traits i.e. days to 50% flowering, days to 80% maturity, plant height (cm), no. of primary branches/plant, no. of secondary branches/plant, number of siliqua/plant, siliqua length (cm), number of seeds/siliqua, thousand seed weight (g), yield/plant (g), palmitic acid content (%), stearic acid content (%), oleic acid content (%), eicosenoic acid content (%), erucic acid content (%), linoleic acid content (%) and linolenic acid content (%). The mean values of ten randomly selected plants used for recording observations were computed for each of ten traits for each population in each replication and were subjected to statistical analysis. Mean, range and co-efficient of variation (CV %) were also estimated using MSTAT C software.

3.7.1 Analysis of variance

The analysis of variance for different characters was carried out using mean data in order to assess the genetic variability among populations as given by Cochran and Cox (1957). The level of significance was tested at 5% and 1% using F test. The model of ANOVA used is presented below:

Sources of variation	Degrees of freedom (D.F.)	Mean sum of squares (MS)	Expected MS
Replication	(r-1)	Mr	p б ^2_r+ б^2_e
Population	(p-1)	Mp	r б^2_p+ б^2_e
Error	(p-1) (r-1)	Me	б^2_e
Total	(rp-1)		

Where,

r = number of replications

p = number of treatments (population)

$б\,\frac{2}{r}$ = variance due to replications

$б_p^2$ = variance due to treatments (population)

$б_e^2$ = variance due to error

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

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

Where, S. E = Standard error of mean

Me = Mean sum of square for error (Intra block)

r = Number of replications

q = Number of population in each sub-block

u = Weightage factor computed

3.7.2 Study of variability parameters in mustard populations

The variability among the populations for traits related to yield per plant in *Brassica rapa* L. were estimated as mentioned below.

3.7.2.1 Genotypic variance and phenotypic variance

Phenotypic and genotypic components of variance were estimated by using the formula given by Cochran and Cox (1957).

Genotypic variance (σ^2g) = $\frac{\text{MSS due to genotypes} - \text{MSS due to error}}{R}$

Phenotypic variance = Genotypic variance (σ^2g) + Error variance (σ^2e)

3.7.2.2 Co-efficient of variability

Both phenotypic and genotypic co-efficient of variability for all characters were estimated using the formula of Burton (1952).

Phenotypic Co efficient of Variability (PCV %) = $\frac{\sqrt{\text{Phenotypic variance}}}{\text{Grand mean}} \times 100$

Genotypic Co efficient of Variability (GCV %) = $\frac{\sqrt{\text{Genotypic variance}}}{\text{Grand mean}} \times 100$

PCV and GCV were classified into three following categories as suggested by Sivasubramanian and Madhamenon (1973).

Categories Low: Less than 10% Moderate: 10-20% High: More than 20%

3.7.2.3 Heritability in broad sense (h^2)

The broad sense heritability (h^2_{bs}) was estimated for all characters as the ratio of genotypic variance to the total of phenotypic variance as suggested by Lush (1949) and Hanson *et al*. (1956).

$$h^2 = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

Heritability estimates in cultivated plants could be placed in the following categories as suggested by Robinson *et al*. (1966).

Categories Low: 0-30%; Moderate: 30-60%; High: >60%

3.7.2.4 Genetic advance (GA)

The expected genetic gain or advance for each character was estimated by using the following method suggested by Johnson *et al*. (1955).

$$GA = h^2_{bs} \times б_p \times K$$

Where,

h^2_{bs} = Heritability estimate in broad sense

$б_p$ = Phenotypic standard deviation of the trait

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

Categories High (>20%) Moderate (10-20%) Low (<10%)

Further the Genetic advance as per cent of mean was computed by using the following formula

$$\text{GA as per cent of mean} = \frac{\text{GA}}{\text{Grand mean}} \times 100$$

Genetic advance as per cent mean was categorized into following groups as suggested by Johnson *et al.* (1955).

Categories Low - Less than 10% Moderate -10-20% High - More than 20%

3.7.3 Correlation coefficient analysis

To determine the degree of association of characters with yield and also among the yield components, the correlation coefficients were calculated. Both genotypic and phenotypic coefficients of correlation between two characters were determined by using the variance and covariance components as suggested by Al-Jibouri *et al*. (1958).

$$r_g(xy) = \frac{Cov_g\, xy}{\sqrt{\sigma^2_x}.\sqrt{\sigma^2_y}}$$

$$r_p(xy) = \frac{Cov_p\, xy}{\sqrt{\sigma^2_x}.\sqrt{\sigma^2_y}}$$

Where,

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

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

σ^2_g and σ^2_p are the genotypic and phenotypic variance of x and y, respectively.

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

3.7.4 Path coefficient analysis

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

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

$$r_{yx1} = P_{yx1} + P_{yx2}r_{x1x2} + P_{yx3}r_{x1x3}$$
$$r_{yx2} = P_{yx1}r_{x1x2} + P_{yx2} + P_{yx3}r_{x2x3}$$
$$r_{yx3} = P_{yx1}r_{x1x3} + P_{yx2}r_{x2x3} + P_{yx3}$$

Where, r's denote 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 x_1 and y is thus partitioned as follows:

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

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

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

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

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

Where,

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

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

r_{iy} = Correlation of the character with yield

Categories

Negligible 0.00 to 0.09; Low 0.10 to 0.19; Moderate 0.20 to 0.29;

High 0.30 to 1.0; Very High >1.00

CHAPTER IV
RESULTS AND DISCUSSION

The present experiment was undertaken with a view to select short duration population by comparing the performance of 15 populations on ten characters of *Brassica rapa* L. The study was also conducted to find out the phenotypic and genotypic variability, co-efficient of variation, heritability, genetic advance, correlation, path co-efficient to estimate direct and indirect effect of yield contributing traits on yield. The study was also taken to find out the beneficial effect of analyzed acids. The data were recorded on different characters such as days to 50% flowering, days to 80% maturity, plant height (cm), no. of primary branches per plant, no. of secondary branches per plant, no. of siliqua per plant, no. of seeds per siliqua, siliqua length (cm), thousand seed weight (g), yield per plant (g), palmitic acid (%), stearic acid (%), oleic acid (%), eicosenoic acid (%), erucic acid (%), linoleic acid (%) and linolenic acid (%). The data were statistically analyzed and thus obtained results are described below under the following headings:

4.1 Mean performance and genetic variability
4.2 Correlation analysis
4.3 Path co-efficient analysis
4.4 Nutrient component analysis
4.5 Selection

4.1 MEAN PERFORMANCE AND GENETIC VARIABILITY

The success in any crop improvement program depends on the ability of the breeder to define and assemble the required genetic variability, and to select for yield indirectly through yield associated and highly heritable characters after eliminating the environmental component of phenotypic variation (Mather, 1949). Therefore, it is necessary to have prior information on both PCV and

GCV, so that the estimate of heritability that helps the breeder to foretell the expected GA possibly by selection for a character can be enumerated.

The results are pertained to mean values grand mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2) and expected genetic advance as per cent of mean (GA) for all the ten characters are embellished in Table 4. Genotypic and phenotypic variability is shown in Figure 1; heritability and genetic advance as per cent of mean is shown in Figure 2. Out of the ten characters studied, plant heights, number of primary branches per plant, number of secondary branches per plant were considered as growth attributing characters. Days to 50% flowering and days to 80% maturity were regarded as earliness attributes. Number of siliquae per plant, length of siliqua, number of seeds per siliqua and thousand seed weight were reckoned as reproductive traits. Yield per plant was the economic trait. The analysis of variance and mean performance of the data on different yield components and yield of fifteen populations was significant (Appendix III). The mean performance and range for all the characters were also significant (Table 3).

4.1.1 Days to 50% flowering

Significant variance were observed in days to 50% flowering (Appendix III). The maximum duration to days to 50% flowering was found in P6 with 39.33 DAS and the minimum in P14 with 30.67 DAS (Table 3). The mean value was 34.29. Ali *et al.* (2002) found days to 50% flowering for parents and it was ranged from 39 to 46 days. The earliness of 50% flowering of population indicates that the plant matures early. Minimum days to 50% flowering was found in P14 (30.64) indicates that flower came early DAS and it is short durable population.

The genotypic variance (5.10) was higher than phenotypic variance (1.26). High genotypic and phenotypic co-efficient of variation was recorded by Lekh *et al*. (1998). Thus, genes controlling this trait experienced less influence of

environment on the expression of the character. The GCV (Genotypic co-efficient of variation) and PCV (Phenotypic co-efficient of variation) were low with value of 6.59 and 7.35 per cent, respectively along with high heritability of 80.25% with moderate genetic advance as per cent mean of 12.16%` and low genetic advance (4.17) (Table 4). This moderate value might be due to moderate values for phenotypic variability as the heritability is high for these characters and selection differential is always constant (Nadarajan and Gunasekaran, 2005). Sikawar *et al.* (2017) found that days to flowering showed low PCV and GCV. The flowering trait of the plant was very much sensitive and influenced by the temperature fluctuation which is reflected in the present study. High heritability and low genetic advance indicating that the traits were being exhibited due to favorable influence of environment rather than genotype. Thus, it is indicative that non-additive gene action might be controlling the trait of expression and selection for this trait may not be recommended. In the contrast to the present results, High heritability was being exhibited due to favorable influence of environment rather than genotype. Thus, selection for this trait may not be rewarding. But, Sikarwar *et al*. (2017) reported high heritability and low genetic advance for days to flowering.

4.1.2 Days to 80% maturity

The average of 82.67 days with a range of 78.67 to 90.67 days was recorded for days to 80% maturity. The P14 required least number of days to mature (78.67 days) followed by P4 (79.00 days), whereas maximum number of days to 80% maturity was observed in the population P3 and P7 (82.33 days) followed by P9 (82.67 days) (Table 3). The shortest time required for 80% maturity in Tori-7 (81 days) were reported by Ali *et al.* (2002). P14 showed lowest days to maturity (78.67) which indicating that it matures early rather than the other populations.

Days to 80% maturity exhibited low GCV and PCV of 4.14 and 4.37 per cent, respectively along with high heritability of 90.02 per cent, low genetic advance 6.69 and low genetic advance as per cent mean of 8.10 per cent (Table 4).This high heritability with low genetic advance was indicative of non-additive gene

action. High heritability is less influenced by the environment. Thus, the selection for improvement of such trait might not be useful. Jahan *et al.* (2014) observed high heritability with low genetic advance in per cent of mean for days to maturity. The genotypic and phenotypic variance were recorded as 11.73 and 1.30, respectively. Genotypic variance was higher than phenotypic variance which means that there is least influence of environment in the expression of genes for this trait. Ara *et al.* (2010) found high heritability with low genetic advance and genetic advance in percentage of mean.

4.1.3 Plant height (cm)

Plant height was observed highest in P12 (116.11 cm) and lowest in P14 (84.14 cm). The mean value was recorded as 104.46 cm and mean of sum of square was 224.73 indicating significant differences among the populations for this trait (Table 3). The lowest plant height was found in P14 (84.14 cm) which showed least leaning than the other populations.

Genotypic and phenotypic variance was observed 69.59 and 15.95, respectively for plant height with large environmental influence. Ara *et al.* (2010) found the highest difference between genotypic and phenotypic variance in plant height. Naznin *et al.* (2015) also found the similar results. The plant height exhibited low genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) of 7.99 and 8.85 per cent, respectively (Table 4). High heritability of 81.36 per cent, moderate genetic advance 15.50 along with moderate genetic advance as per cent mean (14.84%) was recorded. High heritability with moderate genetic advance showed that it is controlled by non-additive gene effects and the selection may be ineffective for improvement of *Brassica rapa* L. Jahan *et al.* (2014) found high heritability with moderate genetic advance in per cent of mean for plant height. But, Fayyaz *et al.* (2014) found highest heritability coupled with higher genetic advance in plant height. Ara *et al.* (2010) also found that plant height had high heritability with high genetic advance, genetic advance in percentage of mean.

Table 3. Mean performance of various growth parameter and yield components of *Brassica rapa* L.

Populations	DF	DM	PH	NPB/P	NSB/P	NS/P	LS	NS/S	TSW	Y/P
P1	35.00	81.33	100.29	6.10	0.90	170.60	4.86	19.10	2.75	12.20
P2	35.33	80.67	107.08	5.83	0.87	157.00	5.18	18.00	2.67	10.40
P3	34.33	82.33	114.45	4.43	0.90	101.13	5.23	12.33	2.98	6.42
P4	31.67	79.00	101.35	4.97	1.33	116.67	5.44	13.73	3.57	7.58
P5	35.00	81.67	110.43	5.53	0.47	134.33	5.32	17.89	1.71	9.77
P6	39.33	90.67	104.89	4.97	1.27	117.83	5.50	14.57	2.22	8.37
P7	35.33	82.33	110.43	5.10	0.80	132.50	5.97	16.97	3.43	9.77
P8	33.33	83.00	101.04	5.07	0.70	121.00	5.97	16.43	3.10	9.57
P9	34.00	82.67	100.66	4.70	0.53	99.27	5.41	17.00	3.17	7.00
P10	32.33	80.33	90.17	3.63	0.27	80.37	5.53	10.67	1.59	5.22
P11	32.67	80.67	109.92	4.20	1.00	100.20	5.34	17.52	1.50	6.11
P12	33.00	81.67	116.11	6.10	1.70	179.00	5.29	18.43	3.55	13.48
P13	38.67	90.00	110.22	4.97	2.17	117.33	4.90	12.71	2.80	7.37
P14	30.67	78.67	84.14	7.03	3.37	196.07	6.28	20.50	2.87	14.00
P15	33.67	85.00	105.76	4.00	1.07	75.07	4.93	15.35	3.37	5.73
Min	**30.67**	**78.67**	**84.14**	**3.63**	**0.27**	**75.07**	**4.86**	**10.67**	**1.50**	**5.22**
Max	**39.33**	**90.67**	**116.11**	**7.03**	**3.37**	**196.07**	**6.28**	**20.50**	**3.57**	**14.00**
Average	**34.29**	**82.67**	**104.46**	**5.11**	**1.16**	**126.56**	**5.41**	**16.08**	**2.75**	**8.87**

DF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), NPB/P = Number of primary branch per plant, NSB/P = Number of secondary branch per plant, NS/P = Number of siliquae per plant, LS = Length of siliqua (cm), NS/S = Number of seeds per siliqua, TSW = Thousand seed weight (g), Y/P = Yield per plant (g)

Table 4: Estimation of mean performance and genetic parameters in ten characters of fifteen populations of *Brassica rapa* L.

Traits	Gen MS	Min	Max	Mean	CV (%)	σ^2_g	σ^2_e	σ^2_P	GCV	ECV	PCV	h^2_b	GA	GA (% mean)
DF	16.57**	30.67	39.33	34.29	3.27	5.10	6.36	1.26	6.59	3.27	7.35	80.25	4.17	12.16
DM	36.48**	78.67	90.67	82.67	1.38	11.73	13.03	1.30	4.14	1.38	4.37	90.02	6.69	8.10
PH	224.73**	84.14	116.11	104.46	3.82	69.59	85.54	15.95	7.99	3.82	8.85	81.36	15.50	14.84
NPB/P	2.42*	3.63	7.03	5.11	3.35	0.80	0.83	0.03	17.47	3.34	17.79	96.47	1.81	35.34
NSB/P	1.82^{NS}	0.27	3.37	1.16	23.46	0.58	0.65	0.07	65.74	23.37	69.77	88.78	1.48	127.59
NS/P	379.87**	75.07	196.07	126.56	5.65	109.59	160.68	51.09	8.27	5.65	10.02	68.21	17.81	14.07
LS	0.49^{NS}	4.86	6.28	5.41	4.49	0.14	0.20	0.06	7.03	4.49	8.34	71.00	0.66	12.20
NS/S	23.16**	10.67	20.50	16.08	6.65	7.34	8.48	1.14	16.85	6.65	18.11	86.54	5.19	32.28
TSW	1.46^{NS}	1.50	3.57	2.75	5.28	0.48	0.50	0.02	25.15	5.28	25.70	95.77	1.39	50.70
Y/P	23.07**	5.22	14.00	8.87	2.00	7.68	7.71	0.03	31.27	2.00	31.34	99.59	5.70	64.29

** = Significant at 5% level, * = Significant at 1% level, NS = Non-significant, CV = Coefficient of variation, σ^2_g = Genotypic variance, σ^2_P = Phenotypic variance, σ^2_e = Environmental variance, GCV = Genotypic co-efficient of variance, PCV = Phenotypic co-efficient of variance, h^2_b = Heritability in broad sense, GA = Genetic advance, GA (% of mean) = Genetic advance as per cent of mean

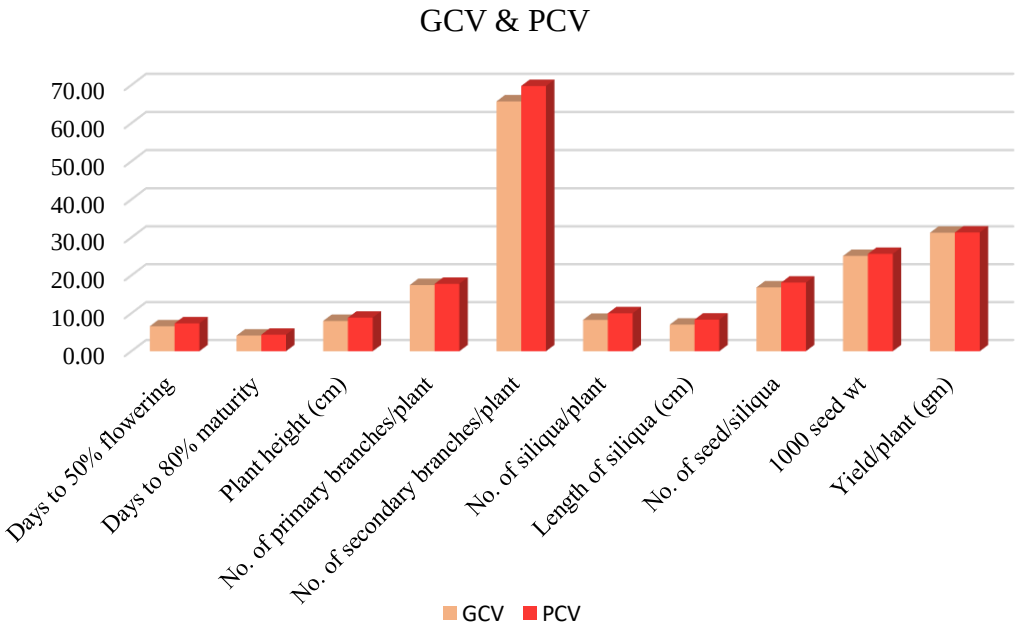


Figure 1: Genotypic and phenotypic variability in *Brassica rapa* L.

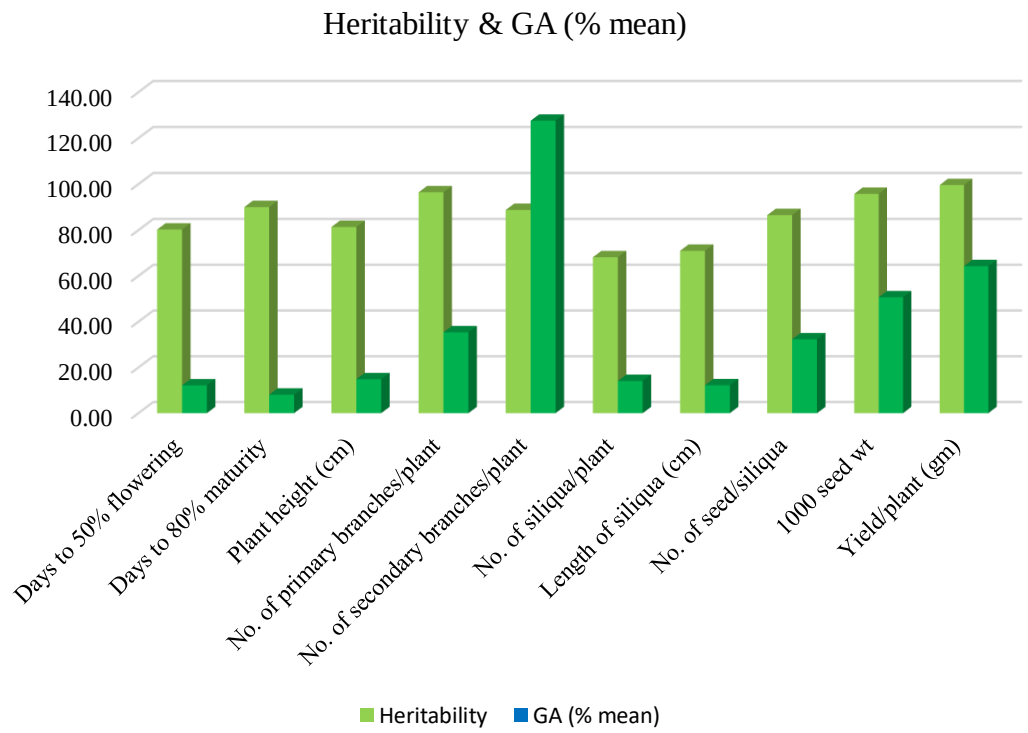


Figure 2: Heritability and genetic advance as percent over mean in *Brassica rapa* L.

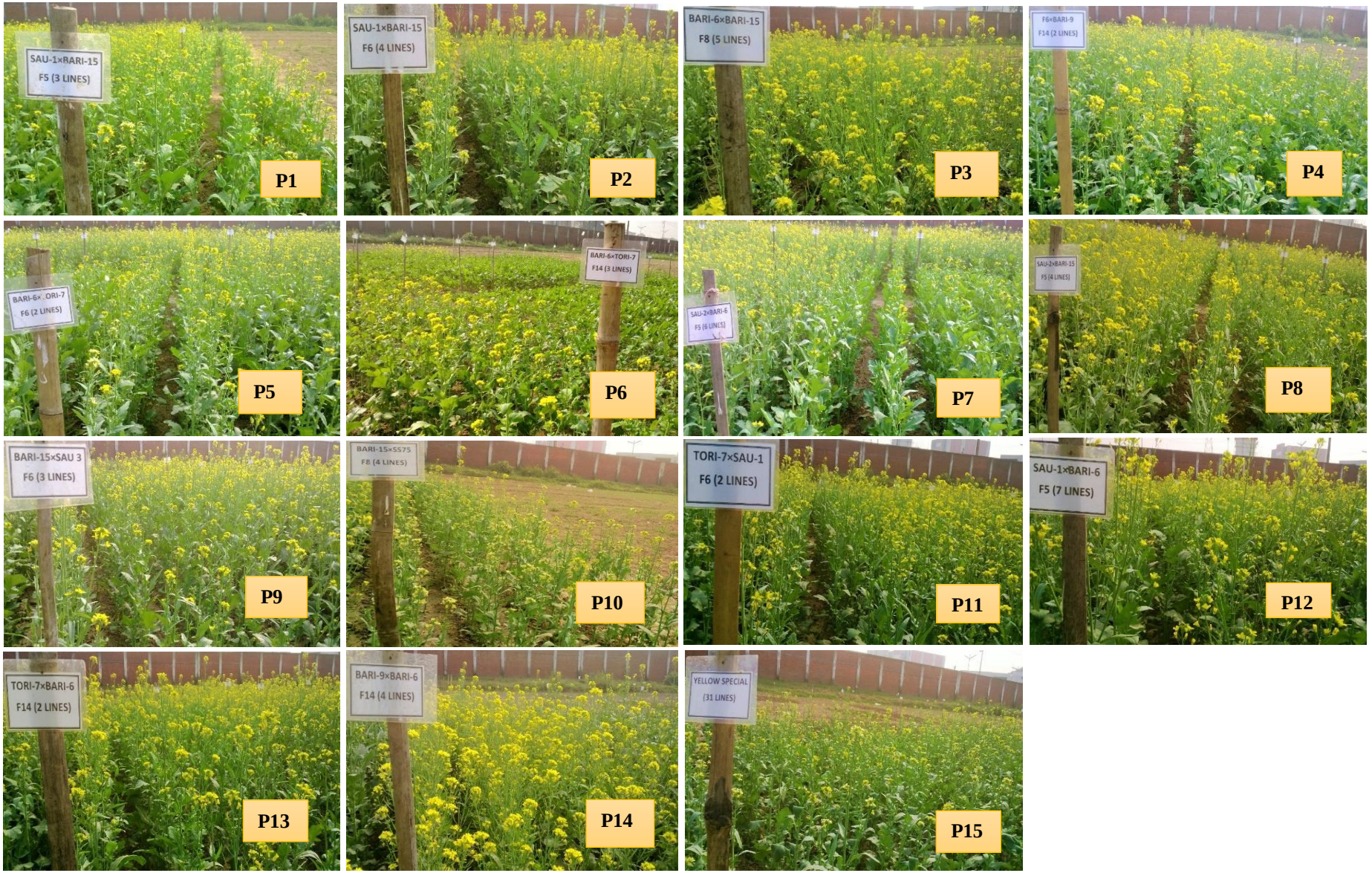


Plate 7: Photograph showing flowering stages of different populations of *Brassica rapa* L.

4.1.4 Number of primary branches per plant

The mean of sum of square for number of primary branches per plant was significantly recorded as 2.42. Maximum number of primary branches per plant were found in P14 (7.03) and minimum number of primary branches per plant were found in P10 (3.63) followed by P15 (4.00), P11 (4.20), P3 (4.43), P9 (4.70), P4 (4.97), P6 (4.97) and P13 (4.97) with mean value 5.11 (Table 3). P14 showed maximum no. of primary branches per plant (7.03) indicating more siliqua than the other populations which ultimately increased yield per plant.

The genotypic and phenotypic variance was recorded as 0.80 and 0.03, respectively. Moderate genotypic co-efficient of variation (GCV) and high phenotypic co-efficient of variation (PCV) of 17.47 and 17.79 per cent were observed, respectively (Table 4). Naznin *et al.* (2015) found that number of primary branches/plant showed low differences between the phenotypic variance (1.27) and genotypic variance (0.86) which indicated that there was less influence of environment on this character. Findings of Hosen *et al.* (2008) was also agreed with this result. High heritability 96.47%, low genetic advance (1.81) high genetic advance as per cent mean 35.34% shows that non-additive gene effects were present, making selection ineffective for this trait.

4.1.5 Number of secondary branches per plant

The mean sum of square for number of secondary branches per plant was significantly recorded as 1.82. Maximum number of secondary branches per plant were found in P14 (3.37) and minimum number of secondary branches per plant were found in P10 (0.27) followed by P5 (0.47), P7 (0.80), P8 (0.70), P9 (0.53), P2 (0.87), P1 (0.90) and P3 (0.90) with mean value 1.16 (Table 3). Maximum no. of secondary branches per plant was showed by P14 (3.37) which is a good sign for increasing the yield and ultimately it showed maximum the yield rather than the others population.

The genotypic and phenotypic variance was recorded as 0.58 and 0.07, respectively. High genotypic co-efficient of variation (GCV) and high phenotypic co-efficient of variation (PCV) of 65.74 and 69.77 per cent were observed, respectively (Table 4). Dash *et al*. observed that secondary branches per plant reflected high estimates of GCV and PCV. This is an agreement with Parveen *et al*. (2015) and Nazneen *et al.* (2015). High heritability 88.78%, low genetic advance (1.48) and high genetic advance as per cent mean 127.59% shows that non-additive gene effects were present, making selection ineffective for this trait.

4.1.6 Number of siliquae per plant

Number of siliquae per plant ranged from 75.07 to 196.07 with mean value 126.56 in different populations. The maximum number of siliquae per plant was noticed in population P14 (196.07) followed by population P1 (170.60). The population P15 recorded minimum number of siliquae per plant (75.07) (Table 3). Naznin *et al.* (2015) observed that the number of siliquae/plant showed the highest range of variation (78.00 -180.33) which means the presence wide range of variation for this character. The mean sum of square reported significant for this trait (379.87) (Table 4). The maximum no. of siliqua per plant was found in P14 (196.07) than the other populations which demonstrated more yield than the others. So, selection for this trait of this population will be effective.

The phenotypic variance (51.09) was lower than genotypic variance (109.59). This indicates less influence of environment on this character. The higher phenotypic coefficient of variation (10.02%) and lower genotypic coefficient of variation (8.27%) (Table 4) indicated presence of less considerable variability among the populations. High genotypic variance indicates the better transmissibility of the character from parent to their offspring (Ushakumari *et al.,* 1991). The heritability (68.21%) estimates for this trait was high, moderate genetic advance (17.81) and moderate genetic advance in per cent of mean (14.07) were found (Table 4), revealed that high heritability coupled by moderate

genetic advance may be due to moderate values for phenotypic standard deviation as the heritability is high for these characters and selection differential is always constant (Nadarajan and Gunasekaran, 2005). Thus, these traits could be exploited for future trial.

4.1.7 Length of siliqua (cm)

The mean of siliqua length was 5.41 cm and ranged from 4.86 to 6.28 cm. The P14 had long length of 6.28 cm followed by P7 (5.97) and P8 (5.97). The siliqua were shorter in P1 (4.86 cm) followed by P13 (4.90 cm) and P5 (4.93 cm) (Table 3). The mean sum of square was not significant (0.49) which indicated less considerable amount of variation for this trait in the populations (Table 4). Length of siliqua was found maximum in P14 (4.86 cm) showed maximum seeds per siliqua. So, selection will be effective for this trait of this population.

The genotypic and phenotypic variance for siliqua length were seen as value of 0.14 and 0.06, respectively. Siliqua length exhibited low GCV (7.03%) and PCV (8.34 %) values. As PCV is higher than GCV thus we can conclude that the trait is controlled by its genotype as well as influence of environment. A high heritability estimates of 71.00%, low genetic advance 0.66 and a moderate genetic advance as per cent of mean of 12.20% were observed. High heritability with combination of moderate genetic advance as per cent of mean allow us to speculate the presence of non-additive gene effects on this trait. Sikarwar *et al.* (2017) found high heritability with moderate genetic advance in case of length of siliqua. The experimental findings of Naznin *et al.* (2015) also found it.

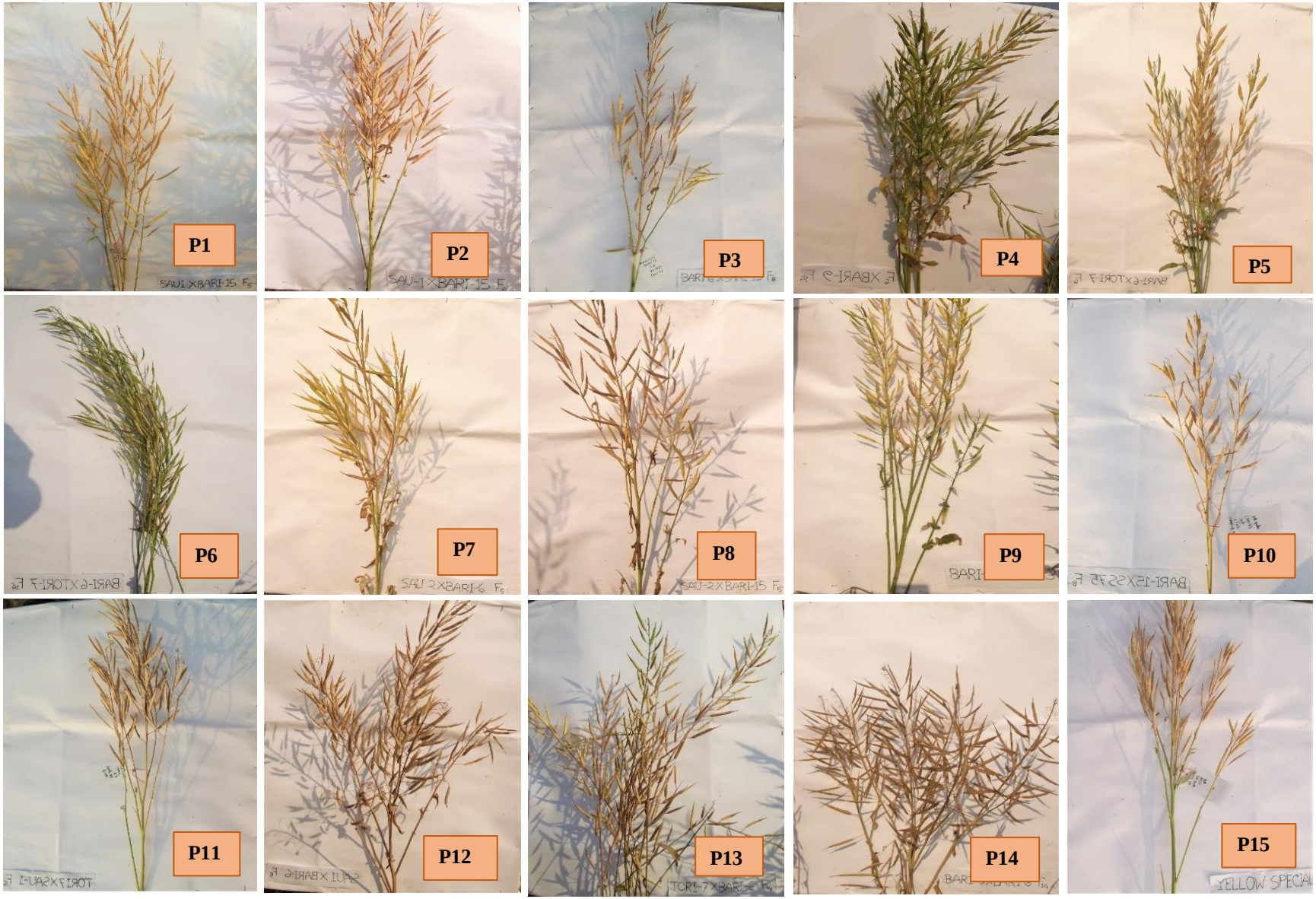


Plate 8: Difference in branching of 15 populations *Brassica rapa* L.

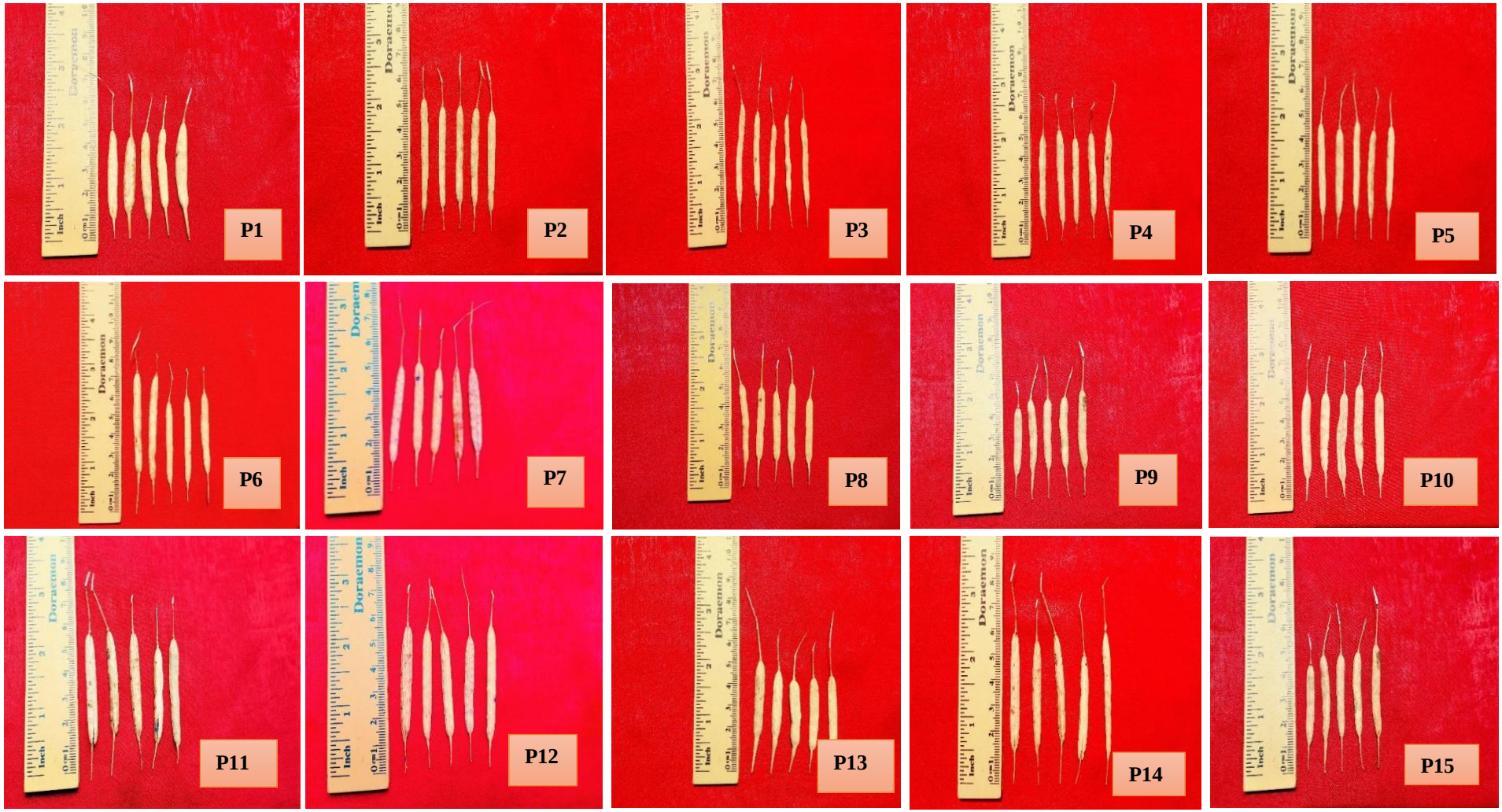


Plate 9: Length variation in siliqua of different populations of *Brassica rapa* L.

4.1.8 Number of seeds per siliqua

Number of seeds per siliqua ranged from 10.67 to 20.50 in different populations. The maximum number of seeds per siliqua was recorded in population P14 (20.50) followed by population P1 (19.10). However, minimum number of seeds per siliqua exhibited in population P10 (10.67) (Table 3). The mean observed for this trait was 16.08. Ali *et al.* (2002) observed that the hybrid of *Brassica rapa* L. produced an excellent number of seeds per siliqua (25.06) which was much higher than the parents. Number of seeds per siliqua was found maximum in P14 (20.50) indicated higher yield than the others. So, selection for this trait of this population will be effective.

The genotypic variance was (7.34) and phenotypic variance was (1.14). Moderate GCV and PCV were observed as 16.85 and 18.11 respectively (Table 4). This indicates very little influence of environment upon the character. Whereas, it showed high heritability (86.54%), low genetic advance (5.19) and high genetic gain as per cent of mean (32.28%) for this trait. High heritability with low genetic advance indicates that high heritability occurs due to environmental effects. Thus, selection is ineffective for the improvement of the crop. Larik and Rajput (2000) estimated the low genetic advance for seeds per siliqua irrespective of their high heritability. Akbar *et al.* (2007), Kumar *et al.* (2007) and Acharya and Pati (2008) also conceded with it.

4.1.9 Thousand seed weight (g)

Thousand seed weight of different populations ranged from 1.50 g to 3.57 g. The population P4 was exhibited maximum thousand seed weight (3.57 g) followed by population P12 (3.55 g), P7 (3.43 g), P9 (3.17 g) and P8 (3.10 g). Whereas, the population P11 was recorded minimum seed weight of (1.50 g) followed by population P10 (1.59 g) and P5 (1.71 g). The grand mean found for this trait was (2.47 g) (Table 3). The mean sum of square was not significant (1.46) in *Brassica rapa* L. which allows to show the presence of less considerable variation for this trait. Ali *et al.* (2002) found variation in thousand seed weight in *Brassica rapa* L. with some extent i.e. from 5.33 to 5.83 g in parent and from 3.60 to 6.33 g in

hybrid. The maximum thousand seed weight was found in P4 (3.57) indicating that the seeds of this population is bigger than others and seeds are filled more than the others indicated ultimate higher oil than the others. So, selection for this trait of P4 population will be effective.

Thousand seed weight recorded high PCV (25.70%) and GCV (25.15%) (Table 4). As PCV is greater than GCV, there is considerable influence of environment on this trait (Table 4). High heritability (95.77%), low genetic advance (1.39) and high genetic gain as percent of mean (50.70%) was found for this trait. High heritability with low genetic advance suggests that the character is governed by the non-additive gene action. Thus, selection may be ineffective in this trait for the improvement of the crop. High heritability with low genetic advance in thousand seed weight was observed by Parveen *et al.* (2015) which indicated the possibility of non-additive gene action.

4.1.10 Yield per Plant (g)

Yield ranged from P14 (14.00 g) to P10 (5.22 g), with a mean value of 8.87 g. The maximum yield was recorded by the population P14 (14.00 g) followed by P12 (13.48 g). The lowest yield was recorded by the population P10 (5.22 g) followed by P15 (5.73 g) (Table 3). The mean sum of square was significant (23.07). P14 showed maximum yield (14.00) than the other population which indicates that selection for this trait will be rewarding for improvement.

Yield per plant exhibited high estimates of PCV (31.34%) and GCV (31.27%) in Table 4. Jahan *et al*. found high genotypic co-efficient of variation (GCV) for yield per plant by considering genetic parameters. Whereas, it also recorded high heritability (99.59%), low genetic advance (5.70) and high genetic gain as per cent of mean (64.29%) for this trait. Hussain *et al.* (1998) observed the high estimates for heritability and genetic advance for yield per plant. Selection would be ineffective for this trait as there is non-additive gene effects on the gene controlling this trait

4.2 CORRELATION ANALYSIS

Improvement of a target character in all the breeding programs can be achieved by indirect selection via other characters. This needs a good understanding of the association of different characters with the target character and among the different characters themselves. It is necessary to have the estimation of correlation of yield with other characters for which the population could be assessed visually. The phenotypic and genotypic correlation reveals the extent of association between different characters, thus, it helps to base selection procedure to a required balance, when two opposite desirable characters affecting the principal characters are being selected. A positive correlation happens due to coupling phase of linkage and negative correlation arises due to repulsion phase of linkage of genes controlling different traits. No correlation indicates that genes concerned are located far apart on the same chromosome or they are located on different chromosomes. Yield being a complex character, is governed by a large number of genes. The influence of each character on yield could be known through correlation studies with a view to determine the extent and nature of relationships prevailing among yield and yield attributing characters.

So, the genotypic and phenotypic correlation co-efficient values for 10 characters in 15 *Brassica rapa* L. populations studied are presented in Table 5 and 6, respectively and in Figure 3.

4.2.1 Days to 50% flowering

Days to 50% flowering showed highly significant and positive correlation with days to maturity (r_g = 0.9051, r_p= 0.8698). Narayan *et al.* (2006) reported that yield per plant had highly significant and positive correlation with days to 50% flowering. It exhibited non-significant and positive correlation with plant height (r_g = 0.4681, r_p = 0.4477). It also presented non-significant and negative correlation with number of primary branches per plant (r_g = -0.0854, r_p = -0.0773), number of secondary branches per plant (r_g = -0.1239, r_p = -0.1127),

number of siliquae per plant (r_g= -0.1178, r_p = -0.1075), siliqua length (r_g = -0.4476, r_p = -0.3994), number of siliquae per plant (r_g= -0.2335, r_p = -0.2295), thousand seed weight (r_g = -0.1229, r_p = -0.1173) and yield per plant (r_g= -0.1337, r_p = -0.1247) (Table 5 and 6).

4.2.2 Days to 80% maturity

Days to 80% maturity showed non-significant and positive correlation with plant height (r_g = 0.3575, r_p = 0.3316), number of secondary branches per plant (r_g = 0.0501, r_p = 0.0553) at genotypic and phenotypic level. It had non-significant and negative correlation with number of primary branches per plant (r_g = -0.2472, r_p = -0.243), number of siliquae per plant (r_g = -0.3046, r_p = -0.2961), length of siliqua (r_g = -0.3516, r_p = -0.3237), number of seeds per siliqua (r_g = -0.3753, r_p = -0.3598), thousand seed weight (r_g = -0.3753, r_p = -0.3598) and yield per plant (r_g = -0.2744, r_p = -0.2688. (Table 5 and 6). Insignificant association of these traits indicated that the association between these traits was largely influenced by environmental factors. Lodhi *et al.* (2014) also revealed that days to maturity had non-significant and positive interaction with yield per plant. Naznin *et al.* (2015) also agreed with it.

4.2.3 Plant height (cm)

Plant height showed non-significant and positive correlation with thousand seed weight (r_g = 0.158, r_p = 0.1435. It was non-significant and negatively associated with number of primary branches per plant (r_g= -0.184, r_p = -0.1666), number of secondary branches per plant (r_g= -0.2783, r_p = -0.2766), number of siliquae per plant (r_g= -0.1348, r_p= -0.1235), siliqua length (r_g = -0.5316, r_p = -0.4887), number of seed per siliqua (r_g= -0.3753, r_p = -0.0728) and yield per plant (r_g= -0.1289, r_p= -0.1228) (Table 5 and 6).

Table 5: Genotypic correlation coefficient for ten characters of *Brassica rapa* L.

	DM	PH	NPB/P	NSB/P	NS/P	LS	NS/S	TSW	Y/P
DF	0.9051**	0.4681	-0.0854	-0.1239	-0.1178	-0.4476	-0.2335	-0.1229	-0.1337
DM		0.3575	-0.2472	0.0501	-0.3046	-0.3516	-0.3753	-0.0213	-0.2744
PH			-0.184	-0.2783	-0.1348	-0.5316*	-0.0709	0.158	-0.1289
NPB/P				0.6125*	0.9877**	0.3052	0.7816**	0.263	0.9653**
NSB/P					0.5756*	0.2781	0.3207	0.2792	0.5133*
NS/P						0.2686	0.7697**	0.2222	0.9819**
LS							0.2644	0.0692	0.3306
NS/S								0.1275	0.7956**
TSW									0.2865

*= significant at 5% level of probability, **= significant at 1% level of probability

DF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), NPB/P = Number of primary branch per plant, NSB/P = Number of secondary branch per plant, NS/P = Number of siliquae per plant, LS = Length of siliqua (cm), NS/S = Number of seeds per siliqua, TSW = Thousand seed weight (g), Y/P = Yield per plant (g)

Table 6: Phenotypic correlation coefficient for ten characters of *Brassica rapa* L.

	DM	PH	NPB/P	NSB/P	NS/P	LS	NS/S	TSW	Y/P
DF	0.8698**	0.4477	-0.0773	-0.1127	-0.1075	-0.3994	-0.2295	-0.1173	-0.1247
DM		0.3316	-0.243	0.0553	-0.2961	-0.3237	-0.3598	-0.0136	-0.2688
PH			-0.1666	-0.2766	-0.1235	-0.4887	-0.0728	0.1435	-0.1228
NPB/P				0.5983*	0.9761**	0.2667	0.7624**	0.2619	0.9599**
NSB/P					0.5636	0.2603	0.2987	0.2671	0.5044*
NS/P						0.2536	0.7422**	0.2178	0.9763**
LS							0.2387	0.0619	0.3106
NS/S								0.1242	0.7748**
TSW									0.2832

*= significant at 5% level of probability, **= significant at 1% level of probability

DF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), NPB/P = Number of primary branch per plant, NSB/P = Number of secondary branch per plant, NS/P = Number of siliquae per plant, LS = Length of siliqua (cm), NS/S = Number of seeds per siliqua, TSW = Thousand seed weight (g), Y/P = Yield per plant (g)

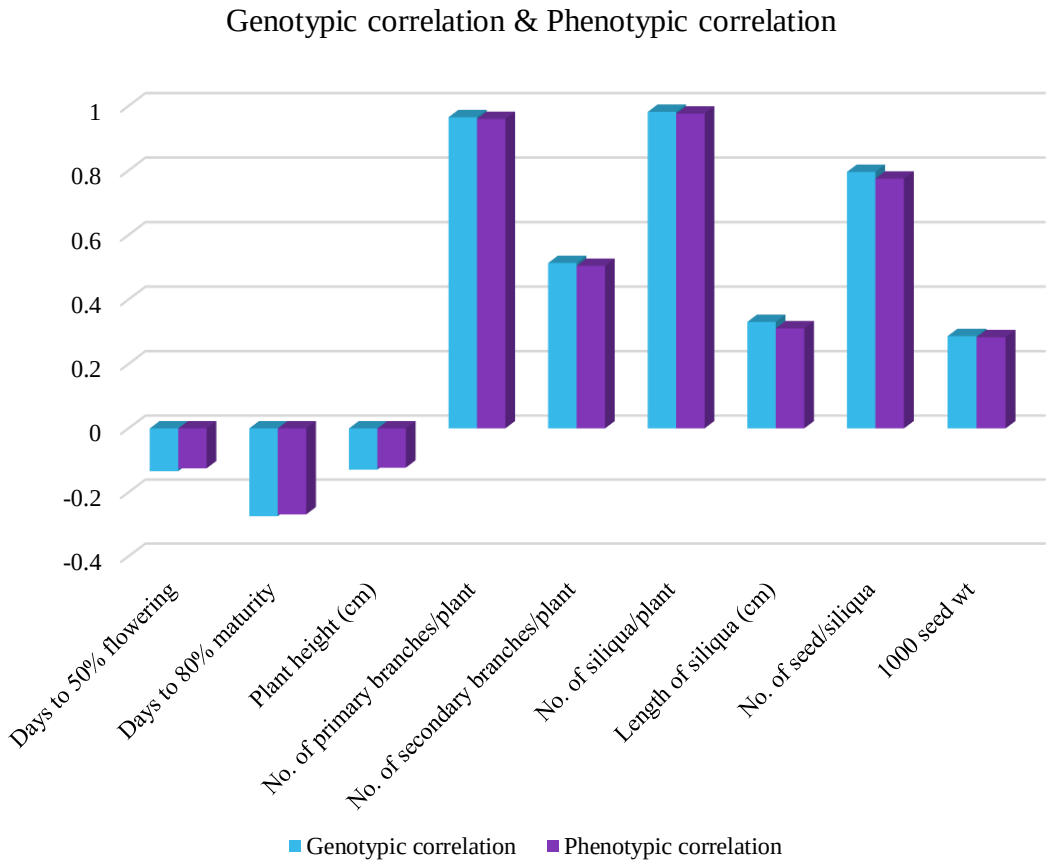


Figure 3: Genotypic and phenotypic correlation of *Brassica rapa* L.

4.2.4 Number of primary branches per plant

Number of primary branches per plant was found to be positively and significantly correlated with number of secondary branches per plant (r_g = 0.6125, r_p = 0.5983), number of siliquae per plant (r_g = 0.9877, r_p = 0.9761), number of seeds per siliqua (r_g = 0.7816, r_p = 0.7624) and yield per plant (r_g = 0.9653, r_p = 0.9599). Naznin *et al.* (2015) reported that yield/plant had significant positive correlation with number of primary branches/plant. Number of primary branches per plant had non-significant and positive interaction with length of siliqua (r_g = 0.3052, r_p= 0.2667) and thousand seed weight (r_g= 0.263, r_p= 0.2619) (Table 5 and 6). Rashid *et al.* (2007) found number of primary branches had positive and significant correlation with yield per plant.

4.2.5 Number of secondary branches per plant

The correlation of number of secondary branches per plant with number of siliquae per plant (r_g = 0.5756, r_p = 0.5636) and yield per plant (r_g= 0.5133, r_p = 0.5044) was significant and positive which indicated that the traits were less influenced by environment. These findings showing similar to the reports of Rashid *et al*. (2007). It also had positive and non-significant correlation with siliqua length (r_g = 0.2781, r_p = 0.2603), number of seeds per siliqua (r_g = 0.3207, r_p = 0.2987), thousand seed weight (r_g = 0.2792, r_p = 0.2671) (Table 5 and 6). Non-significant association of these traits indicated that the association between these traits is largely influenced by environmental factors.

4.2.6 Number of siliquae per plant

Siliqua per plant exhibited highly significant and positive correlation with number of seeds per siliqua (r_g = 0.7697, r_p = 0.7422) and yield per plant (r_g = 0.9819, r_p = 0.9763). Ara *et al.* (2010) reported that number of siliquae per plant had positive and significant effect on yield per plant. Islam *et al.* (2016) revealed that number of siliquae per plant had significant positive association with yield per plant. Naznin *et al.* (2015) also found it. The non-significant and positive interaction was found with siliqua length (r_g = 0.2686, r_p = 0.2536) and thousand

seed weight (r_g = 0.2222, r_p = 0.2178) (Table 5 and 6). Non-significant association of these traits indicated that the association between these traits is largely influenced by environmental factors.

4.2.7 Siliqua length (cm)

Siliqua length was found non-significant and positive association with number of seed per siliqua (r_g = 0.2644, r_p = 0.2387), thousand seed weight (r_g = 0.0692, r_p =0.0619) and yield per plant (r_g = 0.3306, r_p = 0.3106) indicating very little contribution of this trait towards the increase in number of seeds per siliqua and ultimately to yield per plant (Table 5 and 6).

4.2.8 Number of seeds per siliqua

Number of seeds per siliqua showed highly significant and positive interaction with yield per plant (r_g= 0.7956, r_p = 0.7748). Ara *et al.* (2010) observed that seed yield had positive and highly significant association with number of seeds per siliqua both at genotypic and phenotypic levels. It showed positively non-significant association with thousand seed weight (r_g = 0.1275, r_p = 0.1242) (Table 5 and 6). Lodhi *et al*. (2014) also revealed that number of seeds per siliqua had non-significant and positive correlation with yield per plant.

4.2.9 Thousand seed weight (g)

Thousand seed weight showed non-significant and positive interaction with yield per plant (r_g = 0.2865, r_p = 0.2832) (Table 5 and 6). Naznin *et al.* (2015) reported that thousand seed weight had non-significant and positive interaction with yield per plant. Positive associations between thousand seed weight and yield per plant indicate that yield per plant would increase if thousand seed weight increases. Interestingly, thousand seed weight exhibited significant positive correlation with siliqua length and seeds per siliqua observed by Kumari *et al*. (2017). However, Parveen *et al.* (2015) revealed that thousand seed weight had highly significant positive association with yield per plant both genotypic and phenotypic level.

4.3 PATH COEFFICIENT ANALYSIS

Simple correlation does not consider the complex relationships between the various traits related to the dependent variable. Correlation coefficients show relationships among independent variables and the linear relationship between these variables. But it is not sufficient to describe these relationships when the causal relationship among variables is needed. It has been suggested that yield components have either a direct or an indirect effect on yield per plant. Therefore, it was essential to determine the effects of yield components on yield per plant. Consequently, path coefficient analysis is the most common statistical method used for this purpose.

Thus, it is possible to calculate both direct and indirect effects of yield components on yield per plant through the other components. Genotypic and phenotypic paths were worked out in the present study (Table 7) considering yield per plant as dependent character and its attributes as independent characters *viz*. days to 50% flowering, days to 80% maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, length of siliqua, number of seeds per siliqua and thousand seed weight. Each component has two path actions *viz.* direct effect on yield and indirect effect through components which are not revealed by correlation studies.

4.3.1. Days to 50% flowering

Days to 50% flowering showed negligible negative direct effect (-0.3497) towards yield per plant. Islam *et al.* (2016) found that days to 50% flowering had the negative direct effect on yield per plant. It showed highly positive indirect effect towards yield per plant via days to 80% maturity (0.4152). Further, it showed negligible positive indirect effect towards yield per plant via number of primary branches per plant (0.0307), number of secondary branches per plant (0.0271) (Table 7). However, it was recorded negligible negative indirect effect yield per plant via plant height (-0.0260), number of siliquae per plant (-0.1619), siliqua length (-0.0178), number of seeds per siliqua (-0.0285), thousand seed

weight (-0.0227). It showed negative and non-significant genotypic correlation (-0.1337) with yield per plant.

4.3.2. Days to 80% maturity

Days to maturity found highly positive direct effect (0.4772) towards yield per plant. Rashid *et al*. (2013) demonstrated that days to maturity had positive direct effect towards yield per plant. Naznin *et al.* (2015) also found it. Further, it recorded negligible positive indirect effect towards yield per hectare via number of primary branches per plant (0.0920) (Table 7). However, it was recorded negligible negative indirect effect towards yield per plant via days to 50% flowering (-0.3043), plant height (-0.0191), number of secondary branches per plant (-0.0148), number of siliquae per plant (-0.4415), siliqua length (-0.0142), number of seeds per siliqua (-0.0446) and thousand seed weight (-0.0052). It showed negative and non-significant genotypic correlation (-0.2744) with yield per plant.

4.3.3 Plant height (cm)

Plant height recorded negligible negative direct effect (-0.0578) towards yield per plant. Uddin *et al.* (2013) found that plant height had the negative direct effect on yield per plant. In the present study the correlation was negative and non- significant (-0.1289) with yield per plant (Table 7). Further, it was recorded low positive indirect effect towards yield per plant via days to 80% maturity (0.1575). However, it was found negligible positive indirect effect towards yield per plant via number of primary branches per plant (0.0652), number of secondary branches per plant (0.0690), number of seeds per siliqua (0.0087) and thousand seed weight (0.0087). Naznin *et al.* (2015) observed positive indirect effect on seed yield/plant through length of siliqua. It showed negligible and negative indirect effect towards yield per plant via days to 50% flowering (-0.1574), number of siliquae per plant (-0.1766) and siliqua length (-0.0218).

4.3.4 Number of primary branches per plant

Number of primary branches per plant recorded negligible negative direct effect (-0.3835) towards yield per plant. Islam *et al.* (2013) was recorded that number of primary branches per plant had negative direct effect on yield per plant. Further, it was recorded negligible positive indirect effect towards yield per plant via days to 50% flowering (0.0285), plant height (0.0098), length of siliqua (0.0120), number of seeds per siliqua (0.0941), thousand seed weight (0.0249) and negligible negative indirect effect yield per plant via days to 80% maturity (-0.1145), number of secondary branches per plant (-0.1479) (Table 7). However, it was found highly significant and very high positive indirect effect towards yield per plant via number of siliquae per plant (0.870). The correlation of number of leaves was highly significant and positive (0.9653) with yield per plant.

4.3.5 Number of secondary branches per plant

Number of secondary branches per plant observed negligible negative direct effect (-0.2465) towards yield per plant. It was also recorded negligible positive indirect effects to yield per plant via days to 50% flowering (0.0385), days to 80% maturity (0.0286), plant height (0.0162), length of siliqua (0.0116), number of seeds per siliqua (0.0372) and thousand seed weight (0.0337) (Table 7). On the other hand, it was found negligible negative indirect effect towards yield per plant through number of primary branches per plant (-0.2301) and highly positive significant indirect effect via number of siliquae per plant (0.8242). Naznin *et al.* (2015) observed number of secondary branches/plant had high positive indirect effect on yield. The genotypic correlation of number of secondary branches per plant (0.5133) with yield per plant was positive and significant.

Table 7: Path coefficient analysis showing direct and indirect effects of different characters on yield of *Brassica rapa* L.

Characters	Direct effect	Indirect effect									Genotypic correlation with yield
		DF	DM	PH	NPB/P	NSB/P	NS/P	LS	NS/S	TSW	
DF	-0.3497		0.4152	-0.0260	0.0307	0.0271	-0.1619	-0.0178	-0.0285	-0.0227	-0.6067
DM	0.4772	-0.3043		-0.0191	0.0920	-0.0148	-0.4415	-0.0142	-0.0446	-0.0052	-0.2744
PH	-0.0578	-0.1574	0.1575		0.0652	0.0690	-0.1766	-0.0218	-0.0087	0.0017	-0.1289
NPB/P	-0.3835	0.0280	-0.1145	0.0098		-0.1479	0.870**	0.0120	0.0941	0.0249	0.9653**
NSB/P	-0.2465	0.0385	0.0286	0.0162	-0.2301		0.8242**	0.0116	0.0372	0.0337	0.5133*
NS/P	0.870**	0.0385	-0.1432	0.0069	-0.3758	-0.1380		0.0116	0.0916	0.0185	0.9819**
LS	0.0444	0.1399	-0.1527	0.0283	-0.1035	-0.0641	0.3827		0.0297	0.0259	0.3306
NS/S	0.1238	0.0804	-0.1718	0.0040	-0.2915	-0.0739	1.0892**	0.0107		0.0246	0.7956**
TSW	0.0819	0.0420	-0.0048	-0.0081	-0.0997	-0.0665	0.3238	0.0031	0.0149		0.2865

Residual Effect= 0.025

*= significant at 5% level of probability, **= significant at 1% level of probability

DF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), NPB/P = Number of primary branch per plant, NSB/P = Number of secondary branch per plant, NS/P = Number of siliquae per plant, LS = Length of siliqua (cm), NS/S = Number of seeds per siliqua, TSW = Thousand seed weight (g), Y/P = Yield per plant (g)

4.3.6 Number of siliquae per plant

Number of siliquae per plant exhibited highly significant and very high positive direct effect (0.870) towards yield per plant. Uddin *et al*. (2013) observed that number of siliquae per plant had the positive direct effect on seed yield per plant. However, it showed negligible positive indirect effect towards yield per plant via days to 50% flowering (0.0385), plant height (0.0069), length of siliqua (0.0116), number of seeds per siliqua (0.0916), thousand seed weight (0.0185) and negligible negative indirect effect of days to 80% maturity (-0.1432), number of primary branches per plant (-0.3758) and number of secondary branches per plant (-0.1380) (Table 7). Islam *et al.* (2015) found negative indirect effect on number of siliquae per plant. The genotypic correlation of number of siliquae per plant (0.9819) with yield per plant was low positive and highly significant.

4.3.7. Siliqua length (cm)

Siliqua length showed negligible positive direct effect (0.0444) towards yield per plant. Ara *et al.* (2010) revealed that siliqua length had direct effect and high positive correlation with yield per plant. Islam *et al.* (2016) also got this findings. It was found negligible positive indirect effect towards yield per plant via days to 50% flowering (0.1399), plant height (0.0283), number of seeds per siliqua (0.0297), thousand seed weight (0.0259) and high positive indirect effect of number of siliquae per plant (0.3827). Islam *et al.* (2016) also found positive indirect effect of plant height towards yield. On the other hand, it was also recorded negligible negative indirect effects to yield per plant via days to maturity (-0.1527), number of primary branches per plant (-0.1035), number of secondary branches per plant (-0.0641) (Table 7). The genotypic correlation of leaf area (0.3306) with yield per plant was highly positive and non-significant. Islam *et al.* observed negative indirect effects to yield per plant.

4.3.8 Number of seeds per siliqua

Number of seeds per siliqua showed low positive direct effect (0.1238) towards yield per plant. Islam *et al.* (2016) observed that this trait showed positive indirect effect on length of siliqua. Further, it was recorded negligible positive indirect effect towards yield per plant via days to maturity (0.0804), plant height (0.0040), length of siliqua (0.0107), thousand seed weight (0.0246) and very high positive significant indirect effect of number of siliquae per plant (1.0892) (Table 7). It also found low negative indirect effect towards yield per plant via days to maturity (-0.1718) and negative moderate effect to number of primary branches per plant (-0.2915). It also recorded negligible negative effect towards yield per plant via number of secondary branches per plant (-0.0739). It had highly significant and positive genotypic correlation (0.7956) with yield per plant.

4.3.9 Thousand seed weight (g)

Thousand seed weight showed negligible non-significant and positive direct effect (0.0819) towards yield per plant. Parveen *et al.* (2015) revealed that thousand seed weight had the maximum direct effect towards yield per plant. Further, it was recorded negligible positive indirect effect towards yield per plant via days to 50% flowering (0.0420), length of siliqua (0.0031), number of seeds per siliqua (0.0149) (Table 7). It also reported negligible negative indirect effect towards yield per plant via days to maturity (-0.0048), plant height (-0.0081), number of primary branches per plant (-0.0997) and number of secondary branches per plant (-0.0665). Naznin *et al.* (2015) found negative indirect effect for thousand seed weight towards yield per plant. The trait was genotypically moderate positive and non- significant (0.2865) correlated with yield per plant.

4.3.10 Residual effect

The magnitude of residual effect (0.025) indicated that traits included in the path analysis explained about 97.5% of the variation in yield. However, the remaining variation in yield (2.5%) can be attained by incorporating other yield related traits in the path analysis as far as studies involving association of traits is

concerned. Naznin *et al.* (2015) found residual effect 0.45 in case of yield per plant. Islam *et al.* (2016) found 0.430 in case of yield per plant.

4.4 NUTRIENT COMPONENT ANALYSIS

Nutrient component analysis is one of the important features of this study. In oil seed crops, the quality seed production is the major objective beside a high yielding variety. The quality of oil seed *Brassica sp.* depends on high percentage of oil, protein, oleic acid, linoleic, linolenic and low percentage of palmitic, stearic, eicosenoic acid and erucic acid. Oils high in oleic and linolenic acids are valued for edible purposes, and those with proportionately higher quantity of stearic, linoleic, eicosenoic, and erucic acids are valued for industrial purposes. Erucic acid is believed to be responsible for health hazards of human being. For edible oil, high concentration of protein, oleic acid and low concentration of erucic acid and linolenic acid are required (Ahmad *et al.,* 2012). Carbohydrates, lipids and proteins, which are stored during the later stages of seed formation, are considered the major reserves in most seeds (Lima *et al*. 2008). The relationship between various pairs of fatty acids has so far been established by various workers (Genet *et al.,* 2004; Sial *et al.,* 2004). The decrease in erucic acid causes an increase in both oleic and linoleic acids and along with the decrease in erucic acid, eicosenoic acid decreases considerably (Rahman, 1976).

4.4.1 Saturated fatty acid (%)

In the present investigation, saturated fatty acid content in the population of *Brassica rapa* L. ranged from 5.76% to 2.37%. The highest was found in P3 (5.76%) and the lowest was found in P13 (2.37%) statistically similar with P14 (2.53%) (Table 8).

4.4.1.1 Palmitic acid (C16:0)

Population P6 was observed to have highest amount of palmitic acid (2.84%) followed by P15 (2.76%), P14 (2.53%), P10 (2.39%), P13 (2.37%), P4 (2.23%) and the lowest found in P3 (1.98%) (Table 8). Higher amount of consumption of

palmitic acid increases the risk of developing cardiovascular disease which indicates that it may increase LDL levels in the blood. So, population P3 (1.98%) is better than the others which can be selected for this trait. Figure 4 is presented showing relative content of palmitic acid percentage.

4.4.1.2 Stearic acid (C18:0)

The highest amount of stearic acid was found in P6 (1.50%) statistically similar with P3 (1.40%) and lowest was found in P10 (0.82%) also statistically similar with P4 (0.80%). Ko *et al.* (2017) noticed 20.4% stearic acid in his experiment. Stearic acid is mainly used in the production of detergents, soaps, and cosmetics such as shampoos and shaving cream products. It is also used to produce dietary supplements. So, population P6 (1.50%) can be selected for this trait. Figure 5 is presented showing relative content of stearic acid percentage.

4.4.2 Unsaturated fatty acid (%)

Unsaturated fatty acid ranged from 97.62% to 94.23%. Population P3 was found the lowest amount of unsaturated fatty acid (94.23%) statistically similar with P6 (94.56%), P4 (94.89%) and P13 was found the highest (97.62%) followed by P14 (97.47%).

4.4.2.1 Oleic acid (C18:1)

Population P6 (13.49%) had the lowest amount of oleic acid content statistically similar with P14 (14.0%), P4 (14.51%) and population P15 (17.27%) had the highest statistically similar with P10 (16.43%), P3 (16.08%) (Table 8). Khan *et al.* (2008) found that oleic acid contents in their experiment ranged from 38 to 49 %. Oleic acid has been associated with decreased low-density lipoprotein (LDL) cholesterol, and possibly increased high-density lipoprotein (HDL) cholesterol. For this reason, population P10 (16.43%) can be selected for this traits. The range of oleic acid contents (8.9-58.7%) determined by Ahmad *et al.* (2008). Figure 6 is presented showing relative content of oleic acid percentage.

4.4.2.2 Eicosenoic acid (C20:1)

Population P6 was showed to have highest amount of eicosenoic acid (8.04%) followed by P10 (7.50%), P14 (7.12%) and population P13 (4.07%) followed by P15 (4.53%) was found the lowest amount of eicosenoic acid (Table 8). Figure 7 is presented showing relative content of eicosenoic acid percentage.

4.4.2.3 Erucic acid (C22:1)

One of the major undesirable and problematic components of the oil seed *Brassica sp.* is its higher level of erucic acid content. One of the major objectives in the current study was to find out the improved population for low content of erucic acid. It has toxic effect on the heart at high enough doses. Minimum amount of erucic acid was found in P10 (50.21%) statistically similar with P15 (51.29%), P14 (51.65%) and maximum found in P13 (59.04%) among 7 genotypes. Khan *et al.* (2008) found that erucic acid ranged from 48-59% in their experiment. Ko *et al.* (2017) observed 45.3% erucic acid. Figure 8 is presented showing relative content of erucic acid percentage.

4.4.2.4 Linoleic acid (C18:2)

Population P14 (15.40%) showed the highest amount of linoleic acid and population P3 (11.72%) showed the lowest amount. Alud *et al.* (1992) found 2.1% linoleic acid in their experiment. Linoleic acid has become popular for its industrial purposes. So, P14 (15.40%) can be selected for this trait. Scarth *et al.* found 28% linoleic acid. Figure 9 is presented showing relative content of linoleic acid percentage.

Table 8. Fatty acid composition and % of different fatty acids in 7 populations of *Brassica rapa* L.

Population	Saturated fatty acid (%)			Unsaturated fatty acid (%)					
				Monounsaturated			Polyunsaturated		
	Palmitic acid (C16:0)	Stearic acid (C18:0)	Total	Oleic acid (C18:1)	Eicosenoic acid (C20:1)	Erucic acid (C22:1)	Linoleic acid (C18:2)	Linolenic acid (C18:3)	Total
P3	1.98	1.40	5.76	16.08	8.04	52.41	11.72	5.98	94.23
P4	2.23	0.80	5.10	14.51	6.99	52.0	14.97	6.43	94.89
P6	2.84	1.50	5.44	13.49	5.16	54.22	13.85	7.83	94.56
P10	2.39	0.82	4.40	16.43	7.50	50.21	11.97	9.48	95.60
P13	2.37	_	2.37	15.05	4.07	59.04	12.92	6.54	97.62
P14	2.53	_	2.53	14.0	7.12	51.65	15.40	9.30	97.47
P15	2.76	_	4.85	17.27	4.53	51.29	14.0	8.04	95.14

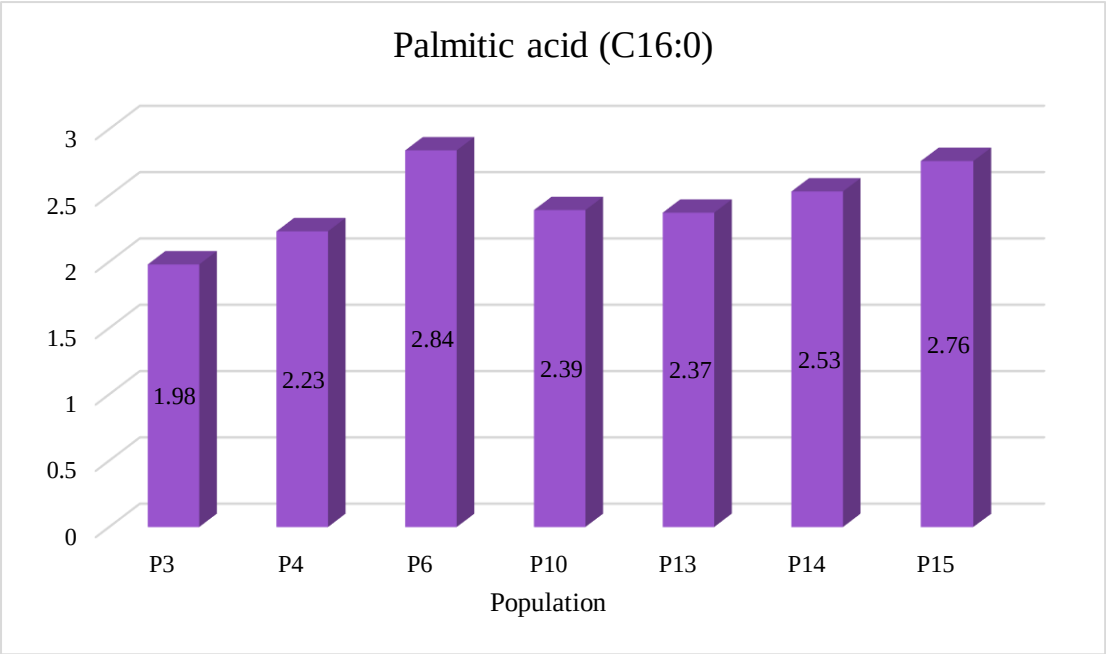


Figure 4. Palmitic acid content (%) of seven populations

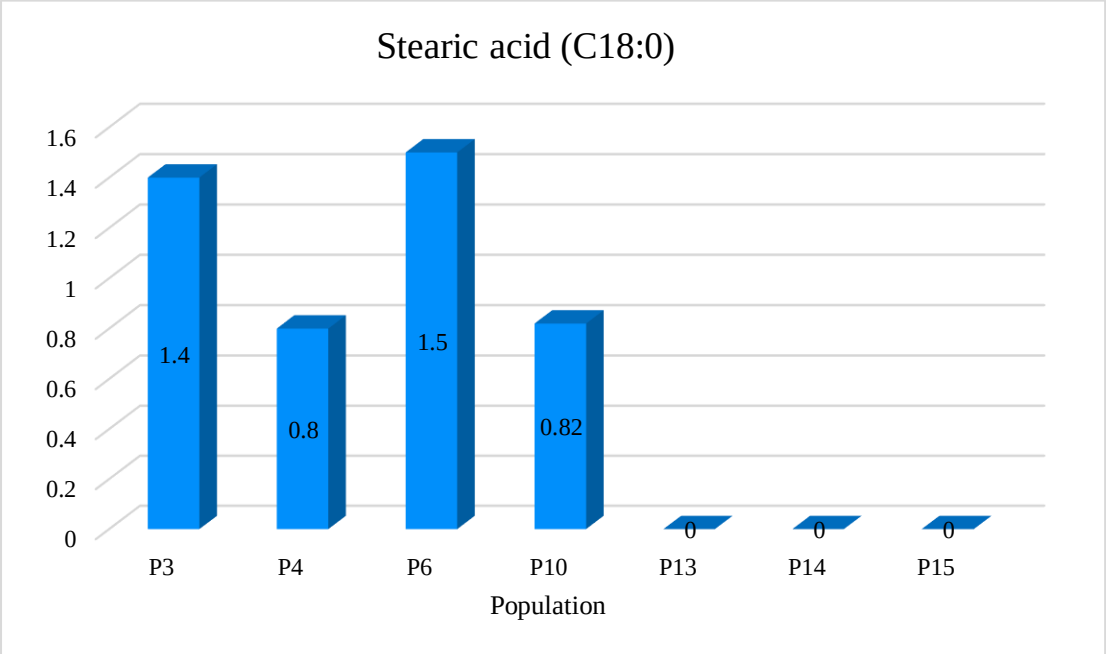


Figure 5. Stearic acid content (%) of seven populations

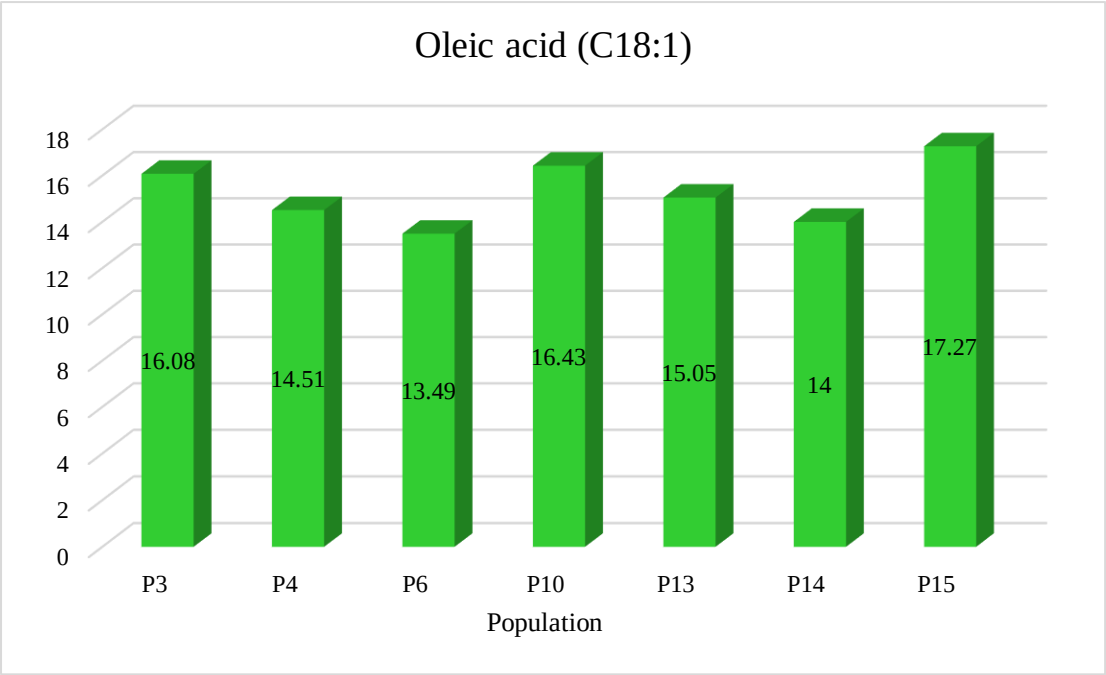


Figure 6. Oleic acid content (%) of seven populations

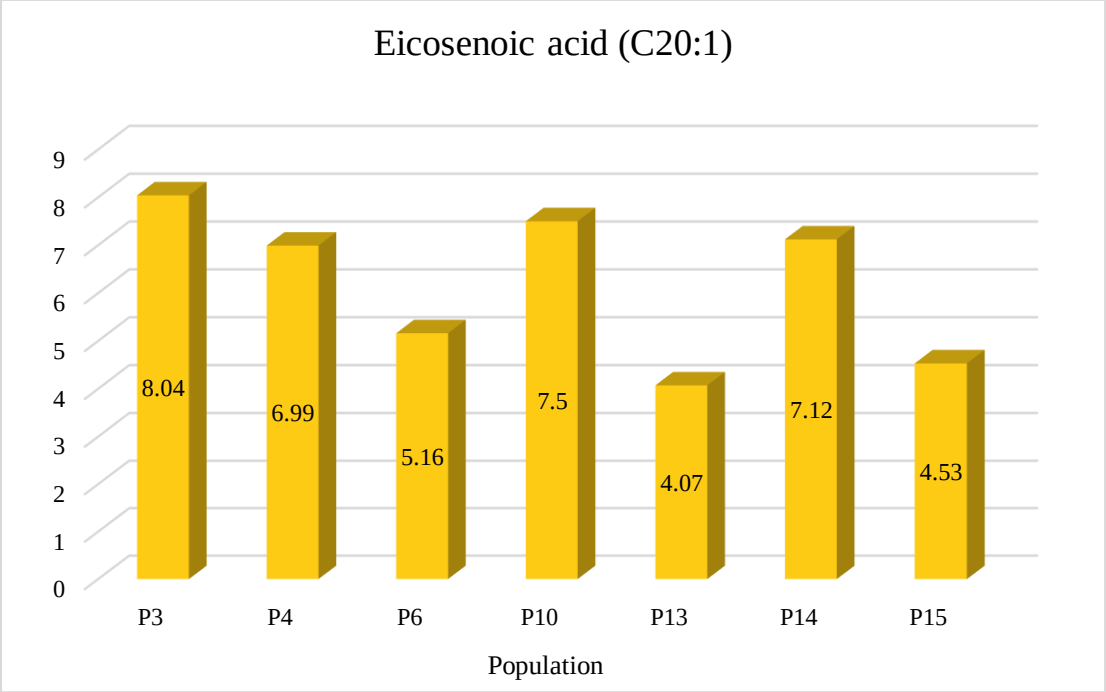


Figure 7. Eicosenoic acid content (%) of seven populations

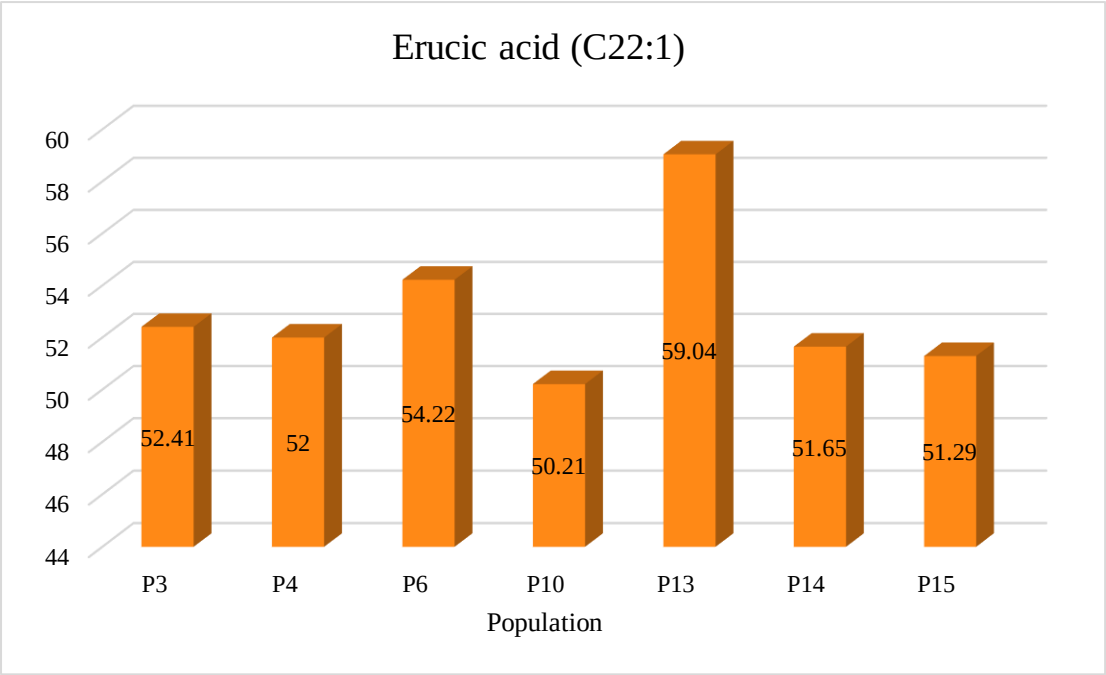


Figure 8. Erucic acid content (%) of seven populations

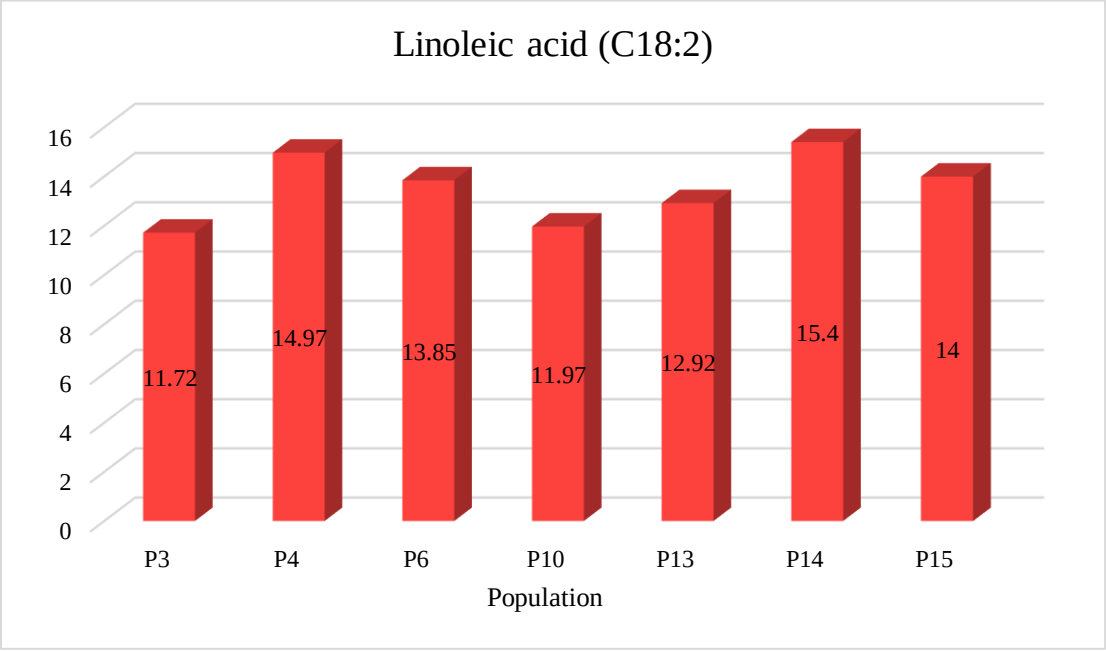


Figure 9. Linoleic acid content (%) of seven populations

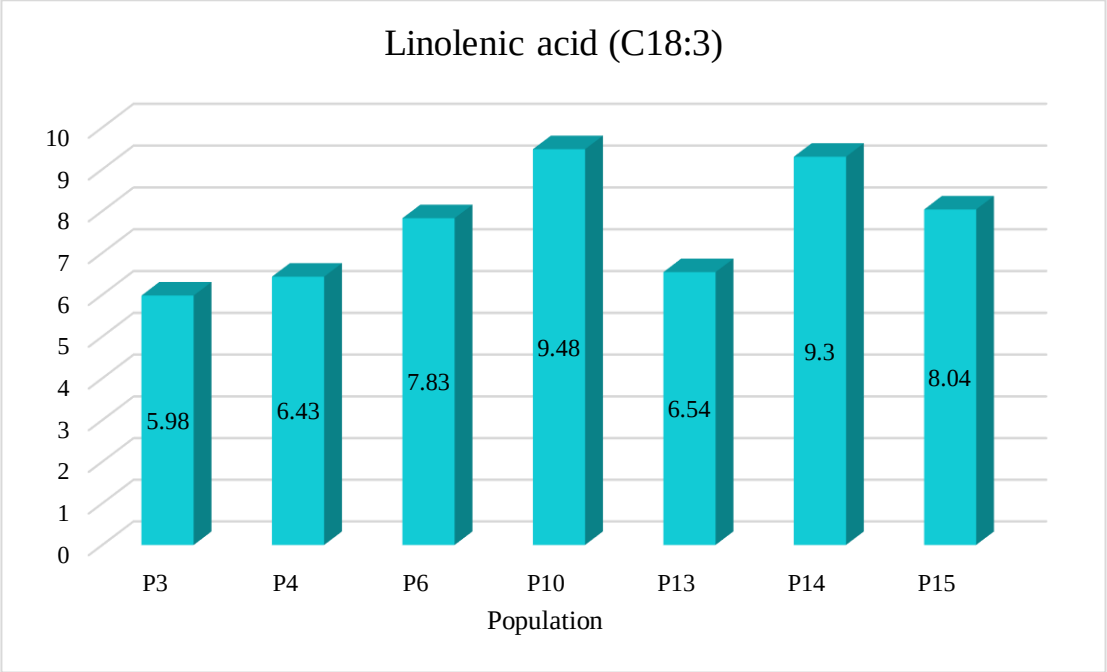


Figure 10. Linolenic acid content (%) of seven populations

4.4.2.5 Linolenic acid (C18:3)

Higher amount of linolenic acid was found in P10 (9.48%) statistically similar with P14 (9.30%) and lower was found in P3 (5.98%) statistically similar with P4 (6.43%), P13 (6.54%). It prevents cardiovascular disease. So, P10 (9.48%) can be selected for this trait. Khan *et al*. (2008) observed that linolenic acid ranged from 9-11% in their experiment. Figure 10 is presented showing relative content of linolenic acid percentage.

4.5 SELECTION

At present, the cultivation of *Brassica sp.* is decreasing in Bangladesh due to pressure of boro rice. The existing high yielding varieties such as BARI sarisha-6 is long durable which occupy land during boro season as a result transplantation of boro rice become delayed. Therefore, farmers prefer short durable and high yielding varieties which can fit with Aman- Mustard- Boro cropping system. The leading early variety of *Brassica rapa* L. in Bangladesh is Tori-7. It has low yield per plant like 6.82 g. Another variety of *Brassica rapa* L. is BARI sarisha-15 which matures by 84 days with 8.45 g yield per plant. Now-a-days, this variety is popular for its high yield and short duration.

The objectives of our study were to select short duration and high yielding population of *Brassica sp.* which fit in the Aman-Mustard-Boro cropping system. Variability was found for most of the characters of different cross combinations. Selection was carried out among the 15 populations as per objectives. The most promising advanced plant populations with high yielding and short duration were selected from the materials of the different cross combinations (Table 9).

4.5.1. SAU sarisha-1 × BARI sarisha-15 F_5 (P1)

Average number of siliqua of P1 was recorded 171 (Table 9) which was higher than BARI sarisha-15 (120.40). The average thousand seed weight was recorded as 2.75 g (Table 9) which was higher than Tori-7 (2.13 g) that meant seeds of this population were larger than tori-7 and had comparatively higher oil content.

Yield per plant was recorded 12.20 g (Table 9) which was close to Tori-7 (6.82 g)(plate 10).

4.5.2. SAU sarisha-1 × BARI sarisha-15 F_6 (P2)

Average number of siliquae per plant of P2 was recorded 157.00 (Table 9) which was higher than BARI sarisha-15 (120.40). This population was recorded with average thousand seed weight 2.67 g by the duration 80.67 days (Table 9) which was higher than Tori-7 (2.13 g) that meant seeds of selected plant were larger than tori-7 and had comparatively higher oil content and the selected population were short durable than Tori-7 (82 days) and BARI sarisha-15 (84 days)(plate 11).

4.5.3. SAU sarisha-2 × BARI sarisha-6 F_5 (P7)

Average number of siliquae per plant of P7 was recorded 132.50 (Table 9) which was higher than BARI Sarisha-15 (120.40). Average thousand seed weight was 3.43 g (Table 9) which was higher than Tori-7 (2.13 g) and BARI sarisha-15 (3.41 g) that meant seeds of P7 were larger than tori-7 and BARI sarisha-15 and had comparatively higher oil content. Average yield per plant was 9.77 g (Table 9) which was higher than BARI Sarisha-15 (8.45 g) and Tori-7 (6.82 g) indicating that this selected population were high yielding than BARI sarisha-15 and Tori-7 (Plate 12).

4.5.4. SAU sarisha-2 × BARI sarisha-15 F_5 (P8)

Average number of siliquae per plant of P8 was recorded 121.00 (Table 9) which was higher than BARI sarisha-15 (120.40). Average thousand seed weight was 3.10 g (Table 9) which was higher than Tori-7 (2.13 g) that meant seeds of P8 were larger than tori-7 and BARI sarisha-15 and had comparatively higher oil content. Average yield per plant was recorded 9.57 g (Table 9) which was higher than BARI sarisha-15 (8.45 g) and Tori-7 (6.82 g) which indicating that this population were high yielding than Tori-7 and BARI sarisha-15 (Plate 13).

4.5.5. SAU sarisha-1 × BARI sarisha-6 F_5 (P12)

Average number of siliquae per plant of P12 was recorded 179.00 (Table 9) which was higher than BARI sarisha-15 (120.40). The population had average thousand seed weight 3.55 g (Table 9) which was higher than Tori-7 (2.13 g) that meant seeds of P12 was larger than tori-7 and had comparatively higher oil content. Average yield per plant was recorded 13.48 g (Table 9) which was higher than BARI sarisha-15 (8.45 g) and Tori-7 (6.82 g) indicating that this population were high yielding than BARI sarisha-15 and Tori-7 (Plate 14).

4.5.6. BARI sarisha-9 × BARI sarisha-6 F_{14} (P14)

Average number of siliquae per plant of P14 was recorded 196.07 (Table 9) which was higher than BARI sarisha-15 (120.40). This population had average thousand seed weight 2.87 g (Table 9) which was higher than Tori-7 (2.13 g) that meant seeds of P14 was larger than tori-7 and had comparatively higher oil content. Average yield per plant was recorded 14.00 g (Table 9) which was higher than BARI sarisha-15 (8.45 g) and Tori-7 (6.82 g) indicating that this was high yielding than BARI sarisha-15 and Tori-7 (Plate 15).

Table 9. Selection of promising high yielding short duration population from different cross combinations of *Brassica rapa* L. based on mean performance

Population	DM	NS/P	TSW (g)	Y/P (g)
SAU sarisha-1 × BARI sarisha-15 F_5 (P1)	81	171.00	2.75	12.20
SAU sarisha-1 × BARI sarisha-15 F_6 (P2)	81	157.00	2.67	10.40
SAU sarisha-2 × BARI sarisha-6 F_5 (P7)	82	132.50	3.43	9.77
SAU sarisha-2 × BARI sarisha-15 F_5 (P8)	83	121.00	3.10	9.57
SAU sarisha-1 × BARI sarisha-6 F_5 (P12)	82	179.00	3.55	13.48
BARI sarisha-9 × BARI sarisha-6 F_{14} (P14)	79	196.07	2.87	14.00

Plate 10. Photograph showing plants of SAU sarisha-1 × BARI sarisha-15 (F_5)

Plate 11. Photograph showing plants of SAU sarisha-1 × BARI sarisha-15 (F_6)

Plate 12. Photograph showing plants of SAU sarisha-1 × BARI sarisha-6 (F_5)

Plate 13. Photograph showing plants of SAU sarisha-2 × BARI sarisha-15 (F_5)

Plate 14. Photograph showing plants of SAU sarisha-1 × BARI sarisha-6 (F_5)

Plate 15. Photograph showing plants of BARI sarisha-9 × BARI sarisha-6 (F_{14})

CHAPTER V
SUMMARY AND CONCLUSION

The genetic variability is the raw material in breeding industry on which selection acts to evolve superior populations. The genetic variability that exists in the available populations provides ample scope for selecting the best lines for future trial. Yield being a complex quantitative character, direct selection for yield might not result in successful advancement. Therefore, it was necessary to partition the noticed variability into heritable and non-heritable components by calculating genetic parameters such as genotypic and phenotypic coefficient of variation, heritability and genetic gain.

The present study was investigated to study the nature and magnitude of genetic variability, the pattern of character association among the characters, the direct and indirect effects of component characters on yield per plant and comparison of biochemical components among the populations of *Brassica rapa* L. The material for the present study comprised of 15 advanced lines collected from Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, were evaluated using RCBD design for 10 quantitative characters at Sher-e-Bangla Agricultural University, Dhaka during the period of November, 2016 to February, 2017.

The study exhibited wide range of variability for most of the characters studied. The lowest days to 50% flowering (30.67 days) was found in P14 followed by P4 (31.67 days). The lowest (78.67 days) were observed in P14 followed by P4 (79.00 days). Plant height exhibited lowest (84.14 cm) in P14. The highest number of primary branches per plant (7.03) was recorded in P14. The highest number of secondary branches per plant (3.37) was observed in P14. The highest number of siliquae per plant (196.07) was in P14. The lowest length of siliqua (4.86 cm) was recorded in P1 followed by P13 (4.90 cm), P15 (4.93 cm) and the highest length of siliqua (6.28 cm) was remarked in P14. The number of seeds per siliqua (20.50) was found highest in P14. The thousand seed weight exhibited

the highest (3.57 g) in P4 followed by P12 (3.55 g). The yield per plant was maximum (14.00 g) in P14. So, these populations for this traits can be used for future trial.

The phenotypic variance of the materials was considerably lower than the genotypic variance for all the characters studied. Number of primary branches per plant, number of secondary branches per plant, length of siliqua and thousand seed weight showed least difference between genotypic and phenotypic variance which indicated low environmental influence on these characters. Hence, selection will be beneficial for these traits. Days to 50% flowering, days to 80% maturity, plant height, number of sliliqua per plant, number of seeds per siliqua and yield per plant showed much difference between genotypic and phenotypic variance suggesting high environmental influence on the expression of these characters. Therefore, selection will not be beneficial for these traits.

The low magnitude of genotypic and phenotypic coefficient of variation (GCV and PCV) was observed for the characters e.g. days to 50% flowering (GCV- 6.59%, PCV- 7.35%), days to 80% maturity (GCV- 4.14%, PCV- 4.37%), plant height (GCV- 7.99%, PCV- 8.85%), number of primary branches per plant (GCV- 17.47%, PCV- 17.79%), length of siliqua (GCV- 7.03%, PCV- 8.34%), thousand seed weight (GCV- 25.15%, PCV- 25.70%), yield per plant (GCV- 31.27%, PCV- 31.34%) except number of secondary branches per plant (GCV- 65.74% and PCV- 69.77%), number of siliquae per plant (GCV- 8.27% and PCV- 10.02%) and number of seeds per siiqua (GCV- 16.85% and PCV- 18.11%) (Table 4). The differences between PCV and GCV for the characters were narrow indicating lesser influence of environment on these characters and could be improved by following phenotypic selection.

High values for heritability and genetic advance for various traits designates good genetic potential for selection and for use in future trial. High heritability estimates were observed for days to 50% flowering (80.25%), days to 80% maturity (90.02%), plant height (81.36%), number of primary branches per plant (96.47%), number of secondary branches per plant (88.78%), number of siliquae

per plant (68.21%), length of siliqua (71.00%), number of seeds per siliqua (86.54%), thousand seed weight (95.77%), yield per plant (99.59%) (Table 4). Plant height (15.50) and number of siliquae per plant (17.81) recorded moderate genetic gain and selection based on these characters may result in development of high yielding populations. High heritability coupled with moderate genetic advance was found in plant height and number of siliquae per plant.

In general, genotypic correlation coefficients were higher than their corresponding phenotypic correlation coefficients. Association of the character yield per plant was highly significant and positive with number of primary branches per plant (r_g= 0.9653, r_p= 0.9599), number of siliquae per plant (r_g= 0.9819, r_p= 0.9763), number of seeds per siliqua (r_g= 0.7956, r_p= 0.7748) at both genotypic and phenotypic level (Table 5 and 6). It shows that yield per plant in *Brassica rapa* L. can be improved by making direct selection based on these traits. Number of secondary branches per plant (r_g= 0.5133, r_p=0.5044) had significant positive association with yield per plant.

Path co-efficient analysis for yield per plant revealed that number of siliquae per plant exerted highest direct effect on the yield (0.4718) followed by days to 50% maturity (0.4772). The indirect contribution of component characters *viz.* number of primary branches per plant (0.4424), number of secondary branches per plant (0.8242), number of seeds per siliqua (1.0892) was high through seed yield per plant (Table 7).

Both genetic and environmental factors can have an influence on the contents of fatty acids in *Brassica rapa* L. and also on the crop yield. In the present investigation the lowest amount of palmitic acid was found in P3 (1.98%). The lowest amount of stearic acid was found in P10 (0.82%) statistically similar with P4 (0.80%). Population P15 (17.27%) had the highest amount of oleic acid content statistically similar with P10 (16.43%), P3 (16.08%). Population P13 (4.07%) followed by P15 (4.53%) was found the lowest amount of eicosenoic acid. Minimum amount of erucic acid was found in P10 (50.21%) statistically similar with P15 (51.29%), P14 (51.65%) among 7 populations. Population P14

(15.40%) was found the highest amount followed by P15 (14.0%), P4 (14.97%) of linoleic acid. Higher amount of linolenic acid was found in P10 (9.48%) statistically similar with P14 (9.30%) (Table 8). As low percentage of erucic, eicosenoic, palmitic, stearic acid and high percentage of oleic, linoleic, linolenic acid is beneficial for human health, these populations can be used for future trial.

The possibility to make predictions for the biochemical composition of *Brassica rapa* L. is very limited due to unforeseeable combinatory effects of variety, site (cultivation), and climate (year). It is yet not possible to make predictions with regard to the influence of those combined environmental factors. The effect of the variety is the most certain factor of influence, and is more or less affected by other parameters. But the choice of the variety can be essential with regard to the quality-determining constituents.

Selection was carried out among the populations of *Brassica rapa* L. for most promising populations with having high yield short duration. The performance of the segregating materials was also compared with two check varieties. Based on the variability and as per our objectives six most promising populations (SAU sarisha-1 × BARI sarisha-15 F_5, SAU sarisha-1 × BARI sarisha-15 F_6, SAU sarisha-2 × BARI sarisha-6 F_5, SAU sarisha-2 × BARI sarisha-15 F_5, SAU sarisha-1 × BARI sarisha-6 F_5, BARI sarisha-9 × BARI sarisha-6 F_{14}) with short duration and higher yield were selected from the 15 populations. Among the populations the highest yield per plant (14.00 g) was found in BARI sarisha-9 × BARI sarisha-6 F_{14}. The population BARI sarisha-9 × BARI sarisha-6 F_{14} matured early (78.67 days) and produced higher yield (14.00 g/ plant) which is comparatively better than the two check varieties. So, these population possessed excellent potential for use in future trial.

REFERENCES

Acharya, N.N. and Pati, P. (2008). Genetic variability, correlation and path analysis in Indian mustard (*Brassica juncea* L.). *Environ. Ecol.* **26**: 2165-2168.

Afrin, T., Bhuiyan, M.S.R. and Parveen, S. (2016). Variability and comparative analysis among advanced generations of *'Brassica rapa'* L. *Plant Knowl. J.* **5**(1): 18.

Ahmad, F., Alia, A.K. and Naeem, M. (2016). Appraisal of rapeseed genotypes for yield traits and oil quality under swat valley condition. *J. Nat. Sci. Res.* **6**(1).

Ahmad, H., Islam, M. and Khan, I.A. (2008). Evaluation of advance rapseed line HS-98 for yield attributes and biochemical characters. *Pakistan J. Bot.* **40**(3): 1099-1101.

Ahmad, M., Naeem, M., Khan, I.A. and Mashwani, M.A. (2012). Biochemical quality study of genetically diversified *Brassica* genotypes. *Sarhad J. Agric.* **28**(4).

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

Akbar, M., Mahmood, T., Yaqub, M., Anwar, M., Ali, M. and Iqbal, N. (2003). Variability, correlation and path coefficient studies in summer mustard. *Asian J. Plant Sci.* **2**(9): 696-698.

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

Ali, M.A., Bhuiyan, M.S.R., Rashid, H.U.M., Parveen, S., Robbani, M.G. and Sonom, M. (2016). Breeding for an ideal plant type in *Brassica rapa* L. *Plant Knowl. J.* **5**(1**)**: 36-43.

Ali, N.A.A.Z.A.R., Javidfar, F. and Attary, A.A. (2002). Genetic variability, correlation and path analysis of yield and its components in winter rapeseed (*Brassica napus* L.). *Pakistan J. Bot*. **34**(2): 145-150.

Al-Jibouri, H., Miller, P.A. and Robinson, H.F. (1958). Genotypic and environmental variances and co-variances in an upland cotton cross of interspecific origin. *Agron. J.* **50**(10): 633-636.

Ara, S. (2010). Variability, correlation and path coefficient in segregating population of *Brassica rapa* L. obtained through inter-varietal crosses. M.S. (Agril.) thesis, SAU, Dhaka, Bangladesh.

Ara, S., Afroz, S., Noman, M.S., Bhuiyan, M.S.R. and Zia, M.I.K. (2015). Variability, correlation and path analysis in F_2 progenies of inter-varietal crosses of *Brassica rapa* L. *J. Environ. Sci. Nat. Res.* **6**(1): 217-220.

Auld, D.L., Heikkinen, M.K., Erickson, D.A., Sernyk, J.L. and Romero, J.E. (1992). Rapeseed mutants with reduced levels of polyunsaturated fatty acids and increased levels of oleic acid. *Crop Sci.* **32**(3): 657-662.

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

Bhardwaj, H.L. and Hamama, A.A. (2000). Oil, erucic acid, and glucosinolate contents in winter hardy rapeseed germplasms. *Indust. Crops Prod.* **12**(1): 33-38.

Burton, G.W. (1952). Qualitative inheritance in grasses. Proc. Int. symp. on Grassland: Aug. 17-23, PSC, Pennsylvania, USA, pp.17-23.

Cochran, W.G. and Cox, G. (1957). Experimental design. W.S John,(2nded.). New York. p.615.

Dabholkar, A.R. (1992). Elements of biometrical genetics. CPC, New Delhi, India. p.493.

Dash, S.S. (2007). Genetic divergence studies for earliness and other yield attributes in toria (*Brassica rapa* L. Var. toria). Ph.D. thesis, RPCAU, Samastipur, India.

Dewan, D.B., Rakow, G. and Downey, R.K. (1998). Growth and yield of doubled haploid lines of oilseed *Brassica rapa. Canadian J. Plant Sci.* **78**(4): 537-544.

Dewey, D.R. and Lu, K. (1959). A correlation and path-coefficient analysis of components of crested Wheat grass seed production. *Agron. J.* **51**(9): 515-518.

Dorrell, D.G. and Downey, R.K. (1964). The inheritance of erucic acid content in rapeseed (*Brassica campestris*). *Canadian J. Plant Sci.* **44**(6): 499-504.

Falconer, D.S. and Mackay, T.F. (1996). Introduction to quantitative genetics. *Genetics.* **167**(4): 1529-1536.

Fayyaz, L. and Afzal, M. (2014). Genetic variability and heritability studies in indigenous *Brassica rapa* L. accessions. *Pakistan J. Bot*. **46**(2): 609-612.

Genet, T., Labuschagne, M.T. and Hugo, A. (2004). Capillary gas chromatography analysis of Ethiopian mustard to determine variability of fatty acid composition. *J. Sci. Food Agric.* **84**(13): 1663-1670.

Guoping, Z. and Chongling, Z. (1999). Genetic correlation and path analysis of several main agronomic characters in *Brassica rapa spp.* parachinensis. *China Veg.* **5**: 003.

Halder, T., Bhuiyan, M.S., Islam, M.S. and Hossain, J. (2016). Analysis of relationship between yield and some yield contributing characters in few advanced lines of rapeseed (*Brassica rapa* L.) by using correlation and path analysis. *Adv. Agric. Bot.* **8**(1).

Hanson, C.H., Robinson, H.F. and Comstock, R.E. (1956). Biometrical studies of yield in segregating populations of Korean lespedeza. *Agron. J.* **48**(6), 268-272.

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

Hortus, T. (1976). A Concise Dictionary of Plants Cultivated in the United States and Canada. L.H. Bailey,(1st ed.). MPC, Cornell University, New York, USA. pp. 903-04.

Hosen, M. (2008). Variability, correlation and path analysis in F_3 materials of *Brassica rapa* L. M.S. (Agril.) thesis, SAU, Dhaka, Bangladesh.

Hossain, M.D. (2013). Food for the poor: achievement and challenges. The Daily Star. March 24.

http://bbs.portal.gov.bd/sites/default/files/files/bbs.portal.gov.bd/page/1b1eb817_9325_4354_a756_3d18412203e2/Yearbook-2016-Final-19-06-2017.pdf

http://nmoop.gov.in/Publication/StatusPaper_RandM_2017.pdf

http://www.banglapedia.com

http://www.fao.org/3/a-I7695e.pdf

http://www.thebangladeshpost.com/national/5046/pdf

https://drive.google.com/file/d/1x07AMUkjglHIaeqyQlZAUvsnoXluR_AU/view?ts=5a684f26

https://drive.google.com/file/d/1x07AMUkjglHIaeqyQlZAUvsnoXluR_AU/view?ts=5a684f26

https://www.pfaf.org/user/Search_Use.aspx?glossary=Oil

Hussain, S., Hazarika, G.N. and Barua, P.K. (1998). Genetic variability, heritability and genetic advance in Indian rapeseed (*Brassica campestris*). *J. Assam Agril. Univ.* **11**(2): 260-261.

Iqbal, A.M., Shikari, A.B., Ashaq, H. and Dar, Z.A. (2015). Genetic variability in *Brassica rapa* L. Var. Brown sarson for maturity, yield and yield attributing traits. *Environ. Ecol.* **33**(1): 267-270.

Islam, M.S., Haque, M.M., Bhuiyan, M.S.R. and Hossain, M.S. (2015). Estimation of genotypic and phenotypic coefficient variation of yield and its contributing characters of *Brassica rapa* L. *Am Eruasian J. Agric. Environ. Sci*. **15**(10): 2029-2034.

Islam, M.S., Rahman, L. and Alam, M.S. (2009). Correlation and path coefficient analysis in fat and fatty acids of rapeseed and mustard. *Bangladesh J. Agric. Res*. **34**(2): 247-253.

Islam, S., Haque, M.M., Bhuiyan, S.R. and Hossain, S. (2016). Path coefficient analysis and correlation coefficients effects of different characters on yield of *Brassica rapa* L. *Plant.* **4**(6): 51-55.

Jahan, N., Bhuiyan, S.R., Talukder, M.Z.A., Alam, M.A. and Parvin, M. (2013). Genetic diversity analysis in *Brassica rapa* L. using morphological characters. *Bangladesh J. Agric. Res*. **38**(1): 11-18.

Jahan, N., Khan, M.H., Ghosh, S., Bhuiyan, S.R. and Hossain, S. (2014). Variability and heritability analysis in F_4 genotypes of *Brassica rapa* L. *Bangladesh J. Agril. Res.* **39(2)**: 227-241.

Jamali, K.H., Mari, S.N., Soomro, Z.A., Soomro, S. and Khanzada, A. (2016). Correlation study on yield and yield contributing traits in *Brassica compestris* L. *Life Sci. Intl. J.* **10**(1): 1-7.

Jan, S.A., Shinwari, Z.K., Rabbani, M.A., Niaz, I.A. and Shah, S.H. (2017). Assessment of quantitative agro-morphological variations among *Brassica rapa* L. diverse populations. *Pakistan J. Bot.* **49**(2): 561-567.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Genotypic and phenotypic correlations in Soybeans and their implications in selection. *Agron. J.* **47**(10): 477-483.

Jombart, T., Devillard, S. and Balloux, F. (2010). Discriminant analysis of principal components: a new method for the analysis of genetically structured populations. *BMC genetics.* **11**(1): 94.

Kashyap, S.C. and Mishra, M.N. (2004). Correlation and path co-efficient analysis studies in toria (*Brassica campestris* Var. toria). *An. Agri. Bio. Res*. **9**(2): 123-126.

Katiyar, A.P. and Singh, B. (1974). Interrelationship among yield and its components in Indian mustard. *Indian J. Agric. Sci*. **44**: 287-290.

Khan, M.H., Bhuiyan, M.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. Agric*. *Res.* **38** (4): 647-657.

Khan, M.M.A., Robin, A.B.M.A.H.K., Dowla, N.U., Talukder, S.K. and Hassan, L. (2009). Agrobacteium-mediated genetic transformation of two varieties of *Brassica*: optimization of protocol. *Bangladesh J. Agril. Res.* **34**(2): 287-301.

Khan, S., Farhatullah, R., Khalil, I.H., Khan, M.Y. and Ali, N. (2008). Genetic variability, heritability and correlation for some quality traits in F_3: 4 *Brassica* populations. *Sarhad J. Agric*. **24**(2): 223-231.

Ko, H.C., Sung, J.S., Hur, O.S., Baek, H.J., Lee, M.C., Luitel, B.P. and Rhee, J.H. (2017). Variation in agronomic traits and fatty acid compositions of

the seed oil in germplasm collection of *Brassica spp.* *한국자원식물학회지*. **30**(6): 590-600.

Kumari, S., Kumar, K. and Kumari, K. (2017). Study on correlation among different character pairs and path coefficient analysis in yellow sarson (*Brassica rapa*. Var. Yellow Sarson). *Prog. Agric.* **17**(1): 15-20.

Larik, A.S. and Rajput, L.S. (2000). Estimation of selection indices in *Brassica juncea* L. and *Brassica napus* L. *Pakistan J. Bot.* **32**(2): 323-330.

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

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

Luhs, W.W., Voss, A., Seyis, F. and Friedt, W. (1999). Molecular genetics of erucic acid content in the genus *Brassica*. Proc. Int. symp. on rapeseed research: Sep. 20-25, JLU, Ludwigstr, Giessen, Germany, pp.26-29.

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

Mahalanobis, P.C. (1928). Statistical study at Chinese head measurement in India. **8**: 32-64.

Mahmud, M.A.A. (2008). Inter-genotypic variability study in advanced lines of *Brassica rapa*. M.S. (Agril.) thesis, SAU, Dhaka.

Mandal, N. and Khajuria. M (2000). Genetic variability and path coefficient analysis in mustard. *Annual of Agric. Res*. 19(1): 107-109.

Mather, K. (1949). Biometrical Genetics: The study of continuous variation. J.K. Jinks,(1st ed.). Methuen and Co., Ltd., London. p.162.

Miah, M.A.M. and Mondal, M.R.I. (2017). Oilseeds sector of Bangladesh: Challenges and Opportunities. *SAARC J. Agric*. **15(1)**: 161-172.

Miah, M.A.M., Shiblee, S.A.M. and Rashid, M.A. (2015). Socioeconomic impacts of oilseeds research and development in Bangladesh. *Bangladesh Inst. Dev. Stud.* **38(1)**: 1-31.

Mondal, M.R.I. and Wahhab, M.A. (2001). Yield and yield attributes of rapeseed as influenced by date of planting. *Int. J. Sustain. Crop Prod.* **3**(3): 25-29.

Mukesh, K., Sinha, T.S. and Vipin, K. (2007). Genetic variability, heritability, genetic advance and character association in Indian mustard (*Brassica juncea* L.) grown in semi-reclaimed alkali soils. *J. Farm. Sys. Res. Devel.* **13**(2): 284-287.

Mumtaz, A., Sadaqat, H.A., Saeed, M., Yousaf, M.I., Shehzad, A. and Ahmed, H.G.M.D. (2017). Genetic behaviour of qualitative and seed yield-related traits in *Brassica rapa* L. *Zemdirbyste Agric.* **104**(2): 147-156.

Nadarajan, N. and Gunasekaran, M. (2005). Quantitative genetics and biometrical techniques in plant breeding. KP, Ludhiana, New Delhi, India. pp. 50-54.

Naznin, S., Kawochar, M.A., Sultana, S. and Bhuiyan, M.S.R. (2015). Genetic variability, character association and path analysis in *Brassica rapa* L. *Bangladesh J. Agric. Res*. **40**(2): 305-323.

Pankaj, S., Gyanendra, T., Gontia, A.S., Patil, V.D. and Shah, P. (2002). Correlation studies in Indian mustard. *Agric. Sci. Digest*. **22**(2): 79-82.

Parveen, S., Rashid, M.H. and Bhuiyan, M.S.R. (2015). Assessment of breeding potential of rapeseed germplasm using D^2 analysis. *J. Expt. Bio. Sci.* **6**(1): 59-64.

Parveen, S., Rashid, M.H. and Bhuiyan, M.S.R. (2015). Genetic variation and selection criteria for seed yield related traits in rape seed (*Brassica napus* L.). *Bangladesh J. Plant B. Genetics*. **26**(2): 15-22.

Pauw, R.D. and Baker, R.J. (1978). Correlations, heritabilities and components of variation of four traits in *Brassica campestries*. *Canadian J. Plant Sci.* **58**(3): 685-690.

Prakash, S. and Hinata, K. (1980). Taxonomy, cytogenetics and origin of crop *Brassica*, a review. *Opera. Bot.* **55**: 3-57.

Price, A.L., Patterson, N.J., Plenge, R.M., Weinblatt, M.E., Shadick, N.A. and Reich, D. (2006). Principal components analysis corrects for stratification in genome-wide association studies. *Nat. Genetics.* **38**(8): 904-909.

Rahman, L. (1976). Breeding for oil content and composition in Oleiferous *Brassica*. M.S. (Agril.) thesis, BAU, Mymensingh.

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

Rao, C.R. (1952). Advanced statistical methods in biometrical research. J. Willey,(1sted.). CMP, London. p.402.

Rashid, M.H.U., Parveen, S. and Bhuiyan, M.S.R. (2015). Morphological attributes species identification of oleiferous *Brassica sp.* and better parents selection criteria for *Brassica Juncea. Intl. J. Curt. Res.* **7**(9): 19847-19854.

Rashid, M.K.S.B.M., Huda, M.S. and Ahmed, I. (2013). Multivariate analysis in F_4 lines of *Brassica rapa* L. *Eco-friendly Agril. J.* **6**(9): 199- 204.

Robinson, H.F., Comstock, R.E. and Harvey, P. (1966). Quantitative genetics in relation to breeding on the centennial of mendelism. *Indian J. Genetics.* **26**: 171-177.

Salam, J.L., Mehta, N., Tomar, N.S., Saxena, R.R. and Sarawagi, A.K. (2017). Genetic variability analysis of yield and its components in *Brassica compestris* Var. toria. *Electronic J. Plant B.* **8**(1): 320-323.

Saleh, M.A. (2009). Variability analysis and selection from F_2 materials generated through inter-varietal crosses of *Brassica juncea*. M.S. (Agril.) thesis, SAU, Dhaka.

Scarth, R.P.B.E., Vetty, M.P.B.E., Rimmer, S.R. and Stefansson, B.R. (1988). Stellar low linolenic-high linoleic acid summer rape. *Canadian J. Plant Sci.* **68**(2): 509-511.

Shah, A.H., Gilani, M.M. and Khan, F.A. (2000). Comprehensive selection of yield and yield influencing characters in *Brassica sp. Int. J. Agric. Biol.* **2**(3): 245-247.

Sial, P. (2004). Analysis of genetic divergence for quality improvement in toria (*Brassica rapa* L. *spp.* toria). *Environ. Ecol*. **22**(2): 283-286.

Sial, P., Singh, B., Sachan, J.N. and Pattnaik. R.K. (2004). Correlation among quality traits in toria (*Brassica rapa* L. *sp.* toria). *Environ. Ecol.* **22**(2): 316-318.

Siddique D.M., Chandio, S.A., Ahmed, N.S., Karloo, W.M., Pathan, K.A., Meghwar, L.B. and Laghari, M.A. (2017). Character association of *Brassica campestries* L. *J. Agric. Res.* **55**(2): 249-265.

Sikarwar, R.S., Satankar, N., Kushwah, M.K. and Singh, A.K. (2017). Genetic Variability, Heritability and Genetic Advance Studies in Yellow Sarson (*Brassica rapa* Var. Yellow Sarson). *Int. J. Agric. Innov. Res.* **5**(5): 2319-1473.

Singh, A.P., Verma, O.P. and Kumar, K. (2017). Estimates of genetic variability parameters and interrelationships of morpho-physiological traits in yellow sarson (*Brassica rapa* L. Var. yellow sarson). *Electronic J. Plant B.* **8**(2): 629-635.

Singh, R.K. and Chaudhary, B.D. (1985). Biometrical methods in quantitative genetic analysis. (revised ed.). KP, Ludhiana, New Delhi, India. p.318.

Sivasubramania, S. and Menon, M. (1973). Heterosis and inbreeding depression in rice. *Madras Agric. J*. **60**: 1139.

Sohail, A., Zabta, K., Malik, A. R. and Sabbir, H. (2017). Assessment of quantitative agro-morphological variations among *Brassica rapa* diverse populations. *Pak. J. Bot.* **49**(2): 561-567.

Suman, S. (2014). Genetic divergence and character association of elite lines of indian mustard. M.S. (Agril.) thesis, OUAT, Odisha, Bhubaneswar, India.

Tollenaar, M.F., Ahmaedzedahand, A. and Lee, E.A. (2004). Physiological basis of heterosis for grain yield in maize. *Crop Sci.* **44**: 2086–2094.

Uddin, M.S., Bhuiyan, M.S.R., Mahmud, F. and Kabir, K. (2013). Study on Correlation and Path Co-efficient in F Progenies of Rapeseed (*Brassica rapa*). *Acad. J. Plant Sci.* **6**(1): 13-18.

Ullah, N., Khan, J., Khan, M.W., Raza, H., Alam, M., Ullah, H. and Ali, F. (2017). Genetic variability for biochemical traits among advanced lines of *Brassica*. *Pure Applied. Biol*. **6**(1): 1.

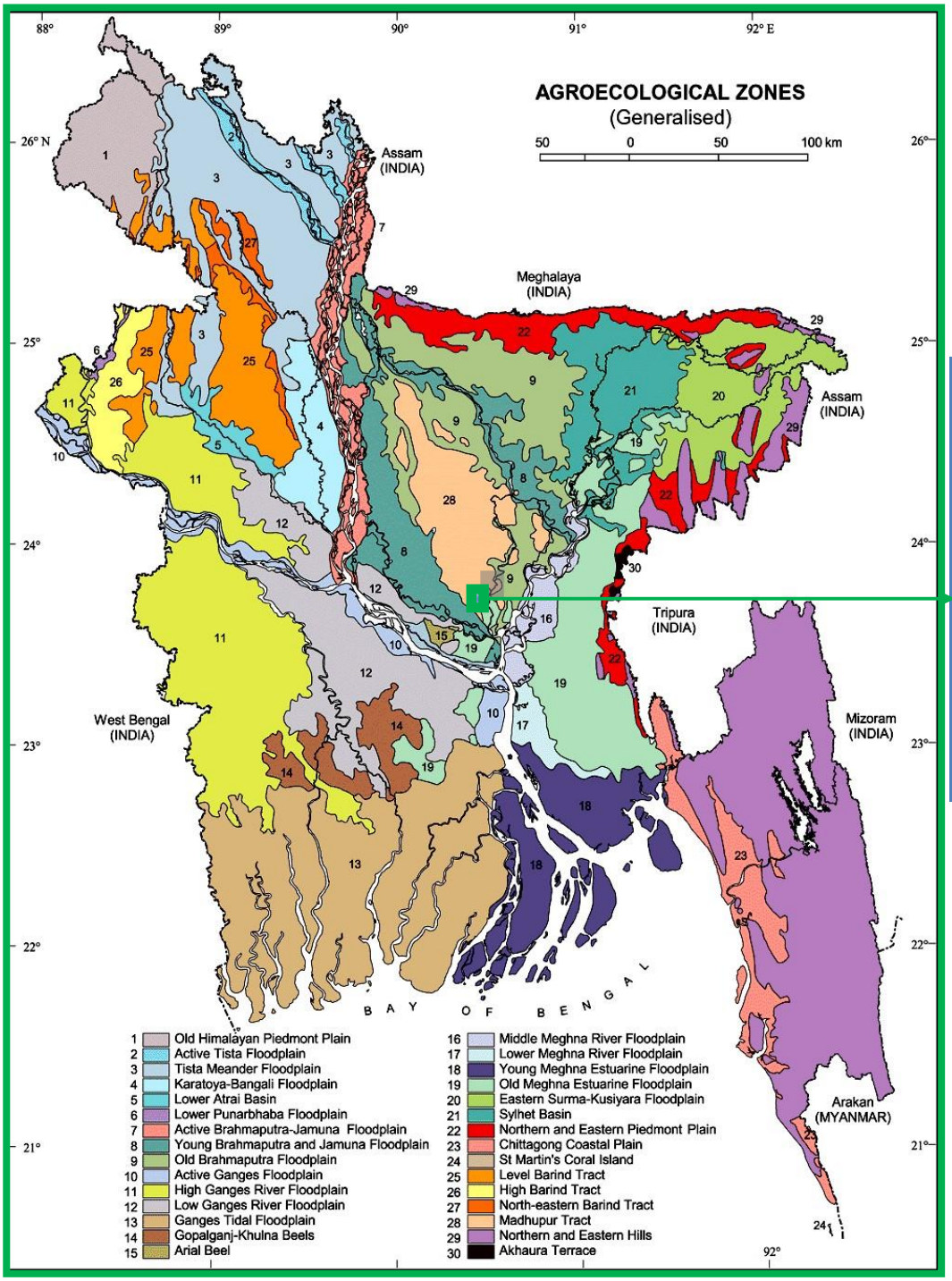
Ushakumari, R.M., Subramanian, M. and Subramaniam. (1991). Studies on coefficient of variation and heritable components of some quantitative characters of Brinjal. *Indian J. Hort.* **48**(1): 75-78.

Velasco, L., Goffman, F.D. and Becker, H.C. (1998). Variability for the fatty acid composition of the seed oil in a germplasm collection of the genus *Brassica*. *Genetic Res. Crop Evol.* **45**(4): 371-382.

Wang, Y., Sun, S., Liu, B., Wang, H., Deng, J., Liao, Y., Wang, Q., Cheng, F., Wang, X. and Wu, J. (2011a). A sequence-based genetic linkage map as a reference for *Brassica rapa* L. pseudo chromosome assembly. *BMC Genomics.* **12**(1): 239.

APPENDICES

Appendix I. Map showing the experimental site of the study



The experimental site

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

Month	Air temperature (°C)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
November, 2016	28.10	6.88	58.18	1.56	5.8
December, 2016	25.36	5.21	54.30	0.63	7.9
January, 2017	21.17	15.46	64.02	0.00	3.9
February, 2017	24.30	19.12	53.07	2.34	5.7

Source: Weather station, Sher-e-Bangla Agricultural University, Dhaka-1207.

Appendix III. Analysis of variance of ten important characters in respect of 15 populations of *Brassica rapa* L.

Source of variation	D.F.	DF	DM	PH	NPB/P	NSB/P	NS/P	LS	NS/S	TSW	Y/P
Replication	2	1.089	2.467	32.720	0.001	0.062	27.558	0.043	1.043	0.002	0.024
Population	14	16.57**	36.48**	224.73**	2.42*	1.82	379.87**	0.49	23.16**	1.46	23.07**
Error	28	1.256	1.300	15.947	0.029	0.074	51.086	0.059	1.142	0.021	0.031

** Significant at 1% level of significance
* Significant at 5% level of significance

DF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), NPB/P = Number of primary branch per plant, NSB/P = Number of secondary branch per plant, NS/P = Number of siliquae per plant, LS = Length of siliqua (cm), NS/S = Number of seed per siliqua, TSW = Thousand seed weight (g), Y/P = Yield per plant (g)

Appendix IV: Maximum, minimum, mean, CV and LSD value with standard error of ten parameters of *Brasssica rapa* L.

	Minimum	Maximum	Mean	CV (%)	SE	$LSD_{0.05}$
DF	30.67	39.33	34.29	3.27	0.915	3.391
DM	78.67	90.67	82.67	1.38	0.931	3.451
PH	84.14	116.11	104.46	3.82	3.260	12.085
NPB/P	3.63	7.03	5.11	3.35	0.140	0.517
NSB/P	0.27	3.37	1.16	23.46	0.221	0.820
NS/P	75.07	196.07	126.56	5.65	5.840	21.631
LS	4.86	6.28	5.41	4.49	0.199	0.736
NS/S	10.67	20.50	16.08	6.65	0.873	3.234
TSW	1.50	3.57	2.75	5.28	0.119	0.439
Y/P	5.22	14.00	8.87	2.00	0.145	0.536

DF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), NPB/P = Number of primary branch per plant, NSB/P = Number of secondary branch per plant, NS/P = Number of siliquae per plant, LS = Length of siliqua (cm), NS/S = Number of seed per siliqua, TSW = Thousand seed weight (g), Y/P = Yield per plant (g)