GENETIC STUDY ON YIELD AND QUALITY TRAITS OF ADVANCED BREEDING POPULATIONS IN *Brassica rapa* L.

DEBOSREE KARMOKAR

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

June, 2018

GENETIC STUDY ON YIELD AND QUALITY TRAITS OF ADVANCED BREEDING POPULATIONS IN *Brassica rapa* L.

BY

DEBOSREE KARMOKAR

REGISTRATION NO: 12-04882

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

MASTER OF SCIENCE

IN

GENETICS AND PLANT BREEDING

SEMESTER: JANUARY-JUNE, 2018

Approved by:

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

(Prof. Dr. Jamilur Rahman)

Chairman
Examination Committee
Department of Genetics and plant breeding, SAU, Dhaka

Dr. Md. Shahidur Rashid Bhuiyan
Professor
Department of Genetics and Plant Breeding
Sher-e-Bngla-Agricultural University
Dhaka-1207

CERTIFICATE

This is to certify that thesis entitled, " **GENETIC STUDY ON YIELD AND QUALITY TRAITS OF ADVANCED BREEDING POPULATIONS IN *Brassica rapa* L.**" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING**, embodies the result of a piece of bona fide research work carried out by **Debosree Karmokar**, Registration No. **12-04882** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: June, 2018
Place: Dhaka, Bangladesh

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

DEDICATED
TO
MY BELOVED PARENTS

ACKNOWLEDGEMENTS

All praises are due to the Supreme ruler of the universe, the most benevolent, the merciful Almighty God whose blessings enabled the author to complete this research work successfully.

It is immense privilege for the author to express her deepest sense of gratitude to her honorable supervisor ***Prof. Dr. Md. Shahidur Rashid Bhuiyan****, Department of Genetics & Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka-1207, for extending her generous help, scholastic guidance, innovative suggestions, constructive criticism, intensive supervision, critical comments and continued inspirations during the research work and also in preparing the manuscript of the thesis.*

The author is grateful to respectable co-supervisor ***Prof. Dr. Firoz Mahmud****, Department of Genetics & Plant Breeding, Sher-e-Bangla Agricultural university, for his immense help, constant cooperation and invaluable advice in completing the study. The author is also grateful to* ***Prof. Dr. Jamilur Rahman****, Chairman, Department of Genetics & Plant Breeding, Sher-e-Bangla Agricultural University. A special appreciation is extended to honorable teachers of the Department of Genetics & Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for their kind co-operation throughout the tenure of the study.*

The author expresses her humble gratitude to Vice Chancellor of sher-e-Bangla Agricultural University. Special Thanks to Ministry of Science and Technology, Government of the People's Republic of Bangladesh for financial Support to conduct the research.

The author desires to express her special gratitude to the farmers of the study area for their cordial co-operation during the collection of data.

The author has the pleasure to express cordial appreciation to all her friends and well wishers particularly Anwesha shreoshi Nath and Aliya Adiba Khanam and Ahmad Ullah for their kind help and co-operation. The author is highly indebted to her beloved mother Tanusri Chowdhury, father Nanda Kumar Karmokar, younger sister Nibedita Karmokar for their blessings, inspirations and co-operation in all phases of this academic pursuit from beginning to the end.

June, 2018

SAU, Dhaka **The Author**

GENETIC STUDY ON YIELD AND QUALITY TRAITS OF ADVANCED BREEDING POPULATIONS IN *Brassica rapa* L.

By

DEBOSREE KARMOKAR

ABSTRACT

The experiment was conducted with 13 advanced breeding populations of *Brassica rapa* L. during rabi season from November 2017 to February 2018 in research farm of Sher-e-Bangla Agricultural University to evaluate morphological and biochemical traits of the selected populations. The analysis of variance showed significant variation in all the traits. High genotypic and phenotypic coefficient of variation was observed for the characters viz; number of secondary branches per plant, number of siliquae per plant and yield per plant. High heritability coupled with high genetic advance in percent of mean was found for days to 50% flowering, number of secondary branches per plant, siliqua per plant, number of seeds per siliqua and yield per plant. The correlation studies revealed that yield per plant had highly significant positive relation with number of primary branches per plant, secondary branches per plant and number of siliquae per plant at both genotypic and phenotypic level. 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 five populations was done. Among the populations lowest amount of palmitic, stearic and erucic acid was found in P7 (Tori-7 x BARI sarisha-15 F_6) (1.68%), P9 (BARI sarisha-9 X BARI sarisha-6 S_5F_{15}) (0.49%) and P12 (SAU sarisha-1 X BARI sarisha-15 F_6) (54.08%) respectively. The highest amount of oleic, linoleic and linolenic acid was found in P12 (15.16%), P13 (BARI sarisha-6 X BARI sarisha-15 F_9) (14.27%) and P13 (8.65%) respectively. In case of short duration P1 (SAU sarisha-2 X BARI sarisha-15 F_7) (78.00 days) showed the best result. Higher yield per plant was found in P1 (7.31 g), P9 (6.53 g) and P12 (5.40 g) chronologically. Among the populations P1 was found as the best on the basis of days to 80% maturity, number of secondary branches per plant, number of siliquae per plant and yield per plant. Based on biochemical analysis for saturated fatty acids populations P7 and P9 were good. For unsaturated fatty acids population P12 was better enough than other populations. By comparing, it might be concluded that populations P1, P7, P9 and P12 had potential for improvement based on yield contributing traits and fatty acid content.

TABLE OF CONTENTS

TABLE OF CONTENTS (CONT'D)

TABLE OF CONTENTS (CONT'D)

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

SOME COMMONLY USED ABREVIATIONS

Full word	Abbreviation
Percent	%
Degree Celsius	^{0}C
At the rate	@
Phenotypic variance	σ^2_p
Genotypic variance	σ^2_g
Environmental variance	σ^2_e
Heritability in broad sense	h^2_b
Agro Ecological Zone	AEZ
Agriculture	Agric.
Agricultural	Agril.
Analysis of variance	ANOVA
Bangladesh Bureau of Statistics	BBS
Percentage of coefficient of variation	CV%
Cultivars	cv.
Degrees of freedom	Df
And others	*et al.*
Etcetera	etc.
The sixth generation of a cross between two dissimilar homozygous parents	F_6
Food and Agriculture Organization	FAO
Gram	g
Genotype	g
Genetic advance	GA
Genotypic coefficient of variation	GCV
Harvest Index	HI
Journal	*J.*
Kilogram	Kg
Meter	M
Distinctness uniformity and stability	DUS

SOME COMMONLY USED ABREVIATIONS (Continued)

Full word	Abbreviation
Mean sum of square	MS
Science	*Sci.*
Murate of Potash	MoP
Ministry of Agriculture	MoA
Square meter	m^2
Phenotypic coefficient of variation	PCV
Randomized Complete Block Design	RCBD
Sher-e-Bnagla Agricultural University	SAU
Triple Super Phosphate	TSP

CHAPTER I
INTRODUCTION

Rapeseed is a major oilseed crop and the third leading source of edible oil in the world (Sood *et al.*, 2010). It contributes a lion share to the total edible oil production in Bangladesh. It is belonging to the family *Brassicaceae* and third most important oil crop in the world. 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). Among the oilseed crops, mustard and rape seed is in the second position after soybean. The total area of mustard and rapeseed in the world is 34.33 million hectares. Global consumption of oils/fats has reached around 211 million tons in 2015-16 (FAOSTAT, 2017).

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. 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).

Mustard oil contains a high amount of selenium and magnesium, which gives anti-inflammatory properties. It also helps stimulating sweat glands and helps lowering body temperature. In traditional to the medicine value, it is used to relieve the pain associated with arthritis, muscle sprains and strains. Seed paste applied on wounds whereas paste of leaf said to heal cattle wounds (Sood *et al.*, 2010). Rapeseed also supplies fat soluble vitamins (A, D, E and K) in the body. Poor intake of fat and oil reduce the availability of fat soluble vitamins and caused dietary imbalance and food wastage.

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). Per capita consumption of edible oil is 11.25 kg per year (FAOSTAT, 2017). Bangladesh import 70% oil from foreign countries and spend a huge amount of foreign exchange to meet the increasing demand of its population. 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 (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 mustard so that they can successfully cultivate oilseed crops in three cropped cropping pattern. Future edible oil requirement can only be achieved through the improvement of seed quality by breeding *Brassica sp*. and using appropriate 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).

Rapeseed-mustard consists of saturated fatty acid such as palmitic (C16:0), stearic (C18:0) and monounsaturated fatty acids such as oleic (18:1) eicosenoic (C 20:1) and erucic acid (C 22:1) and polyunsaturated fatty acids such as linoleic (C 18:2) and linolenic acid (C 18:3), known as essential fatty

acids (USDA, 2000). The presence of high erucic acid in oil is considered anti-nutritional, as it has been reported to cause lipidosis in children and myocardial fibrosis in monkeys (Ackman *et al.*, 1977).

Breeding program should be maintained to produce high-yielding and better-quality lines for release as cultivars to farmers. Analysis of variability and the association among the traits contributing to yield of a crop would be of great importance for a successful breeding program (Mary and Gopalan, 2006). Development of high-yielding cultivars requires knowledge of the existing genetic variation (genetic and environmental) for yield and its components and quality traits. However, estimates of heritability in conjunction with genetic advance, the change in mean value among successive generations should be considered (Shukla *et al*., 2006). Determination of correlation coefficients is an important statistical procedure to evaluate breeding programs for yield (Ali *et al*., 2003). Path coefficient technique splits the correlation coefficients into direct and indirect effects via alternative characters or pathways (Sabaghnia *et al*., 2010).

The present study was undertaken for genetic and fatty acid composition characterization of the advanced populations. The 13 advanced populations obtained were in F_6, F_7, F_9, F_{10}, F_{16} generations and used in this experiment. The goal of the investigation is to select the early maturating yield potential mustard varieties with low erucic acid containing for hybridization programme. To meet the goal the following objectives were addressed:

1. To study the genetic variability of the advanced populations selected from the cross breeding programmes,
2. To analyze the fatty acids composition of *Brassica rapa* advanced populations for comparisons and
3. To select the yield potential short-durable and low erucic acid containing advanced populations for further study.

CHAPTER II

REVIEW OF LITERATURE

Brassica species has received much attention by a large number of researchers on various aspects of its production and utilization. *Brassica* species is the most important oil crop in Bangladesh and many other countries of the world. Many studies on the genetic variability, interrelationship, path co-efficient analysis, genetic diversity and fatty acid composition of *Brassica* spp. have been carried out in many countries of the world. The review of literature concerning the studies presented under the following heads:

2.1 Genotypic and phenotypic variability
2.2 Heritability and genetic advance
2.3 Correlation among different characters
2.4 Path co-efficient analysis
2.5 Fatty acid content

2.1 Genotypic and phenotypic variability

Katiyar *et al.* (1974) studied in *Brassica rapa* L. var. sarson grain on ten characters in 54 plants from each of 40 varieties; seed yield per plant showed a high genotypic coefficient of variation. While working with 65 strains of *B. rapa* by Nanda *et al.* (1995) and reported that days to first flowering varied both by genotypes and date of sowing. In another study, Lekh *et al.* (1998) reported that secondary branches showed highest genotypic co- efficient of variation. High genotypic and phenotypic co-efficient of variation was recorded for days to 50% flowering.

Thousand seed weight is also an important trait of *Brassica* oil crops, where highest consideration is on the seed yield. This trait has been found to vary widely from genotype to genotype and from environment to environment including macro and micro environments. The coefficient of variation was high for thousand seed weight, pod length and number of seed per pod for both genotypic and phenotypic variability (Masood *et al.* 1999).

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

Tyagi *et al.* (2001) evaluated forty-five hybrids of Indian mustard obtained from crossing 10 cultivars for seed yield and yield components. Highest variation for plant height of parents and their hybrids was reported. The seed yield per plant exhibited the highest coefficient of variation (41.1%). Genetic variability for nine traits in 25 genotypes study by Pant and Singh (2001). Analysis of variance revealed highly significant genotypic differences for all traits studied, except for days to flowering, number of primary branches and oil content. Seed yield per plant had the highest coefficient of genotypic and phenotypic variability. The genotypic coefficient of variation estimates for oil content and days to flowering suggest that these traits cannot be improved effectively merely by selection.

Ghosh and Gulati (2001) studied genetic variability in Indian mustard among 12 yield components for 36 genotypes selected from different geographical regions. The genotypic and phenotypic coefficients of variability (GCV and PCV, respectively) were high in magnitude for all the characters except plant height. The differences between the PCV and GCV were narrow for all the characters studied except plant height, indicating the usefulness of phenotypic selection in improving these traits. Shen *et al.* (2002); tested 66 F_1 hybrids of *Brassica rapa* and significant differences were found between F_1s and their parents for yield per plant and seed oil content.

Choudhary *et al.* (2003) studied variability in Indian mustard for 10 characters during rabi season in India. A wide range of variability was observed for all characters, except for primary branches per plant, siliqua length, number of seeds per siliqua and thousand seed weight. Genotypic and phenotypic coefficient of variability was recorded high for secondary branches per plant, seed yield per plant and number of siliqua per plant. Afroz *et al.* (2004); studied genetic variability of 14 genotypes of mustard and rape. The highest genetic advance was observed in percent of pollen sterility.

Mahak *et al.* (2004) conducted an experiment on genetic variability for eight quantitative characters. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all characters. Niraj and Srivastava (2004) studied on variability in Indian mustard of 21 genotypes of *Brassica juncea*. RH-9704 and IGM-21 recorded the highest seed yield. Phenotypic coefficient of variation was high for oil yield per plant, seed yield per plant and seed weight.

Akbar *et al.* (2007) evaluated eight advanced lines of *Brassica junea* in Pakistan and studied variability of different yield components that were under experiment. The highest GCV was found in seed yield per plant followed by plant height, siliqua per plant and thousand grain weight while lowest GCV

was in number of primary branches per plant. Rashid (2007) studied variability of forty oleiferous *Brassica* species. Result revealed that genotypes showed wider variation for morphological characteristics and thus were categorized under three cultivated species - *B. rapa, B. napus and B. juncea* considering genetic parameters. High GCV (Genotypic Co-efficient of Variation) value was observed for days to 50% flowering, days to maturity, plant height and number of siliqua per plant.

Parveen (2007) studied variability in F_2 progenies of the inter-varietal crosses of 17 *Brassica rapa* genotypes. The result revealed that there were significant variations among the different genotypes used in the experiment. A study was conducted by Hosen (2008) using five parental genotypes of *Brassica rapa* and their ten F_3 progenies including reciprocals. The result revealed that there were large variations present among all the genotypes used in the experiment. Number of primary branches per plant, number of secondary branches per plant, days to 50% flowering, length of siliqua, number of seeds per siliquae, thousand seed weight and yield per plant showed least difference between phenotypic and genotypic variances. The values of GCV and PCV indicated that there was considerable variation among the all characters except days to maturity. The plant height, days to 50% flowering and number of siliquae per plant showed high heritability with high genetic advance and genetic advance in percentage of mean.

Dash *et al.* (2007) conducted an experiment on fifty genotypes of toria with 14 characters to estimate genetic variability 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.

A field experiment was conducted by Jahan (2008) to study on inter-genotypic variability in 10 F_4 lines obtained through intervarietal crosses along with eight released varieties of *Brassica rapa* L. Significant variation was observed among all genotypes for all the characters studied. Considering genetic parameters i.e. high genotypic coefficient of variation (GCV) was observed for number of secondary branches/plant, siliquae/plant, yield/plant whereas days to maturity showed very low GCV. An experiment was carried out by Mahmud (2008) with 58 genotypes of *Brassica rapa* L. to study inter-genotypic variability. Significant variation was observed among all the genotypes for all the characters studied except thousand seed weight. High GCV value was observed for number of secondary branches per plant.

Singh *et al.* (2010) studied sixty two F_1 and twenty four parental lines of *Brassica juncea* and observed that higher genotypic variation were found in seed per plant, secondary branches per plant, primary branches per plant, thousand seed weight and seed per siliqua. Roy *et al.* (2011) conducted an experiment on rapeseed mustard (*Brassica* spp.) and studied variability. The result revealed that significant varietal difference except the number of siliqua on main recyme. The PCV and the GCV was high in secondary branches per plant and number of siliqua per plant.

Ali *et al.* (2013) conducted an experiment with thirty lines of *Brassica carinata* and reported that PCV and GCV ranged from 4.92-48.24% and 3.2-38.1%, respectively. Ahmad *et al.* (2013) studied thirty five advanced mutant lines along with a cheek variety of *Brassica napus* called Abasin-95 for variability analysis and reported that seed yield and days to flowering showed high genetic variability. The mutant lines 0A5, G1 and 06 showed their superiority in high seed yield, thousand seed weight and earliness in flowering.

Khan *et al.* (2013) evaluated thirty F_7 segregating lines and two parents of *Brassica rapa* to study variability. The result revealed that except thousand seed weight, significant variation was presented among all the genotypes for all the characters. Highest genotypic, phenotypic and environmental variances were observed in plant height while lowest one was in length of siliquae followed by thousand grain weight. Considering important performances, the genotypes G-15, G-19, G-1, G-3, G-4, G-10, G-18, G21, and G-24 were found suitable for future breeding program. Abideen *et al.* (2013) studied with eight genotypes of *Brassica napus* and observed that there were highly significant variations among the genotypes for most of the traits studied. Non-significant differences were in primary branches per plant and pods per plant among the genotypes.

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.

Walle *et al.* (2014) carried out a study with thirty six genotypes of Ethiopian mustard (*Brassica carinata*) and result revealed that there were significant difference in days to 50% flowering, plant height and primary branches per plant. GCV was lower than the PCV for all yield related characters studied. Mekonnen *et al.* (2014) evaluated thirty six genotypes of Ethiopian mustard, *Brassica carinata* to study variability. The GCV ranged from 4.3% to 44.14% and PCV from 8.3% to 91.7%. Comparatively high GCV estimates were observed for number of pods per plant, primary and secondary braches per plant, seed yield per plot, and seed yield per hectare. The highest PCV was in primary branches per plant. Higher GCV and PCV for seed yield, number of

pods per plant, primary and secondary branches which indicated that, it might provide better scope for improvement through selection.

Muhammad *et al.* (2014) studied with four parental genotype along with twelve F_2 generation of *Brassica napus* and reported that days to 50% flowering were significantly different at 5% level of significance. Plant height and pod length showed high heritability and days to 50% flowering showed moderate heritability. lqbal *et al*. (2014) conducted an experiment with ten indigenous variety associated with eight important yield contributing characters of *Brassica rapa* in Pakistan to study variability. The trails showed highly significant differences in almost all traits. It was observed that indigenous accessions had great proportion of genetic variability.

Yared and Misteru (2016) studied on sixty four *Brassica* breeding lines for investigated of some morphological characters to identify the extent and nature of genetic variability during 2014 cropping season. Analysis of variance showed the existence of considerable genetic variation among the lines for further selection and hybridization efforts. The maximum number of secondary branches/plant was observed by the breeding line code≠64. The highest yield/plot was recorded by the breeding line code≠48 followed by the breeding line code≠25 and code≠64. Breeding line code≠53 exhibited the maximum 1000 seed weight.

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. 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.

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.

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.

2.2 Heritability and genetic advance

Katiyar *et al.* (1974) reported that heritability in the broad sense was associated with high genetic advance for number of siliquae on the main shoot and for seed yield per plant was found. Shalini *et al.* (2000) conducted an experiment to study the heritability and genetic gain and found that heritability values and genetic gain were moderate to high for 1000 seed weight, number of siliquae per plant and number of secondary branches per plant, indicating that the response to selection would be very high for these yield components. For the other characters, medium to low heritability and low genetic gain were observed.

An experiment was conducted by Khulbe *et al.* (2000) to estimates of heritability and genetic advance for yield and its components in Indian mustard revealed maximum variation for seed yield. All the characters except oil content exhibited high heritability with high or moderate genetic advance, suggesting the role of additive gene action in conditioning the traits. Non-additive gene action appeared to influence the expression of days to maturity, while environment had a major influence on oil content. The use of pedigree selection or biparental mating in advanced generations was advocated to achieve substantial gains. Pant and Singh (2001) studied in experiment with nine traits in 25 genotypes. All traits showed high heritability with the highest value estimated for seed yield per plant. The estimates of genetic advance were comparatively low for oil content and days to flowering. The heritability estimates for oil content and days to flowering suggest that these traits cannot be improved effectively merely by selection.

Heritability studied of yield components in Indian mustard among 12 yield components for 36 genotypes selected from different geographical regions by Ghosh and Gulati (2001). All the characters studied estimates of high heritability except plant height. High heritability, coupled with high genetic

advance was observed for oil content, harvest index, number of primary branches, number of siliquae on main shoot, main shoot length and number of seeds per siliqua. This result suggests the importance of additive gene action for their inheritance and improvement could be brought about by phenotypic selection. In a study of heritability in Indian mustard for 10 characters during rabi season in India by Choudhary *et al.* (2003). High heritability coupled with high genetic advance as percentage of mean was observed for secondary branches per plant, seed yield per plant and number of siliquae per plant, indicating preponderance of additive gene action.

An experiment was conducted by Mahak *et al.* (2004) on heritability and genetic advance for eight quantitative characters. High heritability coupled with high genetic advance in percentage of mean was observed for days to flowering, followed by thousand seed weight, days to maturity and plant height. Niraj and Srivastava (2004), studied on heritability in Indian mustard of 21 genotypes of *Brassica juncea*. Heritability was high for test weight, days to flowering, days to maturity and plant height.

An experiment was conducted with eight advanced lines of *Brassica junea* in Pakistan and studied heritability and genetic advance of different yield components by Akbar *et al.* (2007). Highest heritability was found yield per plant followed by plant height, thousand grain weight, siliqua per plant and number of primary branches per plant. The maximum genetic advance was found in seed yield per plant followed by siliqua per plant, plant height, thousand grain weight and minimum in primary branches per plant. Parveen (2007), studied heritabilityin F_2 progenies of the inter-varietal crosses of 17 *Brassica rapa* genotypes. The result revealed that number of primary branches per plant and secondary branches per plant showed high heritability coupled with high genetic advance and very high genetic advance in percentage.

Dash *et al.* (2007) conducted an experiment on fifty genotypes of toria with 14 characters to estimate heritability for earliness and other yield attributes in toria (*Brassica rapa* L. Var. toria). 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.

Hosen (2008) studied heritability using five parental genotypes of *Brassica rapa* and their ten F_3 progenies including reciprocals. The result revealed that plant height, days to 50% flowering and number of siliquae per plant showed high heritability with high genetic advance and genetic advance in percentage of mean. Jahan (2008), conduced field experiment to study heritability in 10 F_4 lines obtained through intervarietal crosses along with eight released varieties of *Brassica rapa* L. Significant variation was observed among all genotypes for all the characters studied. High heritability with low genetic advance in percent of mean was observed for days to maturity which indicated that non-additive gene effects were involved for the expression of this character and selection for such trait might not be rewarding. High heritability with moderate genetic advance in percent of mean was observed for plant height and days to 50% flowering indicating that this trait was under additive gene control and selection for genetic improvement for this trait would be effective.

Mahmud (2008) carried out an experiment with 58 genotypes of *Brassica rapa* L. to study heritability. Significant variation was observed among all the genotypes for all the characters studied except thousand seed weight. High heritability values along with high genetic advance in percentage of mean were obtained for days to 50% flowering, number of secondary branches per plant, seeds per siliqua, and siliqua length. **Singh *et al.* (2010)** studied sixty two F_1 and twenty four parental lines of *Brassica juncea* and observed that high heritability and high genetic advance were found in seed per plant,

secondary branches per plant, primary branches per plant, thousand seed weight and seed per siliqua.

Alam (2010) conducted an experiment by using twenty six F_4 populations of some inter-varietal crosses of *Brassica rapa* L. to study the variation among them. Higher phenotypic variation was present than the genotypic variation. High heritability with high genetic advance was found plant height, number of primary branches per plant, number of secondary branches per plant and number of siliquae per plant. Afrin *et al.* (2011) conducted an experiment in *Brassica napus* and studied heritability. The plant height showed highest value of broad sense heritability while the number of primary branches per plant, number of secondary branches per plant, siliqua length, number of seed per siliquae, number of siliqua per plant, thousand seed weight and seed yield per plant showed moderate broad sense heritability. Days to 80% maturity showed lowest heritability.

Roy *et al.* (2011) conducted an experiment on rapeseed mustard (*Brassica* spp.) and studied heritability. High heritability along with high genetic advance as percent of mean was reported in plant height, seed yield, secondary branches per plant, siliqua per plant and seeds per siliqua. Tahira *et al.* (2011) conducted an experiment with ten wide genetic ranged variety of *Brassica juncea* to study heritability in broad sense and showed siliqua length, plant height and seed yield had high values.

Ali *et al.* (2013) conducted an experiment with thirty lines of *Brassica carinata* and reported that the highest heritability values were recorded for pod length (0.83) followed by pods on main raceme and the genetic advance as percent of mean was the highest for seed yield per plant and pods on main raceme. Ahmad *et al.* (2013) studied thirty advanced mutant lines along with a cheek variety of *Brassica napus* called Abasin-95 for heritability. High heritability and advance was recorded for seed yield.

Khan *et al.* (2013) evaluated thirty F_7 segregating lines and two parents of *Brassica rapa* to study heritability and genetic advance. Thousand seed weight, number of secondary branches per plant, seeds per siliquae, and siliquae length showed high heritability along with low genetic advance in percent of mean. Walle *et al.* (2014) carried out a study with thirty six genotypes of Ethiopian mustard (*Brassica carinata*). High heritability with high genetic advance was observed in plant height, number of secondary branches per plant and days to 80% maturity.

Mekonnen *et al.* (2014) evaluated thirty six genotypes of Ethiopian mustard, *Brassica carinata* to study heritability. Higher heritability along with higher genetic advance was observed in days to maturity, days to flowering, grain-filling period, number of pods per plant, secondary branches per plant, plant height, seed yield/plot and hectare and lowest one was in primary branches per plant. Muhammad *et al.* (2014) studied with four parental genotype along with twelve F_2 generation of *Brassica napus* and reported that plant height and pod length showed high heritability and days to 50% flowering showed moderate heritability.

lqbal *et al.* (2014) conducted an experiment with ten indigenous variety associated with eight important yield contributing characters of *Brassica rapa* in Pakistan to study heritability. The highest heritability with higher genetic advance was reported in plant height while the seed per siliqua was found medium heritability along with tower genetic advance. It was observed that indigenous accessions had great proportion of genetic heritance. Ejaz-Ul-Hasan *et al.* (2014) studied on heritability of *Brassica napus* and the result stated that plant height, yield per plant and days to 50% flowering showed high heritability.

Jahan *et al*. (2014) conducted a field experiment to study heritability in 10 F_4 lines of *Brassica rapa* L. 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.

Yared and Misteru (2016) studied on sixty four *Brassica* breeding lines for investigated of some morphological characters to identify the extent and nature of genetic heritability during 2014 cropping season. Number of secondary branches/plant and yield/plot were among the major positive contributor while 1000 seed weight recorded high heritability values in broad sense along with high genetic advance as percent of mean for which early generation selection would be effective in improvement program.

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 heritability. 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.

2.3 Correlation among different characters

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

Days to maturity showed insignificant correlation with seed yield at both genotypic and phenotypic levels. The number of branches per plant and number of siliquae per plant showed significant negative correlation with number of seeds per siliqua and 1000 seed weight was reported by Malek *et al.* (2000) while studied correlation analysis. Badsra and Chaudhary (2001) studied correlation on 14 traits of 16 Indian mustard genotypes. Seed yield was positively correlated with stem diameter, number of siliquae per plant and oil content, while oil content was positively correlated with harvest index only. Among the characters only three characters positively correlated with seed yield.

Association of yield components in Indian mustard among 12 yield components were studied in 36 genotypes selected from different geographical regions by Ghosh and Gulati (2001). Seed yield exhibited significant positive association with yield contributing traits like days to 50% flowering, days to maturity, plant height, number of secondary branches, number of siliquae on main shoot and oil content. Pankaj *et al.* (2002) studied four parental cultivars and the 174 progenies of resultant crosses for correlation between yield and yield component traits. The genetic correlation was higher than the phenotypic correlation for the majority of the characters. The number of siliqua per plant, which had the strongest positive and significant correlation with yield per plant at both levels, was positively associated with the number of seeds per siliquae and test weight at both levels. The number seeds per siliquae were positively associated with siliqua length and yield per plant at both levels.

Mahak *et al*. (2004) conducted an experiment and showed correlation for eight quantitative characters. Positive correlation was showed in case of seed yield per plant with number of primary branches, length of main raceme, 1000-seed weight and oil content. Selection should be applied on these traits to improve seed yield in Indian mustard. Afroz *et al.* (2004) studied

correlation and found seed yield per plant had significant and positive correlation with number of primary branches per plant and number of siliqua per plant. Path coefficient revealed maximum direct positive effects on plant height followed by number of siliqua per plant, seed yield per plant, number of primary branches per plant, 1000-seed weight and number of siliqua shattering per plant.

An experiment conducted by Niraj and Srivastava (2004) on character association studies in Indian mustard of 21 genotypes of *Brassica juncea*. Seed and oil yields were positively and significantly correlated with plant height and primary branches but negatively correlated with test weight. An experiment on oleiferous *Brassica campestris* L. was conducted by Siddikee (2006) to study the correlation analysis. The results revealed that yield per plant highest significant positive correlation with number of siliqua per plant.

Tusar *et al.* (2006) studied phenotypic correlation and observed that seed yield per plant was positively and significantly associated with plant height, total dry matter production. The number of siliqua per plant, 1000-seed weight, crop growth rate during 60-75 days after sowing and number of branches per plant were also positively associated with seed yield. Zahan (2006) studied correlation and reported that yield/plant had highly significant positive association with plant height, length of siliqua, siliquae/plant and seed/siliquae but insignificant negative association with days to 50% flowering, days to maturity.

Akbar *et al.* (2007) evaluated eight advanced lines and two check variety of *Brassica junea* in Pakistan and reported that siliqua per plant had strong positive correlation with the seed yield followed by plant height while non-significantly negative correlation with thousand grain weight. But significantly negative correlation was present in siliqua per plant and primary branches per plant. Rashid (2007) carried out an experiment with 40

oleiferous *Brassica* species to estimate correlation and observed that, highly significant positive association of yield per plant with number of primary branches per plant , number of secondary branches per plant, number of seeds per siliqua and number of siliquae per plant.

Parveen (2007) conducted an experiment with F_2 population of *Brassica rapa* to study the correlation and observed that yield per plant had non-significant positive association with plant height, number of secondary branches per plant, number of seeds per siliquae and number of siliquae per plant, days to 50% flowering and length of siliqua. A study was conducted by Hosen (2008) using five parental genotypes of *Brassica rapa* and their ten F_3 progenies including reciprocals. He found yield per plant showed highest significant and positive correlation with days to maturity followed by number of seeds per siliquae, number of secondary branches per plant, length of siliqua and number of siliqua per plant.

In an experiment Mahmud (2008) found highly significant positive association of seed yield per plant with number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant. Singh *et al.* (2010); studied sixty two F_1 and twenty four parental lines of *Brassica juncea* and observed that positive correlation was present in plant height, primary branches per plant, secondary branches per plant, seed per siliquae, thousand grain weight with seed yield.

Uddin *et al.* (2013) carried out an experiment with seven parental and twenty one F_2 progenies of *Brassica rapa* to study correlation among different yield component and found that yield per plant had high significant positive correlation with number of primary branches per plant, number of secondary branches per plant and siliqua per plant at both phenotypically and genotypically and significant positive correlation at genotypically in days to flowering and days to maturity. Ali *et al.* (2013) conducted an experiment

with thirty lines of *Brassica carinata* and observed that highly positive phenotypic correlation for seed yield per plant with plant height and primary branches per plant which was the indication that the traits were the most important contributors to seed yield per plant.

Afrin *et al.* (2011) studied on *Brassica napus* and found positive correlation with seed yield per plant in plant height, number of primary branches per plant and number of siliqua per plant. Highest significant positive correlation was found between days to 50% flowering and plant height. Maurya *et al.* (2012) carried out an experiment with one hundred genotypes of *Brassica juncea* and observed that a high positive correlation was presented between length of siliqua, seed yield, thousand grain weight and days to 50% flowering.

Abideen *et al.* (2013) studied with eight genotypes of *Brassica napus* and the resulted that positive phenotypically correlation was observed in plant height, pod length and seed yield . Significant positive correlation was also found in seed yield per plant and pods per plant. Ejaz-Ul-Hasan *et al.* (2014) studied correlation between different traits of *Brassica napus* and found high and positively significant phenotypic correlation between plant height and seeds per plant. Mekonnen *et al*. (2014) studied *Brassica carinata* and found that seed yield per plant were positively correlated with plant height, days to maturity, secondary branches per plant and thousand seed weight at both genotypic and phenotypic level. There were also found that plant height was strongly and positively correlated with number of pods per plant

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

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

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

Srivastava and Singh (2002) reported that number of primary branches per plant, number of secondary branches per plant and 1000 seed weight had

strong direct effect on seed yield while working with Indian mustard (*B. juncea* L. Czern and Coss). Results suggested that number of primary branches and 1000 seed weight were vital selection criteria for improvement-in productivity of Indian mustard. Afroz *et al.* (2004) studied path analysis of 14 genotypes of mustard and observed that maximum direct positive effects on plant height followed by number of siliqua per plant, seed yield per plant, number of primary branches per plant, 1000-seed weight and number of siliqua shattering per plant.

By path analysis, Zahan (2006) reported that siliquae/plant had positive direct effect on yield/plant. And days to 50% flowering had negative direct effect on yield/plant. Khan *et al.* (2006) studied correlation for some quantitative traits relating to yield and quality. The results indicated that a wide range of genetic variation existed among all the characters under study except 1000-grain weight. Correlation analysis revealed that seed yield per plant was positively and significantly correlated with number of primary branches (0.4015), siliqua per plant (0.505), seeds per siliqua (0.79648), siliqua length (0.37037) and seed yield per plot (0.40931). However, it was negatively and non-significantly associated with number of secondary branches (-0.36663) and protein contents (-0.1372) at genotypic level. It was also found that indirect selection for number of seeds per siliqua would be effective in improving the seed yield per plant in present breeding material.

A study was conducted by Tusar *et al.* (2006) to assess the nature and extent of variability of 11 yield related characters of five mustard genotypes. Phenotypic correlation studies indicated that seed yield per hectare was positively and significantly associated with plant height, total dry matter production and husk weight. The number of siliqua per plant, 1000-seed weight, crop growth rate during 60-75 days after sowing and number of branches per plant were also positively associated with seed yield. Path coefficient analysis revealed that the number of siliqua per plant had the

greatest direct contribution on seed yield followed by the number of seeds per siliqua and 1000-seed weight while indirect via number of siliqua per plant and 1000-seed weight. Although plant height and husk weight had a total positive correlation with seed yield, their direct effect on yield was negative. The number of seeds per siliqua showed very high positive direct effect on yield, but its correlation with yield was non-significant and negative.

Rashid (2007) carried out an experiment with 40 oleiferous *Brassica* species to estimate path analysis and observed that yield per plant had the highest direct effect on days to maturity, number of seeds per siliqua, number of siliquae per plant and number of primary and secondary branches per plant. Parveen (2007) conducted an experiment with F2 population of *Brassica rapa* to study the path analysis and observed that number of seeds per siliqua showed highest direct effect on yield per plant.

The path co-efficient analysis by Hosen (2008) exhibited that thousand seed weight had the highest positive direct effect followed by days to 50% flowering, length of siliqua, number of primary branches per plant, number of secondary branches per plant, days to maturity and number of seeds per siliqua while working with five parental genotypes of *Brassica rapa* and their ten F_3 progenies including reciprocals. An experiment was carried out by Mahmud (2008) with 58 genotypes of *Brassica rapa*. Path analysis showed that yield per plant had the highest direct effect on number of primary branches per plant, number of siliquae per plant, number of secondary branches per plant and number of seeds per siliqua.

Aytac *et al.* (2008) evaluated on six genotypes of spring rape seed and studied path coefficient and the result stated that plant height, number of siliqua per plant, seeds per siliquae had highest and positive direct effect on yield per plant for all cultivars except cv. Star. Alam (2010) studied path co-efficient analysis that revealed that plant height, number of primary branches per plant,

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

Afrin *et al.* (2011) studied with *Brassica napus* to identify the path co-efficiant among the characters. The plant height was found the highest positive and direct effect on seed yield per plant followed by number of siliqua per plant and siliqua length. Uddin *et al.* (2013) conducted an experiment with seven parental and twenty one F_2 progenies of *Brassica rapa* to study path coefficient and reported that days to 50% flowering, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, siliquae length, seed per siliquae and thousand seed weight showed direct positive association with seed yield per plant while the plant height and days to maturity had direct negative association.

Mekonnen *et al.* (2014) conducted an experiment to study path co-efficient in *Brassica carinata* and founded that days to maturity and secondary braches per plant had positive and direct genotypic correlation with seed yield. Ejaz-Ul-Hasan *et al.* (2014) conducted an experiment on *Brassica napus* and studied path coefficient. The result revealed that the highest direct positive effect of seeds per plant on yield and followed by days to maturity, days to flowering, seeds per siliquae, siliqua length and thousand seed weight while plant height had direct negative effect on the yield per 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.

Rashid *et al.* (2015) conducted an experiment with 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. Highest positive and highly significant direct association with the yield per hectare followed by number of primary branches per plant were showed by plant height. The high direct effect gave the massage that selection of the traits might be effective for yield improvement.

Islam *et al*. (2016) studied on 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 Fatty acid content

Velasco *et al.* (1998) reported on collecting of 1475 entries from 21 species of Brassica was evaluated for the fatty acid composition of the seed oil. A

total of 358 entries representing the taxonomic variability in the collection were selected and analysed by gas-liquid chromatography (GLC). 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., and in the wild species B. incana Tenore, B. rupestris Raf., and B. villosa Bivona-Bernardi, the three latter belonging to the B. oleracea group (n=9). 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%). The highest levels of these fatty acids were found in samples of B. elongata Ehrh., especially of the var. integrifolia Boiss. The utility of the reported variability for plant breeding is discussed.

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.

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.

Kumar (2013) studied with 24 parents and 80 F1 crosses of Indian mustard to assess the fatty acid profile and oil content. Analysis of variance indicated significant differences for all the quality characters investigated. The environmental effects were significant for erucic and oleic acid content and the influence of environmental factors appeared to be less on other characters. The genotype × environment interactions were non-significant for all the characters, hence, the data were pooled over the years and discussed on the basis of mean of two years. The coefficients of variation at phenotypic level varied from 4.6% for oil content to 50.9% for oleic acid. The genotypic coefficients of variability were high for oleic, palmitic + stearic, erucic and linolenic acid, erucic acid and palmitic acid + stearic acid had the least genotypic variation (GCV: 16.3 to 16.9%). The heritability in broad-sense was relatively high for oleic (61.5%) and erucic acid (56.3%). The high heritability was associated with high genetic advance only for oleic acid suggesting the role of additive gene action in the inheritance of this character. Erucic acid negatively and significantly correlated with the rest of the fatty acids except linolenic acid and significant correlation with oleic (r = -0.536) and eicosenoic acid (r = -0.260). Although, oil content had very low direct effect (-0.011) on erucic acid but its positive association was the result of its strong positive indirect effect through oleic acid (0.435), which was partially neutralized by negative indirect effects (-0.112) through linolenic acid. The implications of these results in the quality-breeding programme were discussed in this paper.

Sharafi, *et al.* (2015) studied on 20 accessions of six Brassica species including cultivated and five wild relatives for oil and fatty acid composition. The results showed that oil content varied from 21 (*B. nigra*) to 46% (*B. napus*). Among wild species, *B. rapa* and *B. oleracea* had highest oil content (31 and 28%, respectively). The main fatty acids of oleic, linoleic, linolenic, erucic, palmitic, and stearic acids accounted for 89–94% of the total fatty acids in all species. Cultivated species of *B. napus* had highest oleic acid

(61%) and lowest erucic acid (1%) content compared to other studied species. *Brassica rapa* and *B. oleracea* had the highest content of erucic acid (41and 46%, respectively). The highest content of linolenic (20%) and linoleic (19%) acid was observed for *B. juncea*. The results showed that there was high genetic variation among the studied species for oil content and fatty acids composition. This indicates that seed oil of these species is possibly suitable for both human consumption and industrial purposes.

Nath *et al.* (2016) reported on rapeseed oil is being utilized from early civilization, but its popularity being declined from the mid-nineteenth century due to presence of erucic acid (C22:1) and glucosinolates. Thereby, several attempts have been made to develop cultivars free from those toxins. In the past 20 years, breeders got success in developing '00'- quality rapeseed, known as 'Canola'. The target mutagenesis of fae-1 and fae-2 of Brassica napus ensured such success. Thereafter, 'canola' regains its market as a healthy vegetable oil. Moreover, high oleic acid rapeseed lines, with 86% oleic acid, have been developed by using chemical mutagenesis of FAD2 alleles responsible for desaturation of oleic acid (C18:1) to linoleic acid (C18:2). Recently, high erucic acid rapeseed oil regained interest for biodegradable plastic, cosmetic, emollient industries and for biodiesel.

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 **"GENETIC STUDY ON YIELD AND QUALITY TRAITS OF ADVANCED BREEDING POPULATIONS IN *Brassica rapa* L.''** 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 2017 to February 2018. The experimental area was situated at 23°46'16" N latitude and 90°22'46" E longitude at an altitude of four 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 13 advanced breeding populations 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 populations 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 replications. The plot size was 300 m^2. Row length was maintained as four meter 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 were 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-2 X BARI sarisha-15 F_7	GEPB, SAU
2	P2	Yellow Special	GEPB, SAU
3	P3	BARI sarisha-15 X SS(Sonali sarisha) 75 F_{10}	GEPB, SAU
4	P4	BARI sarisha-6 X BARI sarisha-15 F_6	GEPB, SAU
5	P5	BARI sarisha-15 X SS(Sonali sarisha) 75 F_{10} BULK	GEPB, SAU
6	P6	BARI sarisha-9 X BARI sarisha-6 F_{16}	GEPB, SAU
7	P7	Tori-7 x BARI sarisha-15 F_6	GEPB, SAU
8	P8	Yellow Special F_9	GEPB, SAU
9	P9	BARI sarisha-9 X BARI sarisha-6 S_5 F_{15}	GEPB, SAU
10	P10	SAU sarisha-1 X BARI sarisha-15 F_7	GEPB, SAU
11	P11	SAU sarisha-1 X BARI sarisha-15 F_7 BULK	GEPB, SAU
12	P12	SAU sarisha-1 X BARI sarisha-15 F_6	GEPB, SAU
13	P13	BARI sarisha-6 X BARI sarisha-15 F_9	GEPB, SAU

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

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 1 November, 2017. The seeds were placed at about 1.5 cm depth in the soil. Clods were removed during sowing. Seeds were started to germinate after three days of sowing on 4 November 2017.

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 one 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 1).

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 12 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. Second thinning was done on 20 November 2019. Thinning was shown in photograph (Plate 2).

Plate 1. Tagging of each population of entire field

Plate 2. Thinning the excess seedling in the experimental field

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 after 22 days of sowing (DAS) before the flower initiation. Third irrigation was given after 40 days of sowing (DAS) when the pod appeared. Fourth irrigation was given after 60 days of sowing (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. First pesticide ripcord 2 ml/liter of water was sprayed on 20 November 2019 to control aphids and later when needed. Insecticide was applied in the afternoon to protect the beneficial insect.

3.5.5 Harvesting

Harvesting was started from 31 January to 7 February, 2018 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. Field view during maturity of *Brassica rapa* L. in Plate 4.

3.5.6 Collection of data

To study different genetic parameters and inter-relationships the following ten characters were taken into consideration: days to 50% flowering, days 80% maturity, plan height (cm), primary branches per plant, secondary branches per plant, siliqua per plant, length of siliqua (cm), seeds per siliqua, 1000 seeds weight (g) and seed yield per plant (g).

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. It was counted as number of days.

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. It was counted as number of days.

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 per plant

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

3.6.5 Number of secondary branches per plant

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

Plate 3. The experimental plot was shown in field during fruiting stage

Plate 4. The experimental field view during maturity stage

3.6.6 Number of siliqua per plant

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

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 per 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. It was counted as number.

3.6.9 Thousand-seed weight (g)

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

3.6.10 Seed yield per 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 Analysis of Fatty Acid

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 Central Laboratory, Oilseed Research Center, Bangladesh Agricultural

Research Institute. 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 110^0 C for about an hour. The plates were 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 ^{o} C and the detector temperature was 260^0C. The temperature of the column was programmed initially at 170^0 C for 8 minutes, then it was allowed to rise to 200^0 C at a rate of 10^0 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:

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

% 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 per plant, no. of secondary branches per plant, number of siliqua per plant, siliqua length (cm), number of seeds per siliqua, thousand seed weight (g), seed yield per 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:

ANOVA (Analysis of variance)

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

Where,

r = number of replications

p = number of treatments (population)

σ^2_r = variance due to replications

σ^2_p = variance due to treatments (population)

σ^2_e = 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) = $\frac{MSS\ due\ to\ genotypes - MSS\ due\ to\ error}{R}$

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 %) = $\frac{\sqrt{Phenotypic\ variance}}{Grand\ mean} \times 100$

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

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).

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

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).

$$GA = h^2_{bs} \times \sigma_p \times K$$

Where,

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

σ_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

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

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).

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

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

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_g^2 and σ_p^2 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):

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

Where,

$P^2_{RY} = R^2$

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

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

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

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 13 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 Analysis of fatty acid
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 thirteen populations was significant. The mean performance and range for all the characters were also significant (Table 3).

4.1.1 Days to 50% flowering

Significant variance was observed in days to 50% flowering. The maximum duration to days to 50% flowering was found in P6 with 57.33 DAS and the minimum in P5 with 33.00 DAS (Table 3). The mean value was 39. 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 P5 (33.00) indicates that flower came early and it is short durable population. Difference of days to flowering at field level was shown in (Plate 5). The phenotypic variance (37.52) was higher than genotypic variance (35.80). Moderate phenotypic coefficient of variation (15.71) and genotypic coefficient of variation (15.34) was observed for this trait. High genotypic and phenotypic co-efficient of variation was recorded by Lekh *et al*. (1998).

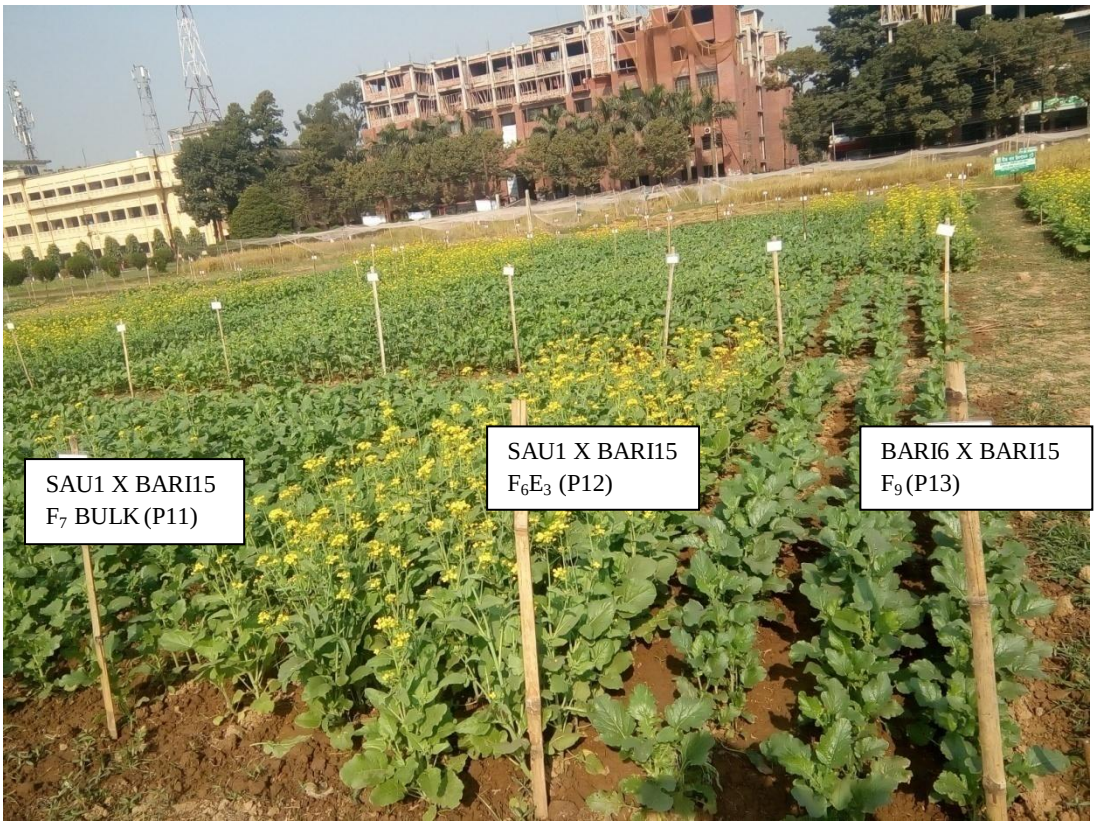


Plate 5. Photograph showing the difference of days to flowering between populations in experimental field level.

Table 3. Mean performance of different characters of 13 *Brasica rapa* advanced breeding populations

Population	D50%F	D80%M	PH	PBP	SBP	SPP	LS	SPS	TSW	SYP
P1	38.00cd	78.00e	111.47a	10.33a	10.93a	104.58ab	5.13bc	13.77f	3.79a-c	7.31a
P2	38.00cd	86.00b	103.90a-c	6.85b-d	0.50b	66.23c-f	5.20bc	17.40cd	3.33c	3.53d
P3	33.67e	80.00d	100.43bc	5.13d	2.77b	59.48e	5.17bc	17.93b-d	3.77a-c	4.37cd
P4	38.00cd	87.00b	105.95ab	6.95b-d	1.57b	87.31bc	4.95c	14.53ef	4.53a	4.52cd
P5	33.00e	82.00c	94.76cd	7.73bc	9.60a	79.51b-e	5.96a	20.43ab	4.01a-c	4.61cd
P6	57.33a	81.00cd	80.77e	5.88cd	8.63a	103.29ab	4.67c	12.83f	4.43ab	4.81cd
P7	39.00b-d	87.33b	104.97ab	7.33b-d	1.77b	82.45b-e	5.03bc	18.60a-c	3.33c	4.91cd
P8	39.00b-d	87.33b	106.17ab	6.29b-d	1.80b	73.17c-e	4.94c	16.53c-e	3.50c	4.50cd
P9	34.00e	81.33cd	88.23de	6.77b-d	8.43a	124.29a	5.57ab	15.40d-f	3.57bc	6.53ab
P10	39.33b-d	86.00b	108.77ab	6.03b-d	1.60b	72.14c-e	4.87c	19.07a-c	3.83a-c	4.45cd
P11	37.00d	86.33b	108.97ab	5.67cd	1.77b	68.47c-e	4.83c	18.06a-d	3.57bc	3.65d
P12	40.00bc	89.00a	107.86ab	8.35ab	1.63b	85.54b-d	5.26bc	18.50a-c	3.60bc	5.40bc
P13	40.67b	89.67a	105.87ab	5.25d	0.87b	60.22de	5.10bc	20.87a	3.33c	3.57d
Min.	**33**	**78**	**80.77**	**5.13**	**0.5**	**59.48**	**4.67**	**12.83**	**3.33**	**3.53**
Max.	**57.33**	**89.67**	**111.47**	**10.33**	**10.93**	**124.29**	**5.96**	**20.87**	**4.53**	**7.31**
Mean	**39**	**84.69**	**102.16**	**6.81**	**3.99**	**82.05**	**5.13**	**17.22**	**3.74**	**4.78**

D50%F = Days to 50% flowering, D80%M = Days 80% maturity, PH = Plan height (cm), PBP = Primary branches per plant, SBP = Secondary branches per plant, SPP = Siliqua per plant, LS = Length of siliqua (cm), SPS = Seeds per siliqua, TSW = 1000 seeds weight (g) and SYP = Seed yield per plant (g).

Table 4. Estimation of mean performance and genetic parameters for ten characters of thirteen advanced breeding populations of *Brassica rapa* L.

Traits	Range		Mean	MS	CV (%)	σ^2p	σ^2g	σ^2 e	PCV	GCV	h^2	GA(5 %)	GA (% mean)
	Min.	Max.											
Days to 50% flowering	33.00	57.33	39.00	109.11**	3.36	37.52	35.80	1.72	15.71	15.34	95.42	12.04	30.87
Days 80% maturity	78.00	89.67	84.69	41.91**	1.08	14.53	13.69	0.84	4.50	4.37	94.24	7.40	8.74
Plan height (cm)	80.77	111.47	102.16	243.38**	5.42	101.54	70.92	30.61	9.86	8.24	69.85	14.50	14.19
Primary branches per plant	5.13	10.33	6.81	6.06**	18.40	3.07	1.50	1.57	25.71	17.96	48.78	1.76	25.83
Secondary branches per plant	0.50	10.93	3.99	44.06**	53.40	17.71	13.17	4.54	105.49	90.97	74.37	6.45	161.62
Siliqua per plant	59.48	124.29	82.05	1096.62**	16.29	484.60	306.01	178.59	26.83	21.32	63.15	28.64	34.90
Length of siliqua (cm)	4.67	5.96	5.13	0.33**	6.18	0.18	0.08	0.10	8.25	5.47	43.98	0.38	7.47
Seeds per siliqua	12.83	20.87	17.22	18.49**	8.70	7.66	5.42	2.24	16.07	13.51	70.71	4.03	23.41
1000 seeds weight (g)	3.33	4.53	3.74	0.45*	12.38	0.29	0.08	0.21	14.51	7.57	27.20	0.30	8.13
Seed yield per plant (g)	3.53	7.31	4.78	3.65**	16.37	1.63	1.01	0.61	26.67	21.06	62.35	1.64	34.26

MS : Mean sum of square
CV (%) :Coefficient of variation
PCV : Phenotypic coefficient of variation
GCV : Genotypic coefficient of variation
** : Significant at 1%

σ^2p : Phenotypic variance
σ^2g : Genotypic variance
σ^2 e : Environmental variance

h^2 : Heritability
GA (5%) : Genetic advance
GA (% mean) : Genetic advance (% mean)

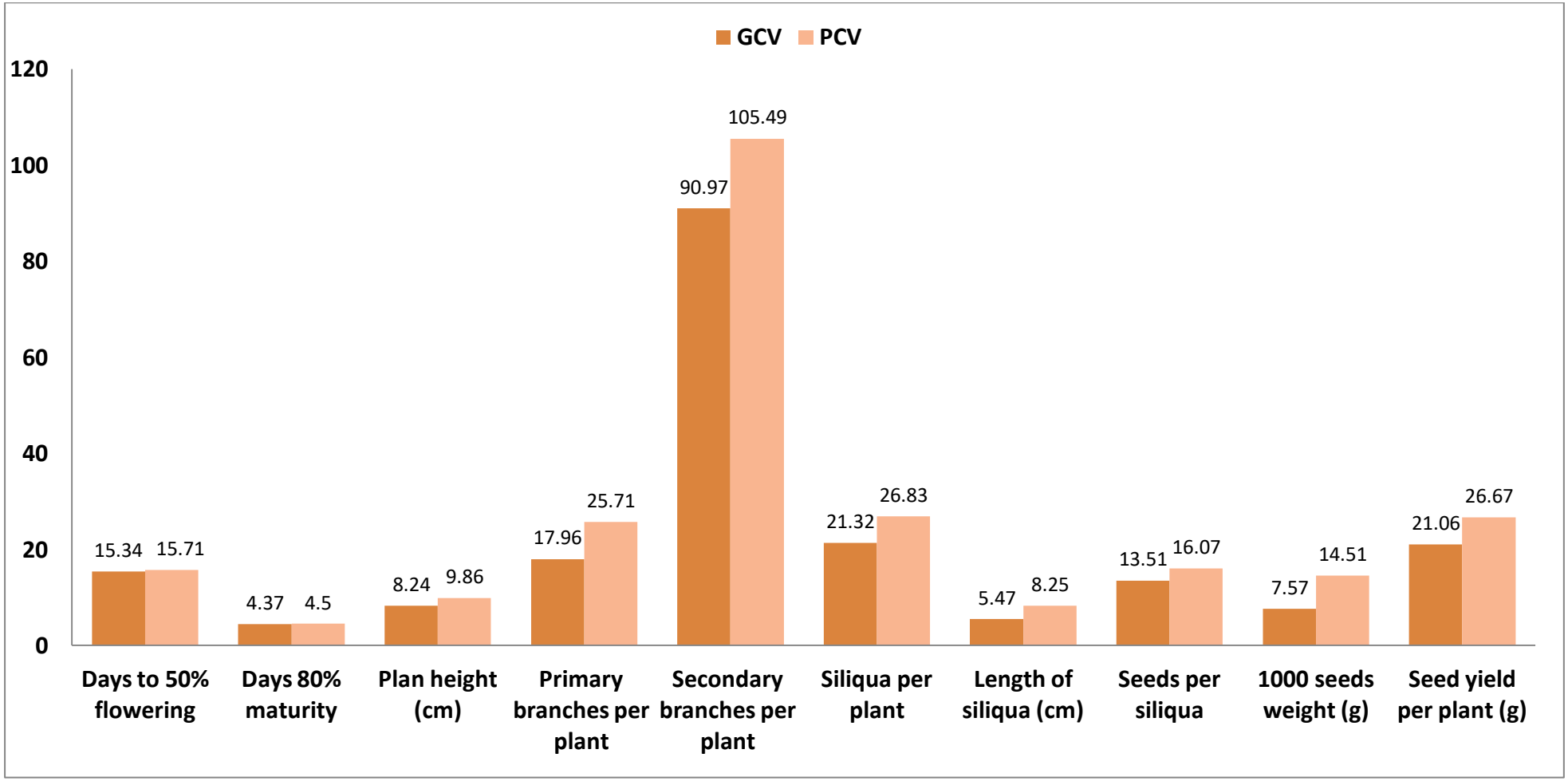


Figure 1. Genotypic and phenotypic variability in *Brassica rapa* L.

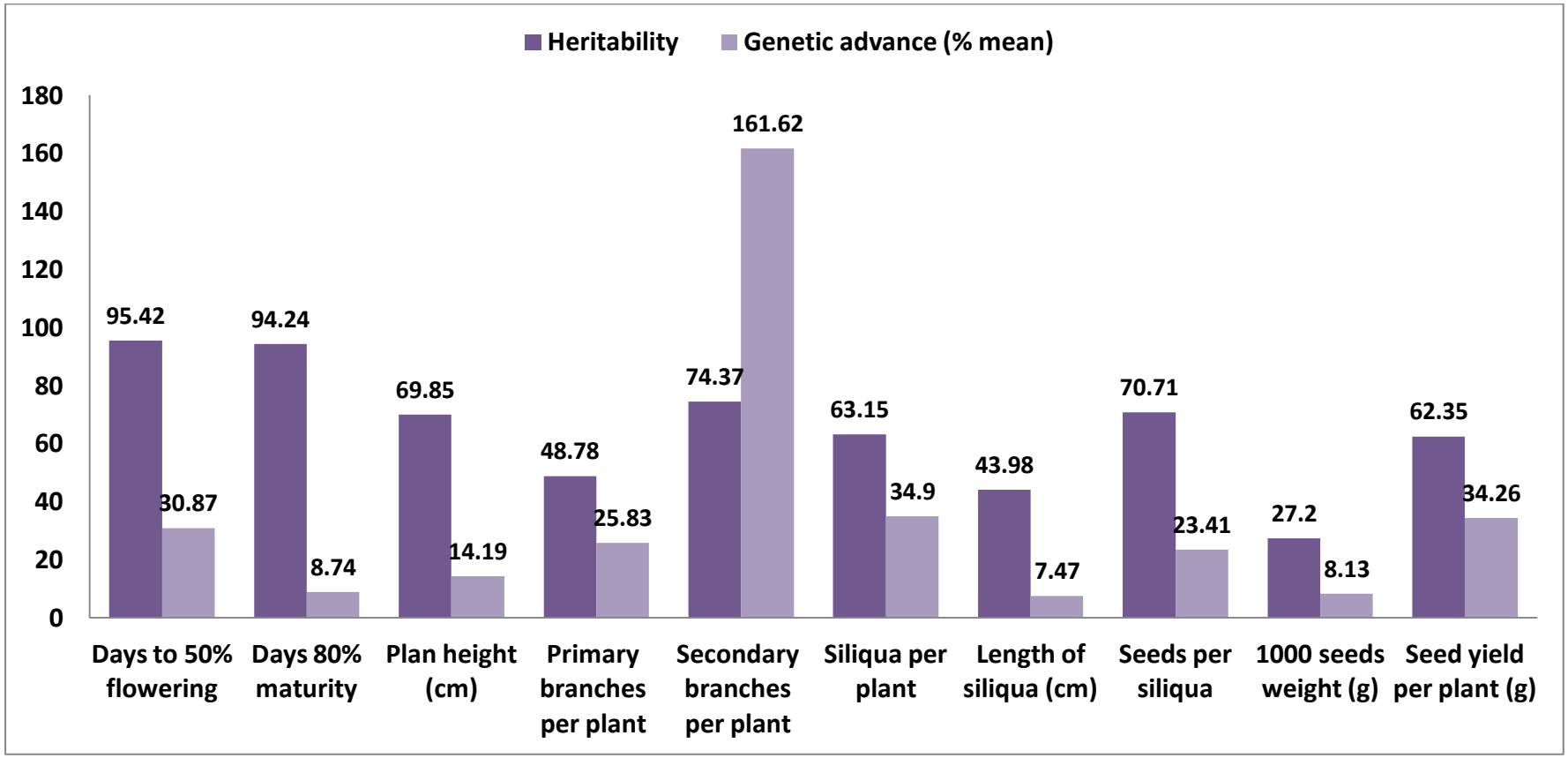


Figure 2. Heritability and genetic advance as percent over mean in *Brassica rapa* L.

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 moderate with value of 15.34 and 15.71 per cent, respectively along with high heritability of 95.42% with high genetic advance as per cent mean of 30.87%` and moderate genetic advance (12.04) (Table 4). So selection differential may be effective for improvement of this trait. Sikarwar *et al.* (2017) found that days to flowering showed low PCV and GCV. High heritability and high genetic advance indicating that the additive gene action might be controlling the trait of expression and selection for this trait may be recommended. Difference in days to flowering between populations was shown in plate 6. P12 showed earlier flowering than P11 and P13 (Plate 5).

4.1.2 Days to 80% maturity

The average days to 80% maturity was observed of 84.69 days with a range of 78.00 to 89.67 days. The P1 required least number of days to mature (78.00 days) and it was significantly different to other lines and followed by P3 (80.00 days). Whereas, the maximum number of days to 80% maturity was observed in the population P13 (89.67 days) and it was statistically similar with P12 (89.00 days) (Table 3). The shortest time required for 80% maturity in Tori-7 (81 days) was reported by Ali *et al.* (2002). P1 showed lowest days to maturity (78.00) which indicated that it matures early rather than the other populations.

The genotypic and phenotypic variance was recorded as 13.69 and 14.53, respectively. Genotypic variance and phenotypic variance was little difference which means that there is least influence of environment in the expression of genes for this trait. Days to 80% maturity exhibited low GCV and PCV of 4.37 and 4.50 per cent, respectively along with high heritability of 94.24 per cent, low genetic advance 7.40 and low genetic advance as per cent mean of 8.74 per cent (Table 4). This high heritability with low genetic

advance was indicated that presence of non-additive gene action. High heritability is less influenced by the environment. Thus, the selection for

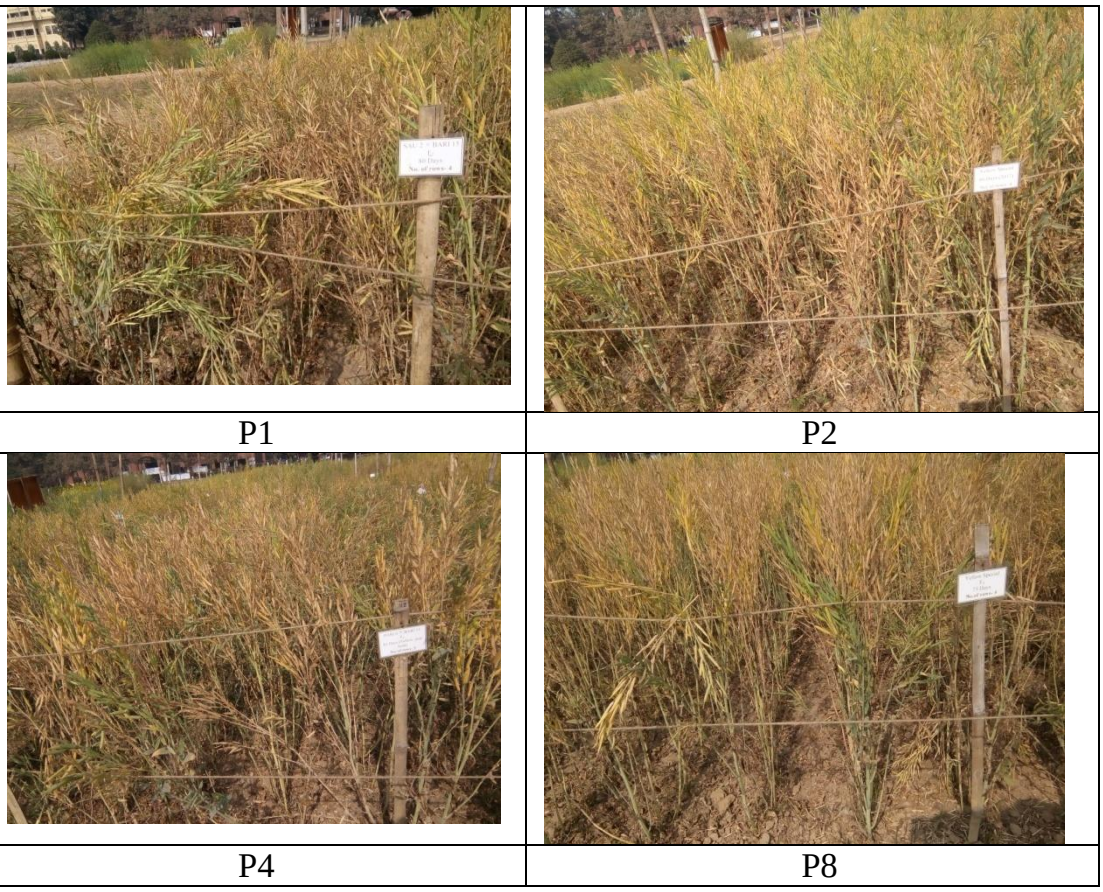


Plate 6. Maturity stage of some advanced breeding populations of *Brassica rapa* L.

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. 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 P1 (111.47 cm) and lowest in P6 (80.77 cm). The mean value was recorded as 102.16 cm. The mean sum of square for treatment was 243.38 indicating significant differences among the populations for this trait (Table 4). The lowest plant height was found in P6 (80.77 cm) which showed shortest plant than the other populations.

Genotypic and phenotypic variance was observed 70.92 and 101.54, respectively for plant height with large environmental influence. Naznin *et al.* (2015) also found the similar results. Ara *et al.* (2010) found the highest difference between genotypic and phenotypic variance in plant height. The plant height exhibited low genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) of 8.24 and 9.86 per cent, respectively (Table 4). High heritability of 69.85 per cent, moderate genetic advance 14.50 along with moderate genetic advance as per cent mean (14.19%) was recorded. High heritability with moderate genetic advance showed that it is controlled by additive and non-additive gene effects and the selection may be effective 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) and Ara *et al.* (2010) found highest heritability coupled with higher genetic advance in plant height.

		
P1	P4	P9

Plate 7. Showing of plant height of some advanced breeding 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 6.06 (Table 4). The Maximum number of primary branches per plant were found in P1 (10.33) which was statistically similar with P12 (8.35) and minimum number of primary branches per plant were found in P3 (5.13) which was statistically similar and followed by P13 (5.25), P11 (5.67) and P6 (5.88).The mean value was 6.81 (Table 3). P1 showed maximum no. of primary branches per plant (10.33) indicating more siliqua than the other populations which ultimately increased yield per plant.

The genotypic and phenotypic variance was recorded as 1.50 and 3.07, respectively. Moderate genotypic co-efficient of variation (GCV) and high phenotypic co-efficient of variation (PCV) of 17.96 and 25.71 per cent were observed, respectively (Table 4). Naznin *et al.* (2015) found that number of primary branches per 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. Moderate heritability 48.78%, low genetic advance (1.76) and high genetic advance as percent mean 25.83% shows that additive and 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 44.06 (Table 4). The maximum number of secondary branches per plant were found in P1 (10.93) and the minimum number of secondary branches per plant were found in P2 (0.50) followed by P13 (0.87) and P4 (1.57) with mean value 3.99 (Table 3). The maximum no. of secondary branches per plant was showed by P1 (10.93) which is a good sign for increasing the yield and ultimately it showed the maximum yield rather than the others population.

The genotypic and phenotypic variance was recorded as 13.17 and 17.71, respectively. High genotypic co-efficient of variation (GCV) and high phenotypic co-efficient of variation (PCV) of 90.97 and 105.49 per cent were observed, respectively (Table 4). This is an agreement with Parveen *et al*. (2015) and Nazneen *et al.* (2015). Dash *et al*. (2007) observed that secondary branches per plant reflected high estimates of GCV and PCV. High heritability 74.37% and high genetic advance as percent mean 161.62% shows that additive gene effects were present, making selection effective for this trait for the improvement.

4.1.6 Number of siliquae per plant

Number of siliquae per plant ranged from 59.48 to 124.29 with mean value 82.05 in different populations (Table 4). The maximum number of siliquae per plant was noticed in population P9 (124.29) which was statistically similar and followed by population P1 (104.58). The population P3 recorded the minimum number of siliquae per plant (59.48) (Table 3). Naznin *et al.* (2015) observed that the number of siliquae per plant showed the highest range of variation (78.00-180.33) which means the presence of wide range of variation for this character. The mean sum of square reported significant for this trait (1096.62) (Table 4). So, selection for this trait of this population will be effective.

The phenotypic variance (484.60) was higher than genotypic variance (306.01). This indicates influence of environment on this character. High value of genotypic variance indicates the better transmissibility of the character from parent to their offspring (Ushakumari *et al.*, 1991). The high phenotypic coefficient of variation (26.83%) and high genotypic coefficient of variation (21.32%) (Table 4) indicated presence of variability among the populations. The heritability (63.15%) estimates for this trait was high, high genetic advance (28.64) and high genetic advance in per cent of mean (34.90) were found (Table 4). It was revealed that high heritability coupled with high

genetic advance may be due to high values for phenotypic standard deviation as the heritability is high for these characters and selection differential is effective. Thus, these traits could be considerable for improvement of this crop.

4.1.7 Length of siliqua (cm)

The mean of siliqua length was 5.13 cm and ranged from 4.67 to 5.96 cm. The P5 had long length of 5.96 cm which was statistically similar with P9 (5.57 cm). The siliqua were shorter in P6 (4.67 cm) followed by P13 (4.90 cm) and P5 (4.93 cm) (Table 3). The mean sum of square was significant (0.34) which indicated considerable amount of variation for this trait in the populations (Table 4)). Length of siliqua was found maximum in P5 (5.96 cm) (table 3) showed the maximum length of siliqua. So, selection will be effective for this trait of this population.

The genotypic and phenotypic variance for siliqua length was seen as value of 0.08 and 0.18, respectively. Siliqua length exhibited low GCV (5.47%) and PCV (8.25 %) 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. Medium heritability estimates of 43.98%, low genetic advance 0.38 and a low genetic advance as per cent of mean of 7.47% were observed. Medium heritability with combination of low genetic advance as per cent of mean allow us to speculate the presence of non-additive gene effects on this trait. The experimental findings of Naznin *et al.* (2015) also found it.

				
P6	P9	P10	P4	P11
				
P3	P8	P12	P7	P2

Plate 8. Photograph showing siliqua length of some *Brssica rapa* advanced breeding populations

4.1.8 Number of seeds per siliqua

Number of seeds per siliqua ranged from 12.83 to 20.87 in different populations. The maximum number of seeds per siliqua was recorded in population P13 (20.87) and it was statistically similar with P5 (20.43). However, the minimum number of seeds per siliqua exhibited in population P6 (12.83) (Table 3). The mean observed for this trait was 17.22. 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 P13 (20.87) indicated higher yield than the others. So, selection for this trait of this population will be effective.

The genotypic variance was (5.42) and phenotypic variance was (7.66). Moderate GCV and PCV were observed as 13.51 and 16.07 respectively (Table 4). This indicates very little influence of environment upon the character. Whereas, it showed high heritability (70.71%) and high genetic gain as per cent of mean (23.41%) for this trait. High heritability coupled with high genetic advance in percent of mean indicates that the selection for this trait is effective for the improvement of the crop. Akbar *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 3.33 g to 4.53 g. The population P4 was exhibited the maximum thousand seed weight (4.53 g) which was identical and followed by population P6 (4.43 g) and P5 (4.01 g). Whereas, the population P7, P13 and P2 were recorded minimum seed weight of (3.33 g). The grand mean found for this trait was (3.74 g) (Table 3). The mean sum of square was not significant (0.45) (Table) in *Brassica rapa* L. which allows to show the presence of 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 (4.53)

indicating that the seeds of this population are 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 medium PCV (14.51%) and low GCV (7.57%) (Table 4). As PCV is greater than GCV, there is considerable influence of environment on this trait (Table 4). Low heritability (27.20%), low genetic advance (0.30) and low genetic gain as percent of mean (8.13%) was found for this trait. Low 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 P2 (3.53 g) to P1 (7.31 g), with a mean value of 4.78 g. The maximum yield was recorded by the population P1 (7.31 g) followed by P9 (6.53 g). The lowest yield was recorded by the population P2 (3.53 g) followed by P13 (3.57 g) (Table 3). The mean sum of square was significant (3.66) (Table 4). P1 showed the maximum yield (7.31) than the other population which indicates that selection for this trait will be rewarding for improvement.

Yield per plant exhibited high estimates of PCV (26.67%) and GCV (21.06%) in (Table 4). Jahan *et al.* (2013) found high genotypic co-efficient of variation (GCV) for yield per plant by considering genetic parameters. Whereas, it also recorded high heritability (62.35%) and high genetic gain as per cent of mean (34.26%) for this trait. Hussain *et al.* (1998) observed the high estimates for heritability and genetic advance for yield per plant. Selection would be effective for this trait as there is additive gene effects on the gene controlling this trait.

4.2 CORRELATION ANALYSIS

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 13 *Brassica rapa* L. populations studied are presented in (Table 5) .

4.2.1 Days to 50% flowering

Days to 50% flowering showed highly significant and positive correlation with 1000 seeds weight (0.490 and 0.314) at both genotypic and phenotypic levels. Naznin *et al.* (2015) reported that yield per plant had highly significant and positive correlation with days to 50% flowering. But in this study it was negatively correlated with yield per plant (-0.092 and -0.028) at both levels. It exhibited non-significant and positive correlation with secondary braches per plant (0.122 and 0.094), siliqua per plant (0.238 and 0.174) and days to 80% maturity (0.01 and 0.013) at both levels. It also presented significant and negative correlation with plant height (-0.491 and -0.346), length of siliqua (-0.735 and -0.508). It exhibited significant and negative correlation with seeds per siliqua (-0.495 and -0.398) (Table 5).

4.2.2 Days to 80% maturity

Days to 80% maturity showed significant and positive correlation with plant height (0.494 and 0.392), seeds per silqua (0.546 and 0.452) (Table 5) at genotypic and phenotypic level. It was indicated that days to 80% maturity increased the plant height and seeds per siliqua. It had significant and negative correlation with number of primary branches per plant (-0.349) at genotypic level but negative and non-significant (-0.211) correlation at phenotypic level. It had also significant and negative correlation with seed yield per plant (-0.636 and -0.503) and secondary branches per plant (-0.884 and -0.735) at both levels. It had significant and negative correlation with 1000 seeds weight (-0.485) and negative but non-significant correlation (-0.276) at phenotypic level (Table 5). It had also significant and negative correlation with siliqua per plant (-0.534 and -0.422) (Table 5). Non-significant 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 primary branches per plant (0.242 and 0.275). It was significant and negatively associated with number of secondary branches per plant (-0.649 and -0.374) at both genotypic and phenotypic level. It had significant and negative correlation with siliqua per plant (-0.669) at genotypic level but negative and non-significant correlation (-0.279) at phenotypic level. It was highly significant and negatively correlated with 1000 seed weight (-0.652) at genotypic level but non-significant and negatively correlated at phenotypic level (-0.192) (Table 5).

Table 5. Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of *Brassica rapa* L.

Characters		D50%F	D80%M	PH	PBP	SBP	SPP	LS	SPS	TSW
D80%M	G	0.01								
	P	0.013								
PH	G	-0.491**	0.494**							
	P	-0.346*	0.392*							
PBP	G	-0.192	-0.349*	0.242						
	P	-0.115	-0.211	0.275						
SBP	G	0.122	-0.884**	-0.649**	0.512**					
	P	0.094	-0.735**	-0.374*	0.480**					
SPP	G	0.238	-0.534**	-0.669**	0.441**	0.724**				
	P	0.174	-0.422**	-0.279	0.554**	0.710**				
LS	G	-0.735**	-0.291	-0.162	0.526**	0.562**	0.290			
	P	-0.508**	-0.193	-0.230	0.169	0.240	0.045			
SPS	G	-0.495**	0.546**	0.391*	-0.342*	-0.471**	-0.770**	0.464**		
	P	-0.398*	0.452**	0.275	-0.198	-0.425**	-0.559**	0.281		
TSW	G	0.490**	-0.485**	-0.652**	-0.052	0.439**	0.489**	-0.115	-0.689**	
	P	0.314*	-0.276	-0.192	0.114	0.366*	0.210	-0.172	-0.427**	
SYP	G	-0.092	-0.636**	-0.225	0.797**	0.718**	0.848**	0.418**	-0.577**	0.142
	P	-0.028	-0.503**	0.020	0.674**	0.697**	0.801**	0.092	-0.452**	0.123

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

D50%F = Days to 50% flowering, D80%M = Days 80% maturity, PH = Plan height (cm), PBP = Primary branches per plant, SBP = Secondary branches per plant, SPP = Siliqua per plant, LS = Length of siliqua (cm), SPS = Seeds per siliqua, TSW = 1000 seeds weight (g) and SYP = Seed yield per plant (g).

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 (0.512 and 0.480), number of siliquae per plant (0.441 and 0.554), length of siliqua (0.526 and 0.169) and seed yield per plant (0.797 and 0.674) at both genotypic and phenotypic level. Naznin *et al.* (2015) reported that yield per plant had significant positive correlation with number of primary branches per plant. Rashid *et al.* (2007) found number of primary branches had positive and significant correlation with yield per plant. Number of primary branches per plant had negative interaction with seeds per siliqua (-0.342 and -0.198) (Table 5). It had negative and non-significant interaction with thousand seed weight (-0.052) at genotypic level but had positive non-significant interaction with thousand seed weight (0.114) at phenotypic level. Non-significant association of these traits indicated that the association between these traits is largely influenced by environmental factors.

4.2.5 Number of secondary branches per plant

The correlation of number of secondary branches per plant with number of siliquae per plant (0.724 and 0.710), length of siliqua (0.562 and 0.240), 1000 seed weight (0.439 and 0.366) and yield per plant (0.718 and 0.697) was significant and positive which indicated that the traits were less influenced by environment. These findings were shown similar reports by Rashid *et al.* (2007). It had negative and significant correlation with seeds per siliqua (-0.471 and -0.425) (Table 5).

4.2.6 Number of siliquae per plant

Siliqua per plant exhibited significant and positive correlation with seed yield per plant (0.848 and 0.801) and 1000 seed weight (0.489 and 0.210). Ara *et al.* (2010) reported that number of siliquae per plant had positive and significant effect on yield per plant. Islam *et al.* (2016) and Naznin *et al.* (2015) revealed that number of siliquae per plant had significant positive

association with yield per plant. The non-significant and positive interaction was found with siliqua length (0.290 and 0.045) (Table 5). Non-significant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Significant negative association was observed of siliqua per plant with seeds per siliqua (-0.770 and -0.559).

4.2.7 Siliqua length (cm)

Siliqua length was found significant and positive association with seeds per siliqua (0.464) and seed yield per plant (0.418) at genotypic level but it had non significant positive correlation with seed per siliqua (0.281) and and seed yield per plant (0.092) at phenotypic level indicating very little contribution of this trait towards the increase in number of seeds per siliqua and ultimately to yield per plant (Table 5). Length of siliqua was negatively associated with 1000 seed weight (-0.115 and -0.172) at both genotypic and phenotypic level.

4.2.8 Number of seeds per siliqua

Number of seeds per siliqua showed significant and negative interaction with 1000 seed weight (-0.689 and -0.427) and yield per plant (-0.577 and -0.452) both levels indicating that if it was increased 1000 seed weight was decreased and vice versa. In the contrast 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.

4.2.9 Thousand seed weight (g)

Thousand seed weight showed non-significant and positive interaction with yield per plant (0.142 and 0.123) at both genotypic and phenotypic levels (Table 5). 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 path was worked out in the present study (Table 6) 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 (**-0.546**) 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 seeds per siliqua (0.47392) and

secondary branches per plant (0.15401). Further, it showed negligible positive indirect effect towards yield per plant via number of primary branches per plant (0.00221), length of siliqua (0.04018) and days to 80% maturity (0.00817) (Table 6). However, it was recorded negligible negative indirect effect towards yield per plant via plant height (-0.0212) and thousand seed weight (-0.19749). It showed negative and non-significant genotypic correlation (-0.092) with yield per plant.

4.3.2. Days to 80% maturity

Days to maturity found highly positive direct effect (**0.763**) towards yield per plant. Rashid *et al.* (2013) and Naznin *et al.* (2015) demonstrated that days to maturity had positive direct effect towards yield per plant. Further, it recorded positive indirect effect towards yield per plant via 1000 seed weight (0.19585) and negligible positive indirect effect towards yield via plant height (0.02131), number of primary branches per plant (0.00402), siliqua per plant (0.01084) and length of siliqua (0.01593) (Table 6). However, it was recorded negative indirect effect towards yield per plant via seeds per siliqua (-0.52292), secondary branches per plant (-1.1182) and days to 50% flowering (-0.0055). It showed negative and significant genotypic correlation (-0.636) with yield per plant.

4.3.3 Plant height (cm)

Plant height recorded negligible positive direct effect (**0.043**) towards yield per plant. In the contrast, Uddin *et al.* (2013) found that plant height had the negative direct effect on yield per plant. In the present study the genotypic correlation was negative and non- significant (-0.225) with yield per plant (Table 6). Further, it was recorded positive indirect effect towards yield per plant via days to 50% flowering (0.26809), days to 80% maturity (0.37692) and 1000 seed weight (0.26297). However, it was found negligible positive indirect effect towards yield per plant via siliqua per plant (0.01359) and length of siliqua (0.00885). Naznin *et al.* (2015) observed positive indirect

effect on seed yield per plant through length of siliqua. It showed negative indirect effect towards yield per plant via secondary branches per plant (-0.8214) and seeds per siliqua (-0.37398) and negligible negative indirect effect towards yield per plant via primary branches per plant (-0.00279).

4.3.4 Number of primary branches per plant

Number of primary branches per plant recorded negligible negative direct effect (**-0.012**) 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 seeds per siliqua (0.32764), days to 50% flowering (0.10483), plant height (0.010406) and thousand seed weight (0.02116) and negligible negative indirect effect towards yield per plant via days to 80% maturity (-0.26629), siliqua per plant (-0.009) and length of siliqua (-0.0288) (Table 6). However, it was found highly positive indirect effect towards yield per plant via number of secondary branches per plant (0.64797). The correlation was highly significant and positive (0.797) with yield per plant.

4.3.5 Number of secondary branches per plant

Number of secondary branches per plant observed highest positive direct effect (**1.265**) under this study towards yield per plant. It was also recorded positive indirect effects to yield per plant via seeds per siliqua (0.45103) (Table 6). Naznin *et al.* (2015) observed number of secondary branches per plant had high positive indirect effect on yield. On the other hand, it was found negligible negative indirect effect towards yield per plant through days to 50% flowering (-0.0666), plant height (-0.02791), number of primary branches per plant (-0.00614), siliqua per plant (-0.0147), 1000 seed weight (-0.17726) and length of siliqua (-0.0307) and highly negative indirect effect via days to 80% maturity (-0.67449). The genotypic correlation of number of secondary branches per plant (0.718) with yield per plant was positive and highly significant.

4.3.6 Number of siliquae per plant

Number of siliquae per plant exhibited low negative direct effect (**-0.02**) towards yield per plant. In distinguish; Uddin *et al*. (2013) observed that number of siliquae per plant had the positive direct effect on seed yield per plant. However, it showed highly positive indirect effect towards yield per plant via secondary branches per plant (0.91586) and seeds per siliqua (0.73709). It was negative indirect effect to yield via days to 50% flowering (-0.1299), days to 80% maturity (-0.40744), plant height (-0.02877), number of primary branches per plant (-0.00529), length of siliqua (-0.0159) and 1000 seed weight (-0.19708) (table 6). Islam *et al.* (2015) found negative indirect effect on number of siliquae per plant. The genotypic correlation of number of siliquae per plant (0.848) with yield per plant was positive and highly significant.

4.3.7. Siliqua length (cm)

Siliqua length showed negligible negative direct effect (**-0.055**) towards yield per plant. It was found negligible positive indirect effect towards yield per plant via 1000 seed weight (0.04657) and high positive indirect effect via secondary branches per plant (0.71093) and days to 50% flowering (0.40131). Islam *et al.* (2016) also found positive indirect effect of siliqua length towards yield. On the other hand, it was also recorded negligible negative indirect effects to yield per plant via days to maturity (-0.22203), plant height (-0.00697), number of primary branches per plant (-0.00631), siliqua per plant (-0.016) and seeds per siliqua (-0.4442) (Table 6). The genotypic correlation of siliqau length (0.418) with yield per plant was positive and highly significant.

Table 6. Partitioning of genotypic correlations into direct (bold) and indirect effects of important characters by path analysis of *Brassica rapa* L.

	D50%F	D80%M	PH	PBP	SBP	SPP	LS	SPS	TSW	Genotypic correlation with yield
D50%F	**-0.546**	0.00817	-0.0212	0.00221	0.15401	-0.0048	0.04018	0.47392	-0.19749	-0.092
D80%M	-0.0055	**0.763**	0.02131	0.00402	-1.1182	0.01084	0.01593	-0.52292	0.19585	-0.636**
PH	0.26809	0.37692	**0.043**	-0.00279	-0.8214	0.01359	0.00885	-0.37398	0.26297	-0.225
PBP	0.10483	-0.26629	0.010406	**-0.012**	0.64797	-0.009	-0.0288	0.32764	0.02116	0.797**
SBP	-0.0666	-0.67449	-0.02791	-0.00614	**1.265**	-0.0147	-0.0307	0.45103	-0.17726	0.718**
SPP	-0.1299	-0.40744	-0.02877	-0.00529	0.91586	**-0.02**	-0.0159	0.73709	-0.19708	0.848**
LS	0.40131	-0.22203	-0.00697	-0.00631	0.71093	-0.016	**-0.055**	-0.4442	0.04657	0.418**
SPS	0.27027	0.4166	0.016813	0.004104	-0.5958	0.04235	-0.0255	**-0.957**	0.27782	-0.577**
TSW	-0.2675	-0.37006	-0.02804	0.000624	0.55534	-0.0269	0.00633	0.65937	**-0.403**	0.142

Residual effect: **0.091** ** = Significant at 1%.

D50%F = Days to 50% flowering, D80%M = Days 80% maturity, PH = Plan height (cm), PBP = Primary branches per plant, SBP = Secondary branches per plant, SPP = Siliqua per plant, LS = Length of siliqua (cm), SPS = Seeds per siliqua, TSW = 1000 seeds weight (g) and SYP = Seed yield per plant (g).

4.3.8 Number of seeds per siliqua

Number of seeds per siliqua showed negative direct effect (**-0.957**) towards yield per plant. Further, it was recorded high positive indirect effect towards yield per plant via days to 80% maturity (0.4166), days to 50% flowering (0.27027) and thousand seed weight (0.27782) and negligible positive indirect effect via plant height (0.016813), primary branches per plant (0.004104) and number of siliquae per plant (0.04235) (Table 6). It also found high negative indirect effect towards yield per plant via secondary branches per plant (-0.5958). It also recorded negligible negative effect towards yield per plant via length of siliqua (-0.0255). It had highly significant and negative genotypic correlation (-0.577) with yield per plant.

4.3.9 Thousand seed weight (g)

Thousand seed weight showed negative direct effect (**-0.403**) towards yield per plant. In contrast, Parveen *et al.* (2015) revealed that thousand seed weight had the maximum direct effect towards yield per plant. Further, it was recorded high positive indirect effect towards yield per plant via seeds per siliqua (0.65937) and secondary branches per plant (0.55534) (Table 6). It also reported negligible negative indirect effect towards yield per plant via days to maturity (-0.37006), days to 50% flowering (-0.2675), plant height (-0.02804) and number of siliqua per plant (-0.0269). Naznin *et al.* (2015) found negative indirect effect for thousand seed weight towards yield per plant. The trait was genotypically positive and non-significant (0.142) correlated with yield per plant.

4.3.10 Residual effect

The magnitude of residual effect (**0.091**) indicated that traits included in the path analysis explained about 90.9% of the variation in yield. However, the remaining variation in yield (9.1%) 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 0.43 in case of yield per plant.

4.4 ANALYSIS OF FATTY ACID

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. 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). Analysis of fatty acids of 5 populations was done and the results were shown below:

4.4.1 Saturated fatty acid (%)

In the present investigation, saturated fatty acid content in the population of *Brassica rapa* L. ranged from 9.22% to 6.92%. The highest was found in P9 (9.22%) and the lowest was found in P7 (2.37%) (Table 7).

4.4.1.1 Palmitic acid (C16:0)

Population P11 was observed to have highest amount of palmitic acid (2.68%) followed by P12 (2.15%) and the lowest found in P7 (1.68%) (Table 7). 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 P7 (1.68%) 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 P11 (0.74%) followed by P12 (0.73%) and lowest was found in P9 (0.49%). 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 P9 (0.49%) can be selected for this trait. Figure.5 is presented showing relative content of stearic acid percentage.

Table 7. Percentage allotments of the most important saturated fatty acids in oil of five *Brassica rapa* genotypes detection by gas liquid chromatography

Population		SATURATED FATTY ACID (%)						
		Myristc ($C_{16:0}$)	Palmitic ($C_{16:0}$)	Stearic ($C_{18:0}$)	Arachidic ($C_{20:0}$)	Behenic ($C_{22:0}$)	Lignoceric ($C_{24:0}$)	Total
Tori-7 X BARI sarisha-15	P7	0.033	1.68	0.567	4.42	0.03	0.19	6.92
BARI sarisha-9 X BARI sarisha-6 (S_5F_{15})	P9	0.04	1.83	0.49	6.6	0.02	0.24	9.22
SAU sarisha-1X BARI sarisha-15 (F_7) BULK	P11	0.19	2.68	0.74	3.61	0.03	0.26	7.51
SAU sarisha-1 X BARI sarisha-15 (F_6)	P12	0.11	2.15	0.73	5.72	0.05	0.19	8.95
BARI sarisha-6 X BARI sarisha-15 (F_9)	P13	0.09	1.84	0.67	5.21	0.08	0.35	8.24

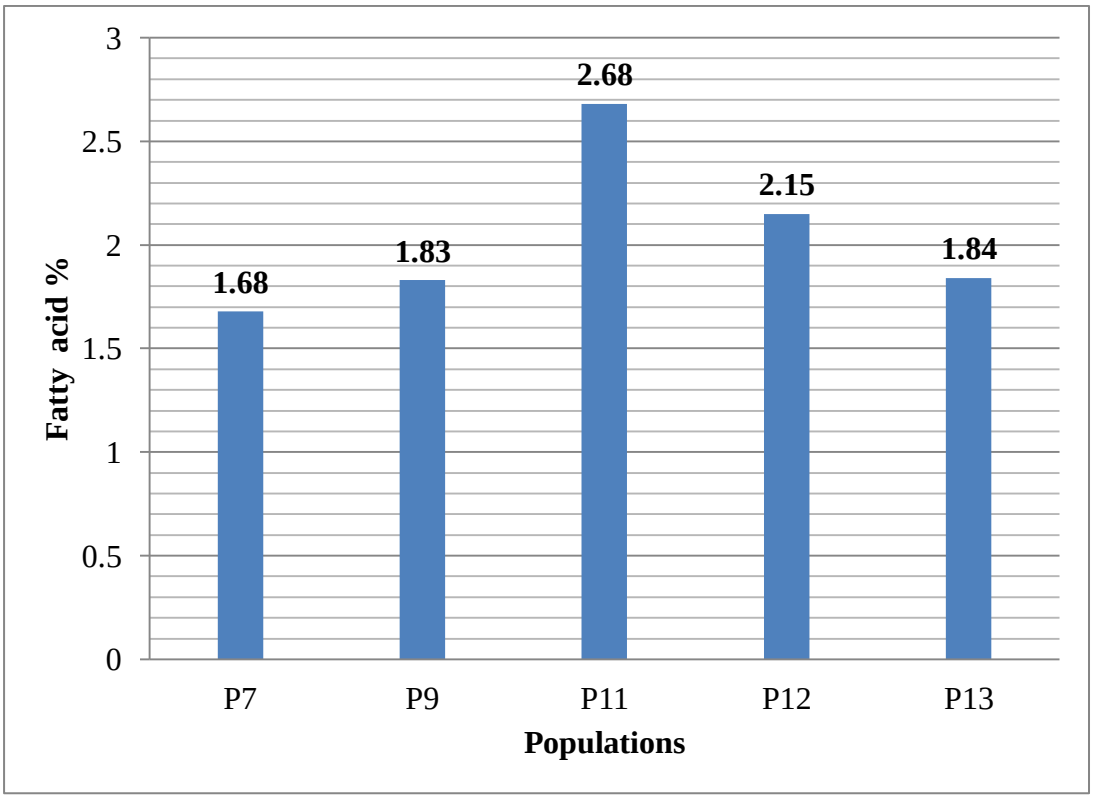


Figure 3. Palmitic acid content (%) of five populations

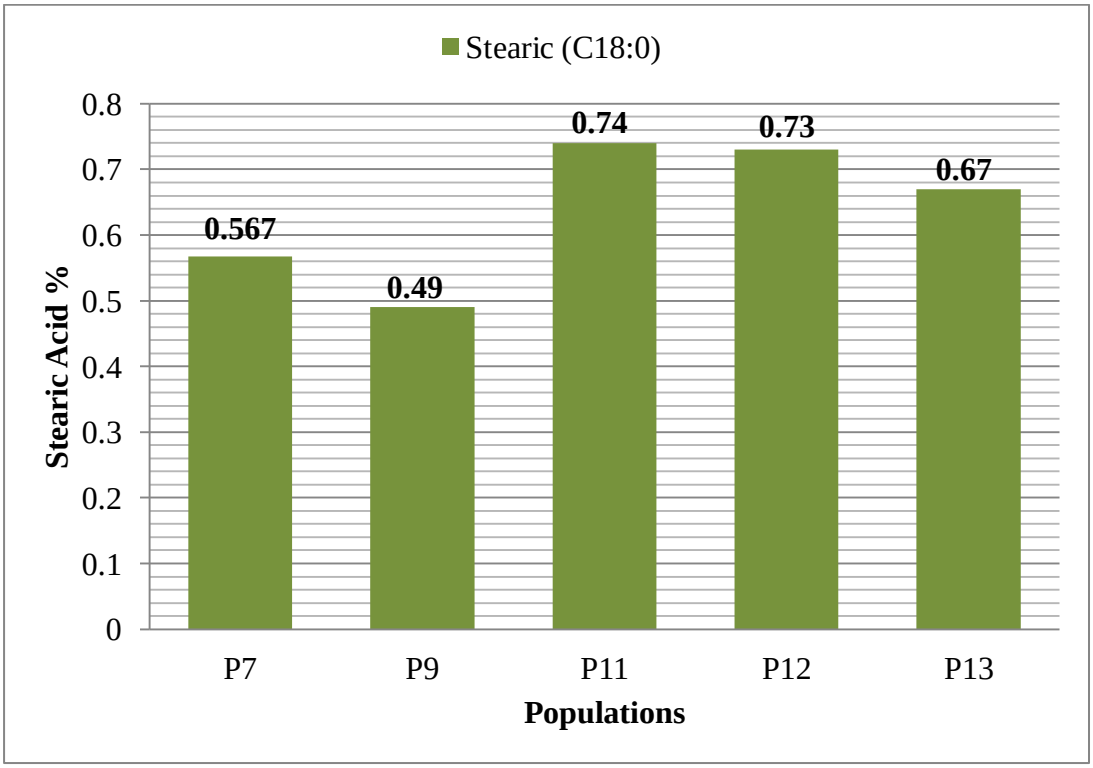


Figure 4. Stearic acid content (%) of five populations

4.4.2 Unsaturated fatty acid (%)

Total unsaturated fatty acid ranged from 93.08% to 90.79%. Population P9 was found the lowest amount of unsaturated fatty acid (90.79%) followed by P12 (91.06%), P13 (91.76%) and P7 was found the highest (93.08%) (Table 8).

4.4.2.1 Oleic acid (C18:1)

Population P7 (11.27%) had the lowest amount of oleic acid content and followed by P13 (13.63%) and population P12 (15.16%) had the highest amount of oleic acid (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 P12 (15.16%) 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 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 P12 (54.08%) follwed by P9 (54.79) and maximum found in P7 (60.75%) among five 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.

Table 8. Percentage allotments of the most important unsaturated fatty acids in oil of six *Brassica rapa* genotypes detection by gas liquid chromatography

Variety	Population	UNSAURAED FATTY ACID (%)					
		Mono			Poly		Total
		Palmitolic ($C_{16:1}$)	Oleic/omega-9 ($C_{18:1}$)	Erucic acid ($C_{22:1}$)	Linoleic/omega-6 ($C_{18:2}$)	Linolenic/omega-3 ($C_{18:2}$)	
Tori-7 X BARI sarisha-15	P7	0.05	11.27	60.75	12.53	8.48	93.08
BARI sarisha-9 X BARI sarisha-6 (S_5F_{15})	P9	0.02	14.77	54.79	12.83	8.38	90.79
SAU sarisha-1X BARI sarisha-15 (F_7) BULK	P11	0.03	14.98	56.95	13.85	6.69	92.5
SAU sarisha-1 X BARI sarisha-15 (F_6)	P12	0.05	15.16	54.08	13.21	8.56	91.06
BARI sarisha-6 X BARI-sarisha15 (F_9)	P13	0.05	13.63	55.16	14.27	8.65	91.76

4.4.2.3 Linoleic acid (C18:2)

Population P13 (14.27%) showed the highest amount of linoleic acid and population P7 (12.53%) showed the lowest amount. Auld *et al.* (1992) found 2.1% linoleic acid in their experiment. Linoleic acid has become popular for its industrial purposes. So, P13 (14.27%) can be selected for this trait. Scarth *et al.* (1988) found 28% linoleic acid. Figure 9 is presented showing relative content of linoleic acid percentage.

4.4.2.4 Linolenic acid (C18:3)

Higher amount of linolenic acid was found in P13 (8.65%) and lower was found in P11 (6.69%). It prevents cardiovascular disease. So, P13 (8.65%) 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.

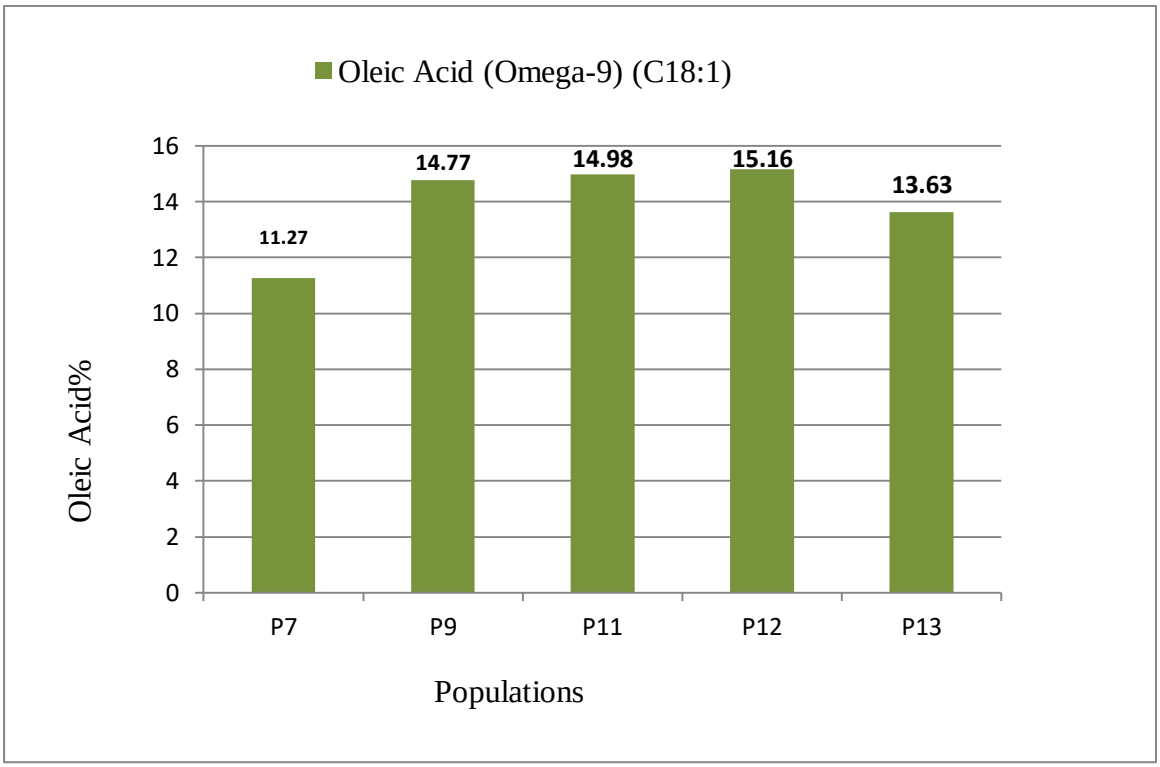


Figure 5. Oleic acid content (%) of five populations

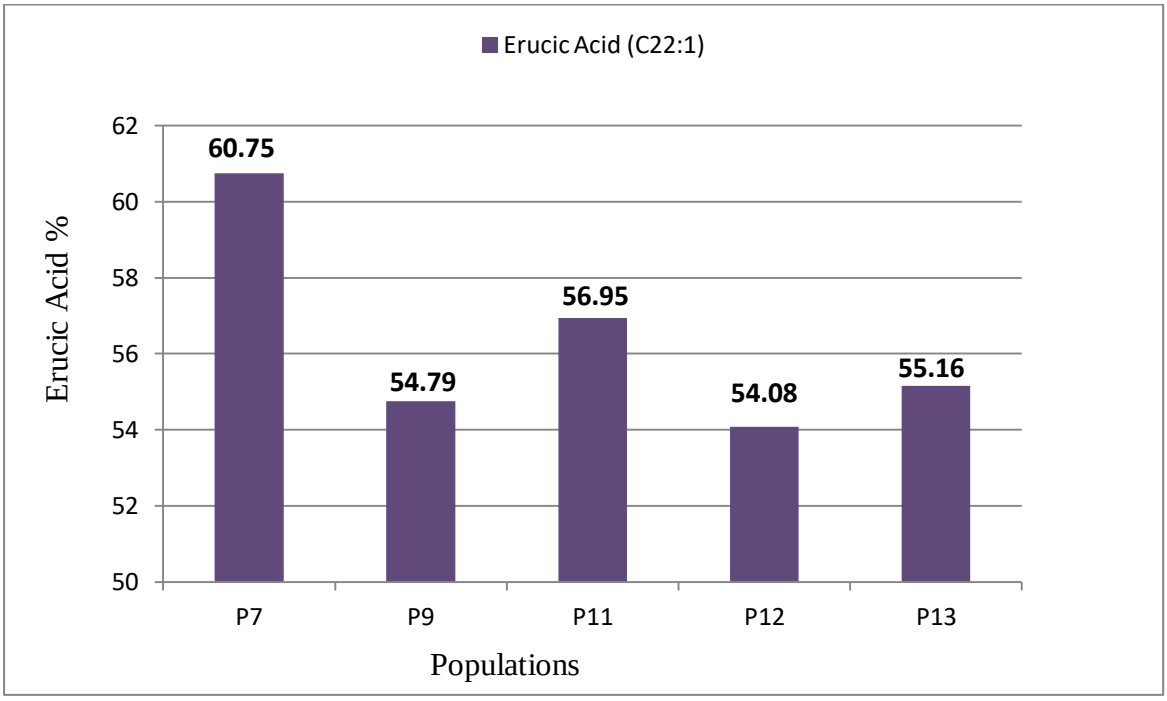


Figure 6. Erucic acid content (%) of five populations

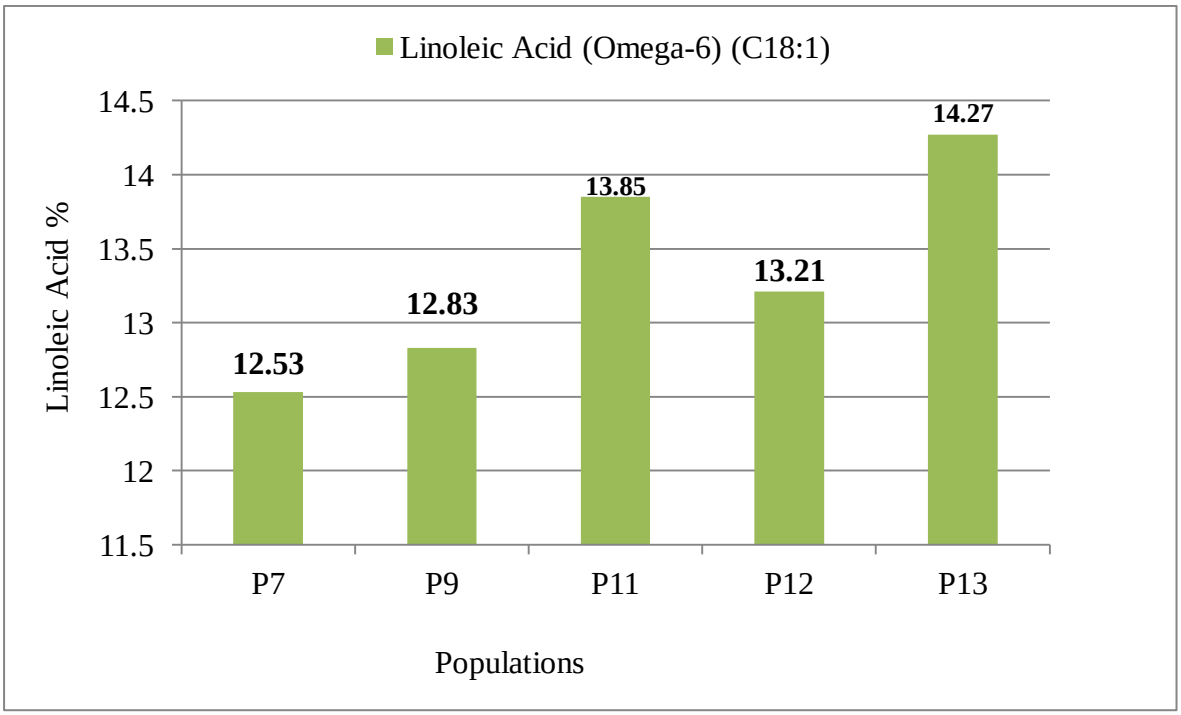


Figure 7. Linoleic acid content (%) of seven populations

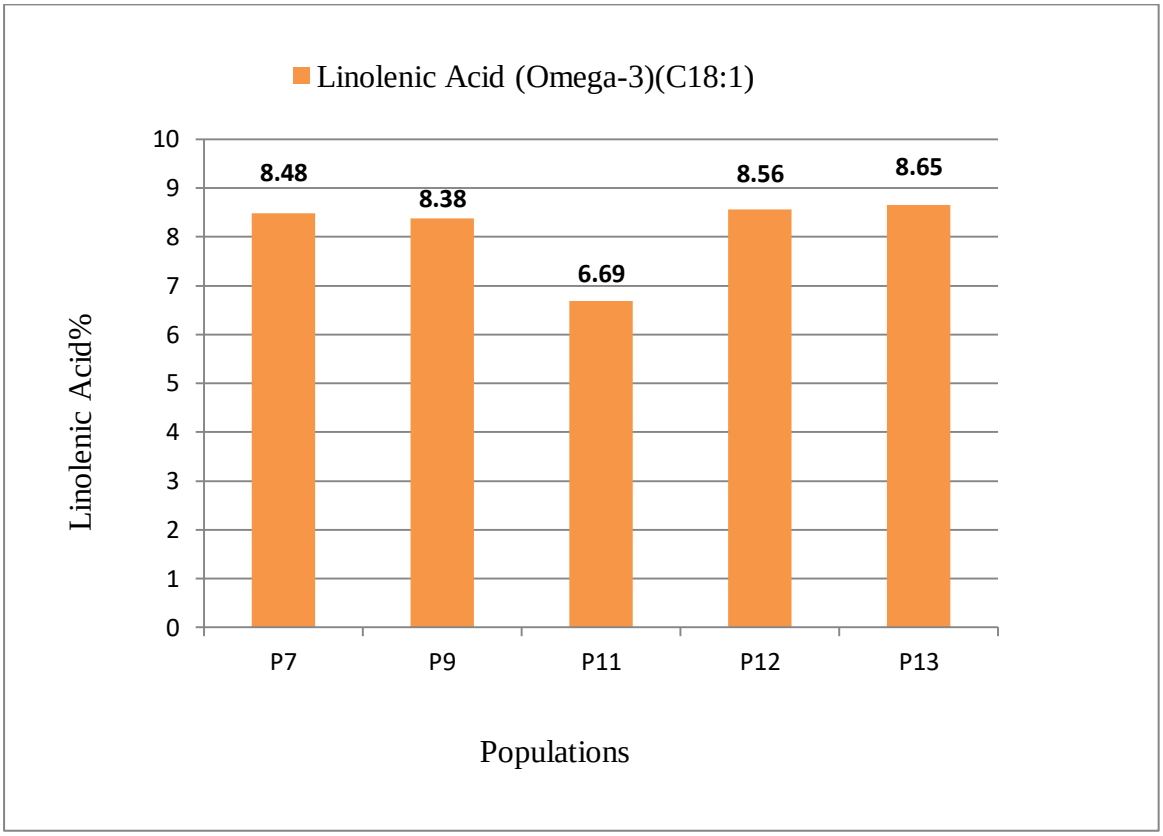


Figure 8. Linolenic acid content (%) of five populations

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 high 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 13 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. P1 (SAU sarisha-2 X BARI sarisha-15 F_7)

Average number of siliqua of P1 was recorded 104.58 (Table 9). The average thousand seed weight was recorded as 3.79 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 7.31 g (Table 9) which was higher than Tori-7 (6.82 g) (plate 9).

4.5.2. P9 (BARI sarisha-9 X BARI sarisha-6 S_5F_{15})

Average number of siliquae per plant of P9 was recorded 124.29 (Table 9) which was higher than BARI sarisha-15 (120.40). This population was recorded with average thousand seed weight 3.57 g by the duration 81.33 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 10).

4.5.3. P12 (SAU sarisha-1 X BARI sarisha-15 F_6)

Average number of siliquae per plant of P12 was recorded 85.54 (Table 9). This population was recorded with average thousand seed weight 3.60 g (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.

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

Population	D80%M	SPP	TSW	SYP
P1 (SAU sarisha-2 X BARI sarisha-15 F_7)	78.00	104.58	3.79	7.31
P9 (BARI sarisha-9 X BARI sarisha-6 S_5 F_{15})	81.33	124.29	3.57	6.53
P12 (SAU sarisha-1 X BARI sarisha-15 F_6)	89.00	85.54	3.60	5.40

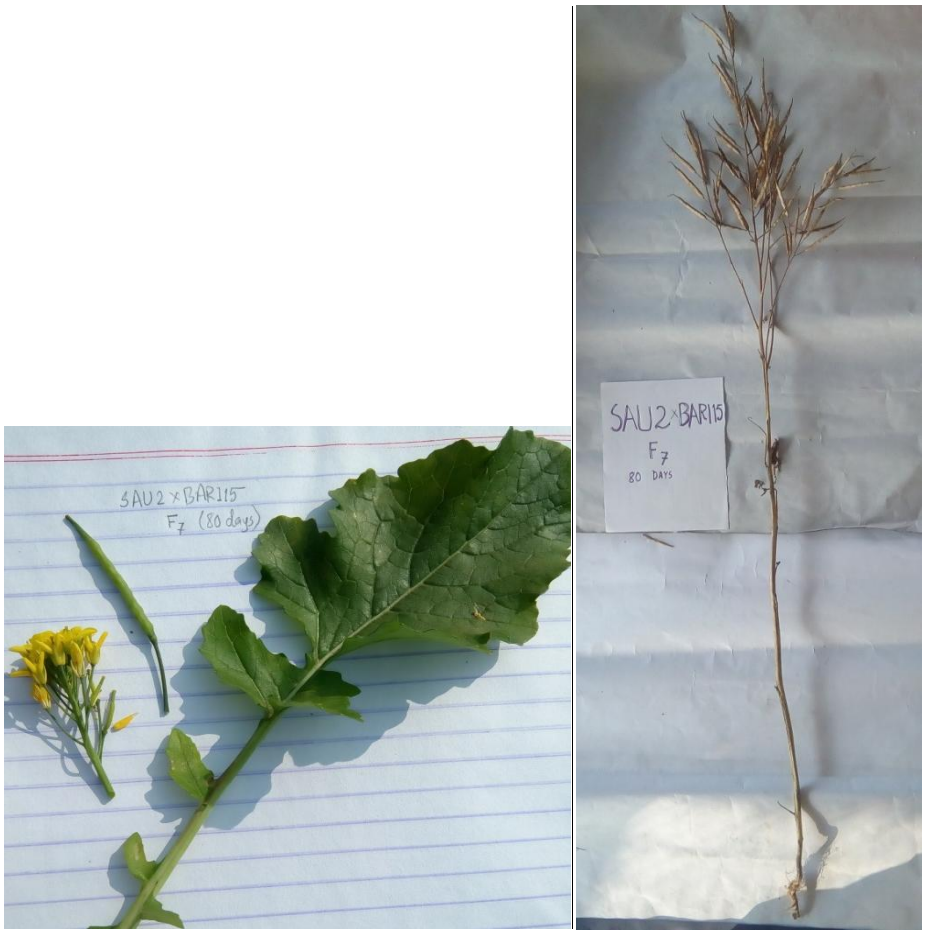


Plate 9. Photograph showing plants of P1

Plate 10. Photograph showing plants of P9

Plate 11. Photograph showing plants of P12

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 13 advanced breeding populations 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, 2017 to February, 2018.

The study exhibited wide range of variability for most of the characters studied. The lowest days to 50% flowering (33.00 days) was found in P5 followed by P3 (33.67 days). The lowest days to maturity (78.00 days) were observed in P1 followed by P3 (80.00 days). Plant height exhibited highest in P1 (111.47 cm) and lowest (80.77 cm) in P6. The highest number of primary branches per plant (10.33) was recorded in P1. The highest number of secondary branches per plant (10.93) was observed in P1. The highest number of siliquae per plant (124.29) was in P9. The lowest length of siliqua (4.67 cm) was recorded in P6and the highest length of siliqua (5.96 cm) was remarked

in P5. The number of seeds per siliqua (20.87) was found highest in P13. The thousand seed weight exhibited the highest (4.53 g) in P4 followed by P6 (4.43 g). The yield per plant was maximum (7.31 g) in P1 followed by P9 (6.53 g). So, these populations for these traits can be used for future trial.

The phenotypic variance of the materials was considerably higher 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 and yield per plant 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 80% maturity, plant height, number of sliliqua 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 high genotypic and phenotypic coefficient of variation (GCV and PCV) was observed for the characters e.g. number of secondary branches per plant (90.97% and 105.49%), number of siliquae per plant (21.32% and 26.83%) and yield per plant (21.06% and 26.67%) indicating these characters 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 coupled with high genetic advance in percent of mean were observed for days to 50% flowering (95.42% and 30.87%), number of secondary branches per plant (74.37% and 161.62%), siliqua per plant (63.15% and 34.90%), number of seeds per siliqua (70.71% and 23.41) and yield per plant (62.35% and 34.26%) and selection based on these characters may result in development of high yielding populations.

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 (0.797 and 0.674), secondary branches per plant (0.718 and 0.697) and number of siliquae per plant (0.848 and 0.801) at both genotypic and phenotypic level (Table 5). It shows that yield per plant in *Brassica rapa* L. can be improved by making direct selection based on these traits.

Path co-efficient analysis for yield per plant revealed that number of secondary branches per plant exerted highest direct effect on the yield (**1.265**) followed by days to 80% maturity (**0.763**). The indirect contribution of component characters *viz.* number of siliqua per plant was high indirect effect via secondary branches per plant (0.91586), number of seeds per siliqua (0.73709) towards seed yield per plant (Table 6).

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 P7 (1.68%). The lowest amount of stearic acid was found in P9 (0.49%). Population P12 (15.16%) had the highest amount of oleic acid content. Minimum amount of erucic acid was found in P12 (54.08) among five populations used in quality test. Population P13 (14.27%) was found the highest amount of linoleic acid. Higher amount of linolenic acid was found in P13 (8.65%) (Table 8). As low percentage of erucic, 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. Based on the variability and as per our objectives three most promising populations P1 (SAU sarisha-2 X BARI sarisha-15 F7 80 DAYS), P9 (BARI sarisha-9 X BARI sarisha-6 S_5F_{15}) and P12 (SAU sarisha-1 X BARI sarisha-15 F_6) with short duration and higher yield were selected from the 13 populations. Among the populations the highest yield per plant (7.31 g) was found in P1 (SAU sarisha-2 X BARI sarisha-15 F7). It was also matured early (78.00 days). So, these populations possessed excellent potential for use in future trial.

REFERENCES

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

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

Ackman, R.G., Eaton, C.A., Sipos J.C., Loew F.W. and Hancock, D. (1977). Comparison of fatty acid from high levels of erucic acid of RSO and partially hydrogenated fish oil in non-human primate species in a short term exploratory study. *Nutr. Diet*. **25**: 170-185.

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

Afrin, 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.

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

Ahmad B., Mohammad S., Azam F., Ali I., Ali J., and Rehman S. (2013). Studies of Genetic Variability, Heritability and Phenotypic Correlations of Some Qualitative Traits in Advance Mutant Lines of Winter Rapeseed (*Brassica napus* L.), American-Eurasian Journal of Agricultural & Environmental Science, **13**(4): 531-538.

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.

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

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

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

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.

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

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.

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

BBS (Bangladesh Bureau of Statistics). (2016). Statistical Yearbook of Bangladesh. Bangladesh Bureau of Statistics, Stat. Div., Ministry Planning, Govt. Peoples Rep. Bangladesh, Dhaka. p. 345.

BBS (Bangladesh Bureau of Statistics). (2017). Statistical Yearbook of Bangladesh. Bangladesh Bureau of Statistics, Stat. Div., Ministry Planning, Govt. Peoples Rep. Bangladesh, Dhaka. p. 477.

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.

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

Choudhary, B.R. and Joshi, P. (2003). Genetic diversity in advanced derivatives of Brassica interspecific hybrids. *Euphytica*. **121**(1): 1-7.

Cochran, W.G. and Cox, G. (1957). Experimental design. W.S John,(2^{nd}ed.). 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.

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

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

FAOSTAT. (2017). Food and Agriculture Organization of the United Nations, FAOSTAT. FAO Statistics Division.

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.

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

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.

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.

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

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. (2013). Variability among advanced lines in Brassica rapa. MS thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

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

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.

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.

Katiyar. B.S.. Lee, J. I. and Chae, Y.A. (1974). Genetic studies on some agronomic characters in rapeseed. *Korean J. Breed.* **21**(1): 22-27.

Khaleque, M.A. (1985). A guidebook on production of oil crops in Bangladesh. DAE and FAO/ UNDP project BGA/79/034, strengthening the Agricultural Extension Service Khamarbari, Farmgate, Dhaka.

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

Khan, M.H., Bhuiyan, 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.

Khulbe, R. K., Pant, D. P. and Naveen Saxena. (2000). Variability, heritability and genetic advance in Indian mustard [Brassica juncea (L.) Czern & Coss]. *Crop Research* (*Hisar*). **20**(3):551-552.

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. J. of the Korean Society of Plant Res.***30**(6): 590-600.

Kramer, J. K. G., Farnworth, E. R., Thompson, B. K., Corner, A. H. and Trenholm. H. L. (1982). Reduction of myocardial necrosis in male albino rats by manipulation of dietary fatty acid levels. *Lipids.* **17**(5):372-382.

Kumar, S. (2013). Genetic analysis of oil content and quality parameters in Indian mustard (Brassica juncea (L.) Czern and Coss). *Scholarly J. Agric. Sci.*, **3**(8): 299-304.

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.

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.

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

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.

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

Mary, S.S. and Gopalan, A. (2006). Dissection of genetic attributes yield traits of fodder cowpea in F3 and F4. *J. Appl. Sci. Res.* **2**: 805-808.

Masood. T.. Gilani. M.M. and Khan, F.A. (1999). Path analysis of the major yield and quality characters in *Brassica canspestris*. *Ant. Pt. Scl*. **9**(4): 69-72.

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

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

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

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.

Muhammad, A., Raziuddin, A Muhammad, I Ali. (2014). Combining Ability and Heritability Studies for Important Traits in F_2 of *Brassica Napus*. *Intl. J. Basic & Appl. Sci.* **14**(01):07-11.

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

Nath, U. K., H T Kim, K. Khatun, Jong-In Park, Kwon-Kyoo Kang, Ill-Sup Nou. (2016). Modification of Fatty Acid Profiles of Rapeseed (*Brassica napus* L.) Oil for Using as Food, Industrial Feed-Stock and Biodiesel. *Plant Breed. Biotech.* **4**(2):123~134.

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.

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

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.

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

Parveen, S. (2007). Variability study in F2 progenies of Inter-varietal crosses of *Brassica rapa*. MS Thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.

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.

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.

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

Rahman, L. 1981. Oil Seed Research & Development Activities at BAU. Proc. of the workshop on Oil Crop Improvement, BARI. Oilseed Research Project. Ed. By Khaleque M.A., A.B.M. Abul Khair, Md. Ali Akbar and Md. Moszammal Haque. Pp. 25.

Rao, C.R. (1952). Advanced statistical methods in biometrical research. J. Willey,(1^{st}ed.). CMP, London. p.402.

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

Rashid, M.H.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.

Roy, S. K., S. Haque, V. A. Kale, D. S. Asabe and S. Dash. (2011). Variability and character association studies in rapeseed-mustard (*Brassica* sp.). *J. Crop and Weed.*, **7**(2).108-112.

Sabaghnia, N., Dehghani, H.B. Alizadeh and Mohghaddam, M. (2010). Heterosis and combining ability analysis for oil yield and its components in rapeseed. *Aust. J. Crop Sci.*, **4**(6): 390-397.

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.

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

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

Shen. J.X.. Fu, 1W., Yang, 0.5.. Shcn, J.X., Pu. T.D. and Y.9. G.S. (2002). 1 - leterosis of double low , self incompatibility in oilsecd rape (lJrcssica rapa L.). *Chinese Agrif. ScL.* **7**(i): 732-737.

Shukla, S., Bhargava, A., Chatterjee, A., Srivastava, A. and Singh, S.P. (2006). Genotypic variability in vegetable amaranth (*Amaranthus*

tricolor L.) for foliage yield and its contributing traits over successive cuttings and years. Euphytica. **151**: 103-110.

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.

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

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, D., Arya, R. K., Chandra, N., Niwas, R. and Salisbury, P. (2010). Genetic diversity studies in relation to seedyield and its component traits in Indian mustard(*Brassica juncea*). J. *Oilseed Brassica*, **1**:19-22.

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.

Sonntag, N. O. V. (1991). Erucic, behenic: Feedstocks of the 21st century. INFORM **2**(5): 449-463.

Sood, S.K., Sharma, D., Kumar, S. and Lakhanpal, T.N. (2010). Healing Herbs: Traditional Medications for Wounds, Sores and Bones. Pointer Publishers, Jaipur, India.

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

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

Tahira, Mahmood, T., Tahir, M. S., Saleem, U., Hussain, M. and Saqib, M. (2011). The estimation of heritability, association and selection criteria for yield components in mustard (*Brassica juncea*). *Pakistan J. Agric. Sci.* **48** (4):251-254.

Technical Report (2003). Food Standards Australia New Zealand. Erucic acid in food: A toxicological review and risk assessment. Tech. Report Series. **21**:1448-3017.

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

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

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.

USDA, (2000). National Nutrient Database. Entry for mustard oil in the USDA. National Nutrient Database for Standard Reference, Release 22.

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.

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

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

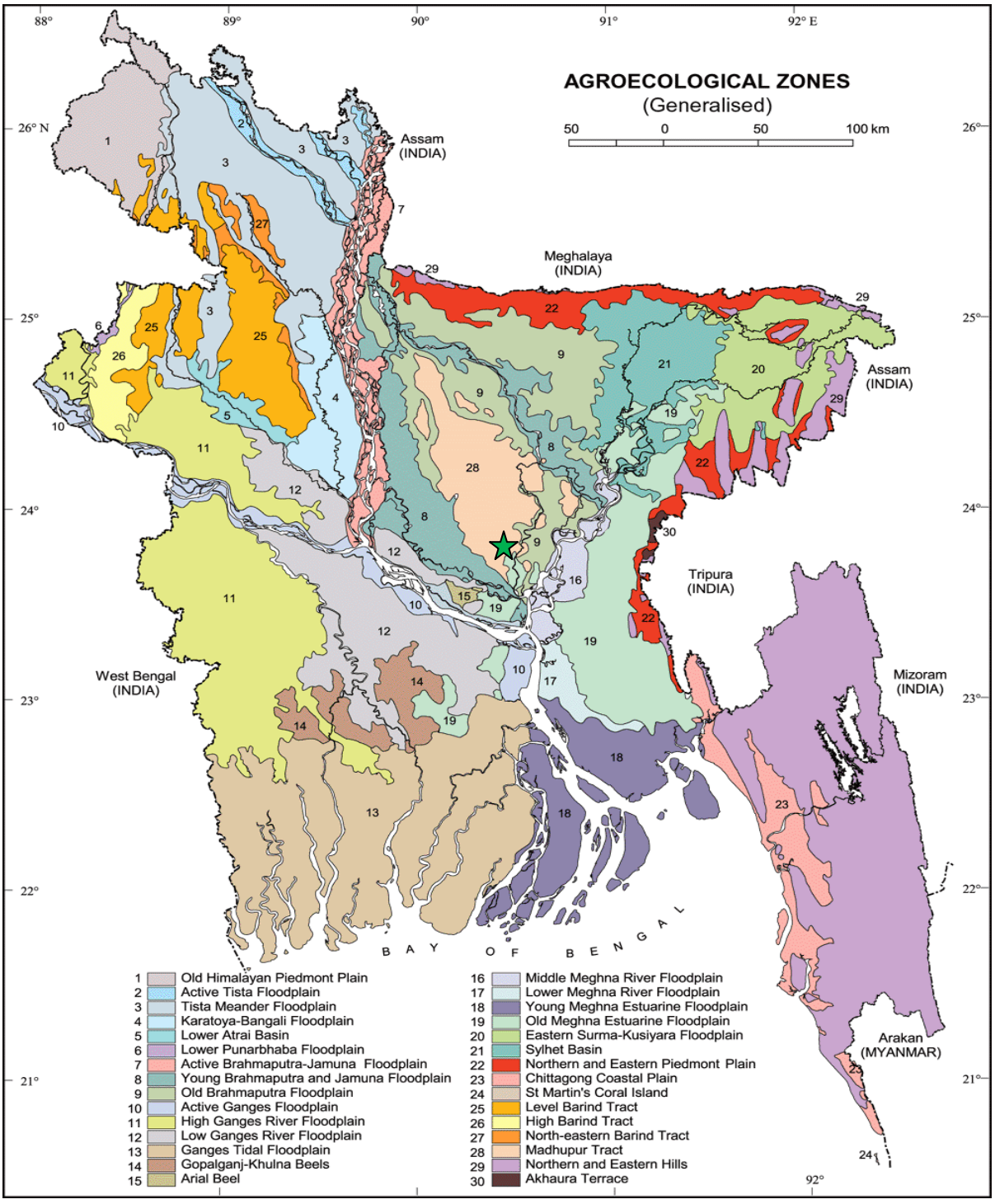
Wright, S. (1921). Correlation and causation. *J. Agric. Res*. **20**: 557-585.

Yadava V.P., Deb S. and Singh H. (1996). Morpho-physiological determinates of yield under water stress conditions in Indian Mustard. *Acta Hort.* **407**: 155-60.

Yared S., and Misteru T., (2016). Variability, Heritability and Genetic Advance Analysis for Some Morphological Characters in Oilseed Brassica Breeding Lines. *Mol. Plant Breed*., **7**(20): 1-8.

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

Appendix I. Map showing the experimental site under the study



★ The experimental site under the study

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

A. Morphological characteristics of the experimental field

Morphological features	Characteristics
Location	Sher-e-Bangla Agricultural University Research Farm, Dhaka
AEZ	AEZ-28, Modhupur Tract
General Soil Type	Deep Red Brown Terrace Soil
Land type	High land
Soil series	Tejgaon
Topography	Fairly leveled

B. Physical composition of the soil

Soil separates	**%**	**Methods employed**
Sand	26	Hydrometer method (Day, 1915)
Silt	45	Do
Clay	29	Do
Texture class	Silty loam	Do

C. Chemical composition of the soil

Sl. No.	**Soil characteristics**	**Analytical data**	**Methods employed**
1	Organic carbon (%)	0.45	Walkley and Black, 1947
2	Total N (%)	0.03	Bremner and Mulvaney, 1965
3	Total S (ppm)	225.00	Bardsley and Lanester, 1965
4	Total P (ppm)	840.00	Olsen and Sommers, 1982
5	Available N (kg/ha)	54.00	Bremner, 1965
6	Available P (ppm)	20.54	Olsen and Dean, 1965
7	Exchangeable K (me/100 g soil)	0.10	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	pH (1:2.5 soil to water)	5.6	Jackson, 1958
10	CEC	11.23	Chapman, 1965

Source: Soil Resource and Development Institute (SRDI), Farmgate, Dhaka

Appendix III. Monthly average temperature, relative humidity and total rainfall and sunshine of the experimental site during the period from November, 2017 to February, 2018.

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
November, 2017		18.0	77	227	**5.8**
December, 2017	32.4	16.3	69	0	**7.9**
January, 2018	29.1	13.0	79	0	**3.9**
February, 2018	**28.1**	**11.1**	**72**	**1**	**5.7**

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