# VARIABILITY STUDY IN EIGHT ADVANCED POPULATIONS OF *Brassica rapa* L.

**SHAKILA AKTER**

**DEPARTMENT OF GENETICS AND PLANT BREEDING**

**SHER-E-BANGLA AGRICULTURAL UNIVERSITY**

**DHAKA-1207**

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# VARIABILITY STUDY IN EIGHT ADVANCED POPULATIONS OF *Brassica rapa* L.

**BY**

**SHAKILA AKTER**

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**Approved by:**

| | |
|---|---|
| **(Prof. Dr. Md. Shahidur Rashid Bhuiyan)** | **(Prof. Dr. Md. Sarowar Hossain)** |
| **Supervisor** | **Co-supervisor** |

**(Prof. Dr. Kazi Md. Kamrul Huda)**
**Chairman**
**Examination Committee**

Dr. Md. Shahidur Rashid Bhuiyan
Professor
Department of Genetics and Plant Breeding
Sher-e-Bngla-Agricultural University
Dhaka-1207
Email: ipbscfc2009@gmail.com
Mobile no.: 01552467945

# CERTIFICATE

This is to certify that thesis entitled, **"VARIABILITY STUDY IN EIGHT ADVANCED POPULATIONS OF *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 **SHAKILA AKTER**, Registration No. **13-05654** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

**Dated: June, 2020**
**Place: Dhaka, Bangladesh**

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

*DEDICATED TO*
*MY*
*BELOVED FAMILY*

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**SAU, Dhaka** **The Author**

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## ABSTRACT

The present study was undertaken by using eight advanced populations of *Brassica rapa* L. to study variability among them at the experimental field of Sher-e-Bangla Agricultural University, Dhaka-1207 during November 2018 – February 2019 to evaluate the magnitude of variations in characters, heritability, genetic advance, correlation, direct and indirect effect of different characters on seed yield per plant for twelve characters. Analysis of variance revealed significant variations among all populations for all the traits. Minimum difference between phenotypic and genotypic variance was observed in root length (cm), number of primary branches per plant, number of secondary branches per plant, length of siliqua (cm) and thousand seed weight (g). However, high genotypic and phenotypic coefficient of variation was observed for the characters viz; number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, seed yield per plant (g). High heritability with low genetic advance was observed in days to first flowering, days to 50% flowering, days to 80% maturity, number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua, length of siliquae, thousand seed weight and seed yield per plant whereas high heritability with high genetic advance was observed in plant height, number of siliquae per plant. Correlation study revealed that seed yield per plant had a significant positive correlation with number of primary branches per plant, number of secondary branches per plant, root length (cm), number of siliquae per plant, number of seeds per siliqua, length of siliquae (cm) and thousand seed weight (g) at the genotypic and phenotypic level. Direct positive effect on seed yield per plant was found in days to first flowering, plant height (cm), number of siliquae per plant and length of siliquae (cm) through path coefficient analysis. According to their yield and yield contributing characters five advanced populations such as Pop$^n$ 3 (BARI Sarisha-6 X BARI Sarisha-15, $F_{10}$, 76.667 days), Pop$^n$ 4 (SAU Sarisha-1 X BARI Sarisha-15, $F_8$, 78.667 days), Pop$^n$ 1 (SAU Sarisha-2 X BARI Sarisha-15, $F_8$, 80 days), Pop$^n$ 6 (SAU Sarisha-1 X BARI Sarisha-15, $F_8$, 78.667 days) and Pop$^n$ 5 (BARI Sarisha-15 X SS 75 (Sonali Sarisha), $F_{11}$, 85.667 days) with higher seed yield per plant were selected from the 8 advanced populations.

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# SOME COMMONLY USED ABBREVIATIONS

| FULL WORD | ABBREVIATION |
|---|---|
| Agriculture | Agric. |
| Agro Ecological Zone | AEZ |
| Analysis of variance | ANOVA |
| And others | *et al.* |
| At the rate | @ |
| Bangladesh Bureau of Statistics | BBS |
| Centimeter | cm |
| Cultivars | cv. |
| Degree Celsius | $^0C$ |
| Degrees of freedom | df |
| Environmental variance | $\sigma^2_e$ |
| Etcetera | etc. |
| Food and Agriculture Organization | FAO |
| Genetic advance | GA |
| Genotypic coefficient of variation | GCV |
| Genotypic variance | $\sigma^2_g$ |
| Gram | g |
| Heritability in broad sense | $h^2{}_b$ |
| Journal | *J.* |
| Kilogram | Kg |
| Mean sum of square | MS |
| Meter | M |
| Ministry of Agriculture | MoA |
| Muriate of Potash | MOP |
| Percent | % |
| Percentage of coefficient of variation | CV% |
| Phenotypic coefficient of variation | PCV |

# SOME COMMONLY USED ABBREVIATIONS (CONT'D)

| FULL WORD | ABBREVIATION |
|---|---|
| Phenotypic variance | $\sigma^2_p$ |
| Randomized Complete Block Design | RCBD |
| Science | *Sci.* |
| Sher-e-Bangla Agricultural University | SAU |
| Square meter | $m^2$ |
| The sixth generation of a cross between two dissimilar homozygous parents | $F_6$ |
| Triple Super Phosphate | TSP |

# CHAPTER I

# INTRODUCTION

*Brassica rapa* L. commonly known as field mustard or turnip mustard belonging to the family Brassicaceae. The Brassicaceae family consists of 338 genera and approximately 3710 species (Beilstein *et al.,* 2008). Six specieses are agronomically important in the *Brassica* genus. Three of them are diploid: *Brassica rapa* (AA genome, 2n=20), containing three main morphotypes (turnip types, leafy types and oil types); *Brassica nigra* (BB genome 2n=16) (black mustard) and *Brassica oleracea* (CC genome 2n=18) including cabbages, broccoli, cauliflower and kohlrabi (above ground turnip) and three are amphidiploids: *Brassica juncea* (AABB genome, 2n=36) (Indian or brown mustard and several leafy types); *Brassica napus* (AACC genome, 2n=38) including oilseed rape and the turnip forming Swede, and *Brassica carinata* (BBCC genome, 2n=34) (Ethiopian mustard). The relationships between these *Brassica* species and their genomes were summarized by U N (1935).

Within those six species *B. rapa* is the species that was domesticated first. The crop is cultivated for the oil content (Yellow Sarson) and for vegetable purposes (Chinese cabbage). Being an important member of Brassicaceae family, *B. rapa* is cultivated extensively for vegetable oil in India, China, and Canada, for leafy vegetables in Korea, China, and Japan, for edible oil in Bangladesh and Indian sub-continents, and as a fodder crop in Europe. In Bangladesh, *B. rapa* is considered as the major oil yielding species of genus *Brassica* (FAO, 2017). *B. rapa* possesses first position in respect of area and production among the oilseed crops in our country (Naznin *et al*., 2015). Total area covered by rapeseed in the world is 36.50 million hectares in 2017-18 whereas in Bangladesh 0.25 million hectares are covered by rapeseed with 0.92 metric tons (MT) per hectares yield which is lower than developed countries (USDA 2019). In 2017-2018, the total esculent oil production is estimated at about 580.7 million tons from major oil producing crops in the world whereas rapeseed supplies 75.4 million tons holding second position after soybean among major edible oil sources (FAO, 2019).

Vegetable oils are a high-value agricultural commodity for use in refined edible oil products and as renewable industrial or fuel oils. Vegetable oils are used mostly for edible purposes and for industrial purposes. After oil extraction, oilseed meals such as rapeseed extraction meal contain a high quality protein that can be used as a valuable animal feed. Mustard oil has anti-inflammatory properties due to the presence of high amount of selenium and magnesium. It stimulates sweat glands and reduces body temperature. However, one of the two essential fatty acids is absent in many edible oils whereas mustard provides both the essential fatty acids named linoleic and linolenic acid to the human body (Khan *et. al.,* 2009). Besides, Seeds of mustard and rapeseeds bear 42% oil and 25% protein and minerals (Kaul and Das, 2006) which serves an eminent role to fulfill the need of the world population. It is also a vital source of raw material for making soaps, paints, hair oils, lubricants, textile auxiliaries, pharmaceuticals and so on.

Among different *Brassica* species, *B. rapa*, *B. napus* and *B. juncea* are cultivated in Bangladesh. In Bangladesh there is a limited scope to increase mustard oil production due to scarcity of land, pressure of other crops and to increase yield due to cultivation of the low yielding varieties. Farmers mostly like to grow tori-7 as Maghi sarisha from long past for its shorter duration (70-80 days) with an average yield of 750 kg/ha and it can fit well in Amon-Mustard-Boro cropping pattern although it has low yield potential. To solve those problems, crosses were made among different mustard varieties and selection has been done for several generations of eight advanced populations of *B. rapa*.

The present study of advanced populations of *B. rapa* is expected to be useful for developing short durational, higher yielding and yellow seeded variety in near future. By comparing among them, it would be possible to select the best one to mitigate the demand of edible oil for future.

The present study was undertaken with 8 advanced populations of *B. rapa*. However, the objectives of the study were-

- To study the variability among the advanced populations of *B. rapa* and
- To study the association between the traits and direct and indirect effects of those traits on seed yield.

# CHAPTER II

# REVIEW OF LITERATURE

*Brassica sp*. is the most important oil crop in Bangladesh and many other countries of the world. Researchers have become more interested in this species on various aspects of its production and utilization. Many studies on the genetic variability, heritability, genetic advance, correlation, path coefficient analysis of *Brassica sp*. have been executed by researchers in many countries of the world. Considering the studies, the review of literature is presented under the following heads:

2.1 Genotypic and phenotypic variability
2.2 Heritability and genetic advance in *Brassica sp.*
2.3 Correlation analysis
2.4 Path co-efficient analysis

## 2.1 Genotypic and phenotypic variability:

It is necessary to introduce successful breeding program with genetic variability to develop high yielding varieties. A lot of research works were done regarding this variability. Some literatures concerning this are discussed here.

Sikarwar *et al*. (2017) performed an experiment for the assessment of the genetic variability in 21 diverse genotypes of yellow sarson (*Brassica rapa* Var. yellow sarson) for ten yield and yield contributing characters. Analysis of variance for the design of the experiment pointed out highly significant differences for all the characters. High Phenotypic Co-efficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were found 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. Days to flowering, plant height and length of siliqua showed low PCV and GCV.

Sohail *et al.* (2017) conducted an experiment to study intra-specific quantitative characters among 253 *Brassica rapa* genotypes. Significant variations were recorded among genotypes for days to flower initiation, days to 50% flowering completion, days to maturity, leaf length and width, plant height, primary branches per plant, main raceme length, pod length, pod width, stem thickness, thousand seed weight, seed yield per plant and pod shattering (stage I-IV). Many elite lines such as Br-505, Br512, Br-536, Br-547, Br-560, Br-760, etc. had excellent morphogenetic responses in both years.

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.

An experiment was conducted by Afrin *et al*. (2016) to study variability among the fifteen $F_4$ population considering different morphological attributes of *Brassica rapa*. Presence of highly significant variation was found among the genotypes for almost all of the characters studied.

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.

Ara *et al.* (2015) executed an experiment by using eight the $F_2$ population of 12 intervarietal crosses with 3 check varieties of the species *Brassica rapa* L. for evaluating the variations in characters. Significant variations were present among different $F_2$ materials used in the experiment. Higher values of phenotypic variances were observed than corresponding genotypic variances. The values of GCV and PCV indicated that there was least variation present among most of the studied characters.

Naznin *et al.* (2015) evaluated on thirty three genotypes of *Brassica rapa* L. to find out their inter-genotypic variability. The character such as plant height was highly influenced by the environment whereas, all other characters influenced the least. The highest phenotypic and genotypic coefficient of variation were found in number of secondary branches/plant.

A research work was undertaken by Parvin (2015) with 30 $BC_1$ $F_4$ genotypes of *Brassica napus* L. to study the genetic variability. Significantly variable genotypes were found for most of the characters. Genotypic variances were comparatively lower than the phenotypic variances for all studied characters. PCV were higher than the GCV for all the studied characters.

To evaluate genetic variation Sharafi *et al.* (2015) performed an experiment with twenty eight winter rapeseed cultivars. They revealed that yield, number of branches per plant and plant height had the highest variation. These findings showed that cultivars with higher number of pod per plant had higher seed production.

Siddika (2015) executed an experiment to study the genetic variability of *Brassica napus* L. with 30 $F_2$ genotypes. The genotypes were found significantly variable for all the characters. Genotypic variances were lower comparatively than the phenotypic variances for all the studied characters. Phenotypic co-efficient of variation (PCV) values were higher than the genotypic co-efficient of variation (GCV) values.

Sultana (2015) performed an experiment by utilizing sixty two $F_4$ genotypes of *Brassica napus* L. to study the variability. Significantly variable genotypes were observed for most of the characters. The high GCV value was observed for number of secondary branches per plant.

Fayyaz and Afzal (2014) studied on indigenous lines to check locally collected *Brassica rapa* (*Brassica campestris* L.) accessions for genetic variability. They got highly significant differences in all traits except siliqua width. Hence, it was noticed that indigenous accessions have great proportion of genetic variability, which can be manipulated for utilizing their genetic potential in future breeding programs.

An experiment was conducted by Helal *et al.* (2014) to study genetic variability of yield and yield contributing characters and coefficient of variance in rapeseed or mustard. The results revealed that varieties produced the highest seed yields and 15% variation at genotypic and phenotypic level.

An experiment was conducted by Hussain (2014) for estimating the magnitude of variations in different characters using 24 genotypes including 4 check varieties of the species *Brassica rapa* L. Existence of significant variation was found among all the genotypes for all the characters studied. Moderate difference between the phenotypic and genotypic variance was seen in days to 50% flowering, days to 80% maturity.

An experiment was undertaken by Iqbal *et al.* (2014) using ten indigenous varieties with eight important yield contributing characters of *Brassica rapa* in Pakistan to study variability. They showed highly significant differences in almost all traits except siliqua width, which showed significant variation.

Jahan *et al.* (2014) executed a field experiment to study variability in 10 $F_4$ lines of *Brassica rapa* L. Significant variation was found among all the genotypes for all the studied characters. Considering genetic parameters, high genotypic coefficient of variation (GCV) was noticed for number of secondary branches per plant, siliquae per plant, yield per plant, whereas days to maturity showed very low GCV.

An experiment was undertaken by Shakera (2014) utilizing twenty $F_3$ and $F_4$ populations produced through inter-varietal crosses, with three check variety of *Brassica rapa* L. to study the variation in different characters good yielding plants of the $F_3$ and $F_4$ material to select high yielding and early mature plants. Considering genetic parameters, comparatively phenotypic variances were higher than the genotypic variances for all the studied characters. Least difference between genotypic and phenotypic variance was noticed in days to maturity, number of primary branches per plant, length of siliqua, thousand seed weight. High phenotypic and genotypic co-efficient of variation were noticed in number of secondary branches per plant, number of siliqua per plant and yield per plant.

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 while non-significant differences were found among the genotypes in primary branches per plant and pods per plant.

Ahmad *et al.* (2013) conducted an experiment with thirty five advanced mutant lines along with a check variety of *Brassica napus* called Abasin-95 for variability analysis and reported that seed yield and days to flowering showed high genetic variability.

Halder (2013) performed an experiment to study the variability in eleven advanced lines of *Brassica rapa* L. She found significant variations among the genotypes for all the characters. Phenotypic variance was higher than the genotypic variance for every character. Difference between phenotypic and genotypic variance was minimum in number of primary branches per plant, length of siliqua, thousand seed weight, seeds per silique, days to 50% flowering and days to 80% maturity.

Khan *et al.* (2013) evaluated thirty $F_7$ segregating lines and two parents of *Brassica rapa* L. to study variability. The result revealed significant variation among all the genotypes for all the characters except thousand seed weight. Plant height showed highest genotypic, phenotypic and environmental variances while lowest were observed in length of siliquae. Thousand seed weight, number of secondary branches per plant, seeds per siliquae, and siliquae length showed high heritability coupled with low genetic advance in percent of mean. On the contrary, moderate heritability along with high genetic advance was observed in number of siliquae per plant.

To study the genetic differences, Nasim *et al*. (2013) evaluated ten *Brassica napus* L. cultivars. Highly significant differences were noticed for morphological parameters of thousand seed weight, days to half flowering, days to full flowering, siliqua width, siliqua length, seed per siliqua and plant height whereas non-significant differences were observed for main raceme length, siliquae on main raceme and primary branches per plant.

Zare and Sharafzadeh (2012) evaluated 8 *Brassica napus* L. genotypes through agro-morphological traits to investigate the differences. Except siliqua length and seeds per siliqua, they found significant genetic differences for the traits of seed yield and related traits.

Roy *et al.* (2011) performed a research work on rapeseed mustard for studying variability. The finding revealed significant varietal difference on main raceme except the number of siliquae. High PCV and the GCV were observed in secondary branches per plant and number of siliqua per plant.

Alam (2010) executed an experiment by using twenty six $F_4$ populations of some inter-varietal crosses of *Brassica rapa* to study the variation among them. Significant variations were noticed in number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, days to

50% flowering, length of siliqua, number of seeds per siliqua, 1000 seed weight and least difference between genotypic and phenotypic variances was observed for yield per plant. Plant height, length of siliqua, number of siliqua per plant, days to 50% flowering exhibited low genotypic and phenotypic coefficient of variation.

Ara (2010) conducted a field experiment by using eight $F_2$ and eight $F_4$ populations generated through inter-varietal crosses along with three check variety of *Brassica rapa* to study the variation. The values of phenotypic variances were higher than corresponding genotypic variances. Days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, length of siliquae, seeds per siliqua, 1000-seed weight and yield per plant showed least difference between phenotypic and genotypic variances. The value of GCV and PCV indicated that there was least variation present among most of the characters.

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 seeds per siliqua.

Saleh (2009) carried out a field experiment by utilizing twenty $F_2$ populations developed through inter-varietal crosses, along with three check variety of *Brassica rapa* L. to find out the variation in different traits. Result unveiled considerable variations present among all the genotypes used in the experiment. The values of phenotypic variances were higher than corresponding genotypic variances. Least difference between phenotypic and genotypic variances was exhibited in days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, length of siliqua, seeds per siliqua, 1000 seed weight and yield per plant. The value of GCV and PCV uncovered that there was least variation existing among most of the characters.

Aytac *et al*. (2008) studied on six genotypes of spring rapeseed and found significant differences among the genotypes to make effective selection. They obtained highest genotypic and phenotypic variances in seed yield per plant.

Jahan (2008) executed a field experiment with 10 $F_4$ lines derived through intervarietal crosses in association with eight released varieties of *Brassica rapa* L. to study genotypic variability. She noticed significant variation among all genotypes for all the studied characters. Number of secondary branches/plant, siliquae/plant, yield/plant showed high genotypic co-efficient of variation (GCV) whereas very low GCV was observed for days to maturity.

Mahmud (2008) conducted an experiment using 58 genotypes of *Brassica rapa* L. to study inter-genotypic variability. Significant variations were viewed among all the genotypes for all the studied characters except thousand seed weight. High GCV value was observed for number of secondary branches per plant.

Parveen (2007) conducted an experiment to study the variability in $F_2$ progenies of the inter-varietal crosses of seventeen genotypes of *Brassica rapa*. Significant variations were discovered among different genotypes. Least difference between genotypic and phenotypic variance was found in genetic parameters like number of primary branches/plant, number of secondary branches/plant, length of siliqua, number of seeds/siliqua, days to 50% flowering, 1000 seed weight and yield/plant.

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.

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.

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.

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.

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.

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 studied 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.

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 was observed.

## 2.2 Heritability and genetic advance in *Brassica spp*.:

Sikarwar *et al*. (2017) performed an experiment for the assessment heritability and genetic advance in 21 diverse genotypes of yellow sarson (*Brassica rapa* Var. yellow sarson) for ten yield and its contributing characters. Higher estimates of broad sense heritability were observed for all the characters. High heritability along with high genetic advance was noticed 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.

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.

Afrin *et al.* (2016) executed an experiment on the fifteen $F_4$ population considering different morphological attributes of *Brassica rapa* L. Highest value for heritability was exhibited in the number of secondary branches per plant while the primary branches per plant revealed lowest value. Moderate heritability was observed in yield per plant, thousand seed weight, siliquae length, days to 50% flowering, days to 80% maturity and plant height.

Ara *et al.* (2015) executed an experiment by using eight $F_2$ population of 12 intervarietal crosses with 3 check varieties of the species *Brassica rapa* L. for evaluating heritability and genetic advance. High heritability along with low genetic advance and genetic advance in percentage of mean were found in the number of branches per plant, days to 50% flowering, days to maturity and length of siliqua with low genetic advance and genetic advance in percentage of mean.

A research work was carried out by Begum (2015) using 31 $BC_1$ $F_5$ genotypes of *Brassica napus* L. and reported highest value of heritability for seed yield per plant whereas days to 50% flowering showed the lowest value of heritability. High heritability coupled with high genetic advance in percent of mean was observed in number of primary branches per plant, number of secondary branches per plant. High heritability with moderate genetic advance was observed in number of siliqua per plant, number of seed per siliquae, thousand seed weight and seed yield per plant.

Nazneen *et al*. (2015) conducted an experiment to evaluate on thirty three genotypes of *Brassica rapa* L and revealed that number of siliquae/plant, number of secondary branches/plant and number of primary branches/plant showed high heritability coupled with high genetic advance in percent of mean.

A research work was undertaken by Parvin (2015) with 30 $BC_1$ $F_4$ genotypes of *Brassica napus* L. and reported that Plant height, number of primary branches per plant, siliqua length and thousand seed weight exhibited high heritability with high genetic advance.

In order to investigate genetic variability Shaukat *et al*. (2015) evaluated eight *Brassica napus* genotypes. High broad sense heritability estimates were exhibited for primary branches per plant, plant height, pods per main raceme, seeds per pod, 1000-seed weight while pod length, pods per plant and seed yield per plant showed moderate heritability.

Sultana (2015) performed an experiment by utilizing sixty two $F_4$ genotypes of *Brassica napus* L. and found highest value of heritability for number of secondary branches followed by seed yield per plant while days to maturity showed the lowest value of heritability.

Fayyaz and Afzal (2014) studied on indigenous lines to check locally collected *Brassica rapa* (*B. campestris,* L.) accessions for heritability and genetic advance. The highest heritability with higher genetic advance was viewed in plant height which provided the evidence that this trait was under the control of additive genetic effects, while rest of the traits exhibited variable trends.

An experiment was conducted by Hussain (2014) for estimating heritability and genetic advance of different characters using 24 genotypes including 4 check varieties of the species *Brassica rapa* L. High heritability along with high genetic advance in percentage of mean was observed in number of secondary branches per plant whereas days to 50% flowering, no. of siliqua per plant, yield per plant while high heritability with moderate genetic advance in percentage of mean. Days to 80% maturity, no. of primary branches per plant, no. of seed per siliqua exhibited high heritability with low genetic advance in percentage of mean.

An experiment was undertaken by Iqbal *et al.* (2014) using ten indigenous varieties with eight important yield contributing characters of *Brassica rapa* in Pakistan. They showed highest heritability in association with higher genetic advance in plant height while the seed per siliquae showed medium heritability along lower genetic advance.

Jahan *et al.* (2014) executed a field experiment in 10 F4 lines of *Brassica rapa* L. and finding revealed high heritability coupled with low genetic advance in percent of mean for days to maturity. High heritability along with moderate genetic advance in percent of mean was found for plant height and days to 50% flowering.

An experiment was undertaken by Shakera (2014) utilizing twenty F3 and F4 populations produced through inter-varietal crosses, with three check variety of *Brassica rapa* L. to study heritability and genetic advance and reported that high heritability coupled with low genetic advance and high genetic advance in percentage of mean were observed in thousand seed weight and yield per plant.

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.

Ahmad *et al*. (2013) conducted an experiment with thirty five advanced mutant lines along with a check variety of *Brassica napus* called Abasin-95 to estimate heritability and genetic advance. High heritability and genetic advance were recorded for seed yield. The mutant lines OA5, G1 and 06 showed their superiority in high seed yield, thousand seed weight and earliness in flowering.

Khan *et al.* (2013) evaluated on thirty $F_7$ segregating lines and two parents of *Brassica rapa* L. to study heritability and genetic advance. High heritability coupled with low genetic advance in percent of mean was exhibited in thousand seed weight, number of secondary branches per plant, seeds per siliquae, and siliquae length. On the other hand, moderate heritability along with high genetic advance was viewed in number of siliquae per plant.

Halder (2013) studied on eleven advanced lines of *Brassica rapa*. High heritability along with moderate genetic advance and genetic advance in mean percentage was found in days to 50% flowering and days to 80% flowering whereas moderate heritability with high genetic advance and genetic advance in mean percentage was noticed in siliquae per plant and yield per hectare. To study the rate of heritability,

Nasim *et al.* (2013) evaluated on ten *Brassica napus* L. cultivars. Flower initiation, fifty percent flowering, complete flowering, plant height, seeds per siliqua and thousand seed weight exhibited high heritability and high heritable advances.

Zare and Sharafzadeh (2012) evaluated 8 *Brassica napus* L. genotypes through agro-morphological traits to investigate heritability among these genotypes for the traits of seed yield and related. Very high heritability in broad sense was found for days to flowering which was 93.3 percent and the lowest of 14.3 percent for siliqua length, while for the rest of parameters they found high heritability.

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.

Patel (2011) experimented with three high yielding varieties and two very low quality varieties and their six generation cross product of *Brassica napus*. The result showed that the heritability in broad sense with high to moderate genetic advance was found in thousand seed weight, seed yield per plant. Moderate to high heritability associated with low genetic advance was recorded in days to maturity and days to flowering.

Roy *et al*. (2011) performed a research work on rapeseed mustard for studying heritability. High heritability with high genetic advance as percent of mean was noticed in plant height, seed yield, secondary branches per plant, siliqua per plant and seeds per siliquae.

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.

Alam (2010) executed an experiment using twenty six $F_4$ populations of some inter-varietal crosses of *Brassica rapa* and observed high heritability coupled with high genetic advance in plant height, number of primary branches per plant, number of secondary branches per plant and number of siliquae per plant.

Ara (2010) conducted a field experiment by using eight $F_2$ and eight $F_4$ populations generated through inter-varietal crosses along with three check variety of *Brassica rapa* to study the heritability and genetic advance. The days to maturity, length of siliquae, seeds per siliquae and 1000-seed weight showed high heritability with low genetic advance and genetic advance in percentage of mean.

Saleh (2009) executed a field experiment by using twenty $F_2$ populations developed through inter-varietal crosses, along with three check variety of

*Brassica rapa* L. High heritability along with low genetic advance and genetic advance in percentage of mean were exhibited in days to maturity, length of siliqua, seeds per siliqua and thousand seed weight.

Aytac *et al*. (2008) studied on six genotypes of spring rape seed and found high heritability with range 87% to 99%. Plant height and siliqua length exhibited high heritability and low genetic advance. Seed yield per plant, seed yield, siliquae per plant showed high heritability with high genetic advance.

An experiment was performed by Hosen (2008) using five parental genotypes of *Brassica rapa* and their ten $F_3$ progenies including reciprocals to estimate heritability and reported that plant height, days to 50% flowering and number of siliquae per plant exhibited high heritability with high genetic advance and genetic advance in percentage of mean.

Jahan (2008) executed a field experiment with 10 $F_4$ lines obtained through intervarietal crosses with eight released varieties of *Brassica rapa L.* to study heritability. High heritability in association with low genetic advance in percent of mean was observed for days to maturity. On the other hand, plant height and days to 50% flowering showed high heritability coupled with moderate genetic advance in percent of mean.

Mahmud (2008) conducted an experiment using 58 genotypes of *Brassica rapa* L. High heritability values in association with high genetic advance in percentage of mean was found in for days to 50% flowering, siliqua length and seed per siliqua.

Parveen (2007) conducted an experiment on $F_2$ progenies of the inter-varietal crosses of seventeen genotypes of *Brassica rapa*. High heritability with high genetic advance in percent of mean was recorded for number of primary branches per plant and secondary branches per plant whereas low heritability was viewed in the yield/plant, days to maturity and length of siliqua.

A research work was performed by Rashid (2007) on forty oleiferous *Brassica* species. High heritability values along with high genetic advance in percentage of mean was obtained for siliqua length, number of seeds/siliqua, number of primary branches/plant and number of secondary branches/plant.

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.

Akbar *et al.* (2007) conducted an experiment with eight advanced lines of *Brassica junea* in Pakistan and studied heritability and genetic advance of different yield components by. 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 heritability in $F_2$ progenies of the inter-varietal crosses of 17 *Brassica rapa* L. 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.

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.

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.

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.

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.

## 2.3 Correlation analysis:

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

A research work was performed by Kumari *et al*. (2017) to study correlation among thirteen quantitative and qualitative characters of forty four genotypes of yellow sarson (*Brassica rapa* var. yellow sarson). Seed yield per plant exhibited significant and positive correlation with biological yield, while positive but non-significant correlation with siliqua length, harvest-index, seeds per siliqua, days 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) carried out a research work to estimate correlation using six genotypes of *Brassica campestris* L. Results revealed that 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. Relationship between plant height and seeds per pod, branches per plant and ripeness days and pods per plant and seeds per pod was negative and significant.

An experiment was performed by Halder *et al.* (2016) to study the interrelationship among the characters of eleven advanced lines and three popular check varieties of *Brassica rapa* L. on yield per hectare .Through genotypic correlation coefficient ,it was observed that yield per hectare had positive and highly significant correlation with days to first flowering, days to 80% flowering and number of primary branches per plant while days to 50% flowering and length of siliquae were negatively correlated with yield .

Jamali *et al.* (2016) conducted a research work to study the 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. Highly significant positive correlation was observed in plant height, days to 75% flowering, number of pods per plant and seed index vs seed yield per plant. Negative and significant correlation was found in plant height vs seeds per pod, branches per plant vs days to 90% maturity and pods per plant vs seeds per pod.

Begum (2015) conducted an experiment with 31 $BC_1$ $F_5$ genotypes of *Brassica napus* L. to study the correlation and found significant positive correlation between seed yield per plant with the number of primary branches, number of secondary branches, number of siliqua per plant and thousand seed weight.

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

Naznin *et al*. (2015) evaluated on thirty three genotypes of *Brassica rapa* L. to study their character association. The seed yield/plant exhibited significant positive correlation with number of siliquae/plant, number of primary branches/plant and number of secondary branches/plant revealing that selection based on these traits would be judicious.

Rameeh (2015) conducted an experiment with 36 rapeseed (*Brassica napus* L.) genotypes including four checks and 32 advanced lines and found that pods per plant, seeds per plant and 1000- seed weight traits were positively associated with seed yield.

An experiment was conducted by Sultana (2015) by using sixty two $F_4$ genotypes of *Brassica napus* L. to study the correlation. The significant positive correlation with seed yield per plant were found with all most all the characters except days to 50% flowering and days to maturity.

Ejaz-Ul-Hasan *et al*. (2014) studied on nine genotypes of *Brassica napus* to determine correlation between different traits and reported high and positively significant phenotypic correlation between plant height and seeds per plant.

An experiment was conducted by Halder *et al.* (2014) with 14 genotypes including 11 advanced lines and 3 check varieties of *Brassica rapa* to study the correlation and reported that days to first flowering had positive non-significant relationship with yield but high positive significant correlation with the days to 50% and 80% flowering. Highly significant negative correlation was observed with number of secondary branches per plant and siliqua length.

Hussain (2014) performed an experiment with 24 genotypes including 4 check varieties of the species *Brassica rapa* L. for estimating the character associations. The significant positive correlation was noticed in thousand seed weight, no. of siliqua per plant, no. of primary branches per plant with seed yield 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

An experiment was carried out by Parvin (2014) with 40 genotypes of *Brassica napus* L. to study the character association. The significant positive correlation with seed yield per plant was found in days to 1st flowering, days to 80%

flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant and siliqua per plant.

Shakera (2014) conducted an experiment using twenty $F_3$ and $F_4$ populations generated through inter-varietal crosses, along with three check variety of *Brassica rapa* L. to study correlation between pairs of different characters to select high yielding and early mature plants. Yield per plant showed significant and the positive correlation with plant height, number of primary branches per plant number of secondary branches per plant, number of siliqua per plant and thousand seed weight.

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.

To determine correlation between various traits, Nasim *et al.* (2013) evaluated on ten *Brassica napus* L. genotypes and noticed that pod length had positive highly significant and significant correlation with thousand seed weight and pod width respectively. Pod width uncovered negative significant correlation with days to flowering initiation whereas positive significant correlations with thousand seed weight.

An experiment using seven parental and twenty one $F_2$ progenies of *Brassica rapa* was executed by Uddin *et al.* (2013) to study correlation among different yield component and revealed 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.

An experiment was performed by Maurya *et al.* (2012) with one hundred genotypes of *Brassica juncea* and noticed a high positive correlation between length of siliquae, seed yield, thousand grain weight and days to 50% flowering.

Afrin *et al.* (2011) studied on 22 *Brassica napus* L. advanced lines and observed positive correlation with seed yield per plant in plant height, number of primary branches per plant and number of siliquae per plant. Highest significant positive correlation was noticed between days to 50% flowering and plant height.

A research work was done by Rameeh (2011) with 36 *Brassica napus* L. cultivars to determine the associations for yield components in these genotypes. Siliqua per plant was significantly and highly correlated with seed yield with correlation value of 0.80.

An experiment was carried out by Tahira *et al.* (2011) with ten wide genetic ranged variety of *Brassica juncea* and the result revealed correlation among the different characters studied. The highest phenotypic correlation was found between plant height, branches per plant, siliqua length and seeds per siliquae. Seed yield was only significantly correlated with plant height and siliquae length. Plant height, branches per plant, siliqua length and thousand seed weight were genotypically correlated with yield per plant. A highly significant and strong positive genetic relation was observed between plant height and branches per plant, siliqua length and seed per siliquae.

An experiment was conducted by Alam (2010) to study correlation using twenty six $F_4$ populations of some inter-varietal crosses of *Brassica rapa* and reported that yield per plant showed significant positive association with plant height, number of primary branches per plant, number of siliqua per plant, seeds per siliquae at both genotypic and phenotypic level.

Ara (2010) executed a field experiment by using eight $F_2$ and eight $F_4$ populations generated through inter-varietal crosses with three check variety of *Brassica rapa* to study correlation between pairs of different characters. Yield per plant exhibited significant and highest positive correlation with length of siliquae, seeds per siliquae and 1000-seed weight.

Esmaeeli Azadgoleh *et al.* (2009) observed positively significant correlation of seed yield with number of pod per plant, number of pods in sub branches and number of seeds per pod.

Saleh (2009) conducted a field experiment by utilizing twenty $F_2$ populations developed through inter-varietal crosses, along with three check variety of *Brassica rapa* L. to detect correlation between pairs of different traits. Yield per plant exhibited significant and highest positive correlation with length of siliqua, seeds per siliqua and thousand seed weight.

A study was conducted by Hosen (2008) using five parental genotypes of *Brassica rapa* and their ten $F_3$ progenies including reciprocations. He found yield per plant showed highest significant and positive correlation with days to maturity followed by number of seeds per siliqua, number of secondary branches per plant, length of siliqua and number of siliqua per plant.

An experiment was performed by Uddin (2008) to study the correlation among seven parental genotypes and their twenty one $F_2$ progenies of *Brassica rapa* and found positive significant correlation in seed yield per plant with number of primary branches per plant, number of secondary branches per plant and number of siliquae per plant.

Jeromela *et al.* (2007) studied on 30 rapeseed varieties and showed that pods per plant had the highest correlation with seed yield.

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

An experiment was executed by Rashid (2007) with forty oleiferous *Brassica* species to estimate correlation and found highly significant positive correlation of yield per plant with number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant and seeds per siliquae.

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.

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.

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.

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.

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.

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.

## 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.

Kumari *et al.* (2017) studied on different character pairs of yellow sarson (*Brassica rapa* Var. Yellow Sarson) and it was revealed that the path coefficient analysis of biological yield exerted maximum direct effect, whereas silique length and oil content showed negative direct effect and days to 50 percent flowering exerted negative indirect effect on seed yield.

Halder *et al.* (2016) undertook an experiment to visualize the inter-relationship of eleven advanced lines and three popular check varieties of *Brassica rapa* L. through path coefficient which indicated that plant height exerted highest positive and highly significant direct association with the yield per hectare followed by number of primary branches per plant and number of siliquae per plant showed highest negative significant direct effect followed by days to maturity. The high direct effect concluded that selection of the traits might be effective for yield improvement. Low residual effect indicated that the considered traits of the study explained almost all the variability towards yield.

Islam *et al*. (2016) conducted an experiment on twenty one (21) $F_9$ populations from inter-varietal crosses of *Brassica rapa* L. and result of path co-efficient analysis concluded that plant height, number of primary branches per plant, number of siliquae per plant, seeds per siliquae, and siliquae length showed the positive direct effect and days to 50% flowering, number of secondary branches per plant and thousand seed weight showed the negative direct effect on yield per plant.

A research work was undertaken by Naznin *et al.* (2015) to evaluate on thirty three genotypes of *Brassica rapa* L. in order to find out their path coefficient of seed yield/plant and its component characters. Path analysis revealed that the number of siliquae/plant, number of primary branches/plant and number of secondary branches/plant were the most important contributors to seed yield/plant.

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.

Sharafi *et al.* (2015) studied on twenty eight winter rapeseed cultivars and observed that number of pods per plant, number of seeds per pod and 1000 seed weight had positive direct effect on seed yield.

Afrin (2014) conducted an experiment to evaluate the variability among fifteen $F_4$ population of *Brassica rapa* of different cross combinations and path coefficient analysis showed that number of primary branches per plant, number of siliquae per plant, number of seeds per siliquae and thousand seed weight had the positive direct effect on seed yield per plant.

Ejaz-Ul-Hasan *et al.* (2014) conducted an experiment with nine genotypes of *Brassica napus* to evaluate path analysis for yield and yield components and reported that the seeds/siliqua, 1000 seed weight, days to flowering, days to maturity and seeds/plant showed direct positive contribution towards seed yield per plant.

Helal *et al.* (2014) carried out an experiment to study the Genetic variability, correlation of yield and yield contributing characters and coefficient of variance in rapeseed or mustard and path coefficient analysis of different yield contributing characters resulted in biological yield contributed maximum direct effect with the highest correlation and Plant height showed the negative direct effect on yield /plant.

Shakera (2014) conducted an experiment using twenty $F_3$ and $F_4$ populations generated through inter-varietal crosses, along with three check variety of *Brassica rapa* L. to study the direct and indirect effect of good yielding plants of the $F_3$ and $F_4$ material to select high yielding and early mature plants. The path co-efficient analysis unveiled that plant height had the highest positive direct effect followed by siliquae per plant, number of seed per siliqua, number of secondary branches per plant.

Uddin *et al.* (2013) studied on seven parental genotypes and their twenty one $F_2$ progenies of *Brassica rapa* L. to detect their variability and Path co-efficient analysis indicated that days to 50% flowering, number of primary branches, secondary branches and siliquae/ plant, siliquae length, seeds /siliqua and thousand seed weight showed the positive direct effect on seed yield /plant whereas Days to maturity and plant height showed the negative direct effect on yield plant.

Tahira *et al.* (2011) performed an experiment with ten wide genetic ranged variety of *Brassica juncea* to study relationship among the characters. The result reported that plant height and siliquae length exhibited positive direct effect on seed yield per plant while positive indirect effect of primary branches per plant through plant height and seed per siliquae provided significant effect on seed yield per plant. Siliqua length contributed negative indirect effect through plant height, seed per siliquae and thousand grain weight.

Afrin *et al.* (2011) conducted an experiment with 22 *Brassica napus* L. advanced lines to determine the path co-efficiant among the characters. The plant height exhibited the highest positive and direct effect on seed yield per plant followed by number of siliquae per plant and siliqua length.

An experiment was conducted by Alam (2010) by using twenty six (26) $F_4$ populations of some inter-varietal crosses of *Brassica rapa*. Through path coefficient analysis, it was revealed that plant height, number of primary branches per plant, number of siliqua per plant, seeds per siliqua and siliqua length had the direct positive effect on yield per plant while days to 50% flowering, number of secondary branches per plant and thousand seed weight had the negative direct effect on yield per plant.

Singh (2010) performed a research work to study sixty two $F_1$ and twenty four parental lines of *Brassica juncea* and the path analysis revealed that the highest positive direct effect was observed in secondary branches per plant followed by plant height and seeds per siliquae on seed yield per plant while the highest negative effect was in the plant height on seed yield per plant.

Saleh (2009) performed a field experiment by exploiting twenty $F_2$ populations developed through inter-varietal crosses, along with three check variety of *Brassica rapa* L. to find out direct and indirect effects of different traits on seed yield per plant. The path co-efficient analysis uncovered highest positive direct effect of siliqua per plant followed by number of secondary branches per plant, days to 50% flowering, length of siliqua and plant height.

Mahmud (2008) executed an experiment with fifty eight genotypes of *Brassica rapa*. Path analysis revealed 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.

Uddin (2008) studied on seven parental genotypes and their twenty one $F_2$ progenies of *Brassica rapa* and through path coefficient analysis he showed that the seed yield per plant had positive direct effect on days to 50%flowering, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, siliquae length, seeds per siliquae and thousand seed weight while days to maturity and plant height exhibited direct negative effect on yield per plant.

Parveen (2007) carried out an experiment with $F_2$ population of *Brassica rapa* and through the path analysis it was found that number of seeds per siliqua had highest direct effect on yield per plant.

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

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.

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.

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.

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.

# CHAPTER III

# MATERIALS AND METHODS

The present investigation entitled **"VARIABILITY STUDY IN EIGHT ADVANCED POPULATIONS OF *Brassica rapa* L."** was carried out at the experimental field of Sher-e-Bangla Agricultural University, Dhaka - 1207. The detail information regarding the materials and methodology of this experiment is discussed below:

## 3.1 Experimental site:

The experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka – 1207 during November 2018 to February 2019. The location of the experimental site was situated at $23^0$ 77' N latitude and $90^0$ 37' E longitudes with an elevation of 13.03 meters from the sea level (www.distancesfrom.com). The experimental field belongs to the Agro-ecological zone of "The Modhupur Tract", AEZ-28 (www.banglapedia.com). The photograph showing the experimental site is presented in Appendix I.

## 3.2 Soil and climate:

The land was medium high with medium fertility level. The soil was clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH of the soil was 5.47 to 5.63 and organic carbon content was 0.82% (Appendix II). The experimental site was located in the subtropical climatic zone with wet summer and dry winter. Generally, very few rainfall, moderate temperature and short day length were observed during the Rabi season. The records of air temperature, humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix III).

## 3.3 Experimental materials:

The healthy seeds of eight advanced populations of *B. rapa* were collected from the Dept. of Genetics and Plant Breeding, Sher-e-Bangla Agricultural

University, which were used as experimental materials. These materials cover $F_6$ – $F_{10}$ populations. The materials used in the experiment is shown in Table 1.

**Table 1.** Name of the advanced populations with their abbreviated forms:

| **Advanced populations** | **Abbreviated forms** | **Generations** | **Duration (Days)** | **Source** |
|---|---|---|---|---|
| SAU Sarisha 2 X BARI Sarisha 15 | Pop$^n$ 1 | $F_7$ | 80 | GEPB, SAU |
| SAU Sarisha 1 X BARI Sarisha 15 | Pop$^n$ 2 | $F_6$ | | GEPB, SAU |
| BARI Sarisha 6 X BARI Sarisha 15 | Pop$^n$ 3 | $F_9$ | 75 | GEPB, SAU |
| SAU Sarisha 1 X BARI Sarisha 15 | Pop$^n$ 4 | $F_7$ | 80 | GEPB, SAU |
| BARI Sarisha 15 X SS75 (Sonali Sarisha) | Pop$^n$ 5 | $F_{10}$ | 75 | GEPB, SAU |
| SAU Sarisha 1 X BARI Sarisha 15 | Pop$^n$ 6 | $F_7$ | 75 | GEPB, SAU |
| Tori-7 X BARI Sarisha 15 | Pop$^n$ 7 | $F_6$ | 85 | GEPB, SAU |
| BARI Sarisha 6 X BARI Sarisha 15 | Pop$^n$ 8 | $F_6$ | 85 | GEPB, SAU |

### 3.4 Methods:

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

#### 3.4.1 Land preparation:

The experimental plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about good tilth. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly. The pictorial view of experimental field during land preparation and after seed sowing is presented in Plate 1 and Plate 2 respectively.

#### 3.4.2 Application of manures and fertilizers:

At proper rate and proper time, Urea, Triple Super Phosphate (TSP), Muriate of potash (MOP), Gypsum, Zinc oxide and Boric acid were applied to the field. The first half amount of urea, total amount of Cowdung, TSP, MOP, Gypsum, Zinc Oxide and Boric acid were applied during final land preparation as basal dose. The rest amount of urea was applied as top dressing after 25 days of sowing. A picture of experimental field after the application of fertilizers and manures is presented in Plate 3.

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

| **Sl. No.** | **Fertilizers/ manures** | **Dose** | | **Procedures of application** |
|---|---|---|---|---|
| | | **Applied in the plot** | **Quantity/ha** | |
| 1 | Cowdung | 150kg | 5 ton | As basal |
| 2 | Urea | 7 kg | 250 kg | 50% basal and 50% at the time of flower initiation |
| 3 | TSP | 4.5kg | 170 kg | As basal |
| 4 | MOP | 2.5 kg | 75 kg | As basal |
| 5 | Gypsum | 4 kg | 150 kg | As basal |
| 6 | ZnO | 80g | 3kg | As basal |
| 7 | Boric acid | 300g | 10 kg | As basal |

**Plate 1.** The pictorial view of experimental field during land preparation

**Plate 2.** The pictorial view of experimental field after seed sowing

**Plate 3.** The pictorial view of experimental field after the application of fertilizers and manures

### 3.4.3 Experimental design and layout:

Field lay out was done after final land preparation. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The total area of the experiment was 19m × 13m = 247m$^2$. Each replication size was 19m×3m and distance between replication to replication was 1m. The spacing between line to line was 30cm and plant to plant was 10 cm.

### 3.4.4 Seed selection and sowing:

Pure and healthy seeds were selected by avoiding the unfilled seeds. In the experimental field, seeds were sown in lines in the experimental plots on 28 November, 2018 maintaining a soil depth at about 1.5cm. The seeds were veiled with soil carefully after sowing so that no clods were found to suppress the seeds. Seeds germination were started three to four days after sowing.

### 3.4.5 Irrigation and drainage:

Irrigation was given with sprinkler after sowing of seeds to maintain proper moisture condition of the soil to ensure uniform seed germination. Before the flower initiation, second irrigation was given (22 DAS). Third irrigation was given 40 days after sowing when the pod appeared. Fourth irrigation was given 60 days after sowing when seeds appeared in the pod. Good drainage system was maintained to drain out the excess water. To avoid the water pressure, special care was taken during irrigation.

### 3.4.6 Intercultural operations, insect and disease control:

Various intercultural operations like thinning, weeding were done to ensure normal growth and development of the plants. After fifteen days of sowing, first weeding was done. At the similar time, thinning was done for maintaining 30 cm from line to line and 10 cm from plant to plant. After twenty five days of sowing, second weeding was done. No remarkable disease and pest attack was observed.

### 3.4.7 Crop harvesting:

Harvesting was done from 12th to 23th February, 2019 on the basis of the maturity. When 80% of the plants exhibited symptoms of maturity i.e. straw color of siliquae, leaves, stems desirable seed color in the matured siliqua, the crop was assessed to attain maturity. Ten plants were selected for morphological analysis and 50 plants for biochemical analysis at random from the advanced lines in each replication. The plants were harvested by uprooting and then they were tagged properly. Data were recorded on different parameters from these plants. A pictorial view of experimental field at growth stage, flowering stage and harvesting stage is presented in Plate 4, 5, 6 respectively.

### 3.4.8 Data collection:

For studying different genetic parameters and inter-relationships, twelve characters of ten plants were taken into account such as days to first flowering, days to 50% flowering, days to 80% maturity, plant height, root length, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, length of siliquae, number of seeds per siliqua, thousand seed weight and seed yield per plant.

### 3.4.9 Data collection methods:

The data were recorded on ten selected plants for each cross on the following traits-

**3.4.9.1 Days to 1st flowering:** When the treatments of each row showed the 1st flower bloom, days to 1st flowering was counted. Counting should be started from sowing date to the date of appearance of 1st flower bloom.

**3.4.9.2 Days to 50% flowering:** When near about 50 percent plants had at least one open flower of each line, days to 50% flowering was counted. Counting should be started from sowing date to the date of 50% flowering of every entry.

**Plate 4.** The pictorial view of experimental field during growth stage

**Plate 5.** The pictorial view of experimental field during flowering stage

**Plate 6.** The pictorial view of experimental field during harvesting period

**3.4.9.3 Days to 80% maturity:** From the date of sowing to siliquae maturity of 80% plants of each entry, the data were recorded.

**3.4.9.4 Plant height (cm):** Measurement of plant height was done in centimeter (cm) which was starting from the base of the plant to the tip of the longest inflorescence. After harvesting, data of plant height were taken.

**3.4.9.5 Root length (cm):** Root length was measured from the portion situated just below the starting point of the shoot to the end portion of the plant. It was measured in centimeter (cm) and data were taken after harvesting the plants.

**3.4.9.6 Number of primary branches per plant:** The total number of branches derived from the main stem of a plant were considered as primary branches and record was kept after counting.

**3.4.9.7 Number of secondary branches per plant:** The total number of branches originated from the primary branches of a plant was counted and deliberated as number of secondary branches per plant.

**3.4.9.8 Number of siliquae per plant:** Total number of siliquae of each plant were enumerated and considered as the number of siliquae per plant.

**3.4.9.9 Length of siliquae (cm):** Five representative siliquae were chosen randomly from each selected plant and measurement was taken in centimeter from the base to the tip of a siliqua without break.

**3.4.9.10 Number of seeds per siliqua:** All siliquae were collected from the sample plants and five siliquae were selected randomly. Record was kept after counting the seeds from the siliquae.

**3.4.9.11 Thousand seed weight (g):** Ten plants of each cross were selected. Thousand seeds from each entry were counted and weighted in grams.

**3.4.9.12 Seed yield per plant (g):** Seeds produced by a representative plant were weighted in gram and considered as the seed yield per plant.

### 3.4.10 Statistical analysis:

The data obtained for different characters were analyzed statistically for different components to find out the significance of the difference among the advanced populations of *B. rapa* After evaluating the mean values of all the characters, analysis of variance was performed by the F test. The significance of the differences among the treatments was estimated by least significant difference (LSD) test at 5% level of probability (Gomez and Gomez, 1984). Genotypic and phenotypic variance were estimated by the formula used by Johnson *et al.* (1955). Genotypic and phenotypic coefficient of variation were calculated by the help of the formula of Burton (1952). Heritability in broad sense was computed by using the formula given by Singh and Chaudhary (1985). Genetic advance was measured by using the formula of Allard (1960) while genetic advance in percentage of mean was computed by using the formula given by Comstock and Robinson (1952). Genotypic and phenotypic correlation obtained by the formula that was suggested by Al-Jibouri *et al*. (1958). Path coefficient analysis was done by following the outlined method of Dewey and Lu (1959).

#### 3.4.10.1 Analysis of variance:

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

The model of ANOVA used is presented below:

| **Sources of variation** | **Degrees of freedom (D.F.)** | **Mean sum of squares (MS)** | **Expected MS** |
|---|---|---|---|
| Replication | (r-1) | Mr | $p\,\sigma_r^2 + \sigma_e^2$ |
| Population | (p-1) | Mp | $r\,\sigma_p^2 + \sigma_e^2$ |
| Error | (p-1) (r-1) | Me | $\sigma_e^2$ |
| Total | (rp-1) | | |

Where, p = number of treatments (population)

r = number of replications

$\sigma_r^2$ = variance due to replications

$\sigma_p^2$ = variance due to treatments (populations)

$\sigma_e^2$= variance due to error

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

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

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

### 3.4.10.2 Estimation of Least Significant Differences (LSD):

Least Significant Differences were estimated according to the formula of Gomez and Gomez (1984).

$$LSD_\alpha = t_\alpha\sqrt{\frac{s^2}{r}}$$

Here, α = Level of significance, t= tabulated t value with concerned df at same level of significance, $s^2$= Error Mean Sum of Square and r = Number of replication.

### 3.4.10.3 Study of variability parameters:

Estimation of the variability among the populations for traits related to yield per plant in *B. rapa* were narrated below:

### 3.4.10.3.1 Estimation of Genotypic variance and phenotypic variance:

To estimate phenotypic and genotypic components of variance, Johnson *et al.* (1955) suggested a formula which is mentioned below:

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

Where,
MSG = Mean sum of square for genotypes
MSE = Mean sum of square for error, and
r = Number of replication

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

Where,
$\sigma_p^2$= Phenotypic variance
$\sigma_g^2$= Genotypic variance
$\sigma_e^2$ = Environmental variance = Mean square of error

### 3.4.10.3.2 Estimation of genotypic and phenotypic coefficient of variation:

To compute genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for all the characters, following formula was given by Burton, 1952:

$$\mathrm{GCV} = \frac{\sigma_\mathrm{g} \times 100}{\bar{\mathrm{x}}}$$

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

GCV = Genotypic coefficient of variation
PCV = Phenotypic coefficient of variation
$\sigma_g$= Genotypic standard deviation
$\sigma_p$= Phenotypic standard deviation
$\bar{x}$ = Population mean

Sivasubramanian and Madhavamenon (1973) categorized phenotypic coefficients of variation (PCV) and genotypic coeffcients of variation (GCV) as
Low (0-10%),
Moderate (10-20%) and
High (>20%)

### 3.4.10.3.3 Estimation of heritability in broad sense:

Singh and Chaudhary (1985) suggested a formula to estimate broad sense heritability which is given below:

$$\mathrm{h}_{\mathrm{b}}^2(\%) = \frac{\delta_{\mathrm{g}}^2}{\delta_{\mathrm{p}}^2} \times 100$$

Where,
$\mathrm{h}_{\mathrm{b}}^2$=Heritability in broad sense
$\sigma_{\mathrm{g}}^2$= Genotypic variance
$\sigma_{\mathrm{p}}^2$= Phenotypic variance

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

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

### 3.4.10.3.4 Estimation of genetic advance:

Allard (1960) suggested the following formula which was used to estimate the expected genetic advance for different characters under selection:

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

Where,

GA = Genetic advance

$\sigma_g^2$ = Genotypic variance

$\sigma_p^2$ = Phenotypic variance

$\sigma_p$ = Phenotypic standard deviation

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

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

### 3.4.10.3.5 Estimation of genetic advance in percentage of mean:

Following formula was given by Comstock and Robinson (1952) to compute genetic advance in percentage of mean:

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

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

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

### 3.4.10.4 Correlation coefficient analysis:

To determine the level of relationship of characters with yield and furthermore among the yield parts, the correlation coefficients were computed. Both genotypic and phenotypic correlation coefficients between two characters were determined by utilizing the variance and covariance components as suggested by Al-Jibouri *et al.* (1958).

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

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

Where,

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

$\mathrm{Cov}_g, \mathrm{Cov}_p$ are the genotypic and phenotypic covariance of xy, respectively.

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

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

### 3.4.10.5 Path coefficient analysis:

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

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

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

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

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

Where, r’s denote simple correlation coefficient and P’s denote path coefficient.

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

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

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

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

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

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

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

Hence, residual effect, $R = (P_{RY}^2)^{1/2}$
$P_{iy}$= Direct effect of the character on yield
$r_{iy}$=Correlation of the character with yield

Categories:
Negligible (0.00 to 0.09);
Low (0.10 to 0.19);
Moderate (0.20 to 0.29);
High (0.30 to 1.0);
Very High (>1.00)

# CHAPTER IV

# RESULTS AND DISCUSSION

The present experiment was undertaken to study variability among 8 advanced populations of *B. rapa*. The study was also conducted to detect the phenotypic, genotypic and environmental variance, phenotypic and genotypic coefficient of variation, heritability, genetic advance, genetic advance in percent of mean, correlation coefficient and path coefficient to estimate direct and indirect effect of yield contributing traits on yield. The data were recorded on the basis of different characters such as days to first flowering, days to 50% flowering, days to 80% maturity, plant height, root length, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, number of seed per siliqua, length of siliqua, thousand seed weight and seed yield per plant of 8 advanced populations of *B. rapa*. The data were statistically analyzed and thus acquired results are described below under the following headings:

4.1 Mean performance and genetic variability of the populations
4.2 Heritability, genetic advance and genetic advance in percentage of mean
4.3 Correlation analysis
4.4 Path coefficient analysis
4.5 Selection

## 4.1 Mean performance and genetic variability of the populations:

The achievement in any crop improvement program depends on the efficiency of the breeder to define and aggregate the required genetic variability and to select for yield indirectly through yield associated and highly heritable characters after alleviating the environmental component of phenotypic variation (Mather, 1949). Therefore, it is essential to have prior information on both phenotypic coefficient variation (PCV) and genotypic coefficient variation (GCV), so that the estimate of heritability that helps the breeder to predict the expected GA possibly by selection for a character can be calculated.

The results are related to analysis of variance (ANOVA), mean performance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense ($h^2b$) and expected genetic advance in percent of mean (GA) for all the traits. Analysis of variance for the experimental design pointed out significant differences for all the characters which indicated the presence of considerable genetic variation among the genotypes for all the traits (Appendix IV). Out of the twelve traits studied, plant height, no. of primary branches per plant, no. of secondary branches per plant were considered as growth attributing characters. Days to 1st flowering, days to 50% flowering and days to 80% maturity were considered as earliness attributes. No. of siliquae per plant, length of siliquae, no. of seeds per siliqua and 1000 seed weight were regarded as reproductive traits. Seed yield per plant was the economic trait. The mean values of yield and yield contributing characters of all the genotypes are shown in Table 3. Estimation of some genetic parameters such as genotypic, phenotypic and environmental variance, phenotypic and genotypic coefficient of variation is presented in Table 4 and Figured through line graph (Figure 1). The advanced populations of *B. rapa* evaluated on the basis of yield and yield contributing traits are presented below.

**Table 3.** Mean performance of yield and yield contributing characters of eight advanced populations of *B. rapa*

| **AP** | **DFF** | **DFPF** | **DTM** | **PH (cm)** | **RL (cm)** | **NPB/P** | **NSB/P** | **NS/P** | **LS (cm)** | **NS/S** | **TSW (g)** | **SY (g)** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Pop$^{n}$ 1 | 27.667 cd | 32 cd | 80 cd | 103.28 e | 10.453 cd | 8.9667 a | 5.5333 ab | 182.87 b | 6.44 a | 22.143 a | 3.1 ab | 8.027 bc |
| Pop$^{n}$ 2 | 31.667 b | 40.333 a | 88.667 a | 114.31 c | 11.767 bc | 5.7333 b | 3.7 bc | 110.07 cd | 5.7 b | 18.84 b | 2.4333 bc | 5.773 de |
| Pop$^{n}$ 3 | 25.667 d | 30.667 d | 76.667 e | 120.86 b | 13.733 a | 9.0667 a | 6.8333 a | 217.97 a | 6.0667 ab | 23.3 a | 3.5333 a | 11.7 a |
| Pop$^{n}$ 4 | 29.667 bc | 35.667 bc | 78.667 de | 109.77 d | 12.85 ab | 7.3 ab | 6.8 a | 187.5 b | 6.0433 ab | 23.307 a | 3.3667 a | 9.2 b |
| Pop$^{n}$ 5 | 31.667 b | 40.333 a | 85.667 b | 93.57 g | 9.827 d | 6.2 b | 3.1667 c | 103.61 cd | 6 ab | 18.353 bc | 3.0667 ab | 5.967 de |
| Pop$^{n}$ 6 | 26.667 cd | 34.667 cd | 78.667 de | 110.53 cd | 10.677 cd | 7.4 ab | 4 bc | 125.56 c | 6.0663 ab | 24.433 a | 2.2667 c | 6.667 cd |
| Pop$^{n}$ 7 | 35.333 a | 40.667 a | 89.333 a | 98.67 f | 10.367 cd | 5.0333 b | 2.7 c | 87.91 d | 4.6667 c | 16.1 c | 2.8333 abc | 4.8 e |
| Pop$^{n}$ 8 | 31.667 b | 39.333 ab | 82.333 c | 125.04 a | 12.967 ab | 5 b | 2.5667 c | 100.13 d | 5.0333 c | 18.073 bc | 2.9 abc | 5.467 de |
| **MAX** | **35.3** | **40.67** | **89.333** | **125.04** | **13.733** | **9.0667** | **6.8333** | **217.97** | **6.44** | **24.433** | **3.5333** | **11.7** |
| **MIN** | **25.7** | **30.67** | **76.667** | **93.57** | **9.827** | **5** | **2.5667** | **87.91** | **4.6667** | **16.1** | **2.2667** | **4.8** |
| **MEAN** | **30** | **36.71** | **82.5** | **109.5** | **11.58** | **6.8375** | **4.4125** | **139.45** | **5.752** | **20.569** | **2.9375** | **7.2** |
| **CV%** | **5.85** | **6.37** | **1.89** | **2.15** | **8.37** | **20.07** | **23.88** | **10.12** | **4.81** | **6.58** | **14.96** | **12.51** |
| **SE** | **1.43** | **1.91** | **1.2709** | **1.923** | **0.7916** | **1.1207** | **0.8605** | **11.527** | **0.2259** | **1.1044** | **0.3587** | **0.7356** |
| **LSD** | **3.07** | **4.096** | **2.7257** | **4.1243** | **2.4036** | **1.8456** | **1.6978** | **24.724** | **0.4845** | **2.3687** | **0.7694** | **1.5778** |

AP= Advanced Populations, DFF= Days to first flowering, DFPF = Days to 50% flowering, DTM = Days to 80% maturity, PH = Plant height (cm), RL=Root length, NPB/P = Number of primary branch per plant, NSB/P = Number of secondary branch per plant, NS/P = Number of siliquae per plant, LS = Length of siliqua (cm), NS/S = Number of seeds per siliqua, TSW = Thousand seed weight (g), SY/P= Seed yield per plant (g), CV (%) = Percentage of Coefficient of variation, SE= Standard error, LSD=Least Significant Difference.

**Table 4.** Estimation of some genetic parameters of 8 advanced populations of *B. rapa*

| **Parameters** | **DFF** | **DFPF** | **DTM** | **PH (cm)** | **RL (cm)** | **NPB/P** | **NSB/P** | **NS/P** | **LS (cm)** | **NS/S** | **TSW (g)** | **SY (g)** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| $\sigma_g^2$ | 9.976 | 12.202 | 10.673 | 113.09 | 1.807 | 1.985 | 2.684 | 7.572 | 0.332 | 8.094 | 0.061 | 2.132 |
| $\sigma_p^2$ | 12.184 | 18.065 | 20.602 | 118.64 | 2.747 | 3.869 | 3.795 | 287.572 | 0.406 | 10.372 | 0.326 | 4.5 |
| $\sigma_e^2$ | 2.2083 | 5.8631 | 9.9286 | 5.547 | 0.93991 | 1.88387 | 1.11065 | 280.02 | 0.07438 | 2.2783 | 0.26494 | 2.36755 |
| **GCV** | 10.161 | 10.296 | 5.773 | 9.712 | 11.607 | 20.605 | 37.135 | 34.749 | 10.043 | 14.492 | 11.851 | 31.341 |
| **PCV** | 11.723 | 12.108 | 6.074 | 9.947 | 14.311 | 28.767 | 44.153 | 36.193 | 11.136 | 15.914 | 19.083 | 33.747 |

DFF= Days to first flowering , DFPF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), RL=Root length, NPB/P = Number of primary branch per plant, NSB/P = Number of secondary branch per plant, NS/P = Number of siliquae per plant, LS = Length of siliquae (cm), NS/S = Number of seeds per siliqua, TSW = Thousand seed weight (g), SY/P =Seed yield per plant (g) $\sigma_g^2$= Genotypic variance, $\sigma_p^2$= Phenotypic variance, $\sigma_e^2$ = Environmental variance, GCV= Genotypic Coefficient of variation, PCV =Phenotypic Coefficient of variation.

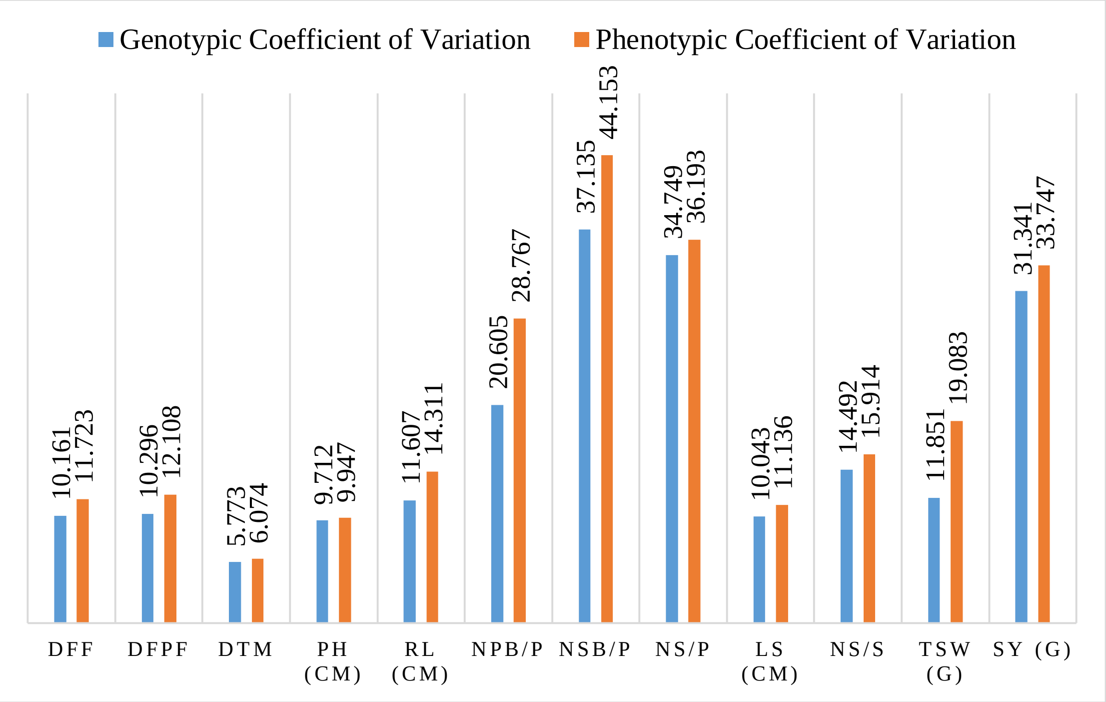


**Figure 1.** Genotypic and phenotypic coefficient of variation of 12 characters of 8 advanced populations of *B. rapa*

### 4.1.1 Days to first flowering:

Highly significant variations were observed among the tested advanced populations for the character of days to first flowering (30.95) (Appendix IV). The minimum duration required for first flowering was found in Pop$^n$ 3 with 25.667 DAS indicating that first flower appeared earlier than other advanced populations sowing in Table 3. It also matured earlier (76.667 DAS) than other populations. On the contrary, maximum duration required for first flowering was noticed in Pop$^n$ 7(35.333 DAS) which also matured later (89.333 DAS) (Table 3). Mean value of 30.00 DAS was recorded. Mean performance of days to first flowering in 8 advanced populations of *B. rapa* is presented in Figure 2 through line graph.

It was observed that there were no significant differences in days to 1st flowering among the populations of Pop$^n$ 2, Pop$^n$ 5 and Pop$^n$ 8 (31.667 DAS). There were very little differences among Pop$^n$ 1 (27.667 DAS), Pop$^n$ 3 (25.667 DAS), Pop$^n$ 4 (29.667 DAS) and Pop$^n$ 6 (26.667 DAS) (Table 3). They showed almost similar performance in days to 1st flowering.

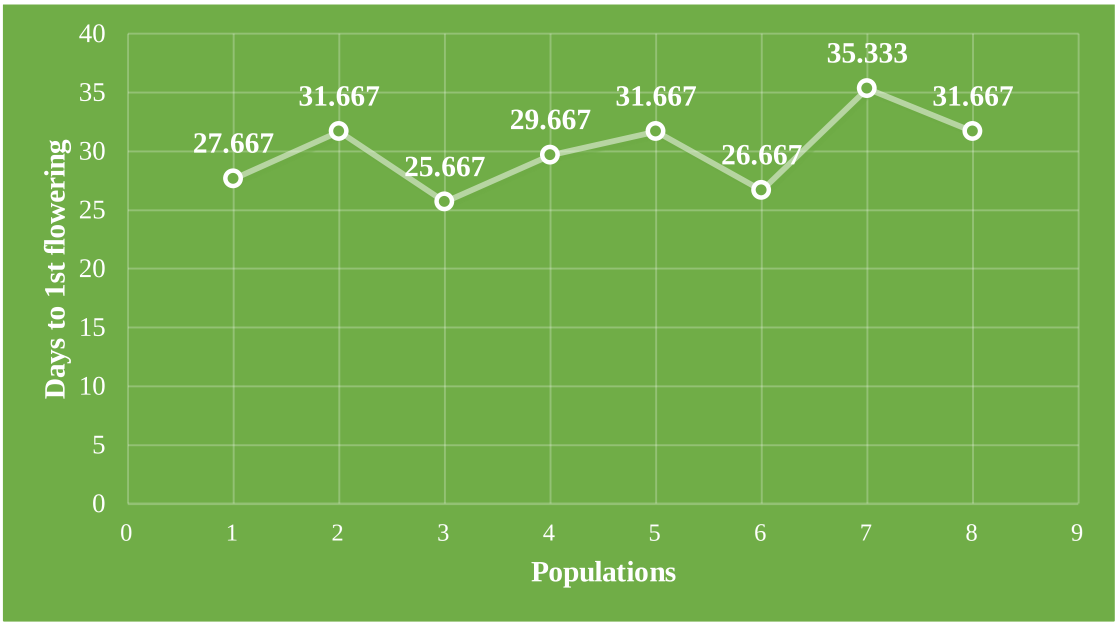


**Figure 2.** Mean performance of days to first flowering in 8 advanced populations of *B. rapa*

The phenotypic variance (12.18) was higher than genotypic variance (9.976) and variation between them was moderate indicating that environment had moderate influence for the expression of this trait (Table 4). Generally, quantitative characters were highly influenced by the environment. The GCV (Genotypic coefficient of variation) and PCV (Phenotypic coefficient of variation) were moderate with 10.16 and 11.72 percent, respectively (Table 4) (Figure 1).

### 4.1.2 Days to 50% flowering:

Significant variations were observed in days to 50% flowering among the 8 advanced populations of *B. rapa* (48.33) (Appendix IV). The minimum duration to days to 50% flowering was found in Pop$^n$ 3 with 30.667 DAS indicating that 50% flowers appeared earlier in Pop$^n$ 3 than other advanced populations after sowing. The earliness of 50% flowering of population indicated that the plants matured early. Pop$^n$ 7 took maximum period for 50 % flowering with 40.67 DAS (Table 3). Mean value was recorded as 36.71 DAS. Ali *et al.* (2002) found days to 50% flowering for parents which was ranged from 39 to 46 days. Mean performance of days to 50% flowering in 8 advanced populations of *B. rapa* is shown in Figure 3 through line graph. A pictorial view showing flowering of different advanced populations is presented in Plate 7.

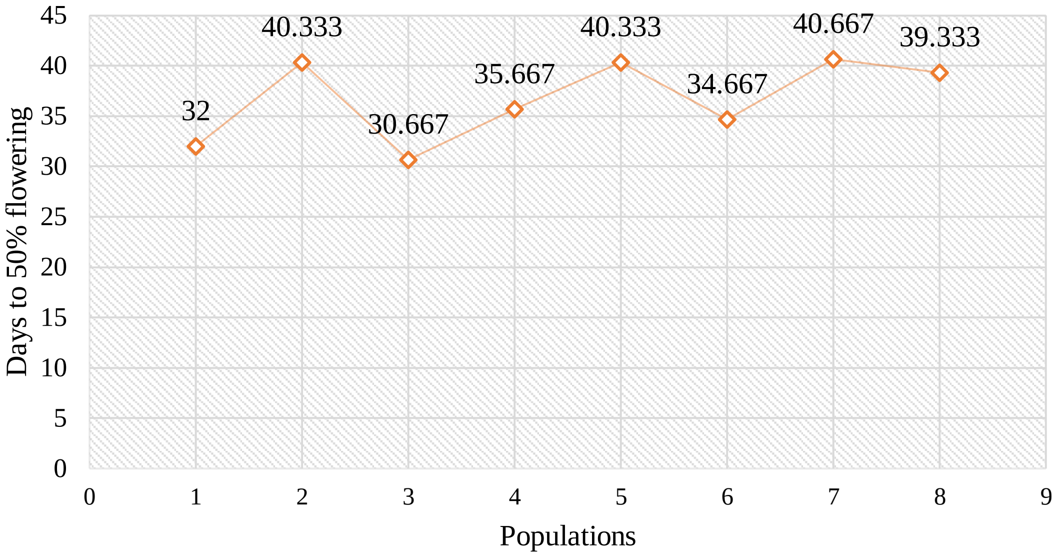


**Figure 3.** Mean performance of days to 50% flowering in 8 advanced populations of *B. rapa*

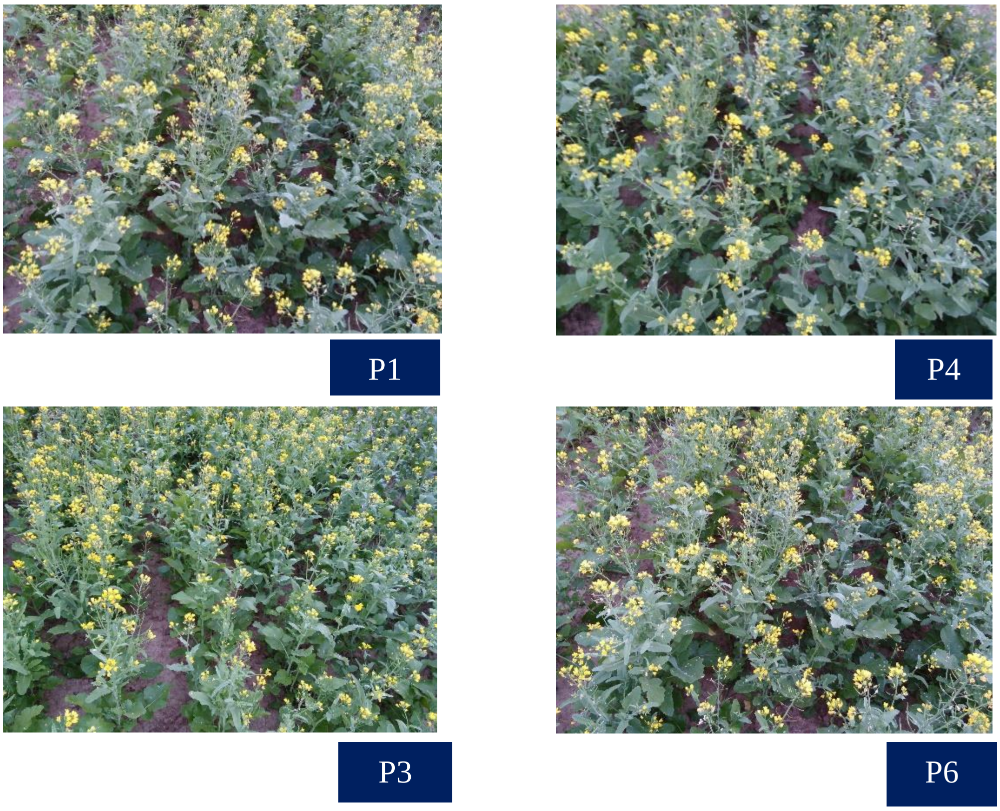


**Plate 7.** A pictorial view showing flowering of different advanced populations

The phenotypic variance (18.07) was higher than genotypic variance (12.20) and variation between them was moderate indicating that environment had moderate influence for the expression of the character (Table 4). The GCV (Genotypic coefficient of variation) and PCV (Phenotypic coefficient of variation) were moderate with value of 10.3 and 12.11 per cent, respectively (Table 4) (Figure 1).

### 4.1.3 Days to 80% maturity:

Highly significant variations were observed among the populations for the character of days to 80% maturity (70.48) (Appendix IV). The Pop$^n$ 3 required least number of days to mature (76.667 DAS). It indicated that Pop$^n$ 3 matured earlier than other populations followed by Pop$^n$ 4 (78.667 DAS), Pop$^n$ 6 (78.667 DAS) and Pop$^n$ 1 (80.00 DAS). Maximum number of days for 80% maturity was observed in the population Pop$^n$ 7 (89.333 DAS) (Table 3). Mean value was 82.5 (Table 3). Mean performance of days to 80% maturity in 8 advanced populations of *B. rapa* is shown in Figure 4 through line graph.

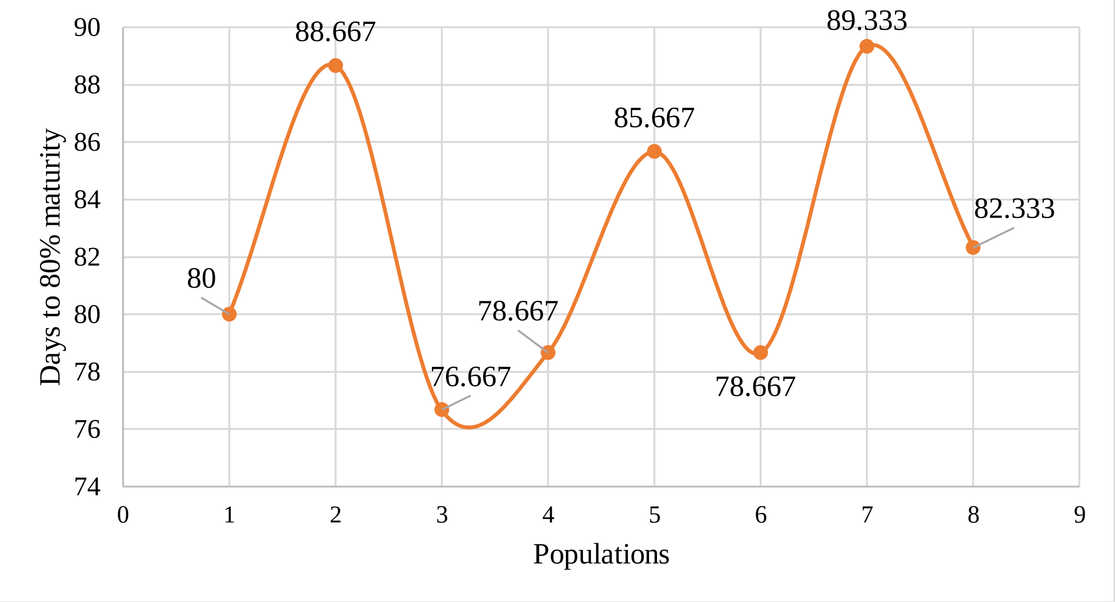


**Figure 4.** Mean performance of days to 80% maturity in 8 advanced populations of *B. rapa*

Phenotypic variance was recorded as 20.6 which was higher than genotypic variance (10.67) with moderate difference between them indicating that there was little influence in the expression of genes for this trait (Table 4). The value of GCV (Genotypic Coefficient of variation) and PCV (Phenotypic Coefficient of variation) was very low, 5.773 and 6.074 percent, respectively for days to 80% maturity (Table 4) (Figure 1).

### 4.1.4 Plant height (cm):

Plant height is an essential characteristic of *Brassica* genotypes being related to flowering time because as more time passes before flowering, more height is obtained through vegetative growth of the primary stem. Highly significant variations (344.83) were observed for this trait among the tested advanced populations (344.83) (Appendix IV). In this study the highest plant height was observed in Pop$^n$ 8 (125.04 cm) (Table 3) whereas the minimum plant height was observed in Pop$^n$ 5 (93.57 cm) (Table 3). Mean performance of plant height in 8 advanced populations of *B. rapa* is presented in Figure 5 through bar graph.

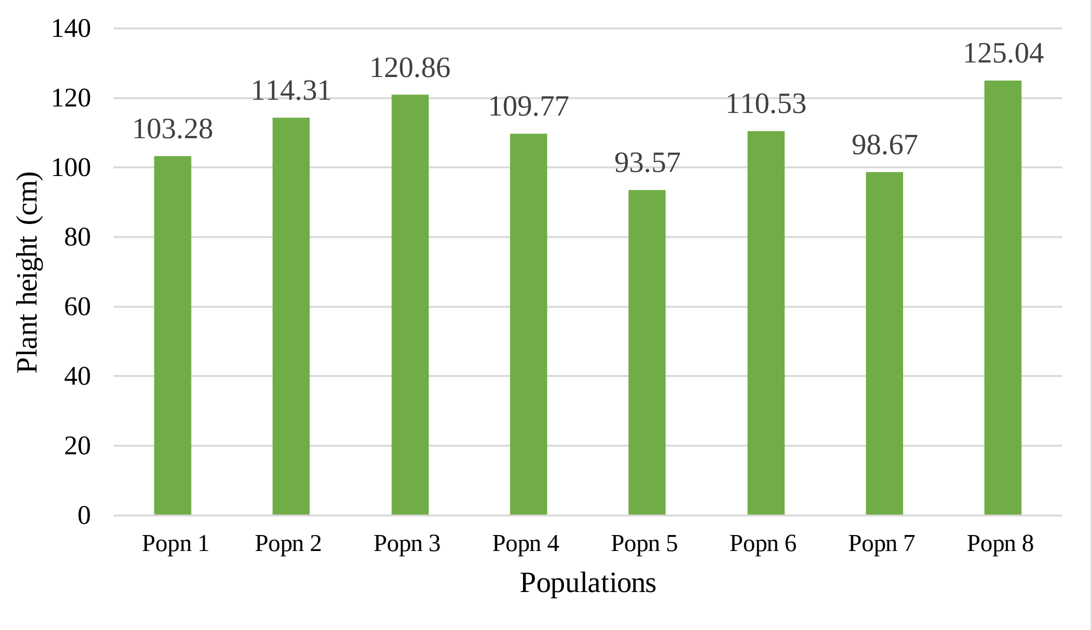


**Figure 5.** Mean performance of plant height (cm) in 8 advanced populations of *B. rapa*

Phenotypic variance and genotypic variance were observed as 118.64 and 113.09, respectively. The phenotypic variance appeared to be higher than the genotypic variance which indicated that considerable influence of environment presents on the expression of the genes controlling this trait. Ara *et al.* (2010) found the highest difference between genotypic and phenotypic variance in plant height. The value of GCV (Genotypic Coefficient of variation) and PCV (Phenotypic Coefficient of variation) was low, 9.712 and 9.947 percent, respectively (Table 4) (Figure 1). The highest variation in plant height among parents and their hybrid was observed by Tyagi *et al*. (2001).

### 4.1.5 Root length (cm):

Highly significant variations were observed among the populations for the character of root length (Appendix IV). Root length showed significant differences among the advanced populations (6.36) (Appendix IV). Maximum length of root was found in Pop$^n$ 3 (13.773 cm) whereas minimum in Pop$^n$ 5 (9.827 cm) (Table 3). Mean value was 11.58 (Table 3). Mean performance of root length in 8 advanced populations of *B. rapa* is shown in Figure 6 through bar graph.

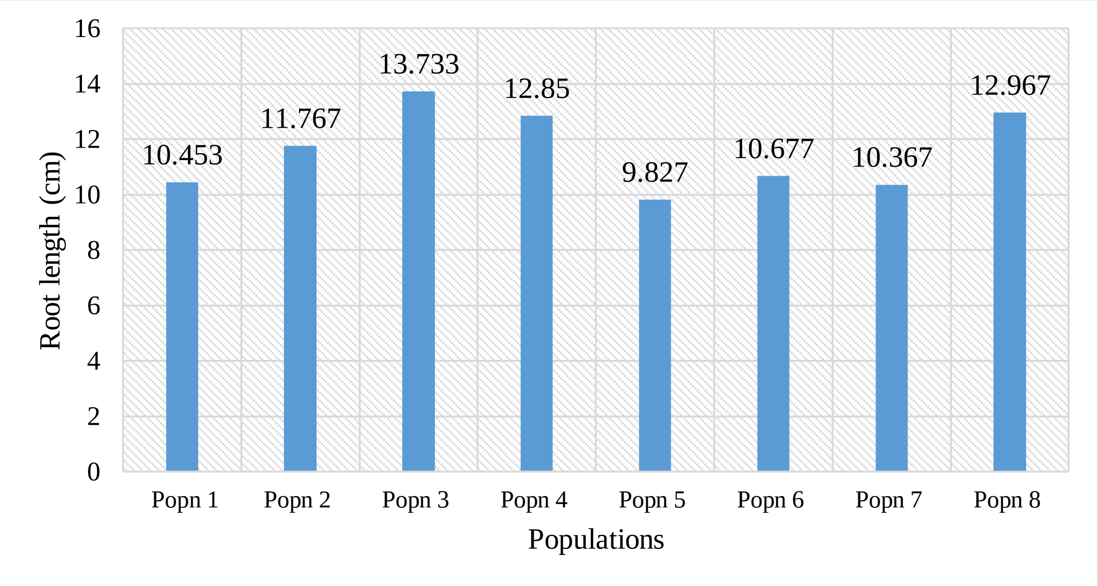


**Figure 6.** Mean performance of root length (cm) in 8 advanced populations of *B. rapa*

Phenotypic variance (2.747) was slightly higher than genotypic variance (1.807) having little difference between them indicated that there was less environmental effect on this trait (Table 4). The value of GCV (Genotypic Coefficient of Variation) and PCV (Phenotypic Coefficient of Variation) were moderate, 11.607 and 14.311 percent (Figure 1), respectively.

### 4.1.6 Number of primary branches per plant:

Number of primary branches per plant showed highly significant variations among the tested advanced populations (7.84) (Appendix IV). Maximum number of primary branches per plant was noticed in Pop$^n$ 3 (9.0667) and minimum number of primary branches per plant were found in Pop$^n$ 8 (5.00) followed by Pop$^n$ 1 (8.9667), Pop$^n$ 6 (7.40), Pop$^n$ 4 (7.30), Pop$^n$ 5 (6.20), Pop$^n$ 2 (5.7333) and Pop$^n$ 7 (5.0333) (Table 3). The mean value was 6.8375 (Table 3). Pop$^n$ 3 showed maximum no. of primary branches per plant (9.0667) indicating more siliquae than the other populations which ultimately increased yield per plant. Mean performance of number of primary branches per plant in 8 advanced populations of *B. rapa* is presented in Figure 7 through line graph.

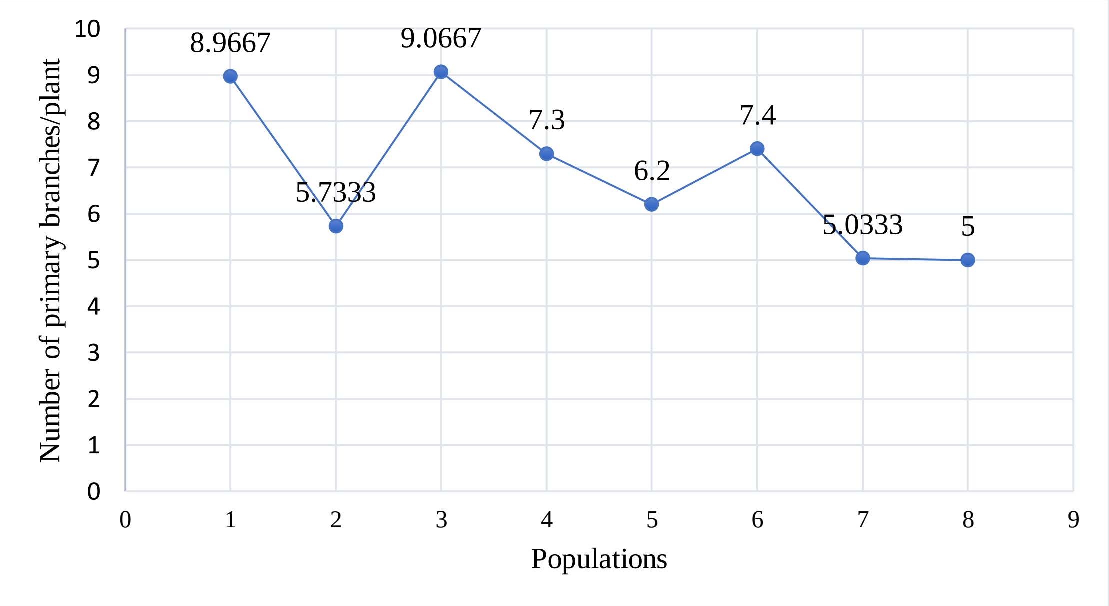


**Figure 7.** Mean performance of number of primary branches per plant in 8 advanced populations of *B. rapa*

The genotypic and phenotypic variance was recorded as 1.985 and 3.869 percent, respectively which suggested that there was less influence of environment on this character (Table 4). Naznin *et al.* (2015) showed least differences between the phenotypic variance (1.27) and genotypic variance (0.86) in case of number of primary branches per plant which indicated that there was less influence of environment on this character. Findings of Hosen *et al.* (2008) was also agreed with this result. The values of GCV (Genotypic Coefficient of Variation) and

PCV (Phenotypic Coefficient of Variation) was high, 20.605 and 28.767 percent (Figure 1), respectively.

### 4.1.7 Number of secondary branches per plant:

Significant variations were observed for the number of secondary branches per plant (9.17) suggesting that large variations are present among the tested advanced populations (Appendix IV). The maximum number of secondary branches were found in Pop$^n$ 3 (6.8333) with more number of siliquae per plant (217.97) which was a good sign for increasing yield and ultimately highest seed yield per plant was found in Pop$^n$ 3 (11.70). The minimum number of secondary branches per plant were found in Pop$^n$ 8 (2.5667). Mean value was 4.4125 (Table 3). Mean performance of number of secondary branches per plant in 8 advanced populations of *B. rapa* is presented in Figure 8 through line graph.

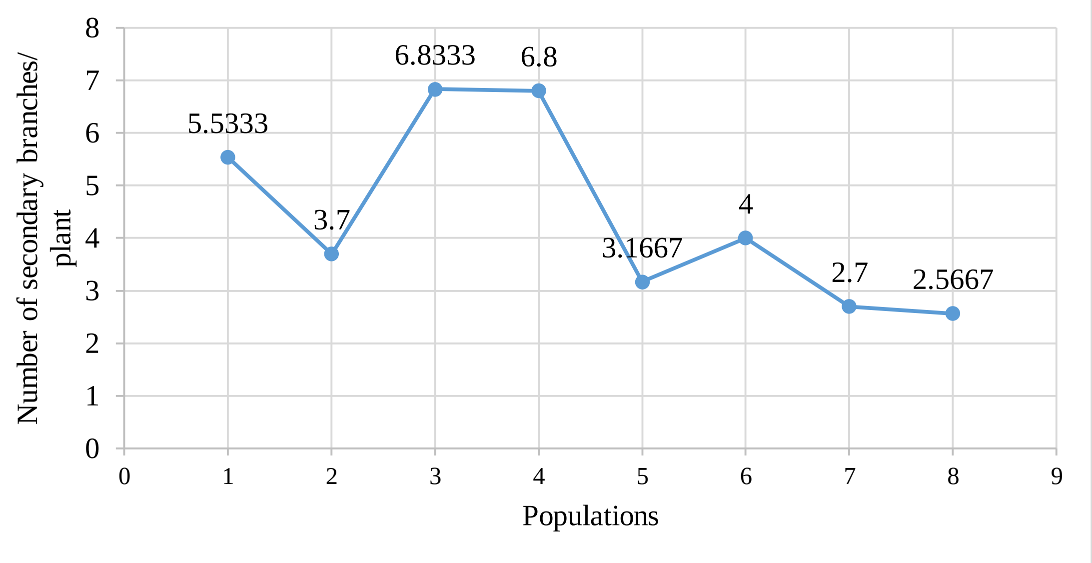


**Figure 8.** Mean performance of number of secondary branches per plant in 8 advanced populations of *B. rapa*

The genotypic and phenotypic variance were recorded as 2.684 and 3.795 respectively and phenotypic variance was slightly higher than genotypic variance. Less environmental influence was found due to little difference between genotypic and phenotypic variance. The value of GCV (Genotypic Coefficient of Variation) and PCV (Phenotypic Coefficient of Variation) were high, 37.14 and 44.15 percent, respectively (Table 4) (Figure 1). Sikarwar *et* al.

(2017) reported high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for number of secondary branches per plant. Naznin *et al.* (2015) showed the same findings.

### 4.1.8 Number of siliquae per plant:

Highly significant variations were observed among the populations for the character of number of siliquae per plant (7243.7) (Appendix IV). The highest number of siliquae per plant was found in population Pop$^n$ 3 (217.97) which was a good sign for increasing yield and ultimately highest seed yield per plant was found in Pop$^n$ 3 (11.70). The population Pop$^n$7 showed lowest number of siliquae per plant (87.91) followed by Pop$^n$ 4 (187.50), Pop$^n$ 1 (182.87), Pop$^n$ 6 (125.56), Pop$^n$ 2 (110.07), Pop$^n$ 5 (103.61) and Pop$^n$ 8 (100.13) (Table 3). Having lowest number of siliquae per plant (87.91), Pop$^n$ 7 showed lowest yield (4.80). the mean value was 139.45 (Table 3). Mean performance of number of siliquae per plant in 8 advanced populations of *B. rapa* is shown in Figure 9 through line graph.

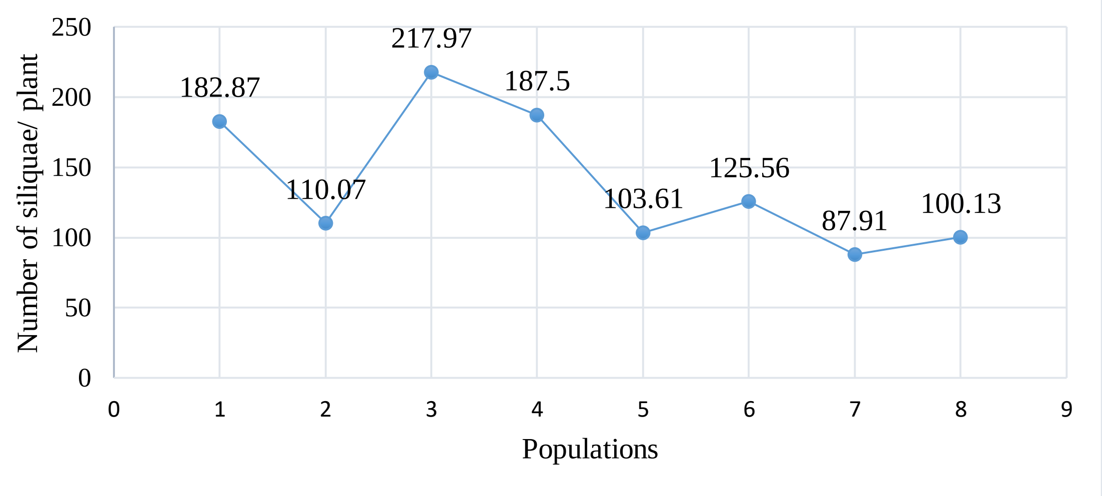


**Figure 9.** Mean performance of number of siliquae per plant in 8 advanced populations of *B. rapa*

The phenotypic variance (7.572) was higher than genotypic variance (287.572). This indicated high influence of environment on this character. Naznin *et al.* (2015) reported high phenotypic variance (661.58) and genotypic variance (616.31) for number of siliquae/plant. The high GCV (Genotypic coefficient of variation) (34.749%) and high PCV (Phenotypic coefficient of variation) (36.193%) (Table 4) (Figure 1) indicated presence of variability among the populations. Rashid (2007) discovered higher estimates of genotypic coefficient of variation for number of siliquae/plant and maximum genotypic and phenotypic coefficients of variations were found for number of siliquae/plant by Ali *et al.* (2003).

### 4.1.9 Length of siliqua (cm):

Highly significant variations were observed among the advanced populations for this trait (1.08) (Appendix IV). Length of siliquae was longer in Pop$^n$ 1 (6.44 cm) and shorter in Pop$^n$ 7 (4.6667 cm) followed by Pop$^n$ 3 (6.0667 cm), Pop$^n$ 6 (6.0663 cm), Pop$^n$ 4 (6.0433 cm), Pop$^n$ 5 (6.00 cm) Pop$^n$ 2 (5.70 cm) and Pop$^n$ 8 (5.0333 cm). Longer length of siliqua increases the possibility of more yield but it had less number of siliqua than Pop$^n$ 3. Having shorter length of siliqua per plant, Pop$^n$ 7 showed lowest yield (4.80). The mean value was 5.752 cm (Table 3). Mean performance of length of siliquae in 8 advanced populations of *B. rapa* is presented in Figure 11 through bar graph. A pictorial view showing length of siliqua (cm) of different advanced populations is presented in Plate 8.

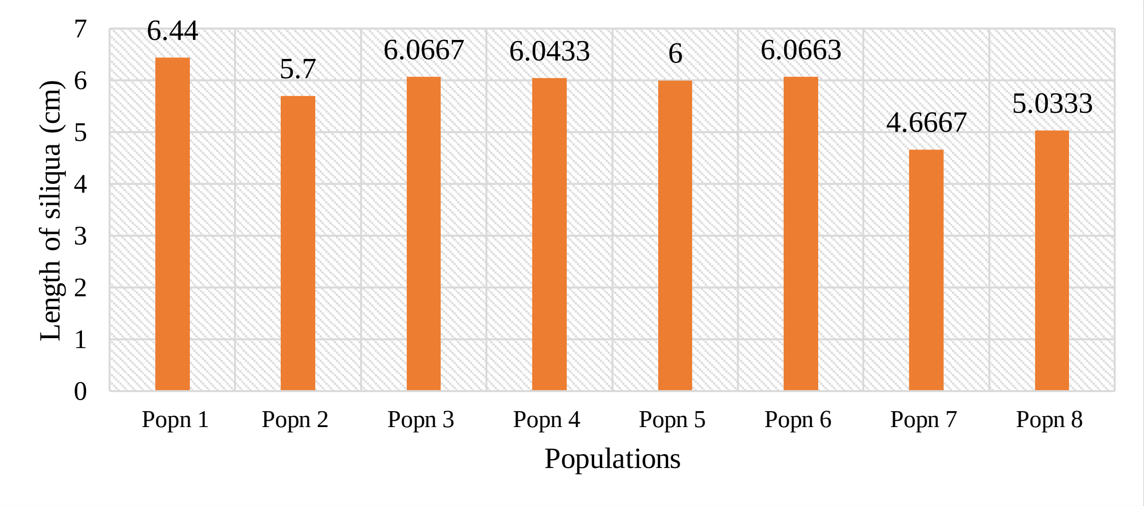
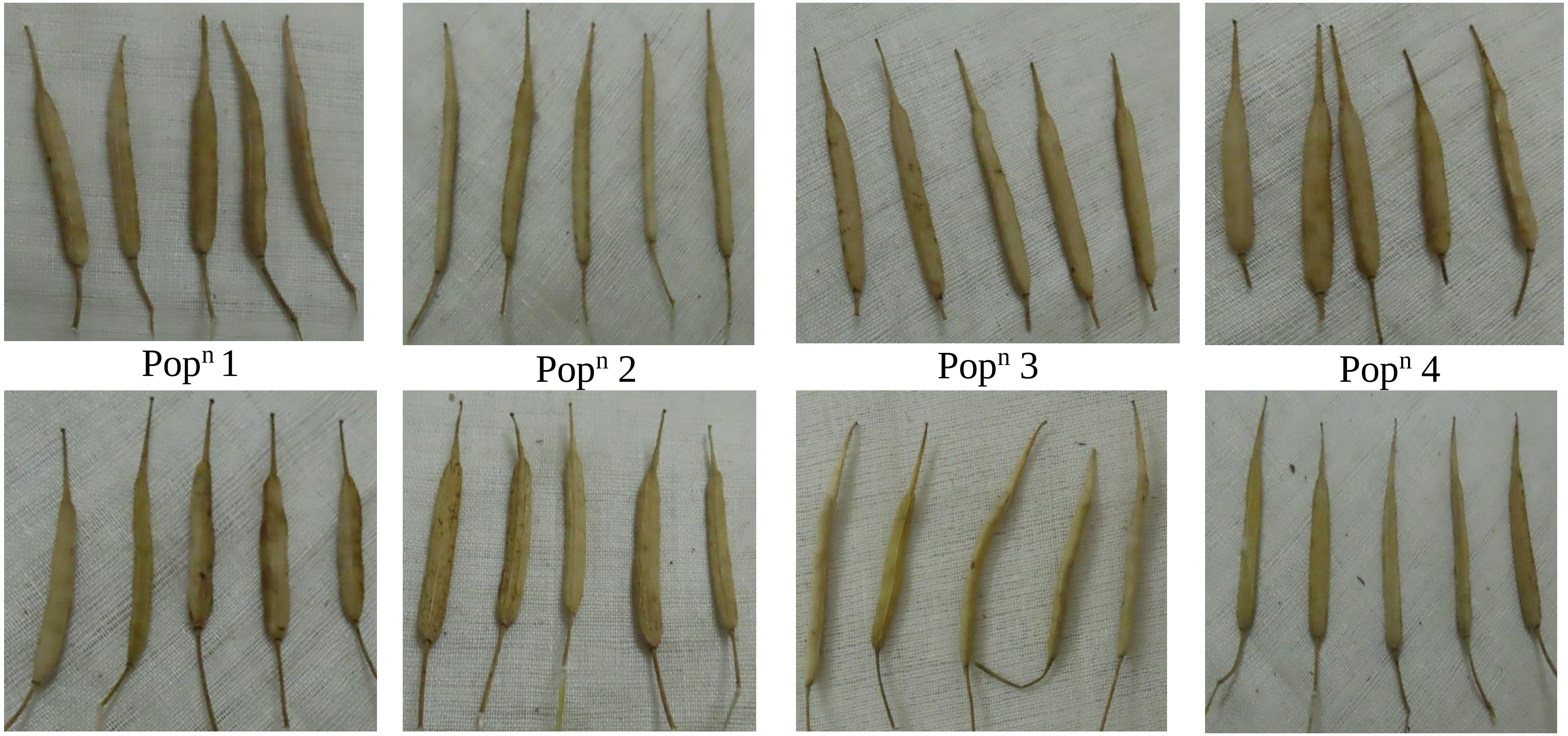


**Figure 10.** Mean performance of length of siliqua (cm) in 8 advanced populations of *B. rapa*



Pop$^n$ 1 Pop$^n$ 2 Pop$^n$ 3 Pop$^n$ 4

Pop$^n$ 5 Pop$^n$ 6 Pop$^n$ 7 Pop$^n$ 8

**Plate 8.** A pictorial view showing siliquae length (cm) of different advanced populations

Phenotypic variance (0.406) was slightly higher than genotypic variance (0.332) for length of siliquae with little difference between them indicating that environment has less influence for the expression of this trait (Table 4). The value of GCV (Genotypic Coefficient of Variation) and PCV (Phenotypic Coefficient of Variation) were moderate, 10.043 and 11.136 percent, respectively (Table 4) (Figure 1). The same finding was also reported by Sikarwar *et al. (*2017).

### 4.1.10 Number of seeds per siliqua:

Number of seeds per siliqua showed highly significant variations (28.48) which indicated the presence of large variations among the tested advanced populations (Appendix IV). The maximum number of seeds per siliqua was found in Pop$^n$ 6 (24.433) but lowest thousands seed weight (2.2667 g) (Table 3) which hampered more yield. The minimum number of seeds per siliqua exhibited in population Pop$^n$ 7 (16.10) with lowest yield (4.80 g) (Table 3). The mean value was 20.569 (Table 3). Mean performance of number of seeds per siliqua in 8 advanced populations of *B. rapa* is presented in Figure 11 through line graph.

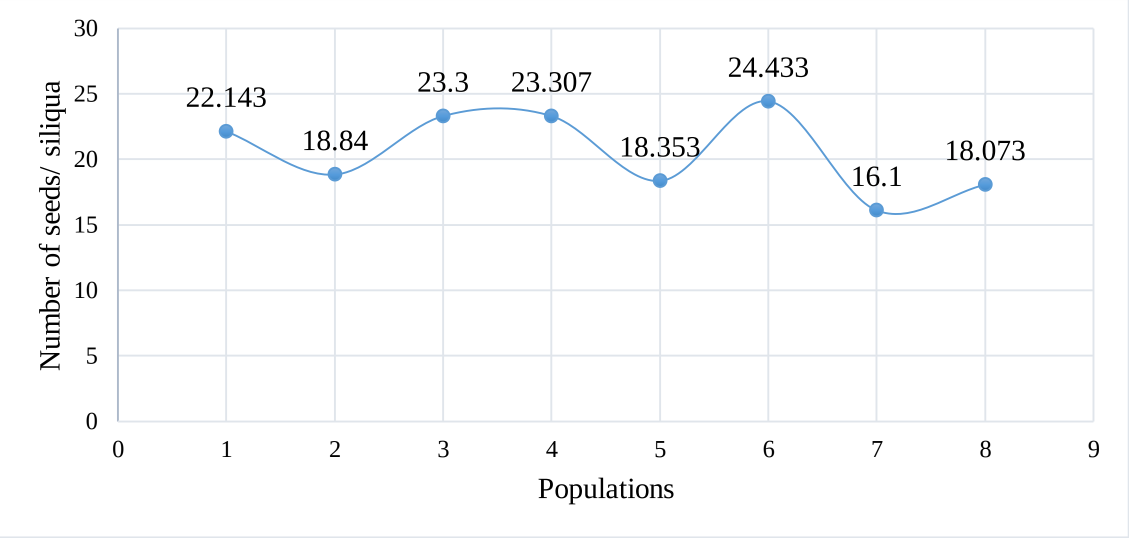


**Figure 11.** Mean performance of number of seeds per siliqua in 8 advanced populations of *B. rapa*

The phenotypic variance was (10.372) higher than genotypic variance was (8.094) having moderate difference between them indicating that there was moderate influence of environment on this trait (Table 4). Moderate GCV (Genotypic coefficient of variation) (17.02) and PCV (Phenotypic coefficient of variation) (19.31) were observed (Table 4) (Figure 1). There was a little difference in the estimates of GCV and PCV for number of seeds per siliqua suggested low environmental effect in the expression of this trait.

### 4.1.11 Thousand seed weight (g):

Thousand seed weight (g) showed significant variations (0.5566) among the tested advanced populations (Appendix IV). Maximum thousand seed weight (g) was found in Pop$^n$ 3 (3.5333 g) which increased the possibility of higher yield and ultimately highest yield was found from Pop$^n$ 3 (11.70 g) whereas minimum thousands seed weight (g) was found in Pop$^n$ 6 (2.2667 g) followed by Pop$^n$ 4 (3.3667 g), Pop$^n$ 1(3.10 g), Pop$^n$ 5 (3.0667 g), Pop$^n$ 8 (2.90 g), Pop$^n$ 7 (2.8333 g) and Pop$^n$ 2 (2.4333 g) (Table 3). The mean value was 2.9375 g (Table 3). Mean performance of thousand seed weight in 8 advanced populations of *Brassica rapa* L. is embellished in Figure 12 through line graph.

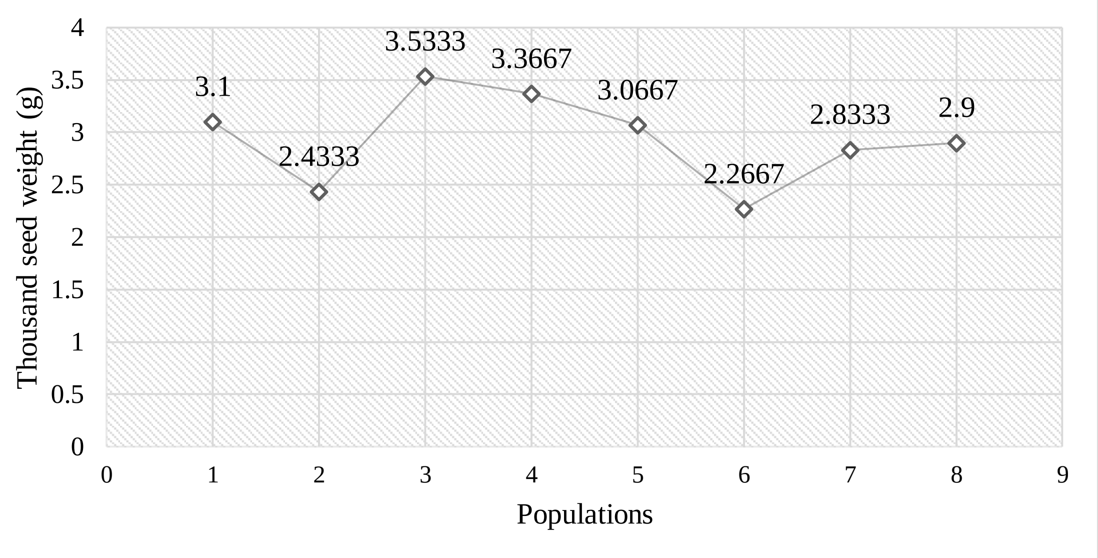


**Figure 12.** Mean performance of thousand seed weight (g) in 8 advanced populations of *B. rapa*

The values of phenotypic variance and genotypic variance were 0.326 and 0.061, respectively. The little difference between them indicates the less influence of environment on this trait. The values of GCV (Genotypic Coefficient of Variation) and PCV (Phenotypic Coefficient of Variation) was moderate, 11.851 and 19.083 percent, respectively (Table 4) (Figure 1).

### 4.1.12 Seed yield per plant (g):

The performance of the advanced populations showed highly significant variations (16.09) for the trait yield per plant (Appendix IV). Maximum seed yield per plant (g) was found in Pop$^{n}$ 3 (11.70 g) followed by Pop$^{n}$ 4 (9.20 g), Pop$^{n}$ 1 (8.027 g), Pop$^{n}$ 6 (6.667 g), Pop$^{n}$ 5 (5.967 g), Pop$^{n}$ 2 (5.773) and Pop$^{n}$ 8 (5.467 g) (Table 3). Pop$^{n}$ 3 showed highest seed yield per plant due to highest number of primary branches per plant (9.0667), highest number of secondary branches per plant (6.8333), highest number of siliquae per plant (217.97), 2nd highest length of siliqua (6.0667 cm), 2nd highest number of seeds per siliqua (23.30) and highest thousand seed weight (3.5333 g). Pop$^{n}$ 7 showed lowest seed yield per plant (4.80 g). The mean value was 7.20 g (Table 3). Mean performance of seed yield per plant in 8 advanced populations of *B. rapa* is shown in Figure 13 through line graph.

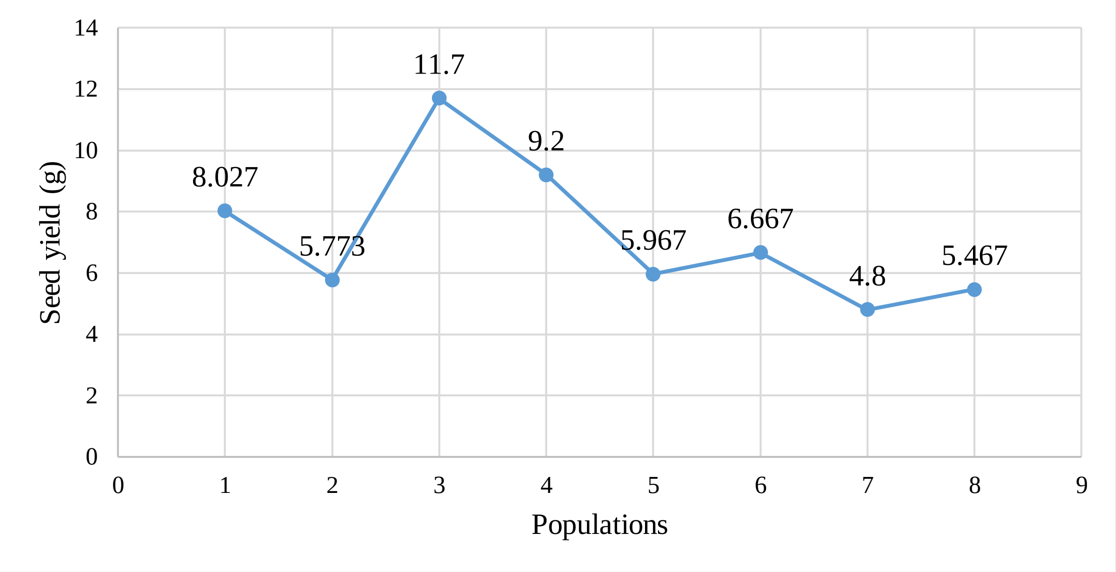


**Figure 13.** Mean performance of seed yield per plant (g) in 8 advanced populations of *B. rapa*

The phenotypic variance was (4.50) higher than genotypic variance was (2.132) having moderate difference between them indicating that there is moderate influence of environment on this trait (Table 4). The similar finding was also reported by Afrin *et al*. (2016). The values of GCV (Genotypic Coefficient of Variation) and PCV (Phenotypic Coefficient of Variation) was high, 31.341 and 33.747 percent, respectively (Table 4) (Figure 1).

### 4.2 Heritability, genetic advance and genetic advance in percentage of mean:

The coefficient of variation does not permit the full opportunity for heritable variation. It can be discerned with greater degree of accuracy when heritability in association with genetic advance is discussed. Hence, heritability and genetic advance are essential parameters to study the scope of improvement in various characters via selection. Heritability, genetic advance and genetic advance in percent of means for yield and yield contributing characters of 8 advanced populations of *B. rapa* is presented in table 5 and also figured through line graph (Figure 14).

**Table 5.** Heritability, genetic advance and genetic advance in percentage of mean for yield and yield contributing characters of 8 advanced populations of *B. rapa*

| **Parameters** | **Heritability** | **Genetic advance** | **Genetic advance in percentage of mean** |
|---|---|---|---|
| **DFF** | 75.12 | 5.442 | 18.141 |
| **DFPF** | 72.311 | 6.621 | 18.037 |
| **DTM** | 90.351 | 9.326 | 11.304 |
| **PH (cm)** | 95.325 | 21.389 | 19.533 |
| **RL (cm)** | 65.778 | 2.246 | 19.392 |
| **NPB/P** | 51.305 | 2.079 | 30.403 |
| **NSB/P** | 70.739 | 2.839 | 64.34 |
| **NS/P** | 92.176 | 95.838 | 68.725 |
| **LS (cm)** | 81.341 | 1.073 | 18.659 |
| **NS/S** | 82.925 | 5.592 | 27.185 |
| **TSW (g)** | 38.568 | 0.445 | 15.161 |
| **SY (g)** | 86.251 | 4.317 | 59.96 |

DFF= Days to first flowering, DFPF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), RL=Root length(cm), NPB/P = Number of primary branch per plant, NSB/P = Number of secondary branch per plant, NS/P = Number of siliquae per plant, LS = Length of siliqua (cm), NS/S = Number of seeds per siliqua, TSW = Thousand seed weight (g), SY/P =Seed yield per plant (g).

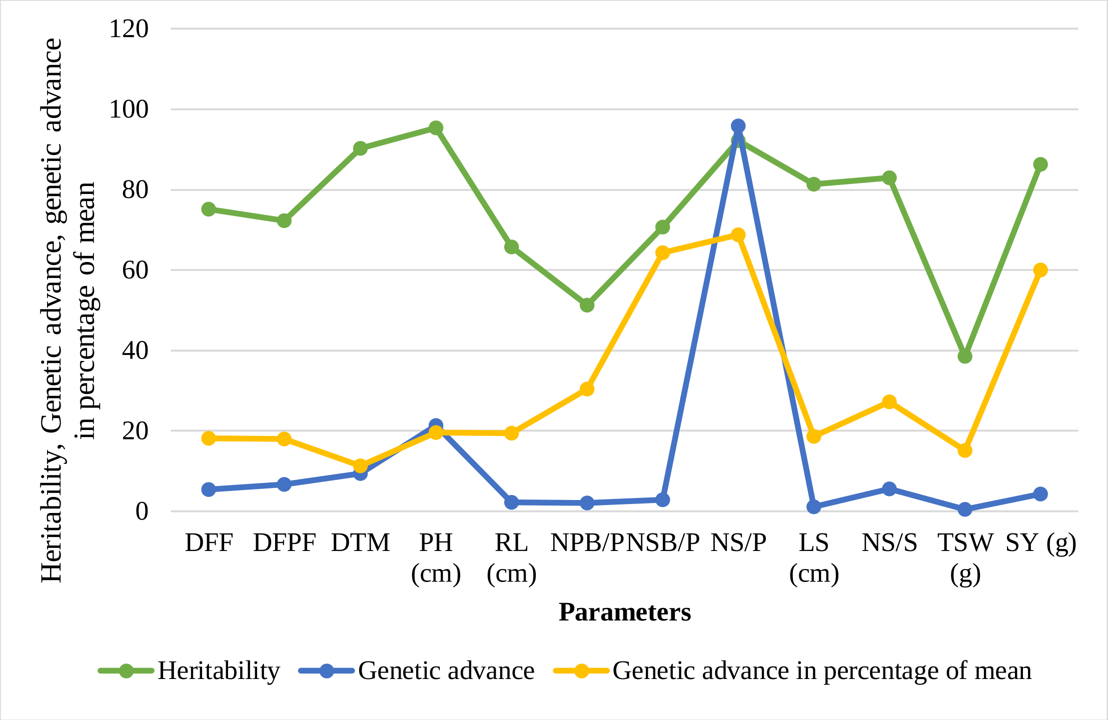


**Figure 14.** Heritability, genetic advance & genetic advance (% mean) of 12 characters of 8 advanced populations of *B. rapa*

### 4.2.1 Days to first flowering:

High heritability (75.12%) in association with low genetic advance (5.442) was noted for this character rendering them unfit for improvement through simple selection due to prevalence of non-additive gene action (Table 5) (Figure 14). Similar result was also reported by Sikarwar *et al.* (2017). Moderate value of genetic advance in percent of mean (18.141) was also recorded in (Table 5) (Figure 14).

### 4.2.2 Days to 50% flowering:

High heritability of 72.3111% with low genetic advance (6.621) was noted for the character and the value of genetic advance in percent of mean was moderate (18.037) (Table 5) (Figure 14). High heritability having low genetic advance suggested the prevalence of non- additive gene action and so, improvement through selection might not be so effective. Akter (2010) reported high heritability (88.86%) and low genetic advance (2.06) for days to 50% flowering which was similar to the findings.

### 4.2.3 Days to 80% maturity:

High heritability of 90.351% with low genetic advance (9.326) was noted for the character and the value of genetic advance in percent of mean was moderate (11.304) (Table 5) (Figure 14). High heritability with low genetic advance suggested the prevalence of non- additive gene action and so, improvement through selection might not be so effective. Environment was mainly responsible for high heritability. Jahan *et al.* (2014) observed high heritability with low genetic advance in per cent of mean for days to maturity.

### 4.2.4 Plant height (cm):

High heritability of 95.325% with moderate genetic advance (21.389) was noted for the character and the value of genetic advance in percent of mean was moderate (19.533) (Table 5) (Figure 14). High heritability with moderate genetic advance supported the opportunity of improvement by direct selection of the trait.

### 4.2.5 Root length (cm):

High heritability of 65.778% with low genetic advance (2.246) was noted for the character and the value of genetic advance in percent of mean was moderate (19.392) (Table 5) (Figure 14). High heritability with low genetic advance suggested the prevalence of non- additive gene action and so, improvement through selection might not be so effective.

### 4.2.6 Number of primary branches per plant:

Moderate heritability 51.305% along with low genetic advance (2.079) (Table 5) (Figure 14) indicating the presence of non-additive gene action which was responsible for the ineffectiveness of the selection for this trait whereas genetic advance in percent mean was recorded high (30.403) (Table 5) (Figure 14).

### 4.2.7 Number of secondary branches per plant:

High heritability 70.739% along with low genetic advance (2.839) (Table 5) (Figure 14) indicating the presence of non-additive gene action which was responsible for the ineffectiveness of the selection for this trait whereas genetic advance in percent mean was recorded high (64.34) (Table 5) (Figure 14).

### 4.2.8 Number of siliquae per plant:

High heritability of 92.176% with high genetic advance (95.838) was noted for the character and the value of genetic advance in percent of mean was also high (68.725) (Table 5) (Figure 14). High heritability with high genetic advance suggested the prevalence of additive gene action. So, improvement through selection might be so effective. Naznin *et al*. (2015) showed high heritability (93.16%) with high genetic advance in percent of mean (37.74%) for number of siliquae/plant which was similar to this finding. Hosen (2008) also agreed to the result.

### 4.2.9 Length of siliquae (cm):

High heritability 81.341% along with low genetic advance (1.073) (Table 5) (Figure 14) indicating the presence of non-additive gene action which was responsible for the ineffectiveness of the selection for this trait whereas genetic advance in percent mean was recorded moderate (18.659) (Table 5) (Figure 14). Naznin *et al*. (2015) reported high heritability coupled with moderate genetic advance in percentage of mean for length of siliquae.

### 4.2.10 Number of seeds per siliqua:

High heritability 82.925% with low genetic advance (5.592) (Table 5) (Figure 14) indicating the presence of non-additive gene action and so selection was not so effective for the improvement of the crop. High value of genetic advance in percentage of mean was recorded as 27.185 for this trait (Table 5) (Figure 14). High heritability values along with high genetic advance in percentage of mean for seeds per siliqua was reported by Mahmud (2008).

### 4.2.11 Thousand seed weight (g):

Moderate heritability 38.568% along with low genetic advance (0.445) (Table 5) (Figure 14) indicating the presence of non-additive gene action which was responsible for the ineffectiveness of the selection for this trait whereas genetic advance in percent mean was recorded moderate (15.161) (Table 5) (Figure 14).

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.

### 4.2.12 Seed yield per plant (g):

High heritability of 86.251% with low genetic advance (4.317) was noted for the character and the value of genetic advance in percent of mean was moderate (59.96) (Table 5) (Figure 14). High heritability with low genetic advance suggested the prevalence of non- additive gene action and so, improvement through selection might not be so effective. Environment was mainly responsible for high heritability.

## 4.3 Correlation analysis:

Correlation coefficient is a numerical measure of some type of interrelation to detect the direction and strength of relationship between the relative movements of two or more variables. The values of correlation coefficient ranges between -1.0 and +1.0. A correlation of -1.0 exhibits a perfect negative correlation, whereas a correlation of 1.0 exhibits a perfect positive correlation. A correlation of 0.0 exhibits no relationship between the movements of the two variables. Yield being a target character is governed by polygene and highly influenced by the environment. So, selection based on only yield itself is unavailing. When selection is done for development of any character highly correlated with yield, it affects a number of other correlated characters simultaneously. Therefore, knowledge regarding association of character with yield and among themselves provides guideline to the plant breeder for making improvement through selection vis-à-vis provide a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factors (Dewey and Lu 1959). Both genotypic and phenotypic correlation coefficient of different characters of eight advanced populations of *B. rapa* are presented in Table 6 and Table 7. It was conspicuous that genotypic correlation coefficients were higher than their analogous phenotypic ones suggested that these traits were strongly correlated genetically and the phenotypic expression of these traits was less influenced by the environment. Similar result was found by Pankaj *et al.* (2002). In many cases, phenotypic correlation coefficient was higher than their corresponding genotypic correlation coefficient suggesting that both environmental and genotypic correlation performed in the same direction and finally maximized their expression at phenotypic level.

**Table 6.** Genotypic correlation coefficient among yield and yield contributing characters of 8 advanced populations of *B. rapa*

| | **DFF** | **DFPF** | **DTM** | **PH (cm)** | **RL (cm)** | **NPB/P** | **NSB/P** | **NS/P** | **LS (cm)** | **NS/S** | **TSW (g)** | **SY (g)** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **DFF** | 1 | | | | | | | | | | | |
| **DFPF** | 0.998$^{**}$ | 1 | | | | | | | | | | |
| **DTM** | 0.976$^{**}$ | 0.934$^{**}$ | 1 | | | | | | | | | |
| **PH (cm)** | -0.397$^{NS}$ | -0.282$^{NS}$ | -0.428$^{*}$ | 1 | | | | | | | | |
| **RL (cm)** | -0.424$^{*}$ | -0.352$^{NS}$ | -0.483$^{*}$ | 0.913$^{**}$ | 1 | | | | | | | |
| **NPB/P** | -0.997$^{**}$ | -0.993$^{**}$ | -0.886$^{**}$ | 0.057$^{NS}$ | 0.209$^{NS}$ | 1 | | | | | | |
| **NSB/P** | -0.802$^{**}$ | -0.971$^{**}$ | -0.827$^{**}$ | 0.223$^{NS}$ | 0.644$^{**}$ | 0.930$^{**}$ | 1 | | | | | |
| **NS/P** | -0.848$^{**}$ | -0.957$^{**}$ | -0.823$^{**}$ | 0.263$^{NS}$ | 0.556$^{**}$ | 0.994$^{**}$ | 0.994$^{**}$ | 1 | | | | |
| **LS (cm)** | -0.895$^{**}$ | -0.775$^{**}$ | -0.641$^{**}$ | -0.087$^{NS}$ | -0.020$^{NS}$ | 0.960$^{**}$ | 0.739$^{**}$ | 0.707$^{**}$ | 1 | | | |
| **NS/S** | -0.995$^{**}$ | -0.912$^{**}$ | -0.947$^{**}$ | 0.283$^{NS}$ | 0.386$^{NS}$ | 0.925$^{**}$ | 0.833$^{**}$ | 0.799$^{**}$ | 0.856$^{**}$ | 1 | | |
| **TSW (g)** | -0.312$^{NS}$ | -0.662$^{**}$ | -0.544$^{**}$ | 0.100$^{NS}$ | 0.664$^{**}$ | 0.859$^{**}$ | 0.891$^{**}$ | 0.884$^{**}$ | 0.307$^{NS}$ | 0.251$^{NS}$ | 1 | |
| **SY (g)** | -0.860$^{**}$ | -0.928$^{**}$ | -0.820$^{**}$ | 0.340$^{NS}$ | 0.664$^{**}$ | 0.981$^{**}$ | 0.997$^{**}$ | 0.984$^{**}$ | 0.632$^{**}$ | 0.780$^{**}$ | 0.830$^{**}$ | 1 |

*= Significant at 5% level of probability, **= Significant at 1% level of probability
DFF=Days to first flowering, DFPF = Days to 50% flowering, DTM = Days to 80% maturity, PH = Plant height (cm), RL=Root length(cm), NPB/P = Number of primary branches per plant, NSB/P = Number of secondary branches per plant, NS/P = Number of siliquae per plant, LS = Length of siliquae (cm), NS/S = Number of seeds per siliqua, TSW = Thousand seed weight (g), SY/P = Seed yield per plant (g).

**Table 7.** Phenotypic correlation coefficient among yield and yield contributing characters of 8 advanced populations of *B. rapa*

| | DFF | DFPF | DTM | PH (cm) | RL (cm) | NPB/P | NSB/P | NS/P | LS (cm) | NS/S | TSW (g) | SY (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DFF | 1 | | | | | | | | | | | |
| DFPF | $0.722^{**}$ | 1 | | | | | | | | | | |
| DTM | $0.748^{**}$ | $0.785^{**}$ | 1 | | | | | | | | | |
| PH (cm) | $-0.319^{NS}$ | $-0.276^{NS}$ | $-0.409^{*}$ | 1 | | | | | | | | |
| RL (cm) | $-0.204^{NS}$ | $-0.330^{NS}$ | $-0.498^{*}$ | $0.795^{**}$ | 1 | | | | | | | |
| NPB/P | $-0.593^{**}$ | $-0.796^{**}$ | $-0.668^{**}$ | $0.093^{NS}$ | $0.156^{NS}$ | 1 | | | | | | |
| NSB/P | $-0.582^{**}$ | $-0.604^{**}$ | $-0.619^{**}$ | $0.180^{NS}$ | $0.307^{NS}$ | $0.749^{**}$ | 1 | | | | | |
| NS/P | $-0.665^{**}$ | $-0.814^{**}$ | $-0.765^{**}$ | $0.284^{NS}$ | $0.461^{*}$ | $0.802^{**}$ | $0.899^{**}$ | 1 | | | | |
| LS (cm) | $-0.650^{**}$ | $-0.551^{**}$ | $-0.598^{**}$ | $-0.087^{NS}$ | $-0.025^{NS}$ | $0.684^{**}$ | $0.600^{**}$ | $0.645^{**}$ | 1 | | | |
| NS/S | $-0.808^{**}$ | $-0.744^{**}$ | $-0.790^{**}$ | $0.249^{NS}$ | $0.189^{NS}$ | $0.714^{**}$ | $0.712^{**}$ | $0.729^{**}$ | $0.666^{**}$ | 1 | | |
| TSW (g) | $-0.123^{NS}$ | $-0.215^{NS}$ | $-0.328^{NS}$ | $-0.034^{NS}$ | $0.256^{NS}$ | $0.101^{NS}$ | $0.393^{NS}$ | $0.473^{*}$ | $0.148^{NS}$ | $0.093^{NS}$ | 1 | |
| SY (g) | $-0.643^{**}$ | $-0.747^{**}$ | $-0.761^{**}$ | $0.320^{NS}$ | $0.510^{*}$ | $0.693^{**}$ | $0.806^{**}$ | $0.938^{**}$ | $0.598^{**}$ | $0.688^{**}$ | $0.586^{**}$ | 1 |

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

DFF=Days to first flowering, DFPF = Days to 50% flowering, DTM = Days to 80% maturity, PH = Plant height (cm), RL=Root length(cm), NPB/P = Number of primary branches per plant, NSB/P = Number of secondary branches per plant, NS/P = Number of siliquae per plant, LS = Length of siliquae (cm), NS/S = Number of seeds per siliqua, TSW = Thousand seed weight (g), SY/P = Seed yield per plant (g).

### 4.3.1 Days to first flowering:

Days to first flowering exhibited highly significant and positive correlation with days to 50% flowering ($r_g = 0.998$, $r_p = 0.722$), pointing out a possible increase in days to 50% flowering by increasing days to first flowering. It showed highly significant and positive correlation with days to 80% maturity ($r_g = 0.976$, $r_p = 0.748$) which indicated a possible increase in days to 80% maturity by increasing days to first flowering. It exhibited highly significant and negative correlation with number of primary branches per plant ($r_g = - 0.997$, $r_p = - 0.593$), number of secondary branches per plant ($r_g = - 0.802$, $r_p = - 0.582$), number of siliquae per plant ($r_g = - 0.848$, $r_p = - 0.665$), length of siliqua (cm) ($r_g = - 0.895$, $r_p = - 0.650$), number of seeds per siliqua ($r_g = - 0.995$, $r_p = - 0.808$) and seed yield (g) ($r_g = - 0.860$, $r_p = - 0.643$) which indicated a possible increase in number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, length of siliqua (cm), number of seeds per siliqua, and seed yield (g) by decreasing days to first flowering. It also showed insignificant and negative correlation with plant height (cm) ($r_g = - 0.397$, $r_p = - 0.319$), and thousands seed weight (g) ($r_g = - 0.312$, $r_p = - 0.123$). Insignificant association of these traits revealed that the combination between these traits was largely influenced by environmental factors.

### 4.3.2 Days to 50% flowering:

Days to 50% flowering exhibited highly significant and positive correlation with days to 80% maturity ($r_g = 0.934$, $r_p = 0.785$), pointing out a possible increase in days to 80% maturity by increasing days to 50% flowering. It exhibited highly significant and negative correlation with number of primary branches per plant ($r_g = - 0.993$, $r_p = - 0.796$), number of secondary branches per plant ($r_g = - 0.971$, $r_p = - 0.604$), number of siliquae per plant ($r_g = - 0.957$, $r_p = - 0.814$), length of siliqua (cm) ($r_g = - 0.775$, $r_p = - 0.551$), number of seeds per siliqua ($r_g = - 0.912$, $r_p = - 0.744$) thousands seed weight (g) ($r_g = - 0.662$) and seed yield (g) ($r_g = - 0.928.$, $r_p = - 0.747$) which indicated a possible increase in number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, length of siliqua (cm), number of seeds per siliqua, thousands seed weight (g) and seed yield (g) by decreasing days to 50% flowering. It also showed insignificant and negative correlation with plant height (cm) ($r_g$ = - 0.282, $r_p$ = - 0.276), root length (cm) ($r_g$ = - 0.352, $r_p$ = - 0.330) and thousands seed weight (g) ($r_p$ = - 0.215). Insignificant association of these traits suggested that the interrelationship between these traits was largely influenced by environmental factors.

### 4.3.3 Days to 80% maturity:

Days to 80% maturity exhibited highly significant and negative correlation with plant height (cm) ($r_g$ = - 0.428, $r_p$ = - 0.409), root length (cm) ($r_g$ = - 0.483, $r_p$ = - 0.498), number of primary branches per plant ($r_g$ = - 0.886, $r_p$ = - 0.668), number of secondary branches per plant ($r_g$ = - 0.827, $r_p$ = - 0.619), number of siliquae per plant ($r_g$ = - 0.823, $r_p$ = - 0.765), length of siliqua (cm) ($r_g$ = - 0.641, $r_p$ = - 0.598), number of seeds per siliqua ($r_g$ = - 0.947, $r_p$ = - 0.790) thousands seed weight (g) ($r_g$ = - 0.544) and seed yield (g) ($r_g$ = - 0.820, $r_p$ = - 0.761) which indicates a possible increase in plant height (cm), root length (cm), number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, length of siliqua (cm), number of seeds per siliqua, thousands seed weight (g) and seed yield (g) by decreasing days to 80% maturity. It also showed insignificant and negative correlation with thousands seed weight (g) ($r_p$ = - 0.328).

### 4.3.4 Plant height (cm):

Plant height (cm) exhibited highly significant and positive correlation with root length (cm) ($r_g$ = 0.913, $r_p$ = 0.795) pointing out a possible increase in plant height by increasing root length (cm). It exhibited insignificant and positive correlation with number of primary branches per plant ($r_g$ = 0.057, $r_p$ = 0.093), number of secondary branches per plant ($r_g$ = 0.223, $r_p$ = 0.180), number of siliquae per plant ($r_g$ = 0.263, $r_p$ = 0.284), ($r_g$ = 0.087, $r_p$ = 0.249), number of seeds per siliqua ($r_g$ = 0.283, $r_p$ = 0.034) thousands seed weight (g) ($r_g$ = 0.100) and seed yield (g) ($r_g$ = 0.340, $r_p$ = 0.320) which indicated that this trait had a very little contribution toward the increase in primary branches per plant, number of secondary branches per plant, number of siliquae per plant, number of seeds per siliqua, thousands seed weight (g) and seed yield (g). It also showed insignificant and negative correlation with length of siliqua (cm) ($r_g$ = - 0.087, $r_p$ = - 0.087) and thousands seed weight (g) ($r_p$ = - 0.034) indicated that environmental factors largely influenced on the association between these traits.

### 4.3.5 Root length (cm):

Highly significant and positive correlation of root length was observed in number of secondary branches per plant ($r_g$ = 0.644), number of siliquae per plant ($r_g$ = 0.556, $r_p$ = 0.461), thousands seed weight (g) ($r_g$ = 0.664) and seed yield (g) ($r_g$ = 0.664, $r_p$ = 0.510) which indicates a possible increase in number of secondary branches per plant, number of siliquae per plant, thousands seed weight (g) and seed yield (g) by increasing root length (cm). It showed insignificant and positive correlation with number of primary branches per plant ($r_g$ = 0.209, $r_p$ = 0.156), number of secondary branches per plant ($r_p$ = 0.307), number of seeds per siliqua ($r_g$ = 0.386, $r_p$ = 0.189), and thousands seed weight (g) ($r_p$ = 0.256). insignificant and negative correlation wsa observed in length of siliqua (cm) ($r_g$ = - 0.020, $r_p$ = - 0.025) indicated that environmental factors largely influenced on the association between these traits.

### 4.3.6 Number of primary branches per plant:

Number of primary branches per plant exhibited highly significant and positive correlation with number of secondary branches per plant ($r_g$ = 0.930, $r_p$ = 0.749), number of siliquae per plant ($r_g$ = 0.994, $r_p$ = 0.802), length of siliqua (cm) ($r_g$ = 0.960, $r_p$ = 0.684), number of seeds per siliqua ($r_g$ = 0.925, $r_p$ = 0.714), thousands seed weight (g) ($r_g$ = 0.859) and seed yield (g) ($r_g$ = 0.981, $r_p$ = 0.693) which indicated a possible increase in number of primary branches per plant increases the number of secondary branches per plant, number of siliquae per plant, length of siliqua (cm), number of seeds per siliqua, thousands seed weight (g) and seed yield (g). Naznin *et al. (*2015) reported that seed yield/plant showed positive significant association with number of primary branches/plant ($r_g$ = 0.5611, $r_p$ =

0.4016) at both genotypic and phenotypic level. Alam (2010) noticed significant and positive correlation of the number of primary branches per plant with the seed yield. The finding suggested that to increase seed yield/plant, branching was an important contributor. It also showed insignificant and positive correlation with length of siliquae ($r_g$=0.142, $r_p$=0.162) indicating that it had a very little contribution toward the increase in length of siliquae. It also showed insignificant and positive correlation with thousands seed weight (g) ($r_p$ = 0.101) indicating that it had a very little contribution toward the increase in thousand seed weight (g).

### 4.3.7 Number of secondary branches per plant:

Number of secondary branches per plant exhibited highly significant and positive correlation with number of siliquae per plant ($r_g$ = 0.994, $r_p$ = 0.899), length of siliqua (cm) ($r_g$ = 0.739, $r_p$ = 0.600), number of seeds per siliqua ($r_g$ = 0.833, $r_p$ = 0.712), thousands seed weight (g) ($r_g$ = 0.891) and seed yield (g) ($r_g$ = 0.997, $r_p$ = 0.806) which indicated a possible increase in number of secondary branches per plant increases the number of siliquae per plant, length of siliqua (cm), number of seeds per siliqua, thousands seed weight (g) and seed yield (g). Naznin *et al.* (2015) reported that seed yield/plant had significant and positive correlation for number of secondary branches/plant ($r_g$ = 0.5160, $r_p$= 0.4098) at both genotypic and phenotypic level. It also showed insignificant and positive correlation with thousands seed weight (g) ($r_p$ = 0.393) indicating that it had a very little contribution toward the increase in thousand seed weight (g).

### 4.3.8 Number of siliquae per plant:

Number of siliquae per plant showed highly significant and positive correlation with length of siliqua (cm) ($r_g$ = 0.707, $r_p$ = 0.645), number of seeds per siliqua ($r_g$ = 0.799, $r_p$ = 0.729), thousands seed weight (g) ($r_g$ = 0.884, $r_p$ = 0.473) and seed yield (g) ($r_g$ = 0.984, $r_p$ = 0.938) which indicates a possible increase in number of siliquae per plant increases the length of siliqua (cm), number of seeds per siliqua, thousands seed weight (g) and seed yield (g). Naznin *et al.* (2015)

also showed highly significant positive association of number of siliquae/plant with seed yield/plant. Rameeh (2011) also confirmed the same finding. Similar result was also discovered by Esmaeeli-Azadgoleh *et al*. (2009) and Marjanovic-Jeromela *et al.* (2007).

### 4.3.9 Length of siliquae (cm):

Highly significant and positive correlation of length of siliqua (cm) was observed in number of seeds per siliqua ($r_g = 0.856$, $r_p = 0.666$) and seed yield (g) ($r_g = 0.632$, $r_p = 0.598$) which indicated a possible increase in length of siliqua (cm) increases the number of seeds per siliqua and seed yield (g). It also showed insignificant and positive correlation with thousand seed weight (g) ($r_g=0.307$, $r_p=0.148$) stated that it had a very little association with thousand seed weight.

### 4.3.10 Number of seeds per siliqua:

Number of seeds per siliqua showed significant and positive correlation with seed yield (g) ($r_g = 0.780$, $r_p = 0.688$) indicates a possible increase in number of seeds per siliqua increases the seed yield (g). It also showed insignificant and positive correlation with thousand seed weight (g) ($r_g=0.251$, $r_p=0.093$) stated that it had a very little association with thousand seed weight.

### 4.3.11 Thousand seed weight (g):

Thousand seed weight exhibited highly significant and positive correlation with seed yield per plant ($r_g = 0.830$, $r_p = 0.586$) at both genotypic and phenotypic level indicating that an increase in thousand seed weight tends to increase seed yield per plant. The similar result was also reported by Parveen *et al.* (2015).

### 4.4 Path co-efficient analysis:

Complex relationships between the various traits related to the dependent variable can’t be figured out through simple correlation. Correlation coefficients exhibit linear association between variables. But it is not enough to describe these relationships when the causal relationship among variables is necessary. Therefore, it was suggested that path coefficient analysis is the most common statistical method utilized to determine the direct or indirect effects of yield contributing characters on seed yield per plant and measure the relative importance of each component on seed yield per plant.

Seed yield per plant is considered as dependent (resultant) variable and its attributes as independent variables (causal) such as days to first flowering, days to 50% flowering, days to 80% maturity, plant height, root length, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, length of siliquae, number of seeds per silique, thousand seed weight. Path coefficient analysis for estimating direct and indirect effects of yield contributing characters on seed yield per plant in 8 advanced populations of *B. rapa* is presented in Table 8. Residual effects of their independent variables have been denoted as ‘R’ which have influenced on seed yield per plant to a medium extent.

**Table 8.** Path coefficient analysis presenting direct and indirect effect of yield contributing characters on seed yield per plant in 8 advanced populations of *B. rapa*

| **Direct Effects** | **DFF** | **DFPF** | **DTM** | **PH (cm)** | **RL (cm)** | **NPB/P** | **NSB/P** | **NS/P** | **LS (cm)** | **NS/S** | **TSW (g)** | **SY/P (g)** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **DFF** | 1.011 | -0.148 | -0.49 | -0.36 | 0.368 | 0.781 | 0.048 | -1.75 | -0.539 | 0.2011 | 0.015 | -0.860$^{**}$ |
| **DFPF** | 1.044 | -0.143 | -0.47 | -0.25 | 0.306 | 0.755 | 0.059 | -1.98 | -0.466 | 0.1844 | 0.032 | -0.928$^{**}$ |
| **DTM** | 0.987 | -0.134 | -0.5 | -0.39 | 0.419 | 0.611 | 0.05 | -1.7 | -0.385 | 0.1915 | 0.026 | -0.820$^{**}$ |
| **PH (cm)** | -0.402 | 0.04 | 0.213 | 0.903 | -0.79 | -0.039 | -0.01 | 0.544 | -0.052 | -0.057 | -0.005 | 0.340$^{NS}$ |
| **RL (cm)** | -0.429 | 0.05 | 0.241 | 0.825 | -0.87 | -0.144 | -0.04 | 1.149 | -0.012 | -0.078 | -0.032 | 0.664$^{**}$ |
| **NPB/P** | -1.144 | 0.156 | 0.442 | 0.052 | -0.18 | -0.69 | -0.06 | 2.053 | 0.577 | -0.187 | -0.041 | 0.981$^{**}$ |
| **NSB/P** | -0.811 | 0.139 | 0.413 | 0.201 | -0.56 | -0.642 | -0.06 | 2.115 | 0.445 | -0.168 | -0.043 | 0.997$^{**}$ |
| **NS/P** | -0.858 | 0.137 | 0.411 | 0.238 | -0.48 | -0.686 | -0.06 | 2.066 | 0.426 | -0.161 | -0.042 | 0.984$^{**}$ |
| **LS (cm)** | -0.905 | 0.111 | 0.32 | -0.08 | 0.018 | -0.663 | -0.04 | 1.461 | 0.602 | -0.173 | -0.015 | 0.632$^{**}$ |
| **NS/S** | -1.005 | 0.13 | 0.473 | 0.255 | -0.34 | -0.638 | -0.05 | 1.65 | 0.515 | -0.202 | -0.012 | 0.780$^{**}$ |
| **TSW (g)** | -0.315 | 0.095 | 0.272 | 0.091 | -0.58 | -0.593 | -0.05 | 1.825 | 0.185 | -0.051 | -0.048 | 0.830$^{**}$ |

Bold figures indicate direct effects
Residual effect: 0.12035

DFF=Days to first flowering, DFPF = Days to 50% flowering, DTM = Days to 80% maturity, PH = Plant height (cm), RL=Root length(cm), NPB/P = Number of primary branches per plant, NSB/P = Number of secondary branches per plant, NS/P = Number of siliquae per plant, LS = Length of siliquae (cm), NS/S = Number of seeds per siliqua, TSW = Thousand seed weight (g), SY/P = Seed yield per plant (g).

### 4.4.1 Days to first flowering:

Path coefficient analysis revealed that days to first flowering had positive direct effect (1.01102) on yield per plant. The trait showed positive indirect effect on seed yield per plant via days to 50% flowering (1.04442) and days to maturity (0.98675) followed by negative indirect effect via plant height (cm) (-0.40164), root length(cm) (-0.42876), number of primary branches per plant (-1.14362), number of secondary branches per plant (-0.8108), number of siliquae per plant (-0.85769), length of siliquae (cm) (-0.90512), number of seeds per silique (-1.00549), thousand seed weight (g) (-0.31503) Finally, the trait showed significant negative genotypic correlation with seed yield per plant (-0.860) which was highly significant.

### 4.4.2 Days to 50% flowering:

Days to 50% flowering showed negligible negative direct effect (-0.143) towards seed yield per plant. Islam *et al*. (2016) showed that days to 50% flowering had the negative direct effect on seed yield per plant which was similar to the result. Zahan (2006) also reported the similar finding. The trait showed positive indirect effect on seed yield per plant via plant height (cm) (0.04036), root length(cm) (0.05034), number of primary branches per plant (0.15636), number of secondary branches per plant (0.13884), number of siliquae per plant (0.13689), length of siliquae (cm) (0.11083), number of seeds per silique (0.13041), thousand seed weight (g) (0.09461). The trait showed negative indirect effect on seed yield per plant via days to 1st flowering (-0.14772) and days to 80% maturity (-0.13358). Finally, the trait showed significant negative genotypic correlation with seed yield per plant (-0.928) which was highly significant.

### 4.4.3 Days to 80% maturity:

Days to 80% maturity showed negative direct effect (-0.49923) towards seed yield per plant. Naznin *et al*. (2015) reported positive direct effect of days to maturity towards yield per plant that was similar to the present finding. Rashid *et al*. (2013) showed the similar result. The trait showed positive indirect effect on seed yield per plant via plant height (cm) (0.21344), root length(cm) (0.24092), number of primary branches per plant (0.44221), number of secondary branches per plant (0.41286), number of siliquae per plant (0.41097), length of siliquae (cm) (0.31993), number of seeds per silique (0.4729) and thousand seed weight (g) (0.27179). The trait showed negative indirect effect on seed yield per plant via days to 1st flowering (-0.48724) and days to 50% flowering (-0.46633). The trait had significant negative genotypic association with seed yield per plant (-0.820).

### 4.4.4 Plant height (cm):

Plant height exhibited positive direct effect (0.90338) on seed yield per plant. Uddin *et al*. (2013) demonstrated that plant height had the negative direct effect on yield per plant which supported the result. The trait showed positive indirect effect on seed yield per plant via root length (cm) (0.82509), number of primary branches per plant (0.05152), number of secondary branches per plant (0.20146), number of siliquae per plant (0.23795), number of seeds per silique (0.25537), thousand seed weight (g) (0.09073). The trait showed negative indirect effect on seed yield per plant via days to 1st flowering (-0.35888) and days to 50% flowering (-0.25499), days to 80% maturity (-0.38624) and length of siliquae (cm) (-0.07863). The trait had insignificant positive genotypic association with seed yield per plant (0.340). Direct effect (0.90338) is positive and higher than the genotypic correlation coefficient (.856) which exhibited true relationship between them and direct selection for this trait will be rewarding for yield improvement.

### 4.4.5 Root length (cm):

Root length showed negative direct effect (-0.86786) towards seed yield per plant. It showed positive indirect effect on seed yield per plant via days to 1st flowering (0.36804) and days to 50% flowering (0.30553), days to 80% maturity (0.41882) and length of siliquae (cm) (0.01776). The trait showed negative indirect effect on seed yield per plant via plant height (cm) (-0.79265), number of primary branches per plant (-0.18123), number of secondary branches per plant (-0.55857), number of siliquae per plant (-0.48291), number of seeds per silique (-0.48291) and thousand seed weight (g) (-0.57598). The trait had significant positive genotypic association with seed yield per plant (0.664).

### 4.4.6 Number of primary branches per plant:

Number of primary branches per plant showed negative direct effect (-0.69034) towards seed yield per plant. The trait showed positive indirect effect on seed yield per plant via days to 1st flowering (0.78087) and days to 50% flowering (0.75481) and days to 80% maturity (0.61149). The trait showed negative indirect effect on seed yield per plant via plant height (cm) (-0.03937), root length(cm) (-0.14416), number of secondary branches per plant (-0.64199), number of siliquae per plant (-0.6863), length of siliquae (cm) (-0.66263), number of seeds per silique (-0.63826) and thousand seed weight (g) (-0.5933). The trait had significant positive genotypic association with seed yield per plant (0.981).

### 4.4.7 Number of secondary branches per plant:

Number of primary branches per plant showed negative direct effect (-0.06038) towards seed yield per plant. Naznin *et al.* (2015) revealed that number of secondary branches per plant had high positive direct effect on yield/plant which supported the present finding. Khan (2010) also agreed to the finding. The trait showed positive indirect effect on seed yield per plant via days to 1st flowering (0.04842) and days to 50% flowering (0.05862) and days to 80% maturity (0.04993). The trait showed negative indirect effect on seed yield per plant via plant height (cm) (-0.01346), root length(cm) (-0.03886), number of primary branches per plant (-0.05615), number of siliquae per plant (-0.06183), length of siliquae (cm) (-0.04463), number of seeds per silique (-0.05027) and thousand seed weight (g) (-0.05377). The trait had significant positive genotypic association with seed yield per plant (0.997).

### 4.4.8 Number of siliquae per plant:

Number of siliquae per plant exhibited negative direct effect (2.06556) on seed yield per plant. The trait showed positive indirect effect on seed yield per plant via plant height (cm) (0.54407), root length (cm) (1.14935), number of primary branches per plant (2.05348), number of secondary branches per plant (2.11512), length of siliquae (cm) (1.46116), number of seeds per silique (1.64963) and thousand seed weight (g) (1.82525). The trait showed negative indirect effect on seed yield per plant via days to 1st flowering (-1.75231) and days to 50% flowering (-1.97733) and days to 80% maturity (-1.70041). The trait had significant positive genotypic association with seed yield per plant (0.984). Direct effect (2.06556) is positive and higher than the genotypic correlation coefficient (0.984) which exhibited true relationship between them and direct selection for this trait will be effective for yield improvement.

### 4.4.9 Length of silique (cm):

Length of siliqua showed positive direct effect (0.60152) on seed yield per plant. The trait showed positive indirect effect on seed yield per plant via number of primary branches per plant (0.57738), number of secondary branches per plant (0.44463), number of siliquae per plant (0.42551), number of seeds per siliqua (0.51512) and thousand seed weight (g) (0.1846). The trait showed negative indirect effect on seed yield per plant via days to 1st flowering (-0.53851) and days to 50% flowering (-0.46618) and days to 80% maturity (-0.38549), plant height (cm) (0.05235) and root length (cm) (0.01231). The trait had significant positive genotypic association with seed yield per plant (0.632).

### 4.4.10 Number of seeds per siliqua:

Number of seeds per siliqua showed negative direct effect (-0.20216) on seed yield per plant. The trait showed positive indirect effect on seed yield per plant via days to 1st flowering (0.20106) and days to 50% flowering (0.18436) and days to 80% maturity (0.1915). The trait showed negative indirect effect on seed yield per plant via plant height (cm) (-0.05715), root length(cm) (-0.07812), number of primary branches per plant (-0.18691), number of secondary branches per plant (-0.16831), number of siliquae per plant (-0.16145), length of siliquae (cm) (-0.66263), number of seeds per silique (-0.17312) and thousand seed weight (g) (-0.05069). The trait had significant positive genotypic association with seed yield per plant (0.780).

### 4.4.11 Thousand seed weight (g):

Thousand seed weight had positive direct effect (0.04798) on seed yield per plant. The trait showed positive indirect effect on seed yield per plant via days to 1st flowering (0.01495) and days to 50% flowering (0.03175) and days to 80% maturity (0.02612). The trait showed negative indirect effect on seed yield per plant via plant height (cm) (-0.00482), root length(cm) (-0.03185), number of primary branches per plant (-0.04124), number of secondary branches per plant (-0.04273), number of siliquae per plant (-0.0424), length of siliquae (cm) (-0.01473) and number of seeds per silique (-0.01203). The trait had significant positive genotypic association with seed yield per plant (0.830).

### 4.4.12 Residual effect:

The residual effect (R) of path co-efficient analysis was 0.12035 which reported that the traits under study contributed 88% of the seed yield per plant. It was said that there were some other factors those contributed 12% to the seed yield per plant that were not included in the present study could had significant effect on seed yield per plant. 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.

### 4.5 Selection:

At present, due to pressure of Boro rice, the cultivation of *Brassica sp.* is decreasing in Bangladesh. The existing high yielding varieties like BARI sarisha-6 is long durable which occupy land during Boro season as a result transplantation of Boro rice become delayed. Therefore, short durable and high yielding varieties are preferred by farmers which can fit with T. Aman- Mustard-Boro cropping system. The objectives of our study was to study variability among the advanced populations and to select short duration and high yielding population of *B. rapa* which fit in the Aman-Mustard-Boro cropping system. Variability was observed for most of the characters of different cross combinations which helps to select the better populations for future study. Selection was conducted among the 8 advanced populations as per objectives.

**Pop$^n$ 3 (BARI Sarisha-6 X BARI Sarisha-15, $F_{10}$, 76.667 Days):**

This population had highest number of primary branches per plant (9.0667), highest number of secondary branches per plant (6.8333), highest number of siliquae per plant (217.97). This population also had highest thousand seed weight (g) (3.5333 g) which suggests seed size of the population was larger and contained more oil content than other advanced populations. Yield per plant was recorded as 11.7 g which was higher than other advanced populations. Moreover, Pop$^n$ 3 took shortest period to mature (76.667 days) compared to other populations.

**Pop$^n$ 4 (SAU Sarisha-1 X BARI Sarisha-15, $F_8$, 78.667 Days):**

Average seed yield per plant of Pop$^n$ 4 was recorded as 7.83 g (Table 9). This population had 2nd highest number of siliquae per plant (187.5) 2nd highest number of seeds per siliqua and 2nd highest thousand seed weight (g) (3.3667 g). This population had moderate plant height (109.77 cm). Pop$^n$ 4 took shorter period to mature (78.667 days) after Pop$^n$ 3 than other advanced populations.

**Pop$^n$ 1 (SAU Sarisha-2 X BARI Sarisha-15, $F_8$, 80 Days):**

Average seed yield per plant of Pop$^n$ 1 was recorded as 8.027 g (Table 9). This population had highest length of siliqua (6.44 cm) but moderate number of seeds per siliqua (22.143). This population also had number of siliqua per plant (182.87), thousand seed weight (g) (3.1 g) which are lower than Pop$^n$ 3 and Pop$^n$ 4. This population took 80 days to mature.

### Pop$^n$ 6 (SAU Sarisha-1 X BARI Sarisha-15, $F_8$, 78.667 Days):

Pop$^n$ 6 had highest number of seeds per siliqua (24.433) with 2nd highest length of siliqua (6.0663 cm) but lowest thousands seed weight (g) (2.2667 g). This population had moderate number of siliquae per plant (125.56) with moderate plant height (110.53 cm). Average seed yield per plant of this population was recorded as 6.667 g (Table 9). It took short period (78.667 days) to mature.

### Pop$^n$ 5 (BARI Sarisha-15 X SS 75 (Sonali Sarisha), $F_{11}$, 85.667 Days):

Average seed yield per plant of this population was recorded as 5.967 g (Table 9). This population had lowest plant height (93.57 cm) with lowest root length (9.827 cm). This population also had moderate length of siliqua (6.0 cm) with moderate thousands seed weight (3.0667 g). Number of siliqua per plant of this population was recorded as 103.61. It took 85.667 days to mature.

**Table 9.** Selection of most promising population from different advanced populations of *B. rapa* based on mean performance

| AP | DTM | NPB/P | NSB/P | NS/P | LS (cm) | NS/S | TSW (g) | SY/P (g) |
|---|---|---|---|---|---|---|---|---|
| **Pop$^n$ 3** | 76.667 | 9.0667 | 6.8333 | 217.97 | 6.0667 | 23.3 | 3.5333 | 11.7 |
| **Pop$^n$ 4** | 78.667 | 7.3 | 6.8 | 187.5 | 6.0433 | 23.307 | 3.3667 | 9.2 |
| **Pop$^n$ 1** | 80 | 8.9667 | 5.5333 | 182.87 | 6.44 | 22.143 | 3.1 | 8.027 |
| **Pop$^n$ 6** | 78.667 | 7.4 | 4 | 125.56 | 6.0663 | 24.433 | 2.2667 | 6.667 |
| **Pop$^n$ 5** | 85.667 | 6.2 | 3.1667 | 103.61 | 6 | 18.353 | 3.0667 | 5.967 |

AP= Advanced Populations, DTM = Days to 80% maturity, NPB/P = Number of primary branch per plant, NSB/P = Number of secondary branch per plant, NS/P = Number of siliquae per plant, LS = Length of siliqua (cm), NS/S = Number of seeds per siliqua, TSW = Thousand seed weight (g), SY/P= Seed yield per plant (g).

# CHAPTER V

# SUMMARY AND CONCLUSION

The present study was undertaken to evaluate eight advanced populations of *B. rapa* for estimating the variability among the characters, heritability, genetic advance and genetic advance in percentage of mean, character association and direct and indirect effect of different considered traits on seed yield per plant. The experiment was performed in the experimental field of Sher-e-Bangla Agricultural University during November 2018 to February 2019 using eight advanced populations of *B. rapa* to study variability among the populations.

In this study, variability analysis revealed that there were significant variations among all advanced populations of *B. rapa* for each character. Among all the advanced populations, Pop$^n$ 3 was the earliest (25.667 DAS) population followed by Pop$^n$ 6 (26.667 DAS), Pop$^n$ 1 (27.667DAS), Pop$^n$ 4 (29.667 DAS), Pop$^n$ 2 (31.667 DAS) and Pop$^n$ 5 (31.667 DAS) in case of days to first flowering. Pop$^n$ 3 took shortest period (30.667 DAS) followed by Pop$^n$ 1 (32 DAS), Pop$^n$ 6 (34.667 DAS) and Pop$^n$ 4 (35.667 DAS). Pop$^n$ 3 took shortest period (76.667 DAS) to mature followed by Pop$^n$ 4 (78.667 DAS), Pop$^n$ 6 (78.667 DAS) and Pop$^n$ 1 (80 DAS). Pop$^n$ 8 was the tallest population (125.04 cm) and Pop$^n$ 5 was the shortest population (93.57 cm). Pop$^n$ 3 had the maximum number of primary branches per plant (9.0667) and maximum number of secondary branches per plant (6.8333) while Pop$^n$ 8 had the minimum number of primary branches per plant (5.0) and minimum number of secondary branches per plant (2.5667). Pop$^n$ 3 showed maximum number of siliquae per plant (217.97) followed by Pop$^n$ 4 (187.5) and Pop$^n$ 1 (182.87) whereas longest length of siliquae was exhibited in Pop$^n$ 1 (6.44 cm) followed by Pop$^n$ 3 (6.0667 cm), Pop$^n$ 6 (6.0663 cm) and Pop$^n$ 4 (6.0433 cm). Maximum number of seeds per siliqua was observed in Pop$^n$ 6 (24.433) followed by Pop$^n$ 4 (23.307), Pop$^n$ 3 (23.3) and Pop$^n$ 1 (22.143). Thousand seed weight was found highest in Pop$^n$ 3 (3.5333 g) followed by Pop$^n$ 4 (3.3667 g), Pop$^n$ 1 (3.1 g) and Pop$^n$ 5 (3.0667 g). Seed yield per plant was found highest in Pop$^n$ 3 due to better performances in important yield contributing characters such as number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, thousand seed weight (g) etc.

Phenotypic variance was considerably higher than the genotypic variance for all the studied characters. Differences between the genotypic and phenotypic variances was minimum in root length (cm), number of primary branches per plant, number of secondary branches per plant, length of siliqua (cm) and thousand seed weight (g) indicating the less environmental effect to control these characters. Days to 1st flowering, days to 50% flowering, days to 80% maturity, number of seeds per siliqua and seed yield per plant (g) showed moderate difference between phenotypic variance and genotypic variance which indicates moderate influence of environment on these traits. Maximum differences between the genotypic and phenotypic variances was found in plant height (cm) and number of siliquae per plant indicating the more environmental effect to control these characters.

The high genotypic and phenotypic coefficient of variation (GCV and PCV) was observed for the character number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, seed yield per plant (g) indicating that these characters can be improved by selection.

High heritability with high genetic advance was found in plant height, number of siliquae per plant suggesting the high possibility of selecting the populations for these trait. High heritability with low genetic advance was observed in days to first flowering, days to 50% flowering, days to 80% maturity, number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua, length of siliquae, thousand seed weight and seed yield per plant indicating the non-effective selection of the populations for these traits.

Significant genotypic and phenotypic positive association with seed yield per plant was observed in number of primary branches per plant, number of secondary branches per plant, root length (cm), number of siliquae per plant, number of seeds per siliqua, length of siliquae (cm) and thousand seed weight (g) through the correlation analysis. On the other hand, significant negative association with seed yield per plant was revealed in days to first flowering, days to 50% flowering and days to 80% maturity at both genotypic and phenotypic level.

According to the path coefficient analysis, direct positive effect on seed yield per plant was observed by days to first flowering, plant height (cm), number of siliquae per plant and length of siliquae (cm). On the other hand, negative direct effect on seed yield per plant was found in days to 50% flowering, days to 80% maturity, root length (cm), number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua and thousand seed weight (g).

Selection was conducted among the advanced populations based on their yield and yield contributing characters. Based on the objectives, five advanced populations such as Pop$^n$ 3 (BARI Sarisha-6 X BARI Sarisha-15, $F_{10,}$ 76.667 Days), Pop$^n$ 4 (SAU Sarisha-1 X BARI Sarisha-15, $F_{8,}$ 78.667 Days), Pop$^n$ 1 (SAU Sarisha-2 X BARI Sarisha-15, $F_{8,}$ 80 Days), Pop$^n$ 6 (SAU Sarisha-1 X BARI Sarisha-15, $F_{8,}$ 78.667 Days) and Pop$^n$ 5 (BARI Sarisha-15 X SS 75 (Sonali Sarisha), $F_{11}$, 85.667 Days) with higher seed yield per plant were selected from the 8 advanced populations.

# CHAPTER VI

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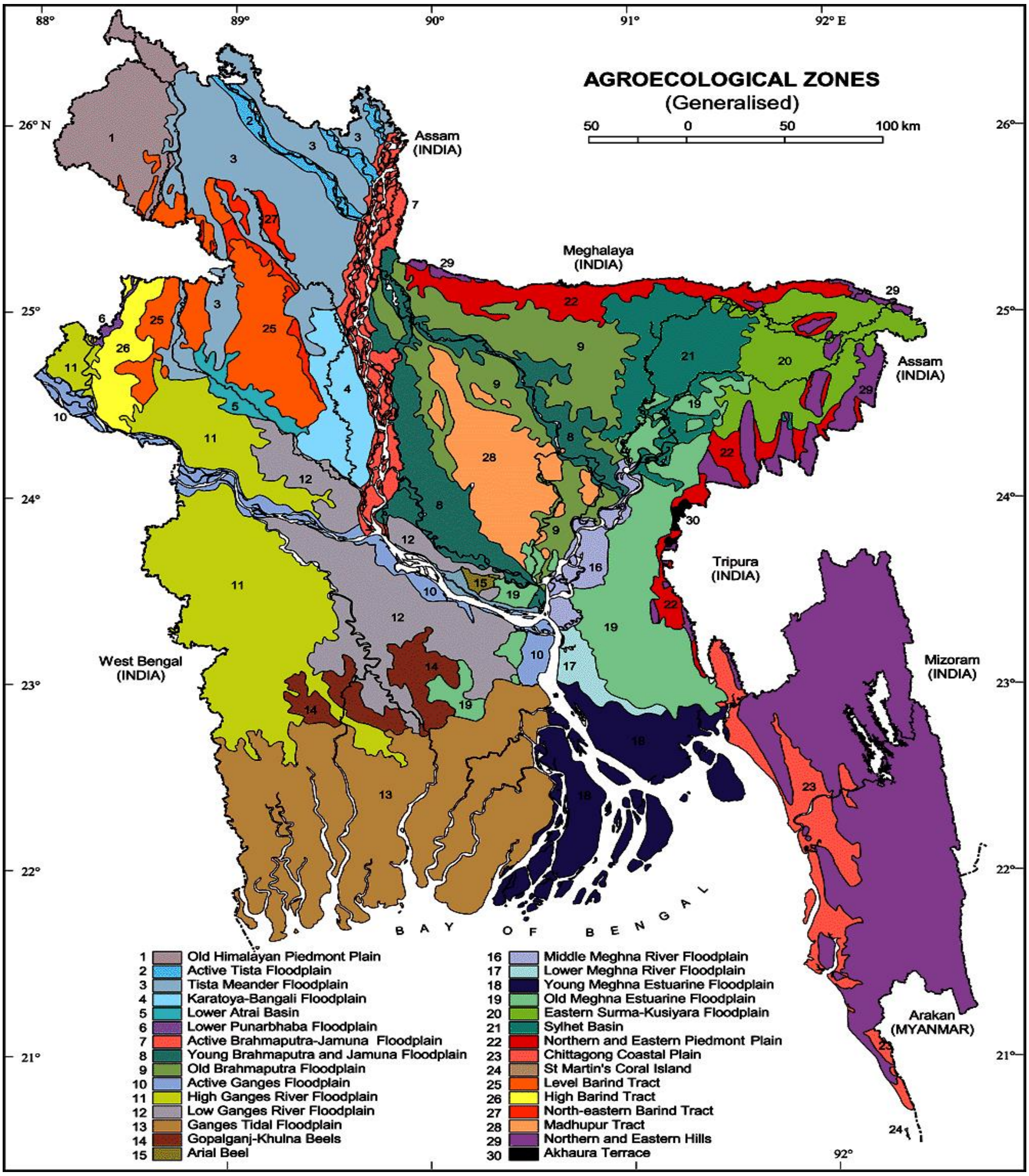
# APPENDICES

**Appendix I.** Map showing the experimental site under the study



🟧 Legend showing the research site

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

A. Physical composition of the soil:

| Soil separates | % | Methods employed |
|---|---|---|
| **Sand** | 36.90 | Hydrometer method (Day, 1915) |
| **Silt** | 26.40 | Do |
| **Clay** | 36.66 | Do |
| **Texture class** | Clay loam | Do |

B. Chemical composition of the soil:

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

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

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

| **Month** | **Air temperature (ºC)** | | **Average relative humidity (%)** | **Rainfall(mm) (total)** | **Total sunshine (hr)** |
|---|---|---|---|---|---|
| | **Minimum** | **Maximum** | | | |
| **November, 2018** | 18 | 31 | 63 | Trace | 216.4 |
| **December, 2018** | 11.56 | 27.12 | 61 | Trace | 212.5 |
| **January, 2019** | 10 | 28 | 65 | Trace | 212.5 |
| **February, 2019** | 12 | 32 | 73.23 | 4.0 | 195.00 |

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

**Appendix IV:** Analysis of variance of 12 important character of 8 advanced populations of *B. rapa*

| Source of Variation | Degrees of freedom | Mean sum of square of characters | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | DFF | DFPF | DTM | PH (cm) | RL (cm) | NPB/P | NSB/P | NS/P | LS (cm) | NS/S | TSW (g) | SY/P (g) |
| **Replication** | 2 | 0.1250 | 10.0417 | 2.38 | 22.18 | 2.11 | 1.3362 | 0.2788 | 125.15 | 0.0162 | 1.21 | 0.0488 | 0.7306 |
| **Populations** | 7 | 30.95** | 48.33** | 70.48** | 344.83** | 6.36** | 7.84** | 9.17** | 7243.7** | 1.08** | 28.48** | 0.5566* | 16.09** |
| **Error** | 14 | 3.078 | 5.47 | 2.42 | 5.55 | 0.9399 | 1.88 | 1.11 | 199.32 | 0.0766 | 1.83 | 0.1930 | 0.8117 |

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

DFF=Days to first flowering, DFPF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), NPB/P = Number of primary branch per plant, NSB/P = Number of secondary branch per plant, NS/P = Number of siliquae per plant, LS = Length of siliqua (cm), NS/S = Number of seed per siliqua, TSW = Thousand seed weight (g), SY/P = Seed yield per plant.